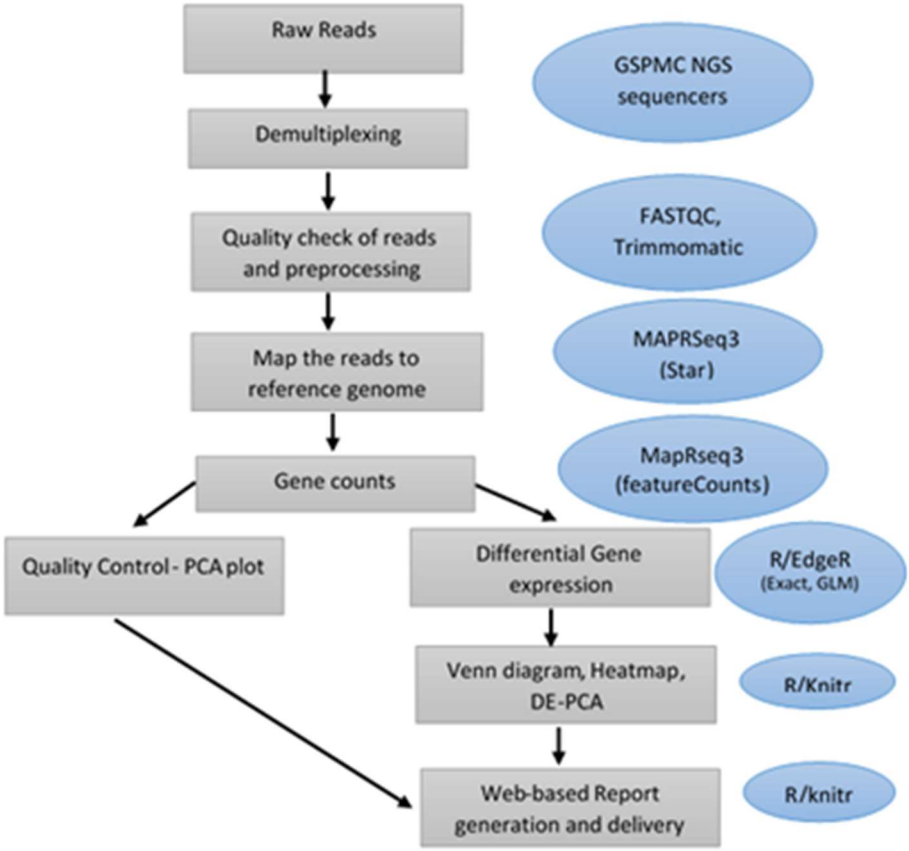

Fig. S1. RNA sequencing and data processing workflow. RNA sequencing and data processing were completed using the standard the Mellowes Center for RNA sequencing and bioinformatic analysis workflow.

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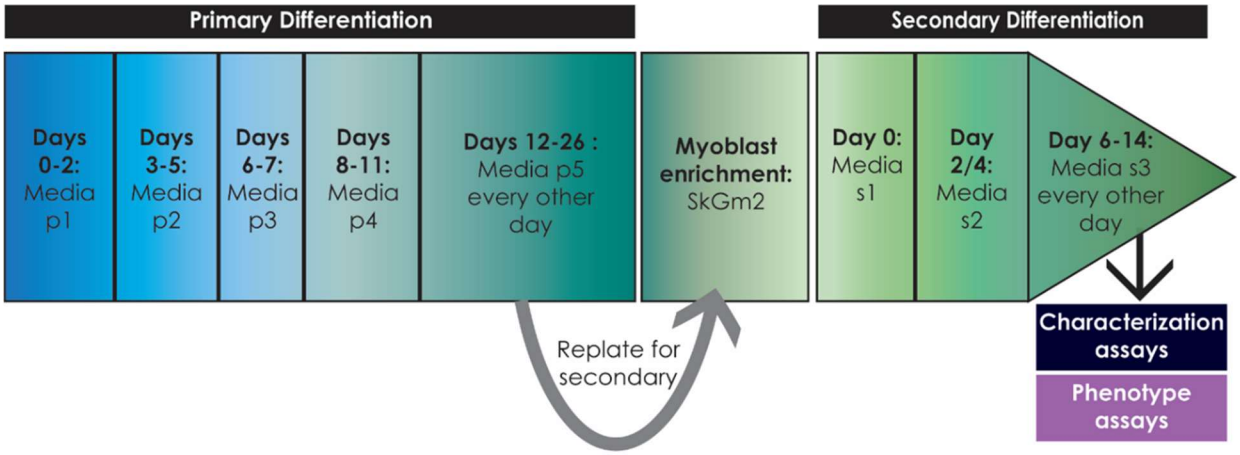

Fig. S2. iSkM differentiation schematic. iPSCs were plated at a desired seeding density and differentiated into myotubes using a two-stage differentiation protocol. Primary differentiation uses a series of five medias to modulate Wnt and BMP signaling to form paraxial mesoderm progenitors and myoblasts. Cells were then replated and enriched for myoblasts. Enriched myoblasts cultures underwent secondary differentiation to form spontaneously contracting myotubes which were then used for endpoint assays.

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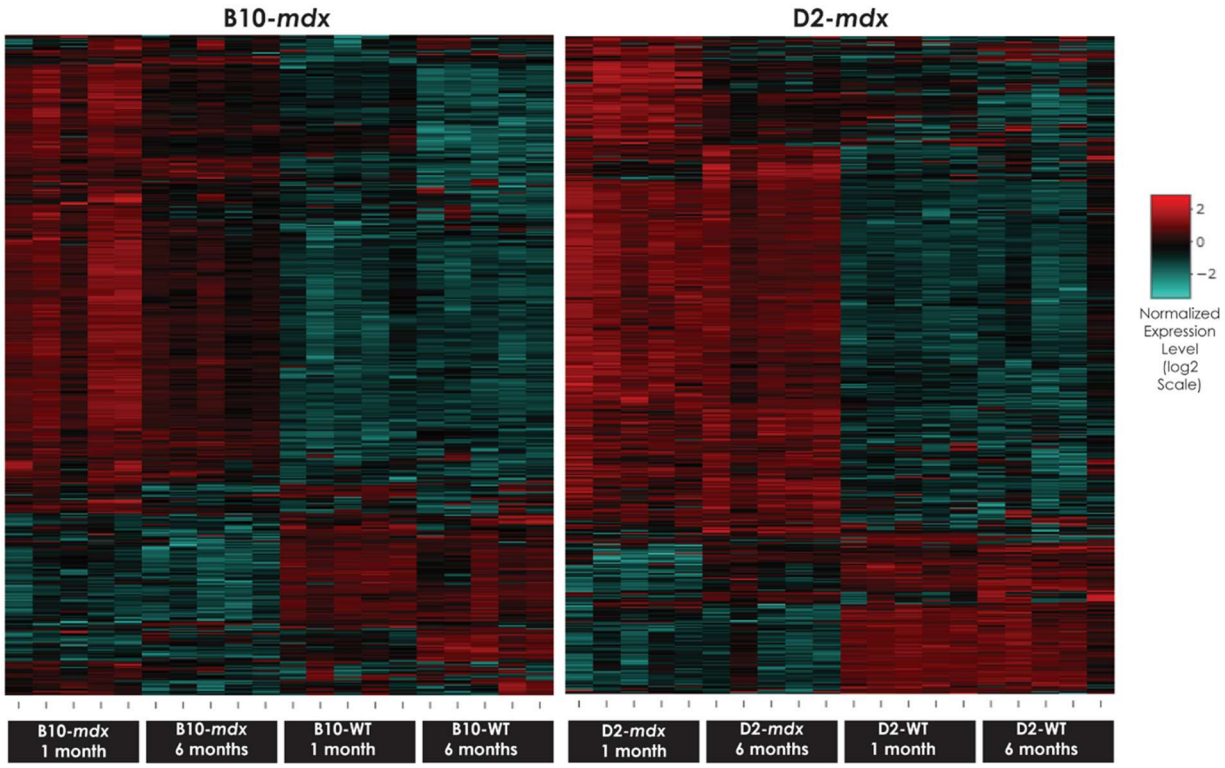

Fig. S3. Heat maps of differentially expressed transcripts in B10-*mdx* and D2-*mdx* muscle at 1 and 6 months of age as compared to WT counterparts.

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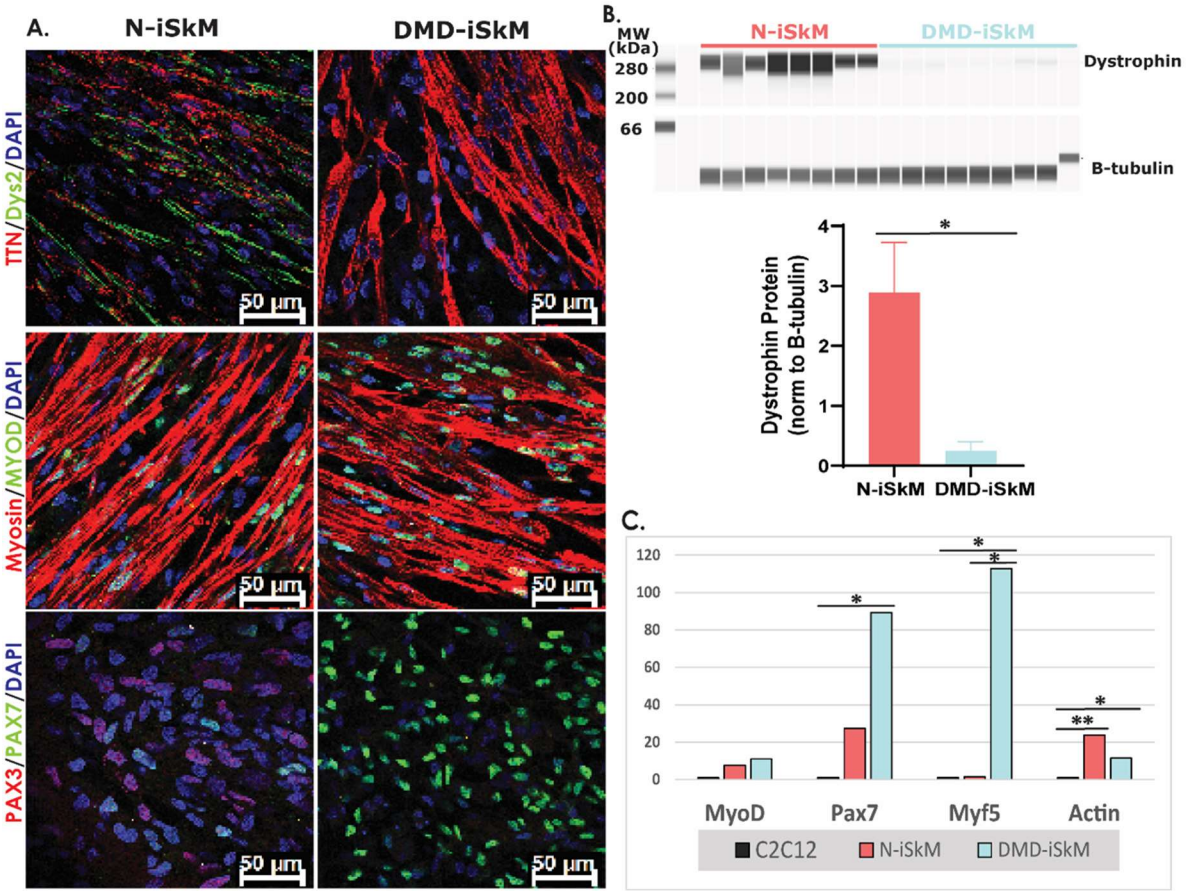

Fig. S4. Characterization of CTRL and DMD iSkMs. A) Differentiated myotubes express normal skeletal muscle markers after secondary differentiation (scale bar = 50 microns). **B)** DMD iSkMs are dystrophin deficient after secondary differentiation as shown by capillary western (p-value = 0.0131). **C)** *MyoD*, *Pax7*, *Myf5*, and *Actin* transcript expression was evaluated by qPCR in CTRL and DMD iSkMs using C2C12s as a control. *Gapdh* was utilized for normalization. (P-value ≤ 0.05 = *, ≤ 0.01 = *)

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Table S1. IPA settings utilized for core analyses. Each dataset was run through IPA individually. Expression log ratio, expression p-value, and expression FDR were used as cut-offs for each core analysis.

Analysis Type	Analysis Settings	Details
Expression	**General Settings**	Expr Log Ratio ≤ -1.5 or ≥ 1.5; Expr p-value ≤ 0.05, Expr FDR ≤ 0.01
	Networks	Interaction and causal networks. Causal networks including Severe DMD, Isolated DMD, Striated muscle disease, Disease of skeletal muscle, Disease of muscle cells, Muscle and heart defects
	Node Types	All; excluding fusion gene/product
	Data Sources	All
	Confidence	Experimentally Observed
	Species	All
	Tissues and Cell Lines	All
	Mutation	All
Core	**Species**	All
	Tissues and Cell Lines	-
	Node Types	All
	Diseases Categories	Inflammatory Response, Metabolic Disease, Skeletal and Muscle Disorders
	Biofluids	Blood, Plasma/Serum, Saliva, Urine
	Biomarkers	Disease progression, Prognosis

Table S2. Media components used for two-phase iSkM differentiation protocol. DMEM F12 + Glutamax was used as basal media for the primary differentiation stage while DMEM High Glucose was utilized for secondary differentiation. Cultures were enriched for myoblasts after primary differentiation and replating using SkGM2.

Media	Stage	Components
Differentiation Media p1	Primary (d0-2)	DMEM F12 + Glutamax, Non-Essential Amino Acids + Insulin-Transferrin-Selenium 1x + CHIR99021 + LDN193189
Differentiation Media p2	Primary (d3-5)	DMEM F12 + Glutamax, Non-Essential Amino Acids + Insulin-Transferrin-Selenium 1x + CHIR99021 + LDN193189 + human basic FGF protein
Differentiation Media p3	Primary (d6-7)	DMEM F12 + Glutamax, Non-Essential Amino Acids + Knockout replacement serum + HGF + IGF-1 + human basic FGF protein + LDN193189
Differentiation Media p4	Primary (d8-11)	DMEM F12 + Glutamax, Non-Essential Amino Acids + Knockout replacement serum (KSR)+ IGF-1
Differentiation Media p5	Primary (d12-26 every other day)	DMEM F12 + Glutamax, Non-Essential Amino Acids + Knockout replacement serum + HGF + IGF-1
SkGm2	Myoblast Enrichment	SkGM2 media + SkBM2 aliquots
Differentiation Media s1	Secondary (d0)	DMEM High Glucose + 5% KSR + HGF + IGF + SB431542
Differentiation Media s2	Secondary (d2/4)	DMEM High Glucose + 2% KSR + HGF + IGF + SB431542
Differentiation Media s3	Secondary (d6-14 every other day)	DMEM High Glucose + 15% KSR + HGF + IGF + SB431542
Treatment media	Secondary (d0 of AAV)	Differentiation media s1 + SGT-001 + 3µM etoposide
Vehicle media	Secondary (d0 of VEH)	Differentiation media s1 + DPBS + 3µM etoposide

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Table S3. Antibody info and conditions used for IF and Jess experiments. Underlined antibodies were used for Jess experiments.

Antibody	Product Number	IF Dilution	IF Secondary	Fixation	Jess Dilution
PAX3	Pax3-s (DSHB)	1:300	A21135	4% PFA	N/A
PAX7	Pax7-s (DSHB)	1:5	A21121	4% PFA	N/A
Myosin	MF-20 (DSHB)	1:20	A21145	4% PFA	N/A
MYOD	554130 (BD Biosciences)	1:200	A21121	4% PFA	N/A
Titin	9D10 (DSHB)	1:250	A10680	Methanol	N/A
DysB	NCL-DysB (Leica)	1:50	A21125	Methanol	N/A
Dys2	NCL-Dys2 (Leica)	1:20	A21121 or 35501BID (1:250)	Methanol	N/A
Dystrophin	Ab218198 (Abcam)	1:50	A11008	Methanol	N/A
Mannex44a	5B2 (DSHB)	1:10	A21141	Methanol	N/A
Mandys106	Mandys106 (Millipore Sigma)	N/A	N/A	N/A	1:100
HMGB1	Ab79823 (Abcam)	1:250	A11012	4% PFA	1:5
VCAM1	Ab134047 (Abcam)	1:250	A11012	4% PFA	1:5
B-tubulin	Ab21058 (Abcam)	N/A	N/A	N/A	1:25

Table S4. Primers used for qPCRs.

Primer	Sequence	
Pax7	Forward	GGG AAG AAA GAG GAG GAG GA
	Reverse	CCT CGC GGG TGT ATA TGT CT
Actin	Forward	AGG TCA TCA CCA TCG GCA ACG A
	Reverse	GCT GTT GTA GGT GGT CTC GTG A
Myf5	Forward	CCA CCT CCA ACT GCT CTG AT
	Reverse	AGG TGA TCC GGT CCA CTA TG
MyoD	Forward	GAC GGC ATG ATG GAC TAC AG-
	Reverse	AGG CAG TCT AGG CTC GAC AC
Hmgb1 human	Forward	GCG AAG AAA CTG GGA GAG ATG TG
	Reverse	GCA TCA GGC TTT CCT TTA GCT CG
Hmgb1 mouse	Forward	CCA AGA AGT GCT CAG AGA GGT G
	Reverse	GTC CTT GAA CTT CTT TTT GGT CTC
Vcam1 human	Forward	GCT ATG AGG ATG GAA GAC TCT GG
	Reverse	ACT TGT GCA GCC ACC TGA GAT C
Vcam1 mouse	Forward	GCT ATG AGG ATG GAA GAC TCT GG
	Reverse	ACT TGT GCA GCC ACC TGA GAT C

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Table S5. RNA sequencing analysis and differential expression data of B10-mdx vs B10-WT mice at 1 month of age. Raw reads were mapped to chromosomes and gene identifiers and subsequent differential analysis was completed (n = 5 per group).

Ensembl ID	Chromosome	Gene Name	Start	End	Length	logFC B10-*mdx* vs. B10-WT 1 mo	logCPM_ B10-*mdx* vs. B10-WT 1 mo	PValue_B 10-*mdx* vs. B10-WT 1 mo	FDR_B10-*mdx* vs. B10-WT 1 mo	Tgw.Disp	UpDown. Tgw	B10-WT.1mo_ Rep1_raw	B10-WT.1mo_ Rep2_raw	B10-WT.1mo_ Rep3_raw	B10-WT.1mo_ Rep4_raw	B10-WT.1mo_ Rep5_raw	B10-*mdx* .1mo_R ep1_raw	B10-*mdx* .1mo_R ep2_raw	B10-*mdx* .1mo_R ep3_raw	B10-*mdx* .1mo_R ep4_raw	B10-*mdx* .1mo_R ep5_raw
ENSMUSG00000046805	chr19	Mpeg1	12460779	12460861	4335	4.811467	6.209129	3.59E-89	4.97E-85	0.047872	1	72	62	82	110	99	2068	3742	2251	4630	4310
ENSMUSG00000061086	chr11	Myl4	1.05E+08	1.05E+08	4637	5.273989	7.256915	2.63E-81	1.82E-77	0.062081	1	81	114	169	117	173	5411	11640	5968	6044	5440
ENSMUSG00000038642	chr3	Ctss	95526786	95526925	1358	4.607479	7.125563	6.06E-68	2.8E-64	0.061644	1	158	99	206	162	320	4505	6898	3811	8353	8161
ENSMUSG00000023992	chr17	Trem2	48346401	48346595	4946	5.006626	3.979895	5.58E-62	1.93E-58	0.065808	1	17	8	16	21	16	458	631	400	1157	979
ENSMUSG00000034652	chr11	Cd300a	1.15E+08	1.15E+08	4738	3.815488	3.496869	4.69E-53	1.3E-49	0.049052	1	19	20	34	16	35	313	503	340	678	631
ENSMUSG00000044811	chr11	AF251705	1.15E+08	1.15E+08	1275	5.079592	2.826981	1.56E-51	3.59E-48	0.071345	1	5	5	13	1	9	213	400	205	393	371
ENSMUSG00000031762	chr8	Mt2	94172618	94172875	556	4.49806	5.599762	2.63E-51	5.21E-48	0.076372	1	58	96	78	48	54	2099	1496	3045	2554	1469
ENSMUSG00000050335	chr14	Lgals3	47367751	47367852	1858	5.960781	7.229387	3.76E-51	6.51E-48	0.120191	1	65	57	90	68	123	3494	3465	3422	13359	12430
ENSMUSG00000061436	chr6	Hipk2	38694390	38698596	8836	-3.72207	5.527373	1.18E-49	1.81E-46	0.058865	-1	1359	946	1893	1592	1416	72	105	189	183	225
ENSMUSG00000054958	chr4	Nt5c1a	1.23E+08	1.23E+08	1220	-4.32504	3.072814	4.3E-49	5.95E-46	0.065209	-1	233	212	273	343	281	11	15	34	26	8
ENSMUSG00000039316	chr17	Rftn1	49992257	49994481	4504	4.127338	4.055458	3.94E-48	4.96E-45	0.066579	1	19	23	47	22	40	553	914	383	1220	639
ENSMUSG00000039126	chr19	Prune2	16956118	16956292	12512	3.534167	3.690042	2.02E-47	2.33E-44	0.050778	1	18	16	42	36	62	449	609	440	716	534
ENSMUSG00000081194	chrX	Gm8424	1.51E+08	1.51E+08	988	-3.44244	3.395947	3.18E-47	3.39E-44	0.048131	-1	306	266	367	417	239	36	40	40	51	40
ENSMUSG00000020961	chr12	Ston2	91638542	91639805	6915	-2.96107	4.131434	6.05E-45	5.98E-42	0.041553	-1	453	325	773	505	583	60	94	119	115	82
ENSMUSG00000049103	chr9	Ccr2	1.24E+08	1.24E+08	6393	3.388932	3.895425	8.2E-44	7.53E-41	0.052241	1	48	35	46	31	53	392	910	412	804	664
ENSMUSG00000090942	chr18	F830016B08Rik	60293380	60293486	3297	-4.36617	5.505781	8.7E-44	7.53E-41	0.086923	-1	865	1472	2367	1212	1412	98	147	41	129	74
ENSMUSG00000040552	chr6	C3ar1	1.23E+08	1.23E+08	4305	3.316841	4.505567	1.08E-43	8.79E-41	0.053014	1	51	42	80	68	110	607	846	666	1411	1363
ENSMUSG00000002985	chr7	Apoe	19696109	19697103	1980	2.897883	8.957201	2.34E-43	1.8E-40	0.045652	1	1587	1151	2071	2127	3140	15325	23839	15622	24508	23702
ENSMUSG00000052837	chr8	Junb	84976909	84978748	1840	2.365369	4.238091	5.01E-41	3.65E-38	0.029601	1	84	87	117	118	101	630	795	684	895	647
ENSMUSG00000040253	chr3	Gbp7	1.43E+08	1.43E+08	5552	-2.4574	4.20954	5.83E-41	4.03E-38	0.032597	-1	390	526	659	456	594	116	143	105	161	140
ENSMUSG00000026414	chr1	Tnnt2	1.36E+08	1.36E+08	7752	4.447036	6.015928	1.34E-40	8.85E-38	0.097758	1	46	56	122	97	172	1835	5490	1903	2947	2338
ENSMUSG00000045103	chrX	Dmd	82948870	82949147	23801	-3.99331	6.718611	1.65E-40	1.04E-37	0.08399	-1	3218	2265	3631	3155	4466	134	276	570	283	204
ENSMUSG00000039704	chr15	Lmbrd2	9140621	9140740	3863	-3.76033	2.752167	7.76E-40	4.67E-37	0.064209	-1	198	132	270	187	280	7	30	27	20	25
ENSMUSG00000049173	chr18	Myoz3	60576316	60576518	870	-2.41622	5.374637	1.21E-37	6.97E-35	0.037295	-1	1016	956	1493	1192	1200	207	354	217	472	312
ENSMUSG00000030579	chr7	Tyrobp	30413788	30413899	564	3.340349	5.192594	1.76E-37	9.76E-35	0.065342	1	94	68	152	75	171	1074	1569	858	2315	2082
ENSMUSG00000023067	chr17	Cdkn1a	29090979	29091101	2223	3.483549	6.390759	2.2E-37	1.17E-34	0.072549	1	199	143	233	211	389	2083	4961	5246	3021	2645
ENSMUSG00000003484	chr8	Cyp4f18	71988482	71988737	1855	5.088533	1.943789	3.59E-37	1.84E-34	0.090533	1	3	2	3	4	5	109	228	96	175	226
ENSMUSG00000024907	chr19	Gal	3409919	3410165	712	5.484438	2.512776	1.66E-36	8.21E-34	0.118607	1	4	0	9	1	6	194	288	114	458	235
ENSMUSG00000020354	chr11	Sgcd	46896253	46897969	8257	-2.48646	4.062642	7.21E-36	3.44E-33	0.038355	-1	456	281	623	501	533	109	111	108	126	132
ENSMUSG00000000682	chr4	Cd52	1.34E+08	1.34E+08	1187	4.690386	3.16678	1.15E-35	5.3E-33	0.106958	1	7	9	12	9	18	295	328	149	545	685
ENSMUSG00000056069	chr15	Fam105a	27655071	27657071	2830	3.179489	2.980274	1.37E-35	6.14E-33	0.053905	1	20	25	37	18	28	214	402	223	446	362
ENSMUSG00000063011	chr17	Msln	25748614	25748830	2114	4.947891	1.896465	1.47E-35	6.37E-33	0.090256	1	6	0	5	4	3	88	242	161	171	144
ENSMUSG00000053063	chr6	Clec12a	1.29E+08	1.29E+08	5139	3.412184	2.955524	6.22E-35	2.61E-32	0.062563	1	22	11	26	23	27	249	449	194	405	329
ENSMUSG00000029816	chr6	Gpnmb	49036518	49036792	3798	5.463234	7.129157	1.02E-34	4.17E-32	0.159201	1	81	56	115	129	148	2884	2319	3278	13189	12105
ENSMUSG00000033685	chr7	Ucp2	1E+08	1E+08	6989	2.480337	6.059381	2.06E-34	8.16E-32	0.043353	1	242	248	388	338	510	1697	2522	2044	4271	3003
ENSMUSG00000033777	chrX	Tlr13	1.06E+08	1.06E+08	4086	4.032944	2.913065	2.46E-34	9.46E-32	0.085026	1	12	9	17	11	22	162	249	220	523	516
ENSMUSG00000079293	chr6	Clec7a	1.29E+08	1.29E+08	2287	3.582119	2.935213	4.06E-34	1.52E-31	0.070005	1	20	16	19	11	30	177	498	247	363	345
ENSMUSG00000007617	chr13	Homer1	93303757	93305302	10502	-2.04901	5.625855	5.68E-34	2.07E-31	0.030572	-1	1111	1144	1699	1345	1361	412	461	437	473	439
ENSMUSG00000073421	chr17	H2-Ab1	34263209	34263405	1637	3.010425	5.53002	1.33E-33	4.73E-31	0.062541	1	142	120	220	197	176	1843	2741	994	2349	1582
ENSMUSG00000079523	chr6	Tmsb10	72957347	72957652	1276	3.129772	7.042024	2.43E-33	8.41E-31	0.068383	1	338	351	562	463	574	4751	8642	2588	6188	5359
ENSMUSG00000031765	chr8	Mt1	94179089	94179338	540	3.456443	5.50351	2.57E-33	8.68E-31	0.079073	1	94	161	108	149	104	1759	1141	2946	2302	1434
ENSMUSG00000039824	chr10	Myl6b	1.28E+08	1.28E+08	1026	3.201044	4.624988	2.67E-33	8.81E-31	0.067867	1	37	67	67	99	141	670	1527	1090	1105	796
ENSMUSG00000042485	chr14	Mustn1	30879257	30879615	1177	2.247913	6.852502	1.11E-32	3.58E-30	0.038533	1	537	417	840	771	849	3304	4406	5384	4698	4459
ENSMUSG00000089929	chr9	Bcl2a1b	89199209	89199779	817	5.008975	1.996337	1.14E-32	3.58E-30	0.109257	1	2	0	4	5	8	110	176	91	234	264
ENSMUSG00000032089	chr9	Il10ra	45253837	45256441	3498	3.073283	3.084344	2.12E-32	6.52E-30	0.057926	1	28	14	35	30	42	318	416	236	345	399
ENSMUSG00000026253	chr1	Chrng	87204657	87204704	4163	5.262472	4.171932	2.67E-32	8.03E-30	0.153035	1	8	13	18	11	27	540	1848	270	905	531
ENSMUSG00000030789	chr7	Itgax	1.28E+08	1.28E+08	4045	5.484143	2.552692	4.46E-32	1.31E-29	0.138064	1	3	5	5	4	3	152	279	78	508	329
ENSMUSG00000028132	chr3	Tmem56	1.21E+08	1.21E+08	7650	-1.96384	5.269027	6.1E-32	1.71E-29	0.029871	-1	875	911	1321	939	1094	293	397	390	379	371
ENSMUSG00000028859	chr4	Csf3r	1.26E+08	1.26E+08	3609	5.061156	1.66552	6.17E-32	1.71E-29	0.101734	1	1	4	1	3	5	89	130	78	174	214
ENSMUSG00000058715	chr1	Fcer1g	1.71E+08	1.71E+08	874	3.223543	4.92485	6.08E-32	1.71E-29	0.072503	1	93	65	105	86	145	1074	1136	557	1789	1873
ENSMUSG00000036594	chr17	H2-Aa	34282744	34283023	1874	2.946654	5.732576	9.59E-32	2.6E-29	0.06417	1	164	144	266	247	203	2135	3218	1244	2605	1666
ENSMUSG00000030707	chr7	Coro1a	1.27E+08	1.27E+08	2783	3.489441	4.520971	2.59E-31	6.89E-29	0.083889	1	54	49	70	46	96	630	865	424	1446	1637
ENSMUSG00000040809	chr3	Chil3	1.06E+08	1.06E+08	1632	8.300759	3.847752	6.89E-31	1.8E-28	0.272315	1	0	1	0	4	2	205	291	194	1258	1552
ENSMUSG00000093327	chr18	Mir5107	60812076	60812163	88	3.058131	4.59645	7.88E-31	2.02E-28	0.067999	1	69	57	100	108	100	992	1470	498	1172	828
ENSMUSG00000040345	chr10	Arhgap9	1.27E+08	1.27E+08	1811	3.020159	2.512802	1.05E-30	2.64E-28	0.054329	1	18	15	24	23	21	163	227	160	316	298
ENSMUSG00000031880	chr8	Rrad	1.05E+08	1.05E+08	1575	3.84582	3.989579	1.99E-30	4.92E-28	0.099519	1	24	27	26	49	45	787	776	375	1152	327
ENSMUSG00000035004	chr7	Igsf6	1.21E+08	1.21E+08	2133	3.070687	2.334221	2.05E-30	4.99E-28	0.055465	1	15	8	22	19	23	120	248	188	276	201
ENSMUSG00000024672	chr19	Ms4a7	11321039	11321582	4453	3.351844	3.760987	2.66E-30	6.34E-28	0.078193	1	35	23	56	31	58	499	842	255	615	620

ENSMUSG00000056888	chr10	Glipr1	1.12E+08	1.12E+08	1543	5.047148	1.665138	3.33E-30	7.82E-28	0.110091	1	1	6	1	2	4	81	195	73	181	157
ENSMUSG00000069516	chr10	Lyz2	1.17E+08	1.17E+08	1266	2.791666	8.656451	3.41E-30	7.88E-28	0.062468	1	1564	1048	2192	1329	2572	9916	18781	9945	27585	18830
ENSMUSG00000020865	chr11	Abcc3	94343295	94343775	5698	3.158963	2.200331	4.96E-30	1.12E-27	0.057109	1	16	11	15	11	21	125	193	140	272	213
ENSMUSG00000037416	chr18	Dmxl1	49832670	49833176	21860	-2.00933	5.217804	5.13E-30	1.15E-27	0.033441	-1	866	818	1094	1005	1224	221	345	455	426	300
ENSMUSG00000091562	chr16	Gm9581	59558013	59560242	2870	-3.96479	2.294675	5.25E-30	1.15E-27	0.094383	-1	124	114	168	174	201	4	8	32	12	13
ENSMUSG00000049625	chr13	Tifab	56173703	56176633	3498	3.514143	2.62054	7.83E-30	1.69E-27	0.076555	1	16	7	13	24	20	185	290	145	352	325
ENSMUSG00000024610	chr18	Cd74	60803848	60804010	1410	3.132942	6.976589	8.41E-30	1.79E-27	0.077131	1	339	270	573	533	466	5211	7862	2532	6352	4207
ENSMUSG00000021886	chr12	Gpr65	98268635	98268714	2049	4.105805	1.699593	1.27E-29	2.66E-27	0.085085	1	3	4	7	4	10	92	162	77	178	176
ENSMUSG00000078949	chr2	R3hdml	1.63E+08	1.63E+08	1094	10.05725	1.815905	2.01E-29	4.15E-27	0.215717	1	0	0	0	0	0	77	385	68	151	103
ENSMUSG00000038147	chr1	Cd84	1.72E+08	1.72E+08	6272	3.35884	3.660748	2.74E-29	5.57E-27	0.081023	1	38	16	42	32	60	326	393	329	883	801
ENSMUSG00000060586	chr17	H2-Eb1	34305877	34306047	1184	2.902351	5.266718	3.06E-29	6.14E-27	0.067013	1	107	104	230	200	121	1430	2177	934	1935	1399
ENSMUSG00000020649	chr12	Rrm2	24708241	24708445	2771	2.462173	3.461143	4.43E-29	8.76E-27	0.045134	1	40	49	60	43	90	281	391	348	656	514
ENSMUSG00000029762	chr6	Akr1b8	34354119	34354296	1499	3.455082	3.38629	4.58E-29	8.93E-27	0.084612	1	19	14	33	24	58	311	559	214	657	499
ENSMUSG00000024912	chr19	Fosl1	5447703	5448055	1707	8.691869	0.546812	4.89E-29	9.4E-27	0.108107	1	0	0	0	0	0	51	34	46	94	78
ENSMUSG00000005580	chr16	Adcy9	4287529	4289089	5197	-2.88039	4.447615	5.55E-29	1.05E-26	0.065701	-1	629	517	747	590	732	59	114	227	125	90
ENSMUSG00000028238	chr4	Atp6v0d2	19876841	19878380	2716	6.392452	3.006986	6.73E-29	1.26E-26	0.206377	1	2	4	1	0	8	123	228	158	794	619
ENSMUSG00000040907	chr7	Atp1a3	24978167	24978576	5972	4.937031	2.561301	1.22E-28	2.25E-26	0.140009	1	2	3	6	11	8	147	197	104	524	374
ENSMUSG00000098112	chr15	Bin2	1.01E+08	1.01E+08	2530	4.198478	1.347723	2.39E-28	4.35E-26	0.082093	1	4	2	7	3	4	73	90	73	156	140
ENSMUSG00000060063	chr5	Alox5ap	1.49E+08	1.49E+08	852	2.751731	4.079135	4.35E-28	7.82E-26	0.060934	1	57	55	85	60	110	462	567	388	1064	1001
ENSMUSG00000021190	chr12	Lgmn	1.02E+08	1.02E+08	2323	2.19864	7.265413	7.09E-28	1.26E-25	0.043954	1	671	740	1068	761	1459	4378	5518	4367	8229	7398
ENSMUSG00000021423	chr13	Ly86	37345345	37345574	997	3.124296	3.623201	9.95E-28	1.74E-25	0.07588	1	34	23	61	37	58	517	759	278	461	479
ENSMUSG00000001864	chr2	Aif1l	31950139	31950381	4032	2.322262	4.644182	2.11E-27	3.64E-25	0.046921	1	97	99	126	159	224	733	1350	906	1109	747
ENSMUSG00000000305	chr2	Cdh4	1.79E+08	1.79E+08	7257	-3.15076	3.147308	2.42E-27	4.13E-25	0.076648	-1	351	179	209	340	224	43	47	28	44	45
ENSMUSG00000043091	chr15	Tuba1c	99029891	99030424	1977	2.818739	4.053252	3.84E-27	6.48E-25	0.066054	1	40	67	58	67	113	376	462	586	1187	869
ENSMUSG00000059498	chr1	Fcgr3	1.71E+08	1.71E+08	1736	2.267681	4.73114	3.91E-27	6.52E-25	0.045549	1	140	85	171	121	260	737	1103	823	1378	1128
ENSMUSG00000056758	chr10	Hmga2	1.2E+08	1.2E+08	6772	6.978298	0.414001	6.67E-27	1.09E-24	0.102803	1	0	1	0	0	0	30	45	51	103	48
ENSMUSG00000062382	chr13	Gm10116	74406396	74407317	922	2.984741	3.337734	6.6E-27	1.09E-24	0.07053	1	30	36	40	25	56	277	274	280	686	595
ENSMUSG00000025473	chr7	Adam8	1.4E+08	1.4E+08	4638	5.004133	4.020248	7.59E-27	1.22E-24	0.173735	1	20	4	21	11	26	356	409	264	1551	1251
ENSMUSG00000040613	chr6	Apobec1	1.23E+08	1.23E+08	2391	2.553997	3.685445	1.03E-26	1.64E-24	0.054766	1	41	40	68	69	97	259	567	389	688	695
ENSMUSG00000034116	chr17	Vav1	57279100	57279401	3688	3.503233	2.810464	1.05E-26	1.65E-24	0.090337	1	15	13	26	15	24	157	294	144	462	454
ENSMUSG00000021665	chr13	Hexb	97176332	97176589	1904	2.143026	5.111411	1.45E-26	2.26E-24	0.042828	1	229	142	230	166	303	893	1428	977	1869	1504
ENSMUSG00000074677	chr3	Sirpb1c	15795145	15795350	3682	5.283462	0.570449	1.74E-26	2.68E-24	0.089306	1	1	1	2	1	0	53	81	39	63	62
ENSMUSG00000031760	chr8	Mt3	94152607	94152830	538	2.98533	2.571499	2.05E-26	3.13E-24	0.066224	1	8	20	30	18	34	229	175	237	276	268
ENSMUSG00000050556	chr2	Kcnb1	1.67E+08	1.67E+08	4060	-2.15643	4.343741	2.62E-26	3.94E-24	0.042453	-1	408	400	641	699	657	140	157	113	244	223
ENSMUSG00000029810	chr6	Tmem176b	48833811	48834139	2049	2.025932	5.643763	2.82E-26	4.16E-24	0.039437	1	282	251	341	322	464	1464	2579	1348	2166	1813
ENSMUSG00000076138	chr9	Gm26377	78478528	78478635	108	1.920919	6.653203	2.83E-26	4.16E-24	0.036177	1	602	563	736	642	1005	2379	3854	3081	5095	4513
ENSMUSG00000006519	chr8	Cyba	1.22E+08	1.22E+08	758	2.784628	5.030441	3.06E-26	4.46E-24	0.069651	1	122	114	176	100	183	904	979	730	2110	2075
ENSMUSG00000020901	chr11	Pik3r5	68432121	68432262	5550	4.010733	2.523194	3.35E-26	4.83E-24	0.113336	1	4	5	11	17	18	143	195	131	436	359
ENSMUSG00000005054	chr10	Cstb	78425670	78425857	599	2.808623	4.610354	5.58E-26	7.92E-24	0.07057	1	79	104	112	93	117	627	735	536	1580	1618
ENSMUSG00000026480	chr1	Ncf2	1.53E+08	1.53E+08	8478	3.095562	3.635746	5.61E-26	7.92E-24	0.080587	1	42	18	35	48	75	331	497	288	763	740
ENSMUSG00000102049	chr1	Zbed6	1.34E+08	1.34E+08	5007	-3.50006	4.832932	6.53E-26	9.13E-24	0.105493	-1	839	523	1050	792	1255	34	117	221	96	80
ENSMUSG00000103229	chr3	Dcun1d1	35895620	35895699	780	-2.08494	3.802634	6.63E-26	9.17E-24	0.03897	-1	323	267	503	384	429	98	146	153	133	89
ENSMUSG00000030306	chr6	Tmtc1	1.48E+08	1.48E+08	8578	-1.97073	6.698836	7.31E-26	1E-23	0.038725	-1	2995	1967	2984	2423	3497	841	1180	833	1229	852
ENSMUSG00000103405	chr1	Unspecified	34160330	34160496	7920	-3.71263	3.190523	8.14E-26	1.1E-23	0.109842	-1	340	120	340	366	253	15	21	44	21	50
ENSMUSG00000101389	chr19	Ms4a4a	11375523	11375631	836	2.901293	3.198228	8.82E-26	1.19E-23	0.069632	1	33	20	66	24	37	332	399	361	281	446
ENSMUSG00000026177	chr1	Slc11a1	74375195	74375321	3705	3.193123	3.554713	9.56E-26	1.27E-23	0.085544	1	29	20	58	39	48	288	392	252	889	705
ENSMUSG00000018774	chr11	Cd68	69664213	69664504	1257	3.703479	5.554568	1.29E-25	1.69E-23	0.118464	1	64	64	113	100	243	1277	1339	982	3841	3117
ENSMUSG00000024411	chr18	Aqp4	15389394	15393729	5082	-2.37961	6.002738	1.29E-25	1.69E-23	0.055309	-1	1344	1879	1886	1904	1942	363	605	246	747	499
ENSMUSG00000063388	chr18	BC023105	60441753	60442361	1227	-2.20234	5.474765	1.77E-25	2.29E-23	0.04782	-1	1000	1578	1437	864	1125	317	374	395	401	356
ENSMUSG00000028581	chr4	Laptm5	1.31E+08	1.31E+08	3788	2.93983	5.392787	2.13E-25	2.73E-23	0.081069	1	114	80	161	181	299	1201	1820	873	2529	2398
ENSMUSG00000084883	chr12	Ccdc85c	1.08E+08	1.08E+08	1547	-2.87973	2.169403	2.22E-25	2.82E-23	0.063541	-1	118	121	148	160	108	19	21	37	27	21
ENSMUSG00000040751	chr5	Lat2	1.35E+08	1.35E+08	1505	4.936203	3.39882	2.32E-25	2.92E-23	0.174849	1	10	12	7	7	18	207	293	146	895	916
ENSMUSG00000004707	chr1	Ly9	1.72E+08	1.72E+08	3307	3.927781	2.52663	2.59E-25	3.23E-23	0.114169	1	8	10	7	7	26	199	234	102	369	333
ENSMUSG00000021091	chr12	Serpina3n	1.04E+08	1.04E+08	2064	4.0058	4.562851	2.83E-25	3.5E-23	0.133973	1	44	21	26	54	89	437	637	1079	991	2102
ENSMUSG00000043157	chr14	Arl11	61309753	61309937	1482	3.222775	1.56843	3.27E-25	4E-23	0.065207	1	6	7	10	9	13	81	94	101	181	142
ENSMUSG00000099906	chr1	Gm28653	20679023	20684298	5276	3.699161	2.018377	3.74E-25	4.54E-23	0.094879	1	11	5	6	7	17	84	263	158	159	182
ENSMUSG00000031838	chr8	Ifi30	70762774	70763040	980	2.250751	5.208408	4.28E-25	5.15E-23	0.050218	1	174	159	254	177	324	1070	1222	897	2103	1930
ENSMUSG00000063142	chr14	Kcnma1	23289431	23289452	6513	-1.81011	4.103583	4.38E-25	5.22E-23	0.031137	-1	421	363	539	396	522	118	204	210	200	163
ENSMUSG00000020546	chr11	Stxbp4	90476492	90480714	11834	-1.9659	4.701672	6.6E-25	7.81E-23	0.038704	-1	640	620	744	591	870	238	307	166	281	236
ENSMUSG00000102573	chr9	RP23-296I6.8	72691549	72695050	3502	-3.52618	2.940857	8.48E-25	9.95E-23	0.104414	-1	234	167	333	272	173	8	30	55	34	19
ENSMUSG00000078771	chr11	Evi2a	79526560	79527802	2297	2.084898	3.371197	1.21E-24	1.41E-22	0.038882	1	59	57	81	45	84	290	353	316	522	463
ENSMUSG00000020399	chr11	Havcr2	46454935	46455058	2721	4.912892	0.839568	1.87E-24	2.16E-22	0.106472	1	5	0	0	3	0	42	83	53	104	89
ENSMUSG00000047497	chr15	Adamts12	11064790	11065157	6234	-2.8566	3.969649	2E-24	2.29E-22	0.077153	-1	439	182	539	423	794	42	123	91	120	78
ENSMUSG00000049723	chr9	Mmp12	7344381	7344437	7237	4.795811	2.772454	2.37E-24	2.69E-22	0.167208	1	8	3	4	13	10	248	245	81	672	303
ENSMUSG00000043832	chr6	Clec4a3	1.23E+08	1.23E+08	1327	2.51196	2.783059	2.41E-24	2.71E-22	0.053624	1	33	24	39	27	45	235	347	185	293	266
ENSMUSG00000006731	chr10	B4galnt1	1.27E+08	1.27E+08	2474	3.397542	2.629539	2.98E-24	3.33E-22	0.094007	1	11	20	17	11	28	157	219	136	418	386

ENSMUSG00000048865	chr1	Arhgap30	1.71E+08	1.71E+08	8591	2.657676	3.415205	3.3E-24	3.65E-22	0.064887	1	52	24	56	44	66	285	382	260	613	616
ENSMUSG00000020437	chr11	Myo1g	6506548	6506832	6957	3.207572	2.75295	3.72E-24	4.05E-22	0.086797	1	24	9	18	19	38	156	286	172	414	390
ENSMUSG00000036905	chr4	C1qb	1.37E+08	1.37E+08	1088	2.421812	6.522331	3.69E-24	4.05E-22	0.060957	1	434	268	593	378	809	3312	4150	2167	4545	3860
ENSMUSG00000048163	chr5	Selplg	1.14E+08	1.14E+08	2604	2.784125	3.404834	4.4E-24	4.76E-22	0.071301	1	42	21	36	50	75	354	419	237	561	565
ENSMUSG00000045136	chr13	Tubb2b	34127008	34128531	1922	3.179426	4.259289	5.08E-24	5.45E-22	0.094783	1	54	60	49	66	85	626	1509	337	893	631
ENSMUSG00000040659	chr4	Efhd2	1.42E+08	1.42E+08	2381	2.299228	5.358004	5.65E-24	6.01E-22	0.055082	1	172	180	239	259	317	970	1236	1074	2567	2321
ENSMUSG00000076036	chr7	Gm22133	45458089	45458197	109	2.718294	7.853153	6.35E-24	6.71E-22	0.076223	1	804	828	1046	1092	1376	6217	5734	5386	16252	14770
ENSMUSG00000037280	chr15	Galnt6	1.01E+08	1.01E+08	3871	5.054345	2.456576	6.88E-24	7.22E-22	0.180696	1	1	3	5	6	11	90	345	73	426	321
ENSMUSG00000028874	chr4	Fgr	1.33E+08	1.33E+08	3863	5.277741	2.157213	7.08E-24	7.37E-22	0.180736	1	0	9	2	3	3	96	189	74	343	305
ENSMUSG00000055541	chr7	Lair1	4007073	4009834	3760	3.143904	2.088637	7.59E-24	7.84E-22	0.076112	1	12	13	12	10	22	118	212	96	243	199
ENSMUSG00000031827	chr8	Cotl1	1.2E+08	1.2E+08	1628	2.845362	5.42958	7.7E-24	7.9E-22	0.081929	1	134	109	193	158	308	1095	1331	942	3117	2628
ENSMUSG00000057191	chr9	AB124611	21526176	21526307	1447	3.369876	2.06112	8.73E-24	8.89E-22	0.086146	1	19	6	8	8	17	125	186	107	226	214
ENSMUSG00000053687	chr8	Dpep2	1.06E+08	1.06E+08	4540	4.090738	2.127539	9.44E-24	9.54E-22	0.123445	1	10	6	2	6	14	99	129	119	329	278
ENSMUSG00000025283	chrX	Sat1	1.55E+08	1.55E+08	2774	1.767439	5.128634	9.9E-24	9.93E-22	0.033399	1	230	240	309	209	340	870	1500	1292	1240	1392
ENSMUSG00000072945	chrX	Ripply1	1.4E+08	1.4E+08	811	6.308961	0.913225	1.09E-23	1.08E-21	0.162735	1	2	0	0	1	0	53	157	39	72	72
ENSMUSG00000028327	chr4	Stra6l	45848664	45848726	9567	4.92218	0.458849	1.11E-23	1.1E-21	0.098195	1	0	1	0	1	4	31	60	43	61	81
ENSMUSG00000033624	chr8	Pdpr	1.11E+08	1.11E+08	5028	-3.36535	6.120781	1.24E-23	1.21E-21	0.111547	-1	1918	1683	2426	2524	2025	110	253	624	312	163
ENSMUSG00000021182	chr12	Ccdc88c	1.01E+08	1.01E+08	6313	-1.68428	5.198468	1.29E-23	1.25E-21	0.030827	-1	739	689	1119	1010	1185	284	488	391	447	434
ENSMUSG00000052160	chr12	Pld4	1.13E+08	1.13E+08	1978	2.517161	4.386354	1.75E-23	1.7E-21	0.064402	1	82	60	121	77	192	669	943	466	1049	1021
ENSMUSG00000053205	chr14	Styx	45351473	45351529	672	-3.13171	2.509359	1.91E-23	1.84E-21	0.086823	-1	167	109	219	189	175	10	39	43	32	14
ENSMUSG00000038451	chr6	Spsb2	1.25E+08	1.25E+08	1658	2.794456	2.623722	1.96E-23	1.87E-21	0.068858	1	17	17	30	16	49	146	324	201	287	280
ENSMUSG00000022952	chr16	Runx1	92601466	92606124	11827	2.221299	3.670252	2.3E-23	2.18E-21	0.048746	1	61	62	70	61	121	313	695	410	640	394
ENSMUSG00000079419	chr19	Ms4a6c	11469366	11469556	2050	2.361698	3.560523	2.68E-23	2.52E-21	0.054866	1	45	40	84	64	90	359	473	266	556	632
ENSMUSG00000072620	chr11	Slfn2	83065112	83065343	1664	3.076015	3.824093	2.93E-23	2.74E-21	0.091487	1	24	36	60	58	76	521	419	287	675	1011
ENSMUSG00000038618	chr7	Rassf7	1.41E+08	1.41E+08	1803	4.223786	1.571283	3.13E-23	2.91E-21	0.118527	1	6	5	5	2	5	88	225	68	122	115
ENSMUSG00000023845	chr17	Lnpep	17527723	17529880	5181	-2.08824	4.518092	3.51E-23	3.24E-21	0.046462	-1	556	416	732	677	750	108	190	310	238	186
ENSMUSG00000032041	chr9	Tirap	35184551	35187930	4929	-1.6217	4.180509	3.93E-23	3.61E-21	0.027407	-1	379	374	537	470	538	170	205	218	211	228
ENSMUSG00000030218	chr6	Mgp	1.37E+08	1.37E+08	598	2.422683	7.291767	4.82E-23	4.39E-21	0.064415	1	827	572	837	712	1207	4109	9159	7812	5876	3844
ENSMUSG00000050708	chr7	Ftl1	45457944	45458283	1340	2.521946	9.173742	5.04E-23	4.56E-21	0.069609	1	2123	2378	3071	2907	4035	14589	14817	14376	39937	35038
ENSMUSG00000017400	chr11	Stac2	98036623	98038070	3139	4.611684	1.763401	5.59E-23	5.03E-21	0.148981	1	6	0	3	1	11	123	203	84	226	91
ENSMUSG00000073016	chrX	Uprt	1.04E+08	1.04E+08	2304	-2.72241	1.746037	7.47E-23	6.67E-21	0.060695	-1	99	63	118	90	119	10	22	23	30	19
ENSMUSG00000024965	chr19	Fermt3	6998958	6999520	2587	2.873826	3.409814	1.09E-22	9.69E-21	0.081388	1	26	30	40	38	81	287	328	253	674	657
ENSMUSG00000002204	chr7	Napsa	44572432	44572689	2158	4.609714	1.799491	1.19E-22	1.05E-20	0.148842	1	6	5	1	0	9	87	123	81	212	251
ENSMUSG00000021339	chr13	Mrs2	24992483	24993188	2035	-1.82549	3.751081	1.27E-22	1.12E-20	0.034874	-1	292	300	456	374	332	111	116	123	210	139
ENSMUSG00000041702	chr12	Btbd7	1.03E+08	1.03E+08	4298	-2.09179	3.376403	1.53E-22	1.33E-20	0.045145	-1	246	210	301	294	366	41	94	125	115	94
ENSMUSG00000056737	chr6	Capg	72544391	72544466	2529	2.643497	5.498935	1.64E-22	1.42E-20	0.076396	1	169	164	248	193	277	1056	1237	1002	3392	2758
ENSMUSG00000004266	chr6	Ptpn6	1.25E+08	1.25E+08	2802	3.061013	3.631446	1.89E-22	1.62E-20	0.093571	1	43	21	43	35	81	285	458	264	832	792
ENSMUSG00000079227	chr9	Ccr5	1.24E+08	1.24E+08	3704	3.744198	2.666125	1.95E-22	1.67E-20	0.123212	1	11	14	7	15	24	141	280	105	458	402
ENSMUSG00000031443	chr8	F7	13026034	13026131	1859	8.541778	1.845548	2.01E-22	1.71E-20	0.301145	1	0	0	0	0	1	53	52	55	380	302
ENSMUSG00000024030	chr17	Abcg1	31057698	31057856	4066	2.30356	2.81146	2.34E-22	1.97E-20	0.050304	1	24	36	37	51	45	240	292	194	334	268
ENSMUSG00000033220	chr15	Rac2	78559169	78561485	3036	3.165425	3.587114	2.59E-22	2.17E-20	0.099955	1	30	20	45	30	80	331	496	214	724	775
ENSMUSG00000030577	chr7	Cd22	30865402	30866662	4987	4.781422	0.341887	3.25E-22	2.71E-20	0.093135	1	1	0	0	3	2	46	41	33	73	57
ENSMUSG00000054178	chr19	Gm9938	23723279	23725034	1756	-3.01134	0.964865	3.84E-22	3.19E-20	0.061714	-1	44	52	64	55	74	7	11	12	7	12
ENSMUSG00000023169	chr15	Slc38a1	96571418	96576812	8391	2.415974	3.147629	3.88E-22	3.19E-20	0.058843	1	39	28	48	35	84	185	398	296	490	383
ENSMUSG00000031101	chrX	Sash3	48146436	48146717	2677	2.921502	2.143595	4.8E-22	3.93E-20	0.075459	1	9	11	14	18	32	119	176	121	237	235
ENSMUSG00000042155	chr2	Klhl23	69821944	69822059	4925	-1.80874	5.135561	5.13E-22	4.18E-20	0.038279	-1	729	789	1135	936	1002	304	482	249	478	318
ENSMUSG00000050919	chr13	Zfp366	99184823	99184864	2763	-3.93979	1.131939	5.61E-22	4.54E-20	0.114242	-1	53	51	70	114	54	1	5	11	6	8
ENSMUSG00000040528	chr11	Milr1	1.07E+08	1.07E+08	2474	3.447886	1.51239	7.91E-22	6.37E-20	0.090185	1	6	9	6	5	11	92	95	65	179	149
ENSMUSG00000037902	chr2	Sirpa	1.3E+08	1.3E+08	4911	2.548474	5.977591	8.1E-22	6.48E-20	0.074374	1	275	197	292	242	566	1452	2239	1566	4331	3402
ENSMUSG00000087591	chrX	Gm14635	12339782	12340861	1614	8.18005	0.087453	9.52E-22	7.57E-20	0.144789	1	0	0	0	0	0	34	75	19	47	35
ENSMUSG00000030144	chr6	Clec4d	1.23E+08	1.23E+08	1336	6.255955	2.590715	1.06E-21	8.41E-20	0.270329	1	1	2	4	4	1	95	85	92	546	600
ENSMUSG00000015745	chr3	Plekho1	95988429	95989633	2172	1.665975	5.209746	1.14E-21	9E-20	0.033011	1	220	279	346	270	371	951	1475	995	1765	1442
ENSMUSG00000102418	chr1	Sh2d1b1	1.7E+08	1.7E+08	2544	6.259774	-0.23018	1.28E-21	1E-19	0.091715	1	0	0	1	0	0	22	42	24	33	41
ENSMUSG00000028843	chr4	Sh3bgrl3	1.34E+08	1.34E+08	821	2.35851	4.983221	1.48E-21	1.15E-19	0.064426	1	140	154	189	171	206	931	1028	578	2176	1600
ENSMUSG00000015950	chr5	Ncf1	1.34E+08	1.34E+08	3663	2.750947	3.520138	1.72E-21	1.33E-19	0.080432	1	40	35	54	27	94	275	454	267	725	641
ENSMUSG00000000290	chr10	Itgb2	77530252	77530459	3052	3.512421	4.637577	1.97E-21	1.51E-19	0.129609	1	54	30	72	67	120	559	776	398	2007	1809
ENSMUSG00000042460	chr6	C1galt1	7844842	7845394	2452	-2.25478	2.815597	2.34E-21	1.79E-19	0.052833	-1	171	121	213	222	257	32	61	78	68	48
ENSMUSG00000070354	chr11	Gm21975	79513385	79516762	3944	2.303555	2.955663	2.37E-21	1.8E-19	0.054451	1	42	29	51	35	58	195	265	210	454	382
ENSMUSG00000087410	chr11	2310065F04Rik	67112461	67114117	2916	-2.69532	6.111883	2.49E-21	1.88E-19	0.084435	-1	2031	2105	2184	1936	1538	546	554	243	328	404
ENSMUSG00000060216	chr11	Arrb2	70432635	70432753	2845	2.006644	3.92509	2.79E-21	2.1E-19	0.045327	1	89	77	113	87	139	381	565	360	753	796
ENSMUSG00000020634	chr12	Ubxn2a	4879032	4880771	2820	-2.2618	6.197871	2.83E-21	2.12E-19	0.061667	-1	2010	1725	2418	2125	1784	360	572	998	587	449
ENSMUSG00000024696	chr19	Lpxn	12798606	12798679	1675	3.238895	2.276335	3.13E-21	2.33E-19	0.09676	1	16	11	22	11	14	125	176	95	327	288
ENSMUSG00000025019	chr19	Lcor	41482645	41482783	7620	-2.53941	2.221879	3.49E-21	2.59E-19	0.062754	-1	136	75	152	158	146	21	28	44	38	29
ENSMUSG00000001473	chr18	Tubb6	67390717	67390814	1757	2.594696	6.392058	4.21E-21	3.1E-19	0.0799	1	270	284	431	384	678	2504	5656	1647	4205	2941
ENSMUSG00000010307	chr7	Tmem86a	47050640	47050801	1791	1.81165	3.880426	4.24E-21	3.11E-19	0.036945	1	80	98	116	141	103	352	625	446	633	619
ENSMUSG00000042284	chr13	Itga1	1.15E+08	1.15E+08	5984	-1.94698	3.85608	4.68E-21	3.41E-19	0.043731	-1	292	288	476	523	348	110	137	102	205	150

ENSMUSG00000026288	chr1	Inpp5d	87620312	87620631	7602	2.320401	3.602693	4.77E-21	3.45E-19	0.059828	1	54	41	68	82	93	284	494	272	770	581
ENSMUSG00000024679	chr19	Ms4a6d	11586604	11587181	1735	2.525926	3.171197	4.95E-21	3.57E-19	0.06852	1	27	32	51	29	86	290	353	223	465	438
ENSMUSG00000094439	chr4	Gm21969	1.4E+08	1.4E+08	4402	-1.56244	5.955348	5.38E-21	3.86E-19	0.030856	-1	1368	1287	1635	1674	1790	485	722	853	953	698
ENSMUSG00000024726	chr19	2410127L17Rik	18670780	18671202	2090	-1.70359	5.896716	7.01E-21	5.01E-19	0.036659	-1	1242	1524	1592	1757	1430	604	557	674	778	634
ENSMUSG00000093938	chr11	Evi2b	79515056	79516762	1858	2.785247	2.37434	7.65E-21	5.43E-19	0.075691	1	21	16	17	19	33	138	191	117	316	281
ENSMUSG00000066647	chr7	Gm5113	30169875	30170214	3002	-2.37902	2.611355	9.92E-21	7E-19	0.060299	-1	144	136	241	161	180	23	62	47	72	31
ENSMUSG00000033713	chr12	Foxn3	99194980	99196813	4651	-2.58351	4.376137	1.32E-20	9.25E-19	0.078736	-1	592	384	606	676	732	75	99	274	134	114
ENSMUSG00000024803	chr19	Ankrd1	36111965	36112817	1765	2.807194	5.705202	1.42E-20	9.93E-19	0.094087	1	252	79	292	186	298	1638	3052	1864	3115	1087
ENSMUSG00000022372	chr15	Sla	66780819	66782755	9186	2.660814	2.329371	1.51E-20	1.05E-18	0.069247	1	29	14	16	27	23	159	240	127	258	199
ENSMUSG00000015355	chr1	Cd48	1.72E+08	1.72E+08	1189	2.945114	2.550228	1.78E-20	1.23E-18	0.089178	1	21	10	26	15	39	163	194	137	383	324
ENSMUSG00000001131	chrX	Timp1	20870166	20870324	888	3.619286	4.818527	1.8E-20	1.24E-18	0.144003	1	62	27	74	37	170	777	1619	460	1741	1596
ENSMUSG00000036908	chr19	Unc93b1	3935186	3935352	2841	2.157282	5.385991	2.19E-20	1.5E-18	0.058541	1	215	136	297	231	434	1250	1795	975	1883	2080
ENSMUSG00000032511	chr9	Scn5a	1.19E+08	1.19E+08	8764	3.536019	1.819867	2.32E-20	1.57E-18	0.114514	1	6	2	12	10	15	74	232	99	223	112
ENSMUSG00000038179	chr1	Slamf7	1.72E+08	1.72E+08	4577	3.995627	2.110039	2.31E-20	1.57E-18	0.14487	1	7	6	2	14	11	124	152	79	226	337
ENSMUSG00000031387	chrX	Renbp	73922121	73922263	2494	2.769264	2.986909	2.37E-20	1.6E-18	0.083408	1	29	21	30	30	58	196	260	184	458	516
ENSMUSG00000027499	chr3	Pkia	7366669	7366752	3721	-1.5731	8.726408	2.4E-20	1.61E-18	0.033023	-1	10253	9025	11828	10783	10806	4398	5420	5095	5304	4458
ENSMUSG00000031264	chrX	Btk	1.35E+08	1.35E+08	3149	3.340386	1.865763	2.46E-20	1.65E-18	0.102872	1	10	6	10	9	17	94	115	78	261	210
ENSMUSG00000021457	chr13	Syk	52583173	52583605	9362	2.087325	3.668502	2.48E-20	1.65E-18	0.050938	1	68	63	91	59	124	308	515	300	703	599
ENSMUSG00000003882	chr15	Il7r	9506161	9508358	3208	6.071826	1.898344	3.4E-20	2.25E-18	0.255321	1	1	2	0	3	2	48	74	66	331	339
ENSMUSG00000022488	chr15	Nckap1l	1.03E+08	1.03E+08	4717	2.6271	4.245221	4.96E-20	3.24E-18	0.082945	1	73	37	84	100	156	494	743	396	1263	991
ENSMUSG00000041736	chr15	Tspo	83563573	83563644	854	1.978125	5.571266	4.93E-20	3.24E-18	0.050694	1	234	330	347	310	384	1440	1506	1073	2207	2647
ENSMUSG00000046138	chr19	9930021J03Rik	29714402	29719606	8134	-1.47578	4.239509	4.99E-20	3.24E-18	0.027162	-1	396	381	548	436	574	211	217	241	274	216
ENSMUSG00000089672	chr10	Gp49a	51480632	51480753	2107	3.65791	2.92347	4.99E-20	3.24E-18	0.139273	1	13	9	25	20	25	123	192	174	621	574
ENSMUSG00000015090	chr2	Ptgds	25466709	25466831	1649	4.102989	0.859687	5.04E-20	3.26E-18	0.118955	1	0	1	4	3	7	53	117	48	94	54
ENSMUSG00000025531	chrX	Chm	1.13E+08	1.13E+08	6780	-1.84782	4.156741	5.66E-20	3.65E-18	0.042616	-1	493	357	501	456	516	117	193	254	218	130
ENSMUSG00000021384	chr13	Susd3	49230690	49231331	2837	3.347952	1.112455	5.74E-20	3.68E-18	0.089577	1	3	2	8	5	12	53	100	59	103	114
ENSMUSG00000069792	chr11	Wfdc17	83703991	83704173	533	2.664113	3.305371	5.86E-20	3.74E-18	0.081855	1	28	33	42	30	95	307	305	249	574	550
ENSMUSG00000049866	chr1	Arl4c	88673125	88674468	5492	2.097431	3.267132	7.16E-20	4.54E-18	0.050959	1	36	56	65	66	79	261	470	230	503	352
ENSMUSG00000050347	chr7	Gm9844	24862278	24862412	135	3.096549	1.543311	7.7E-20	4.87E-18	0.085389	1	7	8	9	8	16	98	169	72	144	91
ENSMUSG00000079547	chr17	H2-DMb1	34153072	34153453	1485	2.894112	2.819126	8.26E-20	5.2E-18	0.091409	1	29	23	22	27	34	240	453	127	379	223
ENSMUSG00000022500	chr16	Litaf	10959275	10961051	2642	2.125106	4.886653	1.02E-19	6.37E-18	0.058444	1	138	119	169	224	284	647	941	823	1798	1555
ENSMUSG00000026395	chr1	Ptprc	1.38E+08	1.38E+08	18313	2.309716	3.855843	1.08E-19	6.74E-18	0.06533	1	63	51	84	72	141	326	729	318	744	724
ENSMUSG00000026950	chr2	Neb	52136647	52137431	26369	-1.77935	12.05079	1.2E-19	7.48E-18	0.043474	-1	98281	76486	136253	113672	130026	31699	42614	64662	47381	37243
ENSMUSG00000018927	chr11	Ccl6	83587882	83588939	1795	3.212756	5.632086	1.44E-19	8.87E-18	0.125819	1	151	86	233	87	273	1189	1464	914	3851	3439
ENSMUSG00000002897	chr6	Il17ra	1.2E+08	1.2E+08	3970	1.985128	3.073966	1.62E-19	9.93E-18	0.045302	1	55	47	58	47	71	181	310	252	463	371
ENSMUSG00000020326	chr11	Ccng1	40748552	40751059	3512	-1.58538	9.472937	1.62E-19	9.93E-18	0.035118	-1	14266	15960	20686	17931	20599	7696	8684	6039	9644	9176
ENSMUSG00000024556	chr18	Me2	73770040	73770808	2455	2.009676	3.183335	2.04E-19	1.24E-17	0.047772	1	50	47	61	48	94	226	391	238	488	357
ENSMUSG00000032717	chr17	Mdfi	47815328	47816164	3092	2.779067	2.217994	2.3E-19	1.4E-17	0.082655	1	14	6	21	17	40	150	162	193	272	144
ENSMUSG00000020169	chr10	Best3	1.17E+08	1.17E+08	2719	-2.25717	3.410269	2.31E-19	1.4E-17	0.062624	-1	186	244	506	264	294	76	110	52	115	77
ENSMUSG00000007041	chr17	Clic1	35049966	35050486	1799	1.619264	5.559997	2.46E-19	1.47E-17	0.035816	1	332	325	426	345	517	1249	1737	1136	2315	1959
ENSMUSG00000060036	chr15	Rpl3	80077794	80077894	3119	1.66507	7.122932	2.45E-19	1.47E-17	0.038628	1	903	852	1198	977	1756	3168	5481	4260	6587	5661
ENSMUSG00000024885	chr19	Aldh3b1	3913493	3914084	1875	2.883673	2.962155	2.57E-19	1.53E-17	0.096433	1	12	16	44	29	57	205	386	166	453	388
ENSMUSG00000079471	chr17	Gm7325	45600967	45601685	976	4.11305	2.816953	2.77E-19	1.64E-17	0.174078	1	8	17	9	8	20	204	709	131	318	158
ENSMUSG00000024521	chr18	Pmaip1	66458604	66458812	2646	4.215616	1.196944	2.78E-19	1.64E-17	0.147309	1	0	2	5	4	7	58	166	42	109	99
ENSMUSG00000062785	chr7	Kcnc3	44590664	44591758	5344	-1.9347	3.131372	2.87E-19	1.69E-17	0.04514	-1	168	178	294	229	309	76	93	53	105	96
ENSMUSG00000024397	chr17	Aif1	35170991	35171193	1532	2.953426	2.722371	2.89E-19	1.7E-17	0.097894	1	25	20	22	17	39	267	341	104	285	315
ENSMUSG00000023043	chr15	Krt18	1.02E+08	1.02E+08	1400	4.21522	0.341567	2.95E-19	1.72E-17	0.101902	1	1	2	5	1	0	46	36	68	52	41
ENSMUSG00000021998	chr14	Lcp1	75131101	75131204	9504	2.646911	5.6646	2.97E-19	1.73E-17	0.091074	1	178	140	228	247	402	1264	1588	948	3682	3080
ENSMUSG00000001020	chr3	S100a4	90603770	90603806	587	2.833309	5.809213	3.02E-19	1.75E-17	0.102915	1	326	110	301	88	335	1635	2036	1766	3185	3001
ENSMUSG00000028402	chr4	Mpdz	81278500	81279769	12437	-1.5525	6.135139	3.53E-19	2.04E-17	0.033769	-1	1351	1544	2142	1849	1913	659	994	681	1127	746
ENSMUSG00000009214	chr2	Tmem8c	27061636	27062337	1511	3.339716	5.448903	3.56E-19	2.04E-17	0.136369	1	41	98	116	168	258	1344	3613	994	2007	1325
ENSMUSG00000071042	chr17	Rasgrp3	75435905	75436168	4921	-1.49755	5.526278	3.66E-19	2.09E-17	0.031131	-1	943	1171	1221	1231	1061	447	567	543	693	573
ENSMUSG00000059089	chr1	Fcgr4	1.71E+08	1.71E+08	1256	4.391162	1.976616	4.25E-19	2.42E-17	0.178579	1	2	8	6	6	6	190	169	34	207	225
ENSMUSG00000002111	chr2	Spi1	91082390	91082523	2695	2.865733	3.495692	4.66E-19	2.64E-17	0.099867	1	36	18	48	37	93	317	343	252	749	676
ENSMUSG00000028599	chr4	Tnfrsf1b	1.45E+08	1.45E+08	3818	2.136141	4.496434	5E-19	2.82E-17	0.060216	1	91	92	132	165	231	507	913	541	1294	1125
ENSMUSG00000042312	chr3	S100a13	90514435	90514465	715	1.628738	4.169424	5.02E-19	2.82E-17	0.034384	1	129	131	179	139	149	497	596	484	757	826
ENSMUSG00000035697	chr10	Hmha1	80016653	80016918	4478	2.422283	3.468694	5.42E-19	3.04E-17	0.072903	1	54	31	72	38	98	226	467	298	577	630
ENSMUSG00000033192	chr8	Lpcat2	92855350	92855625	3377	3.14423	1.729886	5.53E-19	3.09E-17	0.097989	1	8	5	14	10	17	111	196	70	124	154
ENSMUSG00000022139	chr14	Mbnl2	1.2E+08	1.2E+08	4552	-1.56483	7.066488	6.73E-19	3.74E-17	0.035181	-1	2592	2860	3844	3565	4000	1168	1534	2061	1791	1366
ENSMUSG00000091955	chr7	Gm9844	24862213	24862697	485	2.952003	1.605441	6.83E-19	3.78E-17	0.084683	1	7	11	11	8	18	100	174	75	150	96
ENSMUSG00000104217	chr1	RP24-426M1.3	4807892	4807982	825	-1.8883	4.795095	8.47E-19	4.67E-17	0.049317	-1	673	645	852	693	781	168	263	436	334	191
ENSMUSG00000001025	chr3	S100a6	90612894	90613226	719	1.952486	6.820029	8.74E-19	4.8E-17	0.053847	1	740	544	1078	489	1090	3380	5045	2849	4850	4857
ENSMUSG00000100838	chr9	Gm29094	89199379	89199779	664	2.478223	2.350172	1.12E-18	6.1E-17	0.069407	1	18	18	38	27	25	127	203	123	252	285
ENSMUSG00000042045	chr9	Sln	53850251	53850326	515	4.200359	4.378709	1.46E-18	7.98E-17	0.203126	1	14	27	61	24	59	427	425	2387	542	749
ENSMUSG00000015340	chrX	Cybb	9435252	9438343	5808	2.407292	4.318635	1.51E-18	8.2E-17	0.077104	1	135	44	85	106	157	581	1009	454	1049	840
ENSMUSG00000024298	chr17	Zfp871	32771236	32776008	5376	-2.97905	2.822318	1.68E-18	9.07E-17	0.108311	-1	206	121	228	210	300	13	37	71	52	17

ENSMUSG00000098855	chr11	Mir6923	67099804	67099875	72	8.370313	0.262589	1.97E-18	1.06E-16	0.22338	1	0	0	0	0	0	24	110	16	47	46
ENSMUSG00000002603	chr7	Tgfb1	25687002	25688223	2558	1.990541	4.089517	2.02E-18	1.08E-16	0.053519	1	73	80	124	139	161	398	647	403	1085	712
ENSMUSG00000063193	chr11	Cd300lb	1.15E+08	1.15E+08	2917	3.1571	2.224131	2.03E-18	1.08E-16	0.111991	1	11	11	13	8	34	89	189	119	308	271
ENSMUSG00000027784	chr3	Ppm1l	69316861	69317965	10496	-1.47634	7.050608	2.05E-18	1.09E-16	0.03233	-1	2997	2768	3672	3492	3307	1519	1625	1520	1891	1569
ENSMUSG00000061132	chr19	Blnk	40928927	40929292	5991	2.632072	2.54781	2.04E-18	1.09E-16	0.081866	1	18	18	37	36	23	150	237	120	375	288
ENSMUSG00000036198	chrX	Arhgap36	49463945	49464130	3421	5.050333	2.254643	2.1E-18	1.11E-16	0.24386	1	1	2	3	3	14	115	92	516	195	118
ENSMUSG00000001750	chr19	Tcirg1	3896050	3896192	4470	2.328401	4.519919	2.16E-18	1.14E-16	0.073545	1	125	97	118	105	191	497	811	471	1359	1434
ENSMUSG00000026100	chr1	Mstn	53061640	53062141	2705	-2.20658	5.080916	2.44E-18	1.28E-16	0.068521	-1	915	696	901	873	1292	181	202	510	235	272
ENSMUSG00000013707	chr3	Tnfaip8l2	95139521	95140596	1122	2.461626	2.175255	2.98E-18	1.56E-16	0.068542	1	19	10	25	26	33	121	216	112	229	192
ENSMUSG00000062593	chr10	Lilrb4	51480640	51480753	1491	3.72881	3.418626	3.07E-18	1.6E-16	0.164905	1	13	17	27	32	36	177	251	180	902	897
ENSMUSG00000041515	chr8	Irf8	1.21E+08	1.21E+08	7055	2.039652	3.456372	3.24E-18	1.68E-16	0.054574	1	70	44	91	67	84	287	485	237	498	545
ENSMUSG00000040699	chr11	Limd2	1.06E+08	1.06E+08	3707	1.928149	3.072658	3.38E-18	1.75E-16	0.046615	1	40	58	56	55	79	229	315	210	434	358
ENSMUSG00000052414	chr15	Gm28047	1.03E+08	1.03E+08	1611	-2.21039	2.792113	3.53E-18	1.81E-16	0.061692	-1	192	104	239	193	233	40	51	81	49	64
ENSMUSG00000022788	chr16	Fgd4	16416917	16422820	17517	-1.50416	4.037127	3.68E-18	1.89E-16	0.031025	-1	360	297	552	397	435	159	194	172	283	199
ENSMUSG00000023367	chr6	Tmem176a	48841483	48841589	1119	1.961837	3.886632	3.74E-18	1.91E-16	0.052369	1	67	83	114	94	150	474	769	321	639	511
ENSMUSG00000028337	chr4	Coro2a	46536937	46539267	6459	3.22248	1.412655	4.33E-18	2.21E-16	0.101363	1	7	5	11	8	9	73	104	50	141	164
ENSMUSG00000038127	chr16	Ccdc50	27388869	27389137	8639	-1.41787	6.672384	5.11E-18	2.59E-16	0.030511	-1	2199	2050	3155	2246	2815	1050	1459	1193	1504	1282
ENSMUSG00000073412	chr17	Lst1	35185095	35185310	415	3.47857	2.021141	5.41E-18	2.73E-16	0.132325	1	12	6	13	10	12	146	162	50	205	269
ENSMUSG00000003363	chr7	Pld3	27532000	27532485	2924	1.874182	5.612856	5.81E-18	2.93E-16	0.051723	1	269	257	361	375	514	1085	1586	1193	2890	2470
ENSMUSG00000024300	chr17	Myo1f	33555719	33555856	4914	3.236123	3.987444	6.2E-18	3.11E-16	0.135425	1	49	13	41	62	93	344	550	320	1122	1101
ENSMUSG00000026126	chr1	Ptpn18	34459762	34461056	6492	2.221308	2.314989	6.67E-18	3.33E-16	0.05755	1	18	30	37	26	31	157	163	129	267	216
ENSMUSG00000031441	chr8	Atp11a	12757014	12757352	11150	-1.34612	5.562644	6.7E-18	3.33E-16	0.027215	-1	942	859	1270	1236	1412	446	677	619	765	632
ENSMUSG00000059456	chr14	Ptk2b	66153257	66154269	7398	2.726441	2.571911	6.7E-18	3.33E-16	0.091013	1	21	19	20	28	39	137	199	126	354	385
ENSMUSG00000026956	chr2	Uap1l1	25359889	25361739	4071	2.420274	3.731739	6.75E-18	3.34E-16	0.079369	1	66	40	81	49	116	284	354	376	883	775
ENSMUSG00000029223	chr5	Uchl1	66676098	66676322	1616	2.235425	2.764903	6.95E-18	3.43E-16	0.062483	1	32	39	36	40	46	186	235	397	230	219
ENSMUSG00000018415	chr11	Gid4	60417145	60417844	4864	-1.49805	6.255853	7.62E-18	3.74E-16	0.034155	-1	1897	1451	2275	1892	1890	850	990	842	1038	910
ENSMUSG00000019942	chr10	Cdk1	69336635	69338596	3445	2.253168	3.181214	7.81E-18	3.81E-16	0.066811	1	35	53	48	42	82	270	313	193	578	399
ENSMUSG00000025268	chrX	Maged2	1.51E+08	1.51E+08	3239	2.083804	6.748627	7.79E-18	3.81E-16	0.064382	1	478	549	753	561	1175	2791	4348	6294	4087	2746
ENSMUSG00000028780	chr5	Sema3c	17574281	17574965	7140	-1.81596	6.062505	8.2E-18	3.98E-16	0.049538	-1	1721	972	1905	1437	2862	548	859	668	762	611
ENSMUSG00000029994	chr6	Anxa4	86736840	86737823	4545	1.577552	5.000034	8.73E-18	4.23E-16	0.036817	1	230	222	319	230	346	631	954	1139	1605	1380
ENSMUSG00000004933	chr10	Matk	81252935	81253278	4594	3.300263	0.8107	9.39E-18	4.53E-16	0.090248	1	5	3	7	4	5	38	63	45	108	91
ENSMUSG00000030249	chr6	Abcc9	1.43E+08	1.43E+08	7538	-1.51487	7.921235	9.42E-18	4.53E-16	0.035563	-1	5420	4513	7168	5876	7267	2425	3097	3531	3186	2360
ENSMUSG00000034330	chr8	Plcg2	1.17E+08	1.17E+08	4296	2.645914	2.249825	9.61E-18	4.6E-16	0.08293	1	14	21	19	25	26	105	180	105	282	275
ENSMUSG00000005413	chr8	Hmox1	75093591	75093772	2161	2.358323	4.837911	9.66E-18	4.61E-16	0.079843	1	126	131	186	133	207	572	598	865	1860	1870
ENSMUSG00000037111	chr3	Setd7	51515319	51521487	10813	-1.62168	8.490054	9.78E-18	4.65E-16	0.040637	-1	8593	6955	11073	8150	10855	3197	4395	5497	3918	3439
ENSMUSG00000057230	chr6	Aak1	86849517	86850215	8272	-2.17602	2.490746	9.8E-18	4.65E-16	0.059627	-1	159	91	175	155	193	32	62	59	41	42
ENSMUSG00000031637	chr8	Lrp2bp	45999303	45999505	4338	-2.17251	3.780391	1.04E-17	4.9E-16	0.065538	-1	282	352	400	336	525	161	120	74	96	107
ENSMUSG00000021728	chr13	Emb	1.17E+08	1.17E+08	2253	2.12023	3.184214	1.21E-17	5.68E-16	0.060219	1	52	26	71	41	96	221	323	300	440	435
ENSMUSG00000026458	chr1	Ppfia4	1.34E+08	1.34E+08	6572	2.208362	3.622766	1.22E-17	5.73E-16	0.067274	1	52	56	85	75	98	341	828	286	479	402
ENSMUSG00000009687	chr7	Fxyd5	31032722	31033018	4185	2.383061	4.837034	1.43E-17	6.67E-16	0.081536	1	142	120	160	145	200	624	863	534	1974	1793
ENSMUSG00000026012	chr1	Cd28	60716800	60717001	6122	-2.29386	3.689417	1.49E-17	6.96E-16	0.073472	-1	237	320	428	230	622	118	110	57	101	112
ENSMUSG00000030148	chr6	Clec4a2	1.23E+08	1.23E+08	2860	2.360371	2.266327	1.52E-17	7.04E-16	0.066864	1	30	14	29	17	37	126	207	126	262	201
ENSMUSG00000049988	chr8	Lrrc25	70616844	70617026	1273	2.773029	2.411219	1.55E-17	7.2E-16	0.095595	1	15	9	22	21	46	142	228	115	307	276
ENSMUSG00000026600	chr1	Soat1	1.56E+08	1.56E+08	9791	2.367447	4.119485	1.74E-17	8.02E-16	0.079392	1	77	64	101	81	153	372	549	359	1199	1020
ENSMUSG00000022439	chr15	Parvg	84324026	84324127	3090	3.85783	1.704577	1.84E-17	8.46E-16	0.156716	1	9	4	10	8	1	71	96	71	219	235
ENSMUSG00000030798	chr7	Cd37	45233632	45233978	3538	3.088616	2.747905	1.84E-17	8.46E-16	0.120957	1	22	8	22	17	49	163	222	149	413	454
ENSMUSG00000031540	chr8	Kat6a	22859535	22859632	9180	-1.41922	5.160973	2.07E-17	9.44E-16	0.030867	-1	811	617	872	923	1160	332	485	510	526	428
ENSMUSG00000015501	chr10	Hivep2	13966075	13966220	13720	-1.37168	5.758006	2.09E-17	9.54E-16	0.029289	-1	1183	1000	1467	1273	1644	531	807	749	774	663
ENSMUSG00000030786	chr7	Itgam	1.28E+08	1.28E+08	6377	3.003843	4.643008	2.21E-17	1.01E-15	0.125089	1	70	44	85	93	184	486	912	425	1887	1684
ENSMUSG00000039976	chr11	Tbc1d16	1.19E+08	1.19E+08	7119	-1.60566	5.326622	2.3E-17	1.04E-15	0.03973	-1	757	927	1104	1043	1244	315	383	647	451	520
ENSMUSG00000054342	chr7	Kcnn4	24370263	24370595	2034	3.292802	1.881425	2.32E-17	1.04E-15	0.122613	1	11	8	8	16	10	76	105	85	312	198
ENSMUSG00000051627	chr13	Hist1h1e	23621755	23622502	748	-2.64697	1.849201	2.45E-17	1.1E-15	0.085554	-1	73	80	131	118	122	14	32	8	42	22
ENSMUSG00000035954	chr12	Dock4	40446053	40446394	8063	-1.44911	3.799074	2.89E-17	1.3E-15	0.029921	-1	286	283	379	305	463	125	191	142	237	185
ENSMUSG00000003812	chr8	Dnase2a	84908560	84908874	5389	1.76673	3.897076	2.93E-17	1.31E-15	0.044928	1	91	103	117	89	164	327	410	505	699	766
ENSMUSG00000040747	chr3	Cd53	1.07E+08	1.07E+08	1742	2.544773	3.899238	2.96E-17	1.32E-15	0.09139	1	78	46	71	59	109	273	509	307	1084	903
ENSMUSG00000051910	chr7	Sox6	1.15E+08	1.15E+08	8852	-1.44554	6.8417	3.26E-17	1.44E-15	0.033378	-1	2659	1974	3046	3065	3344	1265	1382	1509	1511	1465
ENSMUSG00000030844	chr7	Rgs10	1.28E+08	1.28E+08	1711	1.920397	3.221354	3.47E-17	1.54E-15	0.050727	1	56	40	73	60	96	275	394	208	461	369
ENSMUSG00000039496	chr2	Cdnf	3513030	3513096	3111	-1.44215	5.071587	3.56E-17	1.57E-15	0.032285	-1	842	682	927	815	809	333	422	489	507	363
ENSMUSG00000022708	chr16	Zbtb20	42875881	42875924	30730	-1.61815	6.762971	3.88E-17	1.7E-15	0.041718	-1	2790	1606	3040	2852	3542	832	1282	1561	1419	1179
ENSMUSG00000034342	chr9	Cbl	44149262	44151737	5083	-2.17126	2.117979	3.89E-17	1.7E-15	0.059334	-1	118	64	143	118	156	22	39	41	47	36
ENSMUSG00000064367	chrMT	mt-Nd5	11742	13565	1824	-1.801	12.09589	4.2E-17	1.83E-15	0.051734	-1	74435	92166	156461	155741	92813	30140	44752	56497	50290	47731
ENSMUSG00000021366	chr13	Hivep1	42052021	42052090	8753	-1.45511	4.492755	4.93E-17	2.15E-15	0.032499	-1	425	412	585	630	738	194	329	299	362	234
ENSMUSG00000019876	chr10	Pkib	57631981	57632207	11800	3.965125	0.389313	5.01E-17	2.17E-15	0.11293	1	3	1	3	2	2	25	41	34	78	80
ENSMUSG00000025326	chr7	Ube3a	59228752	59229271	5097	-1.67039	5.193142	5.26E-17	2.28E-15	0.043848	-1	864	686	1099	924	1107	259	401	622	421	345
ENSMUSG00000001281	chr15	Itgb7	1.02E+08	1.02E+08	2743	3.642557	2.236312	5.3E-17	2.29E-15	0.159311	1	6	12	9	10	19	99	132	75	312	393
ENSMUSG00000091712	chr16	Sec14l5	5147109	5147129	2337	-2.17214	3.643141	5.66E-17	2.44E-15	0.068954	-1	270	231	455	344	439	77	158	43	123	132

ENSMUSG00000016256	chr2	Ctsz	1.74E+08	1.74E+08	1441	2.186831	6.461772	6.08E-17	2.6E-15	0.0744	1	394	350	633	478	870	2321	2854	1708	5283	5103
ENSMUSG00000021624	chr13	Cd180	1.03E+08	1.03E+08	4509	3.522916	2.529709	6.08E-17	2.6E-15	0.153788	1	19	9	7	14	25	133	126	122	442	423
ENSMUSG00000027022	chr2	Xirp2	67446002	67446154	11979	-1.40317	10.35565	6.36E-17	2.71E-15	0.032505	-1	29183	24152	38034	32214	36076	15325	18153	14074	19658	16290
ENSMUSG00000022292	chr15	Rrm2b	37923952	37927397	6437	-1.65	3.877219	6.46E-17	2.74E-15	0.040537	-1	359	340	414	352	382	109	168	241	182	131
ENSMUSG00000025351	chr10	Cd63	1.29E+08	1.29E+08	1031	1.45973	7.277272	6.5E-17	2.75E-15	0.034776	1	1197	1159	1690	1112	1817	4594	5560	4249	6199	5886
ENSMUSG00000037649	chr17	H2-DMa	34135182	34135758	1641	2.660155	3.035872	6.61E-17	2.78E-15	0.096974	1	44	21	52	23	44	306	507	156	374	264
ENSMUSG00000070691	chr4	Runx3	1.35E+08	1.35E+08	5003	4.172278	0.444163	6.6E-17	2.78E-15	0.132959	1	2	1	1	3	3	33	59	20	81	77
ENSMUSG00000047986	chr8	Palm3	84021471	84021528	3612	3.585684	0.57355	6.91E-17	2.9E-15	0.110739	1	1	2	4	1	9	47	84	34	70	52
ENSMUSG00000036887	chr4	C1qa	1.37E+08	1.37E+08	1040	2.060184	6.071499	7.33E-17	3.07E-15	0.066762	1	340	279	546	354	714	2431	2904	1241	3202	2819
ENSMUSG00000005087	chr2	Cd44	1.03E+08	1.03E+08	6776	2.088939	5.424792	8.46E-17	3.53E-15	0.068311	1	224	193	310	225	439	921	1689	854	2714	2202
ENSMUSG00000039981	chr10	Zc3h12d	7832470	7832562	4093	3.519068	0.201487	8.6E-17	3.58E-15	0.081793	1	1	1	4	4	3	35	49	27	55	49
ENSMUSG00000063632	chr12	Sox11	27334264	27342574	8311	3.127039	1.715364	9.35E-17	3.87E-15	0.11388	1	4	10	6	19	14	87	182	73	208	115
ENSMUSG00000067212	chr17	H2-T23	36029773	36030694	2889	1.76702	4.882226	9.5E-17	3.93E-15	0.04916	1	202	167	245	228	278	917	861	748	1082	1655
ENSMUSG00000002992	chr7	Apoc2	19671579	19671848	932	4.967022	1.211298	1.19E-16	4.9E-15	0.23844	1	0	0	1	2	8	61	75	30	141	186
ENSMUSG00000031010	chrX	Usp9x	13071498	13071733	15051	-1.95381	6.360433	1.2E-16	4.93E-15	0.061532	-1	1911	1575	2807	2136	2607	374	889	1240	951	557
ENSMUSG00000031903	chr8	Pla2g15	1.06E+08	1.06E+08	2704	1.590463	4.062602	1.21E-16	4.94E-15	0.038261	1	134	105	131	112	214	397	643	463	759	680
ENSMUSG00000024883	chr19	Rin1	5050808	5050941	4176	2.707105	1.401863	1.22E-16	4.97E-15	0.080456	1	11	8	7	7	22	62	108	111	147	82
ENSMUSG00000048960	chr1	Prex2	10993465	10993909	16609	-1.93762	3.412288	1.22E-16	4.97E-15	0.055696	-1	246	207	319	363	275	46	104	151	123	99
ENSMUSG00000026418	chr1	Tnni1	1.36E+08	1.36E+08	3600	4.116313	6.842962	1.23E-16	4.99E-15	0.227431	1	40	340	57	329	261	3751	8482	4170	5251	3660
ENSMUSG00000038844	chr2	Kif16b	1.43E+08	1.43E+08	6635	-1.56315	5.518634	1.23E-16	4.99E-15	0.039765	-1	828	1080	1252	1294	1282	313	510	726	727	479
ENSMUSG00000058818	chr7	Pirb	3711409	3712830	4471	2.501031	3.455275	1.24E-16	4.99E-15	0.091015	1	38	28	60	44	111	278	352	253	596	706
ENSMUSG00000050199	chr2	Lgr4	1.1E+08	1.1E+08	5884	-1.327	4.92194	1.27E-16	5.09E-15	0.028176	-1	615	660	866	672	811	291	452	444	458	378
ENSMUSG00000024781	chr19	Lipa	34492318	34494213	2969	1.786106	5.142301	1.28E-16	5.14E-15	0.050974	1	218	210	307	267	330	789	1090	802	2093	1787
ENSMUSG00000074994	chr2	Qser1	1.05E+08	1.05E+08	8973	-1.46412	6.253422	1.34E-16	5.35E-15	0.035415	-1	1682	1487	2075	1958	2184	734	874	1252	976	883
ENSMUSG00000041624	chr9	Gucy1a2	3532354	3533099	5273	-3.08689	-0.00684	1.4E-16	5.57E-15	0.068954	-1	26	20	33	30	35	3	8	3	5	4
ENSMUSG00000036067	chr2	Slc2a6	27021363	27022069	3211	4.284594	1.274997	1.63E-16	6.48E-15	0.19132	1	1	1	2	8	6	46	179	37	152	98
ENSMUSG00000054717	chr8	Hmgb2	57511843	57512005	2692	1.470917	3.763339	1.73E-16	6.86E-15	0.032005	1	92	120	137	104	143	315	444	403	643	536
ENSMUSG00000042359	chr2	Osbpl6	76406508	76406689	10063	-1.59523	5.370753	1.9E-16	7.53E-15	0.041682	-1	954	848	1113	1049	1238	505	522	309	504	522
ENSMUSG00000021573	chr13	Tppp	74009407	74009509	5118	-1.51563	4.021741	2.04E-16	8.03E-15	0.035652	-1	275	420	412	422	482	141	206	146	275	227
ENSMUSG00000047466	chr18	8030462N17Rik	77633281	77635328	3418	-1.8056	3.984977	2.11E-16	8.3E-15	0.050774	-1	295	322	501	450	517	91	173	254	200	114
ENSMUSG00000043336	chr16	Filip1l	57353093	57353458	5335	-1.31916	5.173724	2.22E-16	8.7E-15	0.028579	-1	747	672	924	955	1025	369	574	424	588	467
ENSMUSG00000090118	chr8	Gm16163	1.25E+08	1.25E+08	1119	-1.75819	3.173527	2.4E-16	9.39E-15	0.045843	-1	191	189	280	274	229	48	105	123	116	95
ENSMUSG00000034653	chr18	Ythdc2	44828665	44828918	6299	-1.81741	2.950734	2.57E-16	9.98E-15	0.048075	-1	183	150	206	195	279	43	108	90	95	67
ENSMUSG00000042817	chr5	Flt3	1.47E+08	1.47E+08	7760	3.983665	-0.15698	2.57E-16	9.98E-15	0.083871	1	0	1	2	2	2	21	45	29	33	37
ENSMUSG00000047798	chr11	Cd300lf	1.15E+08	1.15E+08	5149	5.672134	1.74455	2.57E-16	9.98E-15	0.317384	1	0	0	4	2	4	62	46	49	217	374
ENSMUSG00000072294	chr14	Klf12	99874486	99875314	1856	-3.82033	1.176355	2.59E-16	1E-14	0.163265	-1	87	38	59	82	85	2	5	19	2	6
ENSMUSG00000090290	chr8	Gm17296	1.26E+08	1.26E+08	5060	-1.84318	2.557864	2.6E-16	1E-14	0.047025	-1	132	112	182	161	186	46	50	80	75	48
ENSMUSG00000034708	chr11	Grn	1.02E+08	1.02E+08	3474	2.113505	7.446076	2.7E-16	1.04E-14	0.073228	1	851	648	1042	1058	2046	4936	5084	4089	10408	9226
ENSMUSG00000002289	chr17	Angptl4	33773750	33775568	3286	3.416784	4.510933	2.75E-16	1.05E-14	0.167892	1	24	34	150	51	81	253	635	1093	1451	1615
ENSMUSG00000017716	chr11	Birc5	1.18E+08	1.18E+08	3402	2.824785	2.498027	2.82E-16	1.08E-14	0.108754	1	20	18	22	15	39	159	187	90	400	315
ENSMUSG00000071203	chr13	Naip5	1E+08	1E+08	5204	2.927368	0.789662	2.82E-16	1.08E-14	0.077943	1	4	7	4	6	9	48	57	46	90	86
ENSMUSG00000026728	chr2	Vim	13573927	13574060	4743	1.671981	8.565933	2.92E-16	1.11E-14	0.047384	1	2553	2456	3166	3017	4065	7793	14153	9022	22430	16251
ENSMUSG00000084349	chrX	Rpl3-ps1	13202571	13203780	1210	1.689508	3.301355	3.16E-16	1.2E-14	0.042031	1	71	45	97	66	111	226	390	299	476	368
ENSMUSG00000034947	chr11	Tmem106a	1.02E+08	1.02E+08	3138	2.520545	3.945287	3.26E-16	1.23E-14	0.096966	1	57	49	97	65	119	443	419	246	1008	989
ENSMUSG00000022534	chr16	Mefv	3707215	3708097	3281	6.373278	-0.11913	3.33E-16	1.26E-14	0.190513	1	0	0	1	0	0	9	59	17	47	49
ENSMUSG00000022584	chr15	Ly6c2	75108158	75110627	2740	5.875733	1.898165	3.49E-16	1.31E-14	0.33095	1	3	3	1	2	0	102	83	30	139	461
ENSMUSG00000019990	chr10	Pde7b	20398004	20400632	7232	-1.32283	4.793505	3.71E-16	1.39E-14	0.028794	-1	523	572	789	710	727	284	434	322	479	342
ENSMUSG00000020098	chr10	Pcbd1	61089343	61089416	809	3.014264	1.891364	3.72E-16	1.39E-14	0.116448	1	1	12	15	12	27	139	191	107	144	145
ENSMUSG00000006589	chr8	Aprt	1.23E+08	1.23E+08	866	1.574713	4.707787	3.88E-16	1.45E-14	0.040572	1	165	224	263	200	239	664	733	698	1303	1215
ENSMUSG00000020657	chr12	Dnajc27	4082574	4082873	4713	-1.40264	6.033588	4.14E-16	1.54E-14	0.033573	-1	1445	1300	1934	1755	1483	684	982	776	966	787
ENSMUSG00000058672	chr13	Tubb2a	34074301	34075528	1584	2.403845	5.504143	4.13E-16	1.54E-14	0.092946	1	230	150	243	220	378	1388	3009	662	2200	1687
ENSMUSG00000035373	chr11	Ccl7	82045712	82045859	801	5.201073	3.792559	4.33E-16	1.6E-14	0.324004	1	8	11	11	8	23	202	290	62	1274	1477
ENSMUSG00000035385	chr11	Ccl2	82035571	82035737	1138	5.40954	4.205802	4.61E-16	1.7E-14	0.348197	1	9	11	5	16	30	209	381	113	1760	2001
ENSMUSG00000030729	chr7	Pgm2l1	1E+08	1E+08	7036	-1.3912	4.243824	5.15E-16	1.89E-14	0.031342	-1	429	366	558	451	486	201	242	299	248	221
ENSMUSG00000071713	chr15	Csf2rb	78325990	78326098	4764	2.372562	3.039629	5.31E-16	1.95E-14	0.083889	1	28	31	39	35	91	160	278	248	471	466
ENSMUSG00000046223	chr7	Plaur	24462500	24462567	1396	3.752366	2.737543	5.4E-16	1.98E-14	0.187237	1	14	14	16	10	20	83	201	94	634	491
ENSMUSG00000018008	chr15	Cyth4	78597047	78597219	2791	2.496129	4.19149	5.98E-16	2.18E-14	0.097902	1	59	36	96	99	186	485	767	355	1054	1006
ENSMUSG00000003283	chr2	Hck	1.53E+08	1.53E+08	2092	3.463355	2.325091	6.17E-16	2.25E-14	0.159655	1	17	4	15	6	26	140	215	71	271	352
ENSMUSG00000032122	chr9	Slc37a2	37229149	37231656	5079	3.231819	4.020083	6.99E-16	2.54E-14	0.155385	1	44	22	60	45	95	268	444	271	1440	1169
ENSMUSG00000047180	chr1	Neurl3	36264597	36266553	3217	2.409649	2.8762	7.06E-16	2.56E-14	0.085465	1	24	31	38	58	39	250	390	138	273	346
ENSMUSG00000015947	chr3	Fcgr1	96282909	96284619	2589	3.291223	3.527038	7.49E-16	2.7E-14	0.158394	1	20	15	35	41	72	453	314	146	594	893
ENSMUSG00000052812	chr12	Atad2b	4917404	4917921	4688	-2.32497	2.978004	7.49E-16	2.7E-14	0.082184	-1	177	158	257	241	277	27	70	111	66	35
ENSMUSG00000055805	chr11	Fmnl1	1.03E+08	1.03E+08	4868	1.724342	3.729166	8.14E-16	2.93E-14	0.046839	1	100	85	96	115	109	303	524	301	760	523
ENSMUSG00000063506	chr14	Arhgap22	33214026	33214293	3876	2.6422	2.14288	8.89E-16	3.19E-14	0.096561	1	20	6	19	15	40	92	209	130	246	198
ENSMUSG00000050022	chr5	Amz1	1.41E+08	1.41E+08	6697	3.968349	1.227564	9.84E-16	3.52E-14	0.174174	1	1	6	3	6	5	38	95	37	194	133
ENSMUSG00000033991	chr13	Ttc37	76098734	76098829	5381	-1.45295	4.187265	1.07E-15	3.82E-14	0.035076	-1	364	342	545	416	590	162	249	298	235	192

ENSMUSG00000022969	chr16	Il10rb	91406164	91406391	3808	1.480224	4.219906	1.15E-15	4.08E-14	0.036265	1	141	119	178	174	210	426	583	500	860	861
ENSMUSG00000033182	chr6	Kbtbd12	88547340	88547915	7153	-1.5561	4.053344	1.17E-15	4.15E-14	0.039726	-1	359	322	535	420	442	165	198	268	194	148
ENSMUSG00000027797	chr3	Dclk1	55242526	55242751	12991	2.800303	5.191769	1.3E-15	4.59E-14	0.125738	1	124	77	173	113	307	906	3173	770	1531	1120
ENSMUSG00000053199	chr9	Arhgap20	51765337	51765611	12685	-1.61049	4.797431	1.32E-15	4.65E-14	0.044488	-1	534	485	719	848	967	272	266	435	294	314
ENSMUSG00000019122	chr11	Ccl9	83572919	83575495	3045	2.918725	5.060542	1.32E-15	4.66E-14	0.135173	1	111	67	164	84	246	762	954	527	2626	2289
ENSMUSG00000045382	chr1	Cxcr4	1.29E+08	1.29E+08	1808	1.64198	3.389091	1.54E-15	5.39E-14	0.041967	1	83	73	92	74	95	234	514	295	417	383
ENSMUSG00000058099	chr15	Nfam1	82997721	82999795	3222	2.449777	2.897017	1.54E-15	5.39E-14	0.091152	1	34	21	34	25	79	200	307	155	433	370
ENSMUSG00000013033	chr8	Lphn1	83900105	83900924	8587	-1.25704	5.351356	1.6E-15	5.6E-14	0.027705	-1	800	786	1095	1019	1133	459	622	579	584	553
ENSMUSG00000034786	chr17	Gpsm3	34589806	34590260	1343	2.265229	2.767024	1.82E-15	6.34E-14	0.077592	1	34	27	43	39	49	193	250	115	386	361
ENSMUSG00000056054	chr3	S100a8	90669071	90669102	392	5.549562	0.238767	1.82E-15	6.34E-14	0.208178	1	0	1	0	1	1	15	24	29	77	95
ENSMUSG00000027009	chr2	Itga4	79255426	79256064	13978	-1.67554	4.972044	1.87E-15	6.49E-14	0.048947	-1	721	495	985	754	1111	267	469	206	456	365
ENSMUSG00000054640	chr17	Slc8a1	81388691	81389067	2934	-1.99083	2.245021	1.9E-15	6.58E-14	0.057022	-1	122	74	149	132	160	27	54	53	53	36
ENSMUSG00000075420	chr11	Smim6	1.16E+08	1.16E+08	978	8.454368	0.34223	2.34E-15	8.09E-14	0.316996	1	0	0	0	0	0	17	147	20	50	26
ENSMUSG00000027782	chr3	Kpna4	69067149	69074187	8940	-1.28891	6.753116	2.43E-15	8.37E-14	0.030322	-1	2258	2294	3054	2531	2624	1132	1446	1641	1711	1397
ENSMUSG00000022651	chr16	Retnlg	48872608	48872700	608	5.624487	-0.16689	2.47E-15	8.47E-14	0.189267	1	1	0	0	0	1	49	20	39	15	40
ENSMUSG00000052336	chr9	Cx3cr1	1.2E+08	1.2E+08	3742	2.943477	2.752778	2.47E-15	8.47E-14	0.130005	1	19	9	16	31	55	224	426	128	355	230
ENSMUSG00000085438	chr2	1700020I14Rik	1.2E+08	1.2E+08	8306	-1.45173	9.522225	2.48E-15	8.48E-14	0.03867	-1	15755	17297	20620	19374	16108	9183	9229	8137	9701	9027
ENSMUSG00000030263	chr6	Lrmp	1.45E+08	1.45E+08	4070	2.474337	1.815088	2.58E-15	8.81E-14	0.084353	1	6	9	23	18	32	94	127	102	179	170
ENSMUSG00000030681	chr7	Mvp	1.27E+08	1.27E+08	2902	1.343813	5.271723	2.63E-15	8.95E-14	0.032028	1	252	319	418	389	459	926	1224	1086	1781	1523
ENSMUSG00000044951	chr13	Mylk4	32700827	32705215	6128	-2.59264	9.243615	2.67E-15	9.05E-14	0.114126	-1	22722	17689	19184	15742	8067	2571	3004	7207	4729	2756
ENSMUSG00000042700	chr12	Sipa1l1	82170016	82170076	7697	-1.45427	4.783623	2.68E-15	9.07E-14	0.037168	-1	503	540	810	661	907	271	387	234	395	436
ENSMUSG00000059326	chr19	Csf2ra	61224402	61225033	1849	3.106636	3.07089	2.72E-15	9.18E-14	0.145847	1	26	15	30	21	54	174	312	110	574	615
ENSMUSG00000025262	chrX	Fam120c	1.51E+08	1.51E+08	5823	-1.97476	3.245683	3.48E-15	1.17E-13	0.063993	-1	220	163	287	252	361	40	111	136	81	84
ENSMUSG00000036478	chr10	Btg1	96617001	96617472	5010	1.324424	4.973385	3.53E-15	1.19E-13	0.031045	1	253	250	323	294	380	609	1053	1088	1307	1251
ENSMUSG00000024737	chr19	Slc15a3	10839727	10839998	5491	3.65951	3.334742	3.6E-15	1.21E-13	0.196924	1	15	20	17	32	38	225	221	102	894	810
ENSMUSG00000036896	chr4	C1qc	1.37E+08	1.37E+08	1931	1.972397	6.110646	3.83E-15	1.28E-13	0.069388	1	403	237	489	394	901	2340	2856	1587	3117	2899
ENSMUSG00000073411	chr17	H2-D1	35262730	35263186	2579	1.837209	7.846527	4.35E-15	1.45E-13	0.061438	1	1439	1231	1752	1678	2424	5561	6579	5611	10380	14471
ENSMUSG00000033792	chrX	Atp7a	1.06E+08	1.06E+08	8734	-2.34869	2.713764	4.43E-15	1.47E-13	0.087952	-1	184	117	204	146	278	15	68	74	56	43
ENSMUSG00000046541	chr7	Zfp526	25221451	25221504	3354	-2.04733	1.951164	4.57E-15	1.52E-13	0.060396	-1	85	67	129	111	133	21	35	38	58	26
ENSMUSG00000010277	chr11	2610507B11Rik	78261752	78261917	8798	-1.24945	8.814501	4.68E-15	1.55E-13	0.029479	-1	8774	9259	11877	11300	11849	5532	6238	5784	7160	6260
ENSMUSG00000014496	chr14	Ankrd28	31700015	31702306	5229	-1.44839	5.658874	4.67E-15	1.55E-13	0.038401	-1	1100	1027	1394	1231	1442	392	574	911	768	552
ENSMUSG00000048779	chr7	P2ry6	1.01E+08	1.01E+08	1938	2.38642	2.941092	5.21E-15	1.72E-13	0.091007	1	28	26	31	31	92	230	342	164	420	334
ENSMUSG00000029925	chr6	Tbxas1	38875404	38875452	9094	2.890356	2.667072	5.41E-15	1.78E-13	0.12729	1	28	7	33	23	33	163	233	99	428	384
ENSMUSG00000023473	chr9	Celsr3	1.09E+08	1.09E+08	12048	4.127063	-0.03274	5.51E-15	1.81E-13	0.120589	1	1	1	2	1	2	21	65	21	41	36
ENSMUSG00000045776	chr14	Lrtm1	29018208	29018609	7318	-1.39114	6.369739	5.75E-15	1.88E-13	0.03604	-1	1733	1673	1771	2231	2622	973	1017	965	1098	1222
ENSMUSG00000103319	chrX	AC055766.1	68821093	68821490	1019	-2.90409	0.40975	5.92E-15	1.93E-13	0.088199	-1	45	26	57	29	34	6	9	6	6	8
ENSMUSG00000053040	chr9	Aph1c	66814994	66819461	5205	2.184128	1.897282	6.07E-15	1.98E-13	0.065403	1	13	24	25	21	24	71	128	141	172	182
ENSMUSG00000073982	chr7	Rhog	1.02E+08	1.02E+08	1356	1.517106	4.67427	6.38E-15	2.07E-13	0.041305	1	168	148	256	259	284	688	846	584	1275	1059
ENSMUSG00000074093	chr7	Svip	51997165	51999777	3059	-1.42668	4.364638	6.58E-15	2.13E-13	0.03618	-1	459	503	561	492	462	230	311	267	257	224
ENSMUSG00000020644	chr12	Id2	25093801	25094576	1270	1.734868	3.259645	6.73E-15	2.18E-13	0.049541	1	66	41	87	55	123	237	335	288	483	376
ENSMUSG00000024338	chr17	Psmb8	34197721	34197761	2736	2.259575	3.746428	6.86E-15	2.21E-13	0.086371	1	56	58	80	89	104	441	377	220	642	889
ENSMUSG00000006411	chr1	Pvrl4	1.71E+08	1.71E+08	3746	4.100163	0.223057	7.19E-15	2.31E-13	0.152376	1	2	0	2	2	3	59	44	17	41	57
ENSMUSG00000037855	chr10	Zfp365	67886103	67889091	5205	3.360862	2.415676	7.61E-15	2.44E-13	0.166458	1	12	9	17	10	30	138	493	91	258	129
ENSMUSG00000025656	chrX	Arhgef9	95048935	95052154	8714	-1.36757	3.423001	8.27E-15	2.65E-13	0.030702	-1	225	225	276	286	272	121	130	128	166	151
ENSMUSG00000097141	chr18	Gm10524	82692284	82694176	1893	-2.20634	2.882224	8.97E-15	2.87E-13	0.080498	-1	202	139	227	211	236	28	35	109	76	63
ENSMUSG00000078453	chr10	Abracl	18011263	18011816	807	1.949857	2.914889	9.97E-15	3.18E-13	0.061346	1	43	44	74	42	51	187	265	165	427	355
ENSMUSG00000030220	chr6	Arhgdib	1.37E+08	1.37E+08	1839	1.729919	4.750834	1.05E-14	3.35E-13	0.054568	1	149	179	227	234	255	676	844	534	1462	1391
ENSMUSG00000029862	chr6	Clcn1	42286685	42286946	5428	-1.27889	6.862701	1.06E-14	3.35E-13	0.031351	-1	2632	2182	2902	2796	3272	1327	1566	1777	1738	1485
ENSMUSG00000029470	chr5	P2rx4	1.23E+08	1.23E+08	3309	1.800062	3.868389	1.11E-14	3.53E-13	0.056706	1	116	50	110	98	174	415	534	371	643	671
ENSMUSG00000020766	chr11	Galk1	1.16E+08	1.16E+08	1406	1.832359	2.992951	1.14E-14	3.61E-13	0.054977	1	54	37	63	38	99	189	288	238	393	338
ENSMUSG00000031376	chrX	Atp2b3	73503086	73503334	4820	-1.35315	3.745345	1.16E-14	3.64E-13	0.031421	-1	298	257	385	325	343	153	156	171	251	152
ENSMUSG00000038886	chr7	Man2a2	80349098	80351851	6553	-1.29279	7.911086	1.15E-14	3.64E-13	0.032342	-1	5255	4290	6627	6050	6457	2707	3180	3715	3427	3167
ENSMUSG00000015533	chr13	Itga2	1.15E+08	1.15E+08	4214	-3.58011	1.22662	1.26E-14	3.97E-13	0.169619	-1	89	16	68	52	144	8	9	8	10	6
ENSMUSG00000060147	chr13	Serpinb6a	33917918	33918442	5409	1.652617	7.563871	1.34E-14	4.19E-13	0.052076	1	1104	1583	1891	1541	1489	5407	4875	9920	7452	5698
ENSMUSG00000020948	chr12	Klhl28	64942440	64943613	2854	-1.82113	2.706293	1.39E-14	4.34E-13	0.054165	-1	166	108	184	174	223	36	92	75	79	57
ENSMUSG00000059182	chr6	Skap2	51859166	51859570	1638	1.933268	3.626245	1.41E-14	4.4E-13	0.065035	1	50	75	127	77	100	283	401	272	671	683
ENSMUSG00000051439	chr18	Cd14	36725074	36726397	1572	2.666454	2.992129	1.44E-14	4.49E-13	0.116136	1	40	16	43	27	53	176	297	128	493	524
ENSMUSG00000023959	chr17	Clic5	44188572	44188961	5870	-1.4448	7.822604	1.45E-14	4.5E-13	0.040417	-1	4224	5300	6952	5607	5604	2280	2718	3743	3174	2243
ENSMUSG00000054428	chr4	Atpif1	1.33E+08	1.33E+08	1441	1.266049	4.874485	1.46E-14	4.53E-13	0.029584	1	235	274	333	268	323	819	1048	774	1154	1018
ENSMUSG00000002489	chr16	Tiam1	89787111	89789591	9911	-1.53492	3.5202	1.5E-14	4.63E-13	0.04091	-1	282	182	338	257	380	89	138	108	189	173
ENSMUSG00000043483	chr12	Gm6863	96922420	96923061	642	1.335129	3.626369	1.5E-14	4.63E-13	0.029942	1	87	121	127	105	139	316	413	397	462	455
ENSMUSG00000025764	chr3	Jade1	41555731	41555819	8492	-1.27392	4.476763	1.51E-14	4.64E-13	0.029737	-1	478	363	581	548	686	214	304	270	413	338
ENSMUSG00000060843	chr10	Ctnna3	63430098	63430179	7227	-1.59213	3.013304	1.55E-14	4.74E-13	0.041945	-1	150	167	228	221	253	91	89	72	134	82
ENSMUSG00000000594	chr11	Gm2a	55098115	55098244	4127	1.610903	4.630245	1.59E-14	4.88E-13	0.047963	1	176	130	204	226	293	575	899	549	1291	1113
ENSMUSG00000084796	chr11	Mir142hg	87755577	87755613	269	4.583461	-0.28059	1.6E-14	4.9E-13	0.132251	1	0	1	2	1	0	17	30	14	45	48
ENSMUSG00000020340	chr11	Cyfip2	46193850	46196467	7103	2.823913	2.425049	1.63E-14	4.96E-13	0.124501	1	11	24	30	22	20	157	243	67	404	223

ENSMUSG00000026656	chr1	Fcgr2b	1.71E+08	1.71E+08	5790	1.970376	4.176715	1.64E-14	5E-13	0.069873	1	89	63	143	90	250	561	881	479	717	685
ENSMUSG00000025241	chr9	Fyco1	1.24E+08	1.24E+08	8653	-1.55998	8.35037	1.79E-14	5.42E-13	0.047232	-1	6540	6458	8727	9629	9632	3218	3237	5686	3519	3395
ENSMUSG00000079104	chr12	Prps1l3	57230412	57230611	1720	-1.2849	3.844934	1.79E-14	5.43E-13	0.028869	-1	279	329	390	328	370	140	196	222	206	211
ENSMUSG00000029685	chr6	Asb15	24528144	24528269	4497	-1.78344	4.26603	1.84E-14	5.57E-13	0.058098	-1	592	362	496	646	341	140	205	259	236	176
ENSMUSG00000015027	chr8	Galns	1.23E+08	1.23E+08	2585	2.186154	2.777762	1.85E-14	5.58E-13	0.079127	1	29	22	42	44	69	156	224	162	458	324
ENSMUSG00000085457	chr13	1110046J04Rik	33935567	33938342	3487	3.335225	0.14658	1.99E-14	5.97E-13	0.095873	1	1	2	4	5	2	34	28	58	51	32
ENSMUSG00000049130	chr7	C5ar1	16246743	16249090	2570	2.573416	3.818396	1.99E-14	5.99E-13	0.114932	1	62	30	72	59	121	278	452	253	982	938
ENSMUSG00000049037	chr6	Clec4a1	1.23E+08	1.23E+08	1558	1.95755	2.654863	2.23E-14	6.68E-13	0.062237	1	42	25	48	30	68	165	266	153	296	272
ENSMUSG00000039542	chr9	Ncam1	49502136	49505563	7995	1.865964	4.75248	2.31E-14	6.92E-13	0.065013	1	200	110	212	164	293	610	1658	894	1055	735
ENSMUSG00000023004	chr15	Tuba1b	98931425	98932562	1875	1.986684	6.53958	2.35E-14	7.02E-13	0.074858	1	510	454	642	505	1093	2607	4014	1517	5303	4217
ENSMUSG00000029204	chr5	Rhoh	65863569	65863881	4960	2.705465	0.616748	2.41E-14	7.18E-13	0.074244	1	7	4	8	7	4	34	67	47	85	51
ENSMUSG00000031146	chrX	Plp2	7667941	7668506	1334	1.278912	5.120209	2.46E-14	7.3E-13	0.031081	1	246	334	381	332	402	847	1078	968	1567	1339
ENSMUSG00000042476	chr5	Abcb4	8893721	8893907	4074	-1.44098	6.272979	2.49E-14	7.38E-13	0.040499	-1	1565	1783	2134	2198	1691	999	928	937	1086	836
ENSMUSG00000010142	chr11	Tnfrsf13b	61126755	61126815	2836	2.325751	1.593699	2.78E-14	8.21E-13	0.075692	1	12	13	19	10	26	70	102	80	163	152
ENSMUSG00000041697	chr5	Cox6a1	1.15E+08	1.15E+08	702	1.739278	5.822077	2.93E-14	8.63E-13	0.058232	1	315	413	452	435	573	1363	1700	1173	3047	3093
ENSMUSG00000032009	chr9	Sesn3	14276301	14276629	2162	-1.83287	2.668687	2.98E-14	8.77E-13	0.055897	-1	141	108	173	158	262	60	76	72	64	48
ENSMUSG00000023349	chr6	Clec4n	1.23E+08	1.23E+08	1420	3.445658	2.466385	3.02E-14	8.86E-13	0.183613	1	10	14	21	5	26	107	209	65	391	416
ENSMUSG00000027107	chr2	Chrna1	73563215	73566307	4386	1.757017	6.249739	3.09E-14	9.07E-13	0.059759	1	535	438	585	516	856	2051	4608	2123	3002	1931
ENSMUSG00000103888	chr1	AC123072.1	33908272	33908452	23154	-1.85033	7.863044	3.15E-14	9.21E-13	0.066513	-1	6444	4035	6814	7175	5877	1339	2389	3955	2306	1876
ENSMUSG00000053158	chr7	Fes	80377758	80378074	2762	1.650005	3.368993	3.17E-14	9.25E-13	0.047483	1	72	55	96	80	113	239	390	235	494	476
ENSMUSG00000049382	chr15	Krt8	1.02E+08	1.02E+08	1805	4.115816	0.379127	3.43E-14	9.99E-13	0.175985	1	1	0	4	3	2	18	46	102	58	31
ENSMUSG00000050965	chr11	Prkca	1.08E+08	1.08E+08	8992	-1.26586	6.006155	3.65E-14	1.06E-12	0.031684	-1	1298	1204	1863	1479	1798	821	933	759	985	872
ENSMUSG00000046230	chr19	Vps13a	16616763	16616915	9656	-1.39601	3.896838	3.7E-14	1.07E-12	0.03576	-1	307	304	426	369	400	100	186	249	244	194
ENSMUSG00000032231	chr9	Anxa2	69453620	69453739	3731	1.680154	7.567818	3.86E-14	1.11E-12	0.055715	1	1293	1188	1603	1460	2070	4919	7288	3388	10299	8554
ENSMUSG00000055782	chr15	Abcd2	91145884	91149205	5527	-1.4725	5.907573	3.86E-14	1.11E-12	0.042755	-1	1160	1272	1562	1533	1901	541	704	491	957	1063
ENSMUSG00000052384	chr16	Nrros	32142785	32145005	4177	2.227197	3.901153	3.92E-14	1.13E-12	0.090031	1	68	59	102	75	140	377	478	227	1004	849
ENSMUSG00000071714	chr15	Csf2rb2	78282517	78285379	4612	2.154578	2.339169	3.99E-14	1.15E-12	0.07472	1	24	21	27	28	52	113	148	137	283	275
ENSMUSG00000018507	chr11	Trpv2	62574486	62574600	4485	2.250965	2.664804	4.05E-14	1.16E-12	0.084945	1	25	28	52	40	35	154	213	118	387	351
ENSMUSG00000046179	chr7	E2f8	48866429	48867229	5443	2.933282	1.559982	4.53E-14	1.3E-12	0.124962	1	5	11	12	8	18	70	204	63	169	79
ENSMUSG00000060487	chr10	Samd5	9627259	9629049	2495	-3.73269	-0.01125	4.52E-14	1.3E-12	0.141233	-1	20	38	33	42	14	4	1	5	3	2
ENSMUSG00000030047	chr6	Arhgap25	87458545	87460133	4250	2.493325	2.447662	4.56E-14	1.3E-12	0.102636	1	19	19	36	30	30	133	144	102	372	330
ENSMUSG00000021188	chr12	Trip11	1.02E+08	1.02E+08	10150	-1.17365	4.969776	4.61E-14	1.31E-12	0.026665	-1	588	592	879	747	845	352	477	476	498	441
ENSMUSG00000034685	chr11	Fam171a2	1.02E+08	1.02E+08	3119	2.34136	2.914001	4.65E-14	1.32E-12	0.09463	1	38	24	46	34	64	194	532	166	357	204
ENSMUSG00000031662	chr8	Snx20	88626828	88627827	1434	3.313321	1.404521	4.71E-14	1.34E-12	0.153804	1	8	3	3	6	18	80	86	45	160	162
ENSMUSG00000026875	chr2	Traf1	34941750	34944091	5051	2.334688	1.191807	4.82E-14	1.36E-12	0.069943	1	9	8	9	13	20	56	103	66	92	100
ENSMUSG00000067158	chr1	Col4a4	82448423	82453394	10612	-2.05528	2.545069	4.85E-14	1.37E-12	0.071652	-1	136	87	220	171	182	48	42	80	48	41
ENSMUSG00000014547	chr14	Wdfy2	62837690	62838057	2011	-2.23033	1.459133	4.89E-14	1.38E-12	0.074221	-1	66	43	104	70	99	10	21	31	30	21
ENSMUSG00000037685	chr5	Atp8a1	67618140	67622696	10962	-1.49005	5.979251	4.99E-14	1.4E-12	0.044132	-1	1393	1171	2219	1320	1748	782	921	671	814	617
ENSMUSG00000026832	chr2	Cytip	58129137	58134193	6744	3.494611	0.605624	5.26E-14	1.48E-12	0.136255	1	1	7	1	1	8	29	67	38	77	86
ENSMUSG00000010461	chr10	Eya4	23104168	23106288	4192	-1.68567	4.516003	5.33E-14	1.49E-12	0.054893	-1	550	426	761	454	759	143	303	384	244	198
ENSMUSG00000021094	chr12	Dhrs7	72650356	72650617	1301	1.396684	4.593626	5.37E-14	1.5E-12	0.037478	1	214	147	239	246	263	548	843	618	1046	1064
ENSMUSG00000022575	chr15	Gsdmd	75862339	75862481	1776	1.806295	3.00824	5.54E-14	1.55E-12	0.056898	1	50	39	68	56	84	212	274	178	373	411
ENSMUSG00000026117	chr1	Zap70	36761798	36761942	2992	3.827514	-0.13229	5.7E-14	1.59E-12	0.120984	1	1	0	0	3	4	24	54	20	43	27
ENSMUSG00000058728	chr11	Cd300c	1.15E+08	1.15E+08	1065	7.665744	-0.36408	5.8E-14	1.61E-12	0.243127	1	0	0	0	0	0	28	63	7	28	19
ENSMUSG00000021939	chr14	Ctsb	63122462	63122565	4739	1.564412	9.756774	6.14E-14	1.7E-12	0.049631	1	6128	5887	7792	7421	9626	21199	24247	19494	48364	41393
ENSMUSG00000034751	chr13	Mast4	1.03E+08	1.03E+08	32204	-1.45893	5.723929	6.14E-14	1.7E-12	0.042512	-1	757	1115	1600	1463	1652	656	687	501	791	626
ENSMUSG00000022089	chr14	Bin3	70100145	70100196	1712	1.370996	3.252174	6.43E-14	1.78E-12	0.032106	1	74	80	106	83	94	229	346	276	384	356
ENSMUSG00000085939	chr18	Cd63-ps	50134726	50135600	875	1.549991	3.276058	6.74E-14	1.86E-12	0.042221	1	89	64	76	67	109	301	380	270	349	345
ENSMUSG00000024087	chr17	Cyp1b1	79706953	79710681	5128	3.027894	2.148056	6.84E-14	1.88E-12	0.146758	1	15	6	17	11	30	57	111	295	292	163
ENSMUSG00000044827	chr5	Tlr1	64924811	64927298	2652	2.677451	1.59534	6.93E-14	1.9E-12	0.106572	1	9	5	14	20	17	79	142	57	138	166
ENSMUSG00000026796	chr2	Fam129b	32876114	32876404	4672	2.001557	5.224752	7.03E-14	1.93E-12	0.077926	1	191	182	261	275	353	687	983	888	2790	1964
ENSMUSG00000037234	chr8	Hook3	26021421	26032030	13132	-1.2533	6.8331	7.61E-14	2.08E-12	0.032245	-1	2449	1935	3170	2838	3118	1222	1560	1840	1742	1497
ENSMUSG00000017697	chr2	Ada	1.64E+08	1.64E+08	2002	2.281088	1.860029	7.8E-14	2.13E-12	0.080422	1	17	17	16	18	31	107	123	77	168	200
ENSMUSG00000039477	chr5	Tnrc18	1.43E+08	1.43E+08	6880	-1.76864	3.940846	8.06E-14	2.2E-12	0.059688	-1	293	254	453	355	689	71	177	222	208	153
ENSMUSG00000020154	chr10	Ptprb	1.16E+08	1.16E+08	11912	-1.40622	5.986014	8.27E-14	2.25E-12	0.040179	-1	1207	1247	1692	2129	1399	564	745	922	1017	844
ENSMUSG00000026251	chr1	Chrnd	87190607	87190742	3288	1.953243	3.458098	8.53E-14	2.31E-12	0.070209	1	60	55	88	71	102	273	718	298	482	257
ENSMUSG00000020623	chr11	Map2k6	1.1E+08	1.1E+08	3444	-1.82783	4.627944	8.79E-14	2.38E-12	0.065506	-1	621	597	762	555	669	291	252	109	354	250
ENSMUSG00000025041	chr19	Nt5c2	46886831	46889051	4475	1.528002	3.923364	9.03E-14	2.44E-12	0.043979	1	122	80	143	155	150	376	706	360	610	571
ENSMUSG00000047230	chrX	Cldn2	1.4E+08	1.4E+08	3325	4.171255	1.130104	9.84E-14	2.65E-12	0.232414	1	0	2	3	2	11	56	200	37	82	72
ENSMUSG00000028367	chr4	Txn1	57943373	57943967	1051	1.26803	6.379709	1.02E-13	2.76E-12	0.033096	1	702	815	958	748	831	2211	2542	2456	3235	3296
ENSMUSG00000035133	chr12	Arhgap5	52516077	52519967	5197	-2.06348	4.321711	1.03E-13	2.78E-12	0.082168	-1	497	428	628	561	585	73	199	346	168	125
ENSMUSG00000034218	chr9	Atm	53439149	53439929	10338	-1.71023	2.919253	1.08E-13	2.89E-12	0.052799	-1	196	132	216	191	235	36	96	98	114	78
ENSMUSG00000038205	chr3	Prkab2	97658193	97658369	5096	-1.6167	8.529273	1.15E-13	3.09E-12	0.053953	-1	9814	8102	11994	7186	9175	3807	4010	5900	3614	3490
ENSMUSG00000025903	chr1	Lypla1	4807788	4807982	7145	-1.44104	5.893973	1.16E-13	3.11E-12	0.042637	-1	1351	1309	1592	1499	1462	450	673	1055	990	628
ENSMUSG00000035885	chr19	Cox8a	7215158	7215484	545	1.485582	6.047648	1.18E-13	3.14E-12	0.045209	1	412	571	665	603	660	1550	2182	1515	3153	3164
ENSMUSG00000026827	chr2	Gpd2	57237635	57237988	6549	-1.29866	7.774806	1.21E-13	3.21E-12	0.035353	-1	4707	4238	5422	4972	6829	2860	2538	2675	3197	3333

ENSMUSG00000022449	chr15	Adamts20	94270163	94270389	8997	-1.71208	4.334278	1.25E-13	3.32E-12	0.058134	-1	400	374	674	387	813	154	326	158	322	159
ENSMUSG00000062380	chr8	Tubb3	1.23E+08	1.23E+08	1868	4.193838	0.860572	1.34E-13	3.55E-12	0.224845	1	0	2	3	3	6	35	136	19	128	58
ENSMUSG00000038506	chr8	Dcun1d2	13255963	13257976	3034	-1.37829	6.313467	1.34E-13	3.56E-12	0.039429	-1	1742	1762	2315	1852	1877	1045	1098	758	1219	983
ENSMUSG00000021242	chr12	Npc2	84754560	84757212	3261	1.619798	6.69046	1.44E-13	3.81E-12	0.054187	1	751	669	801	791	1264	2597	3142	2308	4804	5583
ENSMUSG00000061577	chr8	Gpr114	94923694	94923757	3147	3.335752	0.533232	1.45E-13	3.83E-12	0.129054	1	3	2	7	5	2	39	88	25	53	69
ENSMUSG00000018920	chr11	Cxcl16	70453983	70455444	3021	1.951987	3.243442	1.51E-13	3.96E-12	0.070703	1	49	34	91	71	81	270	538	198	407	321
ENSMUSG00000028518	chr4	Prkaa2	1.05E+08	1.05E+08	7969	-1.28441	7.805947	1.52E-13	3.99E-12	0.034899	-1	4487	4380	6115	5408	6267	2533	2727	3870	3135	2830
ENSMUSG00000021068	chr12	Nin	70011435	70014956	10345	-1.34963	5.172066	1.53E-13	4.02E-12	0.03732	-1	623	591	1010	1022	1162	323	546	375	596	560
ENSMUSG00000091089	chr14	A930018M24Rik	50895942	50896709	1422	-2.02247	4.949889	1.55E-13	4.05E-12	0.081818	-1	858	515	905	929	952	122	223	527	371	215
ENSMUSG00000021027	chr12	Ralgapa1	55602929	55604268	7874	-1.1247	5.360099	1.78E-13	4.65E-12	0.026091	-1	793	778	1079	974	1101	457	633	609	779	557
ENSMUSG00000028063	chr3	Lmna	88481148	88482100	4252	1.25864	7.157133	1.78E-13	4.65E-12	0.03359	1	1155	1097	1543	1293	2042	3273	5394	4174	6269	4698
ENSMUSG00000021948	chr14	Prkcd	30595356	30596025	4983	1.377113	4.033041	1.81E-13	4.72E-12	0.036502	1	151	125	155	153	166	314	610	465	680	715
ENSMUSG00000022831	chr16	Hcls1	36934983	36935074	2525	2.038172	3.903372	1.82E-13	4.72E-12	0.080162	1	76	100	105	83	120	423	456	226	856	871
ENSMUSG00000051236	chr10	Msrb3	1.21E+08	1.21E+08	4048	-1.21969	7.22919	1.84E-13	4.76E-12	0.031659	-1	3124	3036	4397	3350	3636	1793	2173	2201	2376	1937
ENSMUSG00000079465	chr1	Col4a3	82586921	82587431	9967	-2.53105	1.850757	1.85E-13	4.79E-12	0.107464	-1	128	54	108	108	113	11	20	47	22	24
ENSMUSG00000032601	chr9	Prkar2a	1.09E+08	1.09E+08	6378	-1.17873	7.350866	1.9E-13	4.89E-12	0.029671	-1	3106	3173	4075	4233	4402	1787	2269	2561	2877	2239
ENSMUSG00000060131	chr2	Atp8b4	1.26E+08	1.26E+08	6660	3.358311	1.17358	1.91E-13	4.92E-12	0.16259	1	4	3	9	4	11	32	67	47	174	144
ENSMUSG00000024677	chr19	Ms4a6b	11516512	11516545	4485	1.909294	2.946297	1.93E-13	4.96E-12	0.066825	1	41	27	81	42	82	266	320	205	266	316
ENSMUSG00000020256	chr10	Aldh1l2	83487450	83490634	7503	-1.93474	4.106174	1.94E-13	4.97E-12	0.073953	-1	550	268	569	271	646	101	234	199	197	111
ENSMUSG00000022419	chr15	Deptor	55112317	55112619	8874	-1.23574	7.116763	1.94E-13	4.97E-12	0.032518	-1	2546	3164	3884	2842	3912	1529	1820	2216	2146	1935
ENSMUSG00000005142	chr8	Man2b1	85083269	85083488	4325	1.322629	5.350502	1.97E-13	5.03E-12	0.036218	1	333	260	431	344	613	982	1399	1167	1676	1620
ENSMUSG00000027288	chr2	Zfp106	1.21E+08	1.21E+08	10429	-1.20434	9.531857	1.97E-13	5.04E-12	0.031232	-1	14677	14397	18397	20302	18468	8965	10840	10710	11831	9747
ENSMUSG00000030867	chr7	Plk1	1.22E+08	1.22E+08	2203	2.860824	2.026932	1.99E-13	5.08E-12	0.134451	1	14	17	9	6	33	117	134	78	267	222
ENSMUSG00000025899	chr9	Alkbh8	3335478	3335594	3581	-1.67143	2.95893	2.06E-13	5.23E-12	0.051565	-1	178	166	223	189	232	51	82	134	102	67
ENSMUSG00000025877	chr13	Hk3	55005985	55006315	3682	3.40546	3.137494	2.1E-13	5.35E-12	0.201328	1	20	9	29	17	54	236	162	117	697	695
ENSMUSG00000029299	chr5	Abcg3	1.05E+08	1.05E+08	3550	2.541871	1.606446	2.11E-13	5.35E-12	0.099418	1	16	10	15	11	18	73	183	58	164	106
ENSMUSG00000064267	chr5	Hvcn1	1.22E+08	1.22E+08	3563	2.230395	2.190509	2.23E-13	5.65E-12	0.085302	1	20	17	35	20	39	70	150	146	288	226
ENSMUSG00000021745	chr14	Ptprg	11553532	11554332	10917	-1.29905	4.565465	2.26E-13	5.71E-12	0.034385	-1	430	406	702	694	606	207	378	318	417	298
ENSMUSG00000040061	chr2	Plcb2	1.19E+08	1.19E+08	6597	3.233532	0.636786	2.27E-13	5.73E-12	0.129517	1	2	2	6	8	4	25	53	38	86	100
ENSMUSG00000039153	chr17	Runx2	44495987	44497243	8837	2.390109	1.245842	2.38E-13	6E-12	0.081511	1	13	8	12	8	18	42	109	68	123	102
ENSMUSG00000082536	chr2	Gm13456	40555752	40557116	1365	1.357586	3.778543	2.69E-13	6.76E-12	0.035486	1	107	91	125	139	182	280	497	399	650	503
ENSMUSG00000030554	chr7	Synm	67730161	67736906	7866	-1.22947	8.981193	2.86E-13	7.18E-12	0.032924	-1	9816	9333	14623	12310	13601	6785	7207	6023	7883	7019
ENSMUSG00000004626	chr8	Stxbp2	3630955	3631204	4159	2.611078	2.533304	2.87E-13	7.19E-12	0.121817	1	18	13	28	30	46	111	170	114	394	382
ENSMUSG00000026068	chr1	Il18rap	40515362	40515476	6752	4.22002	-0.3502	2.95E-13	7.38E-12	0.145303	1	0	1	1	0	3	11	31	25	24	52
ENSMUSG00000011884	chr5	Gltp	1.15E+08	1.15E+08	1757	1.333708	4.53362	2.99E-13	7.45E-12	0.036391	1	171	151	247	234	308	549	760	578	1080	942
ENSMUSG00000038582	chr5	Pptc7	1.22E+08	1.22E+08	4719	-1.3901	6.582525	3.04E-13	7.58E-12	0.041444	-1	1822	2271	2829	2711	1862	1058	1246	1351	1466	1041
ENSMUSG00000024736	chr19	Tmem132a	10857822	10859151	4069	1.918987	4.606696	3.07E-13	7.64E-12	0.075133	1	101	136	178	222	221	600	1434	427	1235	856
ENSMUSG00000002699	chr11	Lcp2	34046920	34047431	4459	2.171829	2.494942	3.1E-13	7.68E-12	0.084068	1	25	35	26	29	51	130	193	114	326	309
ENSMUSG00000030276	chr6	Ttll3	1.13E+08	1.13E+08	5059	1.371476	4.518143	3.12E-13	7.72E-12	0.038479	1	160	197	261	203	245	620	721	504	1120	916
ENSMUSG00000057181	chr11	5730455P16Rik	80360492	80364018	4842	-1.25641	5.844319	3.17E-13	7.84E-12	0.033688	-1	1228	1198	1586	1283	1460	669	830	936	829	664
ENSMUSG00000026979	chr2	Psd4	24367580	24367802	11786	3.153155	1.728294	3.26E-13	8.06E-12	0.158996	1	7	7	7	14	18	68	87	54	251	225
ENSMUSG00000032508	chr9	Myd88	1.19E+08	1.19E+08	2576	1.454665	3.827115	3.28E-13	8.07E-12	0.04147	1	107	112	119	111	182	419	390	345	675	588
ENSMUSG00000102098	chr12	2310016D03Rik	30410559	30411950	1547	-2.78417	1.217167	3.33E-13	8.18E-12	0.123801	-1	54	76	60	101	39	7	19	10	25	9
ENSMUSG00000020580	chr12	Rock2	16894978	16895330	8012	-1.24507	7.002264	3.38E-13	8.29E-12	0.03365	-1	2233	2786	3780	3061	3278	1643	1810	1577	1966	1810
ENSMUSG00000045273	chr13	Cenph	1.01E+08	1.01E+08	1784	4.104431	-0.43287	3.63E-13	8.9E-12	0.12059	1	1	2	0	0	2	27	16	16	37	36
ENSMUSG00000032393	chr9	Dpp8	65032458	65032623	4968	-1.30405	7.292295	3.84E-13	9.4E-12	0.037105	-1	3437	2947	4456	3766	4078	1531	2010	2845	2234	1928
ENSMUSG00000098701	chr10	Mir6914	1.28E+08	1.28E+08	69	-2.74872	1.000434	3.88E-13	9.47E-12	0.115353	-1	53	35	72	59	72	4	19	20	14	3
ENSMUSG00000030465	chr8	Psd3	67689082	67697187	15304	-1.37515	4.472875	4.28E-13	1.04E-11	0.039349	-1	408	460	644	500	693	257	374	185	345	277
ENSMUSG00000058056	chr8	Palld	61513246	61513524	8479	-1.73116	6.172633	4.4E-13	1.07E-11	0.064005	-1	1295	1302	2448	1833	2620	534	1280	488	1041	615
ENSMUSG00000035711	chr13	Dok3	55523235	55524111	1546	2.805319	1.5915	4.53E-13	1.1E-11	0.126447	1	15	6	16	8	14	44	112	75	165	203
ENSMUSG00000017418	chr2	Arl5b	15049395	15049685	10428	-1.20864	4.196959	4.59E-13	1.11E-11	0.029761	-1	406	330	464	448	489	200	289	296	274	229
ENSMUSG00000055489	chr7	Ano5	51511029	51511250	7785	-1.20966	7.987725	4.85E-13	1.17E-11	0.032433	-1	5758	5157	6874	5532	6157	3111	3887	3659	3912	3208
ENSMUSG00000026360	chr1	Rgs2	1.44E+08	1.44E+08	3627	1.7432	4.250239	4.86E-13	1.17E-11	0.062216	1	170	93	163	138	159	364	639	499	821	1140
ENSMUSG00000044583	chrX	Tlr7	1.67E+08	1.67E+08	4082	1.899282	2.52795	4.99E-13	1.2E-11	0.066255	1	33	17	54	30	70	135	223	205	244	236
ENSMUSG00000046432	chrX	Ngfrap1	1.36E+08	1.36E+08	973	1.905422	2.642228	5.1E-13	1.23E-11	0.067521	1	26	21	53	53	67	168	270	155	324	220
ENSMUSG00000050071	chrX	Bex1	1.36E+08	1.36E+08	1186	1.813206	4.713092	5.48E-13	1.32E-11	0.069023	1	148	134	259	214	224	797	1670	593	867	770
ENSMUSG00000030830	chr7	Itgal	1.27E+08	1.27E+08	6380	3.02614	1.927078	5.55E-13	1.33E-11	0.155993	1	11	6	14	7	30	96	214	49	212	198
ENSMUSG00000013076	chr9	Amotl1	14541966	14547898	9798	-1.15284	8.491705	5.57E-13	1.33E-11	0.029736	-1	7681	6199	9016	8085	10847	4329	5306	5038	6411	5024
ENSMUSG00000035929	chr17	H2-Q4	35379617	35379707	2596	1.582437	4.205581	5.59E-13	1.34E-11	0.051914	1	124	131	132	188	191	476	456	570	683	1025
ENSMUSG00000031444	chr8	F10	13037308	13037547	2731	6.655305	2.231557	5.7E-13	1.36E-11	0.538581	1	0	1	0	2	4	30	58	23	459	546
ENSMUSG00000026469	chr1	Xpr1	1.55E+08	1.55E+08	17880	-1.2788	6.203069	6.08E-13	1.45E-11	0.035979	-1	1803	1202	1615	1996	2095	805	959	1027	1137	1089
ENSMUSG00000038775	chr9	Vill	1.19E+08	1.19E+08	4409	2.978152	0.970811	6.1E-13	1.45E-11	0.129156	1	6	1	6	7	14	38	60	49	122	114
ENSMUSG00000025777	chr1	Gdap1	17145362	17145588	7731	-1.62862	2.683119	6.16E-13	1.46E-11	0.049585	-1	167	111	218	140	175	50	94	63	92	69
ENSMUSG00000092035	chr6	Peg10	4747306	4747578	6667	2.140983	3.567535	6.15E-13	1.46E-11	0.091506	1	50	47	78	47	153	402	592	253	373	574
ENSMUSG00000035934	chr9	Pknox2	36890982	36893057	6942	-1.11303	5.146257	6.78E-13	1.6E-11	0.026668	-1	703	669	845	801	1048	439	538	532	609	489
ENSMUSG00000022742	chr16	Cpox	58670208	58670950	3186	-1.13838	4.23081	6.84E-13	1.62E-11	0.026684	-1	359	386	513	443	452	224	300	247	314	281

ENSMUSG00000053398	chr3	Phgdh	98313170	98313457	2486	1.994564	3.417467	7.29E-13	1.72E-11	0.079673	1	71	33	72	63	121	246	330	242	607	590
ENSMUSG00000015396	chr13	Cd83	43785107	43785250	2143	1.931104	2.361121	7.3E-13	1.72E-11	0.067324	1	27	30	38	37	41	116	299	127	202	185
ENSMUSG00000028693	chr4	Nasp	1.17E+08	1.17E+08	7518	1.147024	4.425732	7.49E-13	1.76E-11	0.027371	1	175	197	264	188	297	525	659	676	866	731
ENSMUSG00000056602	chr5	Fry	1.5E+08	1.5E+08	10729	-1.15256	5.785315	7.71E-13	1.81E-11	0.029343	-1	1112	1003	1390	1345	1537	539	778	927	985	804
ENSMUSG00000016319	chrX	Slc25a5	36795651	36795841	1646	1.337065	6.587643	7.74E-13	1.81E-11	0.039751	1	587	890	946	945	1228	2372	3413	2365	4447	3693
ENSMUSG00000032322	chr9	Pstpip1	56089962	56090444	3830	2.464647	2.570784	7.84E-13	1.83E-11	0.113291	1	45	14	35	22	30	130	309	104	326	299
ENSMUSG00000023927	chr17	Satb1	51736187	51740413	19027	-1.22737	5.940602	8.07E-13	1.88E-11	0.0334	-1	1360	1085	1552	1451	1773	688	899	1024	950	718
ENSMUSG00000045165	chr7	AI467606	1.27E+08	1.27E+08	1918	1.923566	2.051724	8.13E-13	1.9E-11	0.064109	1	26	19	28	25	42	109	184	92	204	157
ENSMUSG00000046532	chrX	Ar	98149721	98151334	9096	-1.44248	4.779215	8.73E-13	2.03E-11	0.045001	-1	408	752	884	555	772	329	306	386	379	303
ENSMUSG00000059495	chr9	Arhgef12	42963842	42969192	10483	-1.19289	6.251111	8.78E-13	2.04E-11	0.031838	-1	1526	1328	1954	1951	2160	749	1092	1292	1302	1017
ENSMUSG00000029560	chr5	Snx8	1.4E+08	1.4E+08	2615	1.296264	4.126025	8.95E-13	2.08E-11	0.034892	1	153	156	183	152	191	394	488	478	836	730
ENSMUSG00000059422	chr9	Gm8116	78820638	78821838	1201	-1.51544	3.34041	9.13E-13	2.11E-11	0.046187	-1	192	258	262	324	199	88	128	138	145	115
ENSMUSG00000023505	chr6	Cdca3	1.25E+08	1.25E+08	2866	2.182996	2.316994	9.2E-13	2.13E-11	0.087765	1	25	21	24	18	60	139	174	113	307	208
ENSMUSG00000069515	chr10	Lyz1	1.17E+08	1.17E+08	1264	3.024849	3.838747	9.64E-13	2.22E-11	0.176929	1	54	32	63	44	67	372	982	81	823	746
ENSMUSG00000078496	chr4	Gm13152	1.47E+08	1.47E+08	1488	-3.15945	-0.33031	9.91E-13	2.28E-11	0.101529	-1	19	22	21	32	18	2	6	6	1	2
ENSMUSG00000044795	chr11	Cyb5d1	69391925	69392129	1605	-1.40425	3.063167	9.96E-13	2.29E-11	0.037998	-1	181	166	234	200	231	82	129	119	121	82
ENSMUSG00000001027	chr11	Scn4a	1.06E+08	1.06E+08	7041	-1.24623	8.311301	1.01E-12	2.33E-11	0.035399	-1	6969	5591	8653	7898	8353	3489	4364	5509	4519	4005
ENSMUSG00000035673	chr10	Sbno2	80057416	80057864	4227	1.43047	4.025284	1.04E-12	2.38E-11	0.042823	1	96	109	177	133	233	356	504	491	918	555
ENSMUSG00000031433	chrX	Rbm41	1.4E+08	1.4E+08	6638	-1.99054	1.736456	1.04E-12	2.38E-11	0.069595	-1	84	88	99	79	88	15	46	37	37	22
ENSMUSG00000029570	chr5	Lfng	1.41E+08	1.41E+08	2282	1.64894	3.27034	1.05E-12	2.39E-11	0.053963	1	70	51	77	107	78	218	336	232	498	433
ENSMUSG00000078945	chr13	Naip2	1E+08	1E+08	4846	2.244391	1.266012	1.06E-12	2.41E-11	0.077242	1	12	6	13	13	22	55	113	63	102	105
ENSMUSG00000046402	chr9	Rbp1	98422961	98425051	2652	1.799635	2.787221	1.07E-12	2.43E-11	0.062077	1	51	38	40	48	75	180	299	152	285	315
ENSMUSG00000040204	chr9	2810417H13Rik	65890237	65890474	4813	2.545649	2.121577	1.12E-12	2.54E-11	0.117704	1	14	22	21	10	36	141	148	68	298	195
ENSMUSG00000020097	chr10	Sgpl1	61098642	61101008	6143	1.586208	5.306248	1.2E-12	2.73E-11	0.055524	1	291	226	309	319	528	674	1267	1153	2234	1833
ENSMUSG00000073684	chr4	2610002J02Rik	1.55E+08	1.55E+08	1743	1.406878	3.0195	1.29E-12	2.93E-11	0.037639	1	59	60	77	72	99	210	248	226	345	330
ENSMUSG00000073490	chr1	AI607873	1.74E+08	1.74E+08	3481	1.594467	3.88321	1.37E-12	3.1E-11	0.053475	1	129	67	128	115	175	464	388	447	513	724
ENSMUSG00000050069	chr1	Grem2	1.75E+08	1.75E+08	3745	-2.14105	4.798857	1.38E-12	3.12E-11	0.098522	-1	413	813	902	584	1149	265	246	95	209	357
ENSMUSG00000025232	chr9	Hexa	59539667	59539976	1865	1.332399	6.401861	1.42E-12	3.2E-11	0.040357	1	707	563	945	762	1090	2282	3016	1860	3809	3265
ENSMUSG00000031165	chrX	Was	8081453	8081989	2381	2.109972	1.870166	1.44E-12	3.23E-11	0.077425	1	22	20	24	17	26	73	129	85	210	184
ENSMUSG00000028030	chr3	Tbck	1.33E+08	1.33E+08	4108	-1.73681	2.053618	1.49E-12	3.36E-11	0.054525	-1	82	86	126	132	105	30	52	53	53	35
ENSMUSG00000026771	chr2	Spopl	23506220	23511460	10280	-1.24432	3.763263	1.52E-12	3.41E-11	0.032013	-1	296	271	356	310	357	134	178	246	206	176
ENSMUSG00000004798	chr11	Ulk2	61775649	61777839	5977	-1.17017	6.795808	1.53E-12	3.42E-11	0.031512	-1	2225	1981	2867	2793	3065	1303	1532	1853	1712	1546
ENSMUSG00000075470	chr15	Alg10b	90224311	90224608	3727	-1.76034	3.826579	1.66E-12	3.7E-11	0.066291	-1	303	275	479	338	458	71	195	234	177	89
ENSMUSG00000035933	chr12	Cog5	31654869	31654983	2997	-1.48947	2.782254	1.7E-12	3.79E-11	0.042841	-1	137	109	219	185	206	68	87	90	102	73
ENSMUSG00000026321	chr1	Tnfrsf11a	1.06E+08	1.06E+08	5985	1.989976	2.042547	1.77E-12	3.95E-11	0.070762	1	33	15	29	21	35	108	129	104	232	179
ENSMUSG00000026915	chr2	Strbp	37483228	37483845	18487	-1.16919	4.018131	1.79E-12	3.99E-11	0.028958	-1	360	293	441	342	439	208	246	194	269	240
ENSMUSG00000047945	chr4	Marcksl1	1.3E+08	1.3E+08	1605	1.913842	3.180484	1.83E-12	4.06E-11	0.07504	1	39	49	54	70	106	284	299	166	528	389
ENSMUSG00000037490	chr10	Slc2a12	22645011	22645313	4237	-1.35017	3.336141	1.84E-12	4.08E-11	0.037016	-1	233	190	267	281	231	95	159	140	155	116
ENSMUSG00000031910	chr8	Has3	1.07E+08	1.07E+08	6380	-2.06966	1.916519	1.84E-12	4.08E-11	0.079406	-1	67	92	92	151	104	22	41	22	57	30
ENSMUSG00000032218	chr9	Ccnb2	70407689	70408029	1541	1.881926	2.079731	1.85E-12	4.08E-11	0.063369	1	24	24	33	25	40	137	151	91	229	145
ENSMUSG00000029333	chr5	Rasgef1b	99217426	99218798	3261	2.407301	1.856218	1.88E-12	4.14E-11	0.104697	1	10	11	20	23	29	81	113	73	230	202
ENSMUSG00000029763	chr6	Exoc4	33249085	33249238	12640	-1.15077	5.843712	1.9E-12	4.18E-11	0.030329	-1	1136	1111	1561	1343	1483	689	869	927	955	712
ENSMUSG00000042066	chr1	Tmcc2	1.32E+08	1.32E+08	5692	-1.13827	5.429252	1.9E-12	4.18E-11	0.029358	-1	812	792	1240	1047	1088	542	638	648	644	644
ENSMUSG00000020627	chr12	Klhl29	5077472	5081334	7041	-1.65217	2.100889	2.14E-12	4.7E-11	0.049188	-1	77	95	140	109	123	36	52	57	56	39
ENSMUSG00000031229	chrX	Atrx	1.06E+08	1.06E+08	15190	-1.2639	5.47285	2.15E-12	4.71E-11	0.036543	-1	914	746	1188	976	1494	361	682	747	741	558
ENSMUSG00000037742	chr9	Eef1a1	78478449	78478858	2493	1.323028	10.04616	2.25E-12	4.94E-11	0.04114	1	8266	6914	10183	10225	15906	20746	38584	32355	49381	39400
ENSMUSG00000072812	chr12	Ahnak2	1.13E+08	1.13E+08	14163	1.803916	3.590001	2.27E-12	4.97E-11	0.06891	1	109	46	76	69	146	237	457	589	517	388
ENSMUSG00000038508	chr8	Gdf15	70629393	70630174	1852	4.6479	-0.25794	2.31E-12	5.04E-11	0.206175	1	0	0	1	0	3	22	21	10	39	64
ENSMUSG00000046034	chr15	Otulin	27605919	27606461	1491	1.177026	4.238685	2.31E-12	5.04E-11	0.029926	1	131	191	212	200	230	482	583	695	681	589
ENSMUSG00000100679	chr1	Gm28778	53297111	53297188	785	-1.35903	3.425648	2.45E-12	5.33E-11	0.038473	-1	247	242	309	247	231	100	159	161	174	112
ENSMUSG00000024477	chr18	Pggt1b	46239949	46241701	2736	-1.61951	2.739728	2.46E-12	5.34E-11	0.052519	-1	134	115	235	176	190	48	100	89	89	58
ENSMUSG00000037573	chr11	Tob1	94211454	94211731	2288	-1.32181	6.93989	2.48E-12	5.38E-11	0.040866	-1	2153	2770	3078	3697	2911	1381	2010	1248	1939	1612
ENSMUSG00000019832	chr10	Rab32	10545011	10546451	2108	2.149885	2.355979	2.53E-12	5.47E-11	0.089422	1	21	20	28	33	53	131	176	93	296	269
ENSMUSG00000001247	chr7	Lsr	30957775	30957901	2167	2.679547	0.254408	2.61E-12	5.65E-11	0.076969	1	6	3	5	5	4	27	49	29	61	48
ENSMUSG00000034801	chr12	Sos2	69583762	69585632	8514	-1.2158	5.538841	2.61E-12	5.65E-11	0.034108	-1	958	907	1192	1134	1245	471	642	878	741	541
ENSMUSG00000064344	chrMT	mt-Tm	3845	3913	69	-1.86345	3.828125	2.63E-12	5.67E-11	0.075392	-1	254	302	477	594	225	113	157	92	209	152
ENSMUSG00000009207	chr2	Lnp	74520291	74522297	9154	-1.13219	4.910644	2.66E-12	5.74E-11	0.028991	-1	664	545	719	645	887	338	402	495	556	418
ENSMUSG00000018924	chr11	Alox15	70344152	70344722	2454	4.163308	-0.19954	2.68E-12	5.75E-11	0.174609	1	2	1	0	1	2	46	32	30	12	34
ENSMUSG00000037731	chr4	Themis2	1.33E+08	1.33E+08	3079	2.149427	2.947641	2.72E-12	5.82E-11	0.094631	1	37	34	46	42	77	311	307	107	327	367
ENSMUSG00000095028	chr3	Sirpb1b	15495751	15495956	2877	4.524251	-0.62958	2.72E-12	5.82E-11	0.134639	1	0	3	0	0	0	22	33	10	26	22
ENSMUSG00000030172	chr6	Erc1	1.2E+08	1.2E+08	11598	-1.11637	4.854284	3.04E-12	6.51E-11	0.02827	-1	523	514	752	719	831	308	476	366	542	458
ENSMUSG00000026131	chr1	Dst	33908225	33908452	38847	-1.55598	8.02757	3.13E-12	6.68E-11	0.056788	-1	6792	4445	7251	7652	6264	1999	3039	4877	3064	2503
ENSMUSG00000039478	chr8	Micu3	40307458	40308410	6153	-1.17154	3.915541	3.31E-12	7.06E-11	0.029711	-1	347	303	403	328	350	165	223	243	229	219
ENSMUSG00000060143	chr14	Gm10076	1.06E+08	1.06E+08	384	1.176808	4.041696	3.36E-12	7.16E-11	0.030055	1	119	150	205	149	224	418	548	438	656	597
ENSMUSG00000056290	chr19	Ms4a4b	11443553	11443660	5274	4.053548	-0.09435	3.41E-12	7.25E-11	0.166988	1	2	0	1	4	0	39	34	17	24	56
ENSMUSG00000006585	chr8	Cdt1	1.23E+08	1.23E+08	2189	2.273999	1.768592	3.42E-12	7.27E-11	0.092882	1	19	15	22	16	20	67	111	75	249	151

ENSMUSG00000056413	chr5	Adap1	1.39E+08	1.39E+08	3232	2.639069	2.239259	3.54E-12	7.5E-11	0.134584	1	22	7	26	17	35	100	132	98	257	351
ENSMUSG00000041707	chr14	1810011H11Rik	32785963	32786096	1473	3.668452	0.00933	3.56E-12	7.54E-11	0.150172	1	1	1	2	3	3	27	24	15	57	65
ENSMUSG00000022102	chr14	Dok2	70766036	70766112	2902	2.443252	3.06848	3.61E-12	7.64E-11	0.123279	1	49	21	45	36	64	182	262	125	557	553
ENSMUSG00000042404	chr3	Dennd4b	90265185	90265561	6031	-1.11034	6.616911	3.64E-12	7.68E-11	0.029367	-1	1998	1777	2354	2530	2566	1194	1477	1369	1751	1470
ENSMUSG00000076387	chr5	Mir671	24592114	24592211	98	1.903796	1.488748	4.6E-12	9.7E-11	0.058558	1	14	21	17	17	24	63	101	108	103	116
ENSMUSG00000026358	chr1	Rgs1	1.44E+08	1.44E+08	6947	4.859028	0.934649	4.62E-12	9.71E-11	0.331218	1	2	1	1	2	3	15	46	17	198	142
ENSMUSG00000025044	chr8	Msr1	39581700	39581865	3998	2.87456	3.117464	4.66E-12	9.78E-11	0.169508	1	30	10	36	33	67	173	219	139	698	603
ENSMUSG00000037313	chr5	Tacc3	33658128	33658727	3551	1.895395	2.77183	4.66E-12	9.78E-11	0.074493	1	32	37	56	37	79	169	207	146	417	321
ENSMUSG00000037151	chr10	Lrrc20	61475833	61475889	2619	-1.18772	7.396492	4.7E-12	9.84E-11	0.034119	-1	3494	3587	4755	3819	3826	2240	2465	2295	2572	2301
ENSMUSG00000022309	chr15	Angpt1	42424727	42427130	4256	-1.38163	3.596348	4.95E-12	1.03E-10	0.041711	-1	195	274	293	360	340	127	184	108	220	149
ENSMUSG00000028832	chr4	Stmn1	1.34E+08	1.34E+08	1922	1.637441	3.564893	4.95E-12	1.03E-10	0.058533	1	73	81	95	77	156	336	406	228	685	447
ENSMUSG00000037405	chr9	Icam1	21015960	21016101	2540	1.69757	2.908967	5E-12	1.04E-10	0.059908	1	26	59	60	80	66	170	258	228	394	290
ENSMUSG00000022667	chr16	Cd200r1	44765736	44766072	2034	2.588877	1.126844	5.15E-12	1.07E-10	0.111926	1	8	6	5	12	17	46	58	57	150	107
ENSMUSG00000025789	chr7	St8sia2	73939119	73943464	5384	3.537626	2.06799	5.16E-12	1.07E-10	0.230954	1	5	5	13	8	24	85	435	69	210	80
ENSMUSG00000025932	chr1	Eya1	14168954	14170996	7808	-1.29571	4.12588	5.49E-12	1.14E-10	0.03803	-1	307	400	529	380	462	228	175	274	262	225
ENSMUSG00000035561	chr4	Aldh1b1	45799022	45799169	2298	2.035713	1.256785	5.6E-12	1.16E-10	0.066165	1	8	14	13	21	17	59	82	68	124	93
ENSMUSG00000028278	chr4	Rragd	32983037	32983607	5173	-1.16735	7.879421	5.71E-12	1.18E-10	0.033331	-1	4795	4579	6688	5251	5991	3177	3379	3469	3412	3272
ENSMUSG00000062753	chr17	AI413582	27563575	27564016	1398	1.861702	1.7864	5.9E-12	1.22E-10	0.061596	1	18	23	26	20	32	79	124	89	153	166
ENSMUSG00000060791	chr7	Gmfg	28437447	28437574	2817	1.927636	2.123924	6.21E-12	1.28E-10	0.072059	1	24	22	39	27	35	117	153	84	213	219
ENSMUSG00000044550	chrX	Tceal3	1.37E+08	1.37E+08	3546	2.676924	1.81218	6.23E-12	1.28E-10	0.136544	1	11	7	15	9	36	98	237	72	158	114
ENSMUSG00000038859	chr5	Baiap2l1	1.44E+08	1.44E+08	3366	2.368905	1.610396	6.51E-12	1.34E-10	0.102877	1	10	15	17	18	18	56	208	81	141	90
ENSMUSG00000061232	chr17	H2-K1	33996017	33996476	2608	1.784575	7.207527	6.88E-12	1.41E-10	0.075916	1	953	771	1103	1172	1636	3607	4124	3113	6305	9921
ENSMUSG00000026928	chr2	Card9	26352176	26352411	2293	2.553715	1.12313	6.9E-12	1.42E-10	0.110476	1	8	4	9	15	13	53	58	48	134	119
ENSMUSG00000021775	chr14	Nr1d2	18204054	18206881	5001	-1.29481	6.67716	6.92E-12	1.42E-10	0.040859	-1	2497	2237	2718	2132	2441	1089	1261	1853	1409	1269
ENSMUSG00000030329	chr6	Pianp	1.25E+08	1.25E+08	2753	2.655759	0.597324	6.94E-12	1.42E-10	0.099961	1	7	3	2	5	14	41	74	38	71	52
ENSMUSG00000021470	chr13	Ercc6l2	63815240	63815517	7681	-1.07604	4.440934	7.36E-12	1.5E-10	0.026562	-1	441	432	539	452	597	281	345	319	355	320
ENSMUSG00000040133	chr2	Gpr176	1.18E+08	1.18E+08	3899	2.624572	0.646016	7.44E-12	1.52E-10	0.099211	1	3	10	6	8	5	28	60	40	86	76
ENSMUSG00000073664	chr1	Nbeal1	60180599	60180685	28441	-1.18136	4.633877	7.45E-12	1.52E-10	0.032758	-1	533	435	649	609	659	221	339	461	423	346
ENSMUSG00000035941	chr9	Ibtk	85687360	85688514	8628	-1.17116	6.749976	7.79E-12	1.58E-10	0.033733	-1	2112	1982	2989	2448	3027	1385	1753	1187	1941	1453
ENSMUSG00000025225	chr19	Nfkb2	46304737	46304820	3289	1.097546	4.213967	7.84E-12	1.59E-10	0.027125	1	168	177	215	181	242	424	583	516	828	622
ENSMUSG00000067288	chr17	Rps28	33819027	33819218	1464	1.129352	6.924147	7.97E-12	1.61E-10	0.03145	1	954	1175	1456	1176	1656	3403	3926	3611	4344	4057
ENSMUSG00000042129	chr6	Rassf4	1.17E+08	1.17E+08	6344	1.523146	3.920025	8.16E-12	1.65E-10	0.052885	1	115	70	133	105	242	319	548	609	590	557
ENSMUSG00000026271	chr1	Gpr35	92950865	92950981	4839	3.488756	1.079633	8.54E-12	1.72E-10	0.203938	1	1	6	3	8	8	27	71	34	162	142
ENSMUSG00000029919	chr6	Hpgds	65117293	65120088	3586	2.275587	2.174115	8.52E-12	1.72E-10	0.105192	1	26	6	24	19	53	139	171	128	258	155
ENSMUSG00000053318	chr1	Slamf8	1.73E+08	1.73E+08	3079	4.162017	0.671228	8.54E-12	1.72E-10	0.252917	1	1	2	3	5	1	41	48	10	101	122
ENSMUSG00000051985	chr1	Igfn1	1.36E+08	1.36E+08	8996	2.473583	4.353192	8.6E-12	1.73E-10	0.136609	1	151	53	92	53	169	399	494	1595	932	643
ENSMUSG00000071715	chr15	Ncf4	78244801	78245087	2021	2.81766	2.193257	9.08E-12	1.82E-10	0.159317	1	16	8	19	10	41	97	195	67	243	319
ENSMUSG00000067071	chr1	Hes6	91411483	91412802	1808	1.527646	4.185589	9.37E-12	1.88E-10	0.054347	1	112	172	173	151	165	436	1000	412	758	553
ENSMUSG00000028381	chr4	Ugcg	59189257	59189741	5212	1.167368	4.342291	9.91E-12	1.98E-10	0.031607	1	188	154	227	207	269	457	676	507	894	770
ENSMUSG00000029730	chr5	Mcm7	1.38E+08	1.38E+08	4426	1.172845	3.948264	9.92E-12	1.98E-10	0.031059	1	146	125	168	129	224	341	462	506	701	503
ENSMUSG00000045636	chr8	Mtus1	40990914	40993633	10078	-1.13857	7.035766	9.99E-12	2E-10	0.032335	-1	2439	3095	3083	3013	3375	1525	1749	2137	2267	1900
ENSMUSG00000046006	chr13	Gapt	1.1E+08	1.1E+08	2055	3.106023	-0.12679	1.01E-11	2.01E-10	0.099522	1	2	2	4	2	3	23	34	16	43	47
ENSMUSG00000039987	chr5	Phtf2	20758663	20761075	6929	-1.15893	7.130108	1.02E-11	2.03E-10	0.033521	-1	2889	2800	3573	3403	3469	1836	1935	2255	2038	1930
ENSMUSG00000044786	chr7	Zfp36	28376784	28378493	1792	1.441673	4.482807	1.06E-11	2.11E-10	0.049331	1	124	138	226	317	204	528	807	675	870	939
ENSMUSG00000026972	chr2	Arrdc1	24925352	24925676	2510	1.686247	2.567284	1.07E-11	2.12E-10	0.059051	1	35	27	63	58	48	111	188	231	260	257
ENSMUSG00000071547	chr14	Nt5dc2	31134853	31134923	1407	1.803275	3.063383	1.08E-11	2.15E-10	0.071353	1	42	49	60	67	91	180	324	158	526	351
ENSMUSG00000021140	chr12	Pcnx	81860030	81860524	12139	-1.13503	6.137141	1.1E-11	2.17E-10	0.03194	-1	1409	1338	1769	1810	1754	758	1049	1236	1178	933
ENSMUSG00000029304	chr5	Spp1	1.04E+08	1.04E+08	1648	6.906915	8.708802	1.1E-11	2.18E-10	0.720549	1	39	29	55	81	436	1958	2595	1410	57754	44330
ENSMUSG00000068220	chr15	Lgals1	78926725	78926804	800	1.252987	8.865667	1.11E-11	2.2E-10	0.039472	1	3304	4263	6218	4151	5329	12821	16884	10692	19099	17463
ENSMUSG00000030341	chr6	Tnfrsf1a	1.25E+08	1.25E+08	2591	1.130803	5.781982	1.15E-11	2.27E-10	0.031484	1	495	449	590	562	810	1194	1581	1812	2362	1978
ENSMUSG00000041058	chr4	Wwp1	19608303	19611813	6453	-1.26745	7.488742	1.18E-11	2.33E-10	0.040305	-1	3809	3682	4432	4821	4357	1886	2132	3410	2611	2234
ENSMUSG00000026355	chr1	Mcm6	1.28E+08	1.28E+08	4666	1.747036	3.861559	1.23E-11	2.41E-10	0.070702	1	79	91	127	80	187	388	524	244	804	678
ENSMUSG00000049658	chr13	Bdp1	1E+08	1E+08	11005	-1.18087	3.999231	1.27E-11	2.49E-10	0.032326	-1	303	297	439	384	441	171	262	277	256	175
ENSMUSG00000019987	chr10	Arg1	24915208	24915779	1476	4.358827	0.474715	1.28E-11	2.52E-10	0.26808	1	2	1	2	0	4	8	34	34	90	118
ENSMUSG00000057113	chr11	Npm1	33152287	33152852	2665	1.098818	7.083577	1.28E-11	2.52E-10	0.030442	1	1283	1271	1624	1344	1696	3198	3861	4935	5095	4577
ENSMUSG00000030796	chr7	Tead2	45215753	45215832	4668	1.594584	2.456831	1.36E-11	2.65E-10	0.051178	1	34	45	55	44	43	122	234	154	270	173
ENSMUSG00000100975	chr12	Gm28875	1.05E+08	1.05E+08	642	2.000146	1.341911	1.37E-11	2.67E-10	0.067856	1	16	15	10	14	24	62	69	92	124	103
ENSMUSG00000034595	chr17	Ppp1r18	35865593	35865694	4317	1.323219	4.16871	1.39E-11	2.71E-10	0.041337	1	142	129	180	171	239	403	587	399	896	756
ENSMUSG00000022307	chr15	Oxr1	41447482	41447589	5165	-1.12147	5.631265	1.44E-11	2.8E-10	0.031278	-1	986	1088	1269	1086	1221	484	745	902	873	670
ENSMUSG00000028630	chr10	Dyrk2	1.19E+08	1.19E+08	2137	-1.47294	4.545766	1.45E-11	2.81E-10	0.052575	-1	426	368	704	597	843	167	310	440	286	247
ENSMUSG00000102351	chr16	Cd47	49913193	49913570	1815	1.274362	4.053798	1.5E-11	2.92E-10	0.038029	1	162	125	156	151	212	473	540	377	650	678
ENSMUSG00000020300	chr11	Cpeb4	31872211	31873412	6369	-1.37288	5.786045	1.54E-11	2.98E-10	0.047022	-1	1212	958	1407	1475	1640	393	695	1080	841	628
ENSMUSG00000040118	chr5	Cacna2d1	15934691	15935108	7514	-1.34695	8.895142	1.56E-11	3.03E-10	0.046088	-1	10373	9229	12763	11542	13375	4637	6028	9520	6209	4838
ENSMUSG00000040322	chr3	Slc25a24	1.09E+08	1.09E+08	3431	1.543597	3.827374	1.66E-11	3.21E-10	0.055799	1	105	76	114	114	202	290	754	425	595	415
ENSMUSG00000097391	chr12	Mirg	1.1E+08	1.1E+08	7292	1.854395	2.561642	1.69E-11	3.27E-10	0.074216	1	34	32	37	22	88	164	243	206	227	210
ENSMUSG00000063646	chr5	Jakmip1	37028335	37028599	6233	7.609507	-0.40572	1.76E-11	3.4E-10	0.339042	1	0	0	0	0	0	22	70	3	28	18

ENSMUSG00000029752	chr6	Asns	7675169	7675524	2735	2.111643	2.766301	1.77E-11	3.4E-10	0.098527	1	33	27	34	31	89	139	263	148	364	378
ENSMUSG00000024978	chr19	Gpam	55069734	55071046	3832	-1.53503	6.581903	1.83E-11	3.53E-10	0.059297	-1	2783	1381	2576	2380	2794	555	1191	1493	1705	965
ENSMUSG00000030793	chr7	Pycard	1.28E+08	1.28E+08	1405	2.492951	2.535815	1.85E-11	3.55E-10	0.13265	1	39	20	21	20	40	146	182	80	393	349
ENSMUSG00000042734	chr12	Ttc9	81631369	81631801	2042	1.462024	4.019411	1.86E-11	3.56E-10	0.05076	1	63	139	190	148	189	424	712	481	691	461
ENSMUSG00000024659	chr19	Anxa1	20373428	20373770	2608	1.571559	5.89939	1.91E-11	3.65E-10	0.061683	1	456	388	539	405	749	1166	1898	1284	3567	2877
ENSMUSG00000042363	chr11	Lgalsl	20823576	20826515	4115	-1.22457	6.157128	1.92E-11	3.67E-10	0.038039	-1	1334	1572	1966	1927	1506	883	971	1121	986	975
ENSMUSG00000039523	chr4	Cep104	1.54E+08	1.54E+08	5279	-1.08907	5.177193	2.06E-11	3.93E-10	0.029591	-1	739	685	936	865	883	363	567	634	680	483
ENSMUSG00000040010	chr8	Slc7a5	1.22E+08	1.22E+08	3708	1.67439	3.345414	2.07E-11	3.94E-10	0.064699	1	75	47	80	60	146	245	440	231	539	361
ENSMUSG00000034636	chr4	Zyg11b	1.08E+08	1.08E+08	9046	-1.18268	6.385411	2.07E-11	3.95E-10	0.035757	-1	1955	1448	2097	2165	1994	883	1160	1449	1462	1045
ENSMUSG00000040212	chr7	Emp3	45918023	45918235	972	1.909876	4.644999	2.11E-11	4.01E-10	0.088699	1	158	105	150	135	350	643	819	450	1569	1234
ENSMUSG00000006360	chr12	Crip1	1.13E+08	1.13E+08	445	1.518095	5.964926	2.12E-11	4.03E-10	0.057977	1	549	417	593	453	692	1641	2349	1054	3226	2706
ENSMUSG00000036676	chr10	Tmtc3	1E+08	1E+08	8939	-1.42718	3.561375	2.14E-11	4.06E-10	0.047706	-1	257	235	333	300	311	87	189	197	187	95
ENSMUSG00000032436	chr9	Cmtm7	1.15E+08	1.15E+08	1136	1.383428	3.448755	2.22E-11	4.21E-10	0.043726	1	87	79	116	82	140	294	370	230	512	431
ENSMUSG00000043252	chr4	Tmem64	15265831	15266749	4670	-1.12434	6.99152	2.37E-11	4.48E-10	0.032727	-1	2395	2480	3459	3179	3096	1679	1961	1941	1996	1680
ENSMUSG00000022905	chr16	Kpna1	35978750	35978850	8486	-1.08741	7.372023	2.39E-11	4.52E-10	0.030748	-1	3234	3217	4648	3650	4132	2139	2446	2631	2748	2344
ENSMUSG00000018654	chr11	Ikzf1	11685003	11685174	5777	1.949081	1.971565	2.48E-11	4.68E-10	0.07766	1	22	16	25	26	42	110	133	81	177	202
ENSMUSG00000068663	chr16	Clec16a	10545339	10545642	8368	-1.19186	5.817858	2.49E-11	4.7E-10	0.036294	-1	971	1198	1574	1416	1419	739	837	569	1008	847
ENSMUSG00000034266	chr12	Batf	85686669	85686973	955	3.204304	0.086904	2.59E-11	4.88E-10	0.143211	1	0	0	4	2	9	24	31	25	59	57
ENSMUSG00000017754	chr2	Pltp	1.65E+08	1.65E+08	2562	1.314098	5.553562	2.6E-11	4.89E-10	0.043883	1	356	313	472	511	627	1336	2053	1036	1678	1664
ENSMUSG00000015575	chr17	Atp6v0e	26676396	26676578	3261	1.189007	4.742326	2.71E-11	5.08E-10	0.035034	1	256	244	326	225	304	633	775	692	1131	1139
ENSMUSG00000047810	chr19	Ccdc88b	6844623	6845119	4959	2.492687	1.695632	2.72E-11	5.1E-10	0.124477	1	10	8	16	25	19	81	130	52	143	210
ENSMUSG00000045205	chr4	Dpy19l4	11261315	11265942	8101	-1.19148	4.208636	2.77E-11	5.17E-10	0.034678	-1	407	361	492	423	457	175	271	353	304	217
ENSMUSG00000098265	chr11	Gm27517	3645286	3645521	236	-1.93441	1.506071	2.87E-11	5.36E-10	0.074177	-1	71	46	84	70	106	14	33	34	40	17
ENSMUSG00000031875	chr8	Cmtm3	1.04E+08	1.04E+08	1616	1.201582	4.361897	2.98E-11	5.56E-10	0.03537	1	211	153	211	177	288	500	718	505	931	712
ENSMUSG00000037946	chr13	Fgd3	49261554	49264035	6012	2.049924	2.281925	2.98E-11	5.56E-10	0.090422	1	18	26	38	29	44	127	257	76	231	204
ENSMUSG00000027907	chr3	S100a11	93520488	93520553	511	1.60327	5.829777	3E-11	5.59E-10	0.065367	1	354	392	466	530	627	1402	2066	902	3213	2638
ENSMUSG00000002043	chr7	Trappc6a	19508670	19508832	1317	1.545778	2.315785	3.08E-11	5.71E-10	0.049235	1	28	38	56	39	46	110	141	168	239	196
ENSMUSG00000073530	chr1	Pappa2	1.59E+08	1.59E+08	10294	-3.31367	2.054045	3.08E-11	5.71E-10	0.226061	-1	153	28	84	54	339	17	17	20	15	17
ENSMUSG00000038663	chr7	Fsd2	81533308	81535248	3985	-1.36002	8.003086	3.15E-11	5.84E-10	0.048319	-1	4835	5511	7263	6625	6706	3549	3333	1937	4243	3569
ENSMUSG00000034993	chr11	Vat1	1.01E+08	1.01E+08	2766	1.826376	5.808099	3.17E-11	5.87E-10	0.084061	1	379	286	360	438	612	1050	1221	1419	3852	3104
ENSMUSG00000055214	chr1	Pld5	1.76E+08	1.76E+08	10094	-2.32127	1.096581	3.22E-11	5.95E-10	0.102639	-1	45	65	49	66	67	12	31	6	17	16
ENSMUSG00000034021	chr5	Pds5b	1.51E+08	1.51E+08	9397	-1.08903	5.067194	3.24E-11	5.98E-10	0.030053	-1	731	522	847	717	1030	400	511	495	591	507
ENSMUSG00000052142	chr17	Rasal3	32390659	32391235	4897	3.443131	0.405069	3.3E-11	6.08E-10	0.185619	1	3	0	1	6	6	24	64	17	87	65
ENSMUSG00000045975	chr16	C2cd2	97855210	97859576	6555	-1.2325	7.462114	3.34E-11	6.14E-10	0.039916	-1	3602	3842	4760	4419	3914	2412	2073	2716	2376	2492
ENSMUSG00000027708	chr3	Dcun1d1	35892105	35895699	4563	-1.02235	5.574977	3.36E-11	6.17E-10	0.026865	-1	907	878	1307	1032	1243	625	784	697	829	722
ENSMUSG00000036792	chr2	Mbd5	48949510	48949549	14221	-1.19014	3.700904	3.4E-11	6.23E-10	0.033379	-1	271	214	306	345	380	144	170	225	202	180
ENSMUSG00000028883	chr5	Sema3a	13396784	13397082	6470	-2.00023	2.748127	3.52E-11	6.45E-10	0.091931	-1	202	94	214	98	307	69	63	58	71	46
ENSMUSG00000043740	chr17	B430306N03Rik	48316141	48316485	6937	4.487031	1.243708	3.55E-11	6.5E-10	0.335984	1	1	2	2	9	1	88	39	18	127	219
ENSMUSG00000078970	chr11	Wdr92	17182107	17182146	2497	-1.08994	5.366227	3.55E-11	6.5E-10	0.030569	-1	821	767	1135	865	1129	401	672	688	829	532
ENSMUSG00000004730	chr17	Emr1	57358686	57358756	3245	1.953048	4.716825	3.62E-11	6.6E-10	0.094991	1	184	64	201	141	337	672	1205	510	1453	1113
ENSMUSG00000025582	chr11	Nptx1	1.2E+08	1.2E+08	5217	2.93449	-0.11673	3.64E-11	6.64E-10	0.110186	1	1	0	4	2	8	16	39	42	39	27
ENSMUSG00000035606	chr9	Ky	1.03E+08	1.03E+08	5879	-1.89168	8.590768	3.67E-11	6.69E-10	0.091316	-1	8198	9432	11218	9613	12495	4546	4282	1246	4013	4566
ENSMUSG00000026207	chr1	Speg	75375297	75375833	12741	-1.05305	8.032619	3.73E-11	6.78E-10	0.029553	-1	4791	4340	6951	6507	7288	3182	4015	3941	4877	3928
ENSMUSG00000010721	chr5	Lmbr1	29229814	29233148	4940	-1.19959	4.01753	3.73E-11	6.78E-10	0.035308	-1	399	275	366	354	490	150	229	289	267	218
ENSMUSG00000054008	chr18	Ndst1	60685978	60689364	6070	-1.22716	5.929949	3.84E-11	6.97E-10	0.039329	-1	1208	1102	1405	1639	1830	515	894	1143	971	779
ENSMUSG00000020954	chr12	Strn3	51608541	51610272	4164	-1.13997	7.287707	3.87E-11	7.02E-10	0.034464	-1	3109	3030	4435	3452	4002	1735	2550	2682	2639	1800
ENSMUSG00000028530	chr4	Jak1	1.01E+08	1.01E+08	7227	-1.06658	7.433296	3.9E-11	7.07E-10	0.03027	-1	3337	3418	4846	3518	4520	2078	3000	2457	3051	2473
ENSMUSG00000057948	chr11	Unc13d	1.16E+08	1.16E+08	4679	2.722658	0.740768	3.93E-11	7.11E-10	0.120793	1	10	6	2	8	6	29	72	39	81	92
ENSMUSG00000029177	chr5	Cenpa	30666777	30667113	2503	1.668959	2.574748	4.02E-11	7.25E-10	0.061369	1	31	47	61	54	38	160	215	132	307	231
ENSMUSG00000031274	chrX	Col4a5	1.41E+08	1.41E+08	6718	-1.76481	4.429949	4.03E-11	7.26E-10	0.078392	-1	603	256	540	449	1002	140	231	346	260	175
ENSMUSG00000049775	chrX	Tmsb4x	1.67E+08	1.67E+08	1371	1.428477	8.368773	4.07E-11	7.33E-10	0.053766	1	2260	3319	3524	2744	3025	9610	12530	6009	15208	13274
ENSMUSG00000092787	chrX	Mir5116	56587852	56587914	63	-1.95793	1.255761	4.14E-11	7.44E-10	0.073243	-1	49	63	78	50	74	17	25	20	40	12
ENSMUSG00000072596	chr14	Ear2	44102654	44102719	719	2.395298	0.596495	4.16E-11	7.48E-10	0.088759	1	7	8	10	2	9	49	52	61	72	33
ENSMUSG00000029616	chr5	Erp29	1.21E+08	1.21E+08	9060	1.231878	5.795747	4.22E-11	7.57E-10	0.039611	1	464	476	659	448	747	1494	1714	1256	2365	2302
ENSMUSG00000027457	chr2	Snph	1.52E+08	1.52E+08	7861	-2.43264	0.745462	4.23E-11	7.58E-10	0.10462	-1	30	40	59	50	55	8	4	18	8	21
ENSMUSG00000020309	chr11	Chac2	30976707	30977746	1315	-1.391	3.073514	4.26E-11	7.63E-10	0.044556	-1	155	206	256	213	179	100	113	84	129	112
ENSMUSG00000045404	chr12	Kcnk13	99964499	99964801	3112	2.195598	1.3814	4.35E-11	7.76E-10	0.09263	1	15	11	15	11	21	53	109	52	168	102
ENSMUSG00000025534	chr5	Gusb	1.3E+08	1.3E+08	4548	1.751659	5.315112	4.41E-11	7.87E-10	0.078427	1	250	237	331	245	482	950	1218	642	2520	2047
ENSMUSG00000035284	chr9	Vps13c	67840396	67840526	11523	-1.10259	4.758672	4.49E-11	7.99E-10	0.031013	-1	546	438	755	627	748	259	361	450	544	423
ENSMUSG00000052920	chr19	Prkg1	30567551	30569336	7799	-2.24745	3.200685	4.55E-11	8.1E-10	0.119959	-1	144	277	276	359	203	51	48	145	96	35
ENSMUSG00000059248	chr11	Sept9	1.17E+08	1.17E+08	7565	1.268721	5.313263	4.61E-11	8.18E-10	0.04181	1	286	293	425	368	612	819	1464	999	2019	1407
ENSMUSG00000003873	chr7	Bax	45461695	45461966	869	1.137377	4.18326	4.65E-11	8.25E-10	0.031853	1	154	168	238	164	223	424	559	458	788	702
ENSMUSG00000104453	chr7	WI1-1616M8.3	81530309	81532521	2213	-1.2797	6.087871	4.66E-11	8.25E-10	0.043146	-1	1304	1529	1760	1789	1633	930	969	593	1191	921
ENSMUSG00000073139	chrX	BC023829	70459753	70461292	2513	-1.08166	5.003417	4.77E-11	8.45E-10	0.030068	-1	621	570	831	736	907	454	525	404	547	451
ENSMUSG00000028414	chr4	Fktn	53713998	53714195	6491	-1.12306	4.041686	4.85E-11	8.57E-10	0.031124	-1	277	364	418	390	438	184	289	194	329	223
ENSMUSG00000098404	chr7	Gm8086	15288251	15289190	940	-1.91428	0.803246	5E-11	8.82E-10	0.059582	-1	39	37	44	46	60	11	21	19	16	16

ENSMUSG00000024675	chr19	Ms4a4c	11404770	11404797	1751	4.891276	1.560309	5.02E-11	8.85E-10	0.407869	1	2	2	3	2	6	149	94	6	66	289
ENSMUSG00000020388	chr11	Pdlim4	54054928	54055239	2560	1.666162	4.015274	5.1E-11	8.98E-10	0.069165	1	118	80	144	106	206	414	969	339	646	492
ENSMUSG00000083405	chr16	Gm15725	37882542	37883631	1090	-2.06548	1.992134	5.19E-11	9.13E-10	0.094177	-1	82	78	107	114	161	11	36	63	41	30
ENSMUSG00000068758	chr14	Il3ra	14346495	14346512	1394	1.841421	2.420381	5.26E-11	9.24E-10	0.075849	1	25	29	32	52	53	157	169	114	228	283
ENSMUSG00000074283	chr7	Zfp109	24228048	24229840	1935	-2.20223	0.410414	5.27E-11	9.25E-10	0.078142	-1	29	31	48	37	32	4	10	17	15	8
ENSMUSG00000041801	chr1	Phlda3	1.36E+08	1.36E+08	1559	1.623135	6.674354	5.44E-11	9.54E-10	0.069177	1	859	711	1050	764	760	2431	2564	6374	3716	2887
ENSMUSG00000020091	chr10	Eif4ebp2	61432497	61433828	1786	-1.42594	5.32749	5.46E-11	9.56E-10	0.053288	-1	861	698	1099	1111	1154	261	421	821	581	494
ENSMUSG00000020733	chr11	Slc9a3r1	1.15E+08	1.15E+08	1925	1.586246	3.118684	5.51E-11	9.63E-10	0.059594	1	56	52	73	68	113	220	205	232	428	432
ENSMUSG00000024644	chr18	Cndp2	84667470	84668100	2119	1.384997	5.375103	5.53E-11	9.66E-10	0.050193	1	316	307	424	392	491	918	983	1023	2200	2040
ENSMUSG00000024640	chr19	Psat1	15904678	15906151	4254	1.848933	4.016637	5.67E-11	9.88E-10	0.085379	1	91	60	113	103	236	332	530	352	997	822
ENSMUSG00000040446	chr18	Rprd1a	24484962	24488331	4297	-1.23277	3.742539	5.85E-11	1.02E-09	0.03729	-1	311	249	404	259	345	116	231	209	222	162
ENSMUSG00000033684	chr1	Qsox1	1.56E+08	1.56E+08	8291	1.117117	5.150218	5.98E-11	1.04E-09	0.032612	1	286	274	429	352	562	795	1098	1326	1358	1118
ENSMUSG00000035164	chr9	Zc3h12c	52111985	52116802	6133	-1.60885	2.534229	5.99E-11	1.04E-09	0.059218	-1	120	117	156	161	175	32	73	101	67	62
ENSMUSG00000052397	chr17	Ezr	6738041	6739467	3290	1.834623	3.305702	6.19E-11	1.07E-09	0.081782	1	67	31	76	67	124	221	329	212	512	541
ENSMUSG00000063856	chr9	Gpx1	1.08E+08	1.08E+08	1441	1.202496	6.857721	6.62E-11	1.15E-09	0.039052	1	951	1184	1294	1047	1385	3047	3241	2831	5021	4865
ENSMUSG00000032245	chr9	Cln6	62838785	62838954	2434	1.084863	3.999085	6.87E-11	1.19E-09	0.028934	1	145	144	193	161	210	338	461	592	574	568
ENSMUSG00000073405	chr17	C920025E04Rik	36109234	36109270	1067	5.265399	1.273281	6.93E-11	1.2E-09	0.44968	1	3	0	3	2	1	96	137	10	22	229
ENSMUSG00000026581	chr1	Sell	1.64E+08	1.64E+08	5911	4.485861	0.61919	7.18E-11	1.24E-09	0.311607	1	2	3	1	2	1	34	17	20	70	169
ENSMUSG00000014498	chr10	Ankrd52	1.28E+08	1.28E+08	8401	-1.06608	6.552863	7.21E-11	1.24E-09	0.030878	-1	1841	1630	2368	2349	2486	900	1523	1468	1833	1469
ENSMUSG00000001228	chr17	Uhrf1	56303321	56303561	4259	1.878987	2.939417	7.25E-11	1.25E-09	0.084379	1	50	40	61	33	88	180	258	146	521	322
ENSMUSG00000064246	chr1	Chil1	1.34E+08	1.34E+08	2804	2.728109	0.6432	7.35E-11	1.26E-09	0.131804	1	5	0	7	10	9	34	65	92	48	46
ENSMUSG00000034854	chr10	Mfsd12	81357491	81357886	3971	2.05992	3.872374	7.4E-11	1.27E-09	0.105633	1	92	60	75	82	166	288	380	276	958	935
ENSMUSG00000034055	chrX	Phka1	1.03E+08	1.03E+08	6259	-1.33041	9.381459	7.52E-11	1.29E-09	0.04829	-1	12940	16130	21326	14668	14321	9098	7086	8453	8244	10494
ENSMUSG00000074476	chr9	Spc24	21755442	21756295	1349	1.804374	1.708626	7.57E-11	1.3E-09	0.066503	1	12	19	24	22	41	91	133	88	154	104
ENSMUSG00000037321	chr17	Tap1	34187553	34188405	5476	1.965864	3.449493	7.62E-11	1.3E-09	0.095281	1	54	42	91	83	105	385	302	170	453	678
ENSMUSG00000063895	chr14	Nupl1	60219204	60220158	2787	-1.0761	4.077655	7.63E-11	1.3E-09	0.029136	-1	305	312	432	420	453	163	268	300	307	240
ENSMUSG00000022946	chr16	Dopey2	93711907	93712068	7313	-1.07623	4.909029	7.69E-11	1.31E-09	0.030344	-1	547	520	823	717	831	386	422	467	451	510
ENSMUSG00000036819	chr11	Jmjd4	59450045	59450512	7115	-1.18949	3.67361	7.73E-11	1.32E-09	0.034673	-1	263	238	381	285	316	161	221	149	224	149
ENSMUSG00000061462	chr11	Obscn	58994256	58994509	28892	-1.23004	10.32925	8.16E-11	1.39E-09	0.041677	-1	28842	21797	33594	32589	34393	13398	16342	25446	19136	15327
ENSMUSG00000023274	chr6	Cd4	1.25E+08	1.25E+08	4032	2.297186	0.918507	8.33E-11	1.42E-09	0.096966	1	6	4	11	10	19	62	71	37	83	84
ENSMUSG00000047454	chr12	Gphn	78226655	78226841	3397	-1.08735	5.244468	8.33E-11	1.42E-09	0.031519	-1	752	727	989	832	1020	408	549	731	598	545
ENSMUSG00000043004	chr14	Gng2	19872559	19875935	4390	1.189895	3.538729	8.89E-11	1.51E-09	0.034018	1	111	98	109	120	146	259	323	363	458	478
ENSMUSG00000024074	chr17	Crim1	78200248	78201099	5995	-1.24423	4.230797	8.97E-11	1.52E-09	0.040255	-1	451	351	424	536	417	179	242	328	352	213
ENSMUSG00000045767	chr13	B230219D22Rik	55693124	55693347	4651	-1.22483	5.679022	9.07E-11	1.54E-09	0.040628	-1	1112	1040	1320	1153	1361	427	790	1014	808	578
ENSMUSG00000020120	chr11	Plek	16971206	16974153	4486	3.261322	4.482271	9.11E-11	1.54E-09	0.248226	1	52	33	66	69	143	226	353	345	2228	1913
ENSMUSG00000055612	chr2	Cdca7	72476159	72476311	3202	1.97605	1.725955	9.23E-11	1.56E-09	0.081793	1	17	20	26	15	29	88	106	63	191	150
ENSMUSG00000096910	chr17	Zfp955b	33289649	33289669	1638	-1.97418	1.272158	9.26E-11	1.56E-09	0.078639	-1	44	46	78	79	74	10	27	33	29	15
ENSMUSG00000027843	chr3	Ptpn22	1.04E+08	1.04E+08	3064	2.631364	0.637595	9.49E-11	1.6E-09	0.118455	1	9	4	2	5	12	32	44	41	80	90
ENSMUSG00000029373	chr5	Pf4	90772435	90772678	586	1.837437	4.265935	9.5E-11	1.6E-09	0.086988	1	134	82	149	105	243	487	471	373	1286	978
ENSMUSG00000037411	chr5	Serpine1	1.37E+08	1.37E+08	3024	1.883804	3.424488	9.56E-11	1.61E-09	0.08835	1	69	38	117	108	45	186	410	324	592	494
ENSMUSG00000046031	chr10	Fam26f	34126069	34126566	1080	3.088203	-0.04861	9.64E-11	1.62E-09	0.127261	1	3	1	1	7	2	38	41	19	30	41
ENSMUSG00000051506	chr14	Wdfy4	32959547	32960004	10512	2.037689	2.507901	9.71E-11	1.63E-09	0.097565	1	20	27	31	39	68	137	165	114	362	290
ENSMUSG00000025888	chr9	Casp1	5298517	5298723	1497	2.331097	1.681229	1E-10	1.68E-09	0.114862	1	13	19	16	19	16	94	92	48	178	189
ENSMUSG00000079445	chr1	B3gnt7	86302832	86304707	4137	3.666615	-0.40881	1.01E-10	1.69E-09	0.15079	1	0	1	0	2	4	13	36	12	50	25
ENSMUSG00000025261	chrX	Huwe1	1.52E+08	1.52E+08	23507	-1.10019	7.429492	1.03E-10	1.71E-09	0.033642	-1	3486	2727	4616	4265	4739	2000	2585	3025	2905	2285
ENSMUSG00000060550	chr17	H2-Q7	35439155	35439284	4265	2.573827	1.807081	1.05E-10	1.75E-09	0.144223	1	14	10	22	18	16	76	101	63	138	296
ENSMUSG00000031506	chr1	Ptpn7	1.35E+08	1.35E+08	6102	3.0649	1.563524	1.05E-10	1.75E-09	0.197067	1	12	3	9	5	21	47	105	43	231	182
ENSMUSG00000101257	chr1	2310015K22Rik	80225044	80225171	1461	-1.40858	2.748446	1.11E-10	1.85E-09	0.046383	-1	142	146	202	160	159	89	88	67	91	86
ENSMUSG00000018042	chr15	Cyb5r3	83153494	83154722	4298	1.069805	6.248293	1.12E-10	1.86E-09	0.031545	1	609	659	894	930	1045	1581	2589	2368	3113	2525
ENSMUSG00000009569	chr16	Mkl2	13256481	13256554	8990	-1.07929	5.275054	1.14E-10	1.89E-09	0.031548	-1	604	862	1001	791	1174	470	565	518	766	600
ENSMUSG00000042439	chr18	Zfp532	65580230	65580510	11192	-1.01954	3.934889	1.15E-10	1.9E-09	0.026043	-1	266	294	384	365	407	189	248	243	257	237
ENSMUSG00000041859	chr1	Mcm3	20802968	20803654	3752	1.70528	3.418209	1.15E-10	1.91E-09	0.073129	1	77	67	75	69	128	278	315	185	646	506
ENSMUSG00000036820	chr17	Amdhd2	24155833	24156085	2728	1.476651	3.360395	1.16E-10	1.92E-09	0.054295	1	67	69	107	95	114	197	254	294	532	510
ENSMUSG00000087107	chr11	AI662270	83223576	83223651	1489	2.759041	2.011202	1.18E-10	1.94E-09	0.169624	1	19	3	13	26	22	92	96	79	279	265
ENSMUSG00000060519	chr1	Tor3a	1.57E+08	1.57E+08	3892	1.174959	4.124778	1.19E-10	1.96E-09	0.035675	1	155	135	197	194	211	572	551	438	591	606
ENSMUSG00000025876	chr13	Unc5a	54949411	54949731	4168	-1.06829	4.211615	1.21E-10	2E-09	0.029575	-1	404	343	376	417	553	231	281	255	363	269
ENSMUSG00000078122	chrX	F630028O10Rik	96239926	96239996	3295	2.628553	0.535288	1.25E-10	2.06E-09	0.114575	1	6	4	8	4	8	49	37	27	60	87
ENSMUSG00000067081	chr1	Asb18	89950220	89952863	3952	-1.14741	4.994077	1.27E-10	2.09E-09	0.035595	-1	615	620	811	918	687	437	434	390	599	445
ENSMUSG00000048442	chr11	Smim5	1.16E+08	1.16E+08	1649	2.713704	1.579411	1.3E-10	2.13E-09	0.159794	1	8	4	26	10	16	70	236	66	121	83
ENSMUSG00000026459	chr1	Myog	1.34E+08	1.34E+08	1495	2.007784	6.096087	1.3E-10	2.13E-09	0.107465	1	217	449	480	412	773	2193	4871	1318	2446	1831
ENSMUSG00000075232	chr10	Amd1	40287458	40289469	3206	-2.25714	7.362518	1.32E-10	2.16E-09	0.134019	-1	2437	6123	7101	4729	1982	1569	1338	631	1411	1541
ENSMUSG00000039745	chr7	Htatip2	49759106	49759311	1465	1.339223	3.071468	1.32E-10	2.17E-09	0.042799	1	82	63	99	64	82	199	239	270	322	360
ENSMUSG00000029202	chr5	Pds5a	65615260	65615604	4146	-1.13558	4.425595	1.33E-10	2.17E-09	0.034284	-1	387	398	550	532	620	178	372	377	382	281
ENSMUSG00000007034	chr17	Slc44a4	34914466	34914520	3112	3.766303	-0.70876	1.36E-10	2.22E-09	0.140508	1	1	0	2	0	2	11	31	25	30	8
ENSMUSG00000028514	chr4	Usp24	1.06E+08	1.06E+08	12350	-1.06141	6.593892	1.39E-10	2.27E-09	0.031572	-1	1939	1747	2473	2337	2440	1170	1310	1733	1628	1449
ENSMUSG00000020737	chr11	Hn1	1.15E+08	1.15E+08	2149	1.229266	6.228977	1.42E-10	2.31E-09	0.04202	1	583	668	892	694	935	2024	3147	1539	3060	2535

ENSMUSG00000015854	chr3	Cd5l	87357881	87358029	2036	4.035322	-0.30992	1.45E-10	2.37E-09	0.216627	1	0	0	2	2	2	29	13	9	40	55
ENSMUSG00000038650	chr7	Rnh1	1.41E+08	1.41E+08	1911	1.211898	6.165718	1.47E-10	2.39E-09	0.04089	1	582	623	849	702	880	1456	2029	1854	3441	3190
ENSMUSG00000027639	chr2	Samhd1	1.57E+08	1.57E+08	9150	1.30638	5.263096	1.48E-10	2.41E-09	0.046809	1	295	250	449	384	495	1165	1079	865	1425	1792
ENSMUSG00000000056	chr11	Narf	1.21E+08	1.21E+08	4806	-1.07953	6.797173	1.54E-10	2.49E-09	0.032874	-1	2321	2354	2974	2449	2426	1479	1710	1641	1812	1636
ENSMUSG00000031897	chr8	Psmb10	1.06E+08	1.06E+08	1270	1.548081	4.134421	1.54E-10	2.49E-09	0.063244	1	113	135	162	175	156	615	524	293	736	838
ENSMUSG00000090066	chr3	1110002E22Rik	1.38E+08	1.38E+08	9998	-1.46579	8.225938	1.56E-10	2.52E-09	0.060118	-1	5267	6125	6731	7135	12205	4048	4168	2162	4050	3822
ENSMUSG00000027287	chr2	Snap23	1.21E+08	1.21E+08	4293	-1.00911	5.392109	1.59E-10	2.57E-09	0.028083	-1	856	784	1091	852	1117	459	771	621	797	632
ENSMUSG00000096727	chr17	Psmb9	34181988	34182351	3659	2.129455	2.515626	1.6E-10	2.58E-09	0.108588	1	31	28	36	34	44	207	152	86	226	375
ENSMUSG00000064356	chrMT	mt-Atp8	7766	7969	204	-2.25767	2.037466	1.6E-10	2.59E-09	0.120389	-1	84	104	101	207	59	16	35	41	35	40
ENSMUSG00000021390	chr13	Ogn	49608071	49608126	2540	-1.56678	6.215897	1.62E-10	2.6E-09	0.06794	-1	1865	1088	1990	1552	2973	576	1090	1289	814	604
ENSMUSG00000026786	chr2	Apbb1ip	22774094	22774521	7414	1.811309	2.974651	1.65E-10	2.65E-09	0.082047	1	57	22	49	58	106	167	260	222	438	350
ENSMUSG00000097296	chr8	Gm26532	84208920	84209609	690	2.490108	0.713416	1.67E-10	2.68E-09	0.111076	1	9	5	14	3	6	26	65	46	79	85
ENSMUSG00000027207	chr2	Galk2	1.26E+08	1.26E+08	6088	1.466479	3.016435	1.68E-10	2.69E-09	0.052664	1	65	52	88	63	87	175	282	176	398	360
ENSMUSG00000025597	chrX	Klhl4	1.14E+08	1.14E+08	3584	-2.26297	1.461969	1.72E-10	2.76E-09	0.11423	-1	38	67	89	114	72	11	28	33	29	10
ENSMUSG00000037337	chr7	Map4k1	28982854	28983054	2699	2.793037	1.280537	1.77E-10	2.83E-09	0.16128	1	4	16	9	12	5	53	66	46	149	160
ENSMUSG00000052698	chr9	Tln2	67217087	67221518	12193	-1.15064	6.848484	1.77E-10	2.83E-09	0.037563	-1	2177	2000	2778	2775	3723	1512	1760	1192	2191	1706
ENSMUSG00000037940	chr8	Inpp4b	81342556	81342797	10176	-1.91054	2.300128	1.78E-10	2.85E-09	0.087974	-1	93	99	133	192	132	27	66	73	47	28
ENSMUSG00000029822	chr6	Osbpl3	50293330	50297161	9023	1.624788	2.393332	1.83E-10	2.91E-09	0.06172	1	41	26	41	37	66	110	250	190	210	149
ENSMUSG00000025355	chr10	Mmp19	1.29E+08	1.29E+08	3410	2.435864	4.499332	1.88E-10	2.99E-09	0.153514	1	96	73	120	93	220	402	583	290	1726	1658
ENSMUSG00000094441	chr17	Zfp955a	33241519	33242950	1638	-2.02167	1.126234	1.89E-10	3E-09	0.085657	-1	44	55	77	55	58	9	17	24	40	12
ENSMUSG00000038121	chr18	Fam210a	68260187	68268952	9813	-1.14196	6.837808	1.91E-10	3.03E-09	0.037137	-1	2163	2491	2994	2992	2429	1380	1676	1963	1895	1387
ENSMUSG00000016559	chr11	H3f3b	1.16E+08	1.16E+08	2976	1.072864	6.725877	2.03E-10	3.23E-09	0.032862	1	906	918	1357	1150	1422	2182	2880	3618	4409	3900
ENSMUSG00000099974	chr9	Bcl2a1d	88723285	88723532	863	3.596737	-0.15062	2.04E-10	3.24E-09	0.173161	1	2	2	0	2	3	19	23	11	63	51
ENSMUSG00000070632	chr5	Btbd8	1.07E+08	1.07E+08	1537	-2.73578	-0.47604	2.06E-10	3.26E-09	0.094381	-1	18	14	29	12	25	2	6	1	7	4
ENSMUSG00000032826	chr3	Ank2	1.27E+08	1.27E+08	35218	-1.18832	5.768857	2.08E-10	3.3E-09	0.03985	-1	984	1180	1547	1482	1111	707	869	609	1013	681
ENSMUSG00000037646	chr15	Vps13b	35371546	35371777	13370	-1.11657	3.811034	2.11E-10	3.33E-09	0.032383	-1	288	236	364	326	399	138	212	265	234	188
ENSMUSG00000022383	chr15	Ppara	85734983	85735145	3836	-2.33102	2.208433	2.13E-10	3.36E-09	0.132223	-1	117	102	94	206	116	11	21	67	48	36
ENSMUSG00000027861	chr3	Casq2	1.02E+08	1.02E+08	2736	1.704455	7.50702	2.21E-10	3.48E-09	0.081384	1	658	1495	1354	2436	1149	4876	8467	6342	7620	5302
ENSMUSG00000038244	chr7	Mical2	1.12E+08	1.12E+08	11510	-1.29497	6.688685	2.28E-10	3.58E-09	0.047852	-1	1581	2425	2966	2513	2849	1578	1180	1190	1356	1489
ENSMUSG00000009471	chr7	Myod1	46376474	46377299	1854	1.331044	4.926223	2.33E-10	3.66E-09	0.049245	1	207	267	328	277	372	864	1422	683	1393	723
ENSMUSG00000036246	chr8	Gmip	69808679	69808820	5552	1.454636	2.817843	2.34E-10	3.68E-09	0.051515	1	57	48	79	51	75	154	258	161	320	308
ENSMUSG00000037475	chrX	Thoc2	41794991	41797779	12666	-1.22902	4.215572	2.43E-10	3.81E-09	0.041285	-1	396	308	475	414	606	142	224	353	350	251
ENSMUSG00000033458	chr7	Fan1	64346758	64346895	5289	-1.50236	2.692534	2.46E-10	3.86E-09	0.056181	-1	178	127	178	141	165	41	97	102	86	70
ENSMUSG00000042744	chr5	Gm15800	1.21E+08	1.21E+08	16416	-1.00831	4.631932	2.53E-10	3.96E-09	0.027876	-1	529	392	609	554	698	268	407	389	484	390
ENSMUSG00000056201	chr19	Cfl1	5490485	5490602	1148	1.466677	7.315101	2.61E-10	4.08E-09	0.061539	1	987	1177	1470	1514	2027	3934	5096	2795	9047	7119
ENSMUSG00000006740	chr18	Kif5b	6201002	6203707	7395	-1.17176	6.936937	2.62E-10	4.09E-09	0.039723	-1	2533	2254	3295	2846	3318	1077	1932	2396	1975	1493
ENSMUSG00000007891	chr7	Ctsd	1.42E+08	1.42E+08	2519	1.138671	9.850982	2.64E-10	4.12E-09	0.037903	1	7971	8753	10920	10026	10537	20731	21960	27809	44081	36548
ENSMUSG00000037860	chr1	Aim2	1.73E+08	1.73E+08	3501	2.572541	0.722372	2.65E-10	4.13E-09	0.1259	1	7	2	13	8	6	54	45	37	58	103
ENSMUSG00000040945	chr4	Rcc2	1.41E+08	1.41E+08	4155	1.221925	4.901691	2.65E-10	4.13E-09	0.041766	1	234	212	312	294	470	689	921	707	1475	1169
ENSMUSG00000096954	chr12	Gdap10	32821872	32825987	5003	-2.8106	-0.59856	2.67E-10	4.15E-09	0.094736	-1	16	17	16	14	26	1	4	7	0	5
ENSMUSG00000070780	chr5	Rbm47	66016549	66019436	6859	2.838717	1.510278	2.71E-10	4.21E-09	0.177124	1	10	7	8	9	21	49	65	48	199	210
ENSMUSG00000031383	chrX	Dusp9	73639419	73639641	2722	3.425289	-0.60621	2.77E-10	4.29E-09	0.134697	1	1	0	2	0	4	9	27	25	40	13
ENSMUSG00000066705	chr9	Fxyd6	45370185	45370488	1791	1.185124	5.54833	2.77E-10	4.3E-09	0.03993	1	505	331	498	465	587	946	1743	1924	1779	1253
ENSMUSG00000057280	chr4	Musk	58285960	58286190	3776	-1.43758	2.940995	2.79E-10	4.32E-09	0.052664	-1	128	165	238	214	194	58	132	114	107	74
ENSMUSG00000066026	chr4	Dhrs3	1.45E+08	1.45E+08	2927	1.205465	5.062531	2.79E-10	4.32E-09	0.040939	1	241	241	376	362	497	639	992	1073	1323	1483
ENSMUSG00000062082	chr16	Cd200r4	44811733	44811844	2045	3.415025	0.02277	2.86E-10	4.42E-09	0.177569	1	1	1	0	4	6	20	21	20	76	54
ENSMUSG00000024789	chr19	Jak2	29251828	29252118	5030	-1.05572	5.236853	2.86E-10	4.42E-09	0.031557	-1	736	840	1069	789	790	453	560	602	706	545
ENSMUSG00000056268	chr1	Dennd1b	1.39E+08	1.39E+08	8314	-1.06849	4.377137	2.87E-10	4.43E-09	0.03115	-1	398	378	560	424	610	280	282	365	330	292
ENSMUSG00000062232	chr3	Rapgef2	79062516	79064561	14051	-1.05473	4.081117	2.92E-10	4.49E-09	0.029887	-1	348	277	413	455	415	190	289	264	300	243
ENSMUSG00000046311	chr11	Zfp62	49203292	49203538	6060	-1.23418	3.912107	3.01E-10	4.62E-09	0.041101	-1	354	303	399	326	370	129	224	296	244	162
ENSMUSG00000048534	chr9	Amica1	45079183	45079296	2457	2.807429	-0.01967	3.05E-10	4.68E-09	0.109318	1	5	3	1	4	4	26	22	31	35	58
ENSMUSG00000028478	chr4	Clta	44004452	44004700	1800	1.079408	5.957648	3.08E-10	4.73E-09	0.03358	1	546	527	734	747	797	1412	1718	1699	2698	2442
ENSMUSG00000018501	chr11	Ncor1	62316426	62318030	12811	-1.11936	6.714855	3.11E-10	4.77E-09	0.03654	-1	1981	1948	2808	2389	3002	1070	1482	2106	1646	1442
ENSMUSG00000028737	chr4	Aldh4a1	1.4E+08	1.4E+08	4907	-1.00312	7.060048	3.13E-10	4.79E-09	0.029507	-1	2582	2639	3133	3162	3338	1778	1936	1964	2511	2171
ENSMUSG00000102040	chr6	Clec7a	1.29E+08	1.29E+08	735	2.351679	0.562939	3.13E-10	4.79E-09	0.095363	1	9	3	7	7	10	22	77	55	57	52
ENSMUSG00000029538	chr5	Srsf9	1.15E+08	1.15E+08	1360	1.32529	3.661569	3.21E-10	4.9E-09	0.046487	1	109	96	150	110	133	339	458	232	573	505
ENSMUSG00000103866	chr18	Setbp1	78755215	78755825	4749	-3.40136	1.216026	3.21E-10	4.9E-09	0.249601	-1	51	39	93	78	100	1	7	30	5	3
ENSMUSG00000039988	chr3	Ankrd13c	1.58E+08	1.58E+08	2668	-0.98964	4.037083	3.41E-10	5.2E-09	0.026155	-1	311	305	424	397	384	198	255	274	314	244
ENSMUSG00000020143	chr11	Dock2	34226815	34227730	11425	2.25747	3.007511	3.43E-10	5.22E-09	0.13182	1	54	15	39	38	86	186	255	140	530	460
ENSMUSG00000033450	chr17	Tagap	7926000	7926108	3076	2.765929	0.362485	3.45E-10	5.25E-09	0.130308	1	6	1	7	7	3	39	62	48	23	55
ENSMUSG00000084899	chr10	Gm15344	86692119	86692202	421	1.458385	5.392049	3.48E-10	5.29E-09	0.06082	1	215	349	448	307	591	1248	1480	790	1748	1906
ENSMUSG00000021486	chr13	Prelid1	55322055	55322281	1088	1.264847	5.340127	3.66E-10	5.56E-09	0.045941	1	277	378	437	390	517	939	1350	801	2067	1648
ENSMUSG00000032754	chr5	Slc8b1	1.21E+08	1.21E+08	3463	1.155766	4.231865	3.67E-10	5.56E-09	0.036825	1	178	131	225	171	274	355	594	672	676	745
ENSMUSG00000022385	chr15	Gtse1	85859707	85859794	2721	2.42453	0.720663	3.72E-10	5.63E-09	0.114751	1	5	3	9	5	18	46	46	35	94	78
ENSMUSG00000024431	chr18	Nr3c1	39410545	39414634	7425	-1.04764	6.304088	3.73E-10	5.65E-09	0.032188	-1	1570	1341	1778	1754	2554	867	1250	1336	1413	1180
ENSMUSG00000047996	chrX	Prrg1	78449613	78453172	11614	-1.55443	2.374251	3.74E-10	5.65E-09	0.059539	-1	117	88	123	142	178	38	49	88	83	51

ENSMUSG00000027994	chr3	Ccdc109b	1.3E+08	1.3E+08	1318	2.428799	1.714518	3.87E-10	5.84E-09	0.138005	1	18	7	13	9	36	87	105	59	220	159
ENSMUSG00000039835	chr10	Nhsl1	18390322	18390510	11056	-1.26692	3.191214	3.87E-10	5.84E-09	0.041577	-1	193	151	217	224	300	85	153	148	133	106
ENSMUSG00000057133	chr2	Chd6	1.61E+08	1.61E+08	19093	-1.00389	4.173283	3.96E-10	5.97E-09	0.027473	-1	344	353	410	374	536	215	322	270	320	274
ENSMUSG00000025647	chr9	Shisa5	1.09E+08	1.09E+08	1955	1.363045	5.266322	4.17E-10	6.28E-09	0.053612	1	270	265	337	405	547	1002	1146	770	1781	1828
ENSMUSG00000087543	chr15	Gm16576	79742698	79742911	5404	-1.70768	2.486404	4.19E-10	6.3E-09	0.07437	-1	137	99	147	185	144	34	61	103	59	49
ENSMUSG00000023015	chr15	Racgap1	99620496	99621464	7079	1.551391	3.313472	4.22E-10	6.33E-09	0.06409	1	69	83	77	56	134	257	311	210	597	371
ENSMUSG00000056515	chr17	Rab31	65651726	65654503	3476	1.202342	4.71261	4.22E-10	6.33E-09	0.041146	1	247	153	301	250	394	556	1079	719	1113	844
ENSMUSG00000025372	chr11	Baiap2	1.2E+08	1.2E+08	4992	1.741489	2.68568	4.26E-10	6.39E-09	0.077909	1	31	32	55	50	79	96	225	182	338	326
ENSMUSG00000026028	chr1	Trak2	58900449	58904182	7088	-1.09373	6.836779	4.29E-10	6.43E-09	0.035509	-1	1951	2491	3185	2924	2426	1433	1871	1574	2116	1529
ENSMUSG00000032359	chr9	Ctsh	90054152	90054219	4499	1.276106	5.48213	4.52E-10	6.75E-09	0.047439	1	399	294	584	324	616	1232	1711	935	1866	1650
ENSMUSG00000028873	chr4	Cdca8	1.25E+08	1.25E+08	5177	1.977634	1.800302	4.53E-10	6.77E-09	0.090813	1	14	27	22	20	29	92	117	62	219	144
ENSMUSG00000047888	chr15	Tnrc6b	80711319	80711488	17327	-1.09956	5.655944	4.75E-10	7.09E-09	0.035528	-1	1095	800	1362	1092	1445	491	780	969	859	672
ENSMUSG00000070577	chr4	Gm572	1.49E+08	1.49E+08	1385	-1.56418	2.336571	4.83E-10	7.19E-09	0.061282	-1	114	120	148	138	100	34	55	80	84	48
ENSMUSG00000035273	chr5	Hpse	1.01E+08	1.01E+08	3516	2.079968	2.469453	4.84E-10	7.2E-09	0.110912	1	27	16	29	21	86	156	215	131	259	262
ENSMUSG00000024617	chr18	Camk2a	60925618	60925840	7465	-1.19429	8.717986	4.91E-10	7.3E-09	0.042831	-1	8904	7924	11435	9285	11644	6152	6262	3776	7138	6254
ENSMUSG00000089075	chr3	Gm23820	1.03E+08	1.03E+08	300	-2.37235	-0.14932	4.97E-10	7.38E-09	0.083918	-1	26	19	33	22	19	3	9	4	7	9
ENSMUSG00000001525	chr17	Tubb5	35833921	35836039	3327	1.384223	6.903838	5.03E-10	7.46E-09	0.056763	1	824	857	1149	1004	1829	2848	4004	2357	6694	4823
ENSMUSG00000039512	chr17	Uhrf1bp1	27856490	27856794	8708	-0.99869	5.228694	5.14E-10	7.62E-09	0.029023	-1	627	684	992	951	951	434	605	646	676	566
ENSMUSG00000038023	chr5	Atp6v0a2	1.25E+08	1.25E+08	3019	-0.99788	4.40064	5.31E-10	7.86E-09	0.028042	-1	386	385	533	464	600	208	379	348	409	319
ENSMUSG00000026669	chr2	Mcm10	4989714	4991476	7692	2.387828	0.709571	5.31E-10	7.86E-09	0.112013	1	3	5	9	11	12	49	42	31	104	70
ENSMUSG00000047419	chr13	Cmya5	93040713	93041560	11850	-1.22913	10.35743	5.33E-10	7.87E-09	0.045568	-1	26574	24283	36193	34908	32070	15154	14091	25864	17178	18317
ENSMUSG00000053347	chr17	Zfp943	21962552	21962819	5277	-1.17034	3.86948	5.41E-10	7.99E-09	0.037795	-1	311	301	395	302	376	142	226	289	228	165
ENSMUSG00000018459	chr2	Slc13a3	1.65E+08	1.65E+08	5215	2.701581	0.249055	5.42E-10	7.99E-09	0.124379	1	3	4	4	4	8	39	66	16	47	42
ENSMUSG00000027533	chr3	Fabp5	10012548	10012718	3567	2.331469	5.833061	5.52E-10	8.14E-09	0.151705	1	203	324	323	453	256	1129	942	1053	3921	4518
ENSMUSG00000038390	chr6	Gpr162	1.25E+08	1.25E+08	2676	2.926148	-0.28348	5.55E-10	8.17E-09	0.114273	1	1	2	4	1	5	18	39	18	24	42
ENSMUSG00000026640	chr1	Plxna2	1.95E+08	1.95E+08	17174	-1.08811	4.070803	5.58E-10	8.19E-09	0.033073	-1	283	285	421	406	543	178	303	264	305	211
ENSMUSG00000000278	chr11	Scpep1	88924020	88924724	2097	1.284765	5.088454	5.69E-10	8.36E-09	0.048285	1	315	206	357	248	558	750	1039	939	1614	1377
ENSMUSG00000032491	chr9	Nradd	1.11E+08	1.11E+08	1162	1.781247	1.268416	5.74E-10	8.41E-09	0.065479	1	12	13	25	12	24	50	94	75	122	76
ENSMUSG00000031885	chr8	Cbfb	1.05E+08	1.05E+08	3480	-1.02552	6.259002	5.75E-10	8.43E-09	0.031518	-1	1608	1283	1874	1798	2051	843	1234	1381	1349	1107
ENSMUSG00000002233	chr3	Rhoc	1.05E+08	1.05E+08	1292	1.108796	5.736208	6E-10	8.78E-09	0.036509	1	425	533	612	566	691	1426	1726	1144	2329	1919
ENSMUSG00000006728	chr10	Cdk4	1.27E+08	1.27E+08	3249	1.074788	5.535356	6.01E-10	8.78E-09	0.034154	1	372	455	540	504	634	1191	1519	1025	2025	1629
ENSMUSG00000054477	chr18	Kcnn2	45268860	45269416	7321	-1.64178	2.037294	6.01E-10	8.78E-09	0.066506	-1	97	104	89	132	84	34	55	34	63	47
ENSMUSG00000038312	chr2	Edem2	1.56E+08	1.56E+08	3463	1.170988	3.441371	6.12E-10	8.92E-09	0.03626	1	87	89	113	129	136	228	301	326	454	450
ENSMUSG00000080741	chr13	Gm11398	23620730	23621049	320	-1.88299	1.938708	6.18E-10	9.01E-09	0.088281	-1	88	94	99	101	117	39	51	17	61	22
ENSMUSG00000022540	chr16	Rogdi	5008730	5009252	1421	1.337796	3.080729	6.2E-10	9.02E-09	0.046781	1	56	74	72	85	109	200	383	218	325	274
ENSMUSG00000038024	chr4	Dennd4c	86748555	86748912	8482	-1.86797	4.41159	6.6E-10	9.6E-09	0.099747	-1	512	428	588	627	640	97	168	467	215	131
ENSMUSG00000060802	chr2	B2m	1.22E+08	1.22E+08	860	1.373384	7.513377	6.71E-10	9.74E-09	0.056874	1	1394	1370	1792	1783	2235	4651	5831	3354	7546	9660
ENSMUSG00000076033	chr13	Mir692-3	74407065	74407173	109	2.75223	0.149623	6.75E-10	9.8E-09	0.119723	1	3	8	6	1	2	28	26	29	58	57
ENSMUSG00000087555	chr2	Gm13997	1.2E+08	1.2E+08	336	-2.58428	0.0521	6.77E-10	9.82E-09	0.118418	-1	18	17	40	30	40	4	10	13	2	3
ENSMUSG00000055024	chr15	Ep300	81585351	81588344	13886	-1.14896	5.234396	6.93E-10	1E-08	0.039251	-1	780	625	965	947	1045	336	489	762	695	484
ENSMUSG00000030592	chr7	Ryr1	29003340	29003553	15371	-1.16142	11.15188	7.07E-10	1.02E-08	0.041425	-1	48029	37651	59437	57201	62173	26520	28127	45657	33385	29316
ENSMUSG00000049313	chr9	Sorl1	41964720	41968670	11321	-1.07724	5.887835	7.08E-10	1.02E-08	0.034956	-1	1193	1038	1410	1678	1382	634	800	933	1024	1078
ENSMUSG00000047746	chr16	Fbxo40	36963460	36966285	5517	-1.17676	8.257546	7.14E-10	1.03E-08	0.042369	-1	5630	5779	8936	8214	7034	3836	3922	5690	4108	4063
ENSMUSG00000025804	chr9	Ccr1	1.24E+08	1.24E+08	2831	2.618108	2.455737	7.26E-10	1.05E-08	0.176867	1	24	9	30	14	51	83	141	107	421	370
ENSMUSG00000029233	chr5	Srd5a3	76140271	76140548	4648	1.23943	3.05542	7.31E-10	1.05E-08	0.039885	1	60	77	89	67	117	200	275	223	331	321
ENSMUSG00000004530	chr5	Coro1c	1.14E+08	1.14E+08	9664	1.452629	5.29174	7.36E-10	1.06E-08	0.062623	1	284	228	356	328	592	846	1126	842	2333	1751
ENSMUSG00000090264	chr18	Eif4ebp3	36664060	36664302	744	1.3914	2.552809	7.44E-10	1.07E-08	0.048289	1	41	45	60	56	63	182	159	226	184	202
ENSMUSG00000074862	chr10	BC025920	81606270	81606390	3306	-1.44877	2.060074	7.58E-10	1.09E-08	0.050127	-1	86	93	135	98	92	40	56	50	54	58
ENSMUSG00000028347	chr4	Tmeff1	48585174	48585641	2549	2.526755	0.922393	7.64E-10	1.1E-08	0.131819	1	12	2	4	15	9	27	81	68	93	85
ENSMUSG00000003949	chr11	Hlf	90336536	90340974	6681	-1.91116	3.029498	7.68E-10	1.1E-08	0.100643	-1	319	132	258	176	171	49	56	139	83	74
ENSMUSG00000004207	chr10	Psap	60277627	60277782	2744	1.186343	10.57183	7.77E-10	1.11E-08	0.043366	1	13673	13483	17870	15535	17119	36161	39358	35088	76129	65204
ENSMUSG00000009585	chr15	Apobec3	79891659	79891822	6083	1.48883	2.923861	7.97E-10	1.14E-08	0.05893	1	43	64	86	71	63	213	262	151	323	337
ENSMUSG00000030029	chr6	Lrig1	94604529	94604779	5585	-0.99725	6.210981	8.06E-10	1.15E-08	0.030312	-1	1458	1555	1975	1432	1813	855	1167	1249	1321	1198
ENSMUSG00000068284	chr16	Gm608	44173246	44173510	13050	-1.05297	5.95851	8.07E-10	1.15E-08	0.033638	-1	1223	1022	1687	1509	1623	767	1001	1107	953	862
ENSMUSG00000102869	chr2	RP24-114E18.7	1.56E+08	1.56E+08	1149	-1.67259	4.283532	8.09E-10	1.15E-08	0.081669	-1	436	409	583	482	575	100	198	437	210	149
ENSMUSG00000026981	chr2	Il1rn	24336853	24336992	5535	5.989943	4.048904	8.28E-10	1.18E-08	0.705007	1	2	1	3	19	19	96	134	34	1970	1888
ENSMUSG00000097705	chr10	Gm26740	22187013	22187143	1724	-1.39777	2.986182	8.3E-10	1.18E-08	0.052578	-1	200	134	243	175	205	82	107	138	88	86
ENSMUSG00000061111	chr11	Fam195b	1.21E+08	1.21E+08	1282	0.941241	5.144321	8.42E-10	1.2E-08	0.026152	1	386	324	460	389	459	816	1112	1116	1268	1118
ENSMUSG00000003206	chr17	Ebi3	55952623	55952928	1170	2.580853	0.496026	8.61E-10	1.22E-08	0.127545	1	4	5	6	5	10	42	34	21	78	80
ENSMUSG00000040952	chr7	Rps19	24884371	24884667	4685	1.011194	7.238717	8.67E-10	1.23E-08	0.031592	1	1391	1674	1908	1399	1993	3837	4745	4182	5800	5057
ENSMUSG00000022263	chr15	Trio	27730652	27733030	11494	-1.01457	5.069912	8.92E-10	1.26E-08	0.030742	-1	591	579	919	752	960	331	602	575	601	510
ENSMUSG00000050299	chr16	Gm9843	76403209	76403712	504	0.978755	3.886012	9.06E-10	1.28E-08	0.02624	1	152	139	182	169	181	366	418	425	573	496
ENSMUSG00000033213	chr2	AA467197	1.23E+08	1.23E+08	1203	2.89703	-0.6056	9.32E-10	1.32E-08	0.092258	1	0	2	2	2	4	17	21	13	33	25
ENSMUSG00000101904	chr1	Gm29427	1.31E+08	1.31E+08	1909	-1.61536	1.823888	9.39E-10	1.33E-08	0.063137	-1	76	82	103	111	65	28	47	42	46	39
ENSMUSG00000006356	chr12	Crip2	1.13E+08	1.13E+08	1437	1.023895	5.924672	9.44E-10	1.33E-08	0.031982	1	525	600	750	724	748	1429	2288	1602	2507	1754
ENSMUSG00000044378	chr6	Slc15a5	1.38E+08	1.38E+08	3088	-4.76118	-0.13148	9.54E-10	1.35E-08	0.393107	-1	13	64	33	26	2	1	0	0	3	3

ENSMUSG00000021822	chr14	Plau	20836662	20836734	2343	1.799186	5.857722	9.6E-10	1.35E-08	0.096392	1	400	319	506	417	530	918	1152	1412	4277	3322
ENSMUSG00000021062	chr12	Rab15	76797960	76800401	4614	1.466538	2.893541	9.86E-10	1.39E-08	0.057544	1	52	57	53	72	90	119	253	297	385	232
ENSMUSG00000001827	chr7	Folr1	1.02E+08	1.02E+08	2297	3.058992	-0.3707	9.88E-10	1.39E-08	0.12465	1	3	1	1	1	5	20	46	25	25	16
ENSMUSG00000037568	chr1	Vash2	1.91E+08	1.91E+08	4314	2.220217	3.401385	9.91E-10	1.39E-08	0.137658	1	38	18	60	76	130	239	777	298	425	279
ENSMUSG00000043467	chr1	Zbtb37	1.61E+08	1.61E+08	18814	-1.18266	3.162702	1.01E-09	1.41E-08	0.037867	-1	196	139	259	222	224	81	138	126	166	134
ENSMUSG00000038248	chr10	Sobp	43002500	43004414	5529	-1.1264	4.852238	1.01E-09	1.41E-08	0.037997	-1	535	535	669	655	952	367	492	282	492	480
ENSMUSG00000019841	chr10	Rev3l	39732118	39732613	13293	-1.21086	5.464934	1.01E-09	1.42E-08	0.044647	-1	857	926	1199	899	1302	427	625	946	596	508
ENSMUSG00000008226	chr2	Scrn3	73312601	73312713	4815	-1.0907	5.480652	1.02E-09	1.43E-08	0.036229	-1	943	927	1277	912	992	565	659	823	704	553
ENSMUSG00000034744	chr6	Nagk	83794982	83795282	3293	1.315683	3.21879	1.06E-09	1.48E-08	0.047351	1	66	76	104	76	122	197	310	213	418	417
ENSMUSG00000045071	chr4	E130308A19Rik	59626211	59626491	12617	-1.21038	2.620628	1.07E-09	1.49E-08	0.037162	-1	119	119	166	138	175	65	93	74	103	97
ENSMUSG00000021477	chr13	Ctsl	64363214	64364200	1971	1.50436	8.233509	1.07E-09	1.5E-08	0.069586	1	2481	1972	2932	2388	3434	5463	6139	17415	12567	11211
ENSMUSG00000003541	chr17	Ier3	35821684	35821928	1131	1.385559	2.75299	1.08E-09	1.5E-08	0.050309	1	47	63	71	53	71	212	191	272	248	178
ENSMUSG00000063953	chr10	Amd2	35708691	35711891	3201	-2.82401	0.748906	1.09E-09	1.51E-08	0.178836	-1	17	72	77	53	21	11	10	6	12	8
ENSMUSG00000096252	chr13	Tes3-ps	49493615	49494819	1205	-2.1885	0.984948	1.09E-09	1.52E-08	0.108104	-1	60	30	74	39	66	15	24	21	13	7
ENSMUSG00000039419	chr6	Cntnap2	45060061	45060386	7183	-1.65542	3.065613	1.09E-09	1.52E-08	0.076772	-1	206	157	165	239	294	89	82	55	83	154
ENSMUSG00000040084	chr2	Bub1b	1.19E+08	1.19E+08	4275	1.744631	2.118295	1.12E-09	1.56E-08	0.077525	1	20	25	28	38	52	120	145	88	258	157
ENSMUSG00000029622	chr5	Arpc1b	1.45E+08	1.45E+08	5103	1.28383	5.960963	1.12E-09	1.56E-08	0.050679	1	504	472	638	581	868	1274	1923	1314	3300	2783
ENSMUSG00000028494	chr4	Plin2	86648386	86648579	3512	1.939618	6.391793	1.14E-09	1.58E-08	0.11237	1	482	506	652	644	610	1529	1565	1615	5930	5659
ENSMUSG00000023031	chr15	Cela1	1.01E+08	1.01E+08	1103	2.9098	0.441564	1.18E-09	1.64E-08	0.1744	1	4	0	7	3	10	47	40	17	67	78
ENSMUSG00000037493	chr9	Cib2	54544794	54545484	1433	-1.35338	7.249797	1.19E-09	1.65E-08	0.056916	-1	3172	3708	4673	3387	3178	2346	1737	1474	1848	2296
ENSMUSG00000056071	chr3	S100a9	90692632	90692934	522	4.391645	0.198893	1.2E-09	1.66E-08	0.328239	1	2	0	0	2	3	16	20	14	50	125
ENSMUSG00000053175	chr7	Bcl3	19808462	19809056	2485	1.912771	1.944069	1.21E-09	1.67E-08	0.092925	1	17	15	26	39	34	129	148	64	186	155
ENSMUSG00000026547	chr1	Tagln2	1.73E+08	1.73E+08	2082	1.441438	6.465528	1.21E-09	1.67E-08	0.064079	1	569	680	814	856	1097	2222	2898	1419	5002	3895
ENSMUSG00000056529	chr4	Ptafr	1.33E+08	1.33E+08	3637	1.945414	3.566693	1.23E-09	1.7E-08	0.108946	1	59	35	73	80	172	250	413	220	651	694
ENSMUSG00000031596	chr8	Slc7a2	40862396	40862557	9135	-1.40517	6.294366	1.25E-09	1.72E-08	0.061077	-1	1508	1939	2107	1635	2344	708	797	1737	968	790
ENSMUSG00000004709	chr1	Cd244	1.72E+08	1.72E+08	4876	3.622032	-0.43062	1.26E-09	1.73E-08	0.182168	1	3	0	2	0	2	15	21	8	49	40
ENSMUSG00000037318	chr1	Traf3ip3	1.93E+08	1.93E+08	5756	1.673963	2.372181	1.27E-09	1.74E-08	0.07295	1	39	29	36	47	49	131	298	126	185	154
ENSMUSG00000040616	chr4	Tmem51	1.42E+08	1.42E+08	1875	1.674353	2.393141	1.28E-09	1.75E-08	0.074172	1	29	27	39	45	67	153	195	94	246	225
ENSMUSG00000043991	chr18	Pura	36281097	36281549	14943	-1.01905	5.360597	1.3E-09	1.78E-08	0.031931	-1	851	621	1009	937	1227	425	669	731	746	622
ENSMUSG00000079426	chr6	Arpc4	1.13E+08	1.13E+08	2323	1.082293	5.852015	1.32E-09	1.8E-08	0.036357	1	483	537	783	603	705	1480	1721	1302	2609	2128
ENSMUSG00000090799	chr14	Klhl33	50891389	50891941	1602	-1.51974	6.042272	1.33E-09	1.81E-08	0.071199	-1	1771	1081	1693	1806	1795	485	542	1408	944	635
ENSMUSG00000035455	chr11	Fignl1	11787431	11789158	4839	2.281381	1.409868	1.35E-09	1.84E-08	0.125338	1	14	6	10	14	28	68	115	43	172	98
ENSMUSG00000066440	chr12	Zfyve26	79232347	79234169	9368	-0.97829	4.253816	1.35E-09	1.84E-08	0.02808	-1	405	324	433	439	513	204	277	317	391	325
ENSMUSG00000032383	chr9	Ppib	66060169	66060400	960	1.230443	6.28712	1.38E-09	1.88E-08	0.04732	1	626	585	853	697	1208	2022	3097	1535	3473	2768
ENSMUSG00000030677	chr7	Kif22	1.27E+08	1.27E+08	2063	1.984519	2.15997	1.39E-09	1.89E-08	0.103015	1	12	33	22	34	45	110	166	85	295	171
ENSMUSG00000018363	chr11	Smurf2	1.07E+08	1.07E+08	6162	-0.98576	4.766324	1.39E-09	1.89E-08	0.029332	-1	547	446	658	655	728	299	459	490	503	391
ENSMUSG00000028822	chr4	Tmem50a	1.35E+08	1.35E+08	1270	0.96043	5.719652	1.4E-09	1.9E-08	0.028578	1	557	488	675	540	733	1246	1626	1795	1759	1678
ENSMUSG00000005470	chr8	Asf1b	83955507	83955937	2338	1.76174	1.538596	1.43E-09	1.93E-08	0.072683	1	11	20	23	18	34	57	86	93	163	111
ENSMUSG00000050721	chr9	Plekho2	65554386	65557079	3271	1.451196	4.626259	1.43E-09	1.94E-08	0.063954	1	155	148	241	243	337	484	692	532	1399	1234
ENSMUSG00000022504	chr16	Ciita	10488178	10488424	5254	2.386167	0.609502	1.44E-09	1.96E-08	0.111621	1	8	8	9	6	5	37	94	35	70	36
ENSMUSG00000033009	chr8	Ogfod1	94037198	94037442	5846	-0.98729	4.679864	1.45E-09	1.96E-08	0.029332	-1	534	519	667	520	589	358	400	341	497	404
ENSMUSG00000042686	chr1	Jph1	16964560	16964577	4998	-1.12436	8.305349	1.46E-09	1.97E-08	0.040248	-1	6934	5968	8504	7133	7638	3874	4482	6177	4335	4098
ENSMUSG00000030745	chr7	Il21r	1.26E+08	1.26E+08	2607	2.942176	0.588747	1.47E-09	1.99E-08	0.174059	1	6	5	4	7	3	46	78	12	65	78
ENSMUSG00000025648	chr9	Pfkfb4	1.09E+08	1.09E+08	3333	-1.11657	5.906738	1.49E-09	2.01E-08	0.039032	-1	1088	1288	1731	1139	1656	860	751	1027	921	793
ENSMUSG00000045752	chr7	Tssc4	1.43E+08	1.43E+08	1760	1.177869	3.819329	1.49E-09	2.01E-08	0.040133	1	95	149	182	107	190	407	513	366	550	421
ENSMUSG00000070000	chr8	Fcho1	71708387	71708831	4467	3.752161	-0.4902	1.49E-09	2.01E-08	0.176993	1	5	0	1	0	0	23	13	16	29	43
ENSMUSG00000024621	chr18	Csf1r	61105572	61105684	4885	1.490992	6.089428	1.51E-09	2.03E-08	0.069074	1	549	253	618	544	1121	1730	2778	1715	3051	2557
ENSMUSG00000093701	chr16	Gm21970	91391721	91391878	884	1.134925	3.785704	1.56E-09	2.09E-08	0.037044	1	108	105	156	169	184	314	387	353	598	569
ENSMUSG00000043263	chr1	Pyhin1	1.74E+08	1.74E+08	3547	2.503652	2.194093	1.59E-09	2.14E-08	0.16723	1	15	9	25	27	38	234	133	58	143	275
ENSMUSG00000032849	chr14	Abcc4	1.18E+08	1.18E+08	5729	-1.01162	4.112714	1.65E-09	2.22E-08	0.030147	-1	361	270	444	377	493	206	242	268	302	320
ENSMUSG00000074925	chr19	Ptar1	23687400	23687545	2064	-1.76184	0.897352	1.68E-09	2.25E-08	0.064158	-1	42	30	56	41	69	18	20	18	24	16
ENSMUSG00000004319	chr8	Clcn3	60910389	60913175	17071	-0.98764	5.432442	1.71E-09	2.29E-08	0.030443	-1	836	879	1032	1026	998	547	640	799	707	668
ENSMUSG00000052688	chr1	5430435G22Rik	1.32E+08	1.32E+08	4624	1.743008	4.001641	1.72E-09	2.3E-08	0.090546	1	114	73	145	103	186	291	395	321	1079	896
ENSMUSG00000085295	chr4	4930430E12Rik	6352105	6352529	1135	4.910828	0.482336	1.72E-09	2.3E-08	0.421602	1	0	1	0	4	1	22	20	8	98	140
ENSMUSG00000002020	chr12	Ltbp2	84783212	84784395	8184	2.899124	2.571661	1.75E-09	2.33E-08	0.224402	1	18	11	16	21	51	98	201	50	447	450
ENSMUSG00000026004	chr1	Kansl1l	66719248	66721006	6664	-1.04638	4.658294	1.75E-09	2.33E-08	0.033419	-1	514	474	612	541	707	312	417	481	398	301
ENSMUSG00000020413	chr11	Hus1	8993137	8996346	6450	-1.02718	3.520432	1.76E-09	2.34E-08	0.029378	-1	216	205	299	252	319	154	186	148	204	184
ENSMUSG00000034981	chr5	Parm1	91517615	91517957	5068	-1.29858	5.128443	1.76E-09	2.34E-08	0.052543	-1	590	896	1090	766	803	401	364	326	574	698
ENSMUSG00000079278	chr5	Tmem233	1.16E+08	1.16E+08	2477	-1.166	7.416049	1.76E-09	2.34E-08	0.0435	-1	3812	3508	4784	3799	3696	2466	2332	1765	2639	2926
ENSMUSG00000020137	chr10	Thap2	1.15E+08	1.15E+08	3408	-1.25706	2.362329	1.81E-09	2.41E-08	0.040215	-1	109	102	138	124	127	51	81	71	87	63
ENSMUSG00000057135	chr11	Scimp	70790932	70791638	1080	3.88806	-0.60534	1.85E-09	2.45E-08	0.193787	1	1	1	0	3	0	26	25	6	18	37
ENSMUSG00000011008	chr3	Mcoln2	1.46E+08	1.46E+08	3288	2.776894	0.399098	1.85E-09	2.45E-08	0.156469	1	3	1	2	6	13	29	45	22	75	72
ENSMUSG00000042529	chr11	Kcnj12	61022564	61022850	2750	-1.15208	5.364556	1.87E-09	2.48E-08	0.041714	-1	863	832	1155	833	1067	425	543	886	581	539
ENSMUSG00000057716	chr6	Tmem178b	39873271	39873452	9729	-1.75309	1.914182	1.87E-09	2.48E-08	0.081368	-1	85	80	67	143	103	26	45	49	56	26
ENSMUSG00000073155	chr6	1810058I24Rik	35252654	35252782	2784	1.020799	5.817675	1.88E-09	2.49E-08	0.032916	1	539	590	724	618	618	1489	1545	2007	1861	1842
ENSMUSG00000067736	chr1	Gm10222	24612407	24612700	294	-2.34712	1.312869	1.89E-09	2.49E-08	0.140664	-1	55	63	62	113	46	13	11	11	46	17

ENSMUSG00000027360	chr2	Hdc	1.27E+08	1.27E+08	6389	2.514155	-0.14293	1.99E-09	2.63E-08	0.094386	1	2	1	6	4	6	27	22	21	40	43
ENSMUSG00000035232	chrX	Pdk3	93764607	93765255	2561	1.598256	1.877112	1.99E-09	2.63E-08	0.062732	1	23	25	34	26	39	84	126	81	169	168
ENSMUSG00000075590	chr15	Nrbp2	76085595	76087144	2495	1.348465	3.30839	2E-09	2.64E-08	0.052142	1	102	68	104	78	107	189	314	480	329	334
ENSMUSG00000079057	chr8	Cyp4v3	45269671	45270093	6246	1.585394	2.333008	2.04E-09	2.69E-08	0.066555	1	47	26	46	35	50	92	149	144	252	241
ENSMUSG00000035735	chr19	Dagla	10245265	10248624	5747	-1.25191	3.446476	2.05E-09	2.69E-08	0.045622	-1	210	210	258	288	319	126	168	82	216	165
ENSMUSG00000020773	chr11	Trim47	1.16E+08	1.16E+08	2735	1.038947	4.186833	2.05E-09	2.69E-08	0.032246	1	191	132	230	196	248	391	653	515	802	524
ENSMUSG00000006304	chr1	Arpc2	74236084	74236322	2033	0.980729	6.485737	2.05E-09	2.7E-08	0.03089	1	843	875	1112	1052	1159	2177	2705	2242	3612	3241
ENSMUSG00000059070	chr7	Rpl18	45715457	45715842	4042	0.990355	7.451634	2.07E-09	2.71E-08	0.031826	1	1427	1751	2239	1845	2646	4637	5426	4725	6537	5835
ENSMUSG00000048677	chr7	Tpcn2	1.45E+08	1.45E+08	2909	2.094059	2.428175	2.1E-09	2.75E-08	0.122027	1	16	22	31	33	69	102	159	110	323	327
ENSMUSG00000041959	chr3	S100a10	93555080	93555211	1212	1.134104	5.956389	2.13E-09	2.78E-08	0.04103	1	629	535	728	542	817	1495	2224	1279	2757	2319
ENSMUSG00000046743	chr3	Fat4	38886940	38892134	17165	-1.58621	3.929223	2.15E-09	2.8E-08	0.076406	-1	402	161	409	354	626	99	186	273	187	149
ENSMUSG00000030451	chr7	Herc2	56050155	56050302	15440	-1.18265	6.177254	2.18E-09	2.85E-08	0.044882	-1	1500	1282	1823	1774	2063	648	993	1561	1139	858
ENSMUSG00000032046	chr2	Abhd12	1.51E+08	1.51E+08	2823	0.944111	5.204987	2.21E-09	2.88E-08	0.027866	1	354	329	481	460	489	777	1101	1113	1477	1252
ENSMUSG00000082519	chr2	Vamp7-ps	1.74E+08	1.74E+08	655	-1.68412	1.863175	2.23E-09	2.91E-08	0.073758	-1	106	71	109	61	112	29	41	58	41	30
ENSMUSG00000033578	chrX	Tmem35	1.34E+08	1.34E+08	1918	2.604897	1.009354	2.24E-09	2.92E-08	0.15789	1	6	8	7	5	18	49	146	30	86	64
ENSMUSG00000018930	chr11	Ccl4	83662584	83662738	660	3.834037	0.913666	2.25E-09	2.92E-08	0.330775	1	1	2	0	4	12	50	47	15	102	166
ENSMUSG00000013878	chr8	Rnf170	26119368	26119600	5032	-1.00277	4.675529	2.26E-09	2.93E-08	0.031023	-1	498	509	715	540	579	380	389	390	439	364
ENSMUSG00000097415	chr7	AU020206	75769762	75770237	656	2.132135	1.508502	2.25E-09	2.93E-08	0.111972	1	7	24	14	22	15	79	90	56	140	151
ENSMUSG00000042599	chr6	Kdm7a	39136623	39143305	10057	-1.01362	5.204413	2.28E-09	2.96E-08	0.032453	-1	776	668	912	834	926	379	549	731	622	582
ENSMUSG00000036875	chr10	Dna2	62947026	62947169	5878	1.936947	1.075994	2.29E-09	2.97E-08	0.080813	1	15	14	12	8	18	50	83	46	90	97
ENSMUSG00000071068	chr17	Treml2	48300038	48300596	4509	4.836955	-0.10707	2.34E-09	3.02E-08	0.376147	1	1	0	0	0	3	34	18	4	31	87
ENSMUSG00000060961	chr5	Slc4a4	88886818	88887324	10815	-1.51125	3.074689	2.43E-09	3.14E-08	0.067309	-1	153	161	310	204	225	50	105	63	165	143
ENSMUSG00000027333	chr2	Smox	1.31E+08	1.31E+08	3894	-1.9998	6.86188	2.49E-09	3.21E-08	0.124319	-1	1899	4202	4720	3197	1196	1184	813	754	1122	1452
ENSMUSG00000021779	chr14	Thrb	17660960	17661024	6555	-1.23613	3.299531	2.5E-09	3.22E-08	0.044163	-1	180	211	247	260	252	119	96	165	130	165
ENSMUSG00000057924	chr8	Gm10033	69372145	69372612	654	-1.84044	0.898432	2.56E-09	3.3E-08	0.077362	-1	41	49	63	36	49	7	23	16	30	19
ENSMUSG00000095306	chr8	Gm21807	68099492	68099560	897	-2.05092	0.003082	2.58E-09	3.33E-08	0.06924	-1	22	19	32	24	32	5	6	7	11	14
ENSMUSG00000090124	chr1	Ugt1a7c	88095062	88095303	4219	2.132258	2.571576	2.66E-09	3.42E-08	0.128971	1	37	15	23	35	73	111	133	205	281	393
ENSMUSG00000055737	chr15	Ghr	3317760	3320722	9053	-1.0164	6.767939	2.7E-09	3.47E-08	0.033852	-1	2419	1991	2579	2437	2719	1150	1523	1640	2020	2167
ENSMUSG00000035840	chr13	Lysmd3	81657806	81657936	3124	-1.52418	2.210649	2.71E-09	3.48E-08	0.063597	-1	103	81	117	124	149	23	70	71	70	48
ENSMUSG00000025508	chr7	Rplp2	1.41E+08	1.41E+08	2072	1.054508	7.73707	2.74E-09	3.52E-08	0.036634	1	1651	2375	2824	2035	2753	6140	6827	5773	7211	7367
ENSMUSG00000036879	chr8	Phkb	85840959	85841103	7417	-1.1876	8.172129	2.76E-09	3.54E-08	0.04634	-1	6154	6274	8043	6197	6638	3757	3484	5646	3799	3513
ENSMUSG00000038143	chr8	Stox2	47180048	47186572	10839	-1.13559	3.723338	2.76E-09	3.54E-08	0.038581	-1	221	215	325	371	403	119	217	233	205	194
ENSMUSG00000096842	chr13	Gm10736	1.12E+08	1.12E+08	78	1.054826	5.380328	2.78E-09	3.56E-08	0.035615	1	368	414	626	374	483	1096	1394	986	1601	1480
ENSMUSG00000032878	chr11	Ccdc85a	28385685	28388948	6971	-1.603	2.922682	2.86E-09	3.66E-08	0.075474	-1	140	168	235	274	126	56	82	130	98	73
ENSMUSG00000028654	chr4	Mycl	1.23E+08	1.23E+08	4038	2.153847	1.222036	2.91E-09	3.72E-08	0.110635	1	13	16	5	8	24	50	125	72	102	71
ENSMUSG00000027962	chr3	Vcam1	1.16E+08	1.16E+08	3398	1.136854	3.841035	2.92E-09	3.73E-08	0.038777	1	140	111	181	133	181	328	548	301	623	510
ENSMUSG00000008496	chr7	Pou2f2	25087344	25093002	8231	2.234661	0.833786	2.94E-09	3.75E-08	0.113509	1	8	3	8	13	16	33	81	35	89	83
ENSMUSG00000030657	chr7	Xylt1	1.17E+08	1.17E+08	3822	-2.08068	0.960607	3.02E-09	3.85E-08	0.104958	-1	48	27	51	44	94	8	12	13	30	24
ENSMUSG00000029575	chr5	Mmab	1.14E+08	1.14E+08	3530	-0.95481	4.846883	3.04E-09	3.87E-08	0.028742	-1	561	530	713	666	699	419	430	395	539	489
ENSMUSG00000019988	chr10	Nedd1	92684746	92686295	3534	-0.99819	4.199949	3.09E-09	3.93E-08	0.030656	-1	387	378	437	424	397	208	281	334	362	253
ENSMUSG00000085022	chr4	Gm5860	82065431	82066040	2714	-1.56878	2.334408	3.14E-09	3.99E-08	0.068091	-1	100	154	129	109	126	68	68	46	62	45
ENSMUSG00000048578	chr5	Mlec	1.15E+08	1.15E+08	6010	-1.02848	8.466308	3.25E-09	4.13E-08	0.035324	-1	6966	6270	9614	6965	10262	4634	6312	4029	6460	5726
ENSMUSG00000096764	chr2	Gm21985	1.12E+08	1.12E+08	4532	-1.99138	3.803651	3.35E-09	4.25E-08	0.121706	-1	375	251	435	399	408	31	134	271	148	88
ENSMUSG00000033467	chr5	Crlf2	1.1E+08	1.1E+08	1325	1.401467	2.497563	3.38E-09	4.27E-08	0.053465	1	41	49	63	46	53	142	175	124	282	223
ENSMUSG00000060096	chr18	Amd-ps3	64448519	64450014	1496	-2.76694	0.894148	3.37E-09	4.27E-08	0.189397	-1	30	72	78	66	17	11	17	4	10	12
ENSMUSG00000024339	chr17	Tap2	34203527	34204623	3781	1.385103	4.103476	3.38E-09	4.28E-08	0.060102	1	117	125	165	192	196	448	523	296	760	881
ENSMUSG00000047407	chr17	Tgif1	70844205	70845272	5625	1.539783	2.876871	3.43E-09	4.34E-08	0.069041	1	53	38	66	72	82	144	194	411	275	236
ENSMUSG00000040596	chr1	Pogk	1.66E+08	1.66E+08	9586	-0.99177	3.824086	3.49E-09	4.4E-08	0.029665	-1	272	313	312	300	366	159	255	186	281	232
ENSMUSG00000042759	chr7	Apobr	1.27E+08	1.27E+08	3779	2.213493	2.211162	3.51E-09	4.43E-08	0.137108	1	21	16	16	33	48	102	134	73	272	301
ENSMUSG00000039599	chr14	Fam149b	20348162	20348394	3146	-0.90513	4.042524	3.55E-09	4.47E-08	0.024663	-1	317	316	382	366	407	207	282	266	317	267
ENSMUSG00000034855	chr5	Cxcl10	92346638	92347385	1520	3.969951	1.885774	3.63E-09	4.57E-08	0.385222	1	7	1	7	10	11	297	54	23	74	265
ENSMUSG00000061603	chr12	Akap6	52699383	52699442	10263	-1.03703	5.762531	3.64E-09	4.58E-08	0.035325	-1	1045	905	1351	1344	1501	713	1053	647	999	736
ENSMUSG00000044066	chr11	Cep68	20227037	20229481	5865	-1.06145	4.839484	3.67E-09	4.61E-08	0.036235	-1	516	554	778	719	671	297	420	585	514	360
ENSMUSG00000085272	chr7	Sbk3	4965260	4968026	3197	3.063478	-0.16844	3.66E-09	4.61E-08	0.159493	1	2	1	3	2	5	12	66	25	35	20
ENSMUSG00000021814	chr14	Anxa7	20455261	20456601	2965	1.211325	6.026333	3.81E-09	4.78E-08	0.048353	1	671	504	737	582	789	1374	1913	3295	2196	1858
ENSMUSG00000052248	chr2	Zeb2os	45111138	45111302	1388	1.710312	1.727241	3.85E-09	4.82E-08	0.075772	1	12	20	36	30	27	92	92	78	163	146
ENSMUSG00000049606	chr5	Zfp644	1.07E+08	1.07E+08	8803	-1.24553	4.03782	3.85E-09	4.83E-08	0.048984	-1	325	298	444	405	470	122	257	353	217	193
ENSMUSG00000034290	chr12	Nek9	85299514	85301926	5386	-0.99719	7.386741	3.86E-09	4.83E-08	0.033395	-1	3003	3485	4567	3690	3891	2333	2595	2810	2702	2469
ENSMUSG00000063450	chr12	Syne2	75818134	75818188	26726	-0.94047	4.548142	3.94E-09	4.93E-08	0.027958	-1	456	406	616	550	543	254	374	421	447	387
ENSMUSG00000046688	chr3	Tifa	1.28E+08	1.28E+08	2527	1.672787	1.840389	4E-09	4.99E-08	0.074392	1	20	13	43	26	38	87	121	101	128	175
ENSMUSG00000008475	chr1	Arpc5	1.53E+08	1.53E+08	2276	1.299464	5.503012	4.06E-09	5.07E-08	0.055363	1	342	387	437	412	626	975	1243	913	2438	2153
ENSMUSG00000090171	chr1	Ugt1a2	88200601	88201500	2211	2.314891	2.279965	4.11E-09	5.12E-08	0.152456	1	28	7	17	28	54	96	108	154	236	337
ENSMUSG00000041460	chr6	Cacna2d4	1.19E+08	1.19E+08	9478	-2.03578	2.446954	4.11E-09	5.13E-08	0.121135	-1	103	155	179	223	56	49	42	34	72	52
ENSMUSG00000059408	chr17	Mrgprh	12876034	12877842	1809	-1.6633	1.401652	4.13E-09	5.14E-08	0.06751	-1	43	53	81	84	72	31	23	29	27	33
ENSMUSG00000071379	chr12	Hpcal1	17690814	17691046	1561	1.150607	3.664756	4.13E-09	5.14E-08	0.040025	1	102	92	134	165	164	264	422	309	545	514
ENSMUSG00000042724	chr12	Map3k9	81714950	81722523	10619	2.656764	-0.05229	4.16E-09	5.17E-08	0.112684	1	2	6	1	7	2	16	45	37	44	26

ENSMUSG00000006333	chr7	Rps9	3703993	3704064	2526	0.946561	8.420816	4.2E-09	5.22E-08	0.030417	1	3229	3733	4579	3567	4472	8973	10443	10129	11335	11518
ENSMUSG00000041762	chr2	Gpr155	73341506	73343757	6679	-1.0354	4.161233	4.21E-09	5.22E-08	0.033564	-1	358	330	453	384	488	240	353	209	308	251
ENSMUSG00000022048	chr14	Dpysl2	66802864	66805436	4520	1.139446	4.021658	4.22E-09	5.23E-08	0.040469	1	195	119	180	132	214	440	630	404	570	533
ENSMUSG00000022197	chr15	Pdzd2	12359711	12362239	21645	-1.09197	5.025722	4.26E-09	5.27E-08	0.038985	-1	662	467	815	790	1024	272	513	594	593	493
ENSMUSG00000043008	chr16	Klhl6	19946499	19947292	2606	1.433922	1.830247	4.26E-09	5.27E-08	0.050697	1	21	28	32	39	34	82	121	103	149	132
ENSMUSG00000089675	chr1	Ugt1a8	88087813	88088721	2227	2.313292	2.278667	4.28E-09	5.28E-08	0.152589	1	28	7	17	28	54	96	108	153	236	337
ENSMUSG00000089943	chr1	Ugt1a5	88166012	88166903	2203	2.313291	2.278667	4.28E-09	5.28E-08	0.152573	1	28	7	17	28	54	96	108	153	236	337
ENSMUSG00000089960	chr1	Ugt1a1	88211959	88212871	2224	2.313291	2.278667	4.27E-09	5.28E-08	0.152567	1	28	7	17	28	54	96	108	153	236	337
ENSMUSG00000090165	chr1	Ugt1a10	88055388	88055664	2267	2.313292	2.278667	4.29E-09	5.28E-08	0.152597	1	28	7	17	28	54	96	108	153	236	337
ENSMUSG00000090175	chr1	Ugt1a9	88070800	88071678	2190	2.313292	2.278667	4.28E-09	5.28E-08	0.152589	1	28	7	17	28	54	96	108	153	236	337
ENSMUSG00000090145	chr1	Ugt1a6b	88103252	88103378	2382	2.326086	2.29968	4.34E-09	5.34E-08	0.154856	1	28	7	17	29	54	96	109	154	240	347
ENSMUSG00000026880	chr2	Stom	35313986	35316055	2787	1.167312	5.97624	4.35E-09	5.34E-08	0.04525	1	425	630	692	834	651	1488	1675	1672	2779	2672
ENSMUSG00000033209	chr5	Ttc28	1.11E+08	1.11E+08	12315	-1.15107	4.598833	4.35E-09	5.34E-08	0.0429	-1	470	389	620	615	729	199	311	511	437	322
ENSMUSG00000025185	chr19	Loxl4	42593982	42595404	4213	-1.83866	2.397606	4.36E-09	5.36E-08	0.099243	-1	157	64	190	67	223	38	60	53	75	44
ENSMUSG00000039701	chr3	Usp53	1.23E+08	1.23E+08	4014	-1.78004	2.807154	4.38E-09	5.37E-08	0.095235	-1	144	180	175	199	201	41	64	149	72	42
ENSMUSG00000055775	chr11	Myh8	67277124	67277234	11772	1.195905	9.292415	4.38E-09	5.37E-08	0.048303	1	3800	6052	6064	7012	9377	19957	20548	19545	26389	14822
ENSMUSG00000041431	chr13	Ccnb1	1.01E+08	1.01E+08	4217	1.84108	1.958019	4.4E-09	5.38E-08	0.093338	1	18	14	38	22	48	93	113	86	243	165
ENSMUSG00000074519	chr2	Etohi1	1.78E+08	1.78E+08	2145	-1.769	1.872594	4.4E-09	5.38E-08	0.086488	-1	71	58	163	56	135	24	46	43	45	35
ENSMUSG00000041180	chr19	Hectd2	36554639	36554915	9066	-1.40116	1.792934	4.41E-09	5.39E-08	0.050174	-1	72	64	90	83	109	28	57	43	53	40
ENSMUSG00000033715	chr13	Akr1c14	4049011	4049132	2973	-1.55745	1.185835	4.42E-09	5.4E-08	0.056099	-1	42	48	62	66	61	20	21	24	39	29
ENSMUSG00000024241	chr17	Sos1	80393752	80398672	8919	-0.96968	4.556001	4.61E-09	5.62E-08	0.030064	-1	430	456	559	571	583	283	397	445	420	309
ENSMUSG00000024349	chr18	Tmem173	35733678	35734698	2302	1.424028	3.305107	4.62E-09	5.63E-08	0.061693	1	69	70	109	82	117	256	437	159	489	340
ENSMUSG00000020986	chr12	Sec23a	58958383	58960086	4840	-1.04908	6.490345	4.64E-09	5.65E-08	0.037043	-1	1926	1565	2448	1792	2454	1031	1479	1739	1423	1150
ENSMUSG00000026278	chr1	Bok	93685660	93685854	1775	1.660669	2.295974	4.7E-09	5.71E-08	0.077697	1	26	42	46	25	53	108	248	104	240	160
ENSMUSG00000033186	chr14	Mzt1	99034544	99036510	2256	-0.955	4.854402	4.74E-09	5.76E-08	0.029572	-1	585	568	712	613	698	352	460	558	515	410
ENSMUSG00000027763	chr3	Mbnl1	60472830	60472884	18717	-1.07856	7.919318	4.76E-09	5.78E-08	0.039552	-1	4826	4763	6434	5425	6025	2784	3194	5085	3639	3372
ENSMUSG00000070565	chr1	Rasal2	1.57E+08	1.57E+08	13740	-1.16486	3.489103	4.76E-09	5.78E-08	0.041431	-1	227	198	288	331	247	96	183	198	193	145
ENSMUSG00000037966	chr13	Ninj1	49187485	49187637	1570	1.19712	4.424938	4.82E-09	5.84E-08	0.046301	1	130	174	257	211	338	478	555	585	947	960
ENSMUSG00000042228	chr4	Lyn	3678115	3678364	4073	1.153335	4.096978	4.89E-09	5.92E-08	0.042073	1	122	170	185	205	199	387	564	359	806	669
ENSMUSG00000046865	chr7	Fbl	28169748	28169818	1159	1.043563	4.523461	4.92E-09	5.96E-08	0.034944	1	181	236	275	254	309	576	585	577	978	910
ENSMUSG00000039747	chr5	Orai2	1.36E+08	1.36E+08	3846	1.454048	2.124233	4.96E-09	6E-08	0.056543	1	32	22	46	37	54	86	187	134	177	147
ENSMUSG00000041134	chr16	Cyyr1	85421533	85422341	8894	-1.86446	3.213228	5.02E-09	6.06E-08	0.107777	-1	182	206	259	357	204	27	83	175	101	90
ENSMUSG00000045763	chr15	Basp1	25363285	25364918	1847	1.760213	3.311481	5.11E-09	6.16E-08	0.096073	1	51	39	100	52	146	266	337	167	546	479
ENSMUSG00000030427	chr7	Lilra6	3908280	3908822	2896	2.720144	0.136231	5.12E-09	6.17E-08	0.151943	1	4	0	4	3	10	25	24	23	62	63
ENSMUSG00000047213	chr3	Ythdf3	16183212	16183520	5363	-0.99138	5.572295	5.19E-09	6.26E-08	0.032847	-1	908	836	1199	1120	1254	485	747	962	919	641
ENSMUSG00000030223	chr6	Ptpro	1.37E+08	1.37E+08	6744	1.732028	1.912307	5.2E-09	6.26E-08	0.081088	1	29	19	17	22	54	107	136	95	160	152
ENSMUSG00000055865	chr3	Fam19a3	1.05E+08	1.05E+08	4484	-1.32941	3.133079	5.28E-09	6.35E-08	0.053665	-1	192	184	247	234	179	116	107	75	177	107
ENSMUSG00000059479	chr7	B3gnt8	25627624	25627722	1475	1.785012	1.399607	5.32E-09	6.4E-08	0.079367	1	16	9	24	25	20	67	112	54	127	96
ENSMUSG00000037674	chr9	Rfx7	72532240	72532980	15302	-1.06583	4.662107	5.34E-09	6.41E-08	0.037096	-1	521	392	684	637	644	289	360	508	448	306
ENSMUSG00000060591	chr7	Ifitm2	1.41E+08	1.41E+08	627	1.075223	5.894401	5.41E-09	6.49E-08	0.038889	1	577	458	626	671	892	1466	1884	1329	2695	2147
ENSMUSG00000039208	chr11	Metrnl	1.22E+08	1.22E+08	1586	1.415728	4.110806	5.45E-09	6.53E-08	0.064589	1	156	115	153	134	228	419	550	284	981	751
ENSMUSG00000022525	chr16	Hrasls	29209695	29209809	3286	-1.1298	5.533062	5.49E-09	6.57E-08	0.042727	-1	967	1041	1133	1186	905	727	650	623	670	645
ENSMUSG00000079105	chr15	C7	4988762	4989006	2709	-2.13836	1.893244	5.52E-09	6.6E-08	0.132076	-1	97	89	125	143	39	16	45	31	51	21
ENSMUSG00000020697	chr11	Lig3	82781108	82781276	7284	-0.91255	5.028915	5.53E-09	6.61E-08	0.027356	-1	631	583	800	715	842	387	562	604	606	491
ENSMUSG00000034792	chr10	Gna15	81502306	81503105	2135	2.16446	0.559769	5.55E-09	6.63E-08	0.097576	1	13	3	7	6	11	46	55	30	76	48
ENSMUSG00000039891	chr10	Txlnb	17796226	17796421	5504	-1.31963	8.157574	5.68E-09	6.78E-08	0.059238	-1	6244	5583	7841	7907	6332	2838	3421	6284	3579	2810
ENSMUSG00000048612	chr19	Myof	37899036	37899767	7109	1.502368	4.883565	5.87E-09	7E-08	0.074557	1	242	132	304	209	428	512	1186	641	1779	1160
ENSMUSG00000099764	chr16	Rps10-ps2	20822145	20822640	496	1.033193	3.287139	6.05E-09	7.21E-08	0.031038	1	81	93	137	95	126	248	318	284	359	302
ENSMUSG00000087150	chr6	BC064078	1.29E+08	1.29E+08	2489	2.595058	-0.36893	6.19E-09	7.37E-08	0.099837	1	0	2	6	2	5	14	35	23	26	31
ENSMUSG00000029401	chr5	Rilpl2	1.24E+08	1.24E+08	1391	1.819878	3.131909	6.2E-09	7.37E-08	0.102211	1	55	47	82	63	72	134	190	213	503	588
ENSMUSG00000041992	chr12	Rapgef5	1.18E+08	1.18E+08	3987	-1.93801	1.352157	6.23E-09	7.4E-08	0.102567	-1	40	50	93	102	51	12	27	22	44	20
ENSMUSG00000051285	chr1	Pcmtd1	7088920	7089216	6654	-0.99406	5.755364	6.23E-09	7.4E-08	0.03349	-1	1131	1032	1358	1238	1219	615	791	1080	911	819
ENSMUSG00000039262	chr2	Prrc2b	32151082	32151291	11262	-0.94906	7.630581	6.31E-09	7.49E-08	0.031199	-1	3703	3392	4888	4591	5419	2480	3517	3438	3589	2765
ENSMUSG00000024835	chr19	Coro1b	4148619	4148722	2372	1.116256	5.26375	6.34E-09	7.51E-08	0.041774	1	334	316	425	453	506	810	1144	852	1733	1702
ENSMUSG00000028053	chr3	Ash1l	88950622	88950995	13076	-1.16396	5.395911	6.72E-09	7.95E-08	0.045867	-1	887	689	1079	1033	1213	373	597	927	673	483
ENSMUSG00000050310	chr15	Rictor	6708381	6708451	9311	-1.07763	3.540615	6.76E-09	8E-08	0.03593	-1	234	177	314	255	353	103	199	194	194	189
ENSMUSG00000060206	chr4	Zfp462	54945048	54945101	10702	-1.08036	3.70457	6.96E-09	8.23E-08	0.036632	-1	260	219	276	365	359	142	228	211	247	153
ENSMUSG00000039323	chr1	Igfbp2	72824503	72824964	1847	2.481926	0.355871	7.04E-09	8.31E-08	0.127902	1	7	6	4	4	7	31	73	17	54	51
ENSMUSG00000037563	chr7	Rps16	28350652	28350851	807	0.944062	6.993351	7.1E-09	8.37E-08	0.030916	1	1156	1311	1516	1433	1905	3395	4056	3370	4754	3963
ENSMUSG00000020620	chr11	Abca8b	1.1E+08	1.1E+08	7423	-1.10707	4.805886	7.11E-09	8.38E-08	0.040966	-1	721	455	635	608	758	327	497	475	370	381
ENSMUSG00000036450	chr19	Hif1an	44562850	44563054	6606	-0.95094	7.77569	7.18E-09	8.46E-08	0.031579	-1	4239	3925	5840	4757	5483	2919	3412	3970	3611	3414
ENSMUSG00000019139	chr8	Isyna1	70594481	70594543	1836	1.761962	3.674824	7.23E-09	8.5E-08	0.099594	1	49	55	86	135	171	255	701	239	687	458
ENSMUSG00000052155	chr2	Acvr2a	48814109	48814826	5686	-1.27374	4.824846	7.22E-09	8.5E-08	0.054562	-1	571	491	710	699	916	201	403	615	460	284
ENSMUSG00000033960	chr18	9430020K01Rik	4634929	4635031	6730	-1.02794	5.118177	7.33E-09	8.61E-08	0.035715	-1	636	641	891	979	739	335	616	521	746	498
ENSMUSG00000030654	chr7	Arl6ip1	1.18E+08	1.18E+08	2134	1.181756	4.93349	7.46E-09	8.76E-08	0.046926	1	267	263	301	282	456	685	873	640	1510	1331
ENSMUSG00000046345	chr16	Smco1	32271468	32271658	1408	-1.16845	5.378107	7.48E-09	8.78E-08	0.046427	-1	900	922	1170	969	787	638	555	422	687	642

ENSMUSG00000052087	chr13	Rgs14	55369732	55369936	2490	2.392993	0.832993	7.51E-09	8.8E-08	0.136985	1	7	6	8	12	10	37	70	21	100	99
ENSMUSG00000058690	chr14	Ccser2	36874936	36879762	8715	-0.94331	6.564524	7.57E-09	8.86E-08	0.030863	-1	1832	1621	2332	2232	2434	1327	1457	1632	1755	1351
ENSMUSG00000039652	chr19	Cpeb3	37021291	37025087	7414	-1.00238	4.880915	7.58E-09	8.88E-08	0.033673	-1	523	561	765	681	769	333	381	613	533	435
ENSMUSG00000024856	chr19	Cdk2ap2	4097182	4097507	1636	0.906267	4.320584	7.59E-09	8.88E-08	0.026268	1	180	215	250	243	268	499	563	605	703	650
ENSMUSG00000021952	chr14	Xpo4	57581002	57582468	7266	-1.52562	2.314728	7.66E-09	8.95E-08	0.06887	-1	108	89	127	132	162	23	72	86	72	50
ENSMUSG00000022636	chr16	Alcam	52248996	52251646	7121	2.82675	2.163551	7.79E-09	9.09E-08	0.22864	1	20	10	9	9	42	82	96	64	364	319
ENSMUSG00000039242	chr13	B3galnt2	13954674	13954919	3681	-1.10668	6.286329	7.9E-09	9.21E-08	0.042355	-1	1280	1711	2330	1663	1974	1204	1259	908	1139	1155
ENSMUSG00000092243	chr17	Gm7030	36109719	36109732	927	6.571079	1.161016	7.91E-09	9.21E-08	0.767513	1	2	0	1	0	0	84	119	1	16	242
ENSMUSG00000041362	chr19	4930506M07Rik	58973358	58975208	4081	1.527607	2.090977	8.03E-09	9.35E-08	0.064818	1	32	21	31	45	49	81	116	162	199	169
ENSMUSG00000026630	chr1	Batf3	1.91E+08	1.91E+08	1597	2.524657	-0.34867	8.08E-09	9.4E-08	0.09921	1	3	0	3	3	7	27	30	20	23	28
ENSMUSG00000052776	chr5	Oas1a	1.21E+08	1.21E+08	1885	2.839436	2.4349	8.21E-09	9.54E-08	0.233857	1	21	15	22	25	24	262	150	28	173	427
ENSMUSG00000040462	chr10	Os9	1.27E+08	1.27E+08	4049	1.073458	5.144166	8.23E-09	9.56E-08	0.039159	1	310	259	375	367	626	753	991	1055	1509	1356
ENSMUSG00000046798	chr5	Cldn12	5505015	5508454	4169	-0.94152	4.277066	8.26E-09	9.58E-08	0.028851	-1	397	395	455	360	515	234	307	360	369	281
ENSMUSG00000026932	chr2	Nacc2	26055535	26060473	7815	-0.9714	5.305592	8.31E-09	9.63E-08	0.032175	-1	645	794	996	882	1090	482	774	488	732	652
ENSMUSG00000046722	chr3	Cdc42se1	95228732	95228865	3258	0.94314	5.080089	8.31E-09	9.63E-08	0.029935	1	330	313	444	393	457	700	1045	864	1449	1209
ENSMUSG00000061859	chr4	Inadl	98395785	98395837	13086	2.104943	1.859501	8.4E-09	9.72E-08	0.126824	1	22	8	26	28	26	69	257	98	159	85
ENSMUSG00000062585	chr4	Cnr2	1.36E+08	1.36E+08	3982	2.146693	0.588493	8.44E-09	9.76E-08	0.10398	1	1	8	9	11	13	30	45	40	71	77
ENSMUSG00000001998	chr2	Ap4e1	1.27E+08	1.27E+08	9810	-1.2135	3.102769	8.56E-09	9.9E-08	0.04557	-1	183	160	218	192	250	64	118	169	146	113
ENSMUSG00000006390	chr4	Elovl1	1.18E+08	1.18E+08	2726	1.094277	4.232282	8.82E-09	1.02E-07	0.039533	1	152	145	219	192	306	384	619	445	912	679
ENSMUSG00000055296	chr4	Tmem245	56866923	56880292	17090	-1.01746	5.340307	8.93E-09	1.03E-07	0.035551	-1	992	684	904	926	992	453	643	775	711	552
ENSMUSG00000034641	chr11	Cd300ld	1.15E+08	1.15E+08	2645	1.667701	2.287094	9.04E-09	1.04E-07	0.080898	1	39	39	37	28	44	119	208	82	206	233
ENSMUSG00000022577	chr15	Ly6h	75551268	75552255	4011	3.354271	-0.64612	9.1E-09	1.05E-07	0.162559	1	1	2	2	1	1	20	21	4	34	29
ENSMUSG00000038274	chr19	Fau	6057888	6058001	815	0.929489	6.880671	9.17E-09	1.05E-07	0.03039	1	1109	1282	1606	1209	1585	2967	3380	3507	4163	3995
ENSMUSG00000027652	chr2	Ralgapb	1.58E+08	1.58E+08	12992	-0.90147	5.392454	9.19E-09	1.06E-07	0.027857	-1	781	744	1035	880	1163	498	734	774	796	629
ENSMUSG00000031147	chrX	Magix	7673164	7675191	2910	-1.40259	3.744576	9.23E-09	1.06E-07	0.064491	-1	284	338	313	437	213	172	116	193	200	166
ENSMUSG00000038178	chr11	Slc43a2	75531694	75531822	10042	1.136175	5.272109	9.31E-09	1.07E-07	0.044335	1	249	331	376	552	528	759	1107	1426	1551	1429
ENSMUSG00000033526	chr2	Ppip5k1	1.21E+08	1.21E+08	12486	-1.0498	5.579774	9.37E-09	1.07E-07	0.038195	-1	967	979	1163	1360	846	536	756	723	971	686
ENSMUSG00000038352	chr11	Arl5c	97989578	97990339	2073	1.966754	0.814075	9.4E-09	1.08E-07	0.09072	1	7	7	12	6	24	47	71	44	64	74
ENSMUSG00000032020	chr9	Ubash3b	41011098	41015036	7326	1.829992	2.277178	9.43E-09	1.08E-07	0.100675	1	23	18	34	36	66	97	183	90	265	244
ENSMUSG00000038485	chr11	Socs7	97362551	97363423	7265	-0.93673	6.381282	9.43E-09	1.08E-07	0.03076	-1	1529	1529	2242	1878	2007	1173	1366	1405	1467	1220
ENSMUSG00000052760	chr1	A630001G21Rik	85717083	85718368	2709	2.352597	0.673597	9.46E-09	1.08E-07	0.130059	1	9	7	5	4	14	28	70	27	77	86
ENSMUSG00000028583	chr4	Pdpn	1.43E+08	1.43E+08	1817	1.542184	4.348681	9.5E-09	1.09E-07	0.079933	1	134	111	183	154	306	459	629	334	1283	934
ENSMUSG00000034525	chr13	Ice1	70588689	70589812	7675	-1.01634	5.311319	9.58E-09	1.09E-07	0.035558	-1	851	601	1022	835	1175	477	701	713	604	554
ENSMUSG00000070034	chr1	Sp110	85576899	85577345	6781	1.969904	2.727811	9.73E-09	1.11E-07	0.120812	1	31	30	52	53	57	267	182	84	242	405
ENSMUSG00000034377	chr17	Tulp4	6106437	6106582	18054	-1.01968	6.266897	1E-08	1.14E-07	0.036541	-1	1557	1247	1901	1824	2154	810	1291	1530	1254	1068
ENSMUSG00000093674	chr10	Rpl41	1.29E+08	1.29E+08	1168	0.949785	7.885698	1E-08	1.14E-07	0.03213	1	2112	2632	2748	2723	3270	6199	7238	6009	9243	7760
ENSMUSG00000021262	chr12	Evl	1.09E+08	1.09E+08	2695	1.332706	3.969797	1.01E-08	1.15E-07	0.058747	1	108	95	197	178	171	344	470	301	849	702
ENSMUSG00000007659	chr2	Bcl2l1	1.53E+08	1.53E+08	4586	1.130591	4.291406	1.02E-08	1.15E-07	0.042694	1	148	189	254	194	241	411	493	487	922	871
ENSMUSG00000054404	chr11	Slfn5	82951349	82951481	4427	-1.09853	4.7186	1.04E-08	1.18E-07	0.041241	-1	476	400	662	765	728	279	421	271	512	496
ENSMUSG00000070031	chr1	Sp140	85600378	85600599	3328	1.89183	1.655506	1.05E-08	1.19E-07	0.099879	1	20	8	28	22	30	95	101	57	133	166
ENSMUSG00000001082	chr5	Mfsd10	34633642	34634014	2752	1.28194	2.681326	1.08E-08	1.23E-07	0.048845	1	59	48	61	51	88	154	196	156	317	232
ENSMUSG00000068130	chr2	Zfp442	1.5E+08	1.5E+08	2922	-2.04913	-0.10384	1.09E-08	1.24E-07	0.075884	-1	23	18	26	18	34	5	9	6	15	5
ENSMUSG00000032312	chr9	Csk	57626647	57627503	2748	1.113957	4.262225	1.1E-08	1.24E-07	0.041585	1	166	155	197	206	294	429	655	391	879	744
ENSMUSG00000054545	chr1	Ugt1a6a	88134809	88134935	4312	2.240951	2.373073	1.11E-08	1.25E-07	0.15316	1	29	9	19	31	62	97	109	167	255	361
ENSMUSG00000007872	chr4	Id3	1.36E+08	1.36E+08	1791	0.91916	4.618005	1.11E-08	1.26E-07	0.028234	1	251	263	330	253	313	559	785	748	1027	651
ENSMUSG00000034845	chr8	Plvap	71497754	71498405	2015	1.155768	4.569215	1.12E-08	1.26E-07	0.045465	1	171	215	246	287	312	546	640	516	1170	1010
ENSMUSG00000021668	chr13	Polk	96480689	96482254	4289	-1.48939	3.068062	1.12E-08	1.27E-07	0.071165	-1	132	248	302	195	144	91	129	86	124	81
ENSMUSG00000031934	chr9	Panx1	15005161	15006217	2997	1.280385	3.461215	1.12E-08	1.27E-07	0.053005	1	79	74	126	118	141	385	401	215	457	322
ENSMUSG00000029313	chr5	Aff1	1.04E+08	1.04E+08	9458	-0.91364	5.406085	1.13E-08	1.27E-07	0.02905	-1	754	801	1129	951	1006	445	662	746	932	700
ENSMUSG00000022148	chr15	Fyb	6579871	6581046	5186	1.119767	3.472176	1.14E-08	1.28E-07	0.039692	1	94	93	124	111	161	280	365	230	478	416
ENSMUSG00000037012	chr10	Hk1	62268855	62270056	8532	1.081337	4.655531	1.15E-08	1.3E-07	0.039962	1	205	180	256	314	415	629	887	595	1099	805
ENSMUSG00000023809	chr17	Rps6ka2	7170115	7170443	5404	-1.00942	7.037406	1.16E-08	1.31E-07	0.0364	-1	2714	2352	2802	3483	3272	1807	1953	2325	2215	1793
ENSMUSG00000028906	chr4	Epb4.1	1.32E+08	1.32E+08	8809	-1.03098	6.34825	1.17E-08	1.31E-07	0.037707	-1	1454	1667	2171	1790	2090	1088	1099	1625	1247	1120
ENSMUSG00000097697	chr7	4833412C05Rik	67784725	67785292	896	2.715339	-0.15234	1.18E-08	1.32E-07	0.14707	1	2	0	2	1	12	21	36	42	30	25
ENSMUSG00000040856	chr12	Dlk1	1.09E+08	1.09E+08	5657	1.796621	4.204329	1.18E-08	1.33E-07	0.10849	1	83	61	109	105	367	598	564	585	986	599
ENSMUSG00000040550	chr4	Otud6b	14809498	14811748	3387	-0.91628	5.830575	1.2E-08	1.35E-07	0.0296	-1	1041	1189	1429	1226	1310	702	987	1006	1059	854
ENSMUSG00000047146	chr10	Tet1	62804570	62813412	14710	-1.70259	2.843715	1.23E-08	1.38E-07	0.093113	-1	128	88	187	198	348	60	76	39	120	103
ENSMUSG00000024068	chr17	Spast	74338987	74339445	4696	-0.87975	5.670738	1.23E-08	1.38E-07	0.027163	-1	922	929	1254	1121	1312	727	817	785	926	909
ENSMUSG00000047747	chr8	Rnf150	82863356	82864490	9685	-1.02397	5.197816	1.24E-08	1.39E-07	0.036641	-1	909	710	815	824	789	421	587	458	687	689
ENSMUSG00000022014	chr14	Epsti1	77904239	77904664	2317	2.228219	2.159005	1.25E-08	1.4E-07	0.150948	1	20	11	19	30	50	183	150	58	159	262
ENSMUSG00000021223	chr12	Papln	83763634	83763716	5635	-1.9981	1.818704	1.33E-08	1.48E-07	0.120968	-1	56	80	96	148	89	14	46	14	61	35
ENSMUSG00000038679	chr15	Trps1	50654752	50661736	13380	-1.07637	3.450846	1.33E-08	1.49E-07	0.037054	-1	215	198	258	206	373	124	134	191	212	162
ENSMUSG00000090213	chr2	Tmem189	1.68E+08	1.68E+08	3265	0.957416	5.281687	1.34E-08	1.49E-07	0.032056	1	361	346	488	431	603	699	1235	1221	1565	1371
ENSMUSG00000043154	chr9	Ppp2r3a	1.01E+08	1.01E+08	12455	-0.9504	7.949123	1.37E-08	1.52E-07	0.0328	-1	5070	4395	5972	6023	5690	3567	4213	3635	4536	3606
ENSMUSG00000048490	chr16	Nrip1	76287400	76295015	11457	-1.03666	4.69041	1.37E-08	1.52E-07	0.037193	-1	608	450	583	553	696	270	365	543	426	374
ENSMUSG00000025017	chr19	Pik3ap1	41274218	41274353	2615	1.993313	2.04176	1.37E-08	1.52E-07	0.120327	1	19	7	31	33	47	95	115	92	216	236

ENSMUSG00000037759	chr14	Ptger2	44988195	44989807	3684	2.492265	-0.03062	1.38E-08	1.53E-07	0.119403	1	1	3	5	4	8	15	29	22	49	55
ENSMUSG00000035258	chr16	Abi3bp	56477846	56477992	4735	-1.74445	5.97288	1.4E-08	1.56E-07	0.105953	-1	1959	689	1849	1140	2607	428	1201	565	834	388
ENSMUSG00000035448	chr9	Ccr3	1.24E+08	1.24E+08	3273	3.417827	-0.7924	1.41E-08	1.56E-07	0.156185	1	2	1	0	0	3	25	23	10	11	24
ENSMUSG00000056394	chr7	Lig1	13277283	13277529	4268	1.869351	2.722193	1.42E-08	1.57E-07	0.111276	1	38	35	55	20	89	153	197	125	428	316
ENSMUSG00000054263	chr15	Lifr	7129559	7129826	10330	-1.1902	5.602036	1.42E-08	1.57E-07	0.05033	-1	756	1537	1307	961	990	479	699	788	782	725
ENSMUSG00000025429	chr18	Pstpip2	77794545	77794750	1395	-1.22038	4.891276	1.42E-08	1.57E-07	0.052217	-1	575	541	915	609	872	271	369	682	443	319
ENSMUSG00000019966	chr10	Kitl	1E+08	1E+08	5765	-1.21001	4.724032	1.43E-08	1.58E-07	0.051224	-1	442	607	685	837	481	219	348	493	470	358
ENSMUSG00000024816	chr19	Frmd8	5849702	5852742	5082	1.107954	3.278135	1.43E-08	1.58E-07	0.038345	1	91	99	103	89	123	181	293	289	468	332
ENSMUSG00000031333	chrX	Abcb7	1.04E+08	1.04E+08	5905	-0.90484	5.824712	1.43E-08	1.58E-07	0.029159	-1	1046	1043	1374	1379	1331	771	889	940	1168	844
ENSMUSG00000070802	chr7	Pnmal2	16944682	16948828	4147	1.725872	3.726889	1.43E-08	1.58E-07	0.099879	1	76	62	92	97	196	345	812	215	652	355
ENSMUSG00000042500	chr4	Ago4	1.26E+08	1.26E+08	6947	-0.94555	3.995905	1.44E-08	1.59E-07	0.029544	-1	310	299	401	388	346	217	272	268	286	221
ENSMUSG00000052949	chr11	Rnf157	1.16E+08	1.16E+08	9537	-1.22222	5.572845	1.45E-08	1.59E-07	0.053045	-1	801	770	1597	993	1551	582	709	371	831	845
ENSMUSG00000021871	chr14	Pnp	50944302	50944593	3085	1.26751	4.335072	1.45E-08	1.6E-07	0.055379	1	171	138	184	205	298	590	534	391	853	945
ENSMUSG00000086247	chr5	Gm15787	1.1E+08	1.1E+08	2992	-1.68512	1.057588	1.46E-08	1.6E-07	0.0704	-1	51	53	55	48	50	21	18	28	17	27
ENSMUSG00000031626	chr8	Sorbs2	45507788	45507957	19432	-1.06891	4.389003	1.46E-08	1.61E-07	0.039376	-1	488	339	595	498	440	203	380	364	386	260
ENSMUSG00000029168	chr5	Dpysl5	30711564	30712002	6867	-1.50871	1.690958	1.48E-08	1.63E-07	0.063476	-1	75	96	72	62	83	29	42	43	46	34
ENSMUSG00000040321	chr2	Zfp770	1.14E+08	1.14E+08	6793	-1.02643	4.623558	1.51E-08	1.65E-07	0.036541	-1	399	505	662	692	496	308	410	408	444	321
ENSMUSG00000028527	chr4	Ak4	1.01E+08	1.01E+08	4646	-1.08944	3.464859	1.51E-08	1.65E-07	0.038379	-1	201	219	272	274	287	145	179	107	190	198
ENSMUSG00000046908	chr14	Ltb4r1	55765962	55766093	1394	2.707342	-0.35974	1.52E-08	1.67E-07	0.122391	1	1	1	3	3	6	15	23	13	44	38
ENSMUSG00000042505	chr6	Acn9	6956004	6956200	5095	-1.15001	3.187071	1.56E-08	1.7E-07	0.042309	-1	181	184	293	199	186	121	136	107	173	120
ENSMUSG00000028444	chr4	Cntfr	41657498	41658152	2782	-1.07425	4.117607	1.56E-08	1.7E-07	0.039445	-1	420	268	462	340	481	177	343	250	336	211
ENSMUSG00000029992	chr6	Gfpt1	87042846	87043005	7419	-0.98085	5.545514	1.61E-08	1.76E-07	0.03439	-1	872	805	1337	807	1441	530	892	662	906	705
ENSMUSG00000027715	chr3	Ccna2	36564866	36566282	3510	1.656294	3.154789	1.62E-08	1.77E-07	0.090198	1	49	63	56	68	121	237	277	135	569	376
ENSMUSG00000019370	chr7	Calm3	16915379	16916976	2423	-0.98961	8.229457	1.63E-08	1.78E-07	0.035945	-1	6191	5409	7866	6207	7797	4278	4918	3364	5611	5219
ENSMUSG00000045620	chr9	Odf3l1	56848659	56849291	1080	3.122346	0.008121	1.66E-08	1.81E-07	0.20285	1	3	4	3	3	1	17	62	11	29	62
ENSMUSG00000017002	chr2	Slpi	1.64E+08	1.64E+08	1180	2.831276	0.194998	1.68E-08	1.82E-07	0.180656	1	7	0	4	3	6	19	53	14	62	61
ENSMUSG00000021880	chr14	Rnase6	51129068	51129164	1072	2.481209	0.041113	1.7E-08	1.85E-07	0.119659	1	2	7	7	5	1	41	36	20	35	41
ENSMUSG00000034765	chr19	Dusp5	53529109	53529696	2473	1.668186	1.52164	1.7E-08	1.85E-07	0.074985	1	16	21	12	24	36	71	77	91	149	103
ENSMUSG00000042444	chr9	Fam63b	70599014	70605289	8081	-0.85983	4.996597	1.73E-08	1.88E-07	0.025949	-1	607	580	770	733	744	383	531	510	689	558
ENSMUSG00000022221	chr14	Ripk3	55784996	55785351	1964	2.205965	1.637558	1.74E-08	1.89E-07	0.142193	1	12	18	16	28	12	61	122	43	166	189
ENSMUSG00000043940	chr5	Wdfy3	1.02E+08	1.02E+08	15351	-0.94935	5.260616	1.75E-08	1.89E-07	0.032149	-1	776	590	945	860	1086	379	659	704	748	600
ENSMUSG00000013419	chr9	Zfp651	1.22E+08	1.22E+08	6353	-0.93141	6.558137	1.75E-08	1.89E-07	0.031659	-1	1755	1834	2227	2343	2136	1294	1488	1643	1642	1454
ENSMUSG00000033793	chr1	Atp6v1h	5070018	5070144	9746	1.273082	4.696776	1.75E-08	1.9E-07	0.057004	1	224	248	288	231	263	466	605	1401	971	868
ENSMUSG00000022003	chr14	Slc25a30	75761999	75762690	1706	-1.46171	1.902472	1.76E-08	1.91E-07	0.063071	-1	67	95	121	84	86	24	53	48	70	40
ENSMUSG00000054003	chr12	Tdrd9	1.12E+08	1.12E+08	5415	3.150537	-0.52153	1.8E-08	1.94E-07	0.167696	1	2	1	6	0	0	12	43	12	29	23
ENSMUSG00000085980	chr4	Gm12408	45639936	45640101	996	2.209881	0.022879	1.8E-08	1.94E-07	0.091927	1	2	3	4	8	9	26	46	23	47	28
ENSMUSG00000030515	chr7	Tarsl2	65644898	65645214	4095	-1.02392	6.094676	1.81E-08	1.95E-07	0.038088	-1	1248	1425	1885	1564	1519	928	989	1312	1111	867
ENSMUSG00000073557	chr1	Ppp1r12b	1.35E+08	1.35E+08	14983	-0.92339	8.205259	1.81E-08	1.95E-07	0.031556	-1	5014	5562	7252	7317	7286	3785	4453	5495	5662	4421
ENSMUSG00000000386	chr16	Mx1	97447035	97448372	3646	3.328738	1.514154	1.82E-08	1.96E-07	0.310236	1	2	5	7	12	16	168	61	25	57	231
ENSMUSG00000025813	chr7	Homer2	81600481	81610441	11149	-1.11707	4.85269	1.82E-08	1.96E-07	0.044332	-1	520	565	589	940	672	366	487	321	585	378
ENSMUSG00000079110	chr2	Capn3	1.2E+08	1.2E+08	5023	-0.99314	7.0805	1.82E-08	1.96E-07	0.036224	-1	2661	2701	3427	3044	3181	2168	2166	1782	2317	1973
ENSMUSG00000029082	chr5	Bst1	43818886	43819093	2419	2.521304	1.274935	1.83E-08	1.96E-07	0.179099	1	7	10	6	12	21	52	62	30	156	163
ENSMUSG00000047045	chrX	Tmem164	1.43E+08	1.43E+08	6851	1.330697	3.842174	1.89E-08	2.03E-07	0.060745	1	113	76	152	111	243	269	484	348	716	622
ENSMUSG00000038664	chr9	Herc1	66350450	66350621	27464	-0.97559	6.22868	1.89E-08	2.03E-07	0.034767	-1	1493	1231	1785	1767	2087	850	1135	1514	1385	1042
ENSMUSG00000006398	chr4	Cdc20	1.18E+08	1.18E+08	1868	1.856255	2.533475	1.93E-08	2.07E-07	0.11098	1	19	37	38	41	73	144	167	92	386	274
ENSMUSG00000031007	chrX	Atp6ap2	12587801	12587935	2618	0.929824	4.818325	1.94E-08	2.08E-07	0.030341	1	290	265	374	286	411	534	811	938	1127	961
ENSMUSG00000027347	chr2	Rasgrp1	1.17E+08	1.17E+08	5600	2.269713	0.249786	1.94E-08	2.08E-07	0.104892	1	10	7	6	2	4	35	52	25	56	35
ENSMUSG00000078861	chr2	Zfp931	1.78E+08	1.78E+08	2299	-1.43852	1.831705	1.99E-08	2.13E-07	0.059396	-1	63	90	110	74	93	38	44	30	67	44
ENSMUSG00000010095	chr19	Slc3a2	8706882	8708094	2958	0.943826	5.417313	2.01E-08	2.15E-07	0.032084	1	396	374	581	453	667	915	1154	1218	1707	1635
ENSMUSG00000026833	chr2	Olfm1	28192992	28193462	3553	1.329475	3.72482	2.01E-08	2.15E-07	0.060689	1	81	67	131	143	221	322	550	289	572	476
ENSMUSG00000061046	chr17	Haghl	25779843	25780154	2643	1.03899	3.338087	2.02E-08	2.16E-07	0.034542	1	85	86	136	105	140	261	259	283	397	372
ENSMUSG00000047843	chr5	Bri3	1.44E+08	1.44E+08	1648	0.960137	4.367862	2.03E-08	2.16E-07	0.031711	1	216	227	246	225	240	526	536	745	700	643
ENSMUSG00000067851	chr1	Arfgef1	10137571	10138996	11318	-1.06412	6.307487	2.04E-08	2.17E-07	0.041566	-1	1522	1525	2045	1943	1922	802	1120	1750	1213	1103
ENSMUSG00000020590	chr12	Snx13	35047189	35047411	7387	-1.13572	5.714463	2.05E-08	2.18E-07	0.046973	-1	1156	1011	1413	1153	1281	514	675	1213	779	653
ENSMUSG00000004591	chr3	Pkn2	1.43E+08	1.43E+08	7420	-1.04643	5.115732	2.05E-08	2.18E-07	0.039426	-1	716	677	852	757	895	329	572	752	556	443
ENSMUSG00000030538	chr7	Cib1	80227156	80227386	2052	1.288328	3.198585	2.06E-08	2.19E-07	0.054456	1	72	89	103	74	100	215	295	176	411	422
ENSMUSG00000031360	chrX	Ctps2	1.63E+08	1.63E+08	4720	1.282008	2.941429	2.11E-08	2.24E-07	0.052621	1	74	58	75	55	107	151	209	323	282	294
ENSMUSG00000057003	chr11	Myh4	67238029	67238079	6016	-1.03254	15.35986	2.12E-08	2.25E-07	0.039885	-1	691721	750863	1071575	974483	1310050	649258	526991	695800	648564	644658
ENSMUSG00000063511	chr7	Snrnp70	45376462	45377278	1676	0.98961	5.842997	2.13E-08	2.26E-07	0.035753	1	557	586	633	547	899	1302	1560	1617	2191	2298
ENSMUSG00000078763	chr11	Slfn1	83116849	83117062	1864	3.643284	1.362062	2.15E-08	2.28E-07	0.368038	1	2	2	7	6	14	136	63	9	74	219
ENSMUSG00000020101	chr10	4632428N05Rik	60346851	60347103	5014	1.165006	5.389158	2.2E-08	2.33E-07	0.049298	1	296	293	484	598	513	844	1447	948	1945	1718
ENSMUSG00000042770	chr6	Hebp1	1.35E+08	1.35E+08	1061	1.445729	2.88619	2.28E-08	2.42E-07	0.068617	1	48	47	70	57	110	144	239	172	314	392
ENSMUSG00000025485	chr7	Ric8	1.41E+08	1.41E+08	4742	0.951799	4.929333	2.29E-08	2.42E-07	0.032362	1	320	264	413	321	421	660	1236	863	1078	863
ENSMUSG00000029190	chr5	D5Ertd579e	36584788	36584836	8215	-0.88553	6.825989	2.31E-08	2.44E-07	0.029212	-1	2059	2198	2858	2505	2688	1563	1941	1888	2100	1780
ENSMUSG00000060032	chr6	H2afj	1.37E+08	1.37E+08	1827	0.999203	3.276115	2.4E-08	2.53E-07	0.03168	1	91	87	125	98	135	226	261	283	382	346
ENSMUSG00000051747	chr2	Ttn	76703980	76705329	116825	-0.93232	12.43171	2.4E-08	2.53E-07	0.032897	-1	117143	89669	155643	114104	131864	74193	90896	88399	93234	94553

ENSMUSG00000030060	chr6	Hmces	87913935	87914011	2308	1.217185	2.447989	2.41E-08	2.54E-07	0.043943	1	45	52	56	48	66	129	197	134	221	194
ENSMUSG00000008090	chr5	Fgfrl1	1.09E+08	1.09E+08	2656	1.037827	5.143724	2.42E-08	2.55E-07	0.039023	1	368	304	331	432	492	718	1008	1486	1230	1124
ENSMUSG00000001270	chr12	Ckb	1.12E+08	1.12E+08	1478	1.72797	4.953568	2.46E-08	2.59E-07	0.106807	1	179	139	228	209	485	898	1878	433	1222	1104
ENSMUSG00000095193	chr17	Gm20939	94873986	94874112	1572	-2.64166	-0.5503	2.47E-08	2.6E-07	0.137386	-1	22	14	25	6	24	0	4	5	4	7
ENSMUSG00000027312	chr2	Atrn	1.31E+08	1.31E+08	13208	-0.89519	4.903139	2.48E-08	2.61E-07	0.028758	-1	579	464	712	685	838	346	462	540	596	514
ENSMUSG00000100131	chr1	Gm28439	24611535	24612410	876	-1.46347	2.33871	2.49E-08	2.61E-07	0.068704	-1	91	107	141	184	89	38	62	63	93	62
ENSMUSG00000003762	chr7	Adck4	27233023	27233173	3175	1.173881	3.027459	2.5E-08	2.63E-07	0.044348	1	77	69	79	77	110	189	263	184	340	335
ENSMUSG00000052146	chr17	Rps10	27630422	27630506	1937	0.964235	7.133026	2.53E-08	2.65E-07	0.034878	1	1240	1498	1945	1342	1974	3878	4428	3678	4633	4871
ENSMUSG00000025747	chr5	Tyms	30058202	30061133	6089	1.842972	1.917199	2.53E-08	2.65E-07	0.102862	1	30	25	24	13	39	95	132	65	233	153
ENSMUSG00000029217	chr5	Tec	72755718	72756379	3632	1.33281	2.681602	2.59E-08	2.71E-07	0.056179	1	63	47	61	53	73	113	166	224	281	286
ENSMUSG00000028557	chr4	Rnf11	1.09E+08	1.09E+08	4263	-0.90444	6.995863	2.6E-08	2.72E-07	0.030754	-1	2198	2595	3222	3018	2850	1674	2157	1914	2445	2199
ENSMUSG00000021306	chr13	Gpr137b	13357623	13359423	2978	1.798654	2.079744	2.64E-08	2.76E-07	0.101501	1	32	18	32	24	47	62	115	112	247	231
ENSMUSG00000022971	chr16	Ifnar2	91372783	91373074	3329	1.022908	4.066299	2.67E-08	2.79E-07	0.036394	1	136	156	190	223	215	359	498	397	733	658
ENSMUSG00000000982	chr11	Ccl3	83647844	83648343	766	4.169299	1.703121	2.72E-08	2.84E-07	0.469779	1	2	4	0	15	5	37	70	18	280	314
ENSMUSG00000032006	chr9	Pdgfd	6168612	6168918	3119	-1.27396	2.208952	2.74E-08	2.86E-07	0.04981	-1	90	96	123	109	125	30	67	73	85	64
ENSMUSG00000033257	chr1	Ttll4	74661745	74661889	11527	-1.05429	4.63208	2.76E-08	2.88E-07	0.040111	-1	391	478	862	447	662	326	444	359	379	355
ENSMUSG00000036902	chr8	Neto2	85636588	85641116	5610	-1.64766	0.954918	2.78E-08	2.9E-07	0.07109	-1	35	53	49	50	52	16	27	12	33	20
ENSMUSG00000030068	chr6	Gm20696	99257484	99260419	3994	-1.17279	2.772472	2.82E-08	2.93E-07	0.044324	-1	139	135	181	173	156	64	74	107	136	113
ENSMUSG00000051457	chr7	Spn	1.27E+08	1.27E+08	4607	2.594057	0.594242	2.83E-08	2.94E-07	0.17241	1	5	4	6	5	12	17	35	31	100	100
ENSMUSG00000033589	chr14	Reep4	70545251	70545738	1668	1.451284	2.365839	2.86E-08	2.97E-07	0.066321	1	39	34	35	38	81	130	159	121	263	197
ENSMUSG00000029322	chr5	Plac8	1.01E+08	1.01E+08	1592	3.315077	2.430891	2.87E-08	2.98E-07	0.337273	1	5	11	7	5	57	173	107	78	216	531
ENSMUSG00000036591	chr2	Arhgap21	20847919	20850385	9271	-0.95824	4.53444	2.9E-08	3.01E-07	0.033032	-1	489	393	551	440	699	220	425	394	474	352
ENSMUSG00000021311	chr13	Mtr	12186542	12187091	4482	-0.97536	3.886013	2.92E-08	3.03E-07	0.032946	-1	296	213	347	342	456	188	203	240	320	217
ENSMUSG00000028656	chr4	Cap1	1.23E+08	1.23E+08	3494	1.11047	6.035466	2.93E-08	3.04E-07	0.046061	1	618	549	695	694	930	1359	1987	1364	3277	2736
ENSMUSG00000034868	chr17	Myl12b	70973920	70974496	1711	0.976651	4.984576	2.96E-08	3.07E-07	0.034821	1	248	304	415	378	451	804	1038	688	1236	1138
ENSMUSG00000045246	chr8	Kcng4	1.2E+08	1.2E+08	3806	-2.24043	5.709013	2.97E-08	3.07E-07	0.176735	-1	1233	1752	1878	1552	593	433	482	80	676	476
ENSMUSG00000000958	chr14	Slc7a7	54369444	54369886	2142	1.372132	2.221712	2.98E-08	3.08E-07	0.057392	1	37	30	41	37	68	99	149	120	208	198
ENSMUSG00000029759	chr6	Pon3	5220852	5221722	3385	-1.0131	4.833221	2.98E-08	3.08E-07	0.037473	-1	529	666	701	677	572	378	357	393	532	541
ENSMUSG00000071748	chrX	Gm14698	68821093	68825318	4226	-1.76674	0.974233	3E-08	3.1E-07	0.084321	-1	59	36	70	40	42	15	30	18	24	15
ENSMUSG00000000244	chr7	Tspan32	1.43E+08	1.43E+08	2848	2.346889	0.705005	3.03E-08	3.12E-07	0.140867	1	13	2	11	6	8	38	67	23	88	78
ENSMUSG00000005447	chr7	Pafah1b3	25295049	25295376	2107	1.814344	1.269472	3.03E-08	3.12E-07	0.08889	1	24	16	12	9	21	61	91	54	110	99
ENSMUSG00000046245	chr5	Pilra	1.38E+08	1.38E+08	3077	2.887808	0.70954	3.03E-08	3.12E-07	0.220174	1	2	5	9	9	4	37	81	10	81	100
ENSMUSG00000025132	chr11	Arhgdia	1.21E+08	1.21E+08	2258	1.063411	7.294097	3.06E-08	3.15E-07	0.042881	1	1338	1322	1692	1814	2430	3685	4576	3417	7620	5947
ENSMUSG00000021816	chr14	Ppp3cb	20499364	20501662	6018	-0.96699	7.452769	3.11E-08	3.2E-07	0.03563	-1	3676	3367	4468	3634	4167	2306	2784	3419	2779	2440
ENSMUSG00000036943	chr9	Rab8b	66843672	66847811	4743	0.940156	4.4156	3.13E-08	3.21E-07	0.031418	1	192	207	296	247	280	440	593	558	903	817
ENSMUSG00000020736	chr11	Nt5c	1.15E+08	1.15E+08	1140	1.189031	3.186759	3.13E-08	3.22E-07	0.04699	1	93	77	99	70	118	255	288	193	356	363
ENSMUSG00000035199	chr6	Arl6ip5	97210689	97210996	1442	0.964487	7.474012	3.18E-08	3.26E-07	0.035489	1	1513	1867	2426	1997	2310	5082	6395	5201	5605	4815
ENSMUSG00000068373	chr2	D430041D05Rik	1.04E+08	1.04E+08	15851	-1.73043	1.988979	3.18E-08	3.26E-07	0.095972	-1	107	92	110	78	116	26	76	18	54	42
ENSMUSG00000029167	chr5	Ppargc1a	51454249	51458283	6641	-1.17239	4.640651	3.18E-08	3.26E-07	0.050358	-1	425	666	648	685	410	309	355	416	400	297
ENSMUSG00000002980	chr7	Bcam	19756131	19756619	3199	1.042339	6.032262	3.23E-08	3.3E-07	0.040851	1	495	626	721	1022	701	1488	2205	1838	2733	2124
ENSMUSG00000042350	chr12	Arel1	84918148	84920580	6044	-0.88885	5.049391	3.26E-08	3.34E-07	0.029013	-1	722	585	832	628	819	408	519	594	637	559
ENSMUSG00000063524	chr4	Eno1	1.5E+08	1.5E+08	5379	1.214362	7.840237	3.26E-08	3.34E-07	0.055967	1	1465	1888	2491	2449	3484	5255	6881	4496	11640	9974
ENSMUSG00000026824	chr2	Kcnj3	55435970	55436510	5215	-1.956	0.145717	3.39E-08	3.46E-07	0.087839	-1	29	33	27	28	21	7	13	7	17	7
ENSMUSG00000071866	chr11	Ppia	6415443	6415979	3508	1.066751	7.388586	3.39E-08	3.46E-07	0.043454	1	1342	1678	2300	1547	2269	4243	5946	3320	6926	6241
ENSMUSG00000100685	chr1	Gm28610	1.52E+08	1.52E+08	406	-2.18342	0.665961	3.44E-08	3.51E-07	0.125581	-1	38	39	40	56	37	24	11	6	10	11
ENSMUSG00000027546	chr2	Atp9a	1.69E+08	1.69E+08	5917	0.900002	4.875177	3.46E-08	3.52E-07	0.029556	1	298	262	367	348	442	683	970	708	1106	1005
ENSMUSG00000103779	chr17	RP24-490B17.7	51766643	51771443	4801	-1.27465	2.230124	3.47E-08	3.53E-07	0.050258	-1	114	88	108	107	131	45	72	79	72	50
ENSMUSG00000038056	chr5	Kmt2c	25271798	25273758	20291	-1.2164	5.13585	3.49E-08	3.55E-07	0.055212	-1	754	544	951	820	1088	281	466	820	490	424
ENSMUSG00000004849	chr5	Ap1s1	1.37E+08	1.37E+08	2198	1.070953	4.916906	3.56E-08	3.62E-07	0.04238	1	298	288	391	279	365	801	896	582	1314	1202
ENSMUSG00000004951	chr5	Hspb1	1.36E+08	1.36E+08	1031	1.211992	7.204866	3.61E-08	3.67E-07	0.055974	1	933	1471	1654	1595	1834	3573	4619	7382	5153	3261
ENSMUSG00000092203	chr17	1110038B12Rik	34950238	34950475	1811	1.432793	3.229798	3.62E-08	3.67E-07	0.071091	1	61	71	117	72	101	192	239	543	276	321
ENSMUSG00000001983	chr11	Taco1	1.06E+08	1.06E+08	1383	-1.01679	5.507907	3.64E-08	3.69E-07	0.03892	-1	818	1015	1235	1041	948	639	800	508	940	628
ENSMUSG00000021636	chr13	Marveld2	1.01E+08	1.01E+08	3382	2.03141	0.590764	3.65E-08	3.7E-07	0.103097	1	7	5	16	7	10	36	86	51	47	35
ENSMUSG00000059900	chr6	Tmem40	1.16E+08	1.16E+08	2196	2.483318	0.253359	3.65E-08	3.7E-07	0.144883	1	9	3	6	2	6	33	80	25	35	33
ENSMUSG00000021245	chr12	Mlh3	85234529	85235729	5446	-0.938	3.58325	3.65E-08	3.7E-07	0.029756	-1	244	208	277	242	347	152	207	190	245	166
ENSMUSG00000030301	chr6	Ccdc91	1.47E+08	1.47E+08	2827	-0.92651	6.358814	3.67E-08	3.71E-07	0.032748	-1	1637	1607	2080	1728	1906	1153	1389	1449	1319	1227
ENSMUSG00000020124	chr10	Usp15	1.23E+08	1.23E+08	3227	-0.8966	6.776408	3.69E-08	3.73E-07	0.030845	-1	1919	2238	2825	2418	2510	1417	1721	2027	2057	1720
ENSMUSG00000064357	chrMT	mt-Atp6	7927	8607	681	-1.59452	3.731273	3.75E-08	3.79E-07	0.091412	-1	241	337	248	612	186	114	134	165	215	151
ENSMUSG00000003178	chr6	Mical3	1.21E+08	1.21E+08	2893	-1.54574	3.165341	3.79E-08	3.82E-07	0.08406	-1	180	137	254	217	352	48	80	195	114	102
ENSMUSG00000033502	chr3	Cdc14a	1.16E+08	1.16E+08	11335	-1.15137	4.123329	3.86E-08	3.89E-07	0.048253	-1	406	388	565	283	343	209	247	295	232	265
ENSMUSG00000034210	chr4	Efcab14	1.16E+08	1.16E+08	8201	-0.9574	5.747741	3.86E-08	3.89E-07	0.034754	-1	950	1049	1359	1243	1340	780	980	604	1015	866
ENSMUSG00000094392	chr3	Gm3788	86672033	86672168	136	3.079853	-0.44091	3.93E-08	3.95E-07	0.170409	1	1	2	0	5	2	14	42	8	36	27
ENSMUSG00000029771	chr6	Irf5	29526625	29526774	2903	1.489952	3.945743	3.97E-08	4E-07	0.080111	1	105	135	182	147	94	415	501	227	769	754
ENSMUSG00000030748	chr7	Il4ra	1.26E+08	1.26E+08	5092	1.332692	4.338022	4.02E-08	4.05E-07	0.065552	1	127	142	159	190	362	410	620	454	1090	883
ENSMUSG00000022876	chr16	Samsn1	75858793	75859639	4534	2.715472	0.191625	4.03E-08	4.05E-07	0.168242	1	9	2	0	4	6	19	33	25	59	70
ENSMUSG00000024251	chr17	Thada	84190056	84192331	7884	-1.08398	2.807246	4.03E-08	4.05E-07	0.038133	-1	146	122	184	161	179	72	114	91	151	100

ENSMUSG00000037086	chrX	Prr32	45090904	45091031	1110	2.504021	0.129558	4.12E-08	4.14E-07	0.147151	1	2	4	3	3	12	24	38	65	22	38
ENSMUSG00000020640	chr12	Itsn2	4593008	4593232	5987	-0.92148	3.764514	4.23E-08	4.25E-07	0.02968	-1	251	239	318	330	349	139	215	256	265	229
ENSMUSG00000096472	chr9	Cdkn2d	21288463	21289332	1271	0.909994	4.166778	4.25E-08	4.26E-07	0.029354	1	188	202	247	183	209	437	533	597	627	521
ENSMUSG00000026384	chr1	Ptpn4	1.2E+08	1.2E+08	11321	-1.06585	4.579036	4.28E-08	4.29E-07	0.04225	-1	375	400	532	683	751	248	316	490	427	331
ENSMUSG00000009185	chr11	Ccl8	82115185	82115312	511	2.299929	3.000395	4.37E-08	4.37E-07	0.182898	1	17	38	50	18	110	376	240	125	274	459
ENSMUSG00000087523	chr11	Gm12319	70654741	70654896	357	-1.0853	4.863611	4.43E-08	4.43E-07	0.044213	-1	591	605	859	639	591	481	438	317	485	414
ENSMUSG00000046761	chr15	Fam83h	76001093	76004749	4627	2.498875	-0.34491	4.51E-08	4.51E-07	0.109407	1	5	1	3	1	6	11	25	38	31	26
ENSMUSG00000026407	chr1	Cacna1s	1.36E+08	1.36E+08	6550	-0.89714	9.515474	4.57E-08	4.56E-07	0.031711	-1	13905	11604	16578	17159	21140	9901	11590	13055	14157	10948
ENSMUSG00000096146	chr7	Kcnj11	46098725	46099897	1173	-0.97225	5.282017	4.71E-08	4.7E-07	0.03596	-1	744	596	1005	890	1124	462	569	813	639	574
ENSMUSG00000022772	chr16	Senp5	31962506	31963537	4426	-1.39157	3.162436	4.82E-08	4.81E-07	0.069028	-1	172	186	236	212	282	53	121	171	179	67
ENSMUSG00000033400	chr3	Agl	1.17E+08	1.17E+08	12803	-1.07963	9.593602	4.83E-08	4.81E-07	0.045778	-1	14069	16010	20876	18118	18679	9443	8987	16889	10909	11120
ENSMUSG00000089788	chr1	Gm16586	1.78E+08	1.78E+08	2640	1.197816	3.013901	4.88E-08	4.86E-07	0.048192	1	87	74	75	68	95	176	234	271	258	354
ENSMUSG00000009292	chr10	Trpm2	77907722	77910322	12323	3.067565	-0.86141	4.89E-08	4.87E-07	0.109838	1	2	1	1	1	2	9	21	9	24	26
ENSMUSG00000024014	chr17	Pim1	29490812	29491225	2638	1.468489	4.002326	4.9E-08	4.88E-07	0.079239	1	79	152	122	183	168	239	471	886	526	636
ENSMUSG00000039115	chr9	Itga9	1.19E+08	1.19E+08	7691	-0.94074	4.349259	4.98E-08	4.95E-07	0.032569	-1	358	310	554	420	637	264	326	262	437	349
ENSMUSG00000027272	chr2	Ubr1	1.21E+08	1.21E+08	9889	-0.97689	4.935729	4.99E-08	4.95E-07	0.036119	-1	654	499	802	661	785	342	472	656	519	418
ENSMUSG00000026185	chr1	Igfbp5	72857932	72862508	6006	-1.61175	9.594714	5.01E-08	4.97E-07	0.099421	-1	13531	14317	16398	18299	37875	8786	10935	3155	10831	10560
ENSMUSG00000044676	chr8	Zfp612	1.1E+08	1.1E+08	2301	-1.80663	1.536057	5.1E-08	5.06E-07	0.101859	-1	81	54	96	65	76	25	16	55	30	21
ENSMUSG00000063550	chr7	Nup98	1.02E+08	1.02E+08	4051	-1.13549	3.378927	5.1E-08	5.06E-07	0.045621	-1	240	142	283	243	293	84	164	190	194	137
ENSMUSG00000026548	chr1	Slamf9	1.72E+08	1.72E+08	1313	2.066861	1.283807	5.14E-08	5.09E-07	0.128768	1	15	4	12	14	30	80	99	39	110	102
ENSMUSG00000027613	chr2	Eif6	1.56E+08	1.56E+08	2702	0.885915	5.208123	5.15E-08	5.1E-07	0.02972	1	367	426	485	385	495	827	964	1227	1447	1163
ENSMUSG00000001542	chr13	Ell2	75707484	75707797	3647	-1.01488	3.919004	5.22E-08	5.17E-07	0.037627	-1	306	282	361	349	389	140	197	319	325	205
ENSMUSG00000042717	chr6	Ppp1r3a	14713822	14719941	7120	-1.50245	7.5703	5.27E-08	5.21E-07	0.087066	-1	4635	3751	5205	4945	4844	1278	1721	4737	2116	1748
ENSMUSG00000031167	chrX	Rbm3	8138975	8141208	4698	1.147116	5.924354	5.35E-08	5.28E-07	0.051031	1	584	495	633	516	958	1142	1501	2785	2179	2245
ENSMUSG00000085795	chr8	Zfp703	26977336	26977611	3304	0.948416	5.082954	5.41E-08	5.34E-07	0.034197	1	343	280	404	463	443	630	1048	1218	1386	1002
ENSMUSG00000002668	chr17	Dennd1c	57066056	57066641	2520	2.219785	1.040908	5.56E-08	5.49E-07	0.142951	1	14	6	9	9	18	44	80	30	80	136
ENSMUSG00000021482	chr13	Aaed1	64291836	64292228	972	-1.33985	3.579165	5.62E-08	5.54E-07	0.065881	-1	274	219	340	300	294	85	193	262	139	111
ENSMUSG00000000555	chr15	Itga5	1.03E+08	1.03E+08	4379	1.031877	5.110815	5.62E-08	5.54E-07	0.040824	1	286	287	364	411	572	669	1204	866	1707	1099
ENSMUSG00000001323	chr11	Srr	74906359	74908843	4560	-0.85628	4.167124	5.64E-08	5.55E-07	0.026583	-1	340	324	460	385	423	237	278	296	405	283
ENSMUSG00000020220	chr4	Vps13d	1.45E+08	1.45E+08	24771	-1.00402	5.90139	5.67E-08	5.57E-07	0.039346	-1	1130	1062	1409	1520	1567	670	838	1315	994	824
ENSMUSG00000018166	chr10	Erbb3	1.29E+08	1.29E+08	6016	1.56279	3.562262	5.7E-08	5.6E-07	0.089	1	114	57	77	103	143	229	618	578	372	244
ENSMUSG00000035992	chr11	Fnip1	54438199	54438388	7119	-1.19975	5.385264	5.78E-08	5.67E-07	0.055771	-1	929	912	908	1183	852	402	504	931	683	451
ENSMUSG00000059975	chr7	Zfp74	29930815	29932240	5628	-1.08765	2.625907	5.84E-08	5.73E-07	0.03858	-1	122	128	147	133	166	59	102	101	114	86
ENSMUSG00000103268	chr9	Map4	1.1E+08	1.1E+08	3165	-1.44413	7.113382	5.86E-08	5.74E-07	0.081166	-1	3077	2376	4117	3780	3666	823	1635	3315	1793	1223
ENSMUSG00000059796	chr11	Eif4a1	69666936	69667617	4334	0.925213	7.201518	5.86E-08	5.74E-07	0.033951	1	1272	1540	1995	1517	2247	2994	4162	4280	6385	5094
ENSMUSG00000024063	chr17	Lbh	72918305	72918578	3207	1.12757	4.467852	5.98E-08	5.86E-07	0.04805	1	177	194	244	285	257	469	832	408	1072	824
ENSMUSG00000065947	chrMT	mt-Nd4l	9877	10173	297	-2.21125	1.048294	6.07E-08	5.94E-07	0.15205	-1	42	28	42	119	49	7	14	18	32	16
ENSMUSG00000094870	chr13	Zfp131	1.2E+08	1.2E+08	3067	-0.86679	4.238123	6.14E-08	6.01E-07	0.02763	-1	360	365	462	385	459	219	369	326	379	275
ENSMUSG00000035621	chr10	Midn	80148272	80148349	4307	1.039066	5.323125	6.17E-08	6.03E-07	0.041834	1	283	431	403	542	529	992	1394	1217	1795	932
ENSMUSG00000078920	chr11	Ifi47	49076587	49076662	2317	2.304325	2.692687	6.17E-08	6.03E-07	0.183912	1	23	27	29	49	52	424	156	67	216	288
ENSMUSG00000028328	chr4	Tmod1	46038935	46039309	3946	-0.91376	8.466009	6.25E-08	6.1E-07	0.033485	-1	6745	6446	9263	6993	9404	5113	6469	5852	6267	4701
ENSMUSG00000022453	chr15	Naga	82329532	82330207	1913	0.912526	3.944859	6.3E-08	6.14E-07	0.030036	1	154	133	183	166	260	309	462	505	598	484
ENSMUSG00000027995	chr3	Tlr2	83836272	83838789	3014	1.713549	2.582271	6.4E-08	6.24E-07	0.103297	1	40	19	48	37	91	110	205	129	343	292
ENSMUSG00000034957	chr7	Cebpa	35119293	35121926	2634	2.498521	4.87183	6.43E-08	6.26E-07	0.224796	1	115	65	97	193	284	343	639	424	1837	2832
ENSMUSG00000022285	chr15	Ywhaz	36770770	36772777	3999	0.945313	6.239548	6.54E-08	6.37E-07	0.035346	1	705	709	900	781	1271	1726	2607	1803	3158	2443
ENSMUSG00000020415	chr11	Pttg1	43420250	43420408	2000	1.61451	2.107245	6.67E-08	6.48E-07	0.085861	1	28	40	29	34	38	157	98	86	224	166
ENSMUSG00000025323	chr12	Sp4	1.18E+08	1.18E+08	5770	-1.59967	2.307212	6.67E-08	6.48E-07	0.088836	-1	127	89	123	142	135	27	49	108	51	51
ENSMUSG00000037868	chr10	Egr2	67535475	67535530	3398	2.122609	1.934168	6.83E-08	6.63E-07	0.152069	1	16	10	27	23	41	42	166	70	277	178
ENSMUSG00000030365	chr6	Clec2i	1.29E+08	1.29E+08	3110	2.726011	-0.4167	6.87E-08	6.67E-07	0.142112	1	1	3	6	2	1	15	35	9	33	34
ENSMUSG00000060716	chr12	Plekhh1	79029163	79029420	6432	1.899436	1.725205	6.92E-08	6.71E-07	0.116649	1	20	16	29	18	29	70	230	92	132	62
ENSMUSG00000038170	chr3	Pde4dip	97689824	97690853	16508	-1.18672	11.48452	6.96E-08	6.74E-07	0.05643	-1	60718	50084	72491	72599	78222	32213	31608	66895	36190	34932
ENSMUSG00000022339	chr15	Ebag9	44619641	44619942	1561	-0.93605	3.595998	7.14E-08	6.92E-07	0.031236	-1	207	256	324	273	259	143	214	203	215	192
ENSMUSG00000042042	chr6	Csgalnact2	1.18E+08	1.18E+08	5438	-0.96197	5.066371	7.28E-08	7.04E-07	0.036042	-1	710	540	865	685	921	406	534	698	558	447
ENSMUSG00000059791	chr17	Nrm	35861318	35861517	1466	1.621427	1.673283	7.3E-08	7.06E-07	0.081991	1	23	20	21	23	38	89	145	68	165	75
ENSMUSG00000041258	chr18	Zfp236	82593593	82597754	10471	-0.97054	3.879548	7.4E-08	7.15E-07	0.034874	-1	306	226	398	304	405	146	238	299	259	224
ENSMUSG00000017561	chr11	Crlf3	80046493	80047737	4261	1.013839	3.158419	7.41E-08	7.15E-07	0.035146	1	70	82	108	113	117	202	325	248	338	270
ENSMUSG00000057036	chr3	Gm7536	24333068	24333511	444	0.866322	5.165922	7.44E-08	7.18E-07	0.029118	1	338	390	522	382	496	923	1147	987	1146	1161
ENSMUSG00000028017	chr3	Egf	1.3E+08	1.3E+08	4757	-0.98111	5.655714	7.48E-08	7.21E-07	0.038092	-1	955	847	1360	1075	1413	656	586	966	782	934
ENSMUSG00000027490	chr2	E2f1	1.55E+08	1.55E+08	3154	1.541083	2.384018	7.56E-08	7.28E-07	0.081999	1	30	34	50	35	72	143	168	84	264	234
ENSMUSG00000046480	chr9	Scn4b	45138437	45139102	4940	-0.90329	8.632748	7.56E-08	7.28E-07	0.033167	-1	8186	7818	9348	9024	8482	5895	6559	6320	7543	5769
ENSMUSG00000048234	chr1	Rnf149	39551296	39552515	2838	1.078026	3.429972	7.57E-08	7.28E-07	0.041433	1	105	102	128	104	132	179	323	303	522	409
ENSMUSG00000063428	chr10	Ddo	40630011	40630091	3000	-1.03979	5.068778	7.72E-08	7.42E-07	0.042384	-1	621	824	776	793	706	510	534	356	610	529
ENSMUSG00000071669	chr16	Snx29	11322908	11322978	6435	-1.48676	1.386494	7.8E-08	7.5E-07	0.066564	-1	56	45	71	74	72	15	32	46	34	32
ENSMUSG00000020572	chr12	Nampt	32820335	32820626	4547	-1.02641	6.565569	7.81E-08	7.5E-07	0.042337	-1	1721	2325	2672	1980	1803	1154	1297	1798	1634	1386
ENSMUSG00000026430	chr1	Rassf5	1.31E+08	1.31E+08	3839	1.913153	1.850716	7.82E-08	7.5E-07	0.123042	1	16	17	14	22	55	91	165	60	178	152
ENSMUSG00000001128	chrX	Cfp	20925454	20925759	1736	1.584074	4.054814	7.83E-08	7.51E-07	0.095474	1	119	94	151	93	249	435	466	241	847	945

ENSMUSG00000033799	chr13	Fam208b	3566036	3566667	8337	-1.11543	3.377204	7.9E-08	7.57E-07	0.045463	-1	225	171	239	242	314	80	159	209	194	134
ENSMUSG00000006095	chr7	Tbcb	30224131	30224347	1442	0.905276	4.651362	7.93E-08	7.59E-07	0.031383	1	224	264	340	265	373	644	758	572	952	889
ENSMUSG00000027765	chr3	P2ry1	61002795	61004599	4291	-1.00628	3.569222	8.23E-08	7.87E-07	0.036951	-1	266	187	247	315	302	116	213	170	233	198
ENSMUSG00000002297	chr5	Dbf4	8396973	8398162	6571	1.610402	1.617748	8.45E-08	8.08E-07	0.080721	1	13	29	29	16	34	76	83	74	163	127
ENSMUSG00000092470	chr16	Gm20518	17835277	17835539	3811	-0.97263	3.934406	8.49E-08	8.11E-07	0.035526	-1	301	263	381	325	430	148	250	330	265	217
ENSMUSG00000075324	chr2	Fign	63971507	63980899	9969	-1.42273	1.734218	8.51E-08	8.13E-07	0.065145	-1	80	56	88	69	110	25	44	27	61	55
ENSMUSG00000020521	chr11	Rnft1	86484657	86484799	4719	-0.81939	5.078522	8.52E-08	8.13E-07	0.026202	-1	634	568	845	700	877	424	618	577	692	555
ENSMUSG00000022799	chr16	Arhgap31	38598340	38603815	11141	-0.92576	5.004246	8.55E-08	8.16E-07	0.033718	-1	586	506	739	855	851	323	510	576	738	484
ENSMUSG00000040351	chr5	Ankib1	3690000	3693496	6610	-0.92074	3.87433	8.58E-08	8.18E-07	0.031498	-1	261	246	376	288	452	143	245	260	306	244
ENSMUSG00000003623	chr5	Crot	8966033	8966972	5456	-0.97647	5.439876	8.6E-08	8.18E-07	0.037974	-1	896	835	1200	815	1063	458	626	940	699	696
ENSMUSG00000020914	chr11	Top2a	98992943	98993413	9013	1.620247	3.946604	8.71E-08	8.28E-07	0.100147	1	92	93	85	113	260	374	531	237	1025	616
ENSMUSG00000062646	chr2	Ganc	1.2E+08	1.2E+08	9096	-0.98595	5.234137	8.72E-08	8.29E-07	0.038535	-1	733	730	1060	801	851	538	583	413	645	747
ENSMUSG00000040797	chr6	Iqsec3	1.21E+08	1.21E+08	13603	1.624176	2.58188	8.81E-08	8.37E-07	0.09365	1	48	27	39	52	75	137	300	93	292	226
ENSMUSG00000026096	chr1	Osgepl1	53313624	53313858	6147	-0.9087	4.868785	8.99E-08	8.53E-07	0.032368	-1	587	639	724	624	568	360	526	492	554	442
ENSMUSG00000071342	chr12	Lsmem1	40176386	40177228	1213	-1.14007	4.774517	8.98E-08	8.53E-07	0.05116	-1	734	452	715	547	677	420	478	269	387	399
ENSMUSG00000035891	chr15	Cerk	86139128	86141612	4812	1.113725	3.983262	9E-08	8.54E-07	0.047349	1	134	118	155	159	278	284	490	408	734	654
ENSMUSG00000061816	chr1	Myl1	66924295	66924557	2074	-0.89399	13.70247	9.09E-08	8.61E-07	0.033031	-1	232289	265911	354082	277526	323598	206834	207782	222848	230976	207031
ENSMUSG00000069184	chr13	Zfp72	74371426	74372827	1629	-1.73282	0.270158	9.09E-08	8.61E-07	0.070486	-1	28	29	30	32	28	7	17	16	11	11
ENSMUSG00000039062	chr7	Anpep	79821803	79822376	3879	1.320064	5.10284	9.17E-08	8.67E-07	0.069139	1	296	159	268	334	627	771	1146	821	1578	1492
ENSMUSG00000034557	chr4	Zfyve9	1.09E+08	1.09E+08	6459	-1.09071	6.034542	9.3E-08	8.79E-07	0.048062	-1	1396	1214	1632	1502	1710	724	887	1532	948	770
ENSMUSG00000037358	chrX	4930578C19Rik	18414881	18416093	3499	-1.57775	1.553839	9.31E-08	8.8E-07	0.080541	-1	38	72	101	91	62	18	32	36	44	42
ENSMUSG00000020700	chr11	Map3k3	1.06E+08	1.06E+08	4023	-1.01291	4.756865	9.45E-08	8.92E-07	0.040513	-1	571	451	654	611	744	239	426	586	524	345
ENSMUSG00000021929	chr14	Kpna3	61365186	61367729	4167	-0.87285	6.98403	9.46E-08	8.92E-07	0.031194	-1	2417	2213	3259	2733	3115	1680	2063	2415	2432	1842
ENSMUSG00000030470	chr7	Csrp3	48830398	48830706	973	2.682375	5.368811	9.49E-08	8.95E-07	0.263059	1	84	108	73	504	156	478	2085	3440	1371	1061
ENSMUSG00000068227	chr15	Il2rb	78480553	78482183	2785	2.806044	-0.18269	9.57E-08	9.02E-07	0.171271	1	2	3	4	2	4	11	34	12	35	62
ENSMUSG00000028184	chr3	Lphn2	1.49E+08	1.49E+08	8403	-0.93578	4.409403	9.59E-08	9.03E-07	0.03389	-1	409	318	484	513	630	245	438	293	415	322
ENSMUSG00000057322	chr11	Rpl38	1.15E+08	1.15E+08	542	0.941301	6.218862	9.64E-08	9.07E-07	0.035971	1	581	879	989	784	1046	2129	2243	2205	2397	2314
ENSMUSG00000041845	chr19	Rhod	4425459	4426256	1714	1.993657	0.774456	9.8E-08	9.21E-07	0.110572	1	14	8	11	4	15	43	82	29	72	68
ENSMUSG00000038342	chr5	Mlxip	1.23E+08	1.23E+08	8206	-0.95754	6.705314	9.81E-08	9.22E-07	0.037509	-1	2023	1777	2311	2278	3234	1259	1423	2179	1875	1547
ENSMUSG00000055053	chr10	Nfic	81396186	81401071	6534	-0.92727	8.356666	9.96E-08	9.35E-07	0.035559	-1	5661	4929	8268	8306	9297	4005	5087	6399	6301	4668
ENSMUSG00000038740	chr2	Mvb12b	33729953	33733531	8741	-0.82539	5.521036	9.98E-08	9.36E-07	0.027297	-1	873	746	1106	1082	1113	617	718	792	971	781
ENSMUSG00000001630	chr6	Stk38l	1.47E+08	1.47E+08	4571	-0.87813	3.601904	1E-07	9.39E-07	0.02773	-1	226	236	261	259	328	147	196	205	228	222
ENSMUSG00000032412	chr9	Atp1b3	96332655	96333694	2389	0.949424	5.952509	1E-07	9.41E-07	0.036545	1	544	614	823	687	887	1317	1849	1425	2607	2466
ENSMUSG00000028044	chr3	Cks1b	89415472	89415963	1126	1.27189	2.693626	1.01E-07	9.49E-07	0.057107	1	40	46	76	54	101	160	206	143	308	243
ENSMUSG00000056629	chr19	Fkbp2	6977741	6977934	663	1.236651	3.505297	1.02E-07	9.57E-07	0.057427	1	88	107	120	85	163	307	320	206	547	480
ENSMUSG00000049339	chr1	Fam134a	75142778	75143128	2999	0.883675	4.467885	1.03E-07	9.61E-07	0.030091	1	205	218	259	258	365	439	637	646	868	790
ENSMUSG00000025492	chr7	Ifitm3	1.41E+08	1.41E+08	678	1.262558	5.978711	1.03E-07	9.65E-07	0.064503	1	468	503	644	627	897	2194	1833	1025	2359	2823
ENSMUSG00000058070	chr12	Eml1	1.08E+08	1.08E+08	7436	-1.07877	6.797727	1.05E-07	9.8E-07	0.047722	-1	1966	2240	2626	2848	2974	1760	1725	997	1880	1864
ENSMUSG00000020747	chr11	2310067B10Rik	1.16E+08	1.16E+08	5920	-0.94384	6.081706	1.05E-07	9.8E-07	0.036351	-1	1176	1346	1702	1609	1621	973	1132	750	1339	1206
ENSMUSG00000027712	chr3	Anxa5	36448926	36449406	1721	1.423189	6.854683	1.05E-07	9.82E-07	0.081974	1	831	658	1045	1055	1801	2779	4057	1668	6086	5537
ENSMUSG00000036304	chr16	Zdhhc23	43969078	43969413	1389	-2.20545	0.242915	1.06E-07	9.89E-07	0.130802	-1	26	30	24	55	19	6	12	15	8	6
ENSMUSG00000015659	chr17	Serac1	6042196	6044250	4576	-1.25687	3.089601	1.07E-07	9.99E-07	0.058641	-1	183	164	228	173	256	66	126	187	121	87
ENSMUSG00000029580	chr5	Actb	1.43E+08	1.43E+08	2679	1.154448	9.0298	1.07E-07	9.99E-07	0.054986	1	4227	4375	5529	5671	7611	12691	15552	9026	27047	21744
ENSMUSG00000056608	chr8	Chd9	90828835	90828914	11565	-0.9611	4.469001	1.07E-07	1E-06	0.036227	-1	450	346	544	471	655	232	417	439	371	299
ENSMUSG00000026313	chr1	Hdac4	91928779	91933386	15375	-0.99986	4.955313	1.08E-07	1E-06	0.039982	-1	593	503	713	605	1101	331	473	639	534	444
ENSMUSG00000006386	chr4	Tek	94739289	94739692	4712	-0.97621	4.833962	1.08E-07	1.01E-06	0.037979	-1	495	522	652	837	649	307	381	564	526	478
ENSMUSG00000010609	chr1	Psen2	1.8E+08	1.8E+08	4332	0.925371	3.860136	1.09E-07	1.01E-06	0.031981	1	127	148	156	175	229	309	419	399	545	551
ENSMUSG00000020170	chr10	Frs2	1.17E+08	1.17E+08	5682	-1.0287	3.808227	1.09E-07	1.01E-06	0.04019	-1	294	208	337	337	404	133	211	298	251	189
ENSMUSG00000030795	chr7	Fus	1.28E+08	1.28E+08	5690	0.899901	6.57747	1.09E-07	1.01E-06	0.033319	1	943	876	1259	1106	1430	1902	2495	2874	3910	3562
ENSMUSG00000032812	chr7	Arap1	1.01E+08	1.01E+08	7564	1.009183	5.071785	1.1E-07	1.02E-06	0.040855	1	322	267	358	360	580	772	1176	728	1357	1251
ENSMUSG00000056234	chr14	Ncoa4	32159865	32160010	4452	-0.92276	4.346309	1.12E-07	1.04E-06	0.033251	-1	365	319	513	440	619	184	368	346	423	346
ENSMUSG00000027035	chr2	Cers6	68861441	68861805	8875	1.633846	2.647094	1.12E-07	1.04E-06	0.097446	1	52	26	55	32	89	127	328	119	282	244
ENSMUSG00000028573	chr4	Fggy	95557507	95557591	5844	1.176621	2.971479	1.13E-07	1.04E-06	0.04931	1	62	79	76	88	88	165	362	205	302	226
ENSMUSG00000034041	chr8	Lyl1	84701457	84701987	1800	1.325763	2.254528	1.12E-07	1.04E-06	0.059864	1	35	29	61	40	59	106	118	132	218	211
ENSMUSG00000091474	chr7	2610021A01Rik	41599261	41599400	4004	-1.11417	2.625823	1.14E-07	1.06E-06	0.042905	-1	122	127	139	147	164	62	108	108	98	77
ENSMUSG00000029552	chr6	Tes	17065149	17065313	3199	1.534145	2.118704	1.15E-07	1.06E-06	0.081152	1	19	36	45	32	50	99	127	85	234	200
ENSMUSG00000037818	chr3	3110057O12Rik	40846970	40847136	5433	-0.97049	3.607071	1.15E-07	1.06E-06	0.03508	-1	235	257	240	293	310	145	215	221	228	151
ENSMUSG00000021767	chr14	Kat6b	21481434	21481553	16826	-0.99209	3.796685	1.15E-07	1.06E-06	0.037574	-1	272	206	343	337	400	139	190	290	255	217
ENSMUSG00000063659	chr1	Zbtb18	1.77E+08	1.77E+08	6138	-0.87565	6.290866	1.16E-07	1.06E-06	0.031597	-1	1471	1516	1947	1789	1716	914	1463	1433	1406	1251
ENSMUSG00000015342	chrX	Xk	9272756	9273234	5076	-1.38269	2.699645	1.17E-07	1.08E-06	0.070309	-1	159	148	160	162	140	53	65	142	94	66
ENSMUSG00000028333	chr4	Anp32b	46450902	46451349	1716	0.87134	6.243823	1.18E-07	1.08E-06	0.031253	1	730	743	1044	847	1148	1687	1897	2441	2934	2563
ENSMUSG00000049764	chr10	Zfp280b	76032654	76032749	5097	-0.89925	3.99159	1.2E-07	1.1E-06	0.030776	-1	269	288	370	308	515	220	269	217	315	272
ENSMUSG00000024851	chr19	Pitpnm1	4099998	4100213	6889	1.300169	2.593888	1.2E-07	1.1E-06	0.059721	1	44	48	49	51	96	116	167	180	267	268
ENSMUSG00000033088	chr15	Triobp	78947724	78948048	10681	-0.88285	5.246419	1.2E-07	1.1E-06	0.031491	-1	600	615	943	843	1188	461	656	670	678	653
ENSMUSG00000051984	chr19	Sec31b	44516957	44517488	3950	-1.11114	4.044885	1.22E-07	1.12E-06	0.048515	-1	374	287	454	369	396	165	208	391	241	210
ENSMUSG00000002015	chrX	Bcap31	73686178	73686595	1219	0.888062	5.884979	1.23E-07	1.13E-06	0.032363	1	589	580	721	688	900	1476	1674	1422	2234	2165

ENSMUSG00000030753	chr7	Prkrir	98703103	98703478	4125	-0.94576	6.948191	1.25E-07	1.14E-06	0.037285	-1	2416	2335	3183	2724	2921	1608	1770	2612	2025	1769
ENSMUSG00000006638	chr5	Abhd1	30950066	30950248	1758	1.794456	0.246578	1.25E-07	1.15E-06	0.066772	1	8	6	7	7	11	26	51	37	41	36
ENSMUSG00000073409	chr17	H2-Q6	35424850	35424940	2085	2.147277	1.580796	1.25E-07	1.15E-06	0.155424	1	13	16	17	25	15	60	54	71	118	244
ENSMUSG00000104047	chr11	Cd300lb	1.15E+08	1.15E+08	768	2.714966	-0.3282	1.26E-07	1.15E-06	0.160377	1	5	1	1	1	6	6	30	23	38	40
ENSMUSG00000028459	chr4	Cd72	43446462	43448036	3422	3.057112	1.20075	1.26E-07	1.15E-06	0.297063	1	6	5	5	12	10	100	85	5	115	136
ENSMUSG00000072640	chr11	Lyrm9	78826584	78826636	8146	-1.02426	3.650417	1.27E-07	1.16E-06	0.039824	-1	236	279	321	258	303	171	213	118	246	216
ENSMUSG00000025930	chr1	Msc	14753346	14754325	2546	1.600894	2.251173	1.3E-07	1.18E-06	0.090878	1	38	27	34	43	49	105	223	244	111	119
ENSMUSG00000001751	chr11	Naglu	1.01E+08	1.01E+08	2658	1.145875	3.58505	1.3E-07	1.19E-06	0.050316	1	118	68	153	100	191	241	350	326	524	503
ENSMUSG00000026341	chr1	Actr3	1.25E+08	1.25E+08	4631	0.956773	6.254844	1.3E-07	1.19E-06	0.037961	1	724	767	929	774	1170	1591	2450	1703	3389	2850
ENSMUSG00000043019	chr1	Edem3	1.52E+08	1.52E+08	6381	-0.97063	5.448804	1.31E-07	1.19E-06	0.038654	-1	830	704	1177	915	1268	457	814	888	769	534
ENSMUSG00000021774	chr14	Ube2e1	18282722	18283439	4457	-0.90573	6.251209	1.32E-07	1.21E-06	0.034088	-1	1380	1582	2110	1361	1885	1131	1140	1279	1358	1224
ENSMUSG00000030031	chr6	Kbtbd8	95117240	95117348	5021	-1.55646	1.172244	1.38E-07	1.26E-06	0.074002	-1	46	59	68	34	69	16	32	30	35	19
ENSMUSG00000004446	chr6	Bid	1.21E+08	1.21E+08	3550	1.805199	1.542162	1.42E-07	1.29E-06	0.108859	1	15	21	24	13	30	62	75	57	140	177
ENSMUSG00000021996	chr14	Esd	74732297	74732388	3366	0.878369	6.08133	1.43E-07	1.3E-06	0.032094	1	632	786	916	746	900	1636	1804	1859	2482	2474
ENSMUSG00000060419	chr5	Rps16-ps2	1.29E+08	1.29E+08	441	0.862202	4.052428	1.43E-07	1.3E-06	0.028358	1	182	173	193	181	247	414	526	410	611	523
ENSMUSG00000032313	chr9	Al118078	55326913	55327000	4714	-2.27732	0.521386	1.48E-07	1.34E-06	0.155801	-1	28	42	60	34	29	13	24	4	7	6
ENSMUSG00000085334	chr4	Gm12940	1.27E+08	1.27E+08	2680	1.234417	2.689597	1.48E-07	1.34E-06	0.054239	1	59	69	58	47	79	168	169	244	199	246
ENSMUSG00000003233	chr16	Dvl3	20516982	20517355	4899	-1.1191	4.124916	1.5E-07	1.35E-06	0.050229	-1	314	317	413	439	529	146	299	380	295	175
ENSMUSG00000000183	chr6	Fgf6	1.27E+08	1.27E+08	1232	-2.2852	1.035765	1.5E-07	1.36E-06	0.171651	-1	41	30	84	53	79	11	34	18	14	2
ENSMUSG00000029553	chr6	Tfec	16833381	16834330	1779	1.855005	0.201569	1.51E-07	1.37E-06	0.072078	1	9	6	6	8	7	22	33	38	44	50
ENSMUSG00000081406	chr2	Rps6-ps4	75191073	75191822	750	0.885843	4.208121	1.53E-07	1.38E-06	0.030546	1	192	222	234	180	243	467	563	495	610	636
ENSMUSG00000058183	chr4	Mmel1	1.55E+08	1.55E+08	3475	2.78112	0.529638	1.54E-07	1.39E-06	0.237392	1	2	0	6	9	11	30	119	21	53	42
ENSMUSG00000051000	chr3	Fam160a1	85660061	85661218	7521	-1.03144	6.059166	1.56E-07	1.41E-06	0.044614	-1	1311	1125	1712	1628	1749	758	918	1539	1035	843
ENSMUSG00000000204	chr11	Slfn4	83175186	83175393	3969	4.937361	1.413693	1.57E-07	1.41E-06	0.672648	1	2	0	4	3	4	44	26	5	46	443
ENSMUSG00000068748	chr6	Ptprz1	22875502	22875884	8068	-2.03232	0.045758	1.57E-07	1.42E-06	0.104048	-1	25	10	28	29	42	4	12	11	13	5
ENSMUSG00000032382	chr9	Snx1	66088133	66088569	4339	0.896918	4.671142	1.59E-07	1.43E-06	0.032429	1	232	241	315	289	422	536	881	599	1021	868
ENSMUSG00000008036	chr7	Ap2s1	16738410	16738538	1333	0.890957	5.595704	1.6E-07	1.44E-06	0.032979	1	425	533	666	562	649	1255	1366	1113	1829	1766
ENSMUSG00000041528	chr9	Rnf123	1.08E+08	1.08E+08	6754	-0.86183	7.122633	1.62E-07	1.46E-06	0.031608	-1	2344	2482	3184	3146	4022	2091	2116	2210	2769	2310
ENSMUSG00000032042	chr9	Srpr	35200175	35200213	3364	-0.8547	8.212225	1.63E-07	1.46E-06	0.031302	-1	5541	5425	6870	6266	7948	4250	4333	5317	5258	5332
ENSMUSG00000057101	chr7	Zfp180	24081924	24082238	3886	-0.87046	3.881787	1.64E-07	1.47E-06	0.029166	-1	284	265	392	321	325	199	211	272	306	227
ENSMUSG00000025278	chr14	Flnb	7817957	7818443	9100	-0.9863	4.635357	1.66E-07	1.49E-06	0.039836	-1	444	419	541	653	724	248	423	278	618	427
ENSMUSG00000000275	chr11	Trim25	88999376	89000082	5754	0.965562	4.774014	1.74E-07	1.56E-06	0.038266	1	211	226	399	338	396	632	741	780	905	1155
ENSMUSG00000032560	chr9	Dnajc13	1.04E+08	1.04E+08	11938	-0.827	5.445029	1.75E-07	1.57E-06	0.028497	-1	822	926	985	809	1092	534	787	768	850	741
ENSMUSG00000005886	chr1	Ncoa2	13139105	13142772	15642	-1.17441	4.554327	1.76E-07	1.58E-06	0.056833	-1	575	339	550	627	629	205	299	546	372	271
ENSMUSG00000027180	chr2	Fbxo3	1.04E+08	1.04E+08	7237	-0.90527	6.463823	1.81E-07	1.62E-06	0.034928	-1	1694	1731	2238	1914	2014	1095	1421	1846	1580	1223
ENSMUSG00000031558	chr5	Slit2	47983155	47985218	15079	-1.83796	0.106073	1.81E-07	1.62E-06	0.077041	-1	21	20	34	22	38	14	8	9	13	7
ENSMUSG00000101188	chr1	Eif4a-ps4	60703932	60705149	1218	0.905142	3.992357	1.82E-07	1.63E-06	0.032098	1	148	150	225	163	243	317	410	465	665	587
ENSMUSG00000018567	chr11	Gabarap	69991143	69991802	1844	0.819874	7.26519	1.83E-07	1.64E-06	0.028884	1	1604	1673	1963	1895	2151	3425	4345	4587	5479	5202
ENSMUSG00000049470	chr11	Aff4	53350833	53351129	13450	-0.94836	6.180812	1.84E-07	1.64E-06	0.038251	-1	1462	1102	1807	1567	2140	799	1238	1496	1273	994
ENSMUSG00000040663	chr19	Clcf1	4214238	4214500	3713	1.827877	0.789738	1.85E-07	1.65E-06	0.096534	1	13	8	12	7	18	21	60	60	78	77
ENSMUSG00000056880	chr9	Gadl1	1.16E+08	1.16E+08	3966	-1.25847	4.022496	1.86E-07	1.66E-06	0.064475	-1	235	472	527	306	366	240	189	169	342	173
ENSMUSG00000064345	chrMT	mt-Nd2	3914	4951	1038	-1.02445	12.22866	1.87E-07	1.67E-06	0.045358	-1	78863	103394	137193	135905	78641	55202	72777	70911	94168	79430
ENSMUSG00000030337	chr6	Vamp1	1.25E+08	1.25E+08	8746	-0.88565	4.827017	1.88E-07	1.67E-06	0.032256	-1	587	515	746	577	642	435	493	368	537	475
ENSMUSG00000020431	chr11	Adcy1	7063489	7064235	12522	-1.33069	2.219097	1.89E-07	1.68E-06	0.06367	-1	115	66	110	114	151	49	65	37	93	66
ENSMUSG00000021796	chr14	Bmpr1a	34410734	34414669	6351	-0.95166	6.316788	1.9E-07	1.69E-06	0.038674	-1	1671	1236	1912	1682	2362	920	1307	1631	1508	1003
ENSMUSG00000026208	chr1	Des	75360329	75360992	3754	0.903291	11.5786	1.9E-07	1.69E-06	0.035471	1	24421	30983	40049	42665	41423	80046	80887	105456	105836	90974
ENSMUSG00000024601	chr18	Isoc1	58659482	58659797	2563	-0.89868	4.37312	1.92E-07	1.71E-06	0.032778	-1	428	361	511	462	485	238	355	249	457	410
ENSMUSG00000052889	chr7	Prkcb	1.22E+08	1.22E+08	4749	1.993618	1.061566	1.93E-07	1.71E-06	0.126698	1	14	5	18	13	15	40	74	31	113	113
ENSMUSG00000040254	chr5	Sema3d	12383166	12383674	6521	-2.15839	1.706208	1.93E-07	1.72E-06	0.168612	-1	77	33	69	53	231	19	36	33	35	15
ENSMUSG00000033152	chr6	Podxl2	88842558	88842976	3948	-0.82024	5.124718	1.96E-07	1.74E-06	0.027892	-1	651	593	865	742	887	546	557	563	682	573
ENSMUSG00000021003	chr12	Galc	98202304	98204087	3822	1.105046	2.942653	1.96E-07	1.74E-06	0.044922	1	63	54	99	99	89	140	245	229	342	274
ENSMUSG00000052151	chr10	Ppap2c	79526430	79527248	1645	1.778789	1.482329	1.96E-07	1.74E-06	0.107893	1	16	10	21	23	31	70	79	45	178	119
ENSMUSG00000035352	chr11	Ccl12	82101845	82101972	537	3.475004	1.151564	1.98E-07	1.75E-06	0.38785	1	0	8	8	1	12	110	51	12	80	176
ENSMUSG00000022629	chr15	Kif21a	90933276	90934543	6475	-0.99552	3.749369	2E-07	1.77E-06	0.03893	-1	202	287	358	351	295	165	205	213	195	261
ENSMUSG00000098900	chr7	Gm18190	7265498	7266077	832	-1.73322	0.236181	2.01E-07	1.78E-06	0.075517	-1	31	24	32	25	32	8	12	20	9	11
ENSMUSG00000002458	chr2	Rgs19	1.82E+08	1.82E+08	2230	1.411792	2.329793	2.06E-07	1.82E-06	0.072374	1	46	36	41	35	65	95	179	101	250	225
ENSMUSG00000098948	chr11	Gm27640	3647179	3647325	147	-2.02136	-0.359	2.06E-07	1.82E-06	0.085015	-1	15	11	23	22	27	2	10	9	7	5
ENSMUSG00000037601	chr11	Nme1	93956979	93959513	3342	0.968393	5.870565	2.07E-07	1.83E-06	0.039943	1	510	736	800	614	612	1631	1764	1397	2306	1917
ENSMUSG00000024013	chr17	Fgd2	29360914	29361157	4134	1.582233	1.976365	2.08E-07	1.84E-06	0.089554	1	37	16	31	25	51	119	157	71	153	161
ENSMUSG00000002565	chr12	Scin	40059769	40060627	2999	-1.38398	1.841947	2.11E-07	1.86E-06	0.066721	-1	91	48	86	91	115	36	50	30	58	56
ENSMUSG00000031309	chrX	Rps6ka3	1.59E+08	1.59E+08	8322	-0.87493	6.580881	2.16E-07	1.9E-06	0.033098	-1	1651	1566	2563	1792	2976	1230	1695	1397	1964	1642
ENSMUSG00000036810	chr8	Cnep1r1	88118769	88118869	3563	-0.83398	4.795149	2.19E-07	1.92E-06	0.028833	-1	548	534	697	549	631	338	487	508	610	404
ENSMUSG00000059811	chr17	Atl2	79848392	79850278	3616	-0.91575	7.399814	2.19E-07	1.93E-06	0.03651	-1	3730	3166	4029	3382	4039	2395	2655	3230	2595	2613
ENSMUSG00000023953	chr17	Polh	46172004	46173096	2569	-0.82082	3.845491	2.19E-07	1.93E-06	0.026161	-1	256	264	374	286	356	178	266	221	297	255
ENSMUSG00000003429	chr7	Rps11	45122388	45122558	602	0.833551	7.652116	2.22E-07	1.95E-06	0.030364	1	1797	2253	2579	2488	3029	5115	6007	5485	7237	6210
ENSMUSG00000032939	chr8	Nup93	94214597	94214631	2882	0.842999	4.235931	2.22E-07	1.95E-06	0.028381	1	163	229	246	207	278	424	590	598	678	528

ENSMUSG00000040466	chr7	Blvrb	27447978	27448196	1414	1.084856	3.555643	2.24E-07	1.96E-06	0.046515	1	114	90	140	105	181	288	287	296	442	540
ENSMUSG00000064358	chrMT	mt-Co3	8607	9390	784	-1.59994	3.800805	2.25E-07	1.97E-06	0.104708	-1	256	343	235	667	205	94	128	160	271	178
ENSMUSG00000045193	chr10	Cirbp	80165985	80166076	2604	1.437264	4.675455	2.26E-07	1.99E-06	0.0864	1	204	177	271	242	255	465	627	1776	709	753
ENSMUSG00000079020	chr15	Slc45a4	73577424	73582130	8471	-0.83783	4.914342	2.27E-07	1.99E-06	0.029347	-1	506	531	694	703	820	321	538	568	635	493
ENSMUSG00000021147	chr13	Wdr37	8802968	8805946	8729	-0.8222	4.973615	2.28E-07	2E-06	0.028207	-1	552	555	784	611	881	448	505	578	626	484
ENSMUSG00000020186	chr10	Csrp2	1.11E+08	1.11E+08	973	1.460156	3.47798	2.29E-07	2.01E-06	0.085932	1	79	65	71	109	175	242	581	190	429	463
ENSMUSG00000037270	chr3	4932438A13Rik	36863106	36863348	26985	-1.05536	5.170278	2.31E-07	2.02E-06	0.047381	-1	775	574	948	865	913	391	538	838	518	431
ENSMUSG00000028613	chr4	Lrp8	1.08E+08	1.08E+08	10514	2.221373	-0.24975	2.34E-07	2.05E-06	0.11114	1	1	1	6	3	10	13	23	27	43	33
ENSMUSG00000018819	chr7	Lsp1	1.42E+08	1.42E+08	5174	1.176481	6.130953	2.35E-07	2.05E-06	0.05961	1	772	431	705	619	1104	1755	2836	1324	2702	2773
ENSMUSG00000019082	chr7	Slc25a22	1.41E+08	1.41E+08	4041	1.060589	4.064111	2.35E-07	2.05E-06	0.045986	1	163	133	196	193	218	321	334	554	786	685
ENSMUSG00000026822	chr2	Lcn2	32384633	32384884	2623	3.00881	2.274727	2.35E-07	2.05E-06	0.322068	1	31	7	10	25	9	56	49	474	139	257
ENSMUSG00000046718	chr8	Bst2	71534264	71534480	764	1.75754	4.788153	2.36E-07	2.06E-06	0.128251	1	111	203	301	189	264	1181	883	299	820	1616
ENSMUSG00000075700	chr3	Selt	58576636	58576873	3436	-0.80513	7.224901	2.39E-07	2.08E-06	0.028422	-1	2626	2900	3626	3155	3614	2044	2561	2521	3047	2561
ENSMUSG00000018126	chr15	Baiap2l2	79258195	79258652	2728	1.98024	1.228045	2.4E-07	2.09E-06	0.132432	1	14	6	11	20	24	80	63	137	57	61
ENSMUSG00000102627	chr7	Snurf	59995449	59995554	216	-0.96152	3.147503	2.43E-07	2.12E-06	0.034753	-1	183	162	199	221	203	120	146	125	167	139
ENSMUSG00000025860	chrX	Xiap	42059679	42059851	9262	-0.81883	4.995067	2.51E-07	2.18E-06	0.028264	-1	655	501	803	656	797	381	549	579	689	518
ENSMUSG00000036990	chr8	Otud4	79639618	79640064	8096	-0.92922	6.1867	2.54E-07	2.2E-06	0.037596	-1	1311	1335	1833	1501	2073	848	1096	1613	1283	1019
ENSMUSG00000074129	chr7	Rpl13a	45125558	45126032	3034	0.837502	8.228047	2.54E-07	2.21E-06	0.031041	1	2984	3428	4373	3115	4108	7445	8979	8462	10042	9852
ENSMUSG00000021268	chr12	Meg3	1.1E+08	1.1E+08	18089	1.391173	6.366976	2.55E-07	2.21E-06	0.083299	1	922	407	756	428	1358	1448	2776	3441	3110	3377
ENSMUSG00000076441	chr2	Ass1	31470207	31470339	2414	1.697011	1.517412	2.58E-07	2.24E-06	0.098225	1	16	11	29	35	16	56	121	64	127	125
ENSMUSG00000071722	chrX	Spin4	95022510	95026682	4173	-2.20672	-0.35676	2.58E-07	2.24E-06	0.120772	-1	22	9	22	15	33	1	12	5	7	5
ENSMUSG00000048583	chr7	Igf2	1.43E+08	1.43E+08	5723	1.5819	8.160634	2.6E-07	2.25E-06	0.107318	1	974	1438	2023	2121	6203	7547	11943	9508	12148	9197
ENSMUSG00000085156	chr11	Gm11974	6525591	6525817	1359	1.522714	0.905576	2.64E-07	2.28E-06	0.064873	1	16	10	22	9	18	47	69	58	70	57
ENSMUSG00000020275	chr11	Rel	23741514	23743040	2799	-1.56074	0.657427	2.69E-07	2.33E-06	0.067396	-1	39	23	38	37	55	11	21	21	18	19
ENSMUSG00000035835	chr10	Lppr3	79860475	79861796	4357	2.497025	-0.60722	2.71E-07	2.34E-06	0.12315	1	1	0	2	4	6	8	22	18	25	33
ENSMUSG00000030486	chr7	Zfp108	24257644	24257658	1929	-1.55632	0.554723	2.78E-07	2.4E-06	0.062746	-1	31	24	47	34	42	13	18	22	15	15
ENSMUSG00000004360	chr10	9330159F19Rik	29211643	29211866	5644	-1.14664	4.106119	2.78E-07	2.4E-06	0.055086	-1	352	283	520	478	347	199	242	357	185	246
ENSMUSG00000024695	chr19	Zfp91	12763660	12764380	10046	-0.938	7.416566	2.79E-07	2.4E-06	0.038981	-1	3211	3459	4457	3892	3666	2067	2472	3722	2892	2497
ENSMUSG00000099398	chr19	Ms4a14	11301249	11304622	4065	2.419779	0.39125	2.79E-07	2.4E-06	0.162422	1	6	12	3	4	4	23	70	19	67	55
ENSMUSG00000028961	chr4	Pgd	1.49E+08	1.49E+08	6447	1.595116	5.497276	2.8E-07	2.41E-06	0.108568	1	263	272	351	456	563	758	984	851	2427	3176
ENSMUSG00000036894	chr3	Rap2b	61361638	61368430	6793	1.265916	3.773961	2.8E-07	2.41E-06	0.066025	1	108	110	133	121	200	271	357	257	764	658
ENSMUSG00000091996	chr9	BC049352	45182007	45182315	2404	-2.16713	0.807484	2.8E-07	2.41E-06	0.154301	-1	36	48	67	57	24	21	22	6	10	11
ENSMUSG00000029651	chr5	Mtus2	1.48E+08	1.48E+08	9905	2.115894	0.089471	2.81E-07	2.42E-06	0.11137	1	4	3	2	8	12	20	34	54	32	36
ENSMUSG00000062248	chr13	Cks2	51645232	51645471	692	1.585868	1.558222	2.86E-07	2.46E-06	0.08582	1	10	33	27	16	31	88	115	71	124	92
ENSMUSG00000037712	chr14	Fermt2	45458792	45460023	3746	-0.86598	7.528529	2.87E-07	2.47E-06	0.033366	-1	3442	3351	4812	3761	4657	2391	3355	3622	3274	2591
ENSMUSG00000040560	chr18	Wdr7	63708695	63708919	7109	-0.79966	5.152372	2.89E-07	2.48E-06	0.027319	-1	667	653	860	695	906	492	583	682	709	558
ENSMUSG00000039967	chr4	Zfp292	34803113	34812043	9986	-1.01986	3.573718	2.92E-07	2.51E-06	0.041976	-1	253	170	272	284	362	125	181	248	211	154
ENSMUSG00000068115	chr2	Ninl	1.51E+08	1.51E+08	5952	1.637746	0.975264	2.93E-07	2.51E-06	0.08134	1	12	13	19	13	17	42	99	42	89	55
ENSMUSG00000050777	chr1	Tmem37	1.2E+08	1.2E+08	1311	1.39423	4.454637	2.96E-07	2.54E-06	0.082344	1	182	272	187	205	121	625	532	1052	975	500
ENSMUSG00000026426	chr1	Arl8a	1.35E+08	1.35E+08	2299	1.046863	4.506352	2.97E-07	2.54E-06	0.046477	1	210	199	269	246	316	389	543	1064	878	738
ENSMUSG00000018750	chr11	Zbtb4	69765912	69766085	8117	-0.8019	5.300114	2.98E-07	2.55E-06	0.027696	-1	762	659	983	836	954	508	739	719	758	631
ENSMUSG00000035683	chr4	Melk	44300876	44301072	2972	2.02064	1.084295	3.08E-07	2.64E-06	0.136062	1	13	14	9	8	20	30	73	38	145	99
ENSMUSG00000033658	chr8	Ddx19b	1.11E+08	1.11E+08	6742	-0.80218	4.789503	3.16E-07	2.7E-06	0.027263	-1	514	500	729	511	693	384	504	444	533	482
ENSMUSG00000038034	chr1	Igsf8	1.72E+08	1.72E+08	5217	1.043575	4.199618	3.21E-07	2.74E-06	0.045989	1	164	129	228	205	288	402	530	379	921	704
ENSMUSG00000027961	chr3	Lrrc39	1.17E+08	1.17E+08	5230	-0.91279	6.157568	3.23E-07	2.75E-06	0.036894	-1	1265	1565	1910	1545	1458	1112	1116	1153	1232	1092
ENSMUSG00000013160	chr8	Atp6v0d1	1.06E+08	1.06E+08	1793	0.826592	5.624988	3.27E-07	2.79E-06	0.029867	1	519	519	629	571	736	1146	1265	1267	2001	1743
ENSMUSG00000027940	chr3	Tpm3	90072649	90072850	6085	1.283507	6.622495	3.27E-07	2.79E-06	0.072636	1	542	1022	625	1407	1180	2364	2277	3501	5185	3281
ENSMUSG00000025188	chr19	Hps1	42755105	42755796	5855	1.451067	1.927158	3.3E-07	2.81E-06	0.076397	1	25	22	34	34	51	86	109	76	191	176
ENSMUSG00000074909	chr19	Ranbp6	29808108	29812974	4867	-0.86462	3.781279	3.32E-07	2.82E-06	0.030106	-1	238	267	375	282	320	194	260	215	264	198
ENSMUSG00000018377	chr11	Vezf1	88068279	88068433	4601	-0.94582	5.831934	3.34E-07	2.85E-06	0.03956	-1	1160	885	1381	1377	1496	658	818	1252	906	898
ENSMUSG00000015755	chr10	Tab2	7905653	7907577	6135	-0.87432	6.646873	3.35E-07	2.85E-06	0.034163	-1	2101	1718	2474	2213	2309	1287	1674	2022	1693	1547
ENSMUSG00000025384	chr11	2310003H01Rik	1.2E+08	1.2E+08	5212	-1.03696	4.12972	3.36E-07	2.86E-06	0.045615	-1	283	407	531	362	379	207	320	165	363	295
ENSMUSG00000061273	chrX	Mmgt1	56585512	56589303	4234	-0.80455	5.466369	3.39E-07	2.88E-06	0.028289	-1	855	793	1082	915	1051	669	767	634	919	758
ENSMUSG00000097188	chr19	Snhg1	8723496	8725256	2947	1.584725	3.378493	3.39E-07	2.88E-06	0.103802	1	81	78	120	52	98	188	266	737	307	298
ENSMUSG00000025794	chr9	Rpl14	1.21E+08	1.21E+08	935	0.82148	7.667346	3.41E-07	2.89E-06	0.030443	1	1910	2291	2650	2395	3085	5390	6177	5663	6955	5957
ENSMUSG00000029465	chr5	Arpc3	1.22E+08	1.22E+08	2581	0.900982	5.948211	3.41E-07	2.89E-06	0.035936	1	561	702	916	622	801	1559	1725	1468	2402	2256
ENSMUSG00000022033	chr14	Pbk	65805837	65806134	1791	1.885531	1.77423	3.43E-07	2.91E-06	0.133397	1	16	14	17	16	57	82	111	62	223	140
ENSMUSG00000044734	chr13	Serpinb1a	32842092	32843222	1943	1.592138	5.138124	3.43E-07	2.91E-06	0.109451	1	182	331	400	177	386	1261	1654	383	1590	1226
ENSMUSG00000007836	chr13	Hnrnpa0	58125879	58128556	2678	0.808794	5.648577	3.45E-07	2.92E-06	0.028734	1	450	530	721	599	771	1164	1463	1348	2113	1433
ENSMUSG00000022194	chr14	Pabpn1	54892500	54892738	3035	0.839401	5.129653	3.46E-07	2.93E-06	0.030474	1	379	388	514	364	440	790	982	1015	1167	1283
ENSMUSG00000027327	chr2	1700037H04Rik	1.31E+08	1.31E+08	2286	2.049528	3.484945	3.48E-07	2.94E-06	0.172086	1	53	46	61	100	103	190	244	127	696	907
ENSMUSG00000071083	chr8	Gm10311	69373528	69373914	387	-1.75797	0.132639	3.49E-07	2.95E-06	0.078486	-1	22	25	36	29	22	7	17	13	9	9
ENSMUSG00000101152	chr9	Gm28305	1.04E+08	1.04E+08	365	-1.31873	1.903218	3.51E-07	2.96E-06	0.062916	-1	67	77	97	97	105	30	63	64	61	31
ENSMUSG00000024302	chr18	Dtna	23415415	23415625	6587	-0.82976	6.698291	3.55E-07	2.99E-06	0.030912	-1	2007	1928	2449	2230	2475	1607	1842	1620	1956	1632
ENSMUSG00000024854	chr19	Pold4	4231899	4232188	910	0.968967	3.891566	3.59E-07	3.03E-06	0.038677	1	163	165	198	160	133	350	503	530	480	404
ENSMUSG00000012819	chr10	Cdh23	60302748	60303700	16939	-1.60836	1.378933	3.62E-07	3.05E-06	0.091112	-1	61	28	78	90	68	19	44	26	33	26

ENSMUSG00000040675	chr10	Mthfd1l	3973118	3973478	4435	1.635484	1.502413	3.62E-07	3.05E-06	0.093697	1	21	18	19	12	40	50	77	82	153	126
ENSMUSG00000032050	chr9	Rdx	52047150	52047235	4841	-0.95818	7.196144	3.63E-07	3.06E-06	0.041422	-1	2716	2585	3537	3238	4254	1454	2256	3332	2699	1999
ENSMUSG00000018334	chr11	Ksr1	79013440	79016263	6621	-0.8561	6.940446	3.65E-07	3.07E-06	0.033047	-1	2178	2090	2947	2781	3342	1806	2039	1921	2003	2329
ENSMUSG00000044948	chr19	Cfap43	47737561	47737887	9955	1.493593	1.567665	3.71E-07	3.12E-06	0.076202	1	27	18	32	13	34	63	78	95	118	137
ENSMUSG00000062901	chr16	Klhl24	20097554	20097671	6683	-1.30433	6.718668	3.75E-07	3.15E-06	0.075836	-1	2215	1991	2409	2931	3000	797	1229	2706	1353	1025
ENSMUSG00000099697	chr7	Gm4790	39552496	39556305	4345	-1.89964	0.127104	3.77E-07	3.17E-06	0.101219	-1	23	18	38	31	28	6	11	19	12	3
ENSMUSG00000067653	chr1	Ankrd23	36530188	36531641	2697	-1.11202	11.59939	3.78E-07	3.18E-06	0.056022	-1	64070	57990	94880	67664	70632	51059	52261	25894	49498	45933
ENSMUSG00000006221	chr4	Hspb7	1.41E+08	1.41E+08	2769	1.474294	8.523295	3.79E-07	3.18E-06	0.096465	1	1723	2644	3153	6062	2706	8252	11625	20770	12769	9806
ENSMUSG00000085411	chr2	Gm14319	1.68E+08	1.68E+08	703	-1.90888	-0.01496	3.79E-07	3.18E-06	0.093813	-1	22	14	32	32	24	8	16	9	7	5
ENSMUSG00000025316	chr8	Banp	1.22E+08	1.22E+08	6632	-1.004	3.444604	3.82E-07	3.2E-06	0.040917	-1	203	259	235	227	276	140	213	182	175	127
ENSMUSG00000026094	chr1	Stk17b	53755506	53757770	5185	1.072759	4.125103	3.83E-07	3.21E-06	0.049197	1	163	127	241	165	251	342	871	459	620	478
ENSMUSG00000023827	chr17	Agpat4	12118704	12118840	2701	1.311657	3.187423	3.84E-07	3.22E-06	0.0708	1	87	42	81	73	157	188	377	208	398	348
ENSMUSG00000051550	chr7	Zfp579	4983483	4983540	4159	0.963814	3.155342	3.86E-07	3.23E-06	0.035883	1	96	72	110	100	121	180	309	237	345	301
ENSMUSG00000068747	chr3	Sort1	1.08E+08	1.08E+08	7560	-0.86147	7.012749	3.86E-07	3.23E-06	0.033646	-1	2619	2055	3311	2535	3515	1540	1994	2328	2327	2546
ENSMUSG00000033964	chr1	Zbtb41	1.39E+08	1.39E+08	8362	-0.89662	3.961534	3.87E-07	3.23E-06	0.03349	-1	318	259	365	296	464	198	292	295	271	208
ENSMUSG00000000902	chr10	Smarcb1	75896769	75897088	7930	0.781511	4.428381	3.91E-07	3.26E-06	0.025554	1	228	229	271	251	342	469	659	605	769	678
ENSMUSG00000030104	chr6	Edem1	1.09E+08	1.09E+08	5858	1.112105	4.56235	3.92E-07	3.27E-06	0.053776	1	264	182	228	223	348	396	604	642	1146	1079
ENSMUSG00000026840	chr2	Lamc3	31887291	31887743	6091	-1.81955	1.006211	3.96E-07	3.3E-06	0.112775	-1	50	26	72	39	74	15	21	33	10	20
ENSMUSG00000001173	chrX	Ocrl	47912387	47912691	9486	-0.814	4.24836	3.99E-07	3.32E-06	0.027796	-1	372	347	475	364	463	246	326	368	333	328
ENSMUSG00000028584	chr4	Lrrc38	1.43E+08	1.43E+08	2324	-1.13328	4.76504	3.99E-07	3.32E-06	0.056359	-1	626	470	690	652	673	466	415	220	395	439
ENSMUSG00000028692	chr4	Akr1a1	1.17E+08	1.17E+08	2750	0.860993	8.039462	4.07E-07	3.39E-06	0.03393	1	2725	2733	3816	2798	3587	6171	6731	6656	10862	9602
ENSMUSG00000035629	chr16	1700021K19Rik	32821703	32824146	7478	-0.78535	5.440028	4.09E-07	3.4E-06	0.027294	-1	744	730	1067	897	1201	582	782	800	854	703
ENSMUSG00000038970	chr5	Lmtk2	1.44E+08	1.44E+08	8114	-0.88844	4.797298	4.2E-07	3.49E-06	0.03453	-1	549	485	668	651	659	353	427	609	465	409
ENSMUSG00000025790	chr7	Slco3a1	74275419	74276088	8474	-1.094	5.150352	4.23E-07	3.51E-06	0.053259	-1	582	777	913	1104	628	529	602	369	617	499
ENSMUSG00000031807	chr8	Pgls	71592176	71592504	3770	0.880174	4.692995	4.23E-07	3.51E-06	0.033594	1	205	316	343	313	339	616	704	652	1017	933
ENSMUSG00000031168	chrX	Ebp	8185329	8185833	2310	1.010599	3.780254	4.24E-07	3.52E-06	0.042603	1	113	143	144	135	226	378	452	275	541	479
ENSMUSG00000032705	chr12	Exd2	80463095	80463280	3323	-0.8736	5.001503	4.38E-07	3.64E-06	0.033684	-1	655	536	965	616	697	450	554	530	533	550
ENSMUSG00000029311	chr5	Hsd17b11	1.04E+08	1.04E+08	3265	0.876525	3.848762	4.43E-07	3.67E-06	0.031719	1	151	132	211	164	187	263	435	492	488	503
ENSMUSG00000022674	chr16	Ube2v2	15552677	15556543	4275	-0.92613	3.482338	4.53E-07	3.75E-06	0.03494	-1	221	230	305	210	248	150	208	159	231	150
ENSMUSG00000103661	chr1	ANKRD23	36530193	36531641	2327	-1.10378	11.56956	4.58E-07	3.79E-06	0.056018	-1	62562	56697	92831	66149	69128	50253	51345	25473	48580	45225
ENSMUSG00000017861	chr2	Mybl2	1.63E+08	1.63E+08	4632	2.125173	0.625151	4.68E-07	3.87E-06	0.151158	1	2	3	13	7	20	35	52	28	104	54
ENSMUSG00000032388	chr9	Spg21	65460937	65461154	2690	0.975606	4.550498	4.68E-07	3.87E-06	0.041832	1	220	184	295	217	425	437	880	589	932	835
ENSMUSG00000027863	chr3	Cd2	1.01E+08	1.01E+08	1741	2.628375	-0.67595	4.68E-07	3.87E-06	0.131533	1	0	3	2	5	1	12	21	9	29	30
ENSMUSG00000024276	chr18	Zfp397	23954688	23954861	5487	-0.82344	3.95709	4.69E-07	3.87E-06	0.028342	-1	332	269	348	318	382	187	283	295	299	246
ENSMUSG00000035151	chr8	Elmod2	83312632	83316461	11138	-0.84146	3.560576	4.69E-07	3.87E-06	0.028453	-1	219	227	297	239	278	153	208	167	243	216
ENSMUSG00000028096	chr3	Gpr89	96868281	96871594	5365	-0.79103	4.285127	4.7E-07	3.88E-06	0.026537	-1	338	367	476	399	487	282	285	344	411	341
ENSMUSG00000025574	chr11	Tk1	1.18E+08	1.18E+08	5198	1.24827	2.699685	4.73E-07	3.9E-06	0.06148	1	52	66	64	51	81	161	167	147	382	213
ENSMUSG00000055639	chr14	Dach1	97786853	97789619	7317	-1.39975	1.982479	4.74E-07	3.91E-06	0.074309	-1	54	68	130	142	85	39	45	47	66	55
ENSMUSG00000037139	chr4	Myom3	1.36E+08	1.36E+08	6038	1.626274	6.09104	4.78E-07	3.94E-06	0.117617	1	411	484	395	1090	345	1356	3570	1812	4010	1653
ENSMUSG00000000134	chrX	Tfe3	7762560	7762630	9261	0.937898	4.125572	4.8E-07	3.95E-06	0.037787	1	147	157	196	215	292	333	502	449	792	644
ENSMUSG00000030689	chr7	Ino80e	1.27E+08	1.27E+08	4648	0.841369	3.779823	4.84E-07	3.98E-06	0.029044	1	131	140	170	164	215	313	420	339	575	416
ENSMUSG00000039168	chr15	Dap	31224314	31224583	1925	1.290139	4.855721	4.84E-07	3.98E-06	0.074309	1	271	155	271	238	496	720	1117	463	1354	1194
ENSMUSG00000048410	chr18	Zfp407	84128027	84128353	15167	-1.08799	2.688624	4.87E-07	4E-06	0.046756	-1	135	99	179	145	176	52	119	91	128	97
ENSMUSG00000055027	chr6	Smyd1	71213940	71215909	4546	-0.95025	9.112387	4.9E-07	4.02E-06	0.041926	-1	8885	11960	14740	12520	12947	9176	8901	6257	10167	8987
ENSMUSG00000065460	chr2	Mir133a-2	1.8E+08	1.8E+08	104	1.526998	1.694592	4.9E-07	4.02E-06	0.085089	1	16	29	40	18	31	90	124	76	91	150
ENSMUSG00000034297	chr11	Med13	86267033	86271118	10840	-1.05856	5.688987	4.93E-07	4.04E-06	0.050961	-1	1080	834	1340	1142	1477	467	738	1271	800	648
ENSMUSG00000084329	chr11	Gm6733	72833461	72835380	1920	-1.50778	0.87955	4.98E-07	4.08E-06	0.07196	-1	36	37	49	42	59	15	14	15	34	32
ENSMUSG00000059588	chr2	Calcrl	84330626	84333678	4882	-1.24417	4.035066	5.07E-07	4.15E-06	0.068359	-1	337	337	357	480	399	110	178	392	306	172
ENSMUSG00000025195	chr19	Dnmbp	43847967	43848278	4882	-0.98173	3.722382	5.08E-07	4.15E-06	0.040841	-1	280	192	342	284	376	144	210	284	230	167
ENSMUSG00000032038	chr9	St3gal4	35046579	35047519	2029	1.188266	3.162085	5.11E-07	4.18E-06	0.058298	1	113	61	84	85	102	204	350	180	367	345
ENSMUSG00000040430	chr11	Pitpnc1	1.07E+08	1.07E+08	6612	-0.90964	6.171392	5.12E-07	4.19E-06	0.037994	-1	1541	1371	1423	1883	1542	918	1091	1392	1268	1162
ENSMUSG00000062519	chr6	Zfp398	47835661	47835920	6478	-1.38225	1.481019	5.12E-07	4.19E-06	0.067563	-1	51	58	62	69	94	24	27	47	56	26
ENSMUSG00000016541	chr15	Atxn10	85336381	85336580	2425	0.79923	5.627359	5.14E-07	4.2E-06	0.02892	1	551	439	664	550	838	1101	1541	1351	1824	1547
ENSMUSG00000003824	chr8	Syce2	84872111	84872253	1968	1.883179	0.351249	5.14E-07	4.2E-06	0.104014	1	6	2	7	9	17	26	43	30	74	41
ENSMUSG00000085882	chr11	2610507I01Rik	59199836	59200302	1360	-1.24131	1.553561	5.2E-07	4.24E-06	0.052118	-1	55	67	80	59	78	29	36	47	42	46
ENSMUSG00000027366	chr2	Sppl2a	1.27E+08	1.27E+08	8665	-0.79556	6.26921	5.23E-07	4.27E-06	0.029124	-1	1452	1441	1822	1738	1694	996	1268	1413	1654	1289
ENSMUSG00000030697	chr7	Ppp4c	1.27E+08	1.27E+08	1293	0.862415	4.807008	5.23E-07	4.27E-06	0.032886	1	271	322	369	325	362	650	874	612	1113	988
ENSMUSG00000040565	chr19	Btaf1	36926079	36926401	7204	-0.92008	3.680247	5.25E-07	4.27E-06	0.035652	-1	272	206	329	241	359	117	198	240	276	219
ENSMUSG00000092907	chrX	Mir5132	74023528	74023598	71	-1.99563	0.136768	5.27E-07	4.29E-06	0.121902	-1	29	22	29	29	31	2	13	17	16	2
ENSMUSG00000015002	chr15	Efr3a	65787034	65787246	11091	-0.77313	5.473766	5.3E-07	4.31E-06	0.027016	-1	805	700	1005	1007	1205	592	761	777	943	771
ENSMUSG00000022186	chr15	Oxct1	4026383	4026849	3701	-1.0566	8.715226	5.42E-07	4.41E-06	0.052002	-1	7845	10082	10637	10620	7548	5826	7590	4122	8659	5728
ENSMUSG00000027248	chr2	Pdia3	1.21E+08	1.21E+08	3139	1.045237	7.313399	5.44E-07	4.42E-06	0.050711	1	1352	1329	1908	1554	2704	4207	5647	2816	6774	5738
ENSMUSG00000026490	chr1	Cdc42bpa	1.8E+08	1.8E+08	21522	-0.82415	4.928569	5.47E-07	4.44E-06	0.030388	-1	557	472	718	687	849	332	544	592	640	485
ENSMUSG00000087080	chr11	Gm12199	50717670	50717976	517	-2.19058	2.247132	5.47E-07	4.44E-06	0.194973	-1	123	124	156	117	124	52	47	2	41	51
ENSMUSG00000099083	chr15	Atf7	1.03E+08	1.03E+08	10988	-0.84493	5.730397	5.47E-07	4.44E-06	0.032674	-1	1036	814	1319	1098	1490	666	808	1094	1046	829
ENSMUSG00000000028	chr16	Cdc45	18780447	18780573	2252	1.321206	2.186924	5.59E-07	4.53E-06	0.066917	1	44	33	39	34	61	121	173	87	221	142

ENSMUSG00000026062	chr1	Slc9a2	40680574	40682165	6984	-0.9329	5.581397	5.59E-07	4.53E-06	0.039828	-1	750	888	1285	1117	1265	751	895	508	906	749
ENSMUSG00000027368	chr2	Dusp2	1.27E+08	1.27E+08	2003	1.540086	0.801966	5.66E-07	4.58E-06	0.069447	1	8	14	17	10	20	34	56	58	60	73
ENSMUSG00000042594	chr5	Sh2b3	1.22E+08	1.22E+08	4734	0.801669	5.201147	5.65E-07	4.58E-06	0.028875	1	392	388	483	472	497	714	1109	1217	1435	1042
ENSMUSG00000029577	chr5	Ube3b	1.14E+08	1.14E+08	5264	-0.80741	7.542903	5.68E-07	4.59E-06	0.030572	-1	3386	3268	4413	4493	4293	2608	2891	3317	3628	3364
ENSMUSG00000029461	chr7	Fam168a	1.01E+08	1.01E+08	6632	-0.80648	5.505912	5.71E-07	4.61E-06	0.029684	-1	821	726	1161	1036	1121	535	836	875	954	690
ENSMUSG00000059423	chr4	Zfp933	1.48E+08	1.48E+08	4270	-0.95027	3.003864	5.8E-07	4.68E-06	0.036131	-1	146	168	200	163	201	94	117	127	189	116
ENSMUSG00000060636	chr16	Rpl35a	33056453	33056510	3526	0.881293	7.053932	5.83E-07	4.71E-06	0.036312	1	1305	1555	2007	1239	1701	3683	4090	3690	4304	4137
ENSMUSG00000025986	chr1	Slc39a10	46807544	46810111	6095	-0.95673	3.449912	5.85E-07	4.72E-06	0.038343	-1	216	206	238	214	332	145	164	162	270	132
ENSMUSG00000057469	chr12	E2f6	16810965	16811315	2421	-0.90774	6.700355	5.85E-07	4.72E-06	0.03843	-1	1885	2282	2735	2280	2065	1546	1696	1880	1787	1438
ENSMUSG00000051007	chr7	Pddc1	1.41E+08	1.41E+08	2871	0.962706	3.150284	5.86E-07	4.72E-06	0.037199	1	81	77	130	83	131	178	265	270	331	321
ENSMUSG00000026683	chr1	Nuf2	1.69E+08	1.69E+08	6341	1.77547	1.52539	5.87E-07	4.72E-06	0.11926	1	13	11	16	20	46	66	97	53	178	113
ENSMUSG00000021569	chr13	Trip13	73912462	73913339	2267	2.139376	0.494421	5.92E-07	4.77E-06	0.144995	1	5	3	8	11	12	22	30	36	116	48
ENSMUSG00000019768	chr10	Esr1	4611593	4612155	13661	-1.04695	4.450389	5.94E-07	4.77E-06	0.049193	-1	403	416	442	492	727	297	413	180	421	352
ENSMUSG00000005410	chr8	Mcm5	75109528	75109621	3422	1.457674	2.904736	5.94E-07	4.77E-06	0.089619	1	42	60	71	47	114	161	226	125	444	341
ENSMUSG00000072235	chr15	Tuba1a	98949841	98951014	1647	1.414994	7.05654	5.97E-07	4.8E-06	0.092044	1	923	837	1091	1118	2269	3754	7053	1826	5560	4485
ENSMUSG00000097431	chr14	Gm26782	50870364	50870556	2650	-1.07485	2.649373	5.98E-07	4.8E-06	0.045513	-1	103	138	172	152	140	71	81	112	98	105
ENSMUSG00000057762	chr13	Gm6169	97098237	97099296	1060	1.491916	1.445292	6.09E-07	4.89E-06	0.078546	1	8	25	29	24	28	73	81	67	139	90
ENSMUSG00000039004	chr13	Bmp6	38345716	38346587	2410	-1.11994	2.815888	6.1E-07	4.89E-06	0.051221	-1	116	118	212	206	155	72	90	131	114	109
ENSMUSG00000045690	chr12	Wdr89	75630596	75633508	3192	0.898006	4.20664	6.18E-07	4.95E-06	0.03525	1	155	213	199	253	248	524	478	494	662	610
ENSMUSG00000036745	chr3	Ttll7	1.47E+08	1.47E+08	8105	-1.24172	6.556167	6.19E-07	4.96E-06	0.071528	-1	2033	1828	2673	2286	2212	835	1131	2434	1099	996
ENSMUSG00000059866	chr5	Tnip2	34496087	34496950	2879	1.065884	2.53649	6.21E-07	4.97E-06	0.043257	1	55	54	67	51	80	135	152	198	256	164
ENSMUSG00000041774	chr16	Ydjc	17144621	17144938	5556	2.225508	0.197342	6.23E-07	4.99E-06	0.145612	1	5	2	8	11	3	25	34	17	78	45
ENSMUSG00000020440	chr6	Arf5	28423560	28423755	1116	0.821942	5.937455	6.29E-07	5.03E-06	0.031301	1	597	716	863	706	809	1589	1701	1651	2064	2079
ENSMUSG00000036095	chr12	Dgkb	37880705	37880954	5544	-1.79165	-0.07127	6.32E-07	5.05E-06	0.085022	-1	32	18	23	18	24	6	12	9	14	6
ENSMUSG00000029467	chr5	Atp2a2	1.22E+08	1.22E+08	5293	1.114373	7.488435	6.35E-07	5.07E-06	0.058229	1	1011	1696	1554	2762	2564	3924	7231	5397	7573	4929
ENSMUSG00000026628	chr1	Atf3	1.91E+08	1.91E+08	2154	1.885442	3.815259	6.47E-07	5.17E-06	0.155676	1	50	59	53	144	207	290	738	176	840	600
ENSMUSG00000062054	chr12	Iah1	21316392	21316512	924	1.113166	3.084937	6.53E-07	5.21E-06	0.05157	1	64	73	114	79	117	164	259	192	366	379
ENSMUSG00000018585	chr11	Atox1	55446641	55446784	541	0.8709	4.538643	6.55E-07	5.22E-06	0.033772	1	242	259	316	251	293	617	663	503	902	809
ENSMUSG00000000782	chr11	Tcf7	52252371	52253962	2625	1.609798	0.844414	6.61E-07	5.27E-06	0.081789	1	8	15	14	14	17	29	88	53	73	53
ENSMUSG00000061601	chr5	Pclo	14514918	14515460	19182	-1.98121	0.104742	6.62E-07	5.27E-06	0.120061	-1	40	25	22	13	35	9	9	5	11	14
ENSMUSG00000064340	chrMT	mt-Tl1	2676	2750	75	-1.06326	5.4509	6.63E-07	5.28E-06	0.052462	-1	765	963	1047	1434	654	476	627	714	844	672
ENSMUSG00000101746	chr1	2310043L19Rik	1.78E+08	1.78E+08	698	1.959603	0.400709	6.7E-07	5.33E-06	0.112928	1	2	13	9	7	9	44	59	25	45	44
ENSMUSG00000069769	chr11	Msi2	88339382	88344660	10405	-0.8225	6.98137	6.73E-07	5.35E-06	0.032013	-1	2381	2389	3251	2667	2777	1747	2414	2179	2467	1836
ENSMUSG00000057236	chr4	Rbbp4	1.29E+08	1.29E+08	8744	0.792996	6.43278	6.74E-07	5.35E-06	0.029544	1	930	858	1250	958	1319	2014	2505	2855	2911	2488
ENSMUSG00000087006	chr2	Gm13889	93955810	93957049	1392	1.423146	2.543512	6.77E-07	5.38E-06	0.083938	1	33	41	59	69	58	201	187	88	304	189
ENSMUSG00000063077	chr4	Kif1b	1.49E+08	1.49E+08	17608	-0.81732	8.987883	6.8E-07	5.39E-06	0.031941	-1	9157	8920	11927	11785	12542	7368	8432	9957	9104	7738
ENSMUSG00000085894	chr1	Gm15832	39547570	39547661	1832	1.323321	1.907857	6.81E-07	5.4E-06	0.064494	1	35	34	33	26	43	73	107	98	170	166
ENSMUSG00000046330	chr1	Rpl37a	72711260	72711323	584	0.81503	7.366564	6.87E-07	5.45E-06	0.031561	1	1617	1947	2350	1770	2320	4340	4833	4608	5561	5082
ENSMUSG00000086584	chr11	Gm12002	12314514	12314667	2757	-1.29765	1.829797	6.88E-07	5.45E-06	0.063853	-1	81	83	106	83	58	32	47	52	61	47
ENSMUSG00000025240	chr9	Sacm1l	1.24E+08	1.24E+08	3433	-0.79069	5.178762	6.91E-07	5.48E-06	0.028661	-1	600	707	767	793	979	444	696	663	744	567
ENSMUSG00000002028	chr9	Kmt2a	44803355	44808177	16670	-0.97765	4.679147	6.97E-07	5.52E-06	0.043762	-1	536	408	577	610	719	208	370	573	483	411
ENSMUSG00000038084	chr16	Opa1	29579334	29579571	7875	-0.83225	6.701301	6.99E-07	5.53E-06	0.032794	-1	1777	2172	2279	2609	2222	1386	1660	1831	2158	1730
ENSMUSG00000024588	chr18	Fech	64456550	64458217	2901	-0.9328	7.023546	7E-07	5.53E-06	0.041259	-1	2543	2563	3400	2901	2801	1586	2135	2840	2228	1628
ENSMUSG00000090862	chr7	Rps13	1.16E+08	1.16E+08	582	0.82933	7.078464	7.01E-07	5.54E-06	0.032658	1	1315	1495	1932	1461	1966	3696	4170	3718	4174	4206
ENSMUSG00000064193	chr2	Gm4735	80837141	80838442	1302	1.386216	1.455163	7.04E-07	5.56E-06	0.066366	1	19	23	23	25	30	65	87	55	139	101
ENSMUSG00000040390	chr7	Map3k10	27656375	27656986	4142	-0.76196	4.999254	7.08E-07	5.58E-06	0.02636	-1	603	576	756	678	742	480	560	515	635	566
ENSMUSG00000075415	chr2	Fnbp1	31026206	31033188	10030	0.887032	4.560057	7.08E-07	5.58E-06	0.035519	1	245	175	313	259	409	466	784	645	856	847
ENSMUSG00000029765	chr6	Plxna4	32144268	32150584	12877	-1.18658	2.650336	7.2E-07	5.68E-06	0.058087	-1	130	102	143	188	162	78	99	54	135	82
ENSMUSG00000042349	chr1	Ikbke	1.31E+08	1.31E+08	9018	1.996515	1.990561	7.21E-07	5.68E-06	0.161812	1	25	10	36	15	45	63	120	68	200	283
ENSMUSG00000020635	chr12	Fkbp1b	4833175	4833795	979	1.639838	0.237147	7.26E-07	5.71E-06	0.061513	1	9	8	9	6	10	26	42	32	46	40
ENSMUSG00000026380	chr1	Tfcp2l1	1.19E+08	1.19E+08	9438	-2.16331	1.813267	7.27E-07	5.72E-06	0.189809	-1	91	62	176	109	38	13	19	65	25	27
ENSMUSG00000064493	chr12	Snora28	1.12E+08	1.12E+08	127	-1.79366	0.468232	7.31E-07	5.75E-06	0.103008	-1	34	27	55	30	27	9	18	23	11	8
ENSMUSG00000042473	chrX	Tbc1d8b	1.4E+08	1.4E+08	5211	-1.31304	2.774126	7.37E-07	5.79E-06	0.07367	-1	161	99	211	117	237	53	136	59	128	89
ENSMUSG00000073590	chr18	3222401L13Rik	37655451	37661742	6292	-1.50223	0.562519	7.47E-07	5.87E-06	0.069289	-1	41	25	37	36	36	8	19	19	26	16
ENSMUSG00000051890	chr12	Klhdc1	69241176	69241381	3137	-1.01735	4.146266	7.52E-07	5.91E-06	0.046609	-1	337	337	516	401	386	248	224	381	227	258
ENSMUSG00000039000	chr5	Ube3c	29569242	29569580	5033	-0.78446	6.000399	7.54E-07	5.92E-06	0.028992	-1	1116	1232	1619	1340	1464	871	1222	1074	1264	1060
ENSMUSG00000042377	chr11	Fam83g	61684091	61684168	6659	1.978266	0.70558	7.68E-07	6.02E-06	0.131266	1	5	8	6	19	12	39	33	93	71	42
ENSMUSG00000023965	chr17	Fbxl17	63057452	63060411	5526	-0.82782	5.420111	7.74E-07	6.07E-06	0.031974	-1	710	840	1185	952	889	653	667	713	864	685
ENSMUSG00000025366	chr10	Esyt1	1.29E+08	1.29E+08	3687	0.889467	5.783736	7.78E-07	6.09E-06	0.037267	1	492	517	695	681	876	1084	1650	1294	2599	1918
ENSMUSG00000061983	chr10	Rps12	23785211	23785273	476	0.865188	7.868767	7.78E-07	6.09E-06	0.035994	1	2245	2521	3419	2275	3490	6251	7738	5627	7566	7805
ENSMUSG00000038872	chr8	Zfhx3	1.09E+08	1.09E+08	17569	-0.97146	3.525704	7.8E-07	6.11E-06	0.04073	-1	225	156	246	256	411	128	196	191	208	186
ENSMUSG00000020821	chr11	Kif1c	70700548	70700709	7276	-0.90066	9.467464	7.87E-07	6.16E-06	0.039168	-1	13342	13567	17287	17116	15475	9197	9500	15314	11648	11652
ENSMUSG00000037754	chr2	Ppp1r16b	1.59E+08	1.59E+08	8844	-1.24931	2.406483	7.88E-07	6.16E-06	0.064173	-1	76	110	125	183	126	42	68	82	109	70
ENSMUSG00000092397	chr2	C130080G10Rik	1.14E+08	1.14E+08	2586	-2.784	5.078243	7.89E-07	6.17E-06	0.326568	-1	318	1160	1411	934	1198	310	130	9	208	298
ENSMUSG00000074578	chr2	1500012F01Rik	1.67E+08	1.67E+08	2929	1.341528	3.498744	7.96E-07	6.22E-06	0.079738	1	97	108	144	82	92	235	300	671	295	356
ENSMUSG00000039158	chr4	Akna	63367125	63368286	5765	1.191445	2.441016	8.05E-07	6.28E-06	0.056699	1	41	37	48	63	84	123	197	124	217	207

ENSMUSG00000028108	chr3	Ecm1	95734147	95734470	2521	1.042853	5.260096	8.1E-07	6.31E-06	0.051026	1	422	237	420	348	701	887	1300	865	1623	1405
ENSMUSG00000091086	chr10	Gm5428	1.11E+08	1.11E+08	888	0.880379	4.093106	8.1E-07	6.31E-06	0.034481	1	125	188	264	185	247	422	500	466	558	611
ENSMUSG00000021773	chr14	Comtd1	21845861	21847427	2464	1.280271	2.364367	8.16E-07	6.35E-06	0.065709	1	45	44	48	49	57	141	148	89	242	216
ENSMUSG00000063564	chr11	Col23a1	51289920	51290387	5736	1.253817	2.73583	8.17E-07	6.36E-06	0.065661	1	64	50	60	63	85	135	214	332	257	143
ENSMUSG00000017009	chr2	Sdc4	1.64E+08	1.64E+08	2547	0.819045	5.060419	8.27E-07	6.43E-06	0.031088	1	312	318	407	391	614	741	973	925	1294	1068
ENSMUSG00000032698	chr2	Lmo2	1.04E+08	1.04E+08	2166	1.063271	3.432165	8.27E-07	6.43E-06	0.049104	1	117	75	110	107	173	220	310	257	466	461
ENSMUSG00000036006	chr13	Fam65b	24582189	24582345	11662	-1.38691	3.093258	8.35E-07	6.49E-06	0.084593	-1	138	115	253	153	414	86	121	66	128	149
ENSMUSG00000056498	chr3	Tmem154	84666192	84666415	4738	1.814755	1.580313	8.41E-07	6.53E-06	0.127489	1	24	16	21	15	28	32	91	70	193	155
ENSMUSG00000029915	chr6	Clec5a	40574894	40578080	3840	2.404401	1.272179	8.42E-07	6.54E-06	0.225397	1	8	6	21	7	19	30	72	25	168	169
ENSMUSG00000040524	chr9	Zfp609	65692391	65695694	8268	-1.02205	4.698648	8.47E-07	6.57E-06	0.048654	-1	503	385	579	656	820	230	397	601	453	337
ENSMUSG00000033307	chr10	Mif	75859353	75859543	554	0.844481	5.420382	8.51E-07	6.6E-06	0.033511	1	369	478	505	564	649	1178	1184	1058	1514	1438
ENSMUSG00000040455	chr4	Usp45	21767156	21767244	6226	-1.13809	4.224347	8.54E-07	6.62E-06	0.059738	-1	391	326	519	376	552	156	238	480	287	208
ENSMUSG00000038811	chr11	Gngt2	95837216	95837371	1877	1.485	2.565362	8.54E-07	6.62E-06	0.093055	1	31	64	68	56	31	145	189	115	259	296
ENSMUSG00000021061	chr12	Sptb	76580488	76583392	12147	-1.08101	7.558905	8.69E-07	6.73E-06	0.056265	-1	3775	3324	4434	4917	5010	1973	2297	4738	2735	2340
ENSMUSG00000063047	chr7	Zfp780b	27962708	27964869	3004	-1.57276	0.726439	8.82E-07	6.82E-06	0.081767	-1	37	25	52	37	52	6	25	24	19	21
ENSMUSG00000022489	chr15	Pde1b	1.04E+08	1.04E+08	2954	1.711504	1.271981	8.85E-07	6.84E-06	0.109625	1	19	5	22	22	21	32	82	71	127	107
ENSMUSG00000073647	chr18	Gm10557	4198216	4198611	750	-2.03475	-0.48068	9E-07	6.95E-06	0.101645	-1	10	9	26	20	25	2	5	8	11	4
ENSMUSG00000047343	chr1	Mettl21c	44009408	44010033	4300	-2.02439	5.83952	9.07E-07	7E-06	0.186532	-1	677	2379	2024	1254	1247	959	429	186	434	440
ENSMUSG00000050821	chr16	Fam131a	20693282	20693472	2853	-1.04011	6.866098	9.15E-07	7.06E-06	0.052195	-1	1938	2938	3277	2799	2004	1903	1599	1646	1993	1613
ENSMUSG00000020647	chr12	Ncoa1	4247363	4249750	7328	-0.85559	5.146996	9.16E-07	7.07E-06	0.034446	-1	633	550	882	774	1024	423	644	740	662	480
ENSMUSG00000079165	chr5	Sap25	1.38E+08	1.38E+08	1569	1.358984	1.706373	9.18E-07	7.08E-06	0.069153	1	26	24	32	24	41	55	111	92	116	158
ENSMUSG00000044788	chr11	Fads6	1.15E+08	1.15E+08	6653	-1.07256	3.284499	9.19E-07	7.09E-06	0.05048	-1	181	219	216	285	183	118	153	102	222	144
ENSMUSG00000093402	chr3	Gm18588	68902267	68902758	492	-1.4705	0.812375	9.21E-07	7.1E-06	0.072128	-1	37	45	42	39	45	10	15	29	29	24
ENSMUSG00000025058	chrX	5430427O19Rik	85870354	85870436	3754	2.306281	-0.20853	9.25E-07	7.12E-06	0.137	1	6	2	3	4	5	27	23	9	47	37
ENSMUSG00000092486	chr5	2610524H06Rik	1.15E+08	1.15E+08	947	1.643391	1.035867	9.28E-07	7.14E-06	0.093638	1	10	14	30	8	16	55	70	43	85	86
ENSMUSG00000020476	chr11	Dbnl	5788488	5788642	2346	0.934876	4.435731	9.34E-07	7.19E-06	0.040281	1	223	176	251	248	350	505	681	427	901	823
ENSMUSG00000032875	chr7	Arhgef17	1.01E+08	1.01E+08	10250	-0.81584	6.043128	9.38E-07	7.21E-06	0.031984	-1	1200	1064	1603	1439	1787	791	1061	1365	1375	1024
ENSMUSG00000062098	chr2	Btbd3	1.38E+08	1.38E+08	5776	-0.82506	4.321815	9.4E-07	7.22E-06	0.030997	-1	370	332	528	482	423	222	329	394	417	336
ENSMUSG00000025580	chr11	Eif4a3	1.19E+08	1.19E+08	2122	0.762307	5.262566	9.44E-07	7.25E-06	0.027246	1	373	436	554	453	567	949	1175	1082	1255	1141
ENSMUSG00000033590	chr9	Myo5c	75232014	75232175	6733	-1.12033	2.834045	9.49E-07	7.28E-06	0.053407	-1	160	159	181	135	169	71	81	146	103	120
ENSMUSG00000009555	chr2	Cdk9	32705784	32708289	4611	0.764169	4.701858	9.53E-07	7.31E-06	0.026721	1	272	277	370	296	398	603	667	754	943	855
ENSMUSG00000025330	chr4	Padi4	1.41E+08	1.41E+08	4835	3.603021	-0.23097	9.54E-07	7.31E-06	0.387632	1	0	0	1	1	7	25	25	2	43	59
ENSMUSG00000032661	chr5	Oas3	1.21E+08	1.21E+08	5227	3.771739	1.683877	9.55E-07	7.32E-06	0.519274	1	4	0	7	13	12	216	53	9	58	285
ENSMUSG00000027342	chr2	Pcna	1.32E+08	1.32E+08	2400	0.947334	4.676548	9.59E-07	7.34E-06	0.041863	1	251	247	311	240	417	586	705	532	1255	915
ENSMUSG00000031266	chrX	Gla	1.35E+08	1.35E+08	3265	1.464487	2.836772	9.61E-07	7.35E-06	0.093559	1	55	48	63	71	74	145	154	127	416	397
ENSMUSG00000010066	chr9	Cacna2d2	1.07E+08	1.07E+08	7947	-1.95382	0.700786	9.62E-07	7.36E-06	0.137023	-1	35	16	41	37	88	13	23	6	19	14
ENSMUSG00000030147	chr6	Clec4b1	1.23E+08	1.23E+08	784	2.180837	-0.32149	9.64E-07	7.37E-06	0.117073	1	4	3	1	3	9	30	28	14	34	21
ENSMUSG00000021134	chr12	Srsf5	80945504	80945672	3988	0.840652	6.108282	9.76E-07	7.46E-06	0.034062	1	719	667	986	754	1031	1411	2030	1805	2430	2744
ENSMUSG00000022945	chr16	Chaf1b	93883901	93883975	5001	1.646662	1.047051	9.84E-07	7.51E-06	0.095791	1	14	11	20	12	21	45	60	37	133	76
ENSMUSG00000034584	chr9	Exph5	53301670	53301851	10519	-2.63847	0.297274	9.84E-07	7.51E-06	0.244759	-1	13	13	36	73	40	6	1	17	5	8
ENSMUSG00000027010	chr2	Slc25a12	71271063	71275353	7342	-0.8748	8.648353	9.88E-07	7.54E-06	0.037604	-1	7294	8710	8976	9906	8028	5789	6431	7453	7527	5670
ENSMUSG00000027514	chr2	Zbp1	1.73E+08	1.73E+08	3529	2.787836	2.272241	9.89E-07	7.54E-06	0.318079	1	15	15	9	17	45	254	104	22	140	394
ENSMUSG00000049409	chr6	Prokr1	87578593	87581916	4055	-1.52048	0.593264	9.95E-07	7.58E-06	0.074593	-1	36	22	37	44	42	9	12	18	26	24
ENSMUSG00000002068	chr7	Ccne1	38097984	38098637	2662	1.5699	1.594302	9.99E-07	7.61E-06	0.096951	1	19	16	25	14	50	82	98	58	151	119
ENSMUSG00000042323	chr14	Pbrm1	31019138	31019293	8846	-0.82356	5.490817	1.02E-06	7.75E-06	0.032469	-1	836	746	1129	900	1233	498	815	943	903	662
ENSMUSG00000026385	chr1	Dbi	1.2E+08	1.2E+08	1422	1.088141	7.083592	1.02E-06	7.79E-06	0.057597	1	1143	1490	1536	1562	1464	3176	3178	2852	5754	6851
ENSMUSG00000059775	chr8	Rps26-ps1	1.07E+08	1.07E+08	410	0.940197	3.127244	1.03E-06	7.8E-06	0.037151	1	67	95	101	101	132	229	279	249	287	270
ENSMUSG00000002227	chr3	Mov10	1.05E+08	1.05E+08	4223	1.599504	2.297697	1.03E-06	7.8E-06	0.109034	1	24	37	26	39	75	180	138	77	222	214
ENSMUSG00000033855	chr17	Ston1	88597684	88597741	4521	-1.72677	2.11935	1.03E-06	7.8E-06	0.128165	-1	92	64	127	135	144	15	54	95	36	35
ENSMUSG00000021965	chr14	Ska3	57806561	57807531	2260	2.048815	0.142011	1.03E-06	7.81E-06	0.119544	1	3	10	4	2	12	25	40	22	62	36
ENSMUSG00000017760	chr2	Ctsa	1.65E+08	1.65E+08	4715	0.876851	6.760995	1.05E-06	7.96E-06	0.037586	1	1110	1016	1495	1209	1607	2520	2788	2463	4887	3978
ENSMUSG00000060923	chr11	Acyp2	30505991	30506439	863	-0.92621	5.756041	1.05E-06	7.97E-06	0.041423	-1	1032	1120	1495	1180	1047	875	790	934	799	859
ENSMUSG00000027078	chr2	Ube2l6	84798828	84798932	1996	1.472647	3.318859	1.07E-06	8.07E-06	0.098121	1	62	74	71	101	132	425	248	142	377	453
ENSMUSG00000020646	chr12	Mboat2	24831599	24831774	2802	1.506868	1.8167	1.08E-06	8.16E-06	0.090534	1	16	28	44	30	30	80	192	121	112	78
ENSMUSG00000035357	chr6	Pdzrn3	1.01E+08	1.01E+08	7256	-0.89011	5.579411	1.11E-06	8.4E-06	0.038313	-1	799	848	1077	1453	1002	682	858	776	837	729
ENSMUSG00000033808	chr2	Tmem87a	1.2E+08	1.2E+08	7528	-0.79025	5.561526	1.11E-06	8.43E-06	0.030095	-1	876	786	1272	1013	1072	598	799	940	852	847
ENSMUSG00000073433	chr17	Arhgdig	26196226	26196331	3252	1.450179	1.239589	1.13E-06	8.57E-06	0.0768	1	11	12	22	20	37	69	65	89	74	79
ENSMUSG00000034648	chr6	Lrrn1	1.08E+08	1.08E+08	3756	1.560701	3.831033	1.14E-06	8.59E-06	0.112547	1	99	79	95	204	116	192	688	792	551	281
ENSMUSG00000053007	chr6	Creb5	53573384	53573438	3038	-1.86774	0.294641	1.14E-06	8.63E-06	0.11267	-1	29	11	31	28	59	10	16	12	12	8
ENSMUSG00000034739	chr9	Mfrp	44101738	44101946	4325	1.087683	3.630088	1.15E-06	8.66E-06	0.053593	1	142	87	130	117	182	314	588	278	437	327
ENSMUSG00000027067	chr2	Ssrp1	85037234	85037328	3737	0.778576	5.508078	1.15E-06	8.68E-06	0.029185	1	488	413	617	540	769	990	1299	1211	1734	1527
ENSMUSG00000035439	chr8	Haus8	71248561	71251544	5278	1.396609	2.704752	1.15E-06	8.68E-06	0.085104	1	45	61	64	51	72	176	258	81	317	260
ENSMUSG00000006575	chr11	Rundc3a	1.02E+08	1.02E+08	2941	2.083635	-0.1605	1.15E-06	8.7E-06	0.113873	1	2	7	2	4	9	20	45	29	21	28
ENSMUSG00000027134	chr2	Lpcat4	1.12E+08	1.12E+08	2823	1.470399	1.37096	1.15E-06	8.7E-06	0.078216	1	20	26	15	16	30	53	84	62	136	94
ENSMUSG00000015733	chr6	Capza2	17636234	17636317	5890	-0.79635	8.341183	1.16E-06	8.71E-06	0.031597	-1	6036	6308	8284	6048	7739	5073	5381	5387	5961	5605
ENSMUSG00000060913	chr3	Trim55	19644474	19644776	2659	-0.89729	6.521815	1.17E-06	8.8E-06	0.039631	-1	1690	1771	2215	1864	2493	1392	1927	1059	1645	1408

ENSMUSG00000028896	chr4	Rcc1	1.32E+08	1.32E+08	3848	0.827297	4.156568	1.17E-06	8.81E-06	0.031178	1	178	190	262	198	242	472	422	476	712	567
ENSMUSG00000040022	chr19	Rab11fip2	59902884	59907143	6080	-1.16003	3.331898	1.18E-06	8.85E-06	0.060978	-1	241	185	266	222	238	97	135	245	126	117
ENSMUSG00000030516	chr7	Tjp1	65296165	65297667	7360	-0.97655	4.976188	1.18E-06	8.86E-06	0.045987	-1	570	518	714	916	780	247	527	648	660	448
ENSMUSG00000027293	chr2	Ehd4	1.2E+08	1.2E+08	4007	0.817882	6.384967	1.18E-06	8.87E-06	0.032896	1	649	904	1191	1086	1284	1942	2732	2267	3030	2517
ENSMUSG00000009772	chr1	Nuak2	1.32E+08	1.32E+08	3920	1.625627	1.001329	1.18E-06	8.89E-06	0.096103	1	13	4	20	13	28	53	75	43	85	74
ENSMUSG00000040701	chr14	Ap1g2	55098578	55099161	4177	1.076771	2.853428	1.19E-06	8.92E-06	0.049167	1	53	78	84	81	85	159	212	163	301	303
ENSMUSG00000027536	chr3	Chmp4c	10366907	10367221	10087	-1.6361	0.006261	1.19E-06	8.95E-06	0.069619	-1	26	14	27	25	28	6	12	10	16	10
ENSMUSG00000033159	chr1	Cnppd1	75134554	75136932	5635	1.119599	4.82374	1.21E-06	9.07E-06	0.060197	1	251	226	325	345	345	483	705	1547	904	903
ENSMUSG00000021994	chr14	Wnt5a	28504750	28506114	7822	-1.00232	3.725017	1.21E-06	9.09E-06	0.045989	-1	282	177	267	270	501	153	208	200	223	242
ENSMUSG00000030660	chr7	Pik3c2a	1.16E+08	1.16E+08	8042	-1.00284	3.148633	1.22E-06	9.15E-06	0.044337	-1	190	142	203	204	249	73	151	168	186	121
ENSMUSG00000020897	chr11	Aurkb	69045647	69045810	2946	1.81304	1.549828	1.22E-06	9.16E-06	0.134715	1	11	7	20	22	47	75	92	54	182	114
ENSMUSG00000005583	chr13	Mef2c	83504034	83504376	6760	-0.78806	8.69258	1.23E-06	9.21E-06	0.031143	-1	7439	7592	10135	9280	9360	6447	7565	6619	7807	6705
ENSMUSG00000074238	chr3	Ap1ar	1.28E+08	1.28E+08	2391	-0.74826	4.610478	1.24E-06	9.23E-06	0.026157	-1	466	444	586	515	536	312	432	437	480	470
ENSMUSG00000026739	chr2	Bmi1	18677018	18677469	3974	-0.77087	4.521958	1.24E-06	9.27E-06	0.02782	-1	427	405	543	493	552	243	410	436	505	413
ENSMUSG00000087370	chr13	Tmem170b	41606216	41606312	7160	-0.88947	4.762489	1.25E-06	9.33E-06	0.037775	-1	483	460	673	566	795	362	463	588	414	369
ENSMUSG00000026103	chr1	Gls	52163448	52166314	15057	-0.80224	5.846024	1.25E-06	9.35E-06	0.031536	-1	1071	1174	1476	1165	1184	833	983	987	1087	980
ENSMUSG00000038181	chr5	Chpf2	24586741	24588300	5371	0.840633	4.480266	1.26E-06	9.36E-06	0.033104	1	253	197	284	241	365	404	639	785	820	724
ENSMUSG00000024526	chr18	Cidea	67343564	67343840	1164	3.967686	3.349411	1.26E-06	9.37E-06	0.604419	1	5	24	8	55	4	38	60	193	900	1171
ENSMUSG00000075595	chr11	Zfp652	95712673	95712733	15444	-0.78335	7.805654	1.26E-06	9.37E-06	0.030723	-1	4044	3999	5183	5171	5277	3293	3406	4148	4431	3849
ENSMUSG00000079592	chr9	C1qtnf5	44107245	44107344	1398	1.090603	3.623075	1.26E-06	9.38E-06	0.054348	1	141	86	128	117	182	314	587	275	433	326
ENSMUSG00000036606	chr15	Plxnb2	89155549	89156385	7119	0.951393	5.458783	1.26E-06	9.4E-06	0.0442	1	441	311	499	436	873	862	1521	1236	1812	1437
ENSMUSG00000030432	chr7	Rpl28	4792874	4792998	1138	0.798009	7.331997	1.27E-06	9.46E-06	0.031805	1	1424	1751	2061	2181	2483	4162	4546	4376	5771	4973
ENSMUSG00000033618	chr16	Map3k13	21891969	21892440	6709	-1.84201	-0.25856	1.28E-06	9.51E-06	0.089694	-1	19	10	22	18	34	5	5	11	8	10
ENSMUSG00000027601	chr3	Mtfr1	19187327	19187358	4372	-0.86587	4.62018	1.28E-06	9.53E-06	0.035778	-1	399	526	571	652	482	279	454	381	564	383
ENSMUSG00000015882	chr5	Lcorl	45697181	45701997	10945	-1.18787	1.927002	1.29E-06	9.55E-06	0.055881	-1	83	58	100	99	98	29	52	56	81	55
ENSMUSG00000035953	chr14	Tmem55b	50926070	50928037	4489	0.855534	4.001428	1.29E-06	9.58E-06	0.033346	1	198	152	181	180	231	332	415	580	543	531
ENSMUSG00000006395	chr4	Hyi	1.18E+08	1.18E+08	2209	0.982251	3.184889	1.3E-06	9.65E-06	0.041875	1	69	106	104	107	117	224	207	304	330	325
ENSMUSG00000021375	chr13	Kif13a	46749087	46750626	6866	-0.83175	6.54785	1.31E-06	9.71E-06	0.034394	-1	1654	1663	2345	2134	2256	1282	1438	1989	1606	1489
ENSMUSG00000000901	chr10	Mmp11	75923222	75923490	2572	1.342056	2.440449	1.32E-06	9.79E-06	0.07722	1	40	41	50	54	66	86	187	296	184	141
ENSMUSG00000031358	chrX	Msl3	1.69E+08	1.69E+08	2877	-0.79694	5.222027	1.32E-06	9.79E-06	0.030776	-1	789	696	926	736	778	527	701	633	725	587
ENSMUSG00000005514	chr5	Por	1.36E+08	1.36E+08	4021	1.285665	5.068361	1.32E-06	9.8E-06	0.08025	1	287	202	309	362	490	461	725	1050	1661	1843
ENSMUSG00000015709	chr7	Arnt2	84246281	84250154	5988	-1.57817	2.651992	1.33E-06	9.82E-06	0.112234	-1	157	102	205	102	230	63	118	39	116	34
ENSMUSG00000068335	chr6	Dok1	83030934	83032060	1977	1.362705	3.089834	1.33E-06	9.86E-06	0.084808	1	79	29	92	58	146	205	323	189	356	348
ENSMUSG00000053799	chr19	Exoc6	37550418	37550565	2729	-0.74979	5.522268	1.33E-06	9.86E-06	0.027392	-1	817	806	1133	1004	1065	675	821	844	913	732
ENSMUSG00000044147	chr12	Arf6	69372150	69372223	3730	0.841292	5.241938	1.34E-06	9.89E-06	0.034382	1	359	369	493	439	625	804	1110	861	1707	1281
ENSMUSG00000021557	chr13	Agtpbp1	59449537	59449746	12833	-0.85463	5.446065	1.34E-06	9.92E-06	0.035742	-1	688	863	1123	1010	1020	666	745	524	819	845
ENSMUSG00000032420	chr9	Nt5e	88327197	88328030	8411	-1.43541	1.914909	1.36E-06	1E-05	0.086696	-1	73	61	94	75	163	25	45	77	49	40
ENSMUSG00000031697	chr8	Orc6	85299632	85299992	1653	1.070417	2.656843	1.39E-06	1.02E-05	0.047597	1	63	65	67	56	80	147	153	172	260	253
ENSMUSG00000033538	chr9	Casp4	5308828	5308914	3710	1.530754	0.987155	1.41E-06	1.04E-05	0.0815	1	11	10	23	16	20	46	55	42	83	97
ENSMUSG00000054520	chr5	Sh3bp2	34525838	34525901	4277	1.418635	3.630214	1.41E-06	1.04E-05	0.094404	1	50	174	122	60	149	291	360	299	639	533
ENSMUSG00000044934	chr13	Zfp367	64133022	64135536	5454	-0.74659	4.241486	1.42E-06	1.04E-05	0.025743	-1	361	363	416	392	434	246	351	324	373	355
ENSMUSG00000076617	chr12	Ighm	1.13E+08	1.13E+08	1886	-1.92345	6.568496	1.42E-06	1.04E-05	0.176329	-1	1041	3100	3314	3288	1737	1332	881	229	867	1114
ENSMUSG00000045038	chr17	Prkce	86167785	86168940	7261	-0.86768	3.699161	1.42E-06	1.05E-05	0.034187	-1	240	224	287	327	321	155	173	260	239	245
ENSMUSG00000032300	chr9	1700017B05Rik	57252322	57254329	4934	1.267122	3.322686	1.44E-06	1.06E-05	0.074242	1	73	47	114	118	144	186	241	247	530	474
ENSMUSG00000020988	chr12	L2hgdh	69690436	69692496	3338	-0.96318	5.219775	1.45E-06	1.06E-05	0.045613	-1	727	797	931	757	881	476	523	884	545	487
ENSMUSG00000084516	chr2	Mir1902	1.04E+08	1.04E+08	80	-1.16722	3.228272	1.45E-06	1.06E-05	0.062681	-1	196	175	266	211	233	75	123	234	139	104
ENSMUSG00000031400	chrX	G6pdx	74409483	74410297	3080	1.54093	3.985873	1.45E-06	1.07E-05	0.112824	1	114	86	98	148	237	286	354	275	922	996
ENSMUSG00000022686	chr16	B3gnt5	19760208	19760477	5197	2.088108	0.245545	1.46E-06	1.07E-05	0.136652	1	8	4	9	2	10	17	70	23	47	44
ENSMUSG00000025533	chr5	Asl	1.3E+08	1.3E+08	4563	0.960419	3.323378	1.46E-06	1.07E-05	0.040886	1	102	99	126	92	143	218	292	221	412	401
ENSMUSG00000038943	chr7	Prc1	80294450	80294591	8225	1.379043	2.874507	1.46E-06	1.07E-05	0.085736	1	53	63	59	48	114	151	289	132	464	221
ENSMUSG00000032369	chr9	Plscr1	92249750	92250360	2462	1.624592	1.053572	1.47E-06	1.08E-05	0.09645	1	4	20	22	11	23	58	52	61	97	75
ENSMUSG00000074785	chr10	Plxnc1	94790866	94793290	7836	1.329961	2.400341	1.48E-06	1.08E-05	0.076368	1	53	19	59	46	71	97	211	132	246	192
ENSMUSG00000021196	chr13	Pfkp	6579768	6581592	9395	1.245493	3.662624	1.48E-06	1.08E-05	0.07304	1	111	73	123	140	183	252	381	213	644	625
ENSMUSG00000038545	chr17	Cul7	46650337	46650715	7410	0.892012	4.329934	1.48E-06	1.08E-05	0.037907	1	184	167	247	223	372	451	737	463	826	592
ENSMUSG00000068745	chr3	Mybphl	1.08E+08	1.08E+08	1275	2.425417	-0.29052	1.49E-06	1.09E-05	0.169174	1	4	0	5	1	8	28	36	24	37	9
ENSMUSG00000048279	chr14	Sacs	61138457	61138771	20414	-0.85442	4.926962	1.51E-06	1.1E-05	0.035634	-1	526	499	691	859	704	346	646	486	587	480
ENSMUSG00000026173	chr1	Plcd4	74542888	74543028	7045	-1.42021	6.943861	1.51E-06	1.1E-05	0.099816	-1	2066	2948	3776	2669	3651	1873	1884	502	1484	1857
ENSMUSG00000003680	chr19	Taf6l	8772522	8772834	5884	0.873168	3.612226	1.52E-06	1.11E-05	0.034266	1	121	116	174	111	201	266	374	300	492	418
ENSMUSG00000028923	chr4	Necap2	1.41E+08	1.41E+08	3095	0.857874	4.63982	1.52E-06	1.11E-05	0.035427	1	213	264	337	300	373	602	633	557	1096	890
ENSMUSG00000021036	chr12	Sptlc2	87305058	87310020	8115	0.903103	4.107886	1.54E-06	1.12E-05	0.038484	1	167	140	207	223	271	374	485	382	811	605
ENSMUSG00000032246	chr9	Calml4	62858104	62858161	861	1.226943	1.655955	1.54E-06	1.12E-05	0.057045	1	17	24	36	33	43	87	90	95	137	86
ENSMUSG00000002718	chr2	Cse1l	1.67E+08	1.67E+08	5273	-0.75921	6.195556	1.55E-06	1.12E-05	0.028894	-1	1280	1342	1807	1405	1912	1020	1384	1234	1526	1200
ENSMUSG00000001418	chr3	Glmp	88325023	88325201	6291	0.82435	5.064052	1.56E-06	1.14E-05	0.033203	1	359	335	441	353	536	745	875	812	1366	1237
ENSMUSG00000052387	chr19	Trpm3	22139119	22139301	8061	-1.76432	0.15688	1.57E-06	1.14E-05	0.094231	-1	15	19	35	43	26	11	12	11	8	13
ENSMUSG00000057637	chr4	Prdm2	1.43E+08	1.43E+08	7420	-0.88192	5.279724	1.57E-06	1.14E-05	0.038524	-1	718	669	908	957	966	446	552	881	822	514
ENSMUSG00000020407	chr11	Upp1	9118103	9118284	1961	1.865369	0.432166	1.6E-06	1.16E-05	0.11324	1	3	14	5	7	14	30	54	31	75	36

ENSMUSG00000079139	chr1	Gm4204	1.35E+08	1.35E+08	1231	1.033329	3.179946	1.63E-06	1.18E-05	0.04815	1	68	74	108	105	143	181	219	380	333	300
ENSMUSG00000078532	chr4	Nkain1	1.31E+08	1.31E+08	1426	-0.99697	3.281202	1.64E-06	1.19E-05	0.04537	-1	144	212	291	210	226	118	158	101	225	162
ENSMUSG00000032815	chr8	Fanca	1.23E+08	1.23E+08	8491	2.115857	0.258289	1.64E-06	1.19E-05	0.147831	1	3	4	11	7	8	21	27	18	79	62
ENSMUSG00000026491	chr1	Ahctf1	1.8E+08	1.8E+08	15116	-0.82731	5.224474	1.65E-06	1.19E-05	0.033873	-1	742	613	898	714	1057	455	591	818	688	595
ENSMUSG00000078671	chr7	Chd2	73426691	73430000	9656	-0.88601	5.484613	1.65E-06	1.2E-05	0.039177	-1	808	700	1198	1029	1172	534	674	971	648	819
ENSMUSG00000053332	chr1	Gas5	1.61E+08	1.61E+08	3760	1.207568	5.421709	1.66E-06	1.2E-05	0.072581	1	369	434	486	362	502	855	1148	2584	1063	1270
ENSMUSG00000002059	chr11	Rab34	78188430	78188511	2385	1.086644	3.35404	1.67E-06	1.21E-05	0.054732	1	99	64	98	98	192	180	328	312	402	409
ENSMUSG00000036466	chr9	Megf11	64385626	64385828	11181	-1.81832	-0.0618	1.67E-06	1.21E-05	0.093877	-1	23	18	36	15	26	10	12	6	14	4
ENSMUSG00000028902	chr4	Sf3a3	1.25E+08	1.25E+08	2785	0.765021	4.238655	1.68E-06	1.22E-05	0.02737	1	187	209	286	206	280	444	596	467	669	589
ENSMUSG00000098754	chr2	Gm28045	1.32E+08	1.32E+08	3370	-1.04603	4.078619	1.68E-06	1.22E-05	0.053022	-1	256	373	445	447	377	208	324	161	416	196
ENSMUSG00000026204	chr1	Ptprn	75247027	75247620	4249	2.532565	-0.85038	1.7E-06	1.23E-05	0.119447	1	2	2	2	2	2	4	23	13	24	23
ENSMUSG00000061455	chr4	Stx17	48124915	48124958	5935	-0.85148	4.882589	1.7E-06	1.23E-05	0.035663	-1	607	457	752	618	751	342	464	662	520	468
ENSMUSG00000062980	chr6	Cped1	21985916	21987059	8279	-1.05081	4.646326	1.7E-06	1.23E-05	0.054542	-1	645	384	527	498	768	207	384	574	432	327
ENSMUSG00000027331	chr2	Knstrn	1.19E+08	1.19E+08	5158	1.488902	1.879471	1.71E-06	1.23E-05	0.093276	1	14	32	27	39	44	73	131	73	219	132
ENSMUSG00000055493	chr10	Epm2a	11343404	11343768	3287	-0.90305	5.932458	1.71E-06	1.23E-05	0.041167	-1	1241	1192	1529	1274	1380	810	899	1389	1038	796
ENSMUSG00000005732	chr16	Ranbp1	18239784	18240193	1666	0.889056	4.433199	1.72E-06	1.24E-05	0.038234	1	202	226	280	208	355	510	640	441	928	778
ENSMUSG00000029554	chr5	Mad1l1	1.4E+08	1.4E+08	3390	1.043164	3.2691	1.72E-06	1.24E-05	0.049654	1	101	76	98	106	140	229	429	200	339	302
ENSMUSG00000020218	chr10	Wif1	1.21E+08	1.21E+08	2427	-2.0621	3.883259	1.74E-06	1.25E-05	0.200221	-1	579	113	475	166	698	96	251	142	125	48
ENSMUSG00000027469	chr2	Tpx2	1.53E+08	1.53E+08	4677	1.005028	3.156242	1.74E-06	1.25E-05	0.045464	1	86	61	118	98	132	222	243	200	405	315
ENSMUSG00000047824	chr3	Pygo2	89430214	89430453	3631	0.761308	4.308519	1.74E-06	1.25E-05	0.027312	1	218	189	273	225	327	405	615	528	749	629
ENSMUSG00000086841	chr11	2410006H16Rik	62602877	62603023	462	2.143658	4.13258	1.74E-06	1.25E-05	0.215531	1	89	89	120	106	135	245	370	1970	303	393
ENSMUSG00000021733	chr14	Slc4a7	14703025	14703280	7389	-0.90021	3.551754	1.78E-06	1.28E-05	0.037577	-1	198	201	289	268	329	119	204	218	285	144
ENSMUSG00000037572	chr14	Wdhd1	47240944	47241812	7192	1.491309	1.311933	1.78E-06	1.28E-05	0.084437	1	20	16	12	18	37	60	83	53	113	99
ENSMUSG00000049538	chr13	Adamts16	70727802	70728967	6836	-2.16613	0.203196	1.78E-06	1.28E-05	0.172359	-1	14	14	26	47	54	7	4	3	17	16
ENSMUSG00000002804	chr12	Nudt14	1.13E+08	1.13E+08	793	0.994066	3.165297	1.79E-06	1.28E-05	0.044271	1	84	105	133	75	94	246	274	293	283	264
ENSMUSG00000028495	chr4	Rps6	86854660	86854955	1586	0.759059	7.328823	1.81E-06	1.3E-05	0.029654	1	1545	1775	2247	1966	2515	3966	4771	4417	5296	5066
ENSMUSG00000071176	chr8	Arhgef10	14911663	14911763	9210	-0.98582	3.50482	1.82E-06	1.31E-05	0.045402	-1	261	138	269	239	366	113	211	186	214	171
ENSMUSG00000028992	chr4	Nmnat1	1.49E+08	1.49E+08	3037	-0.77864	4.017639	1.86E-06	1.33E-05	0.028419	-1	273	335	374	353	364	237	259	239	357	299
ENSMUSG00000031133	chrX	Arhgef6	57231485	57233651	8552	-0.77571	5.897897	1.86E-06	1.33E-05	0.030493	-1	1159	925	1428	1302	1509	905	1061	952	1267	936
ENSMUSG00000043262	chr7	Uevld	46923539	46926488	7226	-0.94475	3.332714	1.86E-06	1.33E-05	0.040983	-1	185	195	273	200	254	121	176	207	186	111
ENSMUSG00000023947	chr17	Nfkbie	45555716	45556314	2422	1.502051	1.507956	1.87E-06	1.34E-05	0.091101	1	19	11	26	32	31	61	114	50	144	107
ENSMUSG00000058230	chr7	Arhgap35	16493719	16498010	9147	-0.78047	5.28136	1.88E-06	1.34E-05	0.030461	-1	630	624	887	909	1109	472	649	765	836	644
ENSMUSG00000036273	chr15	Lrrk2	91673175	91673437	11834	-0.89564	3.229903	1.89E-06	1.35E-05	0.036136	-1	202	159	222	207	222	111	192	148	186	129
ENSMUSG00000023982	chr17	Guca1a	47394560	47394820	871	2.249172	-0.27964	1.9E-06	1.35E-05	0.140366	1	5	0	4	3	8	21	36	12	25	39
ENSMUSG00000029238	chr5	Clock	76212177	76216878	7478	-0.87665	4.729717	1.93E-06	1.37E-05	0.038121	-1	420	418	672	572	845	269	564	487	480	400
ENSMUSG00000048920	chr7	Fkrp	16809270	16811976	2803	-0.76907	5.467733	1.96E-06	1.4E-05	0.029784	-1	815	781	1118	917	1037	712	746	632	904	801
ENSMUSG00000031722	chr8	Hp	1.1E+08	1.1E+08	1343	3.659862	6.434532	1.97E-06	1.4E-05	0.560865	1	225	80	63	293	416	237	1016	574	5548	12553
ENSMUSG00000060681	chrX	Slc9a6	56609757	56609820	4961	-0.74167	5.257112	1.98E-06	1.41E-05	0.027504	-1	715	681	975	710	927	531	722	684	753	646
ENSMUSG00000029406	chr5	Pitpnm2	1.24E+08	1.24E+08	12843	-0.8081	4.889972	1.99E-06	1.41E-05	0.032476	-1	479	538	617	799	723	386	452	468	635	588
ENSMUSG00000072501	chr15	Phf20l1	66577572	66577847	6670	-0.932	5.010079	1.99E-06	1.42E-05	0.043708	-1	661	587	826	653	806	322	488	786	485	506
ENSMUSG00000025862	chrX	Stag2	42149317	42149685	8273	-0.92174	6.222965	2E-06	1.42E-05	0.043654	-1	1506	1247	1867	1490	2126	698	1210	1735	1424	1032
ENSMUSG00000062312	chr11	Erbb2	98412470	98412735	5210	1.123069	3.026148	2.04E-06	1.45E-05	0.057754	1	80	82	66	76	115	154	377	268	293	203
ENSMUSG00000026849	chr2	Tor1a	30960627	30961197	1995	0.985045	2.837417	2.06E-06	1.46E-05	0.042518	1	58	56	95	80	111	155	209	181	317	244
ENSMUSG00000039883	chr5	Lrrc17	21543527	21543719	2186	1.293902	4.03609	2.06E-06	1.46E-05	0.082896	1	130	75	163	136	313	400	828	306	663	523
ENSMUSG00000038670	chr7	Mybpc2	44501699	44501842	3624	-0.84983	12.58419	2.06E-06	1.46E-05	0.037865	-1	102466	115105	153727	133891	159842	93929	78047	123480	106646	103478
ENSMUSG00000037486	chr12	Asxl2	3426857	3427212	14574	-0.83469	4.032936	2.07E-06	1.47E-05	0.033494	-1	278	303	458	346	371	186	258	355	344	238
ENSMUSG00000019866	chr10	Aim1	43950307	43951957	7416	1.228103	2.367982	2.09E-06	1.48E-05	0.065525	1	42	47	51	61	48	106	127	126	226	251
ENSMUSG00000017999	chr2	Ddx27	1.67E+08	1.67E+08	4817	0.962036	3.633065	2.1E-06	1.48E-05	0.043688	1	121	118	148	126	187	204	357	541	426	390
ENSMUSG00000021898	chr14	Asb14	26894557	26894672	2549	-1.04602	5.989725	2.11E-06	1.5E-05	0.056181	-1	1393	1349	1670	1357	1303	965	825	1348	769	803
ENSMUSG00000029466	chr5	Anapc7	1.22E+08	1.22E+08	5119	0.758952	4.692751	2.11E-06	1.5E-05	0.028267	1	271	254	359	333	391	562	773	903	867	682
ENSMUSG00000028289	chr4	Epha7	28813131	28813480	9884	-1.62527	1.272971	2.12E-06	1.5E-05	0.108168	-1	66	32	58	75	69	26	38	9	33	29
ENSMUSG00000031778	chr8	Cx3cl1	94772009	94772334	3708	1.67758	1.512645	2.14E-06	1.51E-05	0.118031	1	16	13	26	24	30	88	93	50	204	58
ENSMUSG00000028690	chr4	Mmachc	1.17E+08	1.17E+08	2224	-0.82315	4.845101	2.14E-06	1.51E-05	0.033891	-1	529	617	712	595	586	432	540	408	620	418
ENSMUSG00000028931	chr4	Kcnab2	1.52E+08	1.52E+08	5578	1.815177	2.382232	2.15E-06	1.52E-05	0.152058	1	25	25	35	21	88	121	107	93	382	253
ENSMUSG00000060512	chr5	0610040J01Rik	63812495	63812595	1870	-1.47587	2.244317	2.16E-06	1.52E-05	0.099033	-1	86	117	130	163	74	69	51	32	60	72
ENSMUSG00000035181	chr12	Heatr5a	51875873	51877616	7761	-0.80514	4.642364	2.16E-06	1.53E-05	0.032164	-1	437	401	567	558	717	319	500	318	581	425
ENSMUSG00000051934	chr15	Spats2	99126578	99126887	3065	1.054252	3.304693	2.16E-06	1.53E-05	0.052339	1	68	85	125	109	152	222	444	201	390	295
ENSMUSG00000035275	chr4	Raver2	1.01E+08	1.01E+08	6342	-1.085	2.780203	2.22E-06	1.57E-05	0.054016	-1	145	120	160	186	162	70	135	75	158	82
ENSMUSG00000048520	chr5	Fbxl13	21483847	21484137	3494	1.975572	0.114171	2.24E-06	1.58E-05	0.12385	1	6	1	9	9	7	19	58	24	31	45
ENSMUSG00000032254	chr9	Kif23	61917280	61917679	3423	1.22837	1.919896	2.24E-06	1.58E-05	0.061663	1	34	29	32	33	55	91	122	81	185	127
ENSMUSG00000051220	chrX	Ercc6l	1.02E+08	1.02E+08	5302	1.747532	0.581965	2.25E-06	1.58E-05	0.10894	1	7	4	10	11	21	37	45	25	76	65
ENSMUSG00000071456	chr12	1110002L01Rik	3403878	3406711	4131	-0.98381	3.064477	2.26E-06	1.59E-05	0.044361	-1	156	157	268	180	163	111	148	116	167	111
ENSMUSG00000021738	chr14	Atxn7	14012491	14012750	6847	-0.81295	4.079289	2.26E-06	1.59E-05	0.032015	-1	307	311	408	348	427	174	289	370	315	291
ENSMUSG00000052565	chr13	Hist1h1d	23555087	23555830	744	-1.84838	0.019097	2.28E-06	1.6E-05	0.110563	-1	9	29	37	19	33	9	13	5	12	9
ENSMUSG00000031320	chrX	Rps4x	1.02E+08	1.02E+08	1631	0.764403	8.519431	2.33E-06	1.64E-05	0.030916	1	3570	4207	4854	4065	6210	9081	10788	10189	12291	11447
ENSMUSG00000052516	chr16	Robo2	73892306	73895830	16516	-1.69022	-0.05181	2.37E-06	1.67E-05	0.081947	-1	17	14	28	28	30	7	10	13	16	4

ENSMUSG00000078942	chr13	Naip6	1E+08	1E+08	6827	1.917577	0.041615	2.37E-06	1.67E-05	0.106826	1	6	4	8	6	7	19	37	21	30	59
ENSMUSG00000033004	chr14	Mycbp2	1.03E+08	1.03E+08	19248	-0.86796	5.63726	2.41E-06	1.69E-05	0.038974	-1	835	867	1154	1340	1196	586	700	1129	860	836
ENSMUSG00000030259	chr6	Rassf8	1.46E+08	1.46E+08	5559	-0.75006	4.359618	2.42E-06	1.7E-05	0.027534	-1	386	367	401	445	549	284	369	345	463	331
ENSMUSG00000042807	chr1	Hecw2	53806876	53813333	12947	-1.23251	1.974978	2.44E-06	1.71E-05	0.066024	-1	82	76	107	116	71	28	62	53	81	53
ENSMUSG00000025289	chrX	Prdx4	1.55E+08	1.55E+08	2106	0.905663	4.033675	2.46E-06	1.73E-05	0.040325	1	178	133	210	143	296	420	539	362	630	530
ENSMUSG00000014932	chr5	Yes1	32611171	32611375	4608	-0.86315	3.251378	2.47E-06	1.73E-05	0.033986	-1	179	179	203	231	226	115	166	184	165	154
ENSMUSG00000017830	chr11	Dhx58	1.01E+08	1.01E+08	3272	2.056775	2.225834	2.47E-06	1.73E-05	0.195956	1	13	17	46	39	36	233	100	47	152	288
ENSMUSG00000023905	chr17	Tnfrsf12a	23675447	23676046	963	1.267405	4.973503	2.47E-06	1.73E-05	0.082319	1	200	187	372	339	485	1185	1419	542	1215	702
ENSMUSG00000000605	chr7	Clcn4-2	7282316	7284274	4578	-0.74412	5.909439	2.48E-06	1.74E-05	0.028754	-1	1088	1087	1504	1163	1467	830	1190	1012	1179	1032
ENSMUSG00000060336	chr2	Zfp937	1.5E+08	1.5E+08	2797	-1.63237	-0.22145	2.49E-06	1.74E-05	0.066512	-1	17	17	26	17	24	6	13	7	10	9
ENSMUSG00000024654	chr19	Asrgl1	9109868	9113208	4297	-0.85579	5.844221	2.5E-06	1.74E-05	0.038094	-1	1054	1185	1517	1132	1276	921	898	1079	892	894
ENSMUSG00000033998	chr8	Kcnk1	1.26E+08	1.26E+08	2301	-1.65104	-0.03818	2.51E-06	1.75E-05	0.081691	-1	27	22	21	20	25	4	12	15	14	7
ENSMUSG00000062997	chr2	Rpl35	39001580	39001765	1241	0.790494	6.949487	2.51E-06	1.75E-05	0.032957	1	1145	1540	1774	1387	1722	3273	3683	3336	4152	3721
ENSMUSG00000091649	chr14	Phf11b	59320964	59321283	1184	2.311879	1.489944	2.53E-06	1.76E-05	0.232918	1	10	10	11	17	28	141	60	24	77	194
ENSMUSG00000098926	chr1	Mir6904	1.81E+08	1.81E+08	67	-1.18728	1.333023	2.53E-06	1.76E-05	0.052807	-1	53	44	63	53	75	24	43	29	46	35
ENSMUSG00000031494	chr8	Cd209a	3743395	3744234	1484	1.628429	0.284327	2.55E-06	1.77E-05	0.078032	1	8	8	9	8	11	33	56	25	43	34
ENSMUSG00000074800	chr13	Gm4149	75644864	75645162	362	0.767267	4.386232	2.6E-06	1.81E-05	0.028914	1	233	239	304	219	289	507	602	595	641	698
ENSMUSG00000028890	chr4	Mtf1	1.25E+08	1.25E+08	8907	-0.72816	4.344595	2.61E-06	1.82E-05	0.025935	-1	344	338	497	436	514	275	392	338	397	381
ENSMUSG00000066735	chr5	Vkorc1l1	1.3E+08	1.3E+08	2972	-0.74362	4.319582	2.62E-06	1.82E-05	0.027177	-1	410	343	487	376	466	252	337	371	412	376
ENSMUSG00000022533	chr16	Atp13a3	30312423	30315901	9559	-1.06766	5.904392	2.63E-06	1.83E-05	0.059691	-1	1152	1000	1607	1243	1874	409	1095	1365	1015	712
ENSMUSG00000037851	chr13	Iars	49682100	49682203	5272	-0.76168	6.221698	2.64E-06	1.83E-05	0.03047	-1	1272	1272	1926	1496	1958	1080	1342	1400	1446	1170
ENSMUSG00000062210	chr18	Tnfaip8	49979427	49979626	10328	1.1343	3.236125	2.66E-06	1.85E-05	0.061828	1	105	53	125	81	127	187	324	191	428	392
ENSMUSG00000090150	chr9	Acad11	1.04E+08	1.04E+08	9351	-0.75433	5.645379	2.67E-06	1.86E-05	0.029609	-1	951	950	1161	1063	1098	641	791	1042	1025	864
ENSMUSG00000040681	chr16	Hmgn1	96120618	96122417	3221	0.844311	5.392101	2.72E-06	1.89E-05	0.037032	1	394	402	569	443	736	950	1404	879	1655	1458
ENSMUSG00000075702	chr11	Selm	3514684	3515073	1481	0.84506	4.067548	2.74E-06	1.9E-05	0.035139	1	190	153	208	165	287	417	566	372	618	529
ENSMUSG00000091898	chr14	Tnnc1	31208312	31208378	1041	2.619947	5.30896	2.75E-06	1.9E-05	0.325884	1	27	278	21	375	204	1157	2326	1655	1886	940
ENSMUSG00000062661	chr2	Ncs1	31245823	31246242	4653	0.941518	4.016752	2.78E-06	1.93E-05	0.044287	1	142	131	189	182	293	409	683	376	590	410
ENSMUSG00000050064	chr3	Zfp697	98382481	98382578	5163	1.740896	0.597612	2.79E-06	1.93E-05	0.107301	1	11	8	14	13	6	33	84	39	62	31
ENSMUSG00000074873	chr19	AI606181	41593363	41596158	2796	1.245312	1.915419	2.79E-06	1.93E-05	0.065543	1	21	36	32	49	42	81	124	89	168	144
ENSMUSG00000024663	chr19	Rab3il1	10001669	10002217	4543	0.947243	4.1708	2.8E-06	1.94E-05	0.045146	1	203	120	201	188	325	425	552	412	834	569
ENSMUSG00000028403	chr4	Zdhhc21	82798738	82806461	12972	-0.77987	4.391537	2.82E-06	1.95E-05	0.030392	-1	395	313	565	398	569	257	416	341	404	390
ENSMUSG00000029246	chr5	Ppat	76913249	76915405	4421	-0.75058	4.729954	2.84E-06	1.96E-05	0.028469	-1	446	500	691	517	635	399	477	470	471	470
ENSMUSG00000097451	chr12	Rian	1.1E+08	1.1E+08	17475	1.024477	7.228587	2.85E-06	1.97E-05	0.055851	1	1443	1307	1799	965	2931	3503	5308	5149	5895	3757
ENSMUSG00000027259	chr2	Adal	1.21E+08	1.21E+08	5317	-0.84087	4.309692	2.86E-06	1.97E-05	0.035428	-1	391	382	474	409	457	339	381	269	355	286
ENSMUSG00000036698	chr15	Ago2	73095844	73107016	13705	-0.80009	6.725169	2.87E-06	1.98E-05	0.034119	-1	1801	1604	2503	2381	3121	1306	2218	1772	2103	1660
ENSMUSG00000038267	chr13	Slc22a23	34179158	34183311	6386	-0.91162	3.771517	2.88E-06	1.99E-05	0.041076	-1	225	262	332	399	261	160	278	183	270	220
ENSMUSG00000022978	chr16	Mis18a	90719312	90719978	2863	1.41725	1.410584	2.89E-06	1.99E-05	0.080329	1	18	19	19	32	26	50	91	54	132	111
ENSMUSG00000055044	chr19	Pdlim1	40221173	40222771	5260	1.199413	5.474979	2.92E-06	2.01E-05	0.075229	1	245	476	387	758	357	1191	1637	1090	2154	1222
ENSMUSG00000098906	chr11	Mir7652	55501226	55501281	56	-1.48703	0.454417	2.92E-06	2.01E-05	0.073136	-1	28	25	36	23	52	12	12	19	25	13
ENSMUSG00000023904	chr17	Hcfc1r1	23673596	23673703	958	0.788333	6.639222	2.92E-06	2.01E-05	0.033126	1	921	1058	1527	1281	1356	2759	2660	2725	3319	3133
ENSMUSG00000003970	chr15	Rpl8	76904071	76904109	862	0.739747	8.38179	2.95E-06	2.03E-05	0.029551	1	3337	3714	4540	4038	5390	8304	9242	8829	11548	10724
ENSMUSG00000048572	chr19	Tmem252	24674008	24674343	2462	1.698683	0.693359	2.95E-06	2.03E-05	0.106411	1	7	7	17	21	6	50	42	39	65	67
ENSMUSG00000015112	chr6	Slc25a13	6041218	6042332	3122	1.677975	0.665999	2.99E-06	2.06E-05	0.09963	1	14	10	11	15	6	36	47	31	90	59
ENSMUSG00000066113	chr4	Adamtsl1	86053915	86054120	10870	-1.2683	4.120546	2.99E-06	2.06E-05	0.082503	-1	454	152	435	281	795	188	236	257	276	232
ENSMUSG00000028234	chr4	Rps20	3831334	3834683	4080	0.782533	7.519372	3.02E-06	2.07E-05	0.032968	1	1921	2267	2681	1924	2437	4694	5514	5215	5827	5656
ENSMUSG00000024369	chr17	Nelfe	34850391	34850674	2076	0.915615	3.269808	3.03E-06	2.08E-05	0.039232	1	88	105	122	110	126	164	289	257	413	363
ENSMUSG00000045954	chr1	Sdpr	51289126	51289868	3055	-0.90556	5.829641	3.06E-06	2.1E-05	0.043553	-1	803	1142	1438	1678	1134	601	859	899	1314	1034
ENSMUSG00000041415	chr12	Dicer1	1.05E+08	1.05E+08	9851	-0.74854	5.79797	3.08E-06	2.11E-05	0.029589	-1	934	873	1276	1240	1579	779	967	1024	1102	968
ENSMUSG00000012443	chr19	Kif11	37376403	37376667	4819	1.327695	2.370379	3.09E-06	2.11E-05	0.081785	1	37	36	46	38	87	119	191	97	305	151
ENSMUSG00000022747	chr16	St3gal6	58468125	58470727	6080	-0.87924	6.405226	3.09E-06	2.11E-05	0.041302	-1	1648	1675	2317	1910	1552	1398	1221	1320	1450	1467
ENSMUSG00000026411	chr1	Tmem9	1.36E+08	1.36E+08	2726	0.836585	3.92942	3.1E-06	2.12E-05	0.034453	1	165	135	206	171	237	294	519	571	490	400
ENSMUSG00000038039	chr10	Gcc2	58255497	58255571	9630	-0.76149	4.27832	3.11E-06	2.13E-05	0.028968	-1	339	383	505	375	432	243	359	384	363	330
ENSMUSG00000041161	chr4	Otud3	1.39E+08	1.39E+08	1668	-0.81267	3.447687	3.11E-06	2.13E-05	0.030915	-1	199	185	252	228	300	155	179	205	185	189
ENSMUSG00000006442	chr4	Srm	1.49E+08	1.49E+08	1599	1.004338	3.932725	3.12E-06	2.13E-05	0.050878	1	165	121	161	140	264	369	422	296	740	573
ENSMUSG00000020044	chr10	Timp3	86300372	86300974	8144	-0.95771	6.982869	3.15E-06	2.15E-05	0.049285	-1	2397	2135	2671	2456	4527	1419	1834	2914	2215	1673
ENSMUSG00000039841	chr6	Zfp800	28239931	28241657	4827	-1.19449	1.568196	3.16E-06	2.15E-05	0.058816	-1	65	56	77	65	76	19	43	44	65	41
ENSMUSG00000022474	chr15	Pmm1	81951108	81951612	2776	0.942589	4.145874	3.16E-06	2.16E-05	0.044966	1	176	192	214	184	237	360	408	762	514	654
ENSMUSG00000079553	chr17	Kifc1	33875666	33875869	3407	1.616158	1.47728	3.17E-06	2.16E-05	0.112523	1	13	21	18	15	43	59	100	47	165	107
ENSMUSG00000089857	chr8	Zfp882	71908608	71908738	3569	-1.49674	0.668537	3.17E-06	2.16E-05	0.084873	-1	34	30	41	42	43	9	29	14	33	11
ENSMUSG00000000058	chr6	Cav2	17281185	17281510	3335	-0.96878	4.713435	3.19E-06	2.17E-05	0.049124	-1	494	545	614	714	500	201	380	392	647	518
ENSMUSG00000035847	chrX	Ids	70343069	70346673	5101	-0.77662	4.561398	3.19E-06	2.17E-05	0.03084	-1	473	347	526	530	626	271	386	382	564	458
ENSMUSG00000029413	chr5	Naaa	92257659	92258943	3721	0.939413	3.867676	3.23E-06	2.2E-05	0.044264	1	162	104	179	144	252	361	446	300	635	502
ENSMUSG00000027346	chr2	Gpcpd1	1.33E+08	1.33E+08	7289	-1.08057	6.878501	3.27E-06	2.23E-05	0.062679	-1	2469	2592	2755	2830	2543	1373	1408	2947	1431	1538
ENSMUSG00000020315	chr11	Sptbn1	30099395	30100714	17492	-0.79558	7.371296	3.28E-06	2.23E-05	0.034332	-1	3011	2804	3943	4170	3636	1752	3009	3154	3577	2850
ENSMUSG00000052681	chr10	Rap1b	1.18E+08	1.18E+08	2024	0.814976	5.687849	3.28E-06	2.23E-05	0.035275	1	524	464	720	564	892	1068	1458	1219	2144	1896
ENSMUSG00000048949	chrX	Gm6206	1.03E+08	1.03E+08	2199	-1.06638	2.306505	3.29E-06	2.23E-05	0.050281	-1	86	112	110	131	111	57	67	92	75	77

ENSMUSG00000091985	chr4	Gm17354	1.09E+08	1.09E+08	3039	-1.44753	1.614317	3.3E-06	2.24E-05	0.090062	-1	73	58	97	72	68	52	36	20	36	39
ENSMUSG00000037344	chr5	Slc12a9	1.37E+08	1.37E+08	5020	1.037384	2.488526	3.33E-06	2.26E-05	0.04746	1	57	66	58	46	70	116	198	154	210	190
ENSMUSG00000032086	chr9	Bace1	45838580	45839288	6348	-0.83749	5.903926	3.33E-06	2.26E-05	0.037474	-1	962	976	1671	1090	1854	879	1163	846	1121	980
ENSMUSG00000015094	chr2	Npdc1	25399351	25399536	3906	0.785138	4.926658	3.4E-06	2.3E-05	0.032082	1	366	247	408	336	523	719	908	841	1027	983
ENSMUSG00000022548	chr16	Apod	31296192	31297576	2577	1.772484	6.160291	3.4E-06	2.3E-05	0.162792	1	633	306	613	383	798	1454	1469	6383	1464	1952
ENSMUSG00000029713	chr5	Gnb2	1.38E+08	1.38E+08	3402	0.770197	6.627934	3.41E-06	2.31E-05	0.032033	1	1016	1074	1266	1248	1520	2175	2984	2298	3810	3427
ENSMUSG00000022090	chr14	Pdlim2	70164218	70164793	4486	1.057468	2.491928	3.41E-06	2.31E-05	0.049584	1	60	47	66	65	58	122	223	193	183	146
ENSMUSG00000090100	chr2	Ttbk2	1.21E+08	1.21E+08	11406	-1.1713	3.543751	3.45E-06	2.34E-05	0.069694	-1	274	192	296	256	332	73	155	297	177	144
ENSMUSG00000025223	chr19	Ldb1	46032593	46033341	3583	0.944867	4.842928	3.48E-06	2.36E-05	0.046914	1	295	242	373	309	429	539	693	1356	954	878
ENSMUSG00000048351	chr4	Coa7	1.08E+08	1.08E+08	3851	-0.79713	4.525001	3.5E-06	2.36E-05	0.032717	-1	402	471	597	504	450	351	390	324	518	378
ENSMUSG00000031601	chr8	Cnot7	40492540	40494115	5821	-0.78572	5.099368	3.54E-06	2.39E-05	0.032532	-1	617	634	873	750	746	405	564	756	638	581
ENSMUSG00000056612	chr19	Ppp1r14b	6975048	6975506	919	0.849873	6.016072	3.58E-06	2.42E-05	0.03889	1	552	794	1040	696	776	1722	2007	1620	2090	2197
ENSMUSG00000043613	chr9	Mmp3	7445822	7446008	1798	2.210399	2.597507	3.6E-06	2.43E-05	0.235655	1	11	39	48	26	56	342	130	49	178	377
ENSMUSG00000027177	chr2	Hipk3	1.04E+08	1.04E+08	7987	-0.96512	7.869019	3.61E-06	2.43E-05	0.050834	-1	4393	4113	6166	5404	5912	2477	3002	5962	3557	3468
ENSMUSG00000039765	chr5	Cc2d2a	43662379	43662559	6776	-0.78243	3.640342	3.61E-06	2.43E-05	0.02951	-1	225	193	278	305	319	175	229	213	248	200
ENSMUSG00000064360	chrMT	mt-Nd3	9459	9806	348	-1.58331	0.497814	3.62E-06	2.44E-05	0.09255	-1	29	32	29	54	24	15	17	16	20	11
ENSMUSG00000047617	chr2	BC029214	25455141	25455648	2066	0.871069	3.089061	3.63E-06	2.44E-05	0.035134	1	73	83	120	92	133	187	292	235	286	270
ENSMUSG00000027423	chr2	Snx5	1.44E+08	1.44E+08	4177	0.733768	6.36012	3.66E-06	2.46E-05	0.029137	1	852	927	1273	929	1190	1759	2454	2222	3097	2547
ENSMUSG00000095253	chr17	Zfp799	32815455	32821099	5833	-1.02681	2.384724	3.66E-06	2.46E-05	0.047247	-1	100	75	139	130	142	54	80	99	90	76
ENSMUSG00000023921	chr17	Mut	40934685	40934779	3675	-0.77638	5.96068	3.72E-06	2.5E-05	0.032545	-1	1243	1196	1357	1357	1362	829	976	1263	1156	1125
ENSMUSG00000020810	chr11	Cygb	1.17E+08	1.17E+08	2331	0.83281	4.694784	3.73E-06	2.51E-05	0.036227	1	301	197	298	326	443	507	712	886	948	844
ENSMUSG00000034617	chr13	Mtrr	68560780	68562432	3692	-0.71476	3.996076	3.74E-06	2.51E-05	0.025135	-1	298	289	380	307	378	223	283	284	354	267
ENSMUSG00000031245	chrX	Hmgn5	1.09E+08	1.09E+08	1934	-0.80773	3.547684	3.74E-06	2.52E-05	0.031576	-1	202	221	318	247	252	134	181	225	238	218
ENSMUSG00000021219	chr12	Rgs6	82616925	82617383	8145	-1.80795	-0.1399	3.76E-06	2.52E-05	0.105782	-1	29	8	19	23	32	5	9	7	11	12
ENSMUSG00000058006	chr4	Mdn1	32657119	32657352	21836	-0.82222	3.630138	3.76E-06	2.52E-05	0.033234	-1	243	187	308	228	367	140	233	183	269	228
ENSMUSG00000022789	chr16	Dnm1l	16312235	16314043	4107	-0.74601	6.316447	3.79E-06	2.54E-05	0.030236	-1	1333	1503	2011	1675	1843	1183	1511	1341	1670	1234
ENSMUSG00000029007	chr4	Agtrap	1.48E+08	1.48E+08	4236	0.766664	4.555359	3.8E-06	2.55E-05	0.030292	1	241	220	323	311	365	436	626	801	860	762
ENSMUSG00000055660	chr17	Mettl4	94727080	94727395	2150	-1.1109	2.392381	3.81E-06	2.55E-05	0.057037	-1	117	90	162	95	133	50	99	95	78	63
ENSMUSG00000024791	chr19	Cdca5	6084983	6085208	2129	2.173317	0.547026	3.84E-06	2.57E-05	0.194196	1	5	3	8	6	19	44	56	10	70	73
ENSMUSG00000025959	chr1	Klf7	64029447	64035764	8131	-0.8329	4.091198	3.84E-06	2.57E-05	0.035397	-1	257	302	343	438	498	233	308	219	363	310
ENSMUSG00000041132	chr5	N4bp2l1	1.51E+08	1.51E+08	1906	1.426025	1.691168	3.87E-06	2.59E-05	0.088499	1	34	19	26	25	35	51	93	126	97	163
ENSMUSG00000033392	chr9	Clasp2	1.14E+08	1.14E+08	5690	-0.70107	5.629193	3.88E-06	2.59E-05	0.026337	-1	868	858	1103	1048	1264	703	973	788	1079	869
ENSMUSG00000083567	chr2	Gm11451	1.63E+08	1.63E+08	630	-0.83798	3.548165	3.88E-06	2.59E-05	0.034233	-1	209	235	290	225	290	185	216	145	234	190
ENSMUSG00000038774	chr10	Ascc3	50592669	50592897	7477	-0.73227	4.098313	3.88E-06	2.59E-05	0.026847	-1	308	282	405	370	426	218	353	284	345	305
ENSMUSG00000031617	chr8	Tmem184c	77595982	77597180	2723	-0.86604	3.36307	3.92E-06	2.62E-05	0.03652	-1	224	203	234	185	252	117	183	208	184	157
ENSMUSG00000024691	chr19	Fam111a	12545740	12545855	4125	1.08256	3.132848	3.93E-06	2.62E-05	0.05771	1	77	72	99	81	140	197	308	151	402	336
ENSMUSG00000000374	chr10	Trappc10	78186725	78188094	5048	-0.75752	5.573984	3.93E-06	2.62E-05	0.030883	-1	823	902	1066	1080	1126	584	799	1045	973	751
ENSMUSG00000035726	chr14	Supt16	52160419	52161822	4491	0.788024	4.57963	3.95E-06	2.63E-05	0.032262	1	238	253	283	274	423	545	599	635	1029	755
ENSMUSG00000035078	chr14	Mtmr9	63523616	63524217	2402	-0.86682	3.311347	3.97E-06	2.65E-05	0.036534	-1	195	165	231	234	243	91	164	194	216	166
ENSMUSG00000022769	chr16	Sdf2l1	17130138	17130788	1108	1.321453	3.08245	3.97E-06	2.65E-05	0.087742	1	56	72	88	50	140	226	281	122	437	345
ENSMUSG00000042625	chr17	Safb2	56560965	56561206	8165	0.811417	4.430573	3.98E-06	2.65E-05	0.034044	1	241	217	259	242	346	425	527	791	738	732
ENSMUSG00000029381	chr5	Shroom3	92683435	92683831	7755	1.936004	0.253272	4E-06	2.66E-05	0.129418	1	6	6	2	11	11	24	57	47	51	18
ENSMUSG00000031749	chr8	St3gal2	1.11E+08	1.11E+08	5041	-0.74959	5.833181	4.01E-06	2.67E-05	0.030444	-1	987	974	1432	1218	1400	740	1067	1136	1190	849
ENSMUSG00000032855	chr17	Pkd1	24549950	24550477	14170	-0.93611	5.785369	4.01E-06	2.67E-05	0.047649	-1	1290	766	1273	1091	1683	511	984	1185	1038	756
ENSMUSG00000059714	chr17	Flot1	35823230	35823501	2893	0.80135	6.123619	4.03E-06	2.68E-05	0.034973	1	725	770	971	891	873	1731	1718	2459	2132	2214
ENSMUSG00000020516	chr11	Rps6kb1	86498871	86502962	8658	-0.77838	5.194618	4.03E-06	2.68E-05	0.032396	-1	677	627	937	731	912	417	686	792	697	571
ENSMUSG00000022671	chr16	Mzt2	15848441	15848729	1236	0.785157	3.577312	4.05E-06	2.69E-05	0.029534	1	120	140	167	136	161	303	350	332	449	312
ENSMUSG00000095362	chr2	Gm14325	1.78E+08	1.78E+08	1616	-1.2493	2.665864	4.09E-06	2.71E-05	0.076721	-1	108	103	266	105	178	53	109	110	107	61
ENSMUSG00000080921	chr6	Rpl38-ps2	1.41E+08	1.41E+08	213	0.826943	4.087148	4.1E-06	2.72E-05	0.034814	1	148	227	199	194	245	445	478	514	505	552
ENSMUSG00000056418	chr9	BC043934	96435783	96438138	2356	1.734721	-0.06222	4.12E-06	2.73E-05	0.084849	1	2	6	7	6	11	22	37	18	41	32
ENSMUSG00000046434	chr15	Hnrnpa1	1.03E+08	1.03E+08	1918	0.883843	6.646579	4.14E-06	2.74E-05	0.042946	1	956	965	1328	1102	1595	1836	2610	4412	3545	2915
ENSMUSG00000084098	chr2	Gm13422	23235236	23235739	504	-1.59199	0.557804	4.16E-06	2.76E-05	0.095993	-1	43	31	49	29	24	15	15	17	27	9
ENSMUSG00000026768	chr2	Itga8	12106632	12109201	7368	-1.20656	2.1176	4.18E-06	2.77E-05	0.06759	-1	86	55	110	129	127	39	89	56	70	51
ENSMUSG00000046364	chr7	Rpl27a	1.1E+08	1.1E+08	2774	0.748125	7.1429	4.19E-06	2.77E-05	0.030956	1	1483	1666	2002	1640	2017	3583	4401	3670	4566	4349
ENSMUSG00000029478	chr5	Ncor2	1.25E+08	1.25E+08	10479	-0.82931	6.264616	4.21E-06	2.79E-05	0.037769	-1	1173	1155	1840	2021	2172	878	1442	1439	1650	1126
ENSMUSG00000002032	chr9	Tmem25	44793776	44795048	2902	-0.85964	3.730421	4.22E-06	2.79E-05	0.037409	-1	243	286	297	293	295	191	258	159	305	189
ENSMUSG00000045594	chr9	Glb1	1.14E+08	1.14E+08	2395	1.109194	3.462976	4.22E-06	2.79E-05	0.062802	1	100	58	124	111	199	229	419	221	496	407
ENSMUSG00000024516	chr18	Sec11c	65800549	65800711	3084	0.828409	4.269618	4.24E-06	2.8E-05	0.035461	1	194	223	273	199	265	472	534	417	702	746
ENSMUSG00000085614	chr4	1700123M08Rik	11966565	11966683	1260	-1.08031	2.548777	4.24E-06	2.8E-05	0.055138	-1	137	127	158	105	124	88	100	69	90	82
ENSMUSG00000028673	chr4	Fuca1	1.36E+08	1.36E+08	3276	0.825537	5.145133	4.24E-06	2.8E-05	0.036627	1	355	286	480	394	655	719	1010	898	1445	1278
ENSMUSG00000021987	chr14	Mtmr6	60265205	60265361	3836	-0.75273	5.853035	4.25E-06	2.8E-05	0.030897	-1	1076	1023	1500	1119	1359	697	1065	1181	1168	943
ENSMUSG00000023973	chr17	Cnpy3	46735705	46736908	2659	0.835279	4.061482	4.25E-06	2.8E-05	0.035907	1	151	141	219	178	329	375	487	432	644	564
ENSMUSG00000066232	chr7	Ipo7	1.1E+08	1.1E+08	3117	-0.86382	6.339889	4.25E-06	2.8E-05	0.041051	-1	1447	1462	2013	1795	2064	898	1433	1866	1554	995
ENSMUSG00000037095	chr17	Lrg1	56119680	56120944	1351	1.261337	4.041466	4.27E-06	2.81E-05	0.083637	1	129	159	136	220	148	324	295	404	823	917
ENSMUSG00000041731	chr19	Pgm5	24683016	24684574	3611	1.186306	4.66167	4.28E-06	2.82E-05	0.075323	1	177	214	320	322	259	554	1540	564	900	554
ENSMUSG00000059883	chr15	Irak4	94543643	94543826	5021	1.135222	2.275532	4.3E-06	2.83E-05	0.058935	1	35	40	59	47	68	110	160	92	227	179

ENSMUSG00000020366	chr11	Mapk9	49846751	49846975	6784	-0.69862	5.684847	4.32E-06	2.84E-05	0.02644	-1	932	892	1127	1046	1340	743	894	960	1036	936
ENSMUSG00000017677	chr11	Wsb1	79239372	79240462	3987	0.907468	3.853361	4.34E-06	2.85E-05	0.042262	1	121	128	195	164	239	229	480	361	620	551
ENSMUSG00000079197	chr14	Psme2	55587441	55587565	1764	1.002532	4.93195	4.36E-06	2.86E-05	0.054102	1	272	316	364	338	404	815	817	516	1157	1439
ENSMUSG00000090841	chr10	Myl6	1.28E+08	1.28E+08	665	0.834828	7.488868	4.36E-06	2.86E-05	0.038746	1	1739	2011	2544	2074	2432	4302	5951	3494	7241	6118
ENSMUSG00000099088	chr10	Gm27920	1.23E+08	1.23E+08	96	-1.72368	0.558238	4.37E-06	2.87E-05	0.11725	-1	21	26	58	29	53	6	26	22	14	9
ENSMUSG00000033781	chr13	Asb13	3634032	3634175	3347	-0.8117	3.954642	4.38E-06	2.87E-05	0.033511	-1	285	295	382	366	308	246	250	284	262	250
ENSMUSG00000020889	chr11	Nr1d1	98767932	98768419	3077	-0.88628	6.954759	4.48E-06	2.94E-05	0.043637	-1	2181	1908	2811	3728	2883	1375	1680	2188	2421	2600
ENSMUSG00000063171	chr6	Rps4l	1.48E+08	1.48E+08	943	1.052159	2.8825	4.48E-06	2.94E-05	0.053202	1	68	74	80	69	103	136	295	160	270	296
ENSMUSG00000055435	chr8	Maf	1.16E+08	1.16E+08	8241	-0.75029	7.26562	4.5E-06	2.95E-05	0.031386	-1	2536	2653	3434	3108	4611	2279	2742	2564	3005	2755
ENSMUSG00000090231	chr17	Cfb	34856374	34856582	2825	1.839443	4.397196	4.51E-06	2.95E-05	0.176981	1	85	107	123	120	365	679	492	243	750	1630
ENSMUSG00000003418	chr2	St8sia6	13651021	13657290	7664	-1.48203	0.479849	4.53E-06	2.97E-05	0.076962	-1	31	28	27	41	37	10	26	17	13	16
ENSMUSG00000024548	chr18	Setbp1	78750380	78755825	9953	-1.37765	2.860412	4.54E-06	2.97E-05	0.096296	-1	153	110	200	166	259	53	97	182	70	64
ENSMUSG00000056501	chr2	Cebpb	1.68E+08	1.68E+08	1504	1.033576	4.195989	4.54E-06	2.97E-05	0.056469	1	168	174	218	267	162	573	399	686	496	635
ENSMUSG00000006542	chr1	Prkag3	74738922	74740060	3682	-1.2559	7.43687	4.55E-06	2.97E-05	0.08674	-1	3171	2988	5524	3767	5353	2598	3117	880	2299	2797
ENSMUSG00000040782	chr1	Rfwd2	1.59E+08	1.59E+08	17516	-0.76102	6.313964	4.55E-06	2.97E-05	0.032004	-1	1436	1535	1920	1701	1743	1193	1353	1521	1399	1362
ENSMUSG00000051146	chr16	Camk2n2	20619215	20620243	1291	1.445411	0.535464	4.6E-06	3E-05	0.067391	1	11	12	11	6	19	38	39	43	55	50
ENSMUSG00000019726	chr13	Lyst	13590409	13590496	11806	-1.14126	2.482132	4.65E-06	3.03E-05	0.063313	-1	146	90	137	125	136	34	80	92	104	103
ENSMUSG00000025040	chrX	Fundc1	17556564	17558011	2353	-0.71792	4.257982	4.65E-06	3.03E-05	0.026459	-1	318	373	440	378	479	284	350	310	432	312
ENSMUSG00000100862	chr1	Gm10925	24613974	24614651	678	-1.03103	3.551773	4.72E-06	3.08E-05	0.055084	-1	216	238	322	349	171	123	152	225	225	179
ENSMUSG00000032854	chr3	Ugt8a	1.26E+08	1.26E+08	3583	-1.53491	0.43222	4.73E-06	3.09E-05	0.086467	-1	31	23	26	48	32	9	21	18	20	10
ENSMUSG00000025871	chr13	4833439L19Rik	54551218	54552817	3187	-0.76603	7.696628	4.74E-06	3.09E-05	0.032961	-1	3640	4094	5027	4644	4338	3292	3452	3573	3906	3545
ENSMUSG00000036768	chr9	Kif15	1.23E+08	1.23E+08	4815	1.790456	0.986674	4.78E-06	3.11E-05	0.140017	1	10	4	9	13	35	42	71	40	106	81
ENSMUSG00000093575	chr16	Gm20695	3884648	3884806	1088	-0.91805	3.052038	4.87E-06	3.17E-05	0.041212	-1	186	150	212	171	176	92	162	143	164	110
ENSMUSG00000057551	chr9	Zfp317	19641224	19641254	1824	-1.36017	2.833275	4.88E-06	3.18E-05	0.094651	-1	142	167	176	155	213	31	84	177	108	74
ENSMUSG00000089669	chr11	Tnfsf13	69682846	69683344	1637	1.074755	2.447568	4.88E-06	3.18E-05	0.053052	1	56	52	58	50	69	104	137	150	242	226
ENSMUSG00000026069	chr1	Il1rl1	40429570	40429630	6894	1.653902	1.261734	4.89E-06	3.18E-05	0.121108	1	17	6	15	25	29	63	95	38	88	116
ENSMUSG00000000628	chr6	Hk2	82725025	82727454	5969	-0.82586	7.547532	4.89E-06	3.18E-05	0.038362	-1	3320	4080	3938	4601	3820	2935	2916	2676	4127	3071
ENSMUSG00000070427	chr7	Il18bp	1.02E+08	1.02E+08	1400	1.351252	1.677451	4.9E-06	3.18E-05	0.08085	1	26	21	23	37	37	108	99	60	108	131
ENSMUSG00000031304	chrX	Il2rg	1.01E+08	1.01E+08	2387	1.688363	2.956134	4.92E-06	3.2E-05	0.145635	1	28	63	58	81	72	193	220	72	477	433
ENSMUSG00000027215	chr2	Cd82	93419111	93419942	3005	0.998925	4.778448	4.93E-06	3.2E-05	0.054263	1	200	261	419	246	429	730	1167	495	998	859
ENSMUSG00000006498	chr10	Ptbp1	79854427	79854721	4740	0.992054	5.142311	4.97E-06	3.22E-05	0.053942	1	333	271	380	382	639	699	1055	689	1792	1393
ENSMUSG00000011752	chr19	Pgam1	41911871	41912186	1831	1.195077	3.938988	4.97E-06	3.22E-05	0.076011	1	131	139	161	128	218	297	402	239	845	772
ENSMUSG00000027239	chr2	Mdk	91929805	91930115	1324	1.077708	2.681593	4.96E-06	3.22E-05	0.05648	1	51	49	74	54	117	194	222	159	239	174
ENSMUSG00000028803	chr4	Nipal3	1.35E+08	1.35E+08	7588	-0.87714	3.255454	4.97E-06	3.22E-05	0.038112	-1	183	193	238	229	175	112	139	175	201	161
ENSMUSG00000067336	chr1	Bmpr2	59763400	59764728	17983	-0.8206	6.166553	4.97E-06	3.22E-05	0.037491	-1	1322	1199	1787	1697	1685	868	1122	1655	1294	1125
ENSMUSG00000021719	chr13	Rgs7bp	1.05E+08	1.05E+08	5828	-1.38904	0.579153	5E-06	3.23E-05	0.068253	-1	35	27	28	37	47	11	16	15	29	23
ENSMUSG00000026604	chr1	Ptpn14	1.9E+08	1.9E+08	13413	-0.71533	4.519597	5.03E-06	3.25E-05	0.026957	-1	400	371	489	529	604	291	413	421	526	391
ENSMUSG00000034773	chr11	BC030867	1.02E+08	1.02E+08	3032	2.545533	-0.13562	5.04E-06	3.26E-05	0.24139	1	1	0	3	4	11	13	20	13	70	44
ENSMUSG00000039886	chr5	Tmem120a	1.36E+08	1.36E+08	1553	1.332263	3.530392	5.07E-06	3.27E-05	0.093242	1	89	85	100	102	173	172	257	247	603	701
ENSMUSG00000059493	chrX	Nhs	1.62E+08	1.62E+08	8805	-1.61601	0.805027	5.09E-06	3.29E-05	0.109443	-1	38	21	51	59	47	9	18	31	13	26
ENSMUSG00000022483	chr15	Col2a1	97975602	97976186	6001	-4.22916	5.552289	5.11E-06	3.3E-05	0.764614	-1	345	81	318	125	7757	96	213	73	139	32
ENSMUSG00000018761	chr11	Mpdu1	69656697	69657328	2420	1.04267	3.73196	5.24E-06	3.38E-05	0.056913	1	121	131	169	117	184	256	324	273	629	639
ENSMUSG00000037361	chr12	Sf3b6	4817608	4817819	1115	0.76624	4.252849	5.27E-06	3.4E-05	0.030676	1	235	188	269	190	293	497	553	507	613	597
ENSMUSG00000031962	chr8	Cdh15	1.23E+08	1.23E+08	2843	0.990239	5.070021	5.3E-06	3.42E-05	0.054041	1	246	311	485	312	563	765	1646	834	1145	824
ENSMUSG00000022770	chr16	Dlg1	31663443	31663488	8963	-0.74025	5.640456	5.33E-06	3.43E-05	0.030349	-1	905	841	1185	1065	1240	624	887	1089	931	832
ENSMUSG00000029123	chr5	Stk32b	37446828	37448791	3437	2.832518	-0.48025	5.41E-06	3.48E-05	0.263996	1	2	0	3	0	7	20	53	7	25	14
ENSMUSG00000050288	chr11	Fzd2	1.03E+08	1.03E+08	3663	1.310626	2.710798	5.41E-06	3.48E-05	0.087264	1	42	33	45	73	124	163	284	144	293	193
ENSMUSG00000033972	chr17	Zfp944	22337989	22340107	2784	-0.91424	2.759544	5.45E-06	3.5E-05	0.040028	-1	122	144	189	125	153	77	110	116	131	113
ENSMUSG00000044033	chr2	Ccdc141	77009902	77015247	11717	1.141421	3.899149	5.46E-06	3.51E-05	0.07015	1	95	109	160	128	307	329	754	417	520	367
ENSMUSG00000039844	chr2	Rapgef1	29619720	29620063	7385	-0.76091	7.268372	5.52E-06	3.55E-05	0.03291	-1	2496	2578	3592	3767	3908	2002	2567	3209	3125	2494
ENSMUSG00000027520	chr1	Zdbf2	63273265	63273472	12659	1.213702	4.331574	5.54E-06	3.56E-05	0.080595	1	93	114	225	206	421	557	900	551	626	599
ENSMUSG00000022420	chr15	Dnal4	79761453	79762049	2340	0.800597	3.25663	5.56E-06	3.57E-05	0.030651	1	108	100	128	101	138	218	297	287	345	257
ENSMUSG00000042821	chr2	Snai1	1.68E+08	1.68E+08	1621	1.396714	1.644555	5.6E-06	3.59E-05	0.089591	1	25	11	32	27	45	68	91	64	166	128
ENSMUSG00000072941	chr5	Sod3	52363946	52364052	3570	1.345057	4.997753	5.6E-06	3.59E-05	0.099612	1	258	169	281	286	550	663	922	445	1760	1712
ENSMUSG00000031618	chr8	Nr3c2	76899442	76899567	6474	-0.99507	2.744408	5.65E-06	3.62E-05	0.048432	-1	130	151	139	157	156	84	116	106	145	71
ENSMUSG00000026187	chr1	Xrcc5	72307421	72307567	2555	-0.80366	4.971935	5.67E-06	3.64E-05	0.035403	-1	565	595	729	558	906	522	594	412	593	515
ENSMUSG00000049225	chr4	Pdp1	11958184	11962233	4507	-0.8048	6.058199	5.67E-06	3.64E-05	0.036471	-1	1329	1316	1542	1535	1275	794	1147	1395	1228	1113
ENSMUSG00000029361	chr5	Nos1	1.18E+08	1.18E+08	11151	-1.20021	5.201818	5.68E-06	3.64E-05	0.079947	-1	580	886	972	1154	648	485	370	805	600	314
ENSMUSG00000087380	chr6	2210408F21Rik	31220351	31220519	1476	-0.99041	4.645469	5.73E-06	3.66E-05	0.053815	-1	529	616	612	529	433	446	401	346	348	356
ENSMUSG00000032536	chr9	Trak1	1.21E+08	1.21E+08	4883	-0.80468	7.236738	5.74E-06	3.67E-05	0.036915	-1	2539	2671	3176	4026	3647	2132	2775	2024	3626	2369
ENSMUSG00000019066	chr9	Rab3d	21907491	21910671	4196	1.028348	3.53162	5.85E-06	3.74E-05	0.055262	1	117	79	105	145	189	189	334	315	494	504
ENSMUSG00000091549	chr17	Gm6548	78850792	78851956	1165	1.504925	2.158017	5.86E-06	3.74E-05	0.112753	1	28	19	44	41	61	165	147	58	158	205
ENSMUSG00000040998	chr3	Npnt	1.33E+08	1.33E+08	5026	1.182727	4.924515	5.91E-06	3.77E-05	0.077525	1	217	317	410	259	350	589	1894	789	1024	650
ENSMUSG00000056671	chr18	Prelid2	41875696	41875853	724	1.677796	0.257663	5.92E-06	3.78E-05	0.097481	1	6	6	11	11	8	24	60	20	48	39
ENSMUSG00000023092	chrX	Fhl1	56731787	56731868	3714	1.432731	9.482862	5.97E-06	3.81E-05	0.114919	1	4786	5702	6445	11276	3579	11209	28121	40947	27570	16152
ENSMUSG00000044461	chr14	Shisa2	59625281	59626400	3144	-0.86744	6.33188	5.99E-06	3.82E-05	0.042699	-1	1619	1560	1627	1373	2553	1238	1463	1419	1446	1018

ENSMUSG00000072694	chr5	1500011B03Rik	1.15E+08	1.15E+08	1746	1.242321	1.334766	6.08E-06	3.88E-05	0.062179	1	20	18	26	33	21	60	80	91	75	84
ENSMUSG00000019132	chr13	BC005537	24801657	24803509	3665	0.873204	6.505273	6.12E-06	3.9E-05	0.043398	1	964	899	1225	1057	1217	1567	2288	3978	3230	2823
ENSMUSG00000033910	chr3	Gucy1a3	82092427	82094899	6968	-0.89914	3.628843	6.19E-06	3.94E-05	0.042545	-1	210	196	266	373	302	118	200	248	262	192
ENSMUSG00000079550	chr1	Mpp4	59120935	59121444	7063	1.259466	2.031994	6.23E-06	3.97E-05	0.074943	1	37	29	60	26	44	103	125	185	107	123
ENSMUSG00000027852	chr3	Nras	1.03E+08	1.03E+08	4514	0.737321	5.918853	6.26E-06	3.98E-05	0.030689	1	559	749	894	729	863	1257	1765	1968	2122	1762
ENSMUSG00000045962	chr6	Wnk1	1.2E+08	1.2E+08	15780	-0.73934	8.13959	6.26E-06	3.98E-05	0.031592	-1	4889	4360	7069	6363	7103	4065	5510	4115	6010	5017
ENSMUSG00000039753	chr5	Fbxl5	43744616	43745375	9788	-0.69691	5.174524	6.28E-06	3.99E-05	0.026869	-1	634	641	856	735	875	453	632	738	747	661
ENSMUSG00000063838	chr7	Cdc42ep5	4151260	4151787	1288	1.258157	1.732508	6.29E-06	4E-05	0.071705	1	22	23	43	30	41	77	133	59	151	112
ENSMUSG00000034707	chr10	Gns	1.21E+08	1.21E+08	3855	0.732099	6.085646	6.3E-06	4E-05	0.03039	1	717	684	880	826	1196	1410	1961	1861	2529	2227
ENSMUSG00000037548	chr17	H2-DMb2	34143307	34143529	1710	1.889125	-0.44676	6.31E-06	4.01E-05	0.08016	1	3	5	3	7	3	16	25	17	27	27
ENSMUSG00000029178	chr5	Klf3	64803523	64803791	2479	-1.19367	2.774282	6.31E-06	4.01E-05	0.073709	-1	136	103	167	172	224	38	107	137	143	72
ENSMUSG00000060438	chr3	Rps10-ps1	95622278	95622775	498	1.12768	1.675886	6.32E-06	4.01E-05	0.053068	1	25	38	30	32	34	80	99	94	107	109
ENSMUSG00000038080	chr13	Kdm1b	47043499	47043670	4829	-0.79532	3.422559	6.33E-06	4.01E-05	0.031899	-1	193	173	270	221	285	117	194	210	230	170
ENSMUSG00000053291	chr7	Rab4b	27168424	27168804	1970	0.917404	3.558212	6.33E-06	4.01E-05	0.043783	1	121	112	130	123	192	307	357	219	482	423
ENSMUSG00000101678	chr5	Gm29609	31144739	31144752	3550	-0.72995	4.896174	6.34E-06	4.01E-05	0.029325	-1	555	511	764	558	727	358	561	597	649	470
ENSMUSG00000028643	chr4	Ccdc23	1.19E+08	1.19E+08	1065	1.013589	4.10463	6.38E-06	4.04E-05	0.055961	1	142	179	203	189	236	454	859	325	541	471
ENSMUSG00000049517	chr13	Rps23	90923131	90923199	756	0.71118	7.612449	6.39E-06	4.05E-05	0.02921	1	2121	2165	2953	2217	3005	4534	5676	5557	6436	6152
ENSMUSG00000024247	chr17	Pkdcc	83215292	83216104	2712	-0.81881	6.278562	6.41E-06	4.05E-05	0.038253	-1	1224	1621	1863	1789	1776	1276	1363	1166	1215	1420
ENSMUSG00000049932	chr9	H2afx	44334694	44336077	1384	0.837931	3.349189	6.47E-06	4.09E-05	0.03501	1	88	109	122	143	143	239	261	266	403	349
ENSMUSG00000085201	chr2	Nr6a1os	38823257	38823569	801	-1.81662	-0.20773	6.47E-06	4.09E-05	0.113598	-1	19	22	35	11	18	5	9	3	14	11
ENSMUSG00000016757	chr15	Ttll12	83575119	83577048	4010	0.805623	4.323312	6.48E-06	4.1E-05	0.035031	1	189	218	259	229	324	482	671	400	825	604
ENSMUSG00000066068	chr2	Gm13611	32271845	32272162	318	1.272001	1.119162	6.5E-06	4.1E-05	0.06256	1	16	22	25	18	18	66	65	68	66	67
ENSMUSG00000104344	chr9	RP23-444I6.3	1.05E+08	1.05E+08	3245	-1.34078	1.280888	6.52E-06	4.11E-05	0.078082	-1	56	57	69	37	65	33	36	36	27	22
ENSMUSG00000074088	chr4	Snrnp40	1.3E+08	1.3E+08	3987	0.719913	3.976725	6.53E-06	4.12E-05	0.026806	1	155	170	235	200	232	358	395	495	546	481
ENSMUSG00000002477	chr18	Snrpd1	10617796	10617926	837	0.852788	3.847015	6.53E-06	4.12E-05	0.038509	1	130	151	227	135	216	355	445	292	581	486
ENSMUSG00000040407	chr5	Akap9	3928054	3928342	15848	-0.98713	5.840256	6.53E-06	4.12E-05	0.055458	-1	1087	953	1431	1373	1571	515	858	1503	904	728
ENSMUSG00000024308	chr17	Tapbp	33915899	33915964	3296	0.808976	5.720751	6.54E-06	4.12E-05	0.037087	1	519	520	686	624	882	1265	1492	1130	1902	2064
ENSMUSG00000036391	chr11	Sec24a	51692264	51695241	10683	-1.08576	4.588561	6.54E-06	4.12E-05	0.065785	-1	503	389	647	510	709	200	328	646	392	245
ENSMUSG00000073705	chr4	Apitd1	1.49E+08	1.49E+08	1909	1.946335	0.259228	6.55E-06	4.12E-05	0.134283	1	7	15	5	2	6	38	30	25	60	44
ENSMUSG00000028842	chr4	Ago3	1.26E+08	1.26E+08	16571	-0.74611	3.52195	6.56E-06	4.13E-05	0.027903	-1	216	202	245	233	304	151	200	196	266	192
ENSMUSG00000093156	chr14	Mir3076	30572149	30572208	60	3.263235	3.645148	6.57E-06	4.13E-05	0.508904	1	23	19	12	68	77	101	114	53	893	1608
ENSMUSG00000031748	chr8	Gnao1	93809966	93810129	6785	-0.93227	3.073271	6.63E-06	4.17E-05	0.044188	-1	172	132	194	209	213	80	150	168	174	109
ENSMUSG00000021175	chr12	Cdca7l	1.18E+08	1.18E+08	3258	2.366156	0.960493	6.64E-06	4.17E-05	0.258607	1	6	6	4	5	29	46	50	18	149	100
ENSMUSG00000043241	chr2	Upf2	5951469	5951553	5474	-0.71236	4.625233	6.65E-06	4.17E-05	0.027605	-1	434	428	595	518	591	318	436	525	493	413
ENSMUSG00000070385	chr3	Ampd1	1.03E+08	1.03E+08	2921	-1.12696	10.23311	6.64E-06	4.17E-05	0.073024	-1	26360	21336	31499	25831	33569	22166	18746	7971	18261	18498
ENSMUSG00000039275	chr11	Foxk2	1.21E+08	1.21E+08	5258	-0.70736	5.485078	6.67E-06	4.18E-05	0.028106	-1	752	821	960	923	1207	690	830	798	887	742
ENSMUSG00000045328	chr3	Cenpe	1.35E+08	1.35E+08	7813	1.471493	1.660935	6.67E-06	4.18E-05	0.102163	1	11	27	27	23	48	53	104	72	189	119
ENSMUSG00000103508	chr9	Map4	1.1E+08	1.1E+08	3378	-0.90706	7.605129	6.7E-06	4.2E-05	0.04758	-1	3893	2931	4981	4788	4754	1961	3038	4745	3531	2656
ENSMUSG00000044337	chr1	Ackr3	90203980	90204087	3348	-0.88304	4.644911	6.7E-06	4.2E-05	0.043258	-1	554	303	505	559	822	356	420	364	439	459
ENSMUSG00000034892	chr12	Rps29	69157722	69157821	693	0.76301	7.874734	6.74E-06	4.22E-05	0.033821	1	2421	2733	3531	2542	3346	6396	6953	6090	7250	7420
ENSMUSG00000063065	chr7	Mapk3	1.27E+08	1.27E+08	2163	0.782839	5.307435	6.8E-06	4.26E-05	0.034447	1	382	410	508	580	552	825	1016	988	1629	1463
ENSMUSG00000051469	chr18	Zfp191	24009702	24014685	6271	-0.71242	5.299241	6.81E-06	4.26E-05	0.02842	-1	667	742	942	774	971	589	727	753	740	650
ENSMUSG00000016206	chr17	H2-M3	37270220	37270334	1438	1.180452	2.114242	6.83E-06	4.27E-05	0.065737	1	44	41	33	37	58	109	142	96	142	189
ENSMUSG00000025348	chr10	Itga7	1.29E+08	1.29E+08	4013	0.775949	7.059973	6.85E-06	4.28E-05	0.034854	1	1242	1350	2086	1589	2056	2945	5032	3365	4881	3574
ENSMUSG00000052430	chr3	Bmpr1b	1.42E+08	1.42E+08	5962	-1.34626	1.939435	6.87E-06	4.29E-05	0.08947	-1	111	76	76	70	118	29	43	78	72	32
ENSMUSG00000018736	chr11	Ndel1	68821434	68822665	3253	-0.77078	6.109273	6.88E-06	4.3E-05	0.034065	-1	1376	1239	1746	1346	1552	863	1274	1469	1276	1076
ENSMUSG00000024442	chr18	0610009O20Rik	38250249	38250399	2404	-0.79898	6.624812	6.89E-06	4.3E-05	0.036844	-1	1780	2007	2304	2278	2026	1400	1514	2096	1891	1471
ENSMUSG00000035208	chr11	Slfn8	83002158	83003889	4091	2.110858	1.957256	6.9E-06	4.31E-05	0.22094	1	21	21	15	20	41	197	78	34	108	261
ENSMUSG00000027408	chr2	Cpxm1	1.3E+08	1.3E+08	2432	1.12248	4.376018	6.95E-06	4.34E-05	0.070346	1	201	96	215	199	409	559	788	411	870	689
ENSMUSG00000024056	chr17	Ndc80	71496100	71496353	2201	1.634264	0.993994	6.95E-06	4.34E-05	0.115408	1	5	18	16	12	25	44	89	32	94	73
ENSMUSG00000010290	chr1	AI597479	43098710	43098862	3458	-0.72785	4.393403	7.03E-06	4.38E-05	0.028639	-1	367	424	515	411	461	330	380	357	427	339
ENSMUSG00000018293	chr11	Pfn1	70651850	70652221	2405	0.821263	7.803054	7.04E-06	4.39E-05	0.039284	1	2117	2564	3464	2444	2937	5831	6278	4657	8970	7689
ENSMUSG00000033721	chr3	Vav3	1.09E+08	1.09E+08	6005	1.045151	2.407334	7.09E-06	4.42E-05	0.052158	1	48	39	62	65	70	89	186	140	209	205
ENSMUSG00000022559	chr15	Fbxl6	76535730	76535963	1712	0.872182	3.223673	7.1E-06	4.42E-05	0.038238	1	97	98	143	80	128	194	311	233	364	306
ENSMUSG00000025537	chr5	Phkg1	1.3E+08	1.3E+08	3232	-0.90607	8.968213	7.15E-06	4.45E-05	0.047918	-1	9279	10385	13395	10159	11246	9277	7591	6435	7240	8967
ENSMUSG00000037487	chr15	Ubr5	37967328	37968505	9790	-0.76701	6.698775	7.16E-06	4.46E-05	0.034104	-1	1839	1632	2527	2255	2802	1339	1774	2271	1961	1631
ENSMUSG00000019810	chr10	Fuca2	13499540	13499587	6161	0.761025	4.196733	7.2E-06	4.48E-05	0.031142	1	169	197	283	200	294	389	527	438	762	599
ENSMUSG00000021913	chr14	Ogdhl	32322019	32322116	3449	1.384748	1.587069	7.22E-06	4.49E-05	0.088113	1	25	18	26	29	35	74	89	159	100	59
ENSMUSG00000022555	chr15	Dgat1	76502015	76502388	3054	1.361735	4.050342	7.24E-06	4.49E-05	0.102709	1	139	123	134	175	198	263	312	345	793	1139
ENSMUSG00000028010	chr3	Gar1	1.3E+08	1.3E+08	1714	0.889889	3.058901	7.24E-06	4.49E-05	0.03913	1	81	99	103	84	112	184	207	229	361	280
ENSMUSG00000022322	chr8	Shcbp1	4735980	4736407	2132	1.535771	0.682274	7.28E-06	4.52E-05	0.093214	1	10	7	17	7	23	43	44	38	90	44
ENSMUSG00000021451	chr13	Sema4d	51701246	51703531	6449	-0.70789	5.973859	7.29E-06	4.52E-05	0.02876	-1	1081	1120	1477	1279	1589	853	1038	1234	1248	1201
ENSMUSG00000024900	chr19	Cpt1a	3323301	3323374	4300	0.906043	4.238691	7.31E-06	4.53E-05	0.04535	1	172	141	308	179	318	304	595	585	876	579
ENSMUSG00000064179	chr7	Tnnt1	4504570	4504800	2204	2.324593	6.327645	7.35E-06	4.55E-05	0.288271	1	73	646	72	919	480	2436	3930	3395	3905	1994
ENSMUSG00000030319	chr6	Cand2	1.16E+08	1.16E+08	4810	-0.81885	6.658784	7.39E-06	4.58E-05	0.038973	-1	1721	1660	2543	2367	2589	1500	2010	1173	2323	1561
ENSMUSG00000025138	chr11	Sirt7	1.21E+08	1.21E+08	5148	0.925361	3.244389	7.42E-06	4.59E-05	0.044106	1	101	80	136	85	142	185	253	237	418	366

ENSMUSG00000048368	chr13	Omd	49582766	49582813	1556	-1.65988	0.919326	7.43E-06	4.6E-05	0.125214	-1	55	29	46	26	81	12	17	38	19	17
ENSMUSG00000092412	chr17	Gm20507	33630759	33631463	2860	1.325567	1.675173	7.48E-06	4.62E-05	0.081066	1	21	20	24	37	45	61	95	69	150	146
ENSMUSG00000046058	chr7	Eid2	28267881	28269272	1392	1.001586	2.472181	7.51E-06	4.65E-05	0.047648	1	64	49	51	60	76	159	161	172	192	152
ENSMUSG00000028678	chr4	Kif2c	1.17E+08	1.17E+08	4363	1.688778	1.289472	7.56E-06	4.67E-05	0.132699	1	20	11	11	17	32	57	78	33	158	96
ENSMUSG00000026027	chr1	Stradb	58973522	58973850	7256	-0.76447	6.769563	7.6E-06	4.69E-05	0.034086	-1	2009	2189	2580	2289	2342	1802	2003	1611	2170	1767
ENSMUSG00000020183	chr10	Cpm	1.18E+08	1.18E+08	5964	-1.18069	2.722057	7.62E-06	4.7E-05	0.073047	-1	165	72	167	154	212	52	114	122	118	69
ENSMUSG00000020859	chr11	Spag9	93996091	93996573	11209	-0.9358	7.58899	7.64E-06	4.71E-05	0.051231	-1	3814	3520	4820	4522	4426	2111	2789	4972	2972	2552
ENSMUSG00000020812	chr11	1810032O08Rik	1.17E+08	1.17E+08	2776	1.640674	1.368353	7.71E-06	4.76E-05	0.125813	1	19	11	28	15	27	39	89	164	70	70
ENSMUSG00000031066	chrX	Usp11	20703906	20704119	4732	1.205502	2.204821	7.74E-06	4.78E-05	0.07187	1	35	29	47	47	72	102	219	94	190	132
ENSMUSG00000037098	chr17	Rab11fip3	25989036	25990885	6789	-0.84949	6.163807	7.79E-06	4.8E-05	0.041928	-1	1123	1279	1496	1940	1918	929	1178	1591	1219	1026
ENSMUSG00000043635	chr5	Adamts3	89673841	89677926	7663	-1.3522	2.368872	7.8E-06	4.81E-05	0.094756	-1	138	65	119	79	227	43	91	82	74	48
ENSMUSG00000027649	chr2	Ctnnbl1	1.58E+08	1.58E+08	2705	0.77837	3.479279	7.89E-06	4.86E-05	0.030697	1	103	129	139	156	151	256	293	340	402	341
ENSMUSG00000041189	chr11	Chrnb1	69784036	69784761	2531	0.728557	6.24069	7.91E-06	4.87E-05	0.030852	1	804	774	1159	882	1171	1939	2378	2123	2343	2128
ENSMUSG00000035021	chr12	Baz1a	54892989	54894501	7159	1.051332	2.622438	8E-06	4.92E-05	0.055465	1	59	45	57	68	102	98	199	191	268	216
ENSMUSG00000040481	chr11	Bptf	1.07E+08	1.07E+08	13907	-0.83135	5.069976	8.06E-06	4.95E-05	0.039486	-1	604	471	730	831	1006	385	547	749	639	512
ENSMUSG00000025358	chr10	Cdk2	1.29E+08	1.29E+08	2432	0.86569	3.241927	8.08E-06	4.97E-05	0.038217	1	108	94	112	95	144	210	292	211	409	305
ENSMUSG00000029581	chr5	Fscn1	1.43E+08	1.43E+08	3012	1.033502	5.248378	8.12E-06	4.99E-05	0.061451	1	304	357	424	477	532	872	1331	556	2062	1283
ENSMUSG00000068922	chr3	Msto1	88905107	88905520	5418	0.813961	3.64793	8.12E-06	4.99E-05	0.034625	1	115	154	153	174	151	277	450	312	453	366
ENSMUSG00000031833	chr8	Mast3	70778117	70779937	5334	1.179895	2.938764	8.14E-06	5E-05	0.073782	1	64	37	105	76	113	144	338	150	329	284
ENSMUSG00000048895	chr11	Cdk5r1	80477023	80481184	4162	1.707316	1.798714	8.16E-06	5.01E-05	0.145302	1	19	25	32	14	42	80	241	56	151	74
ENSMUSG00000022200	chr15	Golph3	12321496	12321956	2606	-0.72382	5.910151	8.17E-06	5.01E-05	0.030402	-1	1077	1133	1402	1219	1425	803	1064	1232	1309	908
ENSMUSG00000036144	chr12	Meox2	37108540	37109344	2360	-0.71418	4.10473	8.2E-06	5.03E-05	0.027542	-1	326	273	428	338	427	203	316	299	409	311
ENSMUSG00000028710	chr4	Atpaf1	1.16E+08	1.16E+08	3609	-0.91357	5.202324	8.22E-06	5.04E-05	0.048022	-1	617	859	1003	856	638	613	639	513	714	463
ENSMUSG00000040813	chr9	Tex264	1.07E+08	1.07E+08	2874	0.796821	4.70031	8.23E-06	5.04E-05	0.035637	1	295	269	356	305	353	508	708	1065	821	747
ENSMUSG00000030522	chr7	Mtmr10	64287653	64287841	7474	-0.79844	4.343599	8.25E-06	5.05E-05	0.035488	-1	290	491	460	395	511	266	317	303	484	375
ENSMUSG00000046341	chr4	Gm11223	69925630	69926079	450	1.794828	-0.17244	8.25E-06	5.05E-05	0.095218	1	8	2	7	3	8	18	29	23	49	21
ENSMUSG00000079657	chr17	Rab26	24527241	24527961	2852	-1.51592	-0.03457	8.25E-06	5.05E-05	0.069503	-1	19	20	20	19	36	7	12	11	11	14
ENSMUSG00000056116	chr17	H2-T22	36037128	36039223	3414	0.960555	4.601032	8.34E-06	5.1E-05	0.052319	1	246	244	278	270	330	594	583	466	903	1197
ENSMUSG00000027692	chr3	Tnik	28263214	28263699	19282	-0.74969	5.636222	8.35E-06	5.1E-05	0.032487	-1	949	765	1052	1047	1443	786	952	842	962	751
ENSMUSG00000005871	chr18	Apc	34220924	34221276	15753	-0.71216	5.169221	8.36E-06	5.11E-05	0.028898	-1	575	562	843	881	907	461	696	649	754	639
ENSMUSG00000030022	chr6	Adamts9	92772699	92774576	12527	-0.87782	3.917159	8.47E-06	5.17E-05	0.042603	-1	232	238	374	345	474	157	310	176	378	247
ENSMUSG00000024242	chr17	Map4k3	80580512	80581935	4231	-0.8403	4.189705	8.48E-06	5.18E-05	0.039449	-1	360	366	379	398	436	168	308	415	393	265
ENSMUSG00000035173	chr19	Ccdc186	56787481	56791046	6899	-0.90097	4.75356	8.5E-06	5.19E-05	0.046369	-1	534	449	746	546	675	307	386	690	423	380
ENSMUSG00000050410	chr17	Tcf19	35512734	35513184	1782	1.280126	2.020525	8.51E-06	5.19E-05	0.080804	1	32	32	47	32	49	100	140	58	203	158
ENSMUSG00000036459	chr7	Wtip	34109543	34110239	2233	0.965895	2.543798	8.54E-06	5.21E-05	0.045643	1	50	44	75	63	96	126	212	147	224	180
ENSMUSG00000042515	chrX	Mum1l1	1.39E+08	1.39E+08	4859	-1.08883	2.526069	8.56E-06	5.21E-05	0.060492	-1	89	96	169	118	192	63	129	65	93	77
ENSMUSG00000020792	chr11	Exoc7	1.16E+08	1.16E+08	4367	-0.92394	6.74146	8.59E-06	5.23E-05	0.050281	-1	1571	2070	3412	2097	2736	1813	1818	1111	1943	1811
ENSMUSG00000013155	chr8	Enkd1	1.06E+08	1.06E+08	1272	1.441998	0.566378	8.65E-06	5.27E-05	0.072205	1	14	11	11	8	16	30	47	33	63	60
ENSMUSG00000025759	chr3	Mfsd8	40818070	40819720	3184	-0.72494	3.888227	8.74E-06	5.32E-05	0.027997	-1	288	249	371	288	342	210	274	285	273	251
ENSMUSG00000063316	chr11	Rpl27	1.01E+08	1.01E+08	1535	0.7968	7.08847	8.81E-06	5.36E-05	0.037651	1	1351	1589	2190	1282	1933	3726	4083	3805	4069	4226
ENSMUSG00000056153	chr18	Socs6	88665224	88665382	8225	-0.71362	4.825528	8.82E-06	5.36E-05	0.028822	-1	498	507	638	623	677	360	509	590	630	433
ENSMUSG00000027330	chr2	Cdc25b	1.31E+08	1.31E+08	3728	1.066845	2.9384	8.82E-06	5.36E-05	0.059763	1	68	68	71	59	147	136	224	232	319	303
ENSMUSG00000014074	chr16	Rnf168	32277459	32278415	4462	-0.75267	4.087395	8.85E-06	5.37E-05	0.030995	-1	289	298	504	323	376	216	345	288	347	285
ENSMUSG00000030342	chr6	Cd9	1.25E+08	1.25E+08	2044	1.010305	5.661327	8.97E-06	5.44E-05	0.059654	1	558	383	627	484	776	774	1363	1192	2931	1977
ENSMUSG00000051980	chr16	Casr	36493696	36495974	4718	-1.33927	0.929003	9E-06	5.46E-05	0.075105	-1	29	53	64	36	39	20	23	25	28	26
ENSMUSG00000039943	chr2	Plcb4	1.36E+08	1.36E+08	8970	-0.7922	4.353205	9.06E-06	5.5E-05	0.035315	-1	394	356	505	498	397	222	389	404	458	294
ENSMUSG00000029352	chr5	Crybb3	1.13E+08	1.13E+08	2333	1.908664	-0.57508	9.09E-06	5.51E-05	0.08967	1	2	2	5	5	5	20	15	13	30	23
ENSMUSG00000044201	chr18	Cdc25c	34732997	34733393	1941	1.75125	-0.30622	9.1E-06	5.52E-05	0.083929	1	3	3	6	5	9	14	28	17	39	27
ENSMUSG00000022235	chr15	Cmbl	31568791	31568939	1228	-0.85125	5.67001	9.15E-06	5.54E-05	0.042443	-1	1012	970	1206	1047	1221	801	600	854	792	1123
ENSMUSG00000040721	chr14	Zfhx2	55060262	55063571	18166	-1.12727	2.585401	9.2E-06	5.57E-05	0.066737	-1	134	80	143	160	171	54	96	51	129	116
ENSMUSG00000049871	chr16	Nlrc3	3945007	3947539	7068	1.765889	1.692606	9.21E-06	5.58E-05	0.155384	1	12	18	10	51	25	51	108	78	169	167
ENSMUSG00000057722	chr4	Lepr	1.02E+08	1.02E+08	7049	-1.66669	1.971108	9.24E-06	5.59E-05	0.145042	-1	134	36	104	70	156	25	36	79	54	25
ENSMUSG00000022401	chr15	Xpnpep3	81400138	81400287	6117	-0.92552	2.982826	9.29E-06	5.62E-05	0.044655	-1	142	150	184	194	190	70	125	161	132	150
ENSMUSG00000078584	chr4	AU022252	1.19E+08	1.19E+08	9570	-0.68968	4.74829	9.32E-06	5.63E-05	0.026805	-1	480	487	659	498	652	412	470	500	563	445
ENSMUSG00000073491	chr1	Pydc4	1.74E+08	1.74E+08	6839	2.7316	0.540481	9.33E-06	5.64E-05	0.332087	1	3	5	6	5	10	70	44	7	18	115
ENSMUSG00000092201	chr2	A530058N18Rik	1.14E+08	1.14E+08	1989	-2.59104	4.438053	9.34E-06	5.64E-05	0.354992	-1	202	748	902	559	750	221	99	4	146	218
ENSMUSG00000030850	chr7	Ate1	1.3E+08	1.3E+08	4875	-0.69072	5.313769	9.4E-06	5.68E-05	0.027576	-1	696	670	1054	757	953	536	761	737	822	703
ENSMUSG00000041841	chr15	Rpl37	5116613	5116684	867	0.738535	6.799078	9.42E-06	5.68E-05	0.032472	1	1166	1350	1680	1244	1522	2929	3324	3034	3474	3342
ENSMUSG00000023021	chr15	Cers5	99734881	99736436	3542	0.793994	3.821686	9.56E-06	5.77E-05	0.034285	1	160	116	190	148	255	289	407	373	545	488
ENSMUSG00000022044	chr14	Stmn4	66344296	66344411	1916	-1.53159	1.027826	9.64E-06	5.81E-05	0.107392	-1	51	32	65	34	68	23	35	8	32	21
ENSMUSG00000098569	chr4	Mir7020	1.4E+08	1.4E+08	70	-1.77431	-0.18797	9.65E-06	5.81E-05	0.109297	-1	18	22	9	30	26	7	11	9	11	5
ENSMUSG00000078700	chr11	D030028A08Rik	96916270	96916579	6269	-1.64688	-0.27919	9.73E-06	5.86E-05	0.084405	-1	13	17	29	19	19	8	7	4	16	8
ENSMUSG00000004891	chr3	Nes	87971078	87971988	6416	1.001829	6.853856	9.74E-06	5.86E-05	0.059779	1	989	955	1508	1378	1701	2444	5851	2096	4678	3198
ENSMUSG00000037622	chr4	Wdtc1	1.33E+08	1.33E+08	4800	-0.75292	6.670101	9.75E-06	5.87E-05	0.033856	-1	1834	1808	2360	2318	2366	1381	1485	2224	2035	1728
ENSMUSG00000031555	chr8	Adam9	24949611	24951010	4011	-0.72662	6.151142	9.77E-06	5.88E-05	0.031328	-1	1344	1144	1815	1371	1778	861	1295	1439	1548	1162
ENSMUSG00000054843	chr19	Atrnl1	57611034	57611643	6581	-0.87323	3.895378	9.77E-06	5.88E-05	0.042679	-1	296	192	353	309	483	144	321	237	312	229

ENSMUSG00000024981	chr19	Acsl5	55253369	55254166	3150	1.125452	4.270834	9.83E-06	5.9E-05	0.072791	1	157	164	207	201	290	418	508	280	990	955
ENSMUSG00000090935	chr12	Synj2bp	81497941	81502166	5866	-0.70398	5.652195	9.83E-06	5.9E-05	0.02908	-1	928	959	1234	1037	1018	744	947	847	984	926
ENSMUSG00000041827	chr5	Oasl1	1.15E+08	1.15E+08	2608	2.619767	1.757608	9.86E-06	5.92E-05	0.344241	1	4	13	18	24	18	225	48	18	86	230
ENSMUSG00000090553	chr1	Snrpe	1.34E+08	1.34E+08	1372	0.795566	4.531568	9.86E-06	5.92E-05	0.035862	1	241	310	328	234	279	606	707	546	777	756
ENSMUSG00000025437	chr3	Usp33	1.52E+08	1.52E+08	5950	-0.75661	4.654188	9.9E-06	5.94E-05	0.032794	-1	463	453	643	496	590	246	517	505	502	441
ENSMUSG00000027509	chr2	Rae1	1.73E+08	1.73E+08	2554	0.698312	4.360555	9.92E-06	5.95E-05	0.026991	1	203	249	290	243	321	455	590	643	656	607
ENSMUSG00000070520	chr7	Ndnl2	64867052	64872997	5946	0.843361	3.412345	9.93E-06	5.95E-05	0.037823	1	84	104	192	119	139	236	322	350	383	294
ENSMUSG00000035397	chr10	Klf16	80567124	80569222	2674	1.043938	2.384144	9.94E-06	5.96E-05	0.054381	1	43	45	66	48	79	132	160	103	239	175
ENSMUSG00000103520	chr15	RP23-310L8.1	81584174	81585028	855	1.943421	-0.59762	9.95E-06	5.96E-05	0.093555	1	5	1	2	6	4	11	16	25	24	24
ENSMUSG00000025498	chr7	Irf7	1.41E+08	1.41E+08	3020	2.037934	3.860838	9.95E-06	5.96E-05	0.229475	1	43	68	97	104	177	751	348	99	331	1037
ENSMUSG00000044813	chr4	Shb	45423278	45424123	3199	1.188553	2.796884	9.97E-06	5.97E-05	0.076526	1	46	35	71	76	131	144	316	175	293	194
ENSMUSG00000033940	chr6	Brk1	1.14E+08	1.14E+08	1092	0.741833	5.78319	1E-05	5.99E-05	0.032436	1	579	670	871	637	667	1359	1614	1383	1899	1769
ENSMUSG00000036949	chr2	Slc39a12	14388316	14388498	2998	-1.59698	0.228737	1E-05	5.99E-05	0.099722	-1	27	16	31	24	44	8	20	4	18	15
ENSMUSG00000038884	chr9	A230050P20Rik	20868642	20868936	3417	1.21489	1.741668	1.01E-05	6.01E-05	0.070078	1	29	18	38	35	43	64	92	78	157	144
ENSMUSG00000038949	chr1	Cnst	1.8E+08	1.8E+08	8859	-0.71994	5.537635	1.01E-05	6.01E-05	0.030429	-1	712	883	1187	967	1107	626	734	899	882	951
ENSMUSG00000038095	chr5	Sbno1	1.24E+08	1.24E+08	10197	-0.71603	5.414922	1.01E-05	6.03E-05	0.030045	-1	718	872	1075	819	937	521	790	857	896	729
ENSMUSG00000060012	chr14	Kif13b	64652531	64652656	5603	-1.22499	2.741711	1.01E-05	6.05E-05	0.081624	-1	162	85	147	158	236	34	103	131	115	93
ENSMUSG00000007480	chr18	Mc5r	68337603	68337725	1162	-1.6785	0.642581	1.01E-05	6.05E-05	0.128775	-1	37	23	45	34	56	3	9	30	25	19
ENSMUSG00000009394	chr6	Syn2	1.15E+08	1.15E+08	5646	1.162159	2.394153	1.02E-05	6.06E-05	0.068756	1	45	51	66	64	35	180	157	120	199	159
ENSMUSG00000022361	chr15	Zhx1	58047003	58048785	6031	-0.67957	4.961954	1.02E-05	6.09E-05	0.026548	-1	528	544	754	653	737	398	552	626	647	584
ENSMUSG00000059708	chrX	Akap17b	36608314	36612664	6003	-0.98016	2.304921	1.02E-05	6.09E-05	0.046798	-1	83	98	125	112	126	69	92	54	93	75
ENSMUSG00000068740	chr3	Celsr2	1.08E+08	1.08E+08	11513	-0.8706	3.106906	1.02E-05	6.09E-05	0.039631	-1	164	132	198	233	200	113	158	118	187	135
ENSMUSG00000024887	chr19	Asah2	31984654	31986947	4682	-0.86673	3.230083	1.03E-05	6.11E-05	0.040304	-1	198	169	228	194	215	95	187	130	237	140
ENSMUSG00000042961	chr15	Egflam	7206120	7207802	6121	-0.96042	4.696297	1.03E-05	6.11E-05	0.053679	-1	412	652	734	460	591	415	527	264	425	390
ENSMUSG00000031983	chr8	2310022B05Rik	1.25E+08	1.25E+08	3297	0.930361	4.995757	1.03E-05	6.15E-05	0.05081	1	323	191	433	328	605	632	1191	1091	1231	783
ENSMUSG00000066687	chr9	Zbtb16	48654311	48657371	5100	-1.33092	5.286234	1.04E-05	6.17E-05	0.103942	-1	881	974	1200	871	657	296	318	1064	424	482
ENSMUSG00000022673	chr16	Mcm4	15623897	15624769	3589	0.895466	3.380742	1.04E-05	6.18E-05	0.043212	1	112	87	127	103	179	221	325	238	507	306
ENSMUSG00000029330	chr5	Cds1	1.02E+08	1.02E+08	3939	1.680021	0.749285	1.04E-05	6.2E-05	0.124016	1	10	7	21	8	16	45	44	23	79	86
ENSMUSG00000022177	chr14	Haus4	54541785	54542257	1587	0.971993	2.623048	1.05E-05	6.25E-05	0.047525	1	65	56	79	70	69	158	129	197	229	219
ENSMUSG00000031112	chrX	Stk26	50841047	50841546	5271	-1.36046	1.566668	1.06E-05	6.31E-05	0.091405	-1	71	41	61	69	113	21	41	62	37	30
ENSMUSG00000025937	chr1	Lactb2	13623330	13626904	4566	-0.72282	4.430706	1.06E-05	6.31E-05	0.029645	-1	388	402	500	500	438	281	339	426	500	365
ENSMUSG00000019461	chr11	Plscr3	69846376	69846522	3148	0.745321	4.244904	1.07E-05	6.33E-05	0.031151	1	169	195	270	252	304	417	612	418	747	592
ENSMUSG00000097145	chr5	9230114K14Rik	52190681	52190937	2118	-1.52505	0.535575	1.07E-05	6.33E-05	0.099239	-1	29	16	60	35	36	10	20	17	28	10
ENSMUSG00000040548	chr11	Tex2	1.07E+08	1.07E+08	5576	-0.80079	5.904125	1.07E-05	6.33E-05	0.03831	-1	972	1152	1467	1421	1352	686	928	1400	1113	990
ENSMUSG00000028249	chr4	Sdcbp	6365650	6365759	6904	0.896446	6.328677	1.07E-05	6.34E-05	0.048185	1	760	933	996	909	1080	1486	2153	1696	3752	3445
ENSMUSG00000094410	chr1	Zbed6	1.34E+08	1.34E+08	10156	-0.73141	7.331809	1.07E-05	6.35E-05	0.032428	-1	2922	2581	3896	3073	4528	2239	3173	3052	3000	2634
ENSMUSG00000060538	chr7	Tmem219	1.27E+08	1.27E+08	2292	0.79067	3.452632	1.07E-05	6.35E-05	0.033003	1	119	102	159	135	150	292	309	258	374	361
ENSMUSG00000021978	chr14	Extl3	65052060	65054822	5977	-0.7073	6.07585	1.08E-05	6.38E-05	0.029918	-1	1176	1125	1641	1469	1616	895	1213	1011	1511	1399
ENSMUSG00000071415	chr11	Rpl23	97777527	97778164	1770	0.722382	8.135932	1.08E-05	6.4E-05	0.031795	1	3013	3348	4290	3156	3933	7055	8415	7492	8687	8984
ENSMUSG00000040263	chr8	Klhdc4	1.22E+08	1.22E+08	3708	0.833373	3.514816	1.09E-05	6.45E-05	0.037308	1	101	126	136	151	167	252	302	268	439	446
ENSMUSG00000039476	chr2	Prrx2	30834972	30835252	1961	1.401091	1.822801	1.09E-05	6.46E-05	0.100065	1	32	15	25	25	62	93	162	72	148	103
ENSMUSG00000026980	chr2	Ly75	60292103	60293938	6905	1.766412	-0.39443	1.1E-05	6.47E-05	0.087917	1	2	2	4	8	8	16	20	18	35	27
ENSMUSG00000028417	chr4	Tal2	53779705	53779773	2971	1.932889	0.967194	1.1E-05	6.5E-05	0.177329	1	8	5	15	16	20	42	153	30	58	52
ENSMUSG00000027109	chr2	Sp3	72936427	72938382	4933	-0.8805	4.428871	1.1E-05	6.52E-05	0.0451	-1	366	363	532	465	634	169	361	498	457	320
ENSMUSG00000042208	chr11	0610010F05Rik	23564961	23565136	5226	-0.71183	4.226235	1.11E-05	6.54E-05	0.028443	-1	348	365	443	370	401	240	314	390	397	319
ENSMUSG00000030720	chr7	Cln3	1.27E+08	1.27E+08	5781	0.956728	3.016479	1.11E-05	6.57E-05	0.048301	1	74	91	97	86	103	160	227	176	361	328
ENSMUSG00000046229	chr2	Scand1	1.56E+08	1.56E+08	759	0.779177	3.882863	1.11E-05	6.57E-05	0.033574	1	135	161	229	185	194	432	365	397	512	430
ENSMUSG00000021009	chr12	Ptpn21	98676741	98678678	5738	-0.75168	5.007775	1.12E-05	6.62E-05	0.033086	-1	582	494	711	723	891	473	698	517	638	461
ENSMUSG00000024818	chr19	Slc25a45	5877808	5878095	2650	1.109526	2.119618	1.12E-05	6.62E-05	0.060006	1	48	33	56	40	45	79	146	105	172	181
ENSMUSG00000054400	chr8	Cklf	1.04E+08	1.04E+08	2098	1.6039	0.476158	1.13E-05	6.62E-05	0.097647	1	10	13	12	7	9	39	35	23	64	61
ENSMUSG00000024811	chr19	Tnks2	36834232	36834736	10406	-0.68728	7.392884	1.13E-05	6.67E-05	0.028813	-1	3122	2788	3850	3537	4083	2419	3006	3185	3541	2889
ENSMUSG00000028284	chr4	Map3k7	31964097	31964382	6423	-0.70148	6.044478	1.13E-05	6.67E-05	0.029543	-1	1137	1162	1621	1394	1538	903	1157	1361	1353	1098
ENSMUSG00000063663	chrX	Brwd3	1.09E+08	1.09E+08	12692	-1.05517	2.532538	1.14E-05	6.69E-05	0.058745	-1	133	102	132	121	159	39	99	114	118	75
ENSMUSG00000020671	chr12	Rab10	3247430	3249870	3511	-0.71388	8.052615	1.14E-05	6.7E-05	0.03122	-1	4620	5283	6587	5338	5660	3899	4778	5021	5554	4203
ENSMUSG00000031442	chr8	Mcf2l	12873806	12874061	12760	-0.97453	4.011909	1.15E-05	6.73E-05	0.05488	-1	275	316	504	440	238	167	240	344	285	238
ENSMUSG00000031993	chr9	Snx19	30427329	30429256	5541	-0.68403	5.475086	1.15E-05	6.74E-05	0.027711	-1	804	746	1050	906	1092	624	786	918	865	780
ENSMUSG00000025362	chr10	Rps26	1.29E+08	1.29E+08	447	0.759853	7.086917	1.16E-05	6.83E-05	0.035204	1	1349	1603	1664	1720	2104	3836	4107	3198	4551	4066
ENSMUSG00000005417	chr11	Mprip	59661305	59661418	13327	-0.69542	6.884759	1.17E-05	6.85E-05	0.029471	-1	1933	1981	2650	2628	3128	1479	2217	2023	2707	2225
ENSMUSG00000094786	chr2	Gm14403	1.77E+08	1.77E+08	1656	-1.56575	1.038029	1.18E-05	6.9E-05	0.116757	-1	28	31	79	32	90	14	37	17	32	19
ENSMUSG00000003573	chr8	Homer3	70282827	70283100	3440	1.007437	2.951817	1.19E-05	6.95E-05	0.054582	1	76	49	82	83	140	129	249	238	330	267
ENSMUSG00000011832	chr8	Evi5l	4166567	4166763	8524	-0.72134	4.229642	1.19E-05	6.95E-05	0.029462	-1	344	323	435	421	423	258	366	252	403	378
ENSMUSG00000024042	chr17	Sik1	31844248	31846643	4511	0.879665	4.010337	1.19E-05	6.95E-05	0.044352	1	125	128	181	258	265	381	613	485	486	444
ENSMUSG00000038387	chr7	Rras	45017978	45018168	1103	0.708909	4.693446	1.19E-05	6.95E-05	0.028957	1	235	334	341	331	395	570	680	792	924	784
ENSMUSG00000012519	chr8	Mlkl	1.11E+08	1.11E+08	2303	1.557404	1.450263	1.21E-05	7.08E-05	0.119722	1	24	18	13	22	32	90	74	37	117	132
ENSMUSG00000025511	chr7	Tspan4	1.41E+08	1.41E+08	2178	0.912758	4.130641	1.21E-05	7.09E-05	0.047856	1	208	202	213	165	207	295	415	498	871	657
ENSMUSG00000052276	chr16	Ostn	27307489	27307701	1423	-1.51367	0.836857	1.21E-05	7.09E-05	0.104094	-1	31	57	54	31	40	19	33	12	27	14

ENSMUSG00000039087	chr13	Rreb1	37778400	37778557	13991	-0.76243	4.884956	1.22E-05	7.13E-05	0.034317	-1	449	471	719	693	818	312	550	603	662	467
ENSMUSG00000025875	chr13	Tspan17	54789377	54789681	1657	0.70912	3.972281	1.22E-05	7.13E-05	0.027759	1	142	180	211	218	242	389	426	446	520	468
ENSMUSG00000001229	chr17	Dpp9	56186682	56187461	3509	-0.69073	5.331446	1.23E-05	7.16E-05	0.028363	-1	719	677	956	905	900	595	786	632	932	661
ENSMUSG00000038271	chr6	Iffo1	1.25E+08	1.25E+08	5691	0.809286	4.977965	1.23E-05	7.2E-05	0.038894	1	282	300	455	344	562	675	1311	821	1021	856
ENSMUSG00000029922	chr6	Mkrn1	39397804	39399434	4439	0.697707	4.500067	1.24E-05	7.21E-05	0.02786	1	241	229	328	277	373	442	587	691	839	732
ENSMUSG00000032279	chr9	Idh3a	54586511	54586543	2403	-0.75631	9.18956	1.24E-05	7.23E-05	0.035413	-1	10128	12238	13444	13603	11326	9378	9502	9769	12182	9577
ENSMUSG00000033278	chr17	Ptprm	66666848	66667681	5569	-0.93776	4.430158	1.26E-05	7.32E-05	0.052033	-1	348	355	524	694	448	189	363	435	497	279
ENSMUSG00000039519	chr3	Cyp7b1	18071950	18072753	2166	1.797026	0.03561	1.26E-05	7.34E-05	0.12601	1	2	2	12	5	13	17	23	28	57	41
ENSMUSG00000059436	chr12	Max	76937269	76938755	2005	0.702327	4.593723	1.26E-05	7.34E-05	0.028496	1	252	247	367	295	381	554	573	765	822	765
ENSMUSG00000053580	chr11	Tanc2	1.06E+08	1.06E+08	16494	-0.80957	3.927335	1.26E-05	7.34E-05	0.037171	-1	228	197	386	359	486	204	280	257	303	244
ENSMUSG00000028800	chr4	Hdac1	1.3E+08	1.3E+08	3445	0.795165	4.286574	1.27E-05	7.39E-05	0.036484	1	181	198	252	251	314	408	592	397	787	732
ENSMUSG00000101655	chr6	2310040G24Rik	86483376	86483699	775	-0.91362	6.1514	1.27E-05	7.39E-05	0.050859	-1	1370	1422	1933	1426	1590	1258	1398	719	1217	1048
ENSMUSG00000083563	chr2	Gm13340	22588103	22589647	1545	-1.10876	2.964813	1.28E-05	7.44E-05	0.068989	-1	125	191	212	235	111	71	115	124	172	104
ENSMUSG00000021699	chr13	Pde4d	1.08E+08	1.08E+08	12006	-1.49142	5.479199	1.28E-05	7.44E-05	0.13252	-1	974	866	1749	1097	814	224	438	1267	452	367
ENSMUSG00000013662	chr19	Atad1	32672563	32674364	2813	-0.75626	5.952831	1.28E-05	7.45E-05	0.034805	-1	1106	1278	1534	1268	1274	772	1071	1330	1294	938
ENSMUSG00000051786	chr15	Tubgcp6	89098357	89100503	7965	-0.66885	3.953569	1.28E-05	7.46E-05	0.024634	-1	279	266	357	318	367	208	286	292	342	271
ENSMUSG00000024236	chr18	Svil	4920540	4920874	10640	-0.85237	7.916261	1.29E-05	7.48E-05	0.044899	-1	4612	3501	5739	5562	6894	2745	3831	5862	4252	3452
ENSMUSG00000027953	chr3	Slc50a1	89268246	89268598	1466	0.804256	3.566437	1.29E-05	7.48E-05	0.035365	1	146	114	147	110	199	266	353	300	420	410
ENSMUSG00000039197	chr14	Adk	21052574	21052700	1781	-0.7727	5.581071	1.29E-05	7.48E-05	0.036115	-1	861	1049	984	1128	953	745	784	700	1138	765
ENSMUSG00000040146	chr9	Rgl3	21971527	21972009	2550	1.912115	0.430327	1.29E-05	7.48E-05	0.152139	1	9	7	2	16	7	22	42	30	51	81
ENSMUSG00000052429	chr7	Prmt1	44975989	44976983	2521	0.704156	6.488967	1.29E-05	7.48E-05	0.030351	1	894	1008	1462	1009	1381	2210	2638	2517	3029	2557
ENSMUSG00000066324	chr4	Impad1	4762484	4767972	6543	-0.77699	6.342802	1.3E-05	7.5E-05	0.036978	-1	1531	1408	1829	1761	2055	988	1223	1927	1570	1294
ENSMUSG00000037661	chr3	Gpr160	30855950	30856057	4227	1.29766	1.040321	1.3E-05	7.53E-05	0.071282	1	15	13	24	13	29	39	52	61	86	86
ENSMUSG00000054027	chr10	Nt5dc3	86779005	86779311	5952	-0.88002	6.73568	1.31E-05	7.55E-05	0.047606	-1	1992	2157	3234	2045	2081	1378	1406	2424	1728	1765
ENSMUSG00000074824	chr13	Rslcan18	67096613	67099047	8039	-1.54478	0.01824	1.31E-05	7.55E-05	0.085545	-1	20	27	31	18	22	4	13	17	12	11
ENSMUSG00000021222	chr12	Dcaf4	83520466	83520617	2081	-0.71261	4.725595	1.31E-05	7.59E-05	0.029796	-1	465	528	619	578	533	386	472	401	549	529
ENSMUSG00000040761	chr4	Spen	1.41E+08	1.41E+08	14089	-0.93394	4.664425	1.32E-05	7.64E-05	0.052174	-1	488	391	528	668	723	211	412	626	464	346
ENSMUSG00000076236	chr13	Mir682	75645046	75645141	96	0.787611	3.446666	1.32E-05	7.65E-05	0.033241	1	104	146	149	117	141	258	328	322	347	334
ENSMUSG00000068205	chr2	Macrod2	1.4E+08	1.4E+08	10308	-0.90604	3.41597	1.33E-05	7.67E-05	0.04564	-1	204	253	244	225	215	181	152	166	160	186
ENSMUSG00000090659	chr13	Zfp493	67779754	67779819	4693	-1.47783	1.117852	1.33E-05	7.67E-05	0.104364	-1	52	44	63	49	52	34	32	8	29	25
ENSMUSG00000031858	chr8	Mau2	70016123	70019660	5390	-0.94771	4.79081	1.33E-05	7.69E-05	0.053965	-1	592	469	723	598	662	232	400	725	516	361
ENSMUSG00000003037	chr8	Rab8a	72161200	72161482	4678	0.725593	4.393217	1.33E-05	7.69E-05	0.030309	1	254	191	296	272	307	446	638	494	768	722
ENSMUSG00000005481	chr8	Ddx39	83715177	83715337	5155	0.948558	4.272215	1.34E-05	7.72E-05	0.052875	1	188	224	234	197	246	509	593	292	861	725
ENSMUSG00000000804	chr11	Usp32	84984442	84986583	7680	-0.75391	3.892267	1.35E-05	7.76E-05	0.032226	-1	277	248	371	289	377	150	248	318	317	271
ENSMUSG00000020460	chr11	Rps27a	29545846	29546029	1972	0.73213	7.789468	1.35E-05	7.76E-05	0.033325	1	2325	2637	3392	2191	3406	5585	6435	6023	7151	6882
ENSMUSG00000043631	chr13	Ecm2	49504810	49505005	3596	-0.88619	4.8215	1.35E-05	7.76E-05	0.047107	-1	657	369	788	534	740	335	593	511	563	326
ENSMUSG00000022195	chr15	6030458C11Rik	12808177	12810844	3974	-0.70677	5.081592	1.35E-05	7.78E-05	0.029772	-1	687	596	824	609	782	542	582	545	737	584
ENSMUSG00000025812	chr8	Pard3	1.27E+08	1.27E+08	14506	-0.68288	4.808303	1.36E-05	7.79E-05	0.027374	-1	473	478	695	545	713	425	511	527	572	463
ENSMUSG00000035278	chr10	Plekhj1	80796100	80796522	1259	0.739272	3.962994	1.35E-05	7.79E-05	0.030654	1	195	157	245	163	208	375	492	386	525	480
ENSMUSG00000025762	chr3	Larp1b	40950631	40950684	7216	-0.72032	5.914884	1.36E-05	7.83E-05	0.031667	-1	981	1226	1485	1187	1396	968	1003	1013	1167	1123
ENSMUSG00000027365	chr2	Trpm7	1.27E+08	1.27E+08	11315	-0.9285	5.020585	1.36E-05	7.83E-05	0.052128	-1	627	640	796	695	789	297	466	875	524	460
ENSMUSG00000039789	chr16	Zfp597	3858321	3858581	6660	-0.82025	2.871619	1.36E-05	7.83E-05	0.034734	-1	150	118	174	149	186	94	119	129	148	125
ENSMUSG00000052085	chr19	Dock8	24999529	24999703	7810	1.041117	3.053485	1.36E-05	7.83E-05	0.0604	1	69	55	98	82	154	203	243	170	323	353
ENSMUSG00000087038	chr9	2900079G21Rik	1.12E+08	1.12E+08	6718	1.397737	0.672127	1.39E-05	7.95E-05	0.076981	1	15	8	7	15	22	36	45	56	66	46
ENSMUSG00000028796	chr4	Phc2	1.29E+08	1.29E+08	7064	0.675607	5.097529	1.39E-05	7.95E-05	0.027128	1	338	395	466	439	573	682	1004	1010	1245	1011
ENSMUSG00000026082	chr1	Rev1	38052786	38053198	6168	-0.8658	4.397083	1.39E-05	7.96E-05	0.044403	-1	400	401	499	399	578	238	317	540	327	312
ENSMUSG00000085014	chr2	Gm13490	51656966	51658001	2409	-1.66453	-0.16913	1.39E-05	7.97E-05	0.102432	-1	26	16	24	25	13	3	14	9	13	8
ENSMUSG00000007279	chr7	Scube2	1.1E+08	1.1E+08	4153	-1.33928	2.340067	1.39E-05	7.98E-05	0.098847	-1	132	59	153	91	177	39	117	62	75	42
ENSMUSG00000024127	chr17	Prepl	85063477	85064733	3830	-0.83914	5.142568	1.4E-05	8.01E-05	0.042603	-1	552	601	741	708	1261	464	763	616	632	472
ENSMUSG00000022587	chr15	Ly6e	74955051	74955335	3784	1.149903	7.096239	1.41E-05	8.05E-05	0.081344	1	902	1263	1403	1741	1866	4407	3845	1847	5197	6543
ENSMUSG00000046982	chr18	Tshz1	84011627	84016241	5656	-1.00834	3.693899	1.41E-05	8.07E-05	0.059293	-1	284	179	269	305	418	106	175	303	276	160
ENSMUSG00000047123	chr17	Ticam1	56269319	56272217	2992	0.932196	2.863688	1.41E-05	8.09E-05	0.046488	1	63	62	71	92	128	187	187	196	303	228
ENSMUSG00000034738	chr2	Nostrin	69135800	69135916	1888	1.388955	0.7669	1.42E-05	8.1E-05	0.079237	1	8	19	17	11	17	33	58	39	66	72
ENSMUSG00000034317	chr3	Trim59	69035288	69038008	3352	1.310227	1.416459	1.43E-05	8.15E-05	0.081123	1	20	22	20	21	39	58	107	50	136	79
ENSMUSG00000041852	chr15	Tcf20	82808629	82809787	7347	-0.75751	3.87004	1.43E-05	8.15E-05	0.032608	-1	270	225	312	286	457	170	276	249	284	294
ENSMUSG00000053062	chr16	Jam2	84774123	84774553	5872	-0.79835	5.028062	1.43E-05	8.15E-05	0.038539	-1	568	590	742	887	657	361	644	661	683	458
ENSMUSG00000034560	chr10	A230046K03Rik	83543941	83544102	5854	-0.75027	4.16207	1.43E-05	8.16E-05	0.032653	-1	371	277	403	336	495	195	371	331	382	294
ENSMUSG00000018861	chr11	Fdxr	1.15E+08	1.15E+08	2806	0.995938	2.504296	1.43E-05	8.17E-05	0.051392	1	38	51	69	87	66	126	159	177	196	207
ENSMUSG00000042558	chr4	Adprhl2	1.26E+08	1.26E+08	2475	0.763914	3.680049	1.43E-05	8.17E-05	0.032272	1	151	138	174	145	176	246	319	430	449	439
ENSMUSG00000045322	chr9	Tlr9	1.06E+08	1.06E+08	3478	1.888848	0.598407	1.43E-05	8.18E-05	0.165891	1	4	3	6	9	29	46	59	27	54	65
ENSMUSG00000017652	chr2	Cd40	1.65E+08	1.65E+08	3406	1.503478	0.667111	1.44E-05	8.19E-05	0.095354	1	6	9	15	17	17	50	45	26	63	66
ENSMUSG00000064147	chr17	Rab44	29135056	29136362	4109	1.492183	0.414621	1.44E-05	8.19E-05	0.082929	1	6	14	7	12	13	32	56	29	54	37
ENSMUSG00000051735	chr7	Rinl	28788969	28789005	2871	1.494923	1.601622	1.45E-05	8.24E-05	0.112791	1	32	19	21	28	24	65	82	47	151	164
ENSMUSG00000027858	chr3	Tspan2	1.03E+08	1.03E+08	4585	-0.82463	3.275497	1.46E-05	8.33E-05	0.037556	-1	176	181	215	247	205	109	174	156	245	142
ENSMUSG00000030890	chr7	Ilk	1.06E+08	1.06E+08	2744	0.705944	6.287144	1.48E-05	8.4E-05	0.030827	1	835	860	1106	981	1190	1774	2790	1991	2672	2093
ENSMUSG00000032463	chr9	Faim	98986373	98986512	5745	1.154892	1.682582	1.48E-05	8.43E-05	0.063123	1	32	26	35	27	39	66	85	73	150	131

ENSMUSG00000036550	chr8	Cnot1	95719451	95720485	8390	-0.72471	5.982677	1.49E-05	8.47E-05	0.03242	-1	1117	1006	1454	1396	1664	826	1028	1387	1272	1062
ENSMUSG00000037400	chr3	Atp11b	35754138	35754410	4859	-0.67043	4.761256	1.51E-05	8.58E-05	0.026663	-1	495	465	604	581	635	349	569	471	582	484
ENSMUSG00000079470	chr1	Utp14b	78658038	78658103	7679	-1.14782	1.732564	1.51E-05	8.58E-05	0.066073	-1	60	56	78	68	121	37	49	49	75	30
ENSMUSG00000033671	chr1	Cep350	1.56E+08	1.56E+08	16487	-0.87049	5.413226	1.51E-05	8.58E-05	0.046563	-1	884	629	1082	980	1048	483	638	1081	696	612
ENSMUSG00000024228	chr17	Nudt12	58999618	59002291	4401	-1.01835	2.391071	1.51E-05	8.59E-05	0.055082	-1	102	99	121	127	132	40	66	103	96	102
ENSMUSG00000031278	chrX	Acsl4	1.42E+08	1.42E+08	5405	-0.67692	5.213302	1.53E-05	8.66E-05	0.027739	-1	644	624	842	728	1004	477	752	686	816	623
ENSMUSG00000061175	chr3	Fnip2	79455974	79459741	8364	1.115409	3.274107	1.53E-05	8.67E-05	0.071495	1	91	74	99	108	134	150	222	224	492	490
ENSMUSG00000033530	chr12	Ttc7b	1E+08	1E+08	3441	-0.71488	5.951987	1.53E-05	8.7E-05	0.031604	-1	1067	1057	1395	1518	1396	956	1016	972	1301	1211
ENSMUSG00000072949	chr12	Acot1	84009502	84009966	1559	3.114875	0.895646	1.54E-05	8.7E-05	0.468248	1	3	4	5	4	14	13	22	255	24	39
ENSMUSG00000020057	chr10	Dram1	88322804	88324785	3045	1.486479	3.042468	1.54E-05	8.71E-05	0.127841	1	72	33	56	74	127	129	176	169	481	495
ENSMUSG00000060224	chr19	Pyroxd2	42725858	42726989	3119	1.468584	1.011251	1.54E-05	8.71E-05	0.100996	1	16	7	22	11	29	53	88	39	64	77
ENSMUSG00000059555	chr2	Tor4a	25192966	25195925	3301	1.003441	2.463359	1.55E-05	8.76E-05	0.052049	1	61	47	60	63	67	96	174	136	258	196
ENSMUSG00000038843	chr19	Gcnt1	17326141	17330488	5571	1.554934	1.166141	1.55E-05	8.77E-05	0.117978	1	17	4	12	22	36	48	73	61	119	73
ENSMUSG00000038349	chr1	Plcl1	55405921	55406630	6687	-1.01123	2.708199	1.55E-05	8.77E-05	0.056136	-1	123	128	135	175	161	59	137	122	116	73
ENSMUSG00000000957	chr14	Mmp14	54431604	54431973	2597	1.112149	6.181773	1.56E-05	8.8E-05	0.076707	1	640	399	740	582	1628	1521	3270	2146	2823	1945
ENSMUSG00000000318	chr11	Clec10a	70156197	70156262	2899	1.326869	3.615157	1.57E-05	8.86E-05	0.104487	1	100	44	135	85	238	288	285	318	436	705
ENSMUSG00000024780	chr19	Cdc37l1	28990494	28990669	2517	-0.71142	5.339081	1.58E-05	8.92E-05	0.030936	-1	761	773	1040	737	873	613	779	747	776	643
ENSMUSG00000091462	chr13	Gm17084	34033063	34037147	4085	0.999497	2.518561	1.58E-05	8.92E-05	0.052589	1	53	49	63	50	101	114	157	151	255	211
ENSMUSG00000033825	chr17	Tpsb2	25366550	25366621	1081	1.362068	2.490788	1.6E-05	9.05E-05	0.104016	1	42	33	26	61	99	170	113	172	193	264
ENSMUSG00000042249	chr5	Adrbk2	1.13E+08	1.13E+08	6537	-0.89631	3.201264	1.61E-05	9.07E-05	0.045123	-1	163	190	250	184	207	105	155	99	192	204
ENSMUSG00000006930	chr11	Hap1	1E+08	1E+08	3766	1.916192	-0.63426	1.61E-05	9.09E-05	0.094794	1	1	3	3	5	6	18	20	10	24	24
ENSMUSG00000092463	chrX	Gm20489	1.01E+08	1.01E+08	1350	1.593863	2.259532	1.61E-05	9.1E-05	0.141349	1	21	43	38	42	49	120	140	43	272	258
ENSMUSG00000052557	chr8	Gan	1.17E+08	1.17E+08	3300	-1.56486	-0.06027	1.62E-05	9.13E-05	0.084334	-1	18	13	23	22	38	8	8	6	17	14
ENSMUSG00000051517	chr4	Arhgef39	43496142	43496717	2675	1.865433	-0.09106	1.64E-05	9.23E-05	0.131861	1	7	2	5	3	12	19	35	12	42	42
ENSMUSG00000025464	chr7	Paox	1.4E+08	1.4E+08	1765	1.102455	2.454044	1.64E-05	9.25E-05	0.065323	1	51	43	56	59	76	84	137	202	192	250
ENSMUSG00000033107	chr18	Rnf125	20944625	20944757	1334	-1.9188	0.545165	1.65E-05	9.27E-05	0.181482	-1	19	31	41	75	20	4	9	23	24	11
ENSMUSG00000024420	chr18	Zfp521	13687013	13689024	6152	-0.84425	4.137895	1.65E-05	9.3E-05	0.042481	-1	353	257	457	365	471	188	364	388	299	232
ENSMUSG00000057396	chr13	Zfp759	67128228	67128314	3482	-1.13532	1.292595	1.65E-05	9.31E-05	0.058703	-1	56	44	60	62	51	28	27	41	44	35
ENSMUSG00000047246	chr13	Hist1h2be	23583742	23585970	4374	-1.15004	4.243809	1.66E-05	9.33E-05	0.080375	-1	359	403	511	419	489	297	352	105	426	190
ENSMUSG00000024664	chr19	Fads3	10041548	10041956	3269	1.174	3.634256	1.67E-05	9.39E-05	0.081808	1	112	83	112	127	206	215	583	185	568	491
ENSMUSG00000040325	chr9	Vprbp	1.07E+08	1.07E+08	7786	-0.74199	4.198862	1.68E-05	9.44E-05	0.032485	-1	350	309	414	371	479	218	326	416	385	266
ENSMUSG00000022519	chr16	Srl	4480216	4483284	5325	-0.69698	11.10943	1.69E-05	9.49E-05	0.03115	-1	38483	36393	53600	44478	57619	32384	41998	43913	43728	34164
ENSMUSG00000028228	chr4	Cpne3	19519254	19523294	7131	-0.72273	4.014751	1.7E-05	9.54E-05	0.030445	-1	309	247	332	347	454	177	286	286	382	312
ENSMUSG00000019773	chr10	Fbxo5	5799160	5799822	2003	1.563806	0.805027	1.71E-05	9.57E-05	0.109018	1	11	13	16	8	20	38	56	24	86	82
ENSMUSG00000058799	chr10	Nap1l1	1.11E+08	1.11E+08	4086	0.757724	6.305402	1.72E-05	9.67E-05	0.036155	1	869	784	1188	906	1193	1643	1996	3071	2514	2388
ENSMUSG00000039633	chr8	Lonrf1	36216064	36217601	3930	-0.93392	3.377147	1.74E-05	9.73E-05	0.050317	-1	132	290	273	185	252	139	177	164	180	166
ENSMUSG00000025558	chr14	Dock9	1.22E+08	1.22E+08	8199	-0.81593	4.79707	1.74E-05	9.75E-05	0.040876	-1	470	503	733	707	544	298	382	625	566	501
ENSMUSG00000066861	chr5	Oas1g	1.21E+08	1.21E+08	2340	3.290371	0.251996	1.74E-05	9.76E-05	0.488577	1	2	4	0	3	7	64	25	2	22	99
ENSMUSG00000052102	chr18	Gnpda1	38327558	38328973	2392	0.729681	4.115752	1.75E-05	9.77E-05	0.031027	1	199	170	230	215	273	344	494	410	689	610
ENSMUSG00000031226	chrX	Pbdc1	1.05E+08	1.05E+08	6098	0.831358	3.579074	1.75E-05	9.78E-05	0.039481	1	101	145	159	130	179	269	298	325	384	494
ENSMUSG00000040287	chr10	Stac3	1.28E+08	1.28E+08	2543	-0.77284	8.145631	1.75E-05	9.79E-05	0.038177	-1	5399	5074	7734	5506	6170	4721	5611	3895	5114	4757
ENSMUSG00000006273	chr8	Atp6v1b2	69088646	69088928	5305	0.852895	6.737866	1.76E-05	9.83E-05	0.046086	1	910	1318	1519	1201	1410	2201	2410	2597	4896	4273
ENSMUSG00000022016	chr14	Akap11	78492246	78495946	9419	-0.71595	4.3604	1.76E-05	9.83E-05	0.030552	-1	362	337	470	433	543	226	367	451	429	356
ENSMUSG00000028788	chr4	Ptp4a2	1.3E+08	1.3E+08	4377	-0.71388	9.63512	1.77E-05	9.89E-05	0.032774	-1	14756	15498	19614	15287	17091	12920	13604	14353	14855	13849
ENSMUSG00000092511	chr17	Gm20547	34856412	34856582	3902	1.52418	4.717209	1.77E-05	9.89E-05	0.141955	1	143	150	182	188	514	763	606	382	916	1853
ENSMUSG00000051855	chr6	Mest	30723547	30723646	3935	1.276825	5.496049	1.77E-05	9.89E-05	0.10133	1	269	360	490	404	734	1209	2724	607	1893	1049
ENSMUSG00000100755	chr3	Rps23-ps	37714740	37715164	425	0.723133	4.201525	1.77E-05	9.89E-05	0.030731	1	202	191	314	195	257	410	602	518	548	575
ENSMUSG00000018412	chr11	Kansl1	1.04E+08	1.04E+08	6874	-0.80089	4.497106	1.79E-05	9.97E-05	0.03904	-1	393	346	547	540	592	230	331	533	490	362
ENSMUSG00000040722	chr9	Scamp5	57441328	57443864	3190	1.055007	3.054372	1.79E-05	9.99E-05	0.0644	1	74	50	99	69	165	177	288	181	362	302
ENSMUSG00000003731	chr4	Kpna6	1.3E+08	1.3E+08	6729	-0.68006	6.710448	1.8E-05	0.0001	0.02938	-1	1752	1955	2472	2210	2398	1567	1859	2011	2135	1795
ENSMUSG00000042938	chr2	Gm14117	1.46E+08	1.46E+08	843	-1.26264	1.418832	1.8E-05	0.0001	0.0795	-1	45	67	56	89	48	36	34	35	38	35
ENSMUSG00000002835	chr17	Chaf1a	56040416	56040551	3308	1.427609	1.966023	1.82E-05	0.000101	0.111406	1	25	22	31	32	64	70	112	65	232	185
ENSMUSG00000003779	chr18	Kif20a	34624624	34624852	3796	1.145026	2.340723	1.82E-05	0.000101	0.071409	1	46	31	46	60	76	95	158	108	287	171
ENSMUSG00000025172	chr19	Ankrd2	42036038	42036122	1100	1.912838	6.539166	1.82E-05	0.000101	0.220529	1	348	836	518	1246	192	1606	2734	7520	3159	2222
ENSMUSG00000042496	chr9	Prdm10	31280538	31280662	6075	-1.11447	1.016594	1.83E-05	0.000102	0.052347	-1	34	42	49	48	52	20	28	29	40	29
ENSMUSG00000029335	chr5	Bmp3	98854439	98855422	3112	-1.90741	0.316733	1.83E-05	0.000102	0.173186	-1	31	4	34	37	56	4	12	15	15	13
ENSMUSG00000049791	chr7	Fzd4	89404366	89404971	3685	-1.35706	5.192278	1.85E-05	0.000103	0.114466	-1	730	867	690	841	1268	173	365	1007	616	296
ENSMUSG00000000600	chr5	Krit1	3803165	3803483	6151	-0.71835	4.06772	1.87E-05	0.000104	0.030491	-1	291	341	389	357	350	195	352	297	378	271
ENSMUSG00000001036	chr11	Epn2	61517249	61519707	5228	-0.68916	4.789642	1.88E-05	0.000104	0.028948	-1	507	420	672	592	677	360	449	570	563	534
ENSMUSG00000035000	chr2	Dpp4	62330073	62332719	6319	-1.0789	3.120433	1.88E-05	0.000104	0.067795	-1	173	94	203	173	370	112	138	112	133	149
ENSMUSG00000042622	chr15	Maff	79347541	79347754	2119	1.508859	1.249113	1.89E-05	0.000105	0.115399	1	13	9	22	32	22	40	49	125	99	79
ENSMUSG00000039252	chr5	Lgi2	52537864	52538780	1950	-1.28559	1.720082	1.89E-05	0.000105	0.087853	-1	68	47	86	76	114	34	43	19	58	68
ENSMUSG00000026687	chr1	Aldh9a1	1.67E+08	1.67E+08	3383	1.069596	3.41308	1.89E-05	0.000105	0.067701	1	81	100	110	105	179	165	267	246	566	483
ENSMUSG00000004939	chr10	Nmrk2	81198170	81199446	1840	1.673564	5.893292	1.9E-05	0.000105	0.172101	1	171	394	891	522	457	2478	1912	453	3021	2577
ENSMUSG00000039831	chr3	Arhgap29	1.22E+08	1.22E+08	5088	-0.71864	4.709796	1.91E-05	0.000106	0.031595	-1	440	453	566	597	674	288	497	487	483	567
ENSMUSG00000076437	chr2	2700094K13Rik	84669215	84669397	1131	0.880932	3.218393	1.91E-05	0.000106	0.043966	1	86	101	139	92	124	213	265	188	390	350

ENSMUSG00000028480	chr4	Glipr2	43957401	43957773	2320	1.248966	3.75771	1.92E-05	0.000106	0.094613	1	123	73	128	105	252	364	576	170	574	531
ENSMUSG00000026107	chr1	Nabp1	51465862	51469086	8498	-0.77604	4.795007	1.93E-05	0.000107	0.037269	-1	380	569	722	601	674	348	429	376	664	602
ENSMUSG00000030499	chr7	Kctd15	34639014	34640449	2991	-0.71221	5.929292	1.95E-05	0.000108	0.032129	-1	1002	1074	1610	1197	1491	944	983	1129	1100	1185
ENSMUSG00000048440	chr17	Cyp4f16	32536558	32536655	3017	1.135247	1.998863	1.95E-05	0.000108	0.066614	1	38	43	36	34	49	98	122	74	182	151
ENSMUSG00000021712	chr13	Trim23	1.04E+08	1.04E+08	5747	-1.01988	4.655019	1.95E-05	0.000108	0.064907	-1	574	442	679	563	544	228	365	691	384	278
ENSMUSG00000044308	chr2	Ubr3	69897246	69897839	9719	-1.14182	8.00126	1.95E-05	0.000108	0.083178	-1	5370	4587	6850	6084	6678	2280	2906	7529	3139	2725
ENSMUSG00000046567	chr10	4930430F08Rik	1.01E+08	1.01E+08	2419	-0.98332	2.064338	1.95E-05	0.000108	0.049136	-1	72	77	97	98	117	49	82	57	87	51
ENSMUSG00000033352	chr11	Map2k4	65688243	65690804	4664	-0.68597	6.555315	1.96E-05	0.000108	0.030106	-1	1585	1751	2242	1892	2248	1393	1564	1913	1877	1638
ENSMUSG00000030428	chr7	Ttyh1	4119408	4119424	6345	-1.34838	0.898502	1.97E-05	0.000109	0.083174	-1	35	42	62	39	39	16	32	33	17	20
ENSMUSG00000024927	chr19	Rela	5637483	5637841	2716	0.680221	4.583361	1.97E-05	0.000109	0.027958	1	240	243	337	305	427	495	643	678	944	714
ENSMUSG00000048668	chr6	Rhno1	1.28E+08	1.28E+08	2486	0.873704	2.770469	1.98E-05	0.000109	0.040971	1	74	61	77	69	117	164	202	178	267	206
ENSMUSG00000035898	chr5	Uba6	86110720	86112788	6726	-0.92123	2.526306	1.99E-05	0.000109	0.045422	-1	110	80	149	124	170	79	97	78	125	83
ENSMUSG00000039879	chr10	Heca	17900466	17902377	3667	-1.14326	3.747487	1.99E-05	0.00011	0.07974	-1	251	240	299	354	409	84	199	368	177	155
ENSMUSG00000078619	chr11	Smarcd2	1.06E+08	1.06E+08	3589	0.694729	4.535248	1.99E-05	0.00011	0.029074	1	271	253	308	294	345	487	645	558	846	825
ENSMUSG00000029860	chr6	Zyx	42349828	42350119	3739	0.803675	5.673128	2E-05	0.00011	0.040995	1	443	459	590	656	1020	1171	1726	1174	2113	1460
ENSMUSG00000078486	chr4	Perm1	1.56E+08	1.56E+08	3901	-1.00488	7.332437	2E-05	0.00011	0.064829	-1	2580	3894	3822	4895	2488	2663	2445	1777	3145	2342
ENSMUSG00000028552	chr4	Eps15	1.09E+08	1.09E+08	6931	-0.73676	6.193161	2.02E-05	0.000111	0.034734	-1	1416	1296	1814	1475	1629	892	1260	1657	1390	1223
ENSMUSG00000072844	chrX	G530011O06Rik	1.7E+08	1.7E+08	2380	2.632524	-0.30475	2.02E-05	0.000111	0.300393	1	2	1	3	3	7	38	21	15	4	52
ENSMUSG00000026812	chr2	Tsc1	28641228	28641319	11833	-0.97793	5.301545	2.02E-05	0.000111	0.060574	-1	859	694	948	877	983	384	480	1102	602	533
ENSMUSG00000031647	chr8	Mfap3l	60632827	60633058	6837	-0.89996	3.126915	2.02E-05	0.000111	0.046697	-1	156	161	173	260	190	94	172	136	191	124
ENSMUSG00000029417	chr5	Cxcl9	92321331	92323906	2905	1.970386	2.046472	2.02E-05	0.000111	0.217777	1	21	22	27	37	28	197	190	16	167	150
ENSMUSG00000027200	chr2	Sema6d	1.24E+08	1.24E+08	10559	-0.74805	4.177024	2.03E-05	0.000111	0.033797	-1	389	259	418	402	423	215	364	283	448	287
ENSMUSG00000095538	chr7	Gm21983	27168430	27168804	1690	0.865362	3.558237	2.03E-05	0.000112	0.04377	1	119	116	135	122	204	309	344	222	469	419
ENSMUSG00000037225	chr3	Fgf2	37312519	37312585	1801	-2.00933	0.08495	2.04E-05	0.000112	0.190904	-1	24	15	11	25	63	2	15	14	11	5
ENSMUSG00000002781	chr7	Tmem143	45896941	45897101	5636	-0.72978	5.722105	2.05E-05	0.000112	0.033856	-1	876	1110	1150	1289	1022	770	868	860	1145	997
ENSMUSG00000022265	chr15	Ank	27466677	27467099	3608	-0.79833	6.716133	2.06E-05	0.000113	0.041112	-1	2067	1840	2478	2612	2088	1318	1793	2410	1924	1511
ENSMUSG00000042302	chr11	Ehbp1	22005828	22006871	5825	-0.72928	3.689446	2.06E-05	0.000113	0.030761	-1	240	228	282	270	320	168	258	266	236	199
ENSMUSG00000047036	chr9	Zfp445	1.23E+08	1.23E+08	2961	-1.4946	3.351899	2.06E-05	0.000113	0.13518	-1	241	184	294	232	313	42	90	301	116	81
ENSMUSG00000042104	chr14	Uggt2	1.19E+08	1.19E+08	12796	-0.83004	2.881222	2.06E-05	0.000113	0.037817	-1	149	119	173	147	198	85	147	118	161	110
ENSMUSG00000022075	chr14	Rhobtb2	69784990	69787735	5216	-0.70758	5.087431	2.07E-05	0.000113	0.031199	-1	501	562	830	731	951	556	603	552	668	607
ENSMUSG00000030589	chr7	Rasgrp4	29134854	29135095	6359	1.338324	1.474366	2.07E-05	0.000113	0.09048	1	23	18	27	20	38	55	104	46	109	134
ENSMUSG00000042109	chr15	Csdc2	81936759	81936987	4623	1.074674	1.993785	2.09E-05	0.000115	0.059318	1	27	35	52	45	50	100	165	89	129	125
ENSMUSG00000000568	chr5	Hnrnpd	99958426	99961333	4863	0.657584	5.368377	2.12E-05	0.000116	0.027102	1	478	438	561	542	661	868	1121	1092	1582	1290
ENSMUSG00000067279	chr19	Ppp1r3c	36731737	36734354	2719	-0.91007	7.708958	2.13E-05	0.000116	0.053751	-1	3119	3890	6477	5341	4152	3610	3532	2345	3402	3743
ENSMUSG00000022811	chr16	Zfp148	33380775	33381027	9545	-0.76209	4.487208	2.14E-05	0.000117	0.035851	-1	392	370	564	481	565	239	389	535	456	338
ENSMUSG00000031700	chr8	Gpt2	85492576	85492689	5643	-1.14724	7.873214	2.14E-05	0.000117	0.084744	-1	3673	5857	8841	4769	3786	2990	2788	5332	2693	2879
ENSMUSG00000026558	chr1	Uck2	1.67E+08	1.67E+08	5464	0.733281	4.584757	2.14E-05	0.000117	0.03305	1	231	280	301	261	440	496	757	692	986	600
ENSMUSG00000024330	chr17	Col11a2	34039437	34039736	6831	-1.7385	5.9122	2.15E-05	0.000117	0.187411	-1	1940	453	1700	643	3305	532	1170	555	680	288
ENSMUSG00000033478	chr19	Fam160b1	57361009	57361370	5630	-0.77942	4.055157	2.15E-05	0.000117	0.036894	-1	324	346	310	343	413	169	322	358	325	265
ENSMUSG00000031592	chr8	Pcm1	41239759	41239963	8380	-0.74306	5.979205	2.15E-05	0.000117	0.03545	-1	1092	1089	1435	1325	1707	817	1053	1470	1216	951
ENSMUSG00000025735	chr17	Rhbdl1	25834465	25835056	1723	-0.90821	4.589121	2.15E-05	0.000117	0.051644	-1	431	567	639	537	410	415	324	274	464	448
ENSMUSG00000029363	chr5	Rfc5	1.17E+08	1.17E+08	4669	1.345623	1.807864	2.16E-05	0.000117	0.098821	1	21	21	39	29	52	74	99	55	196	155
ENSMUSG00000051495	chr8	Irf2bp2	1.27E+08	1.27E+08	5080	0.770425	4.857709	2.16E-05	0.000117	0.037147	1	265	229	401	474	441	583	810	889	1014	992
ENSMUSG00000027955	chr3	Fam198b	79884533	79884690	9598	-0.6803	5.177217	2.16E-05	0.000118	0.029043	-1	622	569	874	756	935	524	737	599	845	553
ENSMUSG00000042745	chr2	Id1	1.53E+08	1.53E+08	1160	0.854712	3.501697	2.16E-05	0.000118	0.042457	1	107	129	132	178	113	237	342	329	498	305
ENSMUSG00000037795	chr5	N4bp2	65763521	65763590	9871	-0.82676	3.525597	2.17E-05	0.000118	0.040153	-1	204	161	244	283	351	132	231	219	232	158
ENSMUSG00000024824	chr19	Rad9a	4195198	4196082	2046	0.917553	2.416061	2.17E-05	0.000118	0.043845	1	46	60	67	60	68	125	155	124	218	180
ENSMUSG00000057604	chr6	Lmcd1	1.12E+08	1.12E+08	1730	0.909999	6.904471	2.18E-05	0.000119	0.05368	1	1022	1130	1418	2128	1229	2832	3677	4551	4531	2706
ENSMUSG00000025786	chr9	Zdhhc3	1.23E+08	1.23E+08	11846	-0.69336	6.200322	2.19E-05	0.000119	0.030984	-1	1181	1315	1627	1676	1829	1054	1151	1482	1595	1285
ENSMUSG00000032112	chr9	Trappc4	44403761	44404098	1166	0.768041	4.353718	2.22E-05	0.00012	0.036067	1	213	247	304	225	264	480	571	423	783	754
ENSMUSG00000039182	chr13	AW209491	14630245	14630284	2023	-0.71831	3.548433	2.23E-05	0.000121	0.02955	-1	209	228	290	240	238	159	195	221	245	210
ENSMUSG00000081344	chr2	Gm14303	1.73E+08	1.73E+08	171	0.670163	5.129742	2.23E-05	0.000121	0.028106	1	365	436	498	437	513	904	983	913	1166	1011
ENSMUSG00000021373	chr13	Cap2	46501848	46502211	3322	-0.72512	8.081875	2.23E-05	0.000121	0.034503	-1	4587	4292	7474	5183	7093	4169	5437	4551	5613	3991
ENSMUSG00000098098	chr18	Gm20748	61639542	61639732	699	1.196951	1.623029	2.24E-05	0.000122	0.071218	1	23	35	42	25	23	73	121	107	103	74
ENSMUSG00000099081	chr11	Gm27624	3644776	3644952	177	-1.09493	1.313303	2.24E-05	0.000122	0.055484	-1	40	52	58	62	65	23	40	39	36	43
ENSMUSG00000019731	chr8	Slc35e1	72480641	72483993	4470	-0.66791	5.899569	2.26E-05	0.000122	0.028661	-1	1047	972	1404	1314	1411	823	1065	1202	1264	1040
ENSMUSG00000037686	chr12	Aspg	1.12E+08	1.12E+08	2732	3.338454	0.695876	2.26E-05	0.000122	0.537035	1	1	1	1	8	11	4	10	41	132	141
ENSMUSG00000074280	chr9	Gm6166	57483913	57484223	669	2.423863	1.032382	2.26E-05	0.000122	0.305073	1	3	13	7	17	8	23	25	28	145	169
ENSMUSG00000022441	chr15	Efcab6	83866712	83867171	6408	-1.06022	2.854238	2.28E-05	0.000123	0.066155	-1	184	127	123	202	163	77	136	117	151	69
ENSMUSG00000001829	chr7	Clpb	1.02E+08	1.02E+08	7855	-0.74197	5.573306	2.3E-05	0.000124	0.03535	-1	779	891	1120	1250	916	626	706	916	970	952
ENSMUSG00000031622	chr8	Sin3b	72723288	72723408	4298	0.673966	5.067805	2.3E-05	0.000124	0.028482	1	346	366	436	484	529	689	957	1079	1086	1006
ENSMUSG00000017499	chr11	Cdc6	98907801	98907981	5229	1.611962	0.881582	2.3E-05	0.000124	0.125214	1	10	13	20	10	17	34	55	25	124	73
ENSMUSG00000063273	chr3	Naa15	51415148	51416376	15427	-0.67225	6.194124	2.3E-05	0.000124	0.029269	-1	1220	1307	1811	1353	1886	993	1466	1244	1619	1306
ENSMUSG00000021660	chr13	Btf3	98309896	98310201	1739	0.699506	7.115661	2.31E-05	0.000124	0.032038	1	1447	1635	2171	1557	2051	3500	3729	4169	4295	4189
ENSMUSG00000005107	chr5	Slc2a9	38349273	38351337	5083	1.313287	0.556326	2.34E-05	0.000126	0.065668	1	11	12	8	14	19	34	48	40	46	55
ENSMUSG00000021221	chr12	Dpf3	83213745	83215811	4225	-0.87013	3.135999	2.35E-05	0.000127	0.043698	-1	159	175	190	170	253	111	131	198	139	138

ENSMUSG00000025538	chr5	Sumf2	1.3E+08	1.3E+08	2667	0.834033	3.118482	2.35E-05	0.000127	0.039279	1	80	94	115	108	118	155	227	313	337	268
ENSMUSG00000007039	chr17	Ddah2	35059035	35059272	1593	0.801117	4.302677	2.35E-05	0.000127	0.039853	1	194	163	240	225	399	485	714	471	667	570
ENSMUSG00000030555	chr7	Ttc23	67647410	67647845	6343	-0.76744	3.241319	2.35E-05	0.000127	0.033433	-1	140	169	265	193	234	123	168	167	206	153
ENSMUSG00000026810	chr2	Dpm2	32570858	32570912	1971	0.716812	3.535182	2.36E-05	0.000127	0.029229	1	131	121	174	135	166	235	315	308	441	386
ENSMUSG00000032344	chr9	Mb21d1	78430526	78433267	4126	2.007531	0.163449	2.37E-05	0.000128	0.184678	1	6	2	9	4	12	29	26	9	64	59
ENSMUSG00000031887	chr8	Tradd	1.05E+08	1.05E+08	1866	1.131818	2.053954	2.39E-05	0.000129	0.069422	1	29	43	46	32	62	95	156	75	170	155
ENSMUSG00000028680	chr4	Plk3	1.17E+08	1.17E+08	2531	1.894724	1.374201	2.39E-05	0.000129	0.192826	1	17	11	12	26	19	31	60	36	172	172
ENSMUSG00000036052	chr4	Dnajb5	42949814	42950004	5936	-0.80948	7.447273	2.4E-05	0.000129	0.043132	-1	3221	3085	3981	3607	4789	2984	3717	2072	3058	2742
ENSMUSG00000039232	chr10	Stx11	12939983	12941983	2396	1.620357	0.222566	2.43E-05	0.00013	0.106266	1	3	6	10	7	17	20	31	25	63	48
ENSMUSG00000023908	chr17	Pkmyt1	23726336	23726641	2039	1.34929	1.201515	2.46E-05	0.000132	0.089109	1	19	17	11	19	36	49	71	48	108	93
ENSMUSG00000039395	chr1	Mreg	72159442	72161019	2284	-0.92431	4.390571	2.46E-05	0.000132	0.054	-1	342	418	428	675	409	287	328	454	304	291
ENSMUSG00000062933	chr9	Gm10123	96895658	96896147	490	0.811532	4.111305	2.46E-05	0.000132	0.040574	1	152	205	233	194	262	405	520	322	686	643
ENSMUSG00000028792	chr4	Ak2	1.29E+08	1.29E+08	2140	0.83008	5.525003	2.47E-05	0.000132	0.044579	1	402	540	584	561	687	994	1165	944	1861	1998
ENSMUSG00000033943	chr2	Mga	1.2E+08	1.2E+08	15340	-0.83604	5.118905	2.47E-05	0.000133	0.044933	-1	595	539	848	785	1006	418	603	858	586	437
ENSMUSG00000017057	chrX	Il13ra1	36112110	36112275	3712	1.021005	3.630767	2.48E-05	0.000133	0.064522	1	96	94	129	108	271	303	467	237	512	415
ENSMUSG00000021598	chr13	Med10	69809882	69810052	862	0.794172	3.12062	2.48E-05	0.000133	0.035073	1	99	83	117	120	103	196	254	243	339	247
ENSMUSG00000024098	chr17	Twsg1	65923066	65926466	4046	-0.68346	5.235392	2.49E-05	0.000133	0.029851	-1	676	582	853	747	1061	508	734	736	824	585
ENSMUSG00000040712	chr11	Camta2	70669463	70670262	5207	-0.6663	5.564186	2.5E-05	0.000134	0.028606	-1	764	772	1087	1075	1190	699	846	734	1016	977
ENSMUSG00000042254	chr9	Cilp	65265180	65265223	4252	1.090033	7.202375	2.51E-05	0.000134	0.077881	1	1420	848	1952	1175	2719	3293	7790	3331	5588	3588
ENSMUSG00000061613	chr17	U2af1	31647082	31647355	974	0.682063	4.967848	2.54E-05	0.000136	0.029478	1	320	341	474	354	533	805	880	846	961	957
ENSMUSG00000096493	chr1	Gm10031	1.57E+08	1.57E+08	2568	-0.97371	2.036593	2.55E-05	0.000136	0.049596	-1	74	75	113	83	106	44	75	78	67	55
ENSMUSG00000101523	chr1	Csnk2a1	1.57E+08	1.57E+08	2653	-0.97371	2.036593	2.55E-05	0.000136	0.049601	-1	74	75	113	83	106	44	75	78	67	55
ENSMUSG00000056124	chr18	B4galt6	20684599	20688468	5808	1.057884	3.261797	2.57E-05	0.000137	0.06795	1	105	49	120	83	167	190	353	194	446	343
ENSMUSG00000035566	chr14	Pcdh17	84443563	84448653	9509	-1.44033	2.076046	2.57E-05	0.000137	0.120954	-1	43	99	106	185	76	41	39	49	96	43
ENSMUSG00000030059	chr6	Tmf1	97155266	97155497	3465	-0.72403	4.255319	2.57E-05	0.000137	0.032453	-1	330	312	457	382	523	208	359	428	371	324
ENSMUSG00000038201	chr7	Kcna7	45405960	45407015	3494	-0.74059	7.514159	2.57E-05	0.000137	0.036435	-1	3147	3564	4380	4158	3791	3201	3191	2798	3746	2863
ENSMUSG00000086040	chr6	Wipf3	54429603	54429860	7114	-0.80526	4.056074	2.57E-05	0.000137	0.040151	-1	269	337	333	460	352	266	279	289	351	216
ENSMUSG00000020358	chr11	Hnrnpab	51600100	51601478	2782	0.694028	7.048627	2.58E-05	0.000137	0.031905	1	1294	1511	2026	1557	2136	3194	3579	3234	4849	4293
ENSMUSG00000021218	chr13	Gdi2	3538075	3538343	2681	0.664126	7.049103	2.6E-05	0.000138	0.029225	1	1400	1498	1878	1661	2173	2662	3665	4105	4652	4027
ENSMUSG00000035692	chr4	Isg15	1.56E+08	1.56E+08	756	2.3646	2.996507	2.6E-05	0.000139	0.328248	1	19	41	54	48	55	593	128	38	139	500
ENSMUSG00000056708	chr1	Ier5	1.55E+08	1.55E+08	3276	0.854397	3.96519	2.6E-05	0.000139	0.045287	1	154	140	144	188	309	382	531	352	666	420
ENSMUSG00000063714	chr2	Sp3os	72979424	72979595	892	1.346997	0.806264	2.6E-05	0.000139	0.078612	1	14	17	18	14	12	31	43	77	63	59
ENSMUSG00000041453	chr5	Rpl21	1.47E+08	1.47E+08	3400	0.676047	7.963881	2.62E-05	0.000139	0.030512	1	2558	2963	3724	3051	3830	6285	7397	6627	7842	7476
ENSMUSG00000021374	chr13	Nup153	46679905	46681242	6914	-0.76966	5.229594	2.62E-05	0.00014	0.038336	-1	697	633	931	791	913	459	610	929	702	538
ENSMUSG00000025491	chr7	Ifitm1	1.41E+08	1.41E+08	1094	1.821142	-0.23885	2.67E-05	0.000142	0.114254	1	2	8	4	4	8	10	24	24	33	42
ENSMUSG00000024073	chr17	Birc6	74528295	74528801	28830	-0.90715	5.645477	2.67E-05	0.000142	0.054009	-1	953	776	1329	1091	1367	417	745	1318	972	675
ENSMUSG00000038555	chr18	Reep2	34840589	34840787	1926	1.665109	0.194199	2.71E-05	0.000144	0.116514	1	2	6	18	7	8	23	56	25	42	35
ENSMUSG00000035798	chr10	Zdhhc17	1.11E+08	1.11E+08	4948	-0.73384	4.322855	2.72E-05	0.000145	0.03377	-1	406	338	505	390	442	220	390	438	369	343
ENSMUSG00000020116	chr11	Pno1	17203198	17204001	1717	-0.68371	5.09363	2.73E-05	0.000145	0.030029	-1	669	645	821	657	695	537	645	568	722	572
ENSMUSG00000022464	chr15	Slc38a4	96994823	96997091	3952	-0.89085	6.997273	2.76E-05	0.000146	0.052814	-1	1568	2623	3883	2626	3411	1924	2002	2635	1752	1931
ENSMUSG00000034037	chr6	Fgd5	91978878	91979042	6292	-0.85814	3.8858	2.76E-05	0.000146	0.046111	-1	247	285	306	433	307	146	217	340	287	246
ENSMUSG00000035614	chr12	Fam179b	64965742	64968028	6434	-0.8921	3.875665	2.76E-05	0.000146	0.050064	-1	273	281	389	287	364	122	278	348	299	170
ENSMUSG00000020273	chr11	Papolg	23862646	23864056	5491	-0.97043	2.309214	2.77E-05	0.000147	0.052221	-1	105	101	106	116	109	50	90	100	75	72
ENSMUSG00000028152	chr3	Tspan5	1.39E+08	1.39E+08	3917	0.81911	3.248595	2.8E-05	0.000148	0.039204	1	83	99	150	101	140	198	242	358	350	260
ENSMUSG00000024660	chr19	Incenp	9872297	9872873	3217	1.309376	2.879812	2.8E-05	0.000149	0.104828	1	50	47	61	69	128	142	211	107	461	328
ENSMUSG00000026622	chr1	Nek2	1.92E+08	1.92E+08	4516	1.589277	1.398811	2.82E-05	0.000149	0.138654	1	6	26	34	19	19	53	78	45	169	107
ENSMUSG00000041977	chr3	Arhgef11	87617559	87618792	7918	-0.67276	5.085788	2.82E-05	0.000149	0.029198	-1	643	513	754	719	876	412	561	656	809	655
ENSMUSG00000029405	chr5	G3bp2	92052146	92055053	4677	-0.69033	6.641248	2.84E-05	0.000151	0.031796	-1	1680	1723	2509	1900	2583	1391	1879	1411	2251	2042
ENSMUSG00000037348	chr4	Paqr7	1.34E+08	1.34E+08	4259	1.059758	2.512115	2.86E-05	0.000151	0.064429	1	53	46	82	52	71	138	161	101	299	198
ENSMUSG00000019947	chr10	Arid5b	68095593	68098669	4494	-1.26037	2.864055	2.88E-05	0.000152	0.097903	-1	136	95	203	244	186	33	105	167	116	88
ENSMUSG00000022204	chr14	Ngdn	55015454	55015588	1198	0.685527	3.938248	2.88E-05	0.000152	0.028351	1	141	179	242	209	207	354	441	467	496	429
ENSMUSG00000040522	chrX	Tlr8	1.67E+08	1.67E+08	3586	1.30739	1.146468	2.9E-05	0.000153	0.085982	1	13	13	22	17	37	40	94	70	99	49
ENSMUSG00000030536	chr7	Iqgap1	80711583	80713945	7359	0.900982	5.954293	2.9E-05	0.000153	0.053872	1	607	476	763	742	1087	1054	1763	1331	2938	2623
ENSMUSG00000054484	chr2	Tmem62	1.21E+08	1.21E+08	3348	1.049778	2.32171	2.91E-05	0.000154	0.061419	1	48	57	59	39	60	99	225	128	198	126
ENSMUSG00000031600	chr8	Vps37a	40511783	40512233	6379	-0.88579	5.968163	2.92E-05	0.000154	0.052128	-1	1129	1118	1765	1383	1421	821	872	1615	912	848
ENSMUSG00000029610	chr5	Aimp2	1.44E+08	1.44E+08	1654	-1.06299	7.328454	2.93E-05	0.000155	0.075408	-1	3047	3298	4768	3449	3608	2934	2483	1017	2935	2529
ENSMUSG00000101941	chr9	Gm28979	1.01E+08	1.01E+08	1540	-1.59299	-0.01384	2.94E-05	0.000155	0.104827	-1	17	28	34	21	16	11	13	4	17	9
ENSMUSG00000070469	chr7	Adamtsl3	82335694	82335910	7732	-1.33663	2.732341	2.95E-05	0.000156	0.110214	-1	165	67	167	135	277	45	124	112	121	44
ENSMUSG00000052144	chr6	Ppp4r2	1.01E+08	1.01E+08	3641	-0.71864	5.187903	2.95E-05	0.000156	0.033724	-1	591	669	860	715	982	419	680	836	722	577
ENSMUSG00000028701	chr4	Lurap1	1.16E+08	1.16E+08	5886	-0.85301	3.169991	2.96E-05	0.000156	0.04352	-1	142	214	193	173	239	108	149	119	235	147
ENSMUSG00000042650	chr11	Alkbh5	60536381	60536637	5987	-0.67663	7.05728	2.96E-05	0.000156	0.030801	-1	2423	2212	3100	2700	3325	1953	2205	2785	2682	2308
ENSMUSG00000040046	chr7	Tph1	46647130	46647600	3682	-1.19712	1.981621	2.97E-05	0.000156	0.080349	-1	67	111	106	70	97	64	49	38	50	69
ENSMUSG00000031543	chr8	Ank1	22974844	22975261	13527	-0.85764	9.269648	2.99E-05	0.000157	0.049759	-1	10458	11763	16824	12431	15487	10959	11247	5944	11279	10993
ENSMUSG00000053436	chr17	Mapk14	28691342	28691855	4361	-0.70657	6.949957	2.99E-05	0.000158	0.033593	-1	1993	2382	3031	2444	3018	1990	2356	1712	2638	2231
ENSMUSG00000059552	chr11	Trp53	69580359	69580515	4045	0.729321	4.380797	3E-05	0.000158	0.033639	1	198	231	282	236	370	489	651	437	818	646
ENSMUSG00000022225	chr14	Cma1	55941453	55941797	1074	1.091882	2.553888	3E-05	0.000158	0.070026	1	62	45	58	53	90	189	108	190	180	228

ENSMUSG00000046096	chr7	BC030336	1.21E+08	1.21E+08	4842	-0.69824	3.965401	3E-05	0.000158	0.029985	-1	291	264	340	328	390	185	311	335	321	243
ENSMUSG00000028572	chr4	Hook1	95967240	95967556	8318	-1.08661	3.655496	3E-05	0.000158	0.074916	-1	290	254	318	254	301	107	137	357	160	177
ENSMUSG00000022901	chr16	Cd86	36603869	36605338	3661	1.383218	1.784158	3.05E-05	0.00016	0.109699	1	25	15	28	27	62	53	143	72	141	161
ENSMUSG00000090733	chr3	Rps27	90212725	90212753	255	0.796702	7.17861	3.06E-05	0.000161	0.042826	1	1719	1732	2178	1464	1658	3940	4373	4929	3996	3876
ENSMUSG00000045679	chr12	Pqlc3	16988648	16989895	5408	1.277697	2.474874	3.07E-05	0.000161	0.096924	1	79	34	42	34	72	90	157	146	290	242
ENSMUSG00000015165	chr7	Hnrnpl	28808541	28808859	5953	0.660302	6.273562	3.08E-05	0.000162	0.02915	1	770	884	1113	969	1313	1573	2152	2327	2692	2393
ENSMUSG00000027194	chr2	Ttc17	94300767	94301867	8984	-0.6806	4.697869	3.08E-05	0.000162	0.029707	-1	423	493	708	511	535	346	513	488	530	453
ENSMUSG00000019944	chr10	Rhobtb1	69151434	69151488	6075	-0.70861	3.882633	3.09E-05	0.000162	0.030837	-1	285	240	383	295	323	186	258	322	292	248
ENSMUSG00000004085	chr2	Zak	72285637	72285855	10175	-0.75147	7.958435	3.1E-05	0.000162	0.038352	-1	4854	4234	6042	5419	5504	3833	4079	5451	4182	3813
ENSMUSG00000033863	chr19	Klf9	23141226	23142259	3263	-1.32613	6.41862	3.13E-05	0.000164	0.116502	-1	1950	1616	2343	2138	2159	507	925	2624	990	679
ENSMUSG00000040883	chr9	Tmem205	21921010	21921349	862	0.888763	3.438078	3.15E-05	0.000165	0.048823	1	87	80	155	134	187	250	231	329	378	441
ENSMUSG00000028476	chr4	Reck	43875530	43875705	4779	-1.25077	3.269511	3.15E-05	0.000165	0.098763	-1	265	81	201	170	444	86	161	158	154	109
ENSMUSG00000037197	chr2	Rbm17	11585437	11585728	2405	0.638668	5.123446	3.16E-05	0.000165	0.026468	1	370	390	542	461	518	828	960	1021	1097	1016
ENSMUSG00000039219	chr13	Arid4b	14063232	14063489	13702	-0.8076	3.83205	3.16E-05	0.000165	0.041017	-1	277	241	341	275	384	147	234	353	285	197
ENSMUSG00000033880	chr11	Lgals3bp	1.18E+08	1.18E+08	2847	1.194366	5.514274	3.17E-05	0.000166	0.094677	1	326	328	490	404	841	1471	1372	561	1644	2289
ENSMUSG00000027935	chr3	Rab13	90213695	90213822	1651	0.731336	3.438764	3.19E-05	0.000167	0.031417	1	103	115	177	128	156	218	303	336	354	360
ENSMUSG00000038403	chr3	Hfe2	96525185	96525330	2021	-0.70186	9.158777	3.19E-05	0.000167	0.033713	-1	10148	10831	13361	11535	13258	10051	10036	9646	10270	9980
ENSMUSG00000071302	chr8	2610044O15Rik8	1.29E+08	1.29E+08	3858	-0.7176	4.033897	3.22E-05	0.000168	0.032215	-1	314	367	364	302	326	246	276	293	341	282
ENSMUSG00000005779	chr3	Psmb4	94884093	94884440	1384	0.799535	7.061173	3.23E-05	0.000168	0.043362	1	1354	1612	1882	1486	1785	3251	3314	5556	3764	3701
ENSMUSG00000044927	chr6	H1fx	87980421	87981637	1217	1.318011	0.634166	3.25E-05	0.00017	0.073134	1	10	13	9	13	23	29	39	50	72	51
ENSMUSG00000074749	chr2	Kiz	1.47E+08	1.47E+08	2278	-0.73086	4.021502	3.26E-05	0.00017	0.033506	-1	315	302	345	385	325	236	251	347	311	269
ENSMUSG00000026235	chr1	Epha4	77367185	77369671	8054	-1.10194	1.934823	3.27E-05	0.000171	0.067852	-1	72	54	92	72	150	39	68	63	68	43
ENSMUSG00000038374	chr3	Rbm8a	96629928	96630028	2604	0.700998	5.203157	3.27E-05	0.000171	0.032382	1	322	445	595	432	565	957	1038	1004	1152	1116
ENSMUSG00000098269	chr17	Mir8094	35251289	35251405	117	0.831438	3.77353	3.28E-05	0.000171	0.043375	1	130	135	140	186	229	385	414	270	469	474
ENSMUSG00000049164	chr19	Zfp518a	40894705	40894790	6840	-1.03893	2.690152	3.29E-05	0.000171	0.065379	-1	123	138	137	136	186	43	98	152	122	84
ENSMUSG00000027827	chr3	Kcnab1	65109384	65109992	8593	-1.23373	1.20431	3.29E-05	0.000171	0.078196	-1	66	28	60	56	53	22	26	41	36	32
ENSMUSG00000042390	chr3	Gatad2b	90341654	90341994	1906	-1.50116	2.900392	3.29E-05	0.000171	0.141826	-1	167	112	186	179	291	36	81	212	76	50
ENSMUSG00000045094	chr18	Arhgef37	61493794	61495049	3234	-1.24655	1.756158	3.29E-05	0.000171	0.088836	-1	58	54	107	60	122	20	39	74	51	49
ENSMUSG00000020570	chr12	Sypl	32953891	32954018	7535	-0.6921	7.140923	3.3E-05	0.000171	0.032632	-1	2221	2712	3479	3019	3172	2123	2601	2801	2736	2267
ENSMUSG00000022144	chr15	Gdnf	7811011	7811114	3509	1.646059	0.072463	3.3E-05	0.000171	0.109309	1	7	5	5	8	12	14	41	50	39	21
ENSMUSG00000037112	chr9	Sik2	50892801	50893389	9539	-1.22819	3.755687	3.3E-05	0.000172	0.098004	-1	275	231	360	353	369	57	110	197	266	348
ENSMUSG00000030142	chr6	Clec4e	1.23E+08	1.23E+08	4965	3.654664	1.36505	3.31E-05	0.000172	0.681691	1	2	3	1	14	9	15	20	5	243	273
ENSMUSG00000006576	chr1	Slc4a3	75546266	75546382	8599	0.910168	3.355376	3.31E-05	0.000172	0.051239	1	90	88	169	90	161	231	430	310	353	220
ENSMUSG00000037070	chr8	Rbmxl1	78505271	78506863	1723	0.79471	2.945081	3.31E-05	0.000172	0.036046	1	78	79	98	78	134	171	237	216	283	222
ENSMUSG00000040181	chr1	Fmo1	1.63E+08	1.63E+08	6304	0.780794	4.46078	3.34E-05	0.000173	0.03935	1	210	252	276	284	327	352	608	558	940	862
ENSMUSG00000024985	chr19	Tcf7l2	55741810	55742530	8739	0.8287	2.913858	3.34E-05	0.000173	0.039609	1	74	76	85	87	127	154	209	201	276	278
ENSMUSG00000035776	chrX	Cd99l2	71420060	71422749	4902	-0.65404	6.642506	3.34E-05	0.000173	0.029023	-1	1802	1792	2333	1922	2371	1584	1797	1806	2076	1756
ENSMUSG00000022305	chr15	Lrp12	39870603	39872878	4574	0.997758	3.077391	3.36E-05	0.000174	0.061167	1	91	60	88	83	147	140	300	183	393	314
ENSMUSG00000090093	chr2	Gm14399	1.75E+08	1.75E+08	2561	-1.38129	0.46903	3.37E-05	0.000175	0.085414	-1	26	31	27	43	32	11	21	20	10	23
ENSMUSG00000017291	chr11	Taok1	77529162	77538328	12421	-0.67562	5.848556	3.37E-05	0.000175	0.030654	-1	1069	941	1327	1205	1397	768	1168	1167	1202	888
ENSMUSG00000030513	chr7	Pcsk6	65861734	65861766	5144	-0.91885	5.014374	3.38E-05	0.000175	0.056242	-1	700	358	588	724	1235	413	596	423	694	501
ENSMUSG00000039294	chr11	BC017643	1.21E+08	1.21E+08	4213	0.873142	3.521502	3.39E-05	0.000175	0.04738	1	139	103	156	100	175	269	369	213	451	428
ENSMUSG00000097328	chr11	Tnfsf12	69686250	69687091	1515	0.780451	4.409997	3.41E-05	0.000177	0.039416	1	236	183	282	279	330	456	532	452	938	798
ENSMUSG00000075585	chr5	6330403L08Rik	1.39E+08	1.39E+08	5522	-0.72359	4.192174	3.43E-05	0.000177	0.033328	-1	303	362	436	403	388	254	278	408	334	324
ENSMUSG00000032763	chr10	Ilvbl	78574500	78574665	2325	0.701153	3.693696	3.44E-05	0.000178	0.029647	1	156	138	207	150	163	287	354	347	465	410
ENSMUSG00000025255	chr3	Zfhx4	5218526	5218927	15737	-1.29436	4.04987	3.45E-05	0.000178	0.110021	-1	524	157	365	264	683	101	317	304	242	172
ENSMUSG00000022822	chr16	Abcc5	20331303	20332705	10592	-0.66069	5.631565	3.46E-05	0.000179	0.029244	-1	953	829	1242	917	1140	654	955	755	1138	1022
ENSMUSG00000026623	chr1	Lpgat1	1.92E+08	1.92E+08	7610	-0.66068	5.167717	3.47E-05	0.000179	0.02885	-1	613	640	824	794	806	510	773	552	813	616
ENSMUSG00000024121	chr17	Atp6v0c	24163866	24164608	3384	0.701279	6.212738	3.47E-05	0.000179	0.033336	1	777	812	1066	872	1224	1552	1824	1907	2908	2657
ENSMUSG00000018752	chr11	Tnfsf12Tnfsf13	69682577	69683344	2235	0.757145	4.059456	3.49E-05	0.00018	0.036336	1	184	148	220	227	256	322	415	404	723	615
ENSMUSG00000031337	chrX	Mtm1	71210767	71210952	13935	-0.82685	3.585676	3.51E-05	0.000181	0.042924	-1	200	213	327	260	287	121	175	291	262	171
ENSMUSG00000028378	chr4	Ptgr1	58965439	58966763	2296	1.005133	3.151127	3.55E-05	0.000183	0.062604	1	76	85	108	92	129	221	287	129	431	318
ENSMUSG00000094595	chr4	Fsbp	11579665	11580107	4358	-1.1957	1.085791	3.58E-05	0.000184	0.072322	-1	53	37	65	44	40	21	38	21	41	27
ENSMUSG00000024143	chr17	Rhoq	86963082	86963747	4151	-0.64271	7.918346	3.6E-05	0.000185	0.028568	-1	4366	4271	5394	5055	5548	3540	4688	4381	5338	4152
ENSMUSG00000028396	chr4	2310002L09Rik	73939371	73939598	2158	-0.83276	5.756833	3.6E-05	0.000185	0.047055	-1	1330	961	1223	1144	1032	718	920	1230	935	708
ENSMUSG00000047141	chr16	Zfp654	64780351	64783276	4741	-1.15865	3.597448	3.59E-05	0.000185	0.087098	-1	270	209	335	248	338	95	141	357	137	139
ENSMUSG00000026883	chr2	Dab2ip	35558266	35558612	8366	-0.74361	6.274161	3.61E-05	0.000186	0.037741	-1	1088	1390	1855	1909	1934	1060	1144	1714	1525	1304
ENSMUSG00000086859	chr11	2810008D09Rik	1.17E+08	1.17E+08	2166	1.092834	1.531698	3.61E-05	0.000186	0.059622	1	27	24	35	29	32	52	86	100	87	116
ENSMUSG00000074896	chr19	Ifit3	34583531	34583604	1745	1.983664	3.959803	3.65E-05	0.000188	0.250076	1	77	72	133	122	125	1244	282	146	231	666
ENSMUSG00000058600	chr15	Rpl30	34440505	34440604	3020	0.674004	7.450608	3.66E-05	0.000188	0.031372	1	1947	2087	2672	1948	2621	4427	5088	4645	5465	5305
ENSMUSG00000025967	chr1	Eef1b2	63176825	63177291	2532	0.685514	7.802204	3.68E-05	0.000189	0.03254	1	2432	2739	3333	2393	3422	5481	7063	5973	6779	6636
ENSMUSG00000051212	chr14	Gpr183	1.22E+08	1.22E+08	2942	1.637922	0.756779	3.68E-05	0.000189	0.134019	1	12	12	6	14	18	28	38	31	91	94
ENSMUSG00000079435	chrX	Rpl36a	1.35E+08	1.35E+08	1655	0.673485	6.310559	3.69E-05	0.00019	0.030971	1	852	960	1128	980	1186	1974	2476	1969	2454	2438
ENSMUSG00000003184	chr7	Irf3	44997648	44997908	3187	0.669312	4.269559	3.69E-05	0.00019	0.028402	1	204	223	261	242	311	408	566	442	714	645
ENSMUSG00000019820	chr10	Utrn	12382188	12384196	12382	-0.80271	5.273294	3.69E-05	0.00019	0.043531	-1	745	490	913	970	1036	340	800	695	847	677
ENSMUSG00000021820	chr14	Camk2g	20734875	20736852	3703	-0.73988	7.236231	3.7E-05	0.00019	0.037793	-1	2934	2600	3785	3107	3324	2166	2643	3384	2826	2089

ENSMUSG00000022987	chr15	Zfp641	98285588	98289220	4254	-0.82313	4.336402	3.7E-05	0.00019	0.044416	-1	399	303	478	343	664	273	328	463	347	277
ENSMUSG00000020522	chr11	Mfap3	57518664	57518712	5801	-0.66856	4.086971	3.71E-05	0.00019	0.028294	-1	315	260	407	350	417	204	305	308	438	298
ENSMUSG00000020978	chr12	Klhdc2	69296681	69297147	5438	-0.75093	6.861011	3.71E-05	0.00019	0.038827	-1	2089	2289	3174	2237	2365	1786	1949	2432	1976	1848
ENSMUSG00000035268	chr2	Pkig	1.64E+08	1.64E+08	3990	0.713135	5.746136	3.72E-05	0.000191	0.034468	1	504	624	773	764	733	1329	1919	1254	1755	1487
ENSMUSG00000020029	chr10	Nudt4	95547007	95549490	3231	-0.6734	7.994746	3.73E-05	0.000191	0.03149	-1	5335	4044	5638	5097	6057	3938	4809	4169	5138	4808
ENSMUSG00000021957	chr14	Tkt	30548359	30548614	6533	2.673658	6.450221	3.78E-05	0.000193	0.436803	1	228	153	236	722	707	668	982	488	6429	10284
ENSMUSG00000025395	chr10	Prim1	1.28E+08	1.28E+08	3868	1.388532	1.031621	3.8E-05	0.000195	0.096073	1	19	20	15	16	16	37	51	42	108	93
ENSMUSG00000047675	chr4	Rps8	1.17E+08	1.17E+08	1726	0.68667	8.177323	3.81E-05	0.000195	0.032837	1	2910	3459	4483	3108	4723	7296	8537	7327	9374	8954
ENSMUSG00000019971	chr10	Cep290	1E+08	1E+08	8006	-1.19793	1.278024	3.83E-05	0.000196	0.076849	-1	67	40	58	51	58	16	27	47	46	35
ENSMUSG00000024909	chr19	Efemp2	5473973	5474323	2648	1.053536	4.269139	3.86E-05	0.000198	0.074013	1	186	126	233	154	370	478	676	280	874	751
ENSMUSG00000063236	chr15	1110038F14Rik	76948539	76948544	1010	0.690788	3.91554	3.87E-05	0.000198	0.029762	1	163	183	204	190	214	394	474	363	470	440
ENSMUSG00000028116	chr3	Myoz2	1.23E+08	1.23E+08	3399	1.469592	6.251597	3.88E-05	0.000198	0.145204	1	301	772	353	1440	428	1686	2524	3617	3348	2030
ENSMUSG00000037628	chr14	Cdkn3	46760541	46760648	773	1.604431	-0.19541	3.9E-05	0.000199	0.087873	1	4	4	6	5	12	25	26	16	41	24
ENSMUSG00000031902	chr8	Nfatc3	1.06E+08	1.06E+08	6014	-0.6629	5.302096	3.93E-05	0.000201	0.029601	-1	737	598	880	819	1032	500	747	829	829	677
ENSMUSG00000035473	chr17	Galm	80127471	80127905	2476	1.049737	2.047871	3.97E-05	0.000202	0.061994	1	26	39	52	47	56	83	105	98	198	160
ENSMUSG00000039585	chr9	Myo9a	59750896	59751345	13034	-0.74183	4.271823	3.97E-05	0.000202	0.035969	-1	349	268	446	408	576	220	375	421	377	301
ENSMUSG00000028820	chr4	Sfpq	1.27E+08	1.27E+08	4743	0.652408	5.957951	3.97E-05	0.000203	0.02911	1	655	710	879	741	1080	1431	1771	1583	2255	1856
ENSMUSG00000101493	chr4	2810405F17Rik	1.37E+08	1.37E+08	1117	1.716422	-0.16974	3.98E-05	0.000203	0.10701	1	7	7	6	3	6	15	28	46	23	24
ENSMUSG00000042286	chr14	Stab1	31139013	31139203	10288	1.055633	6.160567	4E-05	0.000204	0.076614	1	677	380	938	721	1282	1568	2145	1193	3892	2793
ENSMUSG00000030446	chr13	Zfp273	67813740	67813896	3799	-1.37223	0.715028	4.02E-05	0.000205	0.094212	-1	50	21	57	28	35	13	27	19	27	18
ENSMUSG00000009291	chr10	Pttg1ip	77581720	77581927	3426	0.700751	5.662084	4.03E-05	0.000205	0.033526	1	613	446	642	616	935	972	1520	1641	1809	1442
ENSMUSG00000028081	chr3	Rps3a1	86137940	86138110	977	0.668393	8.513775	4.04E-05	0.000205	0.031358	1	4040	4295	5224	4233	5873	9054	10555	8953	11659	11942
ENSMUSG00000021256	chr12	Vash1	86678700	86680326	2599	-1.14021	2.510612	4.05E-05	0.000206	0.081226	-1	73	118	143	168	154	39	120	59	139	69
ENSMUSG00000049881	chr1	2810025M15Rik	1.57E+08	1.57E+08	1410	0.922179	2.964105	4.06E-05	0.000207	0.051713	1	56	93	90	121	80	178	274	202	262	259
ENSMUSG00000034075	chr2	Zdhhc5	84687970	84689444	5047	-0.64879	6.250766	4.08E-05	0.000207	0.029058	-1	1347	1307	1788	1620	1716	1141	1478	1248	1785	1295
ENSMUSG00000046027	chr7	Stard5	83631959	83632139	5450	0.868551	2.680308	4.11E-05	0.000209	0.043461	1	59	83	63	73	91	148	173	190	234	206
ENSMUSG00000027751	chr3	Supt20	54693105	54693208	1968	-0.92569	2.534532	4.12E-05	0.000209	0.051468	-1	120	107	124	135	140	47	121	86	132	87
ENSMUSG00000015095	chr2	Fbxw5	25500750	25500886	3052	-0.65798	6.123321	4.13E-05	0.00021	0.029881	-1	1246	1245	1553	1517	1555	998	1121	1408	1575	1230
ENSMUSG00000038831	chr2	Ralgps1	33133417	33137709	7657	-0.96659	1.848404	4.13E-05	0.00021	0.050634	-1	59	80	80	84	88	35	55	66	72	55
ENSMUSG00000067203	chr17	H2-K2	33974831	33974877	1049	1.373412	0.861046	4.16E-05	0.000211	0.092192	1	16	9	22	17	14	25	55	63	58	86
ENSMUSG00000026944	chr2	Abca2	25428703	25428835	8346	-0.76941	4.700654	4.17E-05	0.000211	0.039829	-1	476	434	643	533	667	267	381	656	520	440
ENSMUSG00000031971	chr8	Ccsap	1.24E+08	1.24E+08	2767	1.512842	-0.20456	4.17E-05	0.000211	0.070526	1	5	5	9	6	7	21	25	29	36	18
ENSMUSG00000026705	chr1	Klhl20	1.61E+08	1.61E+08	12847	-0.697	3.901418	4.2E-05	0.000213	0.031033	-1	243	285	354	312	348	163	325	294	309	249
ENSMUSG00000009112	chr6	Bcl2l13	1.21E+08	1.21E+08	6933	-0.64647	6.247527	4.23E-05	0.000214	0.028966	-1	1354	1320	1774	1608	1691	1089	1334	1526	1636	1337
ENSMUSG00000042694	chr19	Obfc1	47501033	47501717	4045	0.887702	3.08641	4.25E-05	0.000216	0.048663	1	101	73	101	86	131	204	330	173	339	231
ENSMUSG00000002984	chr7	Tomm40	19701313	19701857	4239	0.666424	5.026793	4.28E-05	0.000217	0.029838	1	312	385	455	468	485	724	853	810	1312	1006
ENSMUSG00000035620	chr10	Ric8b	84917616	84917825	3068	-0.67366	5.007698	4.28E-05	0.000217	0.030569	-1	594	562	714	768	643	520	552	557	645	596
ENSMUSG00000042043	chr13	Tbca	94788943	94789002	503	0.723515	4.512004	4.29E-05	0.000217	0.034634	1	240	288	379	251	266	574	731	561	728	690
ENSMUSG00000043895	chr9	S1pr2	20965952	20968570	2815	0.857238	3.432702	4.33E-05	0.000219	0.046831	1	118	81	115	117	214	244	332	243	430	373
ENSMUSG00000014039	chr16	Prdm15	97791467	97794656	10547	-0.88398	2.776321	4.33E-05	0.000219	0.04724	-1	168	101	154	139	173	81	105	138	121	113
ENSMUSG00000059970	chr12	Hspa2	76404176	76404289	2520	0.90365	2.93503	4.33E-05	0.000219	0.049994	1	56	92	78	114	96	197	218	255	283	189
ENSMUSG00000032271	chr9	Nnmt	48591877	48592182	1576	1.364627	3.437804	4.34E-05	0.000219	0.122788	1	90	68	85	87	179	249	298	123	449	705
ENSMUSG00000027684	chr3	Mecom	29951296	29952850	12427	-1.02329	2.265071	4.37E-05	0.000221	0.06198	-1	80	75	113	144	125	46	64	106	76	75
ENSMUSG00000030084	chr6	Plxna1	89316316	89319471	9025	-0.80542	5.86151	4.37E-05	0.000221	0.045089	-1	823	909	1435	1273	1893	675	1066	685	1460	1153
ENSMUSG00000076270	chr14	Mir719	60228806	60228915	110	-1.04301	1.273753	4.41E-05	0.000223	0.053611	-1	44	45	59	51	68	19	42	38	44	39
ENSMUSG00000046152	chr8	Fut10	31187331	31187462	5007	-0.7026	3.663262	4.45E-05	0.000224	0.030866	-1	219	212	318	237	331	198	209	254	233	217
ENSMUSG00000042834	chr18	Nrep	33437019	33438839	2513	-1.19479	8.385915	4.46E-05	0.000225	0.099427	-1	7241	7544	8425	7146	8261	5136	7238	1542	5960	3614
ENSMUSG00000019932	chr10	Kera	97607205	97607377	1950	-2.14829	5.964955	4.47E-05	0.000225	0.300725	-1	2700	434	2231	547	2750	277	1256	572	488	113
ENSMUSG00000079055	chr12	Slc8a3	81197915	81199867	5332	-0.7481	5.435181	4.47E-05	0.000225	0.038637	-1	838	753	1070	939	917	548	659	1071	834	657
ENSMUSG00000036202	chr2	Rif1	52072837	52072866	10527	-1.06056	3.365223	4.48E-05	0.000226	0.07401	-1	184	164	324	210	298	61	150	266	177	137
ENSMUSG00000074141	chr7	Il4i1	44816370	44816483	4097	-1.19378	2.354755	4.49E-05	0.000226	0.088192	-1	60	95	189	114	146	66	87	34	110	65
ENSMUSG00000036223	chr18	Ska1	74195299	74197051	2669	1.96199	-0.20538	4.49E-05	0.000226	0.160629	1	3	4	5	4	9	25	22	6	53	33
ENSMUSG00000078238	chr4	Gm12854	1.16E+08	1.16E+08	297	1.468973	0.100308	4.51E-05	0.000227	0.082866	1	4	7	11	8	12	21	33	20	44	46
ENSMUSG00000017404	chr11	Rpl19	98026710	98026762	1022	0.639191	7.936193	4.52E-05	0.000227	0.028989	1	2538	2908	3833	2991	3822	5491	6855	6940	8150	7445
ENSMUSG00000070639	chr5	Lrrc8b	1.05E+08	1.05E+08	2841	-1.40514	0.356152	4.52E-05	0.000227	0.094546	-1	28	14	32	34	42	7	10	24	23	15
ENSMUSG00000043531	chr19	Sorcs1	50143301	50144147	8317	-1.37015	-0.15527	4.52E-05	0.000227	0.06286	-1	17	20	18	21	24	9	10	11	15	9
ENSMUSG00000068270	chrX	Shroom4	6399854	6400261	8880	-0.77859	3.193227	4.53E-05	0.000228	0.037595	-1	181	161	210	228	172	117	147	146	199	178
ENSMUSG00000049265	chr5	Kcnk3	30588170	30588599	3810	3.048178	2.276817	4.54E-05	0.000228	0.538285	1	10	12	13	31	17	10	31	39	412	555
ENSMUSG00000057375	chr4	Yipf1	1.07E+08	1.07E+08	6783	0.730759	3.454103	4.55E-05	0.000228	0.033019	1	121	108	157	117	184	230	292	279	403	390
ENSMUSG00000018974	chr5	Sart3	1.14E+08	1.14E+08	3586	0.70844	3.63149	4.58E-05	0.00023	0.031476	1	139	111	179	144	215	233	382	350	491	351
ENSMUSG00000042810	chr6	Krba1	48395586	48395887	9314	-0.73113	4.478772	4.58E-05	0.00023	0.035871	-1	469	445	501	393	489	279	394	503	391	383
ENSMUSG00000022037	chr14	Clu	65968483	65968688	3438	0.795522	7.003789	4.58E-05	0.00023	0.044659	1	1369	1290	1979	1393	1857	3099	3916	2267	5772	4215
ENSMUSG00000015880	chr5	Ncapg	45669922	45670133	7061	1.665536	1.3031	4.59E-05	0.00023	0.161591	1	12	13	14	9	48	61	74	41	170	79
ENSMUSG00000021579	chr13	Lrrc14b	74359578	74361399	2755	-0.85518	6.655571	4.59E-05	0.00023	0.051469	-1	1902	1974	2585	2399	1908	1424	1536	2450	1497	1349
ENSMUSG00000015652	chr5	Steap1	5736317	5736673	1377	2.446986	-0.31965	4.6E-05	0.00023	0.281494	1	1	0	3	6	7	6	24	8	65	35
ENSMUSG00000032777	chr7	Gtf3c1	1.26E+08	1.26E+08	6960	-0.63155	5.632366	4.6E-05	0.00023	0.027567	-1	835	814	1121	1025	1280	617	996	889	1235	869

ENSMUSG00000033114	chr13	Slc35d2	64096310	64097684	2276	1.390084	0.521465	4.61E-05	0.000231	0.085082	1	11	8	20	11	10	23	34	45	58	64
ENSMUSG00000036093	chr2	Arl5a	52397951	52402432	5409	-0.64639	5.422011	4.63E-05	0.000231	0.028728	-1	725	702	1035	874	1067	565	903	853	834	749
ENSMUSG00000040687	chr2	Madd	91137360	91138401	9086	0.775707	3.504468	4.63E-05	0.000232	0.037857	1	110	119	122	168	174	214	322	285	478	388
ENSMUSG00000033382	chr18	Trappc8	20817224	20818311	5482	-0.77397	5.034352	4.63E-05	0.000232	0.041221	-1	608	576	763	737	769	347	551	841	620	480
ENSMUSG00000089726	chr14	Mir17hg	1.15E+08	1.15E+08	3536	1.917227	-0.33458	4.66E-05	0.000233	0.150129	1	3	5	4	1	10	10	23	14	33	45
ENSMUSG00000028907	chr4	Utp11l	1.25E+08	1.25E+08	4711	0.750038	4.40463	4.7E-05	0.000235	0.037543	1	204	286	305	262	244	471	624	779	629	569
ENSMUSG00000078193	chr1	Gm2000	1.56E+08	1.56E+08	445	0.69145	3.502255	4.72E-05	0.000236	0.029413	1	122	114	149	154	181	285	315	302	379	330
ENSMUSG00000000486	chr7	Sept1	1.27E+08	1.27E+08	2060	1.443834	0.77931	4.76E-05	0.000238	0.106041	1	5	19	10	15	22	41	37	48	64	81
ENSMUSG00000041193	chr4	Pla2g5	1.39E+08	1.39E+08	2884	-1.77436	-0.03444	4.76E-05	0.000238	0.145504	-1	38	10	23	13	35	13	7	7	8	12
ENSMUSG00000044229	chr9	Nxpe4	48362041	48362175	3173	-0.9143	2.539232	4.8E-05	0.000239	0.050653	-1	100	97	136	179	116	64	96	94	123	94
ENSMUSG00000002257	chr17	Def6	28207778	28207938	2524	1.16405	1.88542	4.82E-05	0.00024	0.07941	1	35	21	45	31	54	76	124	64	170	152
ENSMUSG00000017299	chr2	Dnttip1	1.65E+08	1.65E+08	2122	0.709905	4.186724	4.82E-05	0.00024	0.033269	1	190	188	259	219	301	431	455	679	572	472
ENSMUSG00000079304	chr6	4933413G19Rik	1.28E+08	1.28E+08	1875	1.730278	-0.44525	4.83E-05	0.000241	0.11237	1	0	2	7	4	11	17	24	15	28	26
ENSMUSG00000030353	chr6	Tead4	1.28E+08	1.28E+08	3596	1.048013	2.980683	4.84E-05	0.000241	0.070706	1	42	66	89	108	127	166	382	204	285	194
ENSMUSG00000032030	chr9	Cul5	53614582	53618010	8165	-0.69877	6.187649	4.85E-05	0.000241	0.034395	-1	1389	1321	1779	1428	1600	1123	1306	1528	1312	1152
ENSMUSG00000089832	chr7	Shkbp1	27342133	27342544	4230	1.136178	2.627844	4.86E-05	0.000242	0.0813	1	41	60	55	90	69	150	188	96	278	271
ENSMUSG00000061119	chr7	Prcp	92875253	92875500	2956	0.700382	4.181374	4.87E-05	0.000242	0.032216	1	172	219	251	257	248	428	584	398	702	510
ENSMUSG00000055723	chr7	Rras2	1.14E+08	1.14E+08	2272	0.702106	4.471465	4.88E-05	0.000243	0.03306	1	221	254	367	212	365	510	732	542	811	612
ENSMUSG00000031239	chrX	Itm2a	1.07E+08	1.07E+08	1744	-0.68653	8.6119	4.89E-05	0.000243	0.033818	-1	7063	6326	8944	6837	11701	5886	7093	7603	8083	6247
ENSMUSG00000022295	chr15	Atp6v1c1	38661904	38662083	2097	0.741512	5.072271	4.89E-05	0.000243	0.037814	1	356	397	449	468	413	624	765	986	1360	1255
ENSMUSG00000027806	chr3	Tsc22d2	58415689	58417613	8829	-0.74126	4.73305	4.9E-05	0.000244	0.037579	-1	454	470	617	574	676	319	495	647	508	357
ENSMUSG00000087221	chr15	BC037032	4020114	4024492	7125	-1.25869	0.71003	4.9E-05	0.000244	0.078617	-1	27	38	38	47	35	15	23	24	36	12
ENSMUSG00000038608	chr1	Dock10	80501073	80501826	18267	1.008589	3.290165	4.93E-05	0.000245	0.066701	1	106	49	109	110	172	161	309	237	443	397
ENSMUSG00000023971	chr17	Rrp36	46667458	46668086	1195	0.70232	3.627694	4.93E-05	0.000245	0.031142	1	115	150	188	145	184	322	377	312	408	341
ENSMUSG00000102340	chr9	RP24-496O17.2	21275069	21277764	2696	-1.30727	0.272937	4.99E-05	0.000248	0.073259	-1	21	27	25	34	29	6	20	14	20	18
ENSMUSG00000042079	chr6	Hnrnpf	1.18E+08	1.18E+08	3047	0.672248	5.349888	4.99E-05	0.000248	0.031315	1	400	480	523	498	743	802	1122	1367	1444	1154
ENSMUSG00000074417	chr7	Gm14548	3884242	3884427	2128	1.803893	-0.47633	5E-05	0.000248	0.115331	1	1	2	9	5	5	10	26	13	34	27
ENSMUSG00000039304	chr3	Tnfsf10	27317028	27317290	5266	-1.04228	2.997206	5.02E-05	0.000249	0.070425	-1	107	223	230	186	138	111	86	140	124	138
ENSMUSG00000032355	chr9	Mlip	77102081	77102393	8916	-0.66949	6.523179	5.02E-05	0.000249	0.031823	-1	1676	1777	2086	1789	2071	1529	1588	1577	1745	1761
ENSMUSG00000030811	chr7	Fbxl19	1.28E+08	1.28E+08	4293	0.987786	2.164891	5.04E-05	0.000249	0.056184	1	42	36	55	46	67	77	139	109	221	149
ENSMUSG00000027665	chr3	Pik3ca	32397671	32397800	9088	-0.68677	5.899644	5.04E-05	0.00025	0.03321	-1	976	984	1388	1247	1626	820	1099	1322	1130	954
ENSMUSG00000075706	chr10	Gpx4	80047166	80047375	1724	0.688108	7.786623	5.05E-05	0.00025	0.033985	1	2358	2761	3347	2683	2933	5680	5656	6925	6734	6511
ENSMUSG00000019906	chr10	Lin7a	1.07E+08	1.07E+08	5952	-1.09868	1.730605	5.08E-05	0.000252	0.068554	-1	69	64	71	92	73	44	49	67	43	36
ENSMUSG00000030760	chr7	Acer3	98213658	98216890	4319	0.892347	2.534397	5.12E-05	0.000253	0.047097	1	68	52	76	53	83	104	169	160	227	214
ENSMUSG00000030815	chr7	Phkg2	1.28E+08	1.28E+08	3998	0.727445	3.33685	5.12E-05	0.000253	0.032529	1	114	101	147	122	146	199	278	351	364	274
ENSMUSG00000039001	chr2	Rps21	1.8E+08	1.8E+08	810	0.772182	6.888374	5.13E-05	0.000254	0.042597	1	1313	1501	1841	1028	1596	3339	3724	3127	3474	3514
ENSMUSG00000035860	chr12	Cdhr3	33033796	33034148	2953	2.868196	0.132225	5.17E-05	0.000256	0.431885	1	2	3	2	5	7	19	3	123	23	25
ENSMUSG00000052214	chr7	Opa3	19228334	19228584	4554	-0.70382	6.718434	5.19E-05	0.000256	0.035406	-1	1690	2227	2595	2194	2148	1731	1878	1573	2213	1902
ENSMUSG00000020133	chr10	2310011J03Rik	80318254	80319547	1649	0.715255	3.78754	5.25E-05	0.000259	0.033119	1	141	155	195	152	229	286	377	315	536	498
ENSMUSG00000042680	chr18	Garem	21127201	21130022	4923	-1.24839	2.328106	5.25E-05	0.000259	0.098943	-1	115	75	112	120	169	37	64	132	73	40
ENSMUSG00000039414	chr17	Heatr5b	78752906	78753336	6437	-0.78012	3.419629	5.25E-05	0.000259	0.039251	-1	230	144	219	240	298	120	206	170	259	175
ENSMUSG00000031931	chr9	Ankrd49	14780209	14781611	1753	-0.80317	2.714548	5.26E-05	0.00026	0.038837	-1	123	130	166	128	142	78	119	106	154	103
ENSMUSG00000031392	chrX	Irak1	74013914	74015501	4716	-0.63632	5.922337	5.28E-05	0.00026	0.028616	-1	1091	1026	1353	1195	1524	823	1100	1257	1248	1124
ENSMUSG00000027130	chr2	Slc12a6	1.12E+08	1.12E+08	10165	-0.79994	5.021409	5.29E-05	0.000261	0.044812	-1	691	499	716	759	775	299	525	802	615	556
ENSMUSG00000045411	chr7	2410002F23Rik	44246722	44246823	5233	0.802849	3.210719	5.29E-05	0.000261	0.040615	1	102	72	125	97	169	181	291	237	351	314
ENSMUSG00000036672	chr8	Cenpt	1.06E+08	1.06E+08	1767	1.164424	1.91842	5.32E-05	0.000262	0.079758	1	34	29	33	35	58	84	128	60	191	138
ENSMUSG00000044197	chr5	Gpr146	1.39E+08	1.39E+08	6786	-0.69111	5.680395	5.33E-05	0.000262	0.033735	-1	918	990	1435	937	995	798	864	820	1204	898
ENSMUSG00000025816	chr2	Sec61a2	5870987	5872021	4572	-0.66996	5.1966	5.38E-05	0.000265	0.031257	-1	718	653	908	654	819	590	730	636	732	589
ENSMUSG00000028291	chr4	Akirin2	34550937	34551273	1711	0.722772	4.870829	5.4E-05	0.000266	0.036165	1	310	326	420	323	469	711	776	1118	829	761
ENSMUSG00000046785	chr9	Epm2aip1	1.11E+08	1.11E+08	7169	-0.99155	5.809023	5.4E-05	0.000266	0.069895	-1	1171	948	1426	1155	1572	499	825	1620	819	625
ENSMUSG00000090112	chr10	Shprh	11149427	11149586	14066	-0.76962	3.584069	5.41E-05	0.000266	0.038601	-1	251	175	277	245	316	138	212	266	195	219
ENSMUSG00000079323	chr9	Gm20661	1.08E+08	1.08E+08	2160	1.653681	0.647381	5.44E-05	0.000267	0.14616	1	11	5	12	14	16	44	62	17	42	86
ENSMUSG00000030788	chr7	Rnf141	1.11E+08	1.11E+08	5861	-0.65227	4.387193	5.48E-05	0.000269	0.028723	-1	407	364	451	427	476	246	390	353	473	457
ENSMUSG00000033436	chrX	Armcx2	1.35E+08	1.35E+08	4532	1.027635	4.10326	5.49E-05	0.00027	0.073027	1	156	115	204	158	331	349	868	302	701	496
ENSMUSG00000043251	chr8	Exoc3l	1.05E+08	1.05E+08	2497	1.405786	2.122116	5.5E-05	0.00027	0.123427	1	34	46	40	40	28	71	280	85	195	100
ENSMUSG00000058064	chr18	Gm10036	15832794	15833330	537	0.733456	3.574983	5.5E-05	0.00027	0.034011	1	147	154	156	130	143	278	357	295	418	375
ENSMUSG00000031976	chr8	Urb2	1.24E+08	1.24E+08	6153	-0.73867	3.526278	5.51E-05	0.00027	0.035122	-1	199	161	283	237	339	130	210	233	256	186
ENSMUSG00000020661	chr12	Dnmt3a	3806007	3806232	16642	-0.7336	6.751238	5.51E-05	0.00027	0.03876	-1	1601	1616	2686	2452	3116	1528	2166	1372	2379	2046
ENSMUSG00000030787	chr7	Lyve1	1.11E+08	1.11E+08	2607	-1.11759	3.498034	5.52E-05	0.000271	0.084543	-1	209	127	313	172	522	116	113	231	207	167
ENSMUSG00000092812	chr4	Gm23634	1.34E+08	1.34E+08	91	1.489548	0.159204	5.54E-05	0.000271	0.094592	1	8	5	7	11	12	16	34	23	61	41
ENSMUSG00000075707	chr12	Dio3	1.1E+08	1.1E+08	2030	2.157571	-0.2015	5.55E-05	0.000272	0.218682	1	5	3	6	2	6	12	22	6	44	60
ENSMUSG00000020441	chr11	2310033P09Rik	59208321	59208673	1285	0.99444	2.053868	5.59E-05	0.000274	0.057274	1	42	34	53	37	60	87	147	88	193	122
ENSMUSG00000008683	chr7	Rps15a	1.18E+08	1.18E+08	6262	0.65599	7.450574	5.6E-05	0.000274	0.031208	1	1878	2057	2747	2027	2687	4343	5317	4478	5413	5278
ENSMUSG00000024429	chr17	Gnl1	35979851	35980247	3077	0.618891	4.853663	5.63E-05	0.000276	0.026216	1	315	314	448	386	446	610	780	764	1035	916
ENSMUSG00000030137	chr6	Tuba8	1.21E+08	1.21E+08	2225	-0.87985	7.734746	5.64E-05	0.000276	0.056046	-1	3602	3986	5461	4267	5994	3769	3790	1771	4283	3686
ENSMUSG00000044712	chr12	Slc38a6	73286779	73287032	7783	1.13245	2.268676	5.65E-05	0.000276	0.080241	1	48	31	58	27	86	92	191	110	180	188

ENSMUSG00000048416	chr3	Mlf1	67374097	67374262	1719	-0.85271	7.844923	5.65E-05	0.000276	0.052722	-1	4244	5423	5368	5030	4278	3431	3192	5255	3304	3608
ENSMUSG00000007646	chr11	Rad51c	87376645	87379487	4384	1.616837	-0.09928	5.71E-05	0.000279	0.101019	1	8	4	7	3	11	28	34	14	40	26
ENSMUSG00000025766	chr3	D3Ertd751e	41742611	41742689	5813	-0.99436	1.832708	5.74E-05	0.00028	0.056445	-1	58	70	93	75	97	42	57	34	83	61
ENSMUSG00000045665	chr15	Mfsd5	1.02E+08	1.02E+08	1742	0.69295	4.463287	5.75E-05	0.000281	0.032722	1	249	235	304	272	346	515	558	472	901	751
ENSMUSG00000005103	chr5	Wdr1	38526814	38527912	2948	0.746277	6.732685	5.75E-05	0.000281	0.040291	1	887	1276	1461	1389	1672	2423	3638	2112	4191	3337
ENSMUSG00000082292	chr11	Gm12250	58187739	58189012	1274	2.639256	0.411847	5.77E-05	0.000282	0.388014	1	2	0	4	7	16	70	22	8	41	89
ENSMUSG00000035042	chr11	Ccl5	83525778	83526064	960	2.262044	0.536091	5.78E-05	0.000282	0.29313	1	3	1	3	11	21	34	41	12	67	101
ENSMUSG00000064215	chr12	Ifi27	1.03E+08	1.03E+08	1467	1.135069	5.604782	5.78E-05	0.000282	0.091742	1	422	412	545	485	700	929	1161	672	2314	2937
ENSMUSG00000068246	chr15	Apol9b	77729121	77729246	1545	2.362501	-0.4768	5.79E-05	0.000282	0.251639	1	0	5	4	3	4	36	23	5	13	34
ENSMUSG00000034673	chr17	Pbx2	34591266	34591492	3640	0.632621	4.738243	5.81E-05	0.000283	0.02741	1	291	308	396	333	420	614	734	636	917	881
ENSMUSG00000029804	chr6	Herc3	58831465	58831642	7027	-0.65149	5.53154	5.85E-05	0.000285	0.03014	-1	838	747	1066	1027	1051	606	889	1009	957	750
ENSMUSG00000056130	chr18	Ticam2	46559155	46561072	3928	1.453133	0.633068	5.85E-05	0.000285	0.109092	1	12	5	11	12	24	20	64	35	73	57
ENSMUSG00000061544	chr17	Zfp229	21730795	21731051	5139	-1.17875	2.256318	5.87E-05	0.000286	0.089571	-1	113	106	116	86	123	27	57	122	76	62
ENSMUSG00000078870	chr2	Gm14410	1.77E+08	1.77E+08	2398	-1.31223	0.627465	5.88E-05	0.000286	0.084807	-1	27	21	60	25	48	17	14	24	25	19
ENSMUSG00000039763	chr16	Dnajc28	91614257	91617379	3562	-0.83759	4.359876	5.92E-05	0.000288	0.048919	-1	432	443	495	472	308	262	330	457	379	286
ENSMUSG00000062611	chr14	Rps3a2	88123017	88123808	792	0.779661	3.224986	5.93E-05	0.000288	0.038548	1	97	111	142	86	132	239	304	249	272	285
ENSMUSG00000071078	chr8	Nr2c2ap	70131333	70131599	1175	0.827911	2.592435	5.93E-05	0.000288	0.040431	1	54	73	79	63	87	130	166	161	245	190
ENSMUSG00000052316	chr16	Lrrc15	30269302	30274522	5310	2.345256	1.286718	5.94E-05	0.000289	0.334008	1	6	5	12	15	27	43	236	11	68	90
ENSMUSG00000005057	chr5	Sh2b2	1.36E+08	1.36E+08	2848	1.292021	2.821084	5.97E-05	0.00029	0.111969	1	31	35	83	77	124	139	170	139	344	385
ENSMUSG00000025423	chr18	Pias2	77065208	77065419	5433	-0.63362	5.450669	6.01E-05	0.000292	0.028446	-1	749	737	1047	853	1083	667	792	908	849	759
ENSMUSG00000056342	chr11	Usp34	23306895	23307016	18453	-0.67278	5.925451	6.08E-05	0.000295	0.032594	-1	1118	922	1451	1208	1599	824	1029	1351	1227	1040
ENSMUSG00000015968	chr14	Cacna1d	30039949	30042366	9242	1.521909	0.188071	6.11E-05	0.000297	0.105174	1	3	5	11	11	14	12	43	40	50	34
ENSMUSG00000001739	chr5	Cldn15	1.37E+08	1.37E+08	2124	0.984643	2.037337	6.13E-05	0.000298	0.056717	1	36	31	53	42	64	81	112	117	136	175
ENSMUSG00000005628	chr3	Tmod4	95124476	95124578	1717	-0.69549	8.561259	6.16E-05	0.000299	0.035641	-1	6601	7575	9679	6760	8376	6493	6378	6686	6892	6735
ENSMUSG00000015714	chr3	Cers2	95314791	95314902	3676	0.728216	5.097658	6.17E-05	0.000299	0.037594	1	391	323	431	408	615	626	930	830	1384	1300
ENSMUSG00000037887	chr7	Dusp8	1.42E+08	1.42E+08	4870	-1.04658	5.338157	6.17E-05	0.000299	0.078541	-1	671	683	953	1150	1146	761	785	288	727	444
ENSMUSG00000052459	chr16	Atp6v1a	44085402	44087516	6044	0.789759	5.383845	6.18E-05	0.000299	0.044713	1	418	356	605	515	698	699	973	1111	1951	1614
ENSMUSG00000064351	chrMT	mt-Co1	5328	6872	1545	-0.81532	14.21983	6.18E-05	0.0003	0.048991	-1	303685	394471	525881	510210	281658	234830	305016	369321	379449	334358
ENSMUSG00000001666	chr10	Ddt	75771230	75771506	773	0.718359	4.516077	6.19E-05	0.0003	0.035713	1	229	269	327	304	308	471	498	773	742	835
ENSMUSG00000031954	chr8	Cfdp1	1.12E+08	1.12E+08	1215	0.681172	4.559888	6.2E-05	0.0003	0.031996	1	238	285	371	282	334	479	774	520	848	790
ENSMUSG00000026495	chr1	Efcab2	1.78E+08	1.78E+08	4151	-0.6822	3.722502	6.22E-05	0.000301	0.030383	-1	240	237	280	275	320	214	218	252	236	245
ENSMUSG00000041064	chr9	Pif1	65587160	65587251	4388	1.929015	0.013967	6.22E-05	0.000301	0.178726	1	1	4	4	16	5	20	27	16	51	51
ENSMUSG00000031198	chrX	Fundc2	75382399	75382451	2785	-0.72799	7.197985	6.23E-05	0.000301	0.038847	-1	2760	2966	3505	3085	2835	2486	2527	2790	2568	2326
ENSMUSG00000045817	chr17	Zfp36l2	84183931	84187156	3530	0.794789	4.573711	6.23E-05	0.000301	0.044354	1	270	185	319	273	423	407	720	544	1130	816
ENSMUSG00000028837	chr4	Psmb2	1.27E+08	1.27E+08	1204	0.762972	6.087344	6.24E-05	0.000302	0.042214	1	695	752	1000	900	856	1618	1571	2749	1931	2017
ENSMUSG00000024059	chr17	Clip4	71781947	71782069	4055	-0.70784	6.277199	6.25E-05	0.000302	0.036463	-1	1546	1368	1673	1748	1646	1003	1350	1754	1676	1126
ENSMUSG00000008393	chr16	Carhsp1	8658587	8661103	2849	0.743284	4.786278	6.26E-05	0.000302	0.038962	1	257	260	356	343	534	495	770	695	1090	1046
ENSMUSG00000055447	chr16	Cd47	49855618	49855832	5277	0.647596	5.501015	6.26E-05	0.000302	0.029908	1	571	485	629	531	729	1064	1266	1069	1556	1494
ENSMUSG00000031129	chr9	Slc9a9	94669909	94670236	5679	1.040932	3.172071	6.27E-05	0.000302	0.073269	1	82	56	103	86	171	229	371	143	363	298
ENSMUSG00000099309	chr9	Mir7085	44400423	44400488	66	-1.25158	0.50179	6.29E-05	0.000304	0.073627	-1	41	25	35	25	32	18	21	13	22	19
ENSMUSG00000026020	chr1	Nop58	59684971	59685226	10758	0.657095	4.512017	6.34E-05	0.000305	0.029686	1	273	255	336	224	392	516	712	613	772	637
ENSMUSG00000043614	chr5	Vps37d	1.35E+08	1.35E+08	1544	1.448458	0.000464	6.35E-05	0.000306	0.077753	1	6	4	8	12	9	21	38	21	43	28
ENSMUSG00000070462	chr7	Mesdc1	83879873	83884305	4433	0.833393	3.337377	6.36E-05	0.000307	0.045708	1	84	104	142	116	161	218	330	187	458	328
ENSMUSG00000027188	chr2	Pamr1	1.03E+08	1.03E+08	6046	-0.8899	4.593263	6.38E-05	0.000308	0.056192	-1	503	328	649	406	779	308	508	505	370	265
ENSMUSG00000030126	chr6	Tmcc1	1.16E+08	1.16E+08	7250	-0.80996	5.719438	6.41E-05	0.000308	0.047549	-1	962	918	1330	1195	1212	701	838	1367	786	723
ENSMUSG00000036054	chr8	Sugp2	70234226	70234652	14428	-0.63763	5.295471	6.41E-05	0.000309	0.028912	-1	654	665	915	808	975	596	728	821	772	648
ENSMUSG00000039616	chr18	Mocos	24653691	24654067	2884	1.29857	2.020818	6.42E-05	0.000309	0.106245	1	33	25	49	37	47	78	55	217	167	141
ENSMUSG00000034165	chr17	Ccnd3	47505051	47505266	8775	0.787602	5.73721	6.43E-05	0.000309	0.045002	1	470	499	706	646	1011	1202	1983	998	2057	1708
ENSMUSG00000027513	chr2	Pck1	1.73E+08	1.73E+08	3429	3.517157	5.50116	6.46E-05	0.000311	0.736875	1	63	38	62	282	176	32	261	396	2428	7166
ENSMUSG00000026238	chr1	Ptma	86526726	86526950	1462	0.824826	6.504585	6.47E-05	0.000311	0.049812	1	755	855	1119	1157	1696	1737	2420	1943	4396	3425
ENSMUSG00000049717	chr8	Lig4	9970020	9973807	4255	-0.86562	2.710149	6.53E-05	0.000314	0.04737	-1	130	123	167	128	151	90	130	68	140	111
ENSMUSG00000033488	chr1	BC026585	1.57E+08	1.57E+08	2534	1.279143	1.7013	6.54E-05	0.000314	0.099111	1	37	19	30	21	45	62	133	52	142	136
ENSMUSG00000034201	chr11	Gas2l1	5054132	5056689	6100	0.841301	3.510707	6.53E-05	0.000314	0.047521	1	120	90	124	129	223	200	356	276	508	392
ENSMUSG00000004100	chr9	Ppan	20888175	20888317	2504	0.82261	3.134635	6.54E-05	0.000314	0.043498	1	93	90	106	92	144	216	239	196	415	243
ENSMUSG00000031590	chr8	Frg1	41397457	41397644	1085	0.650523	4.311032	6.55E-05	0.000314	0.028767	1	235	212	288	280	265	470	515	631	613	572
ENSMUSG00000031286	chr3	Glt28d2	85869849	85872190	2732	-0.84777	2.976313	6.56E-05	0.000315	0.046294	-1	128	141	207	202	163	111	120	168	139	109
ENSMUSG00000062006	chr3	Rpl34	1.31E+08	1.31E+08	1179	0.655183	6.962058	6.57E-05	0.000315	0.031594	1	1409	1543	1888	1364	1882	2962	3739	3603	3789	3613
ENSMUSG00000086290	chr4	Snhg12	1.32E+08	1.32E+08	1626	1.391423	2.575658	6.57E-05	0.000315	0.129056	1	52	48	48	39	82	113	137	434	149	144
ENSMUSG00000048373	chr5	Fgfbp1	43978865	43979968	1154	-1.65073	1.577225	6.58E-05	0.000315	0.174441	-1	98	54	86	102	23	35	48	15	40	27
ENSMUSG00000072704	chr6	2700089E24Rik	1.33E+08	1.33E+08	2738	-0.65314	6.682545	6.58E-05	0.000315	0.031337	-1	1836	2037	2354	2089	2102	1612	1808	1844	2101	1912
ENSMUSG00000044320	chr2	1700001O22Rik	30794769	30795009	2788	-2.2409	0.200454	6.6E-05	0.000316	0.280938	-1	11	40	60	32	9	13	16	5	7	2
ENSMUSG00000041261	chr4	Car8	8143362	8146216	3853	-0.99612	2.210863	6.6E-05	0.000316	0.061397	-1	73	78	105	156	98	47	86	69	88	70
ENSMUSG00000066235	chr9	Pomgnt2	1.22E+08	1.22E+08	2369	-0.68916	3.53711	6.6E-05	0.000316	0.030729	-1	207	202	285	209	295	182	233	174	241	199
ENSMUSG00000030101	chr6	Sumf1	1.08E+08	1.08E+08	3405	0.631168	4.208987	6.64E-05	0.000318	0.026862	1	194	208	307	223	281	403	511	493	607	601
ENSMUSG00000031207	chrX	Msn	96096042	96096243	6327	0.788077	6.625133	6.65E-05	0.000318	0.045656	1	951	982	1215	1395	1546	1932	2792	1946	4791	3528
ENSMUSG00000101086	chr14	Gm28651	32685648	32685781	644	-1.21188	1.053093	6.67E-05	0.000319	0.080788	-1	41	53	31	59	48	27	33	21	30	30

ENSMUSG00000040433	chr9	Zbtb38	96682770	96689029	11733	-0.8931	4.637943	6.71E-05	0.000321	0.057156	-1	460	368	596	648	653	224	413	664	460	292
ENSMUSG00000003402	chr9	Prkcsh	22003035	22003088	2013	0.740004	5.08464	6.72E-05	0.000321	0.03927	1	378	320	459	378	607	737	954	679	1415	1229
ENSMUSG00000047832	chr12	Cdca4	1.13E+08	1.13E+08	2417	0.842747	2.56721	6.72E-05	0.000321	0.042839	1	54	60	77	70	88	124	174	134	245	205
ENSMUSG00000020100	chr10	Slc29a3	60712072	60716490	5834	1.075805	3.445511	6.75E-05	0.000322	0.07989	1	111	64	126	108	180	186	364	174	517	515
ENSMUSG00000027281	chr2	Slx4ip	1.37E+08	1.37E+08	5905	-1.05625	2.183966	6.75E-05	0.000322	0.070841	-1	96	104	129	90	82	49	77	38	107	76
ENSMUSG00000049892	chr11	Rasd1	59963181	59964366	1611	2.128822	1.318726	6.85E-05	0.000327	0.283411	1	7	11	13	19	23	18	29	42	192	191
ENSMUSG00000030872	chr7	Gga2	1.22E+08	1.22E+08	9769	0.690308	5.177966	6.85E-05	0.000327	0.034242	1	376	358	528	394	691	739	1243	892	1426	975
ENSMUSG00000028005	chr3	Gucy1b3	82032004	82033281	3951	-0.83724	2.981856	6.86E-05	0.000327	0.045487	-1	122	129	180	226	189	97	120	165	161	117
ENSMUSG00000021959	chr14	Lats2	57642077	57642160	7303	-0.64526	4.517022	6.87E-05	0.000327	0.029012	-1	406	359	542	435	610	306	468	412	564	352
ENSMUSG00000024878	chr19	Cbwd1	24919916	24920702	1944	-0.69536	3.851423	6.87E-05	0.000327	0.032515	-1	280	272	320	288	316	227	276	288	244	231
ENSMUSG00000022893	chr16	Adamts1	85793827	85796100	5302	-0.74784	5.217264	6.88E-05	0.000328	0.040451	-1	725	594	729	810	1054	539	766	638	880	430
ENSMUSG00000098318	chr6	1190002F15Rik	1.35E+08	1.35E+08	708	1.534706	-0.23377	6.89E-05	0.000328	0.086295	1	5	4	12	4	6	20	19	19	37	32
ENSMUSG00000038564	chr5	Ift172	31253280	31253424	5407	-0.61044	4.314586	6.9E-05	0.000329	0.025447	-1	364	311	438	403	498	260	380	372	456	381
ENSMUSG00000061393	chr9	Acvr2b	1.19E+08	1.19E+08	1753	-1.59055	1.328469	6.91E-05	0.000329	0.157296	-1	70	51	49	57	81	14	14	67	20	28
ENSMUSG00000002731	chr2	Prkra	76629898	76630568	2028	0.763141	3.096481	6.92E-05	0.000329	0.036775	1	98	91	116	100	116	202	265	191	292	290
ENSMUSG00000037106	chr15	Fer1l6	58510048	58510126	8053	-1.1163	2.420874	6.92E-05	0.000329	0.081725	-1	121	73	101	158	156	67	86	39	132	73
ENSMUSG00000048264	chr13	Dip2c	9276528	9277066	8223	-0.707	4.382006	6.99E-05	0.000332	0.035041	-1	404	319	466	422	559	251	440	458	393	308
ENSMUSG00000027534	chr3	Snx16	10417817	10419223	2632	-0.82791	2.430105	7.01E-05	0.000333	0.041292	-1	112	97	118	110	131	69	109	86	103	82
ENSMUSG00000014426	chr17	Map3k4	12227621	12228120	5305	-0.63546	4.953127	7.05E-05	0.000335	0.028716	-1	478	527	771	680	711	448	652	491	652	589
ENSMUSG00000040785	chr16	Ttc3	94370618	94370861	15134	-0.66674	5.960242	7.08E-05	0.000336	0.032621	-1	1153	989	1428	1165	1702	847	1281	1270	1236	983
ENSMUSG00000039195	chr2	1110008P14Rik	32377097	32379533	2694	0.701286	4.609127	7.09E-05	0.000336	0.034638	1	238	346	339	303	306	623	702	580	795	794
ENSMUSG00000046791	chr12	2410016O06Rik	83950608	83952953	2346	0.919824	2.202533	7.1E-05	0.000337	0.049828	1	47	49	50	46	66	108	106	138	158	174
ENSMUSG00000092885	chr11	Gm22123	6472225	6472277	53	-1.5877	0.092055	7.12E-05	0.000338	0.128425	-1	14	22	27	18	48	3	23	11	13	9
ENSMUSG00000020721	chr11	Helz	1.08E+08	1.08E+08	15044	-0.68549	4.405446	7.13E-05	0.000338	0.032958	-1	435	314	449	463	520	261	398	471	416	353
ENSMUSG00000002799	chr12	Jag2	1.13E+08	1.13E+08	4054	-0.64787	4.464948	7.19E-05	0.000341	0.029314	-1	368	342	488	547	514	306	453	412	474	365
ENSMUSG00000098465	chr8	Mir1668	83723878	83723984	107	1.046466	2.402402	7.2E-05	0.000341	0.070228	1	39	59	57	43	85	109	220	96	224	175
ENSMUSG00000040592	chr11	Cd79b	1.06E+08	1.06E+08	1431	1.607974	-0.24386	7.22E-05	0.000342	0.109825	1	0	4	5	9	12	18	25	21	30	33
ENSMUSG00000037697	chr14	Ddhd1	45593174	45595664	6759	0.914277	2.56176	7.24E-05	0.000343	0.05281	1	62	44	67	61	105	105	167	167	229	228
ENSMUSG00000048924	chr13	Ccdc125	1.01E+08	1.01E+08	2705	1.524314	0.140837	7.28E-05	0.000345	0.107925	1	6	3	9	13	11	21	24	22	55	50
ENSMUSG00000060675	chr19	Pla2g16	7557459	7557564	6396	-0.78197	7.225682	7.29E-05	0.000345	0.045673	-1	2628	3632	3509	3382	2350	2073	2332	2452	3052	2961
ENSMUSG00000071253	chr10	Slc25a16	62920633	62920881	4799	-0.69212	4.732734	7.32E-05	0.000346	0.034217	-1	436	443	682	600	595	329	461	629	490	462
ENSMUSG00000045838	chr2	A430105I19Rik	1.19E+08	1.19E+08	4779	-0.73157	4.399612	7.33E-05	0.000347	0.037938	-1	312	343	588	548	422	249	343	409	416	443
ENSMUSG00000014776	chr8	Nol3	1.05E+08	1.05E+08	2869	0.780078	6.126272	7.35E-05	0.000347	0.045035	1	633	867	1051	917	807	1707	1680	2801	2043	1967
ENSMUSG00000084416	chr1	Rpl10a-ps1	64993951	64994604	654	0.633524	4.756964	7.35E-05	0.000347	0.028296	1	315	331	340	336	438	625	738	664	1007	809
ENSMUSG00000028671	chr4	Gale	1.36E+08	1.36E+08	2370	1.529948	2.112788	7.38E-05	0.000348	0.15568	1	30	22	28	28	76	80	133	49	237	249
ENSMUSG00000022516	chr16	Nudt16l1	4939111	4939293	1269	0.655155	4.246606	7.4E-05	0.000349	0.029546	1	240	213	248	219	302	486	538	446	650	565
ENSMUSG00000023951	chr17	Vegfa	46016993	46018879	4293	-0.76446	6.241929	7.41E-05	0.00035	0.043429	-1	1365	1564	1603	1783	1566	1022	1461	829	1691	1598
ENSMUSG00000036832	chr3	Lpar3	1.46E+08	1.46E+08	2494	1.787078	0.046068	7.44E-05	0.000351	0.14924	1	13	4	3	2	11	20	52	34	38	20
ENSMUSG00000051853	chr15	Arf3	98737621	98740494	3837	0.748194	5.086886	7.52E-05	0.000354	0.040737	1	335	325	410	471	596	745	882	701	1434	1271
ENSMUSG00000056367	chr5	Actr3b	25759997	25760128	1741	-1.42156	0.588793	7.55E-05	0.000356	0.109503	-1	26	45	54	31	18	10	20	23	24	16
ENSMUSG00000034088	chr1	Hdlbp	93405940	93408259	11320	-0.62745	8.423413	7.55E-05	0.000356	0.029754	-1	6070	5489	7494	7162	8860	4749	5845	7208	7629	6213
ENSMUSG00000020386	chr11	Sar1b	51763687	51763791	1255	-1.02059	8.142251	7.59E-05	0.000358	0.077804	-1	6362	5681	7770	5222	6399	2818	3247	8295	3762	3551
ENSMUSG00000045659	chr7	Plekha7	1.16E+08	1.16E+08	11618	1.314245	1.283601	7.62E-05	0.000359	0.100764	1	15	21	25	23	26	29	132	68	98	65
ENSMUSG00000064373	chr15	Sepp1	3268547	3268768	2845	0.769052	8.211317	7.65E-05	0.00036	0.044605	1	3384	2493	3870	3594	5214	5393	10110	11673	8834	7816
ENSMUSG00000022867	chr16	Usp25	77014069	77014140	4412	-0.74917	6.740942	7.71E-05	0.000363	0.042095	-1	2093	1836	2597	2230	2447	1196	1759	2737	1994	1672
ENSMUSG00000064326	chr12	Siva1	1.13E+08	1.13E+08	782	0.719797	3.208034	7.77E-05	0.000366	0.03315	1	89	110	149	99	131	209	268	242	320	290
ENSMUSG00000025962	chr1	Fastkd2	63730614	63730691	5873	-0.6487	4.261081	7.79E-05	0.000366	0.029303	-1	314	381	465	399	384	308	357	323	399	343
ENSMUSG00000036430	chr17	Tbcc	46890621	46892463	1843	0.832125	3.113263	7.79E-05	0.000366	0.045796	1	62	114	120	104	113	205	265	192	354	270
ENSMUSG00000038812	chr19	Trmt112	6909698	6909855	1233	0.675776	4.196013	7.81E-05	0.000367	0.031824	1	176	216	261	240	284	453	469	629	529	510
ENSMUSG00000098302	chr5	Gm28039	1.07E+08	1.07E+08	254	-1.17576	0.586677	7.86E-05	0.000369	0.065253	-1	29	33	30	36	38	13	17	28	20	25
ENSMUSG00000087014	chr10	Gm16364	39556071	39557285	1313	-1.40421	1.155216	7.87E-05	0.00037	0.117957	-1	49	61	53	58	38	43	24	16	32	20
ENSMUSG00000057219	chr11	Armc7	1.15E+08	1.15E+08	3069	1.018406	1.545182	7.88E-05	0.00037	0.056475	1	28	30	37	28	30	60	85	71	109	115
ENSMUSG00000091964	chr5	Map11	1.38E+08	1.38E+08	3581	0.987247	2.584982	7.88E-05	0.00037	0.063837	1	53	47	102	57	74	113	193	118	292	219
ENSMUSG00000031821	chr8	Gins2	1.21E+08	1.21E+08	4097	1.782476	0.818774	7.89E-05	0.00037	0.190393	1	6	6	9	11	31	38	67	16	104	76
ENSMUSG00000036948	chr5	BC037034	1.38E+08	1.38E+08	3860	0.987247	2.584982	7.89E-05	0.00037	0.063845	1	53	47	102	57	74	113	193	118	292	219
ENSMUSG00000008668	chr17	Rps18	33951999	33952118	2491	0.631969	7.916549	7.89E-05	0.00037	0.030271	1	2593	2838	3579	2736	4216	5446	6978	6926	7714	7208
ENSMUSG00000026737	chr2	Pip4k2a	18842255	18844460	3477	0.788183	3.812935	7.93E-05	0.000372	0.043422	1	149	115	202	154	248	314	523	265	546	433
ENSMUSG00000005611	chr7	Mrvi1	1.11E+08	1.11E+08	6827	-0.86975	2.650605	7.96E-05	0.000373	0.049171	-1	108	87	167	165	153	64	108	92	159	102
ENSMUSG00000037989	chr13	Wnk2	49036303	49036505	8481	-1.25692	5.933097	7.97E-05	0.000373	0.116706	-1	1133	1275	1424	1554	1846	512	410	1920	710	632
ENSMUSG00000057457	chrX	Phex	1.57E+08	1.57E+08	6291	-1.64766	-0.32127	7.97E-05	0.000373	0.127395	-1	28	7	14	21	23	2	11	9	10	10
ENSMUSG00000024122	chr17	Pdpk1	24073680	24079142	10935	-0.72509	5.437804	8.01E-05	0.000375	0.038896	-1	751	794	1016	845	1127	530	715	1111	812	647
ENSMUSG00000029725	chr5	Ppp1r35	1.38E+08	1.38E+08	1085	0.906528	2.248618	8.02E-05	0.000375	0.049329	1	55	54	56	44	57	120	157	109	179	140
ENSMUSG00000043733	chr5	Ptpn11	1.21E+08	1.21E+08	7492	-0.63626	6.951427	8.04E-05	0.000376	0.030557	-1	1894	2250	3030	2698	2769	1712	2211	2499	2680	2249
ENSMUSG00000046876	chr13	Atxn1	45549758	45557585	10605	-0.63165	4.860224	8.04E-05	0.000376	0.028735	-1	544	500	590	672	623	442	562	503	599	543
ENSMUSG00000063457	chr10	Rps15	80292453	80292483	630	0.639905	7.869386	8.05E-05	0.000376	0.031095	1	2458	2927	3539	2859	3510	5945	6375	6018	7732	7021
ENSMUSG00000018572	chr11	Phf23	69995777	69996053	3273	0.655039	4.590905	8.08E-05	0.000377	0.030554	1	272	267	309	286	432	542	576	635	879	813

ENSMUSG00000049553	chr6	Polr1a	71909053	71909239	6105	-0.59883	5.41212	8.08E-05	0.000377	0.02627	-1	718	717	996	867	1004	617	798	698	1007	854
ENSMUSG00000054452	chr10	Aes	81559494	81559668	1411	-0.66921	9.174288	8.09E-05	0.000378	0.034164	-1	9370	11073	13208	13475	12001	9682	9638	9075	12047	11283
ENSMUSG00000036053	chr2	Fmnl2	52857860	52858259	6033	-0.85288	3.118246	8.1E-05	0.000378	0.049149	-1	153	110	226	179	282	83	148	174	165	156
ENSMUSG00000068122	chrX	Agtr2	21484544	21484694	3326	1.890476	1.200861	8.14E-05	0.00038	0.231588	1	5	5	10	9	53	61	67	128	85	52
ENSMUSG00000059901	chr10	Adamts14	61197112	61198959	5197	1.23827	2.784697	8.17E-05	0.000381	0.106309	1	53	44	85	52	110	113	417	112	262	225
ENSMUSG00000017491	chr14	Rarb	16430842	16432267	3034	-0.88256	2.870866	8.18E-05	0.000381	0.051781	-1	126	126	148	165	230	94	134	77	133	159
ENSMUSG00000091449	chr18	Gm10269	20682592	20682963	372	0.979122	1.987356	8.18E-05	0.000381	0.058159	1	35	35	51	28	70	97	100	121	158	121
ENSMUSG00000017446	chr11	C1qtnf1	1.18E+08	1.18E+08	3131	-0.97178	4.189888	8.19E-05	0.000382	0.068713	-1	375	175	383	355	798	181	339	294	345	293
ENSMUSG00000032400	chr9	Zwilch	64137144	64138059	4283	1.468642	0.521574	8.19E-05	0.000382	0.110669	1	6	11	15	8	18	18	53	31	87	43
ENSMUSG00000028653	chr4	Trit1	1.23E+08	1.23E+08	2087	0.753892	3.611045	8.22E-05	0.000383	0.038655	1	131	150	211	104	156	285	359	389	393	343
ENSMUSG00000038507	chr6	Parp12	39086410	39087640	3995	0.911344	3.66518	8.23E-05	0.000383	0.058484	1	131	120	156	153	169	410	357	207	382	523
ENSMUSG00000030987	chr7	Stim1	1.02E+08	1.02E+08	3597	-0.64576	7.649903	8.27E-05	0.000385	0.031751	-1	3650	3429	4542	4270	4597	2691	3670	4333	4574	3136
ENSMUSG00000093661	chr6	Eif4e3	99625135	99627053	2515	-0.63162	5.088574	8.34E-05	0.000388	0.029167	-1	580	651	835	692	681	488	574	573	807	690
ENSMUSG00000009563	chr2	Tor2a	32757234	32757450	3050	0.911269	3.193527	8.43E-05	0.000392	0.057193	1	85	70	103	87	191	156	284	231	392	345
ENSMUSG00000006456	chr19	Rbm14	4800569	4801805	3910	0.672864	3.669733	8.45E-05	0.000393	0.030589	1	125	127	174	171	225	269	325	331	496	409
ENSMUSG00000023892	chr17	Zfp51	21450352	21450421	2600	-0.85304	2.667726	8.52E-05	0.000396	0.046898	-1	122	110	179	133	134	79	98	131	97	116
ENSMUSG00000025487	chr7	Psmd13	1.41E+08	1.41E+08	3395	0.674955	6.687115	8.58E-05	0.000399	0.03456	1	1091	1240	1557	1237	1511	2425	2607	3602	2978	3063
ENSMUSG00000080268	chr19	Brms1	5041404	5041490	1338	0.652486	3.844426	8.59E-05	0.000399	0.028959	1	132	186	226	184	199	312	398	423	475	430
ENSMUSG00000010067	chr9	Rassf1	1.08E+08	1.08E+08	5845	0.636053	4.134852	8.62E-05	0.0004	0.027953	1	233	202	232	212	255	393	494	526	583	485
ENSMUSG00000029826	chr6	Zc3hav1	38305286	38307456	6518	0.723047	4.002641	8.63E-05	0.000401	0.036895	1	164	151	217	212	270	386	388	361	550	631
ENSMUSG00000084939	chr4	Gm830	95464724	95467895	3502	1.814104	0.133479	8.63E-05	0.000401	0.166865	1	4	9	5	6	11	11	70	20	53	26
ENSMUSG00000068036	chr17	Mllt4	13760539	13760778	10223	-0.74134	5.593572	8.66E-05	0.000402	0.04126	-1	745	849	1056	1392	1003	531	709	975	1056	1003
ENSMUSG00000095677	chr17	Dynlt1f	6648941	6649337	807	0.915542	1.932219	8.71E-05	0.000404	0.049021	1	35	35	39	43	63	99	115	107	124	115
ENSMUSG00000029312	chr5	Klhl8	1.04E+08	1.04E+08	3489	-0.63782	5.243857	8.77E-05	0.000407	0.030022	-1	651	611	935	701	993	620	721	607	749	735
ENSMUSG00000037544	chr14	Dlgap5	47387779	47388123	6650	1.784443	0.82265	8.79E-05	0.000407	0.194865	1	9	7	4	6	37	38	55	32	107	70
ENSMUSG00000000740	chr8	Rpl13	1.23E+08	1.23E+08	2352	0.62528	7.926551	8.89E-05	0.000411	0.030071	1	2542	2846	3657	3078	3970	6015	6893	6030	8272	7179
ENSMUSG00000027381	chr2	Bcl2l11	1.28E+08	1.28E+08	8029	0.933545	3.219317	8.88E-05	0.000411	0.060856	1	66	66	117	134	157	155	275	405	336	256
ENSMUSG00000061755	chr5	Bod1l	41787542	41788949	10389	-0.77736	4.794954	8.89E-05	0.000411	0.04477	-1	528	426	675	627	687	267	472	721	503	442
ENSMUSG00000034768	chr11	Asb16	1.02E+08	1.02E+08	2843	-0.70614	6.441937	8.91E-05	0.000412	0.037918	-1	1472	1487	1903	1939	2261	1407	1268	1870	1458	1593
ENSMUSG00000044496	chr4	2510039O18Rik	1.48E+08	1.48E+08	2731	0.601428	4.785752	8.92E-05	0.000412	0.026042	1	291	337	390	372	438	563	743	809	985	799
ENSMUSG00000055485	chr2	Soga1	1.57E+08	1.57E+08	7984	-0.9313	3.161246	8.95E-05	0.000414	0.060526	-1	177	105	169	207	339	84	168	131	196	149
ENSMUSG00000026610	chr1	Esrrg	1.88E+08	1.88E+08	6208	-1.03271	3.478521	8.96E-05	0.000414	0.076669	-1	168	282	223	378	171	133	207	133	265	126
ENSMUSG00000007827	chr6	Ankrd26	1.19E+08	1.19E+08	7253	-0.92463	2.043139	8.98E-05	0.000415	0.052559	-1	98	58	90	84	116	51	69	73	73	61
ENSMUSG00000084215	chr4	Gm11814	10438815	10439743	929	-1.40316	0.060489	8.97E-05	0.000415	0.094242	-1	24	22	24	34	13	11	11	10	19	12
ENSMUSG00000092232	chr14	Gm20521	54883441	54883506	1245	0.627648	5.067037	8.98E-05	0.000415	0.028875	1	386	407	526	418	450	711	906	979	1055	1094
ENSMUSG00000054000	chr4	Tusc1	93334138	93335511	1374	1.194742	1.323819	8.99E-05	0.000415	0.083821	1	17	17	24	26	38	59	51	59	99	120
ENSMUSG00000021908	chr12	Gm6768	1.19E+08	1.19E+08	3339	-1.13357	1.134571	9.03E-05	0.000417	0.0714	-1	48	31	48	39	83	28	31	29	42	26
ENSMUSG00000038005	chr8	2700029M09Rik	60890418	60890536	1701	1.033205	3.050876	9.04E-05	0.000417	0.07436	1	81	94	103	64	103	242	229	120	338	350
ENSMUSG00000016554	chr15	Eif3d	77958998	77959122	1910	0.62231	6.078925	9.05E-05	0.000418	0.029286	1	684	769	1027	862	1143	1464	1945	2123	2229	1814
ENSMUSG00000026792	chr2	Lrsam1	32925216	32926901	5145	-0.67236	3.680853	9.06E-05	0.000418	0.03109	-1	234	203	319	283	275	167	271	187	295	240
ENSMUSG00000092534	chr7	Pagr1b	1.27E+08	1.27E+08	693	0.667109	3.767169	9.07E-05	0.000418	0.030351	1	148	171	178	168	204	309	411	305	476	440
ENSMUSG00000042572	chr3	Ube2q1	89773609	89774038	3081	0.631724	4.803656	9.08E-05	0.000419	0.029004	1	312	315	434	356	411	579	740	668	1049	956
ENSMUSG00000060477	chr6	Irak2	1.14E+08	1.14E+08	4194	0.873131	3.392141	9.09E-05	0.000419	0.053177	1	77	120	124	143	151	247	293	192	412	436
ENSMUSG00000041483	chr1	Zfp281	1.37E+08	1.37E+08	4937	-0.68245	3.613597	9.12E-05	0.00042	0.032035	-1	236	213	263	242	300	140	217	273	269	204
ENSMUSG00000086825	chr1	Gm15675	1.3E+08	1.3E+08	3681	1.221489	1.927621	9.16E-05	0.000422	0.096805	1	18	41	61	39	25	109	83	108	130	165
ENSMUSG00000071793	chr8	2610005L07Rik	20385782	20388402	4163	-1.33437	0.396865	9.26E-05	0.000426	0.092213	-1	22	28	22	43	35	7	13	25	19	20
ENSMUSG00000033871	chr18	Ppargc1b	61298136	61298783	3990	-0.90574	2.93981	9.27E-05	0.000426	0.056468	-1	138	98	183	222	199	81	138	91	202	122
ENSMUSG00000029472	chr5	Anapc5	1.23E+08	1.23E+08	2750	-0.65754	8.463686	9.32E-05	0.000429	0.033512	-1	6782	6210	8112	7025	7897	5778	5319	6902	6800	6878
ENSMUSG00000033475	chr17	Tomm6	47686646	47687008	1131	0.641813	5.622516	9.33E-05	0.000429	0.030968	1	496	623	673	695	717	1266	1251	1264	1605	1568
ENSMUSG00000102813	chr4	RP23-169H13.6	1.5E+08	1.5E+08	2459	2.244169	-0.83512	9.37E-05	0.000431	0.188129	1	0	5	4	3	0	8	20	5	30	23
ENSMUSG00000017817	chr2	Jph2	1.63E+08	1.63E+08	4255	-0.74126	9.715722	9.42E-05	0.000433	0.042654	-1	15405	13696	21364	16154	22186	14439	15336	9211	17671	16299
ENSMUSG00000040618	chr14	Pck2	55540266	55540513	3400	0.743956	3.320032	9.43E-05	0.000433	0.037288	1	128	84	139	120	147	198	240	296	388	339
ENSMUSG00000006457	chr19	Actn3	4861223	4861503	2894	-0.76493	12.82647	9.52E-05	0.000437	0.045505	-1	125695	125066	171884	155044	193113	114475	93574	168014	110201	130871
ENSMUSG00000037331	chr11	Larp1	58009064	58009547	6829	-0.6571	7.102049	9.55E-05	0.000438	0.033339	-1	2145	2246	3174	2911	3759	1845	2271	3050	2839	2471
ENSMUSG00000018899	chr11	Irf1	53770014	53770278	3976	0.842232	4.119493	9.57E-05	0.000439	0.05197	1	144	173	231	232	264	534	503	281	611	631
ENSMUSG00000023882	chr17	Zfp54	21423227	21423561	2832	-1.46851	0.0047	9.59E-05	0.00044	0.09962	-1	20	23	33	12	28	7	19	7	10	15
ENSMUSG00000074505	chr9	Fat3	15910205	15915621	18456	-1.68072	0.515343	9.64E-05	0.000442	0.164294	-1	40	13	52	13	62	8	21	22	15	10
ENSMUSG00000020253	chr9	Ppm1m	1.06E+08	1.06E+08	3485	1.346491	2.925775	9.66E-05	0.000442	0.12906	1	64	39	48	83	123	107	207	132	375	474
ENSMUSG00000021067	chr12	Sav1	69965012	69966347	2524	-0.62026	5.705041	9.66E-05	0.000442	0.029154	-1	887	934	1180	988	1313	617	1035	1110	1128	954
ENSMUSG00000025078	chr19	Nhlrc2	56548261	56548860	3934	-0.81883	2.676739	9.66E-05	0.000442	0.044268	-1	127	107	139	152	150	65	100	130	150	99
ENSMUSG00000030750	chr7	Nsmce1	1.25E+08	1.25E+08	1329	0.685221	3.779641	9.65E-05	0.000442	0.032668	1	156	147	217	162	192	323	358	490	418	360
ENSMUSG00000037253	chr18	Mex3c	73573044	73573776	3738	-0.67016	3.968247	9.68E-05	0.000443	0.031866	-1	283	264	316	288	463	189	305	322	358	246
ENSMUSG00000026678	chr1	Rgs5	1.7E+08	1.7E+08	4546	-0.70788	8.222971	9.71E-05	0.000444	0.038977	-1	4600	5467	7656	7889	5308	4420	5432	4837	6466	5364
ENSMUSG00000027454	chr2	Gins1	1.51E+08	1.51E+08	1516	1.108425	1.006449	9.86E-05	0.000451	0.063174	1	12	18	20	23	27	38	57	72	84	53
ENSMUSG00000021115	chr12	Vrk1	1.06E+08	1.06E+08	3796	0.898517	2.556199	9.89E-05	0.000452	0.052586	1	66	42	69	84	75	106	171	152	262	203
ENSMUSG00000047721	chr7	Bola2	1.27E+08	1.27E+08	1658	0.670691	3.667358	9.89E-05	0.000452	0.030821	1	150	147	181	146	186	308	317	303	471	411

ENSMUSG00000028497	chr4	Ptplad2	88396144	88398219	6756	0.879158	3.208091	9.91E-05	0.000453	0.054175	1	95	52	131	114	156	215	335	192	343	302
ENSMUSG00000047215	chr5	Rpl9	65388364	65388441	3080	0.661357	7.956971	9.93E-05	0.000454	0.034096	1	2841	3035	3961	2698	3534	6470	7254	6152	7885	7511
ENSMUSG00000038658	chr19	Ric1	29522282	29522666	10727	-0.78684	4.898562	0.0001	0.000459	0.046776	-1	517	500	666	725	761	275	421	773	588	529
ENSMUSG00000048732	chr11	Klhl11	1E+08	1E+08	2393	-1.28177	0.448124	0.000101	0.000459	0.08232	-1	34	20	31	27	43	10	20	25	12	21
ENSMUSG00000021413	chr13	Prpf4b	34875494	34875694	4465	-0.66363	4.521813	0.000101	0.00046	0.032396	-1	418	383	564	426	571	264	433	535	459	394
ENSMUSG00000027598	chr2	Itch	1.55E+08	1.55E+08	9709	-0.65446	4.920588	0.000101	0.000462	0.031986	-1	531	507	647	643	777	373	537	710	585	546
ENSMUSG00000099329	chr17	Gm28052	29549799	29549994	380	-1.16064	1.818016	0.000101	0.000462	0.08802	-1	66	72	80	78	107	22	45	92	51	43
ENSMUSG00000025229	chr19	Pitx3	46135685	46136605	1526	0.950136	2.431853	0.000102	0.000463	0.059422	1	49	49	65	61	78	135	130	220	219	108
ENSMUSG00000045045	chr19	Lrfn4	4611785	4612638	3366	0.969608	2.05666	0.000102	0.000465	0.05863	1	32	50	53	36	57	86	156	113	179	98
ENSMUSG00000034333	chr15	Zbed4	88751660	88751802	5764	-0.76789	2.912689	0.000103	0.000468	0.038954	-1	128	131	182	180	167	116	137	106	172	115
ENSMUSG00000037725	chr8	Ckap2	22168152	22168974	2601	1.14583	1.626228	0.000103	0.000469	0.081715	1	21	27	28	30	49	57	116	58	166	92
ENSMUSG00000052917	chr16	Senp7	56075409	56075578	5287	-0.83065	3.166798	0.000103	0.000469	0.048249	-1	202	130	217	177	232	100	161	207	167	118
ENSMUSG00000048758	chr9	Rpl29	1.06E+08	1.06E+08	796	0.635759	7.136398	0.000103	0.00047	0.031505	1	1402	1685	1929	1886	2354	3467	3903	3396	5050	4173
ENSMUSG00000027076	chr2	Timm10	84826997	84827147	815	0.765687	4.388672	0.000103	0.00047	0.043351	1	199	282	295	252	251	587	561	768	605	489
ENSMUSG00000007833	chr7	Aldh16a1	45140684	45142102	5501	0.673882	3.741703	0.000104	0.000472	0.031624	1	156	139	175	171	215	291	339	312	540	444
ENSMUSG00000015087	chr2	Rabl6	25583018	25583988	6379	-0.62226	6.536351	0.000104	0.000473	0.030029	-1	1610	1792	2190	1841	1929	1452	1693	1699	2019	1652
ENSMUSG00000002778	chr7	Kdelr1	45872772	45873101	1873	0.615494	6.061996	0.000104	0.000474	0.029126	1	844	677	946	865	1085	1549	1905	1753	2211	2007
ENSMUSG00000024012	chr17	Mtch1	29332072	29332778	2878	0.630171	6.611219	0.000105	0.000477	0.030861	1	1035	1035	1333	1318	1753	2263	2856	2347	3446	2988
ENSMUSG00000044617	chr10	Zbtb39	1.28E+08	1.28E+08	5946	-0.8481	2.967617	0.000105	0.000477	0.049269	-1	135	119	199	183	208	104	116	185	137	102
ENSMUSG00000050592	chr2	Fam78a	32050055	32050912	5973	-0.74063	5.146838	0.000105	0.000478	0.041757	-1	647	607	830	747	883	563	719	351	796	665
ENSMUSG00000081094	chr8	Rpl19-ps11	19492906	19493623	718	0.607553	4.216158	0.000106	0.000479	0.026284	1	186	223	287	252	280	407	572	513	641	481
ENSMUSG00000071267	chr17	Zfp942	21926960	21929489	5259	-0.86182	2.70084	0.000106	0.000479	0.05012	-1	128	123	139	130	175	59	118	148	116	98
ENSMUSG00000038481	chr10	Cdk19	40349308	40349721	5807	-0.75501	4.075608	0.000106	0.00048	0.041931	-1	248	363	503	349	298	203	253	338	346	330
ENSMUSG00000085385	chr2	9430008C03Rik	1.58E+08	1.58E+08	7052	1.037586	1.751588	0.000106	0.00048	0.064929	1	36	29	46	26	40	57	91	103	120	144
ENSMUSG00000021706	chr13	Zfyve16	92487108	92488623	7082	-0.65412	3.660798	0.000107	0.000484	0.029846	-1	223	237	257	241	330	173	268	196	298	216
ENSMUSG00000031109	chrX	Enox2	49009707	49011634	4356	-0.88841	3.636156	0.000107	0.000486	0.057622	-1	157	341	311	277	246	147	169	266	195	234
ENSMUSG00000045691	chr14	Thtpa	55053884	55054019	5967	-0.62796	4.43505	0.000107	0.000487	0.02886	-1	395	400	543	392	454	332	392	425	477	351
ENSMUSG00000028007	chr3	Snx7	1.18E+08	1.18E+08	2171	1.039967	2.677943	0.000108	0.000488	0.075537	1	69	36	77	50	118	128	290	143	239	196
ENSMUSG00000086741	chr8	Gm15816	23138794	23139575	1688	-1.23646	3.132095	0.000108	0.00049	0.111965	-1	115	178	241	157	364	112	59	68	255	128
ENSMUSG00000053128	chr9	Rnf26	44066327	44067231	4546	0.832923	3.076767	0.000109	0.000492	0.048056	1	102	68	109	87	137	201	269	164	357	265
ENSMUSG00000034544	chr3	Rsrc1	66981390	66981542	12000	-0.59916	4.201939	0.000109	0.000493	0.025731	-1	342	302	435	329	446	265	333	340	431	343
ENSMUSG00000029234	chr5	Tmem165	76183880	76184352	2588	0.610525	4.498891	0.00011	0.000497	0.027202	1	252	271	326	264	381	437	655	617	872	639
ENSMUSG00000089862	chr6	Gm16039	8259288	8259493	10430	-0.65465	3.77372	0.00011	0.0005	0.03046	-1	275	254	314	231	312	161	268	242	311	268
ENSMUSG00000039934	chr5	Gsap	21186267	21186459	3745	1.082907	1.696146	0.00011	0.0005	0.072149	1	29	32	37	29	39	55	121	61	133	133
ENSMUSG00000000631	chr11	Myo18a	77763246	77763379	14864	-0.67025	7.547449	0.000111	0.000501	0.035444	-1	2786	2946	4582	4185	5006	2523	3201	4208	3875	3082
ENSMUSG00000038116	chr2	Phf20	1.56E+08	1.56E+08	9988	-0.69543	4.46582	0.000111	0.000501	0.036084	-1	410	336	500	519	521	263	434	517	391	362
ENSMUSG00000029998	chr6	Pcyox1	86386006	86389371	4797	-0.6159	6.45371	0.000111	0.000501	0.029619	-1	1485	1523	2144	1621	2145	1370	1749	1410	1901	1638
ENSMUSG00000028191	chr3	Bcl10	1.46E+08	1.46E+08	1760	0.640299	3.92216	0.000112	0.000504	0.029187	1	137	162	262	199	235	349	445	426	539	387
ENSMUSG00000014850	chr13	Msh3	92211872	92212546	11254	-0.6226	3.829802	0.000112	0.000505	0.027201	-1	261	232	334	265	349	211	296	231	300	264
ENSMUSG00000003348	chr10	Mob3a	80685256	80687173	2644	0.821972	3.520686	0.000112	0.000506	0.048715	1	103	111	177	118	187	248	383	196	498	397
ENSMUSG00000049482	chr8	Ctu2	1.22E+08	1.22E+08	5164	0.778598	2.985481	0.000112	0.000506	0.040598	1	95	83	104	75	123	159	209	279	266	243
ENSMUSG00000029221	chr5	Slc30a9	67306955	67307197	9861	-0.63051	6.221637	0.000113	0.000508	0.031015	-1	1216	1427	1703	1611	1603	1160	1511	1251	1489	1393
ENSMUSG00000024725	chr19	Ostf1	18579328	18581328	4784	0.712975	5.293832	0.000113	0.000509	0.039043	1	397	442	580	530	531	894	941	833	1493	1560
ENSMUSG00000053510	chr4	Nrd1	1.09E+08	1.09E+08	7140	-0.6254	7.309292	0.000114	0.000514	0.030929	-1	2889	2747	3588	3318	3522	2358	2748	3337	3122	2942
ENSMUSG00000066571	chr7	4931406P16Rik	34236707	34239237	6437	-0.7233	5.261682	0.000116	0.000521	0.040446	-1	675	647	829	939	905	408	666	964	784	587
ENSMUSG00000034686	chr13	Prr7	55464267	55464414	1360	1.635409	-0.26743	0.000116	0.000523	0.10573	1	8	3	9	6	2	15	33	15	34	29
ENSMUSG00000074305	chr9	Peak1	56201126	56207611	12351	-0.64502	4.723774	0.000116	0.000524	0.031345	-1	408	391	572	610	749	365	522	453	653	432
ENSMUSG00000022601	chr16	Zbtb11	55973883	55974371	7440	-0.8827	3.376992	0.000117	0.000524	0.056974	-1	212	201	238	223	240	95	201	261	185	114
ENSMUSG00000033701	chr1	Acbd6	1.56E+08	1.56E+08	6453	0.634791	4.386007	0.000117	0.000526	0.029666	1	224	239	358	278	263	508	548	575	678	634
ENSMUSG00000068856	chr3	Sf3b4	96172332	96172607	2162	0.739802	3.441049	0.000117	0.000527	0.038698	1	120	91	140	133	197	221	278	264	457	375
ENSMUSG00000025592	chrX	Dach2	1.13E+08	1.13E+08	9868	-1.98121	-0.07048	0.000117	0.000528	0.230641	-1	8	21	22	58	10	5	6	12	16	4
ENSMUSG00000062627	chr4	Mysm1	94942040	94947123	8946	-0.77683	2.776393	0.000118	0.000529	0.040585	-1	135	116	148	149	169	71	120	138	156	108
ENSMUSG00000002222	chr6	Rmnd5a	71388634	71393188	6783	-0.9271	7.195372	0.000118	0.000529	0.067877	-1	3045	2577	3667	3347	3389	1448	1916	4328	2146	1944
ENSMUSG00000087590	chr18	2410004N09Rik	33794892	33795124	430	1.687939	1.742451	0.000118	0.000531	0.196465	1	19	17	39	20	34	59	60	295	77	74
ENSMUSG00000075318	chr2	Scn2a1	65620857	65621015	9259	-1.3408	0.289131	0.000118	0.000532	0.090514	-1	17	18	45	24	38	15	20	11	21	9
ENSMUSG00000062040	chr7	Zfp27	29893333	29896426	4224	-0.75726	2.826265	0.000119	0.000532	0.038359	-1	131	117	172	159	161	78	130	145	141	121
ENSMUSG00000024939	chr19	Fam89b	5728087	5728878	1209	0.592994	5.000905	0.000119	0.000533	0.026578	1	351	377	498	408	500	754	840	856	1022	998
ENSMUSG00000102692	chr3	Dchs2	83127948	83129942	10783	-1.69057	0.861393	0.000119	0.000534	0.185622	-1	50	10	60	35	77	8	29	31	21	9
ENSMUSG00000042826	chr11	Fgf11	69796068	69797879	3044	0.793634	4.122136	0.000119	0.000536	0.047236	1	168	170	211	234	283	462	697	303	584	503
ENSMUSG00000033405	chr14	Nudt15	73519864	73521674	2592	-0.9908	1.547377	0.00012	0.000536	0.059533	-1	58	54	89	60	57	33	43	40	48	60
ENSMUSG00000046707	chr8	Csnk2a2	95446096	95448418	3766	0.706156	3.850783	0.00012	0.000539	0.036276	1	156	134	208	182	238	281	386	572	468	374
ENSMUSG00000026475	chr1	Rgs16	1.54E+08	1.54E+08	2339	0.979613	2.188944	0.00012	0.00054	0.063665	1	36	40	51	45	81	114	163	86	201	129
ENSMUSG00000021666	chr13	Gfm2	97137937	97138026	10685	-0.63119	6.217425	0.000121	0.000541	0.031353	-1	1209	1407	1698	1632	1596	1241	1328	1231	1589	1385
ENSMUSG00000031273	chrX	Col4a6	1.41E+08	1.41E+08	7973	-1.52414	0.57136	0.000121	0.000541	0.13655	-1	36	9	40	27	71	17	12	14	22	20
ENSMUSG00000031791	chr8	Tmem38a	72572103	72572227	2094	-0.67028	10.32238	0.000121	0.000541	0.03608	-1	21972	22396	29779	25887	32151	20295	20434	29285	23958	20224
ENSMUSG00000050812	chr4	AI314180	58798911	58800320	11447	-0.80402	8.210426	0.000121	0.000541	0.051558	-1	5450	5365	7594	5953	7238	3759	4158	8034	4388	4615

ENSMUSG00000025571	chr11	Tnrc6c	1.18E+08	1.18E+08	12843	-0.71296	4.817325	0.000121	0.000541	0.039027	-1	558	379	620	613	781	307	472	657	623	463
ENSMUSG00000083836	chr4	Ldha-ps2	1.19E+08	1.19E+08	1057	-0.87929	2.665363	0.000121	0.000542	0.053276	-1	114	136	154	141	131	98	89	69	126	133
ENSMUSG00000029571	chr6	Tmem106b	13069759	13069795	6931	-0.74917	5.739959	0.000122	0.000544	0.044095	-1	1057	942	1211	1187	1175	599	892	1409	986	783
ENSMUSG00000037905	chr5	Bri3bp	1.25E+08	1.25E+08	6975	0.780369	3.030072	0.000122	0.000544	0.042125	1	63	76	124	116	123	167	264	193	307	270
ENSMUSG00000021057	chr12	Akap5	76324891	76324989	6824	-1.57397	1.106075	0.000122	0.000547	0.165363	-1	35	42	65	85	36	17	32	4	39	34
ENSMUSG00000069539	chr10	Scyl2	89638721	89641116	10099	-0.63496	4.188438	0.000123	0.000548	0.029683	-1	325	325	448	374	372	265	329	373	425	276
ENSMUSG00000027889	chr3	Ampd2	1.08E+08	1.08E+08	5069	0.967764	3.501272	0.000123	0.000551	0.069625	1	115	79	121	110	221	232	397	180	521	438
ENSMUSG00000049744	chr2	Arhgap15	43748824	43748899	8818	1.12752	0.713676	0.000124	0.000551	0.06028	1	15	14	19	14	17	31	59	42	55	57
ENSMUSG00000031479	chr8	Vps36	22192809	22192966	3706	-0.60147	5.700255	0.000124	0.000553	0.028243	-1	932	996	1192	1026	1054	798	967	991	1112	942
ENSMUSG00000025287	chrX	Acot9	1.55E+08	1.55E+08	2273	0.609448	5.335112	0.000125	0.000555	0.028691	1	427	478	691	478	605	902	1217	1191	1336	1038
ENSMUSG00000063317	chr7	Usp31	1.22E+08	1.22E+08	10198	-0.6384	3.858294	0.000126	0.00056	0.029491	-1	233	240	317	311	382	169	269	298	357	246
ENSMUSG00000057789	chr17	Bak1	27019810	27021035	2407	0.618123	4.786545	0.000126	0.00056	0.028962	1	256	318	427	386	442	555	703	769	1058	851
ENSMUSG00000043831	chr7	Lysmd4	67222544	67222629	3383	-0.64445	3.829799	0.000126	0.000561	0.029895	-1	245	258	352	274	316	205	233	315	298	238
ENSMUSG00000014846	chr8	Tppp3	1.05E+08	1.05E+08	1848	0.743504	6.025754	0.000126	0.000562	0.043766	1	636	598	890	914	1082	1428	2737	1337	2211	1845
ENSMUSG00000018339	chr11	Gpx3	54902453	54902575	1813	1.06872	7.050258	0.000126	0.000563	0.090474	1	1372	1017	1500	1247	2095	1794	2331	7198	4561	5442
ENSMUSG00000029910	chr6	Mad2l1	66535390	66535599	2203	1.019385	2.133359	0.000127	0.000566	0.069127	1	36	46	46	40	68	99	155	73	206	144
ENSMUSG00000034390	chr8	Cmip	1.17E+08	1.17E+08	4732	0.727222	4.235394	0.000128	0.000571	0.039858	1	188	165	206	306	325	347	509	509	816	604
ENSMUSG00000063628	chr18	Gm7665	16274648	16274944	297	1.738062	-0.04891	0.000128	0.000571	0.16125	1	3	2	6	5	17	24	21	13	56	39
ENSMUSG00000004317	chrX	Clcn5	7153810	7159819	11452	0.961969	3.999044	0.000129	0.000573	0.071044	1	131	98	174	158	374	314	597	325	677	582
ENSMUSG00000021549	chr13	Rasa1	85214780	85216187	7296	-0.69673	4.122844	0.000129	0.000573	0.036476	-1	314	296	419	334	443	174	376	377	388	257
ENSMUSG00000026311	chr1	Asb1	91540544	91540864	6432	-0.61316	4.190298	0.000129	0.000573	0.027736	-1	329	333	420	370	380	253	384	341	413	297
ENSMUSG00000007050	chr17	Lsm2	34981862	34982085	3152	0.78197	3.3014	0.00013	0.000577	0.043906	1	97	86	123	116	186	238	263	204	399	345
ENSMUSG00000069744	chr11	Psmb3	97703399	97703490	2300	0.749006	6.51384	0.00013	0.000579	0.044817	1	944	1142	1426	976	1190	2129	2213	3805	2670	2449
ENSMUSG00000038594	chr10	Cep85l	53278081	53278244	2691	-2.47953	3.439693	0.000131	0.00058	0.437737	-1	361	272	380	270	226	8	34	291	37	17
ENSMUSG00000060860	chr7	Ube2s	4808155	4808484	858	0.629636	4.91062	0.000131	0.00058	0.030399	1	341	344	464	388	430	780	734	733	1141	862
ENSMUSG00000044350	chr14	Lacc1	77024200	77024974	3644	1.393006	2.105633	0.000131	0.000581	0.138423	1	34	10	22	49	83	109	162	89	171	176
ENSMUSG00000074818	chr19	Pdzd7	45026906	45027974	4089	-1.39387	3.165163	0.000131	0.000581	0.146107	-1	167	153	280	176	332	117	154	22	98	173
ENSMUSG00000089945	chr4	Palm2Akap2	57568179	57568415	8456	-0.73835	5.54989	0.000131	0.000582	0.043142	-1	711	909	1073	1270	911	565	1030	590	1116	859
ENSMUSG00000032562	chr9	Gnai2	1.08E+08	1.08E+08	3779	0.727185	6.841449	0.000132	0.000583	0.042425	1	1048	1185	1505	1700	1846	2429	3345	2246	5125	3869
ENSMUSG00000025402	chr10	Nab2	1.28E+08	1.28E+08	2941	0.85458	3.545349	0.000132	0.000583	0.054333	1	125	77	143	125	233	250	407	236	528	348
ENSMUSG00000062604	chr5	Srpk2	23503356	23507720	6436	-0.58771	4.951514	0.000132	0.000583	0.026471	-1	504	524	728	634	727	419	610	638	663	563
ENSMUSG00000041836	chr7	Ptpre	1.36E+08	1.36E+08	5411	1.234044	2.509701	0.000132	0.000585	0.110093	1	63	17	54	61	86	88	150	142	318	247
ENSMUSG00000060429	chr15	Sntb1	55638843	55639427	2869	-1.21185	2.533498	0.000132	0.000585	0.107512	-1	54	165	107	191	152	40	119	95	95	62
ENSMUSG00000022514	chr16	Il1rap	26581704	26581886	11360	-0.93436	2.031783	0.000134	0.000592	0.057713	-1	63	61	122	81	125	39	79	73	75	60
ENSMUSG00000085711	chrX	Gm15163	1.57E+08	1.57E+08	1302	-1.11817	0.858485	0.000134	0.000594	0.068976	-1	29	42	46	50	32	23	26	21	34	25
ENSMUSG00000024776	chr19	Stambpl1	34192229	34192631	5557	1.296057	1.335169	0.000134	0.000595	0.107597	1	25	11	21	18	42	53	96	40	108	105
ENSMUSG00000054752	chr4	Fsd1l	53631471	53631612	9739	-0.70695	4.099072	0.000135	0.000595	0.037649	-1	309	293	449	315	415	257	378	203	408	277
ENSMUSG00000103114	chr1	RP23-103B18.8	1.91E+08	1.91E+08	2385	-1.54617	1.266168	0.000135	0.000597	0.163358	-1	50	56	73	78	33	22	32	6	30	51
ENSMUSG00000033355	chr15	Fkbp11	98724373	98724602	731	1.481756	1.77115	0.000136	0.000601	0.153043	1	27	17	32	21	50	124	120	26	163	127
ENSMUSG00000058838	chr9	Rps27a-ps2	83409660	83410126	467	0.919307	4.154292	0.000136	0.000601	0.065251	1	157	212	347	109	203	473	551	547	460	630
ENSMUSG00000033900	chr3	Map9	82358044	82358171	6671	-1.10368	0.980879	0.000136	0.000602	0.069083	-1	47	37	52	38	43	25	28	17	45	28
ENSMUSG00000045751	chr4	Mms22l	24496451	24497065	6382	1.569659	0.709999	0.000137	0.000603	0.151342	1	6	15	14	11	17	42	40	15	93	77
ENSMUSG00000033769	chr6	Exoc6b	84618487	84621511	11187	-0.59471	3.945712	0.000138	0.000608	0.025576	-1	259	253	331	327	381	218	278	296	323	315
ENSMUSG00000021556	chr13	Golm1	59634996	59637401	3693	-0.88071	4.387279	0.000138	0.00061	0.06038	-1	258	474	552	568	408	342	264	248	377	465
ENSMUSG00000029536	chr5	Gatc	1.15E+08	1.15E+08	1794	-0.62846	4.860237	0.000138	0.000611	0.030498	-1	492	513	657	629	653	510	549	435	624	520
ENSMUSG00000020576	chr12	Nbas	13269127	13269264	7239	-0.61242	4.36252	0.000139	0.000611	0.028204	-1	345	292	481	433	550	285	407	370	491	356
ENSMUSG00000035401	chr7	2210018M11Rik	98590615	98590884	4005	-0.68803	3.586682	0.000139	0.000611	0.03447	-1	242	189	222	263	318	130	223	215	272	245
ENSMUSG00000050312	chr16	Nsun3	62732444	62735418	4816	-0.84247	2.941564	0.000139	0.000612	0.050799	-1	114	149	194	187	178	75	127	183	151	108
ENSMUSG00000006281	chr14	Tep1	50824062	50824290	8168	0.681345	4.488048	0.000139	0.000613	0.035588	1	270	200	304	250	428	403	652	612	797	793
ENSMUSG00000021203	chr12	Otub2	1.03E+08	1.03E+08	3695	-0.83307	2.36501	0.000139	0.000614	0.045444	-1	96	76	121	121	135	77	82	75	88	102
ENSMUSG00000021798	chr14	Ldb3	34526699	34529549	6016	-0.6586	11.00712	0.00014	0.000614	0.035512	-1	34879	35677	52515	41625	47003	38496	36116	32813	41406	34690
ENSMUSG00000057278	chr6	Snrpg	86371583	86371614	350	0.711774	3.421804	0.00014	0.000618	0.036056	1	132	117	161	110	150	264	355	237	383	298
ENSMUSG00000022108	chr14	Itm2b	73362231	73363143	1773	0.591995	8.361152	0.000141	0.000621	0.028649	1	3855	3362	5160	4442	5253	7383	9571	9435	10199	9499
ENSMUSG00000096795	chr10	Zfp433	81718919	81719045	1800	-1.3972	-0.1616	0.000141	0.000621	0.088241	-1	17	16	28	16	24	8	5	18	15	7
ENSMUSG00000002808	chr13	Epdr1	19591709	19593348	2386	-0.70002	6.917817	0.000142	0.000622	0.03973	-1	2558	2346	2735	2522	2145	2071	2134	2073	2385	1968
ENSMUSG00000033083	chr14	Tbc1d4	1.01E+08	1.01E+08	7676	-0.76381	5.135257	0.000142	0.000623	0.04624	-1	658	531	773	652	1137	385	563	862	563	667
ENSMUSG00000031519	chr8	Asb5	54550331	54550640	1579	-0.84529	6.876263	0.000142	0.000625	0.057866	-1	2148	2334	2718	2549	2842	1349	1895	3295	1856	1374
ENSMUSG00000050105	chr4	Grrp1	1.34E+08	1.34E+08	1275	0.953688	1.826096	0.000143	0.000626	0.056931	1	27	46	47	37	36	91	96	95	145	101
ENSMUSG00000020432	chr11	Tcn2	3917192	3917709	2178	0.646026	5.377075	0.000143	0.000626	0.032989	1	419	442	555	616	690	757	1127	1075	1541	1501
ENSMUSG00000074807	chr2	Gm10762	1.29E+08	1.29E+08	1133	-0.72104	3.635982	0.000143	0.000626	0.038266	-1	231	228	287	280	254	203	169	258	214	232
ENSMUSG00000022698	chr16	Naa50	44139830	44140111	4648	-0.60408	8.020119	0.000143	0.000627	0.029837	-1	4212	4686	6775	4669	5990	3830	4689	4940	5917	4751
ENSMUSG00000037736	chr5	Limch1	66745835	66746005	7411	-0.63226	6.904208	0.000143	0.000628	0.032445	-1	2236	1894	2853	2343	2901	1771	2340	2526	2343	1940
ENSMUSG00000029705	chr5	Cux1	1.36E+08	1.36E+08	20024	-0.59298	6.251841	0.000144	0.000632	0.028304	-1	1254	1330	1715	1670	1698	1129	1407	1471	1688	1406
ENSMUSG00000062328	chr18	Rpl17	75000477	75000543	775	0.600625	7.527952	0.000145	0.000633	0.029449	1	2092	2184	2880	2249	2887	4384	5309	5118	5671	5360
ENSMUSG00000034320	chr18	Slc26a2	61192919	61199658	12370	-0.70789	3.779683	0.000145	0.000634	0.037386	-1	252	207	341	250	386	193	284	163	321	261
ENSMUSG00000041949	chr8	Tango6	1.07E+08	1.07E+08	4409	-0.75072	2.866225	0.000145	0.000634	0.038959	-1	140	129	160	167	159	97	141	98	151	145

ENSMUSG00000027424	chr2	Mgme1	1.44E+08	1.44E+08	3348	-0.71324	3.163257	0.000145	0.000635	0.036115	-1	165	154	194	210	199	117	149	130	204	194
ENSMUSG00000079444	chr17	Gm21981	47686739	47687008	2721	0.625021	5.646655	0.000145	0.000635	0.031096	1	508	640	689	710	734	1279	1270	1281	1623	1587
ENSMUSG00000027752	chr3	Exosc8	54728678	54728893	3968	0.789232	3.077979	0.000145	0.000637	0.044069	1	90	97	112	101	107	217	242	161	334	281
ENSMUSG00000008682	chrX	Rpl10	74270812	74270874	2053	0.619238	8.149889	0.000147	0.000645	0.031489	1	2954	3612	4384	3147	4720	6638	8620	7837	9010	7963
ENSMUSG00000032353	chr9	Tmed3	89699205	89699979	2848	0.806363	5.05082	0.000147	0.000645	0.051802	1	364	260	425	326	678	788	1104	604	1338	1119
ENSMUSG00000032185	chr9	Carm1	21546894	21547230	4324	-0.62159	6.257242	0.000148	0.000645	0.031229	-1	1119	1324	1636	1638	2121	1165	1370	1445	1752	1310
ENSMUSG00000025279	chr14	Dnase1l3	7964533	7967875	5151	1.644419	-0.1777	0.000148	0.000646	0.134525	1	4	3	4	8	12	34	31	10	31	26
ENSMUSG00000031575	chr8	Ash2l	25816191	25817508	5236	0.579472	4.750289	0.000148	0.000648	0.02575	1	310	295	435	364	398	545	752	807	928	744
ENSMUSG00000032575	chr9	Manf	1.07E+08	1.07E+08	3524	0.923624	4.976226	0.000149	0.00065	0.068096	1	286	311	382	269	593	919	975	434	1271	1192
ENSMUSG00000056753	chr8	C330011M18Rik	84065236	84066803	1849	-1.32134	-0.15504	0.000149	0.00065	0.07138	-1	14	14	23	24	25	9	6	14	13	13
ENSMUSG00000008658	chr16	Rbfox1	6809222	6809248	4151	-0.86412	7.194613	0.000149	0.000651	0.060892	-1	3022	2517	3383	3350	3503	1816	2147	4084	1907	2015
ENSMUSG00000098992	chr11	Gm27597	98029413	98029492	80	0.600809	7.132358	0.00015	0.000653	0.029511	1	1472	1656	2305	1672	2283	3032	3923	3941	4693	4214
ENSMUSG00000007107	chr1	Atp1a4	1.72E+08	1.72E+08	3667	-1.29913	0.691088	0.00015	0.000655	0.098528	-1	40	22	27	32	66	22	23	18	28	13
ENSMUSG00000029817	chr6	Tra2a	49243921	49244731	1828	0.772507	4.342454	0.00015	0.000655	0.046399	1	262	210	298	177	296	528	651	369	692	722
ENSMUSG00000032114	chr9	Slc37a4	44398176	44398621	2083	-0.7023	7.299278	0.000151	0.000659	0.040422	-1	2779	2866	3683	3133	3892	3044	2475	2142	3059	3017
ENSMUSG00000029004	chr5	Kmt2e	23434441	23434783	7607	-0.87289	4.713381	0.000151	0.00066	0.060741	-1	518	399	544	637	754	199	404	716	491	386
ENSMUSG00000032177	chr9	Pde4a	21165714	21166232	7655	-0.97122	5.887061	0.000152	0.000661	0.076312	-1	1110	1116	1435	1492	1388	954	962	335	1272	1129
ENSMUSG00000046828	chr1	Mettl21e	44204070	44206753	3961	-1.07699	3.648048	0.000152	0.000661	0.08982	-1	246	314	259	373	189	186	100	193	158	282
ENSMUSG00000024083	chr17	Pja2	64281005	64283538	4740	-0.60434	7.020687	0.000153	0.000666	0.029937	-1	2174	2233	2915	2726	3092	1814	2596	2648	2872	2144
ENSMUSG00000028399	chr4	Ptprd	75941238	75945026	22702	-0.90189	3.58149	0.000153	0.000668	0.062601	-1	285	159	283	222	360	84	255	253	202	192
ENSMUSG00000056492	chr17	Gpr116	43389466	43389707	8535	-0.91735	6.084087	0.000154	0.00067	0.068442	-1	1017	1222	1752	2200	1216	622	825	1679	1233	1184
ENSMUSG00000039100	chr15	March6	31455899	31459279	6236	-0.68374	7.139218	0.000154	0.000671	0.038402	-1	2693	2386	3251	2791	3424	2015	2252	3445	2594	2245
ENSMUSG00000079499	chr2	6530402F18Rik	29245107	29248878	5511	-0.9431	2.769007	0.000154	0.000671	0.064772	-1	77	157	172	186	154	99	109	70	139	123
ENSMUSG00000038729	chr4	Akap2	57717657	57717758	8163	-0.72966	5.539677	0.000154	0.000671	0.043032	-1	704	906	1055	1259	903	566	1023	589	1111	856
ENSMUSG00000027900	chr3	Dram2	1.07E+08	1.07E+08	3863	-0.69019	5.614172	0.000154	0.000671	0.038476	-1	993	899	1170	935	1018	593	807	1227	954	806
ENSMUSG00000051674	chr5	Dcun1d4	73481002	73481094	5803	-0.71278	3.51046	0.000155	0.000674	0.037545	-1	238	197	248	207	285	124	226	256	219	185
ENSMUSG00000047676	chr3	Rpsa-ps10	1.5E+08	1.5E+08	1031	0.660148	3.553402	0.000156	0.000676	0.031409	1	113	144	187	143	168	280	334	280	385	381
ENSMUSG00000025246	chrX	Tbl1x	77511013	77511269	7052	-0.61877	4.540023	0.000156	0.000676	0.029682	-1	339	383	521	509	628	279	414	425	571	481
ENSMUSG00000035215	chr10	Lsm7	80852825	80853100	468	0.699797	3.256295	0.000156	0.000679	0.034442	1	119	109	149	97	124	221	285	244	326	289
ENSMUSG00000035437	chr2	Rabgap1	37443279	37443456	7607	-0.66251	5.346615	0.000156	0.000679	0.035242	-1	780	711	968	788	910	494	776	985	798	635
ENSMUSG00000040044	chr4	Orc3	34570796	34571018	6088	-0.61956	4.753587	0.000157	0.000682	0.03005	-1	451	514	663	483	619	372	475	606	547	479
ENSMUSG00000032387	chr9	Rbpms2	65629648	65629722	2041	1.23757	1.791611	0.000157	0.000683	0.106225	1	34	23	28	37	43	73	70	61	162	190
ENSMUSG00000031709	chr8	Tbc1d9	83165352	83166204	5887	1.015951	2.144695	0.000158	0.000686	0.071541	1	33	35	58	60	53	72	135	91	218	175
ENSMUSG00000033389	chr11	Arhgap44	65002039	65003450	5819	-0.76293	2.808297	0.000159	0.000689	0.040419	-1	125	128	147	158	172	98	150	123	122	105
ENSMUSG00000063382	chr9	Bcl9l	44499136	44499273	5304	-0.75567	4.608565	0.000159	0.00069	0.045421	-1	514	341	481	546	688	224	391	583	515	437
ENSMUSG00000064346	chrMT	mt-Tw	4950	5016	67	-0.97161	5.708658	0.000159	0.000691	0.076819	-1	1002	1301	763	1779	751	680	659	846	1181	789
ENSMUSG00000025630	chrX	Hprt	52988137	52988250	1289	0.597153	4.957958	0.00016	0.000694	0.027959	1	387	391	446	371	453	665	789	854	1126	951
ENSMUSG00000058290	chr15	Espl1	1.02E+08	1.02E+08	6630	1.269742	1.416443	0.000161	0.000696	0.109631	1	16	15	21	19	57	55	80	54	139	100
ENSMUSG00000005566	chr7	Trim28	13024152	13025061	4044	0.640043	5.930021	0.000161	0.000699	0.033375	1	623	614	834	741	1237	1330	1625	1715	2301	1759
ENSMUSG00000026536	chr1	Mnda	1.74E+08	1.74E+08	1785	1.252792	2.236707	0.000162	0.000699	0.115371	1	48	20	54	42	66	194	107	75	155	200
ENSMUSG00000029605	chr5	Oas1b	1.21E+08	1.21E+08	1992	1.742947	0.326292	0.000162	0.000701	0.178828	1	5	10	10	10	8	63	26	13	35	57
ENSMUSG00000067780	chr1	Pi15	17601901	17602042	6923	-0.97216	2.712332	0.000162	0.000701	0.069977	-1	127	91	125	123	271	66	109	108	162	78
ENSMUSG00000049739	chr7	Zfp646	1.28E+08	1.28E+08	6727	-0.72723	3.793025	0.000162	0.000701	0.040381	-1	261	193	277	311	413	159	225	326	292	222
ENSMUSG00000041406	chr1	BC055324	1.64E+08	1.64E+08	4148	1.517024	0.188939	0.000163	0.000703	0.125962	1	8	4	13	5	14	22	28	16	62	51
ENSMUSG00000039630	chr1	Hnrnpu	1.78E+08	1.78E+08	8959	0.587711	7.152256	0.000163	0.000704	0.028556	1	1596	1607	2036	1935	2367	2986	3810	4240	4886	4125
ENSMUSG00000079017	chr12	Ifi27l2a	1.03E+08	1.03E+08	463	1.731334	5.070788	0.000163	0.000704	0.234976	1	262	167	192	246	444	668	585	243	1298	3331
ENSMUSG00000027742	chr3	Cog6	52981875	52983191	4957	-0.69526	5.979269	0.000165	0.000714	0.039608	-1	1244	1130	1523	1300	1279	929	1101	1485	1137	922
ENSMUSG00000021893	chr14	Capn7	31336638	31336983	4733	-0.57803	5.574664	0.000166	0.000715	0.026953	-1	797	847	1105	998	1017	751	919	861	988	924
ENSMUSG00000043535	chr2	Setx	29124181	29124269	11380	-0.61771	5.296637	0.000167	0.000719	0.030731	-1	684	642	917	835	910	522	739	886	879	611
ENSMUSG00000049804	chrX	Armcx4	1.35E+08	1.35E+08	7996	-0.9079	5.696607	0.000167	0.00072	0.067503	-1	714	940	1321	984	1841	717	1215	433	1173	700
ENSMUSG00000027602	chr2	Map1lc3a	1.55E+08	1.55E+08	1181	0.755432	7.875483	0.000167	0.000721	0.047473	1	2862	2833	3255	2851	2587	5769	5214	9539	7315	6331
ENSMUSG00000026708	chr1	Cenpl	1.61E+08	1.61E+08	5695	1.226051	0.829389	0.000168	0.000722	0.085248	1	16	17	19	8	22	38	50	34	85	67
ENSMUSG00000020827	chr11	Mink1	70562881	70563126	6286	-0.58323	4.892937	0.000169	0.000727	0.026945	-1	500	534	674	613	651	384	611	511	702	594
ENSMUSG00000026676	chr2	Ccdc3	5137776	5138307	2670	-1.0308	4.115047	0.000169	0.000727	0.085037	-1	525	152	466	228	597	173	267	294	359	253
ENSMUSG00000029128	chr5	Rab28	41624976	41625862	1636	-0.6484	5.958718	0.000169	0.000729	0.034487	-1	1123	1266	1430	1277	1180	1026	1114	1163	1208	1087
ENSMUSG00000033361	chrX	Prrg3	71962624	71962779	6087	-0.72321	3.471733	0.000169	0.000729	0.039347	-1	200	160	260	275	261	118	221	218	275	158
ENSMUSG00000094638	chr1	Gm21972	86133637	86133784	776	0.704952	5.639496	0.000169	0.000729	0.040589	1	525	607	755	609	657	1267	1148	1880	1315	1483
ENSMUSG00000026409	chr1	Pfkfb2	1.31E+08	1.31E+08	7254	-0.73361	3.239305	0.00017	0.00073	0.039435	-1	176	155	244	232	169	125	195	156	184	164
ENSMUSG00000060703	chr2	Cd302	60251993	60252491	1354	0.664924	3.719389	0.00017	0.00073	0.033069	1	160	126	198	135	233	284	384	429	409	363
ENSMUSG00000071573	chr19	Rnls	33137747	33138274	1627	-0.93883	1.872722	0.00017	0.00073	0.058251	-1	65	96	83	75	71	51	60	52	71	54
ENSMUSG00000021302	chr13	Ggps1	14052449	14054455	2367	-0.88823	2.937026	0.00017	0.000732	0.058666	-1	145	113	199	171	206	85	110	191	158	83
ENSMUSG00000033306	chr16	Lpp	24393350	24393604	15994	-0.71039	5.24282	0.000171	0.000734	0.041	-1	652	554	923	722	1145	521	867	452	814	714
ENSMUSG00000030201	chr6	Lrp6	1.34E+08	1.34E+08	9822	-0.60554	6.058201	0.000171	0.000734	0.030136	-1	1167	1129	1520	1235	1707	841	1305	1422	1420	1220
ENSMUSG00000000340	chr3	Dbt	1.17E+08	1.17E+08	3296	-0.76177	5.290152	0.000172	0.000736	0.047373	-1	713	684	852	852	1023	406	572	1059	648	711
ENSMUSG00000036501	chr18	Fam13b	34442352	34442765	3343	-0.73832	3.154251	0.000173	0.000741	0.039971	-1	156	130	227	174	251	97	198	159	177	150
ENSMUSG00000027775	chr3	Mfsd1	67582741	67582977	3042	0.636145	5.016485	0.000173	0.000743	0.032398	1	378	369	493	383	491	649	748	835	1252	1163

ENSMUSG00000086605	chr2	Gm14290	1.67E+08	1.67E+08	1894	-1.13401	4.201999	0.000173	0.000743	0.10332	-1	275	363	452	486	560	311	260	70	380	309
ENSMUSG00000035764	chr16	Fbxo45	32230112	32233268	4179	-0.64617	4.769762	0.000174	0.000746	0.033282	-1	397	574	699	535	571	410	454	544	531	528
ENSMUSG00000050002	chr13	Idnk	58157649	58157736	1511	0.938537	2.426431	0.000175	0.000749	0.061569	1	59	63	62	57	55	141	181	93	218	175
ENSMUSG00000034361	chr8	Cpne2	94532990	94533193	3198	0.75547	3.803726	0.000175	0.000749	0.044397	1	130	121	226	120	288	320	467	415	438	387
ENSMUSG00000030469	chr7	Zfp719	43579610	43579766	4706	-0.89715	2.283415	0.000175	0.000749	0.056141	-1	88	86	116	94	144	47	97	105	87	59
ENSMUSG00000025134	chr11	Alyref	1.21E+08	1.21E+08	3839	0.609961	4.081101	0.000175	0.000749	0.028118	1	203	215	232	194	264	414	437	459	576	480
ENSMUSG00000029551	chr5	Psmg3	1.4E+08	1.4E+08	2893	0.683153	3.31099	0.000175	0.000749	0.033764	1	99	107	142	126	159	276	265	250	323	283
ENSMUSG00000025266	chrX	Gnl3l	1.51E+08	1.51E+08	5570	-0.61677	4.940037	0.000177	0.000756	0.030447	-1	510	508	784	543	789	449	645	612	602	508
ENSMUSG00000033355	chr16	Rtp4	23609919	23610149	1573	1.395115	3.063697	0.000177	0.000756	0.151266	1	59	67	82	77	96	390	182	86	201	468
ENSMUSG00000039968	chr5	Rsbn1l	20893028	20896704	5550	-0.84558	3.388885	0.000177	0.000756	0.055034	-1	204	174	253	224	269	88	193	270	156	168
ENSMUSG00000043126	chr10	D830039M14Rik	61475245	61476937	1693	-0.8702	2.6662	0.000177	0.000756	0.054451	-1	113	128	164	152	118	111	83	107	101	107
ENSMUSG00000096942	chr12	Rps19-ps6	1.11E+08	1.11E+08	438	0.765382	2.907885	0.000177	0.000757	0.04154	1	87	86	118	65	100	184	231	213	237	215
ENSMUSG00000036078	chr4	Sigmar1	41738493	41739580	3136	0.784609	3.767708	0.000179	0.000764	0.04782	1	155	116	139	175	251	268	353	302	554	552
ENSMUSG00000030116	chr6	Mfap5	1.23E+08	1.23E+08	3589	0.79788	5.74587	0.000179	0.000765	0.052652	1	631	395	582	645	1071	1231	2185	1132	1866	1556
ENSMUSG00000060992	chr15	Copz1	1.03E+08	1.03E+08	1669	0.650692	5.766624	0.000179	0.000766	0.034851	1	575	648	735	701	885	1328	1467	1116	1958	1899
ENSMUSG00000079641	chrX	Rpl39	37082520	37082749	1434	0.67979	6.728242	0.000179	0.000766	0.038591	1	1124	1361	1774	991	1571	2550	3489	3034	3067	2979
ENSMUSG00000035849	chr11	Krt222	99232761	99235147	3292	-1.18437	2.593473	0.00018	0.000768	0.106173	-1	91	144	131	173	155	96	50	53	68	149
ENSMUSG00000037447	chr1	Arid5a	36307733	36307836	12540	1.009766	3.527841	0.000181	0.00077	0.080432	1	97	81	149	131	188	244	287	639	413	200
ENSMUSG00000031299	chrX	Pdha1	1.6E+08	1.6E+08	3734	-0.7122	9.534441	0.000181	0.000774	0.042877	-1	12286	16610	16685	17663	12603	10440	12304	15923	15289	11666
ENSMUSG00000073489	chr1	Ifi204	1.74E+08	1.74E+08	3561	1.145572	3.783809	0.000183	0.00078	0.10489	1	159	72	156	120	213	503	329	207	381	714
ENSMUSG00000026790	chr2	Odf2	29889221	29889278	9919	0.780711	3.678219	0.000184	0.000783	0.047189	1	156	115	144	143	226	220	344	543	422	360
ENSMUSG00000030304	chr6	Ergic2	1.48E+08	1.48E+08	6727	-0.60928	5.436344	0.000184	0.000783	0.030393	-1	797	857	1037	778	865	649	879	799	928	742
ENSMUSG00000021322	chr13	Aoah	20794119	20794517	2915	1.59124	-0.13268	0.000185	0.00079	0.134022	1	5	2	8	7	11	23	28	9	33	45
ENSMUSG00000036779	chr8	Papd5	88199213	88199313	4937	-0.66381	4.001543	0.000185	0.00079	0.03424	-1	264	262	381	357	382	197	270	396	332	254
ENSMUSG00000070583	chr4	Fv1	1.48E+08	1.48E+08	1380	-1.09556	1.501903	0.000186	0.00079	0.07913	-1	64	46	84	54	69	38	44	54	49	20
ENSMUSG00000092659	chr7	Mir3100	19086828	19086892	65	-1.10054	1.210323	0.000186	0.000792	0.076411	-1	23	48	55	55	81	23	30	40	41	34
ENSMUSG00000098503	chr11	Gm27937	3646942	3647029	88	-1.3774	0.252606	0.000186	0.000792	0.108582	-1	32	14	25	28	38	6	16	25	19	8
ENSMUSG00000000346	chr15	Dazap2	1.01E+08	1.01E+08	1826	0.690844	6.330205	0.000186	0.000793	0.039882	1	915	895	1167	1098	1045	1572	1969	3259	2571	2264
ENSMUSG00000046753	chr14	Ccdc66	27482412	27482602	2940	-0.78966	2.757553	0.000186	0.000793	0.04517	-1	123	124	129	167	165	73	141	131	132	101
ENSMUSG00000050212	chr4	Eva1b	1.26E+08	1.26E+08	1942	0.652578	3.218806	0.000187	0.000794	0.030192	1	111	98	120	125	143	207	270	261	312	264
ENSMUSG00000036330	chr8	Slc18a1	69037711	69038905	5401	-1.65171	-0.16012	0.000187	0.000794	0.15409	-1	8	24	40	23	11	5	5	15	12	10
ENSMUSG00000063415	chr6	Cyp26b1	84571414	84574659	4849	-2.13335	3.585271	0.000187	0.000794	0.348863	-1	111	43	270	769	517	32	122	80	46	243
ENSMUSG00000020716	chr11	Nf1	79339693	79340059	15820	-0.59175	4.510884	0.000187	0.000795	0.027565	-1	364	369	549	491	528	337	459	451	507	367
ENSMUSG00000028068	chr3	Iqgap3	88081971	88082092	11384	1.24184	1.638088	0.000188	0.000797	0.108034	1	19	29	28	26	47	67	135	39	163	96
ENSMUSG00000025920	chr1	Stau2	16228674	16229866	6747	-0.70052	4.866267	0.000188	0.000798	0.040047	-1	500	615	757	639	468	366	537	607	645	455
ENSMUSG00000025921	chr1	Rdh10	16105774	16106306	4160	0.808319	2.568062	0.000189	0.000804	0.04564	1	62	57	78	76	80	101	227	167	218	163
ENSMUSG00000000402	chrX	Egfl6	1.67E+08	1.67E+08	2704	-1.7739	2.406773	0.00019	0.000804	0.240184	-1	182	26	172	45	282	42	92	63	54	25
ENSMUSG00000023972	chr17	Ptk7	46564451	46565495	4255	0.964085	2.668374	0.00019	0.000805	0.069237	1	69	43	70	54	123	115	249	219	252	141
ENSMUSG00000054277	chr15	Arfgap3	83299740	83300702	2618	0.782065	3.713409	0.00019	0.000805	0.047929	1	139	113	180	118	265	227	390	508	444	371
ENSMUSG00000098399	chr7	Gm27995	1.04E+08	1.04E+08	100	1.706467	-0.01026	0.00019	0.000805	0.158008	1	5	6	8	6	9	42	16	15	24	53
ENSMUSG00000022193	chr14	Psmb5	54614120	54614481	871	0.678257	7.101698	0.00019	0.000806	0.038839	1	1395	1744	2224	1577	1886	3399	3520	4646	3664	4255
ENSMUSG00000074916	chr2	Chst14	1.19E+08	1.19E+08	2090	0.898462	2.764995	0.00019	0.000806	0.059792	1	75	60	72	65	120	132	212	137	341	219
ENSMUSG00000044949	chr11	Ubtd2	32455370	32455546	1012	-0.96986	2.138108	0.000191	0.000808	0.067547	-1	90	69	96	94	136	34	102	78	81	53
ENSMUSG00000038366	chr11	Lasp1	97799000	97799197	6495	0.849523	5.694249	0.000191	0.000808	0.060182	1	484	423	580	657	1002	987	1312	980	2584	2133
ENSMUSG00000032690	chr5	Oas2	1.21E+08	1.21E+08	4451	1.664512	2.200691	0.000191	0.000809	0.210271	1	31	25	50	23	53	194	129	25	137	282
ENSMUSG00000102947	chr2	AL772372.1	93956379	93956441	747	1.282702	1.6543	0.000192	0.00081	0.11814	1	13	21	33	44	38	101	90	42	170	99
ENSMUSG00000037466	chr12	4930427A07Rik	1.13E+08	1.13E+08	3353	1.719192	0.675495	0.000192	0.000811	0.195255	1	14	4	12	6	21	29	48	14	108	72
ENSMUSG00000040829	chr11	Zmynd15	70459433	70460080	4409	1.43176	0.081112	0.000192	0.000811	0.09694	1	13	8	7	6	7	25	41	20	30	42
ENSMUSG00000022096	chr14	Hr	70552212	70552324	6919	-0.85777	5.943594	0.000192	0.000812	0.061582	-1	1029	1170	1775	1223	1477	959	1431	535	1410	779
ENSMUSG00000028898	chr4	Trnau1ap	1.32E+08	1.32E+08	2710	0.702056	3.475576	0.000192	0.000812	0.036892	1	108	126	201	135	132	242	297	373	344	334
ENSMUSG00000061740	chr15	Cyp2d22	82370528	82371725	2771	0.945925	3.474834	0.000192	0.000812	0.070143	1	116	103	121	128	160	156	252	578	346	378
ENSMUSG00000044268	chr10	Gm4895	22153280	22154416	1137	-1.50375	-0.01984	0.000193	0.000815	0.118229	-1	35	13	24	20	21	13	9	17	10	6
ENSMUSG00000015843	chr1	Rxrg	1.68E+08	1.68E+08	2297	-0.74437	5.555694	0.000194	0.000819	0.046112	-1	751	898	1312	971	1004	870	851	508	931	882
ENSMUSG00000025427	chr18	Rnf165	77456110	77462449	10134	-1.38402	0.231393	0.000194	0.00082	0.112822	-1	19	23	21	27	46	8	12	6	32	16
ENSMUSG00000055172	chr6	C1ra	1.25E+08	1.25E+08	2751	0.758968	4.916354	0.000195	0.000821	0.047435	1	360	229	348	310	660	721	812	892	932	1041
ENSMUSG00000046157	chr12	Tmem229b	78961795	78965176	4732	0.708301	3.457124	0.000195	0.000823	0.037911	1	105	91	143	148	216	256	300	270	403	352
ENSMUSG00000029723	chr5	Tsc22d4	1.38E+08	1.38E+08	7509	0.617686	5.828384	0.000195	0.000823	0.031799	1	604	574	887	696	1036	1341	1695	1309	2087	1619
ENSMUSG00000054871	chr9	Tmem158	1.23E+08	1.23E+08	1732	1.229715	1.433725	0.000196	0.000825	0.105347	1	13	17	19	27	56	54	112	78	122	61
ENSMUSG00000030726	chr7	Pold3	1E+08	1E+08	4134	0.791245	2.899712	0.000196	0.000827	0.045312	1	96	72	98	88	92	123	194	237	295	258
ENSMUSG00000073434	chr17	Wdr90	25844771	25845225	8466	1.254994	1.103075	0.000196	0.000828	0.102159	1	20	16	25	7	32	34	73	50	109	75
ENSMUSG00000040029	chr6	Ipo8	1.49E+08	1.49E+08	10623	-0.65727	4.852	0.000197	0.000828	0.035218	-1	480	458	729	508	820	414	622	379	658	554
ENSMUSG00000021294	chr12	Kif26a	1.12E+08	1.12E+08	6918	-0.8987	2.781016	0.000197	0.000828	0.061228	-1	105	135	162	202	136	56	103	135	172	105
ENSMUSG00000028634	chr4	Hivep3	1.2E+08	1.2E+08	17427	1.025821	1.946701	0.000197	0.000829	0.073909	1	36	23	37	38	75	67	105	108	170	146
ENSMUSG00000003161	chr5	Sri	8046078	8046215	3734	0.642365	4.283856	0.000197	0.000829	0.0326	1	207	215	293	238	320	438	511	403	773	660
ENSMUSG00000053565	chr7	Eif3k	28971373	28971438	773	0.605367	6.202193	0.000197	0.00083	0.030756	1	706	892	1101	1047	1156	1747	1924	1982	2429	2263
ENSMUSG00000078779	chr7	Zfp59	27842855	27842887	1962	-1.28562	0.444177	0.000198	0.000831	0.097533	-1	32	20	27	30	46	4	16	19	31	21

ENSMUSG00000035960	chr14	Apex1	50924968	50925029	1422	0.597371	4.654971	0.000198	0.000832	0.028509	1	235	327	391	329	394	566	709	642	953	681
ENSMUSG00000048118	chr12	Arid4a	71015990	71016161	5615	-0.65975	3.456396	0.000198	0.000833	0.032652	-1	209	191	236	232	246	126	237	217	239	179
ENSMUSG00000028840	chr4	Zfp593	1.34E+08	1.34E+08	2088	0.763084	2.936237	0.000198	0.000833	0.042307	1	66	85	113	80	128	176	193	274	257	206
ENSMUSG00000093989	chr11	Rnasek	70238124	70238470	885	0.612492	5.865906	0.000199	0.000837	0.031339	1	585	713	885	807	868	1526	1492	1537	1889	1712
ENSMUSG00000005233	chr2	Spc25	69193895	69194545	3188	1.446538	1.368915	0.0002	0.000838	0.149038	1	10	24	21	16	40	54	98	27	154	97
ENSMUSG00000095438	chr18	Gm21747	10781723	10781939	395	-0.8038	2.970837	0.0002	0.000838	0.048196	-1	151	180	200	135	151	124	133	142	130	124
ENSMUSG00000059327	chrX	Eda	99975606	99976176	6825	-0.72461	2.937093	0.0002	0.000841	0.037989	-1	141	113	164	155	227	113	143	124	164	125
ENSMUSG00000032097	chr9	Ddx6	44604892	44604984	6065	-0.59085	6.873279	0.000201	0.000841	0.029634	-1	2161	2011	2609	2238	2761	1637	2263	2461	2534	2057
ENSMUSG00000020114	chr10	Cand1	1.19E+08	1.19E+08	8357	0.692695	4.720373	0.000202	0.000846	0.039214	1	315	232	316	295	544	579	854	595	986	805
ENSMUSG00000034295	chr18	Fhod3	24709445	24709773	5408	-0.7514	5.544866	0.000202	0.000848	0.047293	-1	689	693	1300	1038	1273	727	1053	510	1059	714
ENSMUSG00000068101	chr15	Cenpm	82233779	82234509	1201	1.655778	-0.00225	0.000202	0.000848	0.142876	1	4	12	9	3	6	17	31	13	55	42
ENSMUSG00000089762	chr2	Ier5l	30471537	30474219	2683	0.985138	2.083161	0.000203	0.000851	0.068258	1	46	40	52	36	56	121	128	72	198	122
ENSMUSG00000022359	chr15	Wdyhv1	58141436	58141581	1322	0.794949	2.293387	0.000203	0.000852	0.041936	1	46	56	60	66	63	100	153	128	173	159
ENSMUSG00000030882	chr7	Dnhd1	1.06E+08	1.06E+08	15578	0.597954	4.4032	0.000203	0.000852	0.02817	1	256	262	311	277	284	505	586	561	644	648
ENSMUSG00000037341	chrX	Slc9a7	20105755	20106214	3819	-0.9217	1.60531	0.000203	0.000852	0.054888	-1	63	49	65	75	74	29	57	50	67	41
ENSMUSG00000032334	chr9	Loxl1	58287723	58288917	3338	1.087851	5.941302	0.000204	0.000852	0.099354	1	421	363	586	703	1346	1496	2682	823	2718	2153
ENSMUSG00000021156	chr13	Zmynd11	9684836	9686984	7055	-0.62385	6.02235	0.000205	0.000857	0.032781	-1	1154	1088	1464	1395	1494	923	1175	1497	1225	1126
ENSMUSG00000005881	chr2	Ergic3	1.56E+08	1.56E+08	2121	0.583668	5.737212	0.000207	0.000865	0.028448	1	646	610	768	647	901	1233	1514	1308	1747	1654
ENSMUSG00000001089	chr4	Luzp1	1.36E+08	1.36E+08	8112	-0.62247	4.65466	0.000207	0.000867	0.031477	-1	412	395	564	552	648	335	558	382	657	412
ENSMUSG00000025353	chr10	Ormdl2	1.29E+08	1.29E+08	2055	0.870994	2.469316	0.000208	0.000868	0.054368	1	47	55	68	61	92	131	159	104	236	196
ENSMUSG00000029720	chr5	Gm20605	1.38E+08	1.38E+08	4464	0.589575	4.771903	0.000208	0.000868	0.028076	1	303	300	400	369	455	534	769	658	1010	896
ENSMUSG00000037103	chr8	Dcaf15	84097075	84097508	2320	0.693342	3.161741	0.000208	0.000868	0.035005	1	111	90	133	95	136	201	232	236	310	299
ENSMUSG00000052727	chr13	Map1b	99421464	99425961	11852	0.920253	4.603695	0.000208	0.000868	0.070333	1	217	151	310	281	483	432	1228	696	868	523
ENSMUSG00000067148	chr17	Polr1c	46243920	46244220	2278	0.615616	3.694177	0.000208	0.000868	0.028432	1	154	158	192	141	201	282	359	335	439	404
ENSMUSG00000040543	chr11	Pitpnm3	72047528	72051360	9815	-0.85714	2.266721	0.000209	0.000871	0.051812	-1	103	65	99	105	144	55	85	64	104	91
ENSMUSG00000031504	chr8	Rab20	11453392	11454526	1446	1.303888	1.311435	0.000209	0.000874	0.115017	1	10	35	23	17	27	55	45	75	97	121
ENSMUSG00000029122	chr5	Evc	37289098	37289654	7701	-0.73316	3.963415	0.00021	0.000876	0.043253	-1	295	249	311	422	340	181	327	245	434	207
ENSMUSG00000100235	chr13	Gm28557	67069399	67071528	5037	-1.12079	1.991751	0.000211	0.000878	0.093399	-1	98	65	97	96	91	26	64	103	55	43
ENSMUSG00000012076	chr12	Brms1l	55836366	55836645	2566	-0.63255	4.220353	0.000212	0.000884	0.03181	-1	354	354	443	324	404	310	382	335	368	291
ENSMUSG00000031295	chrX	Phka2	1.61E+08	1.61E+08	6068	0.748545	3.196874	0.000212	0.000885	0.042292	1	101	79	118	114	158	150	252	262	341	344
ENSMUSG00000007458	chr6	M6pr	1.22E+08	1.22E+08	4170	0.656471	5.58462	0.000213	0.000886	0.036181	1	516	543	706	589	769	822	1175	1212	2103	1712
ENSMUSG00000078348	chr10	Sf3b5	13005343	13009183	3841	0.640198	4.337264	0.000213	0.000887	0.032839	1	194	263	309	239	312	512	537	454	675	671
ENSMUSG00000026219	chr1	Trip12	84721189	84724814	16601	-0.5944	7.322863	0.000213	0.000887	0.030355	-1	2572	2749	3842	3057	4017	2356	3164	3282	3367	2715
ENSMUSG00000001794	chr7	Capns1	30186942	30187533	2397	0.593211	7.75904	0.000213	0.000888	0.030318	1	2208	2592	3071	3003	3643	4949	5406	6454	7309	6317
ENSMUSG00000027650	chr2	Tti1	1.58E+08	1.58E+08	4129	-0.57506	4.484378	0.000213	0.000888	0.026404	-1	402	374	510	464	481	345	440	423	510	377
ENSMUSG00000055305	chr7	Zfp93	24270420	24270681	2666	-0.80834	2.338333	0.000215	0.000893	0.045486	-1	109	99	119	98	101	64	87	99	94	80
ENSMUSG00000021982	chr14	Cdadc1	59560896	59560921	1901	-0.59868	4.518592	0.000215	0.000895	0.028859	-1	393	429	563	458	450	358	452	411	457	435
ENSMUSG00000026754	chr2	Golga1	39016261	39018489	5392	-0.61143	3.904086	0.000215	0.000895	0.02897	-1	260	252	363	285	353	205	340	277	281	273
ENSMUSG00000081643	chr1	Gm11605	63364720	63365365	646	1.466203	-0.4969	0.000215	0.000895	0.079787	1	3	5	7	3	8	17	22	13	25	24
ENSMUSG00000025791	chr4	Pgm2	99929414	99929811	2921	-0.67106	10.13228	0.000216	0.000896	0.039034	-1	18825	22312	27205	22979	23575	20575	17086	16589	22732	22777
ENSMUSG00000046873	chrX	Mbtps2	1.58E+08	1.58E+08	10105	-0.69819	3.953152	0.000216	0.000896	0.038973	-1	280	233	409	289	404	166	272	384	323	243
ENSMUSG00000091264	chr13	Smim13	41249860	41250314	4464	-0.62173	6.157682	0.000216	0.000897	0.032862	-1	1201	1422	1600	1513	1446	1192	1329	1227	1415	1342
ENSMUSG00000021069	chr12	Pygl	70190811	70191156	3828	2.157313	4.344619	0.000218	0.000904	0.365569	1	88	51	66	205	223	137	255	186	1371	2150
ENSMUSG00000056121	chr17	Fez2	78377885	78378745	2020	-0.67317	6.154336	0.000218	0.000905	0.038637	-1	1314	1414	1781	1373	1375	1275	1279	1003	1527	1261
ENSMUSG00000090122	chrX	Kcne1l	1.42E+08	1.42E+08	1543	1.154562	4.400056	0.000219	0.000909	0.111262	1	61	176	190	257	452	629	453	794	634	816
ENSMUSG00000037060	chr7	Prkcdbp	1.05E+08	1.05E+08	1035	0.646734	4.716675	0.000219	0.00091	0.034311	1	311	292	364	310	433	626	938	536	913	723
ENSMUSG00000001333	chr4	Sync	1.29E+08	1.29E+08	2862	-0.76058	5.099972	0.000219	0.00091	0.048656	-1	496	611	939	806	782	392	722	826	621	415
ENSMUSG00000081603	chrX	Gm14681	66778442	66778852	411	0.992284	1.149816	0.00022	0.00091	0.056677	1	18	24	30	18	27	60	64	65	73	61
ENSMUSG00000045761	chr17	Fam179a	71673261	71673499	5624	0.88062	3.046777	0.00022	0.000913	0.059889	1	94	88	89	81	125	221	335	172	339	167
ENSMUSG00000031871	chr8	Cdh5	1.04E+08	1.04E+08	3986	-0.77182	6.597092	0.00022	0.000913	0.05117	-1	1346	1845	2292	3028	1652	1124	1562	1609	2454	1760
ENSMUSG00000036533	chr17	Cdc42ep3	79334025	79335716	1967	-0.63294	4.600758	0.000221	0.000914	0.032775	-1	468	474	504	475	515	377	554	373	500	405
ENSMUSG00000037362	chr15	Nov	54745702	54746037	2869	-1.24841	3.83694	0.000221	0.000914	0.128441	-1	429	151	298	220	607	123	376	192	202	98
ENSMUSG00000097195	chr9	Snhg5	88521050	88521448	1730	1.201238	3.516579	0.000221	0.000914	0.11728	1	97	110	139	99	127	169	258	832	256	322
ENSMUSG00000024440	chr18	Pcdh12	38267092	38269211	6055	-1.01123	3.144613	0.000222	0.000916	0.082301	-1	123	188	227	282	159	98	153	77	260	114
ENSMUSG00000024889	chr19	Rce1	4622551	4623242	1446	0.887396	2.554913	0.000222	0.000916	0.057773	1	58	68	81	55	74	127	192	104	235	224
ENSMUSG00000040312	chr17	Cchcr1	35517100	35517229	5508	1.193968	1.410633	0.000221	0.000916	0.097981	1	19	22	22	26	40	44	85	43	124	125
ENSMUSG00000034940	chr11	Synrg	83964428	83964546	8744	-0.61209	5.66651	0.000223	0.00092	0.031659	-1	842	813	1172	1031	1320	765	899	1163	1024	815
ENSMUSG00000017631	chr11	Abr	76416734	76419193	9730	0.62666	4.521796	0.000223	0.000921	0.03192	1	260	240	307	282	427	463	817	547	816	628
ENSMUSG00000037849	chr1	Gm4955	1.73E+08	1.73E+08	3030	2.576767	0.411825	0.000223	0.000921	0.455486	1	2	2	2	8	16	79	28	5	18	94
ENSMUSG00000006134	chr16	Crkl	17451987	17452788	3863	-0.62659	4.570739	0.000223	0.000921	0.032084	-1	417	382	520	509	589	313	430	571	489	378
ENSMUSG00000037325	chr3	Bbs7	36573142	36573622	3957	-0.75249	3.09018	0.000223	0.000922	0.043182	-1	185	157	234	150	153	116	159	133	174	155
ENSMUSG00000002326	chr14	Gmpr2	55672235	55672384	1543	0.86616	2.477541	0.000224	0.000924	0.05434	1	49	51	85	59	82	127	147	110	236	211
ENSMUSG00000025001	chr19	Hells	38930915	38931075	7205	1.344519	1.398193	0.000227	0.000937	0.127411	1	18	27	22	12	39	52	97	34	149	99
ENSMUSG00000040563	chr9	Lppr2	21937033	21937158	2750	1.397122	0.86846	0.000227	0.000937	0.127552	1	16	10	9	16	27	45	81	22	65	74
ENSMUSG00000024712	chr19	Rfk	17394043	17394392	2603	-0.64013	6.293539	0.000228	0.00094	0.035196	-1	1388	1585	1890	1537	1520	1242	1339	1641	1514	1361
ENSMUSG00000001376	chr6	Ccdc132	3498382	3498555	9936	-0.63819	4.762558	0.000229	0.000946	0.033801	-1	488	559	620	461	615	359	433	625	562	502

ENSMUSG00000036934	chr8	4921524J17Rik	85408759	85409890	1595	-0.65992	3.323778	0.00023	0.000948	0.032731	-1	157	179	252	200	237	136	196	206	213	152
ENSMUSG00000067369	chrX	Trmt2b	1.34E+08	1.34E+08	4648	-0.76209	4.400281	0.000231	0.00095	0.048297	-1	339	488	513	487	360	316	398	229	511	382
ENSMUSG00000099023	chr11	Gm27456	1.02E+08	1.02E+08	63	-1.45712	1.422484	0.000231	0.000952	0.156366	-1	56	47	89	58	76	17	24	78	32	13
ENSMUSG00000034613	chr10	Ppm1h	1.23E+08	1.23E+08	10226	1.096043	2.215374	0.000232	0.000954	0.090807	1	30	31	53	72	57	88	113	91	213	229
ENSMUSG00000090673	chr19	Gm340	41582370	41583105	3729	-1.11018	0.505277	0.000232	0.000954	0.066032	-1	26	18	39	31	43	11	20	18	26	26
ENSMUSG00000023064	chr14	Sncg	34370274	34370565	852	1.422996	2.410262	0.000232	0.000955	0.158916	1	36	35	50	63	51	75	135	81	172	434
ENSMUSG00000042684	chr1	Npl	1.54E+08	1.54E+08	2961	1.008091	1.822326	0.000232	0.000955	0.070064	1	33	43	45	23	44	92	120	72	156	95
ENSMUSG00000020594	chr12	Pum2	8674134	8674170	7260	-0.61588	6.335392	0.000233	0.000957	0.032685	-1	1468	1384	1878	1617	1820	1078	1421	1889	1679	1394
ENSMUSG00000089847	chr7	Timm10b	1.06E+08	1.06E+08	4087	0.595237	4.508316	0.000234	0.000962	0.028679	1	273	281	338	307	298	554	638	619	684	665
ENSMUSG00000029263	chr5	Pigg	1.08E+08	1.08E+08	4573	-0.78729	2.804434	0.000234	0.000963	0.046555	-1	142	106	174	173	136	88	149	120	137	101
ENSMUSG00000023277	chr9	Twf2	1.06E+08	1.06E+08	2129	0.94422	6.608755	0.000235	0.000965	0.076893	1	903	996	1175	1366	1110	2034	2239	5664	2893	2092
ENSMUSG00000025321	chr12	Itgb8	1.19E+08	1.19E+08	11060	-1.4342	0.010311	0.000235	0.000965	0.119391	-1	23	13	18	27	35	5	11	22	17	5
ENSMUSG00000027247	chr2	Arhgap1	91649860	91650252	4275	0.724725	4.210075	0.000235	0.000967	0.043189	1	194	143	259	243	342	342	592	381	797	625
ENSMUSG00000029156	chr5	Sgcb	73632749	73635698	3709	-0.64241	7.436027	0.000236	0.000967	0.035974	-1	3292	3025	4086	2978	4304	2865	3462	3421	3133	2705
ENSMUSG00000020664	chr12	Dld	31331564	31332242	2241	-0.68175	8.048023	0.000236	0.000968	0.040632	-1	4481	5914	6102	5895	4449	3712	4684	5496	5636	4242
ENSMUSG00000049401	chr2	Ogfr	1.81E+08	1.81E+08	2580	0.6158	5.000145	0.000237	0.000971	0.031676	1	302	438	473	408	485	793	803	901	984	995
ENSMUSG00000025743	chr4	Sdc3	1.31E+08	1.31E+08	5989	0.796852	5.818444	0.000237	0.000974	0.054666	1	576	449	669	737	1073	1385	1734	928	2219	2141
ENSMUSG00000026479	chr1	Lamc2	1.53E+08	1.53E+08	8039	0.967418	1.657317	0.000238	0.000975	0.062331	1	23	28	34	37	51	74	124	67	119	86
ENSMUSG00000000420	chr18	Galnt1	24205344	24205518	5519	-0.56702	5.97527	0.000238	0.000976	0.027561	-1	1086	1104	1435	1275	1371	911	1235	1132	1493	1180
ENSMUSG00000002844	chr16	Adprh	38445399	38446104	1583	0.572505	5.486712	0.00024	0.000983	0.027728	1	487	564	699	550	715	1008	1390	1106	1469	1280
ENSMUSG00000099908	chr16	Gm28539	18836584	18836619	2982	-0.57784	4.399443	0.00024	0.000983	0.027022	-1	321	403	465	431	490	305	388	437	476	371
ENSMUSG00000009621	chr2	Vav2	27262104	27264211	6915	0.776935	3.050671	0.00024	0.000983	0.046024	1	78	79	99	109	143	174	297	164	320	263
ENSMUSG00000029071	chr4	Dvl1	1.56E+08	1.56E+08	4996	-0.6148	7.006468	0.00024	0.000984	0.032952	-1	2294	2418	2996	2510	2732	1829	2361	2867	2555	2225
ENSMUSG00000056211	chr1	R3hdm1	1.28E+08	1.28E+08	31486	-0.68464	5.46234	0.000242	0.000989	0.04015	-1	765	761	969	1006	1046	512	723	1164	885	683
ENSMUSG00000035948	chr10	Acss3	1.07E+08	1.07E+08	4549	-1.29158	1.428534	0.000242	0.00099	0.12342	-1	50	46	59	69	93	7	28	38	50	62
ENSMUSG00000041920	chr11	Slc16a6	1.09E+08	1.09E+08	4883	-0.89225	3.873982	0.000244	0.000999	0.066142	-1	160	340	382	252	484	200	283	130	332	259
ENSMUSG00000005320	chr13	Fgfr4	55152640	55152927	3542	0.840469	3.246598	0.000245	0.001	0.055972	1	104	73	121	102	169	167	439	231	322	262
ENSMUSG00000083325	chr2	Gm14121	1.5E+08	1.51E+08	1380	-1.00921	0.717772	0.000246	0.001005	0.054745	-1	31	28	37	36	45	18	25	28	25	26
ENSMUSG00000026234	chr1	Ncl	86344719	86350696	10188	0.608863	7.813131	0.000247	0.001011	0.032614	1	2370	2581	3590	2764	3706	4422	5498	7536	7704	6805
ENSMUSG00000027799	chr3	Nbea	55625205	55626994	10976	-0.89634	2.504057	0.000247	0.001011	0.0603	-1	103	81	157	118	161	65	115	124	84	68
ENSMUSG00000032308	chr9	Ulk3	57589452	57589686	2826	0.78936	2.560236	0.000248	0.001012	0.044973	1	58	74	74	53	95	115	197	176	205	168
ENSMUSG00000038500	chr17	Prr3	35972541	35973803	3783	0.910955	1.759863	0.000249	0.001017	0.055637	1	28	26	41	46	50	62	91	98	151	105
ENSMUSG00000014418	chr7	Hps5	46760466	46761450	6482	-0.68723	4.378817	0.000251	0.001023	0.039259	-1	328	350	555	368	571	322	377	241	470	450
ENSMUSG00000018476	chr11	Kdm6b	69398508	69399849	6954	-0.59868	5.006001	0.000251	0.001024	0.030227	-1	526	535	591	742	852	426	611	669	704	586
ENSMUSG00000074813	chr2	Gm14005	1.28E+08	1.28E+08	2045	1.067618	1.025003	0.000251	0.001025	0.066043	1	20	24	19	21	17	41	56	76	73	57
ENSMUSG00000050107	chr11	Gsg2	73135485	73138294	2810	1.577366	-0.37376	0.000251	0.001026	0.117603	1	5	4	5	3	10	17	28	8	38	24
ENSMUSG00000029683	chr6	Lmod2	24597771	24598155	1967	1.367017	6.350539	0.000252	0.001027	0.159574	1	721	594	545	1455	383	1224	3258	5025	3044	1376
ENSMUSG00000020048	chr10	Hsp90b1	86690209	86691128	4032	0.757119	7.816078	0.000253	0.00103	0.050475	1	2000	2313	3091	2480	4408	5451	7041	3862	8798	8146
ENSMUSG00000052062	chr1	Pard3b	61638824	61639362	13153	-0.90338	2.534497	0.000253	0.001033	0.062834	-1	93	107	122	139	169	49	106	137	113	68
ENSMUSG00000066842	chr1	Hmcn1	1.51E+08	1.51E+08	21191	-0.98861	2.290734	0.000256	0.001043	0.074837	-1	112	56	143	78	159	50	109	72	88	62
ENSMUSG00000049686	chr5	Orai1	1.23E+08	1.23E+08	2289	0.615715	6.12702	0.000257	0.001046	0.033011	1	660	791	1096	997	1106	1863	1909	1749	2399	1880
ENSMUSG00000024989	chr19	Cep55	38055025	38055081	2778	1.147365	0.862258	0.000257	0.001048	0.079157	1	14	15	13	17	29	30	57	42	92	58
ENSMUSG00000040396	chr8	Abhd13	9977707	9978019	5191	-0.60015	4.088684	0.000258	0.001048	0.029113	-1	304	272	403	322	417	205	327	377	383	297
ENSMUSG00000055862	chr10	Izumo4	80702693	80702959	938	1.296754	0.92158	0.000258	0.001048	0.112144	1	16	10	16	15	29	24	60	89	46	75
ENSMUSG00000008167	chr8	Fbxw9	85060055	85060536	3383	0.931187	1.648203	0.00026	0.001056	0.057367	1	26	29	38	35	46	53	115	80	104	114
ENSMUSG00000031609	chr8	Sap30	57482707	57483050	1178	0.802216	3.748525	0.000262	0.001064	0.053063	1	111	171	167	131	238	369	515	263	377	427
ENSMUSG00000076068	chr10	Mir678	76207326	76207409	84	1.312559	0.592697	0.000263	0.001068	0.106816	1	7	14	13	16	16	43	43	18	63	63
ENSMUSG00000053746	chr2	Ptrh1	32775786	32775895	1135	1.179949	1.175078	0.000263	0.001069	0.094217	1	19	13	25	20	33	47	44	46	114	101
ENSMUSG00000043207	chr4	Zmpste24	1.21E+08	1.21E+08	7145	-0.56115	4.96766	0.000264	0.001073	0.026541	-1	517	553	742	598	711	474	620	557	773	538
ENSMUSG00000046721	chr7	Rpl14-ps1	45324941	45325456	710	0.595884	4.931437	0.000265	0.001076	0.030059	1	298	353	449	418	524	783	869	870	901	805
ENSMUSG00000037221	chr5	Mospd3	1.38E+08	1.38E+08	1651	0.732199	3.227456	0.000265	0.001077	0.04155	1	99	88	109	146	140	179	279	212	405	300
ENSMUSG00000058883	chr13	Zfp708	67069398	67071528	2450	-1.23167	1.480571	0.000266	0.001079	0.112712	-1	74	44	73	67	61	21	37	75	35	23
ENSMUSG00000033054	chr9	Npat	53537047	53537188	6248	-0.92986	2.59854	0.000267	0.001082	0.068148	-1	126	91	138	156	148	40	101	143	123	86
ENSMUSG00000021928	chr14	Ebpl	61339763	61341404	2077	0.804573	2.516271	0.000267	0.001085	0.047217	1	73	46	80	56	87	131	165	134	214	192
ENSMUSG00000048027	chr17	Rgmb	15806253	15807801	2633	-0.60878	5.024263	0.000268	0.001086	0.031624	-1	598	554	681	612	845	430	602	762	695	527
ENSMUSG00000029775	chr6	Klhdc10	30401868	30402150	8443	-0.58556	6.05113	0.000268	0.001087	0.029957	-1	1079	1182	1508	1416	1470	1077	1255	1047	1575	1238
ENSMUSG00000018411	chr11	Mapt	1.04E+08	1.04E+08	7531	-0.71163	5.991487	0.000269	0.001091	0.044441	-1	993	1047	1612	1455	1562	1016	1036	684	1571	1347
ENSMUSG00000031561	chr8	Tenm3	48227682	48229201	11132	-0.79902	3.477133	0.000269	0.001091	0.052067	-1	241	129	266	257	294	122	234	243	206	144
ENSMUSG00000092360	chr10	Gm20441	75771451	75771506	756	0.643639	4.373565	0.000269	0.001091	0.034435	1	216	247	293	268	324	419	447	682	657	741
ENSMUSG00000001348	chr9	Acp5	22126731	22127262	1612	2.001807	3.934959	0.00027	0.001092	0.327266	1	54	37	22	93	337	253	509	161	832	1177
ENSMUSG00000022947	chr16	Cbr3	93683215	93683613	1170	1.010488	1.427676	0.00027	0.001092	0.068599	1	28	14	32	26	44	56	95	89	74	85
ENSMUSG00000037005	chrX	Xpnpep2	48108725	48109194	4878	-1.25356	1.38574	0.00027	0.001094	0.11429	-1	66	24	70	47	101	33	44	17	39	42
ENSMUSG00000079334	chr9	Nat6	1.08E+08	1.08E+08	3154	0.642079	4.354978	0.000271	0.001096	0.034279	1	235	206	290	272	333	391	465	740	657	660
ENSMUSG00000048458	chr3	Fam212b	1.06E+08	1.06E+08	4781	-0.81452	3.501032	0.000271	0.001098	0.054404	-1	258	126	233	267	327	139	252	139	259	176
ENSMUSG00000037857	chr11	Nufip2	77686155	77686507	5792	-0.63799	4.694445	0.000274	0.001107	0.034546	-1	458	458	524	514	683	342	501	617	534	371
ENSMUSG00000033032	chr18	Afap1l1	61730261	61731310	3680	-0.62027	6.369337	0.000275	0.00111	0.033939	-1	1098	1605	1964	1773	1992	1284	1718	1377	1766	1446

ENSMUSG00000028031	chr3	Dkk2	1.32E+08	1.32E+08	3694	-1.07741	3.55259	0.000275	0.00111	0.09734	-1	274	113	276	175	533	177	125	201	145	208
ENSMUSG00000048616	chr11	Nog	89300638	89302332	1695	1.035901	1.439441	0.000275	0.00111	0.071275	1	30	30	33	24	22	63	75	88	126	58
ENSMUSG00000019877	chr10	Serinc1	57515774	57517292	5150	-0.8252	7.31073	0.000275	0.00111	0.06048	-1	3159	2758	3834	3198	4059	1457	2476	4592	3014	1986
ENSMUSG00000027406	chr2	Idh3b	1.3E+08	1.3E+08	3422	-0.69134	8.670508	0.000275	0.001112	0.042761	-1	7019	9082	9242	9107	6968	5975	6658	9021	8075	6515
ENSMUSG00000063894	chr13	Zkscan8	21513222	21520962	8901	-0.85156	3.014846	0.000276	0.001115	0.058129	-1	181	130	192	164	195	72	127	210	134	130
ENSMUSG00000042292	chr15	Mkl1	81012281	81013802	6114	-0.77751	5.422602	0.000277	0.001116	0.052869	-1	820	545	1130	997	1090	691	743	397	1008	853
ENSMUSG00000030313	chr6	Dennd5b	1.49E+08	1.49E+08	10621	-0.82372	2.586346	0.000277	0.001119	0.052025	-1	125	81	147	130	157	57	104	134	119	93
ENSMUSG00000025817	chr2	Nudt5	5845019	5845385	6484	0.977645	2.90252	0.000279	0.001126	0.076787	1	59	70	83	105	98	156	217	108	337	343
ENSMUSG00000050714	chr2	Zbtb26	37432168	37436999	5267	-0.82585	2.390597	0.000279	0.001126	0.050114	-1	99	107	143	85	119	82	93	92	86	78
ENSMUSG00000026649	chr1	1700009P17Rik	1.71E+08	1.71E+08	1774	1.161349	0.579686	0.00028	0.00113	0.078943	1	8	8	24	12	20	35	43	34	49	60
ENSMUSG00000028036	chr3	Ptgfr	1.52E+08	1.52E+08	4362	-1.21068	0.777859	0.000281	0.001132	0.093965	-1	36	28	46	39	45	17	11	42	25	21
ENSMUSG00000041308	chr8	Sntb2	1.07E+08	1.07E+08	4423	-0.90686	2.865349	0.000281	0.001132	0.066249	-1	161	87	152	132	272	66	123	101	164	146
ENSMUSG00000011257	chr4	Pabpc4	1.23E+08	1.23E+08	4027	-0.58324	7.819041	0.000281	0.001134	0.030491	-1	3594	4154	5033	4950	4900	3321	4391	4555	5066	3819
ENSMUSG00000025324	chr7	Atp10a	58658202	58658915	5469	-0.93087	2.953734	0.000282	0.001134	0.070104	-1	153	82	214	140	279	103	131	76	169	143
ENSMUSG00000057531	chr13	Dtnbp1	44922079	44922454	1334	0.643148	4.808406	0.000282	0.001135	0.035238	1	307	345	367	398	395	549	603	793	1111	978
ENSMUSG00000032783	chr15	Troap	99074973	99075092	2264	1.42973	0.376567	0.000282	0.001136	0.125535	1	11	6	7	7	22	17	48	24	68	48
ENSMUSG00000030680	chr7	Pagr1a	1.27E+08	1.27E+08	4405	0.582472	4.40312	0.000283	0.001137	0.028074	1	229	258	304	271	351	485	576	522	653	705
ENSMUSG00000029561	chr5	Oasl2	1.15E+08	1.15E+08	3879	1.658565	3.73385	0.000283	0.001138	0.230852	1	59	76	116	118	177	717	330	69	288	794
ENSMUSG00000025314	chr2	Ptprj	90429754	90430046	8352	0.867883	3.684621	0.000284	0.001141	0.063197	1	155	67	177	116	258	249	375	315	546	473
ENSMUSG00000041773	chr13	Enc1	97241105	97241529	4742	0.8573	2.966172	0.000285	0.001145	0.058924	1	86	44	105	87	145	161	281	172	307	251
ENSMUSG00000026051	chr1	1500015O10Rik	43730602	43730963	902	-1.94249	3.504312	0.000286	0.00115	0.31084	-1	486	46	370	69	570	90	228	76	103	44
ENSMUSG00000012017	chr16	Scarf2	17797282	17797527	3302	0.804949	3.791106	0.000287	0.001153	0.054339	1	172	102	174	124	277	242	566	380	510	372
ENSMUSG00000040209	chr3	Zfp704	9427020	9438898	15255	-0.77867	3.887342	0.000287	0.001154	0.05116	-1	304	185	322	323	443	142	233	373	320	219
ENSMUSG00000090272	chr1	Mndal	1.74E+08	1.74E+08	3443	0.899041	3.352272	0.000287	0.001154	0.066828	1	96	103	128	118	146	407	231	210	277	350
ENSMUSG00000024742	chr19	Fen1	10199132	10201097	2422	0.889018	2.894146	0.000288	0.001157	0.062926	1	61	80	103	69	120	167	205	124	357	277
ENSMUSG00000044340	chr1	Phlpp1	1.06E+08	1.06E+08	6752	-0.68903	3.483401	0.000288	0.001157	0.038408	-1	191	182	253	266	260	108	221	250	225	203
ENSMUSG00000021131	chr12	Erh	80634022	80634527	1350	0.601769	4.718906	0.000291	0.001166	0.030759	1	299	311	409	301	428	646	764	561	931	791
ENSMUSG00000039377	chr1	Hlx	1.85E+08	1.85E+08	2278	0.764914	3.089828	0.000292	0.00117	0.046123	1	79	70	112	148	114	186	215	294	299	244
ENSMUSG00000039096	chr11	Rsad1	94539798	94542647	4391	-0.76312	2.605312	0.000292	0.001172	0.044001	-1	122	122	157	113	114	73	107	112	134	100
ENSMUSG00000004677	chr8	Myo9b	71272714	71272829	7297	0.688914	4.432111	0.000292	0.001172	0.040388	1	277	177	307	261	364	370	619	500	902	778
ENSMUSG00000029468	chr5	P2rx7	1.23E+08	1.23E+08	5408	0.834053	2.569134	0.000292	0.001172	0.052961	1	71	36	73	73	100	130	198	146	204	195
ENSMUSG00000038014	chr13	Fam120a	48879219	48881095	5105	-0.56597	7.000056	0.000294	0.001176	0.028716	-1	2108	2115	2855	2641	3129	1752	2344	2568	3099	2394
ENSMUSG00000030203	chr6	Dusp16	1.35E+08	1.35E+08	7650	-0.60144	4.531363	0.000294	0.001177	0.030625	-1	413	393	450	504	564	323	527	420	528	353
ENSMUSG00000022594	chr15	Lynx1	74747852	74751427	4662	-0.7501	7.513759	0.000294	0.001177	0.050576	-1	2680	3968	4044	4893	3411	2986	3258	2206	4612	2899
ENSMUSG00000026933	chr2	Camsap1	25926838	25930028	8368	-0.63252	4.923959	0.000295	0.001179	0.034528	-1	465	466	694	673	825	442	495	713	595	519
ENSMUSG00000022462	chr15	Slc38a2	96687394	96690228	4626	-0.67147	6.43069	0.000295	0.00118	0.040272	-1	1141	1792	1841	1989	2124	1183	1715	1881	1726	1259
ENSMUSG00000057182	chr2	Scn3a	65457118	65461737	12459	-1.35647	0.239417	0.000295	0.001182	0.114437	-1	28	19	29	32	26	10	11	25	24	4
ENSMUSG00000019897	chr10	Ccdc59	1.06E+08	1.06E+08	4314	0.635978	3.72597	0.000297	0.001188	0.032386	1	163	170	191	149	178	302	352	437	413	353
ENSMUSG00000030082	chr6	Sec61a1	88503601	88505293	6407	0.719943	5.666509	0.000298	0.001192	0.045952	1	578	437	691	514	1045	994	1661	1040	2127	1688
ENSMUSG00000023348	chr5	Trip6	1.37E+08	1.37E+08	1760	0.874216	2.92387	0.000299	0.001194	0.061786	1	80	55	89	61	166	154	239	186	301	263
ENSMUSG00000040242	chr6	Fgfr1op2	1.47E+08	1.47E+08	4619	-0.5543	5.683513	0.000299	0.001194	0.026997	-1	825	980	1210	968	1122	769	998	941	1154	1005
ENSMUSG00000020171	chr10	Yeats4	1.17E+08	1.17E+08	1407	0.632565	3.8662	0.000299	0.001196	0.03281	1	146	143	233	197	241	368	424	314	471	468
ENSMUSG00000034973	chr9	Dopey1	86467154	86467296	20476	-0.6941	3.605675	0.0003	0.001197	0.039538	-1	217	204	287	252	297	132	216	313	232	194
ENSMUSG00000009073	chr11	Nf2	4765845	4768273	6825	-0.58656	6.175341	0.000301	0.001202	0.030653	-1	1225	1269	1711	1560	1473	1095	1364	1162	1654	1486
ENSMUSG00000048728	chr11	Zfp454	50872720	50874287	2423	-1.07768	1.279111	0.000301	0.001202	0.080063	-1	48	39	68	55	60	37	42	15	41	41
ENSMUSG00000036617	chr2	Etl4	19909780	19910279	16067	-0.97792	5.571125	0.000302	0.001203	0.084887	-1	974	873	1072	1393	897	419	669	1444	703	510
ENSMUSG00000028841	chr4	Cnksr1	1.34E+08	1.34E+08	2804	1.282399	5.144312	0.000302	0.001204	0.143825	1	329	282	438	376	277	753	672	2855	795	669
ENSMUSG00000031782	chr8	Coq9	94838321	94838497	3055	-0.67622	8.43459	0.000302	0.001204	0.041442	-1	5682	7722	7833	7904	5930	5548	5699	6856	7255	5560
ENSMUSG00000020629	chr12	Adi1	28675231	28675372	1886	-0.66332	5.285779	0.000302	0.001205	0.038631	-1	615	794	999	818	751	729	631	678	735	685
ENSMUSG00000060261	chr5	Gtf2i	1.34E+08	1.34E+08	7120	-0.56692	6.911482	0.000302	0.001205	0.028901	-1	1926	1988	2667	2495	3031	1743	2429	2361	2623	2193
ENSMUSG00000028863	chr4	Meaf6	1.25E+08	1.25E+08	5211	0.668464	3.235891	0.000303	0.001206	0.034531	1	99	104	140	128	130	201	281	212	323	324
ENSMUSG00000045251	chr7	Zfp688	1.27E+08	1.27E+08	2734	0.975379	1.029049	0.000303	0.001207	0.054834	1	17	20	30	18	23	42	57	64	71	64
ENSMUSG00000022174	chr14	Dad1	54235479	54235713	3916	0.589981	5.332652	0.000304	0.00121	0.030386	1	474	500	598	507	595	992	1091	893	1385	1272
ENSMUSG00000040584	chr5	Abcb1a	8660077	8660222	5480	-0.96325	3.107937	0.000304	0.00121	0.077098	-1	129	122	254	274	179	81	117	223	133	126
ENSMUSG00000027339	chr2	Rassf2	1.32E+08	1.32E+08	11993	0.860211	4.234291	0.000304	0.001211	0.064277	1	187	119	226	172	446	471	682	390	679	597
ENSMUSG00000030433	chr7	Sbk2	4956134	4957713	2426	1.016748	4.424558	0.000305	0.001212	0.090135	1	295	116	173	315	272	343	504	1064	933	567
ENSMUSG00000019838	chr10	Slc16a10	40033535	40037404	5394	-0.64798	5.445196	0.000305	0.001214	0.037051	-1	738	639	975	995	1142	619	629	922	787	984
ENSMUSG00000037846	chr10	Rtkn2	67979570	67979812	5547	1.344384	0.944739	0.000305	0.001214	0.12375	1	15	16	23	13	17	35	117	30	73	49
ENSMUSG00000020864	chr11	Ankrd40	94328001	94328387	4255	-0.63077	7.724843	0.000306	0.001217	0.036064	-1	3605	3981	4693	4717	4394	3737	3963	2989	4632	3917
ENSMUSG00000103441	chr3	RP24-179O3.1	21753529	21753959	975	-1.22164	-0.07134	0.000306	0.001217	0.074067	-1	24	17	22	16	24	8	19	9	15	11
ENSMUSG00000018381	chr11	Abi3	95830074	95832876	4153	0.963762	2.305161	0.000307	0.001221	0.071675	1	37	53	49	70	63	112	146	85	260	157
ENSMUSG00000054766	chr2	Set	30057378	30057401	4070	0.57454	6.315327	0.000308	0.001224	0.029523	1	875	959	1260	979	1295	1804	2081	1982	2836	2458
ENSMUSG00000053768	chr6	Chchd3	32790976	32791137	2905	-0.63356	7.722151	0.000309	0.001228	0.036443	-1	3661	4389	4724	4672	3743	3320	3702	4088	4425	3709
ENSMUSG00000024076	chr17	Vit	78508063	78508325	2720	-1.25995	2.0608	0.00031	0.00123	0.127504	-1	110	36	133	67	152	44	61	90	57	29
ENSMUSG00000034243	chr16	Golgb1	36875140	36875263	12639	-0.68525	5.262848	0.000311	0.001234	0.041569	-1	739	580	945	754	962	397	648	994	807	629
ENSMUSG00000032258	chr9	Lca5	83390293	83390670	6306	-1.23669	0.506577	0.000312	0.001236	0.098188	-1	26	27	35	26	47	7	36	13	24	16

ENSMUSG00000039449	chr2	Prpf18	4622058	4624526	5310	-0.60378	5.38186	0.000312	0.001239	0.032132	-1	717	757	942	844	936	597	776	985	795	691
ENSMUSG00000029452	chr5	Tmem116	1.21E+08	1.21E+08	3732	1.126404	0.707656	0.000314	0.001245	0.077194	1	9	15	11	14	31	39	53	44	61	45
ENSMUSG00000026433	chr1	Rab29	1.32E+08	1.32E+08	1468	0.790205	2.830986	0.000314	0.001246	0.048535	1	75	80	107	71	95	148	213	139	287	262
ENSMUSG00000022206	chr15	Npr3	11839896	11845288	6927	0.957162	3.034297	0.000315	0.001246	0.075604	1	105	41	100	106	108	113	294	330	304	227
ENSMUSG00000047878	chr15	A4galt	83226726	83228594	2171	0.831017	2.114272	0.000315	0.001246	0.048612	1	44	40	65	54	50	88	130	108	190	123
ENSMUSG00000039748	chr1	Exo1	1.76E+08	1.76E+08	8422	1.548918	-0.01663	0.000315	0.001249	0.138598	1	7	4	5	2	19	18	30	18	51	36
ENSMUSG00000031994	chr9	Adamts8	30942562	30943601	4613	1.422576	1.581848	0.000316	0.001249	0.155948	1	20	14	17	42	37	41	129	112	182	40
ENSMUSG00000021018	chr16	Polr2h	20717665	20717994	1448	0.754859	3.233446	0.000316	0.001252	0.045632	1	98	120	130	102	124	240	321	173	321	303
ENSMUSG00000019787	chr10	Trdn	33083483	33083745	4514	-0.69202	10.2948	0.000317	0.001255	0.043806	-1	24830	20267	29764	24159	31141	20098	17399	29636	20203	23009
ENSMUSG00000036499	chr10	Eea1	95940663	95940972	7836	-0.70968	4.971952	0.000318	0.001256	0.044506	-1	564	484	695	701	833	288	524	817	642	547
ENSMUSG00000092252	chr5	Gm20499	1.15E+08	1.15E+08	444	1.182297	0.246675	0.000319	0.00126	0.072761	1	7	5	17	11	15	22	42	34	36	39
ENSMUSG00000031751	chr8	Amfr	93971588	93973314	3953	-0.59177	7.1244	0.00032	0.001264	0.03183	-1	2441	2539	3159	2835	3010	1954	2492	3150	2952	2464
ENSMUSG00000042419	chr17	Nfkbil1	35220175	35220976	1746	0.938849	2.699552	0.000321	0.001268	0.070604	1	51	71	73	77	94	111	140	323	222	190
ENSMUSG00000022508	chr16	Bcl6	23965052	23966268	6700	-0.77929	5.75294	0.000321	0.001269	0.054562	-1	1176	488	1493	1322	1290	672	832	1073	1089	989
ENSMUSG00000031529	chr8	Tnks	34829179	34831721	6444	-0.97217	3.682943	0.000321	0.001269	0.081527	-1	293	223	286	280	330	98	183	398	182	153
ENSMUSG00000027088	chr2	Phospho2	69789623	69789956	4335	-0.61014	4.273642	0.000321	0.001269	0.031532	-1	323	374	483	411	344	294	391	336	398	359
ENSMUSG00000032018	chr9	Sc5d	42254177	42255797	2328	-0.6805	4.152356	0.000322	0.001271	0.039624	-1	322	245	422	371	489	198	273	316	364	457
ENSMUSG00000044296	chr11	Zfp879	50832031	50833971	2414	-1.15565	0.829436	0.000322	0.001271	0.088	-1	39	31	38	49	40	12	17	41	26	29
ENSMUSG00000021111	chr12	Papola	1.06E+08	1.06E+08	6595	-0.56071	6.13888	0.000323	0.001274	0.028236	-1	1127	1264	1643	1357	1654	1057	1436	1237	1622	1313
ENSMUSG00000031453	chr8	Rasa3	13566950	13568766	5093	0.67324	4.78658	0.000323	0.001274	0.03971	1	270	274	370	326	565	455	716	808	1062	986
ENSMUSG00000027379	chr2	Bub1	1.28E+08	1.28E+08	4354	1.366558	0.736913	0.000323	0.001275	0.125788	1	7	11	17	10	28	27	39	31	99	71
ENSMUSG00000040820	chr16	Hlcs	94129195	94131965	5060	-0.62443	3.594868	0.000326	0.001285	0.031539	-1	224	213	234	250	295	175	202	262	230	231
ENSMUSG00000028197	chr3	Col24a1	1.45E+08	1.45E+08	7621	-1.01267	2.521172	0.000327	0.001288	0.083592	-1	139	72	137	103	193	53	144	58	120	73
ENSMUSG00000029507	chr5	Pus1	1.11E+08	1.11E+08	2180	0.641995	3.557355	0.000327	0.001289	0.033214	1	98	149	154	164	201	269	314	307	434	343
ENSMUSG00000060798	chr3	Intu	40531286	40531963	7429	-0.92662	1.172701	0.000328	0.00129	0.05466	-1	45	39	57	47	52	28	34	27	54	35
ENSMUSG00000041669	chr12	Prima1	1.03E+08	1.03E+08	1253	-1.21902	1.042202	0.000328	0.001292	0.104611	-1	44	53	36	54	43	23	23	40	15	37
ENSMUSG00000033434	chr5	Gtpbp6	1.1E+08	1.1E+08	2825	0.704054	2.922341	0.000329	0.001295	0.03802	1	78	71	108	97	125	144	191	216	312	235
ENSMUSG00000064127	chrX	Med14	12675369	12677651	8763	-0.58882	4.919078	0.000331	0.0013	0.030314	-1	544	502	650	593	753	408	583	701	629	501
ENSMUSG00000024270	chr18	Slc39a6	24579881	24581077	4073	0.904356	3.131641	0.000332	0.001308	0.068075	1	93	63	95	81	181	157	277	183	449	290
ENSMUSG00000023984	chr17	Gm20517	47611589	47611692	6495	-0.7014	3.090398	0.000333	0.001309	0.039192	-1	157	148	218	167	186	101	169	184	179	124
ENSMUSG00000031262	chrX	Cenpi	1.34E+08	1.34E+08	5681	1.290406	0.377865	0.000333	0.00131	0.099369	1	4	13	11	11	18	25	38	22	62	51
ENSMUSG00000015335	chr2	Zdhhc12	30090944	30091566	1785	0.973889	1.835278	0.000333	0.001311	0.06815	1	39	43	34	32	43	73	91	77	163	138
ENSMUSG00000037876	chr10	Jmjd1c	67096125	67096718	14397	-0.60784	4.675573	0.000334	0.001311	0.032152	-1	430	389	549	525	711	305	476	591	561	448
ENSMUSG00000002825	chr9	Qtrt1	21411837	21412097	1319	0.8182	2.286864	0.000334	0.001314	0.049681	1	51	39	72	58	70	91	122	179	164	158
ENSMUSG00000024188	chr17	Luc7l	26252910	26253091	7509	0.788206	4.042773	0.000335	0.001314	0.053784	1	198	147	229	157	281	284	395	756	481	515
ENSMUSG00000002733	chr2	Plekha3	76675281	76675634	3126	-0.6609	3.321642	0.000335	0.001316	0.035267	-1	174	167	240	207	234	110	210	150	264	184
ENSMUSG00000035365	chr10	Parpbp	88091432	88093186	3594	1.563568	-0.14939	0.000338	0.001326	0.137391	1	4	2	7	6	14	7	28	24	50	31
ENSMUSG00000078716	chr4	Tmem8b	43668971	43669172	5553	-0.59556	4.480315	0.000338	0.001326	0.030617	-1	358	413	463	551	443	301	439	411	543	396
ENSMUSG00000035569	chr8	Ankrd11	1.23E+08	1.23E+08	11637	-0.83582	5.852109	0.000339	0.001329	0.06335	-1	1105	885	1358	1331	1557	545	830	1725	990	780
ENSMUSG00000027201	chr2	Myef2	1.25E+08	1.25E+08	5936	0.888155	2.793986	0.000339	0.001329	0.064472	1	56	66	77	68	140	149	243	128	321	211
ENSMUSG00000042726	chr5	Trafd1	1.21E+08	1.21E+08	4486	0.806976	5.674587	0.000343	0.001346	0.058996	1	532	489	670	618	815	1086	1104	2569	1263	1480
ENSMUSG00000048047	chrX	Zbtb33	38189793	38190082	5122	-0.84344	3.084755	0.000344	0.00135	0.059458	-1	193	134	185	165	228	75	155	216	151	114
ENSMUSG00000007892	chr9	Rplp1	61913284	61913521	495	0.590997	8.89604	0.000346	0.001355	0.032372	1	5184	5922	7647	5378	7808	11973	13532	11727	14863	14330
ENSMUSG00000046312	chr4	AI464131	41495604	41499690	4701	-0.55519	6.857079	0.000347	0.001358	0.028252	-1	1995	1909	2735	2261	2678	1736	2180	2264	2509	2274
ENSMUSG00000046711	chr17	Hmga1	27556620	27556711	1990	0.649334	4.608512	0.000347	0.00136	0.036827	1	264	285	387	331	310	465	499	760	958	834
ENSMUSG00000078915	chr13	Hsp25-ps1	45078498	45078911	594	0.889161	3.002428	0.000349	0.001366	0.065673	1	65	83	94	116	105	178	262	359	247	145
ENSMUSG00000098956	chr9	Gm27855	1.1E+08	1.1E+08	128	-1.56117	-0.26652	0.00035	0.001371	0.140035	-1	19	13	16	22	26	2	15	18	5	5
ENSMUSG00000078439	chr10	Smim24	81393051	81393159	1058	1.509184	-0.22155	0.000351	0.001372	0.10808	1	7	5	4	11	4	19	28	12	38	31
ENSMUSG00000047242	chrX	Taf9b	1.06E+08	1.06E+08	3158	-0.66255	2.927891	0.000351	0.001374	0.033879	-1	132	135	186	152	169	107	150	119	169	140
ENSMUSG00000029633	chr6	Gm5578	1.13E+08	1.13E+08	1236	-1.39013	-0.27457	0.000352	0.001378	0.104524	-1	8	17	26	19	23	3	7	17	11	11
ENSMUSG00000006494	chr2	Pdk1	71873224	71873565	7779	-0.58275	5.847468	0.000355	0.001387	0.030818	-1	947	994	1251	1351	1219	804	961	1195	1314	1133
ENSMUSG00000012117	chr4	Dhdds	1.34E+08	1.34E+08	3784	0.702308	4.118671	0.000355	0.001387	0.042705	1	205	159	265	217	258	375	630	301	626	585
ENSMUSG00000044452	chr7	Zfp507	35772343	35776327	7121	-0.74679	4.046878	0.000355	0.001387	0.04857	-1	318	246	408	343	424	204	276	455	262	231
ENSMUSG00000051518	chr15	Rps19bp1	80260614	80261130	830	0.704816	3.197105	0.000356	0.001389	0.03989	1	86	117	128	124	118	230	272	190	336	283
ENSMUSG00000022427	chr15	Tomm22	79670861	79671008	1113	0.608024	5.967892	0.000358	0.001398	0.033654	1	669	809	1019	798	832	1649	1754	1524	2036	1781
ENSMUSG00000005958	chr16	Ephb3	21204755	21205263	6289	1.187292	2.973385	0.000358	0.001399	0.121199	1	84	44	52	51	172	176	413	151	335	193
ENSMUSG00000004642	chr5	Slbp	33634952	33635175	4472	0.75849	3.275645	0.000359	0.0014	0.047252	1	98	120	125	104	146	189	332	175	388	343
ENSMUSG00000049327	chr5	Setd8	1.24E+08	1.24E+08	4034	-0.73404	6.191553	0.000359	0.001401	0.049464	-1	1118	1604	2146	1546	1162	1046	1184	975	1737	1512
ENSMUSG00000034311	chrX	Kif4	1.01E+08	1.01E+08	5514	1.08798	1.161493	0.00036	0.001404	0.080758	1	19	20	17	20	37	47	65	42	114	74
ENSMUSG00000007038	chr17	Neu1	34931253	34931547	3733	0.594867	4.428218	0.000362	0.001413	0.03056	1	209	272	341	281	329	427	524	567	785	740
ENSMUSG00000058486	chr6	Wdr91	34880426	34880968	2990	0.854813	3.082204	0.000363	0.001415	0.061524	1	70	74	129	75	161	137	190	283	338	333
ENSMUSG00000032315	chr9	Cyp1a1	57697613	57697699	2619	-1.14939	0.19123	0.000363	0.001416	0.068414	-1	18	22	30	20	35	10	11	17	18	22
ENSMUSG00000098274	chr16	Rpl24	55966275	55966438	1030	0.599653	7.73276	0.000363	0.001416	0.033418	1	2278	2894	3279	2597	3035	5432	5684	6087	6557	5893
ENSMUSG00000038145	chr9	Snrk	1.22E+08	1.22E+08	5763	-0.64792	5.219446	0.000364	0.001419	0.037927	-1	662	557	894	919	774	423	566	760	828	852
ENSMUSG00000032507	chr9	Fbxl2	1.14E+08	1.14E+08	4444	1.255618	0.992894	0.000366	0.001423	0.110833	1	20	13	24	16	18	31	111	35	75	59
ENSMUSG00000079109	chr5	Pms2	1.44E+08	1.44E+08	8442	-0.74246	2.669765	0.000367	0.001428	0.043382	-1	120	115	176	123	124	73	132	104	130	116

ENSMUSG00000102059	chr1	Gm20257	58652641	58652689	936	1.543025	-0.04668	0.000369	0.001437	0.141385	1	4	3	4	12	13	16	16	23	45	49
ENSMUSG00000024983	chr19	Vti1a	55316351	55316544	3405	-0.57422	3.912239	0.00037	0.001439	0.027502	-1	258	258	373	306	304	225	315	256	328	284
ENSMUSG00000032076	chr9	Cadm1	47530173	47530505	9684	-0.77467	2.622516	0.000375	0.001459	0.046912	-1	100	95	139	113	209	82	120	103	130	92
ENSMUSG00000022216	chr14	Psme1	55578123	55578248	2209	0.712015	5.241717	0.000376	0.001461	0.045996	1	404	491	484	551	428	985	956	732	1411	1389
ENSMUSG00000026141	chr1	Col19a1	24261890	24264817	6887	-1.3266	-0.2246	0.000377	0.001465	0.087249	-1	12	17	24	16	26	10	10	16	5	10
ENSMUSG00000092274	chr19	Neat1	5824708	5845478	20771	0.847544	8.217812	0.000377	0.001465	0.066865	1	3371	3343	4335	2973	3652	3959	7996	7700	10607	15591
ENSMUSG00000043702	chr14	Pde12	26659958	26665967	7725	-0.66253	3.197724	0.000379	0.001472	0.035639	-1	168	143	220	178	231	111	211	158	205	147
ENSMUSG00000091498	chr12	Mpc1-ps	1.11E+08	1.11E+08	330	-0.65724	4.734109	0.00038	0.001475	0.038716	-1	432	560	660	558	486	346	405	616	516	526
ENSMUSG00000031785	chr8	Gpr56	94977109	94977417	3864	0.629737	4.609737	0.000381	0.001479	0.035087	1	217	281	369	407	326	472	774	596	972	690
ENSMUSG00000026502	chr1	Desi2	1.78E+08	1.78E+08	9156	-0.57111	5.601858	0.000381	0.001479	0.029706	-1	841	823	1085	914	1207	686	1020	1062	1005	786
ENSMUSG00000026958	chr2	Dpp7	25352276	25352566	3337	0.759214	3.424071	0.000381	0.00148	0.04882	1	113	114	156	109	171	250	263	193	481	394
ENSMUSG00000040018	chr19	Cox15	43733254	43736852	4909	-0.56441	5.442646	0.000382	0.00148	0.028884	-1	709	826	923	908	954	669	890	841	1000	696
ENSMUSG00000065497	chr12	Mir410	1.1E+08	1.1E+08	81	1.409595	-0.02873	0.000381	0.00148	0.10944	1	4	10	3	5	17	21	31	21	46	28
ENSMUSG00000073676	chr1	Hspe1	55088132	55088412	1474	0.608924	5.909171	0.000382	0.00148	0.034027	1	675	805	883	740	845	1489	1740	1334	1947	1920
ENSMUSG00000001415	chr3	Smg5	88336260	88336497	6956	-0.57598	6.175566	0.000382	0.001481	0.030596	-1	1148	1330	1735	1394	1643	1027	1311	1510	1447	1474
ENSMUSG00000002325	chr14	Irf9	55603571	55604243	5386	0.758349	3.693489	0.000382	0.001482	0.049722	1	144	145	183	117	210	381	349	232	433	466
ENSMUSG00000024304	chr18	Cdh2	16588877	16590353	8066	1.034248	2.29986	0.000383	0.001484	0.088309	1	40	27	63	45	96	93	244	124	189	112
ENSMUSG00000006373	chrX	Pgrmc1	36598206	36598614	1857	0.725123	4.144781	0.000384	0.001485	0.046398	1	193	151	237	192	355	283	483	438	742	678
ENSMUSG00000022912	chr16	Pros1	62854307	62854504	4088	0.675675	4.702814	0.000384	0.001485	0.040941	1	299	231	306	329	528	536	927	560	992	755
ENSMUSG00000037353	chr15	Letmd1	1E+08	1E+08	2579	0.742198	3.702562	0.000387	0.001496	0.04761	1	119	126	181	180	210	242	283	299	553	549
ENSMUSG00000045312	chr13	Lhfpl2	94057796	94057906	8276	0.987108	4.491461	0.000387	0.001499	0.088393	1	264	104	233	238	445	352	733	441	1082	983
ENSMUSG00000034593	chr9	Myo5a	75071015	75071659	14803	0.814814	4.623235	0.000389	0.001505	0.060183	1	248	189	299	274	512	317	635	835	1053	929
ENSMUSG00000042790	chr9	Rnf214	45863425	45864998	5922	-0.59437	4.071056	0.000393	0.001521	0.030364	-1	290	261	468	323	353	234	333	338	378	282
ENSMUSG00000013483	chr11	Card14	1.19E+08	1.19E+08	4605	1.195551	1.26762	0.000394	0.001525	0.105854	1	33	12	22	19	29	82	53	89	95	46
ENSMUSG00000026213	chr1	Stk11ip	75521529	75521642	5743	0.800413	3.937243	0.000396	0.001532	0.056542	1	166	171	196	198	189	235	416	756	462	405
ENSMUSG00000029502	chr5	Golga3	1.1E+08	1.1E+08	12671	-0.57239	5.637675	0.000397	0.001535	0.030077	-1	784	814	1126	1050	1240	627	965	1134	1055	918
ENSMUSG00000036291	chr14	Ap5m1	49066495	49066864	3165	-0.74691	3.163782	0.000397	0.001535	0.046936	-1	161	162	236	171	205	90	185	211	172	125
ENSMUSG00000021200	chr12	Asb2	1.03E+08	1.03E+08	3542	-0.75887	8.097392	0.000398	0.001536	0.054169	-1	4073	4190	5785	8612	6320	4500	4172	5669	4039	4888
ENSMUSG00000052833	chr7	Sae1	16327053	16327929	1884	0.619091	5.135367	0.000398	0.001538	0.034794	1	388	419	541	448	515	904	1049	669	1240	1085
ENSMUSG00000014355	chr2	Anapc1	1.29E+08	1.29E+08	16714	-0.55585	5.571169	0.000399	0.001539	0.028317	-1	778	769	1057	924	1242	575	924	924	1203	937
ENSMUSG00000030744	chr7	Rps3	99477896	99478951	4483	0.559537	8.376582	0.000399	0.00154	0.0296	1	3736	4275	5212	4099	5142	7833	9355	8588	10436	9876
ENSMUSG00000040359	chr4	Ufl1	25248600	25249969	5706	-0.68247	4.805416	0.000406	0.001567	0.042358	-1	515	499	654	552	655	353	450	763	498	432
ENSMUSG00000004393	chr11	Ddx56	6258919	6259258	2533	0.785177	4.413749	0.000407	0.001569	0.055595	1	234	252	275	273	254	402	530	1048	695	470
ENSMUSG00000000948	chr7	Snrpn	59974149	59974175	5216	-0.61739	4.342123	0.000408	0.001572	0.033688	-1	389	340	411	472	421	351	377	292	486	353
ENSMUSG00000057894	chr7	Zfp329	12804977	12806592	6732	-0.8338	2.577837	0.000408	0.001572	0.056397	-1	85	81	173	125	186	73	128	75	127	97
ENSMUSG00000062257	chr9	Opcml	27790775	27790900	13120	-0.93955	1.380758	0.000408	0.001572	0.062253	-1	49	39	50	67	76	30	33	52	43	45
ENSMUSG00000027966	chr3	Col11a1	1.14E+08	1.14E+08	9657	-1.86974	5.437557	0.000409	0.001575	0.309176	-1	1525	236	1169	375	2620	187	983	424	525	106
ENSMUSG00000066456	chr9	Hmgn3	83109948	83110429	1869	0.80956	2.658794	0.000409	0.001576	0.052747	1	78	63	69	59	107	158	235	140	205	179
ENSMUSG00000022436	chr15	Sh3bp1	78899667	78899961	4649	0.758277	3.501231	0.000409	0.001577	0.049702	1	100	110	171	115	214	295	374	197	439	343
ENSMUSG00000022961	chr16	Son	91647506	91647984	14354	-0.64118	7.227925	0.000411	0.001582	0.038821	-1	2704	2318	3387	3051	3935	1733	2646	3760	2995	2632
ENSMUSG00000000197	chr14	Nalcn	1.23E+08	1.23E+08	7115	-1.45782	-0.25298	0.000412	0.001587	0.123675	-1	24	10	22	15	24	5	8	20	11	4
ENSMUSG00000071540	chr14	3425401B19Rik	32659119	32664178	5547	-0.76921	7.833302	0.000412	0.001587	0.055921	-1	4359	3112	4695	6668	5247	2749	3385	5901	4591	3149
ENSMUSG00000032402	chr9	Smad3	63646767	63650385	5542	-0.80817	6.440161	0.000414	0.001592	0.061287	-1	1377	1506	2127	2086	2226	1568	1702	683	1788	1542
ENSMUSG00000032932	chr16	Hspa13	75755190	75758448	5894	-0.64718	3.754671	0.000415	0.001595	0.03623	-1	246	205	359	238	337	137	266	294	303	242
ENSMUSG00000033016	chr18	Nfatc1	80606205	80608025	7433	-0.61071	5.299132	0.000415	0.001597	0.034222	-1	580	599	880	938	1028	649	713	809	830	608
ENSMUSG00000098371	chr16	Gm28037	55966343	55966438	611	0.594062	7.734918	0.000416	0.001599	0.033467	1	2289	2906	3295	2605	3041	5430	5683	6091	6556	5892
ENSMUSG00000028064	chr3	Sema4a	88435959	88437252	5406	1.131356	2.856393	0.000417	0.0016	0.111719	1	59	42	60	73	149	143	198	114	297	408
ENSMUSG00000087412	chr7	Gm15501	93178983	93179669	687	0.668056	2.979633	0.000416	0.0016	0.035417	1	77	90	115	87	137	168	229	220	298	208
ENSMUSG00000022020	chr14	Naa16	79334204	79336485	6145	-0.65662	3.46658	0.000417	0.001602	0.036239	-1	225	187	260	214	233	159	213	238	183	195
ENSMUSG00000079478	chr19	Sssca1	5728088	5728868	3083	0.547524	5.528032	0.000417	0.001602	0.02754	1	487	560	726	621	749	1099	1187	1271	1430	1367
ENSMUSG00000027285	chr2	Haus2	1.21E+08	1.21E+08	3218	-0.63647	3.696186	0.000418	0.001602	0.034768	-1	220	233	319	242	303	155	219	311	304	203
ENSMUSG00000024579	chr18	Pcyox1l	61696837	61697976	2645	1.251225	1.310267	0.000419	0.001608	0.120578	1	28	11	24	15	39	49	115	37	113	79
ENSMUSG00000097099	chr9	Gm9917	1.08E+08	1.08E+08	6021	-0.98739	0.816796	0.000424	0.001626	0.060786	-1	29	34	38	49	38	19	26	25	30	33
ENSMUSG00000049233	chr13	Apoo-ps	1.07E+08	1.07E+08	903	-0.77051	2.75162	0.000426	0.001633	0.048388	-1	121	146	152	156	119	102	110	132	121	106
ENSMUSG00000022255	chr15	Mtdh	34082694	34083413	12096	-0.69858	6.625408	0.000426	0.001633	0.046133	-1	1909	1619	2343	2058	2291	1112	1783	2672	1790	1457
ENSMUSG00000027983	chr3	Cyp2u1	1.31E+08	1.31E+08	2331	-1.04321	1.254408	0.000427	0.001637	0.078857	-1	41	53	61	60	45	31	25	23	63	38
ENSMUSG00000029321	chr5	Slc10a6	1.04E+08	1.04E+08	2124	1.385907	0.584347	0.000427	0.001638	0.13195	1	14	7	25	11	6	37	24	68	49	52
ENSMUSG00000023341	chr16	Mx2	97535308	97535946	3614	1.949555	0.502688	0.000428	0.001638	0.291592	1	2	11	9	9	14	83	20	19	19	82
ENSMUSG00000021710	chr13	Nln	1.04E+08	1.04E+08	3780	0.627573	3.617255	0.000429	0.001644	0.033176	1	131	140	199	154	177	223	303	319	490	420
ENSMUSG00000039178	chr5	Tbc1d19	53809627	53809858	2688	-0.59818	3.989665	0.00043	0.001646	0.031051	-1	283	273	375	309	354	218	284	382	310	274
ENSMUSG00000071266	chr17	Zfp946	22424222	22424429	3504	-0.91528	2.086184	0.00043	0.001646	0.067163	-1	88	90	120	66	91	58	66	42	81	92
ENSMUSG00000001150	chr10	Mcm3ap	76468971	76469214	6382	-0.54495	4.60082	0.000432	0.001654	0.026465	-1	396	395	527	528	565	321	493	504	550	447
ENSMUSG00000027004	chr2	Frzb	80411970	80413472	3237	-0.85954	4.533733	0.000434	0.00166	0.068132	-1	377	533	526	590	436	401	363	181	606	371
ENSMUSG00000021608	chr13	Lpcat1	73467197	73467517	4131	0.700217	3.120326	0.000435	0.001663	0.040564	1	91	82	119	115	144	171	232	195	371	294
ENSMUSG00000055368	chr8	Slc6a2	92960079	92960181	6176	-1.21257	0.36855	0.000437	0.001669	0.092163	-1	29	15	22	30	49	12	19	24	19	12
ENSMUSG00000025572	chr11	Tmc6	1.18E+08	1.18E+08	4091	0.766356	2.881409	0.00044	0.001683	0.047865	1	94	74	78	107	90	133	188	257	273	228

ENSMUSG00000031813	chr8	Mvb12a	71542930	71543057	1060	0.630267	4.062065	0.000443	0.001693	0.03492	1	158	229	253	214	232	398	392	404	578	583
ENSMUSG00000023961	chr17	Enpp4	44096308	44099677	4560	-0.6709	5.728778	0.000445	0.001698	0.04233	-1	924	1113	1387	1025	942	965	944	720	1115	976
ENSMUSG00000034258	chr12	Mfsd7c	85746539	85747589	3435	-1.3555	0.27144	0.000445	0.001698	0.123982	-1	24	9	23	40	44	7	23	17	14	14
ENSMUSG00000027384	chr2	Ndufaf5	1.4E+08	1.4E+08	1789	-0.73739	5.090536	0.000447	0.001707	0.05068	-1	628	782	861	670	555	664	533	467	659	597
ENSMUSG00000040451	chr19	Sgms1	32122727	32124524	10299	-0.67863	5.36047	0.000449	0.001714	0.043124	-1	707	757	1030	737	1011	531	626	1118	771	633
ENSMUSG00000026730	chr2	Pter	12924041	12924198	4682	-0.60051	3.733686	0.00045	0.001718	0.03109	-1	239	208	271	322	293	168	228	245	326	277
ENSMUSG00000038000	chr8	Acd	1.06E+08	1.06E+08	1425	0.741946	2.865999	0.00045	0.001718	0.044535	1	87	78	82	93	106	128	184	204	273	275
ENSMUSG00000045658	chr1	Pid1	84036296	84038507	8172	0.677612	3.995206	0.000451	0.001721	0.040962	1	195	117	244	182	298	285	494	387	651	505
ENSMUSG00000085348	chr11	Gm12300	67211256	67211846	2027	-0.75271	6.404759	0.000452	0.001723	0.053967	-1	1722	1623	1867	1623	1997	1199	1002	1100	2833	1431
ENSMUSG00000025198	chr19	Erlin1	44034944	44037148	4961	0.617987	3.250088	0.000452	0.001724	0.031022	1	122	96	135	114	154	201	260	257	349	272
ENSMUSG00000046841	chr10	Ckap4	84526305	84528777	2954	0.96624	5.700012	0.000453	0.001726	0.088141	1	551	300	680	398	1107	1295	1941	743	2399	1748
ENSMUSG00000031488	chr8	Rab11fip1	27138773	27143394	7965	1.688062	-0.3003	0.000454	0.001731	0.167253	1	5	2	5	7	8	15	20	9	25	54
ENSMUSG00000089782	chr1	Gm3531	97948901	97949389	489	0.701341	2.525398	0.000455	0.001732	0.037655	1	59	63	76	70	92	136	162	168	179	167
ENSMUSG00000070003	chr8	Ssbp4	70597491	70597768	1474	0.646918	3.890426	0.000457	0.001742	0.036805	1	132	168	245	203	219	287	414	311	610	514
ENSMUSG00000008348	chr5	Ubc	1.25E+08	1.25E+08	2893	1.464255	7.393113	0.000458	0.001743	0.198987	1	1000	1443	1835	1744	1457	2488	2388	16305	3451	3994
ENSMUSG00000032525	chr9	Nktr	1.22E+08	1.22E+08	17457	-0.58226	5.311035	0.000458	0.001744	0.031586	-1	779	544	906	731	1050	511	748	802	865	808
ENSMUSG00000037679	chr12	Inf2	1.13E+08	1.13E+08	4600	0.671405	3.966625	0.000458	0.001744	0.039954	1	211	139	209	184	261	234	444	450	665	495
ENSMUSG00000028382	chr4	Ptbp3	59471868	59477015	7480	0.68258	4.625766	0.000459	0.001746	0.042767	1	258	263	329	345	389	363	608	642	1126	915
ENSMUSG00000071662	chr19	Polr2g	8793129	8793404	868	0.59245	4.766342	0.000459	0.001746	0.03197	1	317	357	444	322	356	673	782	642	872	819
ENSMUSG00000050471	chr9	Fam118b	35216965	35217747	5981	-0.56798	4.394051	0.00046	0.001747	0.028734	-1	362	392	451	398	486	362	380	381	406	422
ENSMUSG00000075227	chr19	Znhit2	6061192	6062472	1281	0.680346	2.969651	0.00046	0.001747	0.037409	1	81	79	131	107	99	193	204	212	268	230
ENSMUSG00000025068	chr19	Gsto1	47854970	47855122	1968	0.646259	4.970502	0.000461	0.001753	0.038654	1	296	429	433	470	393	689	734	1126	1015	886
ENSMUSG00000041891	chr18	Lman1	65980754	65982710	6411	-0.60466	6.160564	0.000463	0.001757	0.034762	-1	1196	1129	1712	1320	1946	1050	1536	982	1727	1376
ENSMUSG00000040904	chr11	Gm21988	70235206	70235468	1692	0.576258	6.194013	0.000463	0.001758	0.031526	1	738	932	1093	1034	1118	1839	1903	1873	2391	2162
ENSMUSG00000056735	chr5	A930024E05Rik	1.23E+08	1.23E+08	1896	1.356394	-0.30273	0.000467	0.001771	0.081255	1	4	8	9	4	7	11	28	27	28	23
ENSMUSG00000048772	chr4	Tmem53	1.17E+08	1.17E+08	1713	0.965687	1.399403	0.000467	0.001772	0.066244	1	24	26	19	38	34	53	79	63	116	83
ENSMUSG00000074829	chr9	2010315B03Rik	1.24E+08	1.24E+08	3914	-0.76643	2.88706	0.000474	0.001797	0.049834	-1	141	134	194	136	168	76	106	177	132	147
ENSMUSG00000034462	chr5	Pkd2	1.04E+08	1.04E+08	10169	-0.77703	4.946813	0.000475	0.001801	0.056845	-1	771	341	725	513	936	324	646	651	574	476
ENSMUSG00000073423	chr17	Zfp414	33629090	33629216	1966	0.791609	2.502616	0.000477	0.00181	0.050407	1	55	55	78	71	82	99	163	124	236	216
ENSMUSG00000063488	chr9	Zkscan7	1.23E+08	1.23E+08	2228	-1.11671	1.093412	0.000478	0.00181	0.092771	-1	42	39	57	46	54	15	28	58	27	25
ENSMUSG00000031796	chr8	Cfap20	95420252	95420669	1292	0.673803	3.179425	0.000478	0.00181	0.038322	1	83	91	139	108	164	217	306	218	307	235
ENSMUSG00000027868	chr3	Tbx15	99240381	99240446	3747	-0.74375	8.087074	0.000481	0.001824	0.053591	-1	5317	4917	7057	4780	6420	3292	4766	7559	4432	3596
ENSMUSG00000033444	chr10	Specc1l	75212073	75212219	6075	-0.55757	5.759358	0.000482	0.001826	0.029432	-1	953	843	1183	1013	1442	779	1051	1131	1083	1063
ENSMUSG00000028121	chr3	Bcar3	1.22E+08	1.22E+08	3298	0.913168	3.282697	0.000483	0.001829	0.07482	1	69	78	106	132	185	169	246	188	473	434
ENSMUSG00000028393	chr4	Alad	62509169	62509310	1871	0.684724	4.843747	0.000484	0.001832	0.04372	1	285	371	331	372	473	552	565	800	1245	1041
ENSMUSG00000023791	chr16	Pigx	32084418	32084626	2394	0.697253	3.088646	0.000484	0.001832	0.040342	1	84	124	122	99	100	189	249	257	282	235
ENSMUSG00000007815	chr9	Rhoa	1.08E+08	1.08E+08	7494	0.554387	7.257268	0.000485	0.001836	0.029749	1	1682	1699	2372	2076	2616	3327	4044	3715	5588	4733
ENSMUSG00000040205	chr7	Cuzd1	1.31E+08	1.31E+08	2256	-1.32875	0.15148	0.000486	0.001836	0.107797	-1	24	14	44	24	20	19	12	9	17	11
ENSMUSG00000047821	chr11	Trim16	62820231	62820999	4568	-0.60745	5.462798	0.000488	0.001846	0.034884	-1	647	815	1214	926	859	752	848	706	929	812
ENSMUSG00000020077	chr10	Srgn	62493833	62495106	2196	0.879805	3.964385	0.000488	0.001846	0.071218	1	142	172	201	230	159	251	405	275	747	744
ENSMUSG00000024908	chr19	Ppp6r3	3454933	3457051	4952	-0.579	6.31774	0.00049	0.001849	0.032208	-1	1439	1236	1766	1617	1969	1028	1478	1848	1739	1419
ENSMUSG00000039982	chr19	Dtx4	12466341	12469709	5765	0.703325	4.220286	0.00049	0.001849	0.045599	1	183	120	262	257	391	369	631	506	651	548
ENSMUSG00000066877	chr1	Nck2	43444579	43444706	4321	-0.61304	4.558113	0.000492	0.001858	0.034508	-1	316	393	531	455	729	369	451	435	549	367
ENSMUSG00000024212	chr17	Mllt1	56892612	56894590	3608	-0.52607	4.904611	0.000493	0.00186	0.025444	-1	523	511	653	562	705	454	605	534	693	583
ENSMUSG00000006191	chr13	Cdkal1	29191746	29193146	12799	-0.68441	3.913833	0.000494	0.001864	0.042283	-1	279	294	386	288	290	224	247	373	285	206
ENSMUSG00000039218	chr17	Srrm2	23790662	23790945	10982	-0.60124	7.247522	0.000494	0.001864	0.035112	-1	2695	2149	3557	3070	4027	1852	2802	3503	3212	2833
ENSMUSG00000035914	chr9	Cd276	58524300	58526361	3297	0.887976	4.026474	0.000497	0.001874	0.073465	1	165	99	200	150	366	350	742	335	652	403
ENSMUSG00000033313	chr8	Fbxl8	1.05E+08	1.05E+08	2103	1.031717	0.664171	0.000498	0.001879	0.062384	1	15	13	17	15	20	33	41	34	68	56
ENSMUSG00000039286	chr3	Fndc3b	27416162	27419602	11485	-0.76735	4.842885	0.0005	0.001884	0.055774	-1	561	301	672	571	991	261	590	574	636	465
ENSMUSG00000038370	chr1	Pcp4l1	1.71E+08	1.71E+08	1577	-0.87878	3.751853	0.0005	0.001886	0.071013	-1	170	277	366	391	251	244	239	115	257	232
ENSMUSG00000025103	chr7	Btbd1	81792075	81793726	3000	-0.57188	7.551075	0.000503	0.001896	0.031903	-1	3346	3274	4036	3787	4278	3125	3536	3880	3777	3138
ENSMUSG00000021536	chr13	Adcy2	68620043	68620872	4211	-0.66517	5.331184	0.000503	0.001897	0.042087	-1	644	752	921	817	1007	602	625	1055	754	565
ENSMUSG00000029270	chr5	Fam69a	1.08E+08	1.08E+08	2892	-0.56102	4.719419	0.000504	0.001899	0.028948	-1	494	431	567	482	650	449	445	456	567	548
ENSMUSG00000073902	chr7	Gm1966	1.07E+08	1.07E+08	7293	1.284572	0.416511	0.000504	0.001899	0.110317	1	10	4	13	9	24	25	32	44	36	63
ENSMUSG00000024231	chr18	Cul2	3382988	3383172	4138	-0.55491	5.590574	0.000506	0.001904	0.029242	-1	873	882	1048	961	994	829	941	869	1049	834
ENSMUSG00000039148	chr19	Sart1	5377523	5380135	5091	0.579455	4.862778	0.000507	0.001908	0.03122	1	253	372	445	416	471	590	736	857	991	909
ENSMUSG00000071347	chr14	C1qtnf9	60768134	60768168	1903	-0.7432	4.811848	0.000508	0.00191	0.052332	-1	399	596	729	764	421	342	477	629	583	432
ENSMUSG00000002083	chr7	Bbc3	16309616	16309861	2008	0.894399	1.617911	0.000509	0.001914	0.057728	1	31	33	33	35	39	57	71	111	103	108
ENSMUSG00000051331	chr6	Cacna1c	1.19E+08	1.19E+08	21191	-0.84573	2.05014	0.000513	0.001929	0.057011	-1	82	57	96	87	121	47	93	51	88	65
ENSMUSG00000017390	chr11	Aldoc	78322968	78323222	3263	1.419445	-0.39781	0.000513	0.001929	0.096683	1	2	4	10	6	7	8	28	23	26	25
ENSMUSG00000022960	chr16	Donson	91677268	91677619	2834	1.270451	0.74774	0.000514	0.001931	0.109793	1	24	18	11	7	13	33	43	43	77	64
ENSMUSG00000041037	chr7	Irgq	24530648	24530904	6123	-0.56545	5.198595	0.000514	0.001932	0.030143	-1	589	659	753	795	866	562	723	781	802	580
ENSMUSG00000029298	chr5	Gbp9	1.05E+08	1.05E+08	3693	-0.86097	2.766073	0.000515	0.001933	0.064271	-1	105	118	173	200	132	108	67	122	129	128
ENSMUSG00000045180	chrX	Shroom2	1.53E+08	1.53E+08	8375	-1.01497	0.948451	0.000519	0.001947	0.07004	-1	43	28	53	42	43	18	27	42	35	23
ENSMUSG00000071646	chr19	Mta2	8941875	8942382	4093	0.547515	5.440424	0.000521	0.001957	0.028427	1	487	480	645	621	727	832	1096	1384	1557	1203
ENSMUSG00000050732	chr6	Vamp8	72385223	72385653	2311	0.635011	4.941865	0.000523	0.001964	0.037943	1	337	436	447	412	345	712	756	772	1033	1081

ENSMUSG00000076432	chr12	Ywhaq	21390071	21391415	3061	0.602814	4.679069	0.000523	0.001964	0.033818	1	296	250	353	372	434	535	807	514	977	802
ENSMUSG00000040732	chr16	Erg	95359169	95361326	3466	-0.70717	3.272647	0.000525	0.00197	0.043885	-1	134	173	240	259	193	111	155	154	243	204
ENSMUSG00000042298	chr11	Ttc19	62281473	62281693	4675	-0.59293	5.193702	0.000526	0.001974	0.03337	-1	633	699	934	713	674	628	672	633	823	628
ENSMUSG00000026946	chr2	Nmi	51948487	51948776	2001	0.797921	2.66008	0.000529	0.001983	0.053118	1	70	76	94	64	71	157	164	132	224	242
ENSMUSG00000051329	chr2	Nup160	90677215	90677470	8761	-0.65941	2.953803	0.000531	0.00199	0.036333	-1	130	130	186	153	193	97	155	154	180	116
ENSMUSG00000066682	chr5	Pilrb2	1.38E+08	1.38E+08	1807	1.745312	-0.3586	0.000531	0.00199	0.178963	1	5	4	6	1	9	20	32	4	30	32
ENSMUSG00000020290	chr11	Xpo1	23256041	23256162	7181	-0.57386	5.279437	0.000533	0.001995	0.031412	-1	710	718	929	638	879	506	843	620	962	756
ENSMUSG00000022883	chr16	Robo1	72663149	72664194	7563	-0.97166	2.3437	0.000533	0.001995	0.081402	-1	87	67	110	99	209	51	117	79	102	51
ENSMUSG00000047284	chr11	Neurl4	69901072	69901148	5889	-0.53949	5.128643	0.000536	0.002005	0.027471	-1	558	614	852	675	773	478	699	748	779	637
ENSMUSG00000003123	chr7	Lipe	25379527	25380173	4518	1.801409	5.621088	0.000536	0.002006	0.30041	1	262	241	267	582	495	230	495	1003	2885	4858
ENSMUSG00000096056	chrX	Gm21986	1.01E+08	1.01E+08	5560	0.744032	2.266845	0.000536	0.002007	0.04258	1	44	51	62	60	78	108	141	112	184	146
ENSMUSG00000051639	chr17	Gm5812	6121208	6122164	957	1.17497	0.916762	0.000537	0.00201	0.097441	1	18	18	11	18	24	41	39	37	102	72
ENSMUSG00000001056	chr11	Nhp2	51619735	51619977	1146	0.660212	4.267795	0.000538	0.002012	0.040438	1	197	223	346	187	299	481	517	389	668	682
ENSMUSG00000026641	chr1	Usf1	1.71E+08	1.71E+08	2806	0.549084	4.353146	0.000538	0.002012	0.0274	1	231	211	321	302	323	488	574	558	601	580
ENSMUSG00000006299	chr1	Aamp	74279840	74280309	3458	0.572206	6.821425	0.000539	0.002015	0.0321	1	1188	1362	1723	1463	1912	2584	2847	3684	3337	3245
ENSMUSG00000050493	chr4	Fam167b	1.3E+08	1.3E+08	959	1.235004	-0.16904	0.000541	0.00202	0.068863	1	5	8	5	9	11	18	26	21	35	27
ENSMUSG00000050900	chrX	Gm7327	61785381	61786032	652	-0.97855	1.201914	0.000541	0.002021	0.070578	-1	36	58	65	49	38	25	38	30	51	34
ENSMUSG00000024960	chr19	Plcb3	6953714	6954299	4201	0.547144	4.507099	0.000541	0.002023	0.027399	1	286	234	343	298	384	433	585	667	795	690
ENSMUSG00000028597	chr4	Gpx7	1.08E+08	1.08E+08	1289	0.685082	3.832704	0.000542	0.002024	0.042983	1	156	120	215	140	295	363	464	312	468	419
ENSMUSG00000028645	chr4	Slc2a1	1.19E+08	1.19E+08	2853	0.806877	3.356513	0.000544	0.00203	0.058619	1	94	105	120	142	157	153	241	469	404	267
ENSMUSG00000061068	chr14	Mcpt4	56059744	56060100	990	1.040673	2.644542	0.000546	0.002036	0.096829	1	47	49	50	67	130	225	107	172	191	242
ENSMUSG00000062647	chr2	Rpl7a	26910764	26910830	1781	0.539281	8.084271	0.000547	0.002042	0.028829	1	2920	3247	3915	3824	4694	6065	7148	7032	9289	8119
ENSMUSG00000022280	chr15	Rnf19a	36239934	36242065	4276	-0.63652	4.325104	0.000548	0.002043	0.037801	-1	339	369	448	402	478	225	400	507	422	289
ENSMUSG00000025290	chr14	Rps24	24490681	24490758	840	0.574127	8.255458	0.000549	0.002048	0.032707	1	3311	3934	5079	3777	4433	7539	8625	8058	8933	9171
ENSMUSG00000025779	chr1	Ly96	16688051	16688169	1021	1.024837	0.65672	0.000549	0.002048	0.06508	1	11	12	24	11	23	37	48	36	55	52
ENSMUSG00000001962	chrX	Fam50a	74313033	74313325	2288	0.540614	4.235617	0.00055	0.00205	0.026183	1	219	235	259	273	285	397	476	532	631	566
ENSMUSG00000030824	chr7	Nucb1	45492874	45493949	5796	0.608181	6.276188	0.000553	0.00206	0.036236	1	803	712	1089	1035	1595	1482	2151	2055	2955	2439
ENSMUSG00000037349	chr19	Nudt22	6993018	6993202	1195	0.654557	3.238044	0.000556	0.00207	0.036541	1	91	127	154	113	118	207	262	285	292	283
ENSMUSG00000060572	chr4	Mfap2	1.41E+08	1.41E+08	1211	0.946908	4.72229	0.000556	0.002071	0.086555	1	257	134	255	221	702	670	957	802	914	685
ENSMUSG00000033862	chr8	Cdk10	1.23E+08	1.23E+08	1643	0.691252	3.147762	0.000558	0.002078	0.041331	1	96	89	132	104	142	189	212	203	325	343
ENSMUSG00000038976	chr11	Ppp1r9b	94991035	94992918	5083	0.618388	5.520771	0.000558	0.002079	0.037046	1	462	452	604	643	910	893	1246	1045	1899	1518
ENSMUSG00000057863	chr17	Rpl36	56613395	56613448	404	0.618703	6.911473	0.000562	0.002091	0.03782	1	1225	1619	2049	1393	1639	3122	3345	3678	3450	3202
ENSMUSG00000035901	chr7	Dennd5a	1.1E+08	1.1E+08	8677	-0.58732	5.999355	0.000562	0.002092	0.033738	-1	1021	977	1353	1508	1615	746	1246	1378	1496	1181
ENSMUSG00000035513	chr2	Ntng2	29194541	29195053	3990	-0.76228	3.73551	0.000563	0.002096	0.053813	-1	167	288	284	354	302	233	215	147	330	222
ENSMUSG00000060002	chr10	Chpt1	88452745	88453097	8324	-0.7117	6.717163	0.000564	0.002098	0.050078	-1	1732	2104	2208	2660	2133	1008	1441	1895	2579	2623
ENSMUSG00000072591	chr5	5930412G12Rik	1.29E+08	1.29E+08	3394	0.895863	2.132711	0.000565	0.002099	0.065492	1	57	39	52	50	48	109	166	109	181	85
ENSMUSG00000004383	chr8	Large	72814599	72816021	7883	-0.53851	4.614657	0.000565	0.0021	0.026922	-1	416	423	536	497	548	411	469	394	582	469
ENSMUSG00000025968	chr1	Ndufs1	63143596	63143922	8086	-0.62872	8.928161	0.000566	0.002102	0.039452	-1	8210	10560	10954	10665	8366	7738	8948	9816	10036	7886
ENSMUSG00000031078	chr7	Cttn	1.44E+08	1.44E+08	4192	0.548679	5.52996	0.000567	0.002106	0.029025	1	558	514	645	562	874	890	1385	1347	1595	1238
ENSMUSG00000018326	chr2	Ywhab	1.64E+08	1.64E+08	3382	0.71493	6.513174	0.000569	0.002114	0.050447	1	922	977	1164	1166	1598	1664	2461	1713	3783	3927
ENSMUSG00000037805	chr17	Rpl10a	28328471	28328618	2349	0.537735	7.346668	0.000571	0.002121	0.028724	1	1889	1924	2389	2090	2859	3622	4387	4248	5517	4785
ENSMUSG00000046822	chr10	Slc39a3	81028538	81031700	4016	-0.53431	4.596186	0.000573	0.002127	0.026595	-1	444	407	501	467	565	338	482	404	565	529
ENSMUSG00000021583	chr13	Erap1	74639872	74639893	4014	-0.56071	4.321965	0.000576	0.002138	0.029056	-1	349	295	482	393	485	253	387	336	467	460
ENSMUSG00000031355	chrX	Arhgap6	1.69E+08	1.69E+08	12128	-0.85103	2.40864	0.000577	0.002139	0.062433	-1	115	69	136	118	130	40	95	113	118	81
ENSMUSG00000028048	chr3	Gba	89202928	89203086	1950	0.594552	4.510742	0.000578	0.002143	0.033155	1	272	214	348	293	400	443	526	600	865	798
ENSMUSG00000043140	chr16	Tmem186	8633884	8636392	2736	-0.59988	4.399544	0.000578	0.002143	0.033706	-1	350	424	466	415	455	290	395	507	439	324
ENSMUSG00000038633	chr1	Degs1	1.82E+08	1.82E+08	2591	0.561986	5.251096	0.00058	0.00215	0.030379	1	433	408	596	491	659	827	1011	847	1377	1266
ENSMUSG00000048826	chr17	Dact2	14195231	14197311	2808	-1.14345	0.746218	0.00058	0.00215	0.094594	-1	35	18	33	48	54	14	28	20	42	16
ENSMUSG00000042063	chr12	Zfp386	1.16E+08	1.16E+08	8753	-0.66169	4.046287	0.000582	0.002155	0.040779	-1	282	321	458	280	346	220	279	416	325	248
ENSMUSG00000043391	chr16	2510009E07Rik	21649045	21653758	5164	-0.54779	5.009197	0.000582	0.002156	0.028616	-1	459	571	768	700	711	477	612	532	783	665
ENSMUSG00000029267	chr5	Mtf2	1.08E+08	1.08E+08	5263	-0.62156	3.362131	0.000584	0.00216	0.034038	-1	200	165	249	207	213	119	215	178	262	182
ENSMUSG00000024581	chr18	Napg	62977836	62978024	5139	-0.53341	4.362781	0.000585	0.002166	0.026204	-1	375	357	456	415	415	303	385	390	474	412
ENSMUSG00000025234	chr9	Arih1	59388258	59393378	7707	-0.59889	6.806939	0.000587	0.002171	0.035658	-1	1920	1876	2681	2210	2640	1553	2047	2757	2220	1804
ENSMUSG00000075054	chr13	Yae1d1	17986640	17989782	3436	-0.61382	3.487495	0.000588	0.002175	0.032956	-1	182	219	265	203	259	179	229	212	199	200
ENSMUSG00000015869	chr11	Prpsap1	1.16E+08	1.16E+08	3407	0.54589	4.15275	0.00059	0.002182	0.027019	1	178	227	276	239	286	395	450	480	598	532
ENSMUSG00000038525	chr5	Armc10	21645813	21646235	3407	0.676556	2.987299	0.00059	0.002183	0.038661	1	97	77	98	117	112	143	218	231	290	255
ENSMUSG00000001098	chr5	Kctd10	1.14E+08	1.14E+08	4046	0.571818	4.890326	0.000591	0.002183	0.03111	1	342	316	423	439	474	543	936	680	1161	881
ENSMUSG00000087404	chr11	Gm11752	1.19E+08	1.19E+08	510	-1.86153	-0.41753	0.000591	0.002185	0.212236	-1	16	20	22	13	19	16	3	1	2	10
ENSMUSG00000008333	chr2	Snrpb2	1.43E+08	1.43E+08	2857	0.608499	4.16097	0.000593	0.00219	0.034228	1	191	232	299	199	256	364	507	619	502	510
ENSMUSG00000021238	chr12	Aldh6a1	84430723	84432548	3340	-1.00335	6.65724	0.000593	0.00219	0.099504	-1	2231	1715	2159	2495	2629	650	928	3174	1581	1622
ENSMUSG00000024180	chr17	Tmem8	26113316	26113567	3464	1.044666	1.903792	0.000593	0.00219	0.09138	1	29	30	38	37	66	76	99	58	188	161
ENSMUSG00000071637	chr16	Cebpd	15887286	15888077	1180	1.476903	4.094364	0.000596	0.002199	0.207498	1	120	72	173	224	171	413	201	1534	314	376
ENSMUSG00000033253	chr4	Szt2	1.18E+08	1.18E+08	11947	-0.62727	3.614563	0.000596	0.0022	0.035493	-1	251	166	276	255	293	144	229	245	238	269
ENSMUSG00000031023	chr7	Akip1	1.1E+08	1.1E+08	1305	0.653826	2.832617	0.000597	0.002203	0.035342	1	71	75	106	101	104	160	191	205	223	220
ENSMUSG00000055884	chr12	Fancm	65075606	65076177	7775	-0.87708	1.317135	0.000599	0.002208	0.054717	-1	38	45	60	54	68	25	48	42	54	33
ENSMUSG00000031631	chr8	Cfap97	46151771	46151913	5157	-0.59599	3.834073	0.0006	0.002214	0.032308	-1	235	248	330	270	354	167	267	345	298	253

ENSMUSG00000047250	chr2	Ptgs1	36230426	36230569	3884	0.788237	2.118053	0.000604	0.002227	0.048731	1	45	37	52	65	60	84	120	115	162	150
ENSMUSG00000020850	chr11	Prpf8	75486816	75487191	7461	-0.54237	7.025621	0.000605	0.002229	0.02942	-1	2135	2017	2839	2742	3293	1878	2610	2557	3074	2334
ENSMUSG00000009927	chr9	Rps25	44407714	44407757	683	0.562716	7.828027	0.000605	0.00223	0.031845	1	2700	2870	3699	2567	3496	5405	6439	6559	6920	6134
ENSMUSG00000026365	chr1	Cfh	1.4E+08	1.4E+08	8383	-0.88113	4.341973	0.00061	0.002247	0.075364	-1	481	225	458	393	668	172	332	560	332	280
ENSMUSG00000036376	chr13	Abt1	23421539	23422335	1278	0.647631	3.417437	0.000612	0.002253	0.036995	1	117	139	157	129	142	287	274	333	303	287
ENSMUSG00000031584	chr8	Gsr	33652523	33652570	2754	0.674588	4.625392	0.000613	0.002257	0.043755	1	264	301	356	307	351	463	565	1068	707	728
ENSMUSG00000003437	chr7	Paf1	28392951	28393254	3438	0.544264	5.012525	0.000614	0.002259	0.028456	1	311	385	528	452	532	713	811	976	1042	916
ENSMUSG00000036087	chr5	Slain2	72914304	72915013	8446	-0.61174	6.671763	0.000618	0.002275	0.037476	-1	1658	1692	2395	2314	2284	1421	1810	2531	2012	1622
ENSMUSG00000078184	chr1	B020018G12Rik	1.76E+08	1.76E+08	1338	1.120898	0.248873	0.000619	0.002276	0.070112	1	8	12	12	9	15	28	43	32	28	38
ENSMUSG00000021945	chr14	Zmym2	56887795	56887857	6876	-0.6263	5.268061	0.000619	0.002277	0.038425	-1	647	598	843	826	1029	518	694	993	710	607
ENSMUSG00000043090	chr8	Zfp866	69761326	69763495	5601	-0.57214	3.655902	0.000623	0.002292	0.029165	-1	207	211	267	236	343	180	203	254	310	239
ENSMUSG00000025006	chr19	Sorbs1	40295049	40295116	3075	-1.02228	4.494266	0.000626	0.002299	0.102408	-1	416	430	499	712	442	143	273	720	356	265
ENSMUSG00000038538	chr6	Ubn2	38433950	38434598	21438	-0.60782	5.031809	0.000626	0.002299	0.035928	-1	648	481	701	624	860	485	581	773	578	580
ENSMUSG00000024843	chr19	Chka	3851773	3852413	12024	0.86054	1.94917	0.000627	0.002303	0.058441	1	43	42	34	38	64	68	117	103	160	125
ENSMUSG00000021357	chr13	Exoc2	30813919	30815391	4427	-0.54433	4.288177	0.000629	0.002309	0.027634	-1	333	323	487	374	421	271	365	339	535	366
ENSMUSG00000069806	chr7	Cacng7	3332955	3333036	2207	-0.69509	3.241893	0.000629	0.002309	0.043689	-1	188	134	222	220	209	105	235	144	195	168
ENSMUSG00000034795	chr14	Ccdc122	77036772	77036971	1985	1.083219	0.362909	0.000629	0.00231	0.066839	1	8	8	13	13	21	24	46	37	45	34
ENSMUSG00000029547	chr5	Ints1	1.4E+08	1.4E+08	7113	-0.55416	5.401792	0.000631	0.002317	0.030096	-1	663	705	902	896	1063	668	789	631	1111	824
ENSMUSG00000028024	chr3	Enpep	1.29E+08	1.29E+08	4706	-0.67795	3.872869	0.000632	0.00232	0.043183	-1	256	247	323	244	450	177	258	209	286	390
ENSMUSG00000027610	chr2	Gss	1.56E+08	1.56E+08	5915	0.682558	2.928845	0.000634	0.002324	0.039714	1	85	92	100	99	102	148	226	170	291	258
ENSMUSG00000039183	chr17	Nubp2	24882611	24883314	1430	0.573595	3.628884	0.000637	0.002335	0.029089	1	136	145	193	160	192	247	290	379	450	362
ENSMUSG00000026281	chr1	Dtymk	93792576	93792943	2631	0.70954	3.474608	0.000637	0.002336	0.046009	1	127	128	162	105	177	282	302	199	417	397
ENSMUSG00000006335	chr7	Tfpt	3620324	3620474	1197	0.665676	3.144353	0.000639	0.00234	0.038706	1	75	115	139	101	137	222	232	263	284	241
ENSMUSG00000079084	chr9	Ccdc82	13246982	13247021	1847	-1.05502	0.864097	0.000639	0.002341	0.083127	-1	40	29	43	44	42	11	29	39	39	18
ENSMUSG00000024177	chr17	Nme4	26091734	26092152	1418	0.874311	1.845597	0.000646	0.002366	0.061514	1	27	29	46	46	60	110	94	82	128	105
ENSMUSG00000049734	chr9	Trex1	1.09E+08	1.09E+08	1314	0.634022	4.186284	0.000646	0.002367	0.038089	1	176	221	229	265	297	478	388	603	529	538
ENSMUSG00000028609	chr4	Magoh	1.08E+08	1.08E+08	770	0.659125	3.850247	0.000647	0.002369	0.040557	1	154	169	286	144	177	356	396	465	436	376
ENSMUSG00000097317	chr2	Gm17281	91250743	91254087	3589	-0.66023	3.852273	0.000647	0.002369	0.040799	-1	261	273	289	350	285	215	224	330	232	286
ENSMUSG00000038708	chr9	Golga4	1.19E+08	1.19E+08	7535	-0.6821	8.401315	0.000647	0.002369	0.047319	-1	5560	6078	8019	7844	7356	4827	4965	9107	5632	5479
ENSMUSG00000078190	chr1	Dnm3os	1.62E+08	1.62E+08	7928	1.231653	1.181897	0.000649	0.002373	0.125019	1	26	6	26	11	40	48	95	64	62	80
ENSMUSG00000021025	chr12	Nfkbia	55489411	55489969	1577	0.846244	4.685069	0.000649	0.002373	0.070472	1	209	265	400	413	242	512	550	1231	678	856
ENSMUSG00000034761	chr12	Map4k5	69803750	69805351	8614	-0.70695	4.93905	0.000649	0.002375	0.049318	-1	554	577	673	633	733	324	538	880	547	439
ENSMUSG00000003500	chr6	Impdh1	29200434	29201219	3294	0.614584	4.730546	0.00065	0.002377	0.036643	1	248	270	406	387	461	514	694	576	1111	914
ENSMUSG00000038453	chr11	Srcin1	97509340	97512648	8386	-0.99236	1.013063	0.000651	0.002378	0.073724	-1	31	42	45	55	44	18	34	19	42	42
ENSMUSG00000032625	chr6	Thsd7a	12311610	12317451	13737	-1.00528	1.444805	0.000653	0.002384	0.08096	-1	36	38	79	81	68	23	32	58	53	43
ENSMUSG00000024642	chr19	Tle4	14448072	14449841	4640	-0.61632	4.305116	0.000655	0.002391	0.03626	-1	317	371	441	442	419	262	326	501	370	355
ENSMUSG00000027589	chr2	Pcmtd2	1.82E+08	1.82E+08	4183	-0.91258	5.170951	0.000656	0.002397	0.083054	-1	778	724	862	842	665	261	480	1125	596	490
ENSMUSG00000037761	chr2	Actr5	1.59E+08	1.59E+08	4186	0.807928	1.693145	0.000657	0.0024	0.04757	1	32	33	37	40	47	70	83	85	117	110
ENSMUSG00000021690	chr13	Jmy	93430097	93435419	8780	-0.94474	5.181614	0.000659	0.002404	0.088984	-1	766	703	799	811	885	301	454	1214	506	425
ENSMUSG00000021510	chr13	A530054K11Rik	67617001	67621849	5217	-0.83571	1.675582	0.00066	0.002408	0.053985	-1	61	52	86	69	68	33	54	66	67	45
ENSMUSG00000031012	chrX	Cask	13517080	13522347	9145	-0.56455	3.815689	0.000662	0.002414	0.028895	-1	217	217	313	275	396	208	285	271	287	268
ENSMUSG00000047090	chr10	Tmem198b	1.29E+08	1.29E+08	3363	0.638822	3.010815	0.000664	0.002422	0.034717	1	89	87	117	103	125	143	235	225	317	229
ENSMUSG00000021133	chr12	4933426M11Rik	80790532	80790815	5001	-0.61329	5.980206	0.000667	0.002431	0.037843	-1	1183	1056	1468	1339	1314	790	1235	1544	1341	946
ENSMUSG00000004655	chr6	Aqp1	55336432	55336874	2627	-0.61691	7.917289	0.000668	0.002433	0.038902	-1	4040	3577	5607	6435	4868	3268	3819	4174	6186	5127
ENSMUSG00000029104	chr5	Htt	34761740	34762109	18808	-0.61842	4.305685	0.000669	0.002436	0.036762	-1	340	285	470	388	541	238	341	279	527	468
ENSMUSG00000055128	chr14	Cgrrf1	46832134	46832379	3291	-0.55084	5.12827	0.000669	0.002438	0.029753	-1	586	667	868	672	660	545	698	652	753	654
ENSMUSG00000047907	chr2	Tshz2	1.7E+08	1.7E+08	7781	-0.65242	3.824018	0.000671	0.002445	0.040146	-1	229	185	311	379	354	155	251	310	340	245
ENSMUSG00000041164	chr11	Zmiz2	6389074	6389140	4655	-0.54613	5.668735	0.000672	0.002447	0.029724	-1	782	811	1079	1161	1249	734	916	838	1248	1128
ENSMUSG00000046994	chr1	Mars2	55237177	55248470	11294	-0.62202	3.642772	0.000675	0.002456	0.035581	-1	193	254	239	277	292	191	288	208	258	195
ENSMUSG00000030935	chr7	Acsm3	1.2E+08	1.2E+08	4936	2.830713	0.9455	0.000675	0.002456	0.64663	1	3	6	2	16	8	1	8	35	175	169
ENSMUSG00000006262	chr5	Mob1b	88720855	88721121	10927	-0.56294	5.39659	0.000675	0.002456	0.031407	-1	643	670	1016	885	1025	616	839	941	919	653
ENSMUSG00000004364	chr1	Cul3	80264923	80267287	4873	-0.66365	7.604306	0.000679	0.002469	0.045042	-1	3366	3916	4535	3958	4051	2796	3171	5104	3430	2937
ENSMUSG00000037553	chr4	Zdhhc18	1.34E+08	1.34E+08	5382	0.536612	4.603654	0.00068	0.002473	0.027496	1	262	287	356	358	394	528	568	673	820	768
ENSMUSG00000040540	chr10	Gm9770	1.3E+08	1.3E+08	810	-1.49703	0.722067	0.000682	0.002478	0.185982	-1	34	36	27	60	38	8	13	49	11	16
ENSMUSG00000068923	chr3	Syt11	88744700	88748010	5205	-0.58928	3.283647	0.000684	0.002485	0.030379	-1	160	154	223	222	216	148	178	171	219	187
ENSMUSG00000035064	chr7	Eef2k	1.21E+08	1.21E+08	7166	-0.65705	5.933005	0.000684	0.002486	0.043601	-1	938	1257	1473	1203	1375	915	890	1550	1065	1056
ENSMUSG00000048644	chr8	Ctxn1	4257648	4258647	1224	1.405984	-0.04963	0.000686	0.002491	0.122406	1	2	12	3	12	9	30	35	23	30	23
ENSMUSG00000034161	chr15	Scx	76457438	76458186	1136	1.075572	3.401807	0.000692	0.002513	0.111589	1	145	44	119	72	191	298	493	167	419	275
ENSMUSG00000041926	chr1	Rnpep	1.35E+08	1.35E+08	6977	0.740402	4.644235	0.000694	0.002521	0.054266	1	253	256	323	319	420	614	646	372	999	1034
ENSMUSG00000040940	chr7	Arhgef1	24902912	24903128	7495	0.591884	5.345201	0.000695	0.002522	0.034864	1	494	449	590	526	649	718	1095	908	1606	1484
ENSMUSG00000029598	chr5	Plbd2	1.2E+08	1.2E+08	6620	0.622568	5.466617	0.000698	0.002532	0.038857	1	507	451	653	603	707	745	1133	1774	1519	1153
ENSMUSG00000033760	chr19	Rbm4b	4756543	4756661	9886	0.793529	1.683187	0.000698	0.002533	0.046716	1	33	29	46	34	48	74	91	79	115	100
ENSMUSG00000038736	chr15	Nudcd1	44375227	44376686	3447	-0.69362	2.964869	0.000711	0.002578	0.042894	-1	117	139	180	143	232	104	180	111	163	136
ENSMUSG00000022208	chr14	Jph4	55106830	55108395	6872	-1.39175	-0.07205	0.000712	0.00258	0.126263	-1	26	8	26	12	37	13	14	7	14	8
ENSMUSG00000055866	chr1	Per2	91415982	91418020	5856	-1.13091	2.473882	0.000712	0.00258	0.120548	-1	209	103	136	72	91	41	81	127	91	69
ENSMUSG00000059291	chr4	Rpl11	1.36E+08	1.36E+08	2697	0.542766	7.225846	0.000714	0.002589	0.030303	1	1817	1845	2392	1782	2348	3378	4379	4138	4515	4246

ENSMUSG00000033082	chr6	Clec1a	1.29E+08	1.29E+08	3268	-0.94484	1.729692	0.000716	0.002596	0.075061	-1	53	54	85	102	65	32	57	75	49	47
ENSMUSG00000034265	chr17	Zdhhc14	5492600	5493691	3115	0.761609	2.199442	0.000717	0.002598	0.047206	1	47	49	66	49	67	94	113	127	152	174
ENSMUSG00000098666	chr14	Mir6950	69692248	69692320	73	-1.23572	2.014637	0.000719	0.002603	0.140736	-1	97	35	103	43	209	39	70	41	81	50
ENSMUSG00000024608	chr18	Rps14	60774510	60774686	1384	0.573677	8.192369	0.00072	0.002606	0.034088	1	3176	3960	4794	3284	4435	6719	7617	9138	8737	8448
ENSMUSG00000038059	chr18	Smim3	60474193	60475585	1984	1.010274	2.411258	0.000723	0.002618	0.093684	1	65	37	57	34	98	144	176	79	248	170
ENSMUSG00000028670	chr4	Lypla2	1.36E+08	1.36E+08	2054	0.55188	5.143428	0.000725	0.002625	0.030227	1	378	446	570	455	546	822	933	777	1236	1137
ENSMUSG00000098789	chr2	Jmjd7	1.2E+08	1.2E+08	1960	0.816481	1.757645	0.000728	0.002634	0.050337	1	35	42	40	40	38	77	86	102	112	108
ENSMUSG00000084535	chr12	Mir1906-1	1.1E+08	1.1E+08	80	1.195736	2.274332	0.000734	0.002653	0.132036	1	73	33	34	16	81	87	132	217	195	144
ENSMUSG00000037815	chr18	Ctnna1	35118888	35118981	3698	0.559764	6.354531	0.000734	0.002653	0.032074	1	898	914	1079	1294	1358	1570	2565	2398	2835	2116
ENSMUSG00000087408	chr8	Cers1	70315775	70316108	3171	-0.64735	4.537209	0.000734	0.002654	0.041347	-1	404	350	568	465	602	400	468	249	543	443
ENSMUSG00000031312	chrX	Itgb1bp2	1.01E+08	1.01E+08	1799	0.563924	8.303115	0.000736	0.00266	0.033081	1	3365	4057	5270	3747	4946	8001	9260	8510	9862	8012
ENSMUSG00000039210	chr1	Gpatch2	1.87E+08	1.87E+08	7684	-0.57025	3.469568	0.000737	0.002664	0.029155	-1	180	188	244	227	266	144	208	240	250	200
ENSMUSG00000097715	chr13	Gpr137b-ps	12619084	12621408	2997	1.316066	1.478491	0.000738	0.002665	0.151365	1	26	8	18	35	41	41	61	58	151	146
ENSMUSG00000027569	chr2	Mrgbp	1.81E+08	1.81E+08	3499	0.736135	2.382006	0.000741	0.002674	0.044665	1	68	55	77	53	64	112	154	153	197	132
ENSMUSG00000046618	chr2	Olfml2a	38931978	38932181	5579	-0.80431	3.950221	0.000741	0.002674	0.063781	-1	322	154	347	300	556	168	344	304	319	188
ENSMUSG00000038379	chr9	Ttk	83834689	83834759	4919	1.400119	0.232106	0.000742	0.002679	0.139329	1	5	12	11	3	17	20	41	20	73	29
ENSMUSG00000049550	chr5	Clip1	1.24E+08	1.24E+08	9801	-0.8192	7.898867	0.000745	0.002688	0.069478	-1	4555	4081	5881	5454	5525	2795	3072	7440	3623	3097
ENSMUSG00000019795	chr10	Pcmt1	7629373	7630976	4718	-0.56719	6.797151	0.000747	0.002693	0.033225	-1	1986	2058	2609	2054	2351	1997	2089	2027	2335	1900
ENSMUSG00000032691	chr11	Nlrp3	59541568	59541603	4057	1.482616	-0.30244	0.000747	0.002694	0.124829	1	6	3	5	6	10	7	22	18	33	41
ENSMUSG00000069895	chr8	Atxn1l	1.1E+08	1.1E+08	7526	-0.5658	4.566368	0.00075	0.002703	0.031421	-1	397	340	519	533	591	281	453	529	563	428
ENSMUSG00000024959	chr19	Bad	6941861	6942440	2007	0.547437	3.816145	0.000752	0.00271	0.027593	1	161	169	220	165	238	309	390	400	412	421
ENSMUSG00000038482	chr8	Tfdp1	13339674	13339739	1700	-0.52286	5.297812	0.000755	0.002719	0.027457	-1	638	656	901	787	909	498	806	709	990	816
ENSMUSG00000075122	chr16	Cd80	38458933	38459289	1701	1.538623	-0.3668	0.000759	0.002733	0.149378	1	6	1	5	4	12	11	27	10	29	38
ENSMUSG00000029283	chr5	Cdc7	1.07E+08	1.07E+08	4128	1.220874	0.819829	0.00076	0.002736	0.11467	1	18	16	18	10	19	32	65	21	81	74
ENSMUSG00000074151	chr8	Nlrc5	94472763	94473054	7646	1.302101	1.184567	0.000761	0.002739	0.142226	1	23	12	17	23	28	64	44	28	91	129
ENSMUSG00000078578	chr3	Ube2d3	1.35E+08	1.35E+08	2675	-0.58233	7.680076	0.000761	0.002739	0.03538	-1	3585	3690	4964	3855	4457	2740	3820	4999	4279	3387
ENSMUSG00000029687	chr6	Ezh2	47530274	47530601	6197	0.770708	2.744555	0.000763	0.002747	0.05384	1	74	52	89	64	135	146	191	150	257	234
ENSMUSG00000026775	chr2	Yme1l1	23156369	23156731	8009	-0.58128	5.931462	0.000765	0.002752	0.034692	-1	1146	1061	1336	1156	1400	807	1256	1439	1273	947
ENSMUSG00000015957	chr7	Wnt11	98835112	98835348	3633	0.906857	2.973455	0.000768	0.002763	0.078043	1	81	82	72	93	120	174	185	416	226	167
ENSMUSG00000036980	chr5	Taf6	1.38E+08	1.38E+08	3779	-0.50912	4.898092	0.000769	0.002764	0.025578	-1	493	525	663	588	653	466	559	566	703	579
ENSMUSG00000006344	chr10	Ggt5	75589340	75589882	4736	0.804155	3.417113	0.00077	0.002767	0.062445	1	100	72	151	117	222	190	226	408	360	400
ENSMUSG00000024622	chr18	Hmgxb3	61131279	61132595	5101	-0.57125	4.317687	0.00077	0.002767	0.031794	-1	379	360	385	392	459	261	370	478	407	356
ENSMUSG00000020868	chr11	Xylt2	94663851	94664909	3979	0.635593	3.220887	0.000771	0.00277	0.036525	1	103	83	135	136	151	167	266	242	331	320
ENSMUSG00000032307	chr9	Ube2q2	55148854	55149826	4305	-0.60042	5.128834	0.000771	0.002771	0.036426	-1	619	661	869	632	728	497	617	860	620	628
ENSMUSG00000030672	chr7	Mylpf	1.27E+08	1.27E+08	885	-0.59272	14.42443	0.000776	0.002785	0.037018	-1	356921	413333	556752	393319	497554	412905	382543	410946	410059	393510
ENSMUSG00000022019	chr14	Tdrd3	87416639	87416848	5643	-0.55227	4.162465	0.000777	0.002789	0.029151	-1	315	280	406	348	434	279	352	392	355	302
ENSMUSG00000013663	chr19	Pten	32757497	32758523	11507	-0.5771	5.190472	0.000781	0.0028	0.033761	-1	639	595	856	716	860	443	673	887	883	573
ENSMUSG00000029186	chr5	Pi4k2b	52741587	52741968	3751	0.814976	2.319418	0.000781	0.0028	0.057981	1	60	37	51	59	90	82	144	141	212	162
ENSMUSG00000048489	chr6	8430408G22Rik	1.17E+08	1.17E+08	1317	2.977422	4.970417	0.00078	0.0028	0.780456	1	58	54	135	286	57	136	91	5588	161	415
ENSMUSG00000041718	chrX	Alg13	1.44E+08	1.44E+08	5964	-0.72577	2.289452	0.000782	0.002804	0.044289	-1	80	90	123	106	104	61	94	101	93	76
ENSMUSG00000046603	chr9	Tcaim	1.23E+08	1.23E+08	3126	-0.57259	5.482387	0.000783	0.002809	0.033428	-1	731	835	1010	925	954	699	817	1049	905	697
ENSMUSG00000022641	chr16	Bbx	50191844	50197646	14205	-0.61453	3.378016	0.000784	0.00281	0.034863	-1	186	154	237	197	282	133	216	167	281	172
ENSMUSG00000022895	chr16	Ets2	95702075	95702644	4710	-0.56664	5.884158	0.000785	0.002813	0.033064	-1	965	993	1140	1400	1400	791	1000	1303	1450	1065
ENSMUSG00000045039	chr7	Megf8	25317164	25317693	10159	-0.54125	5.480166	0.000785	0.002813	0.029812	-1	679	652	1003	922	1235	587	923	805	1096	880
ENSMUSG00000079462	chr6	Gm15737	92869357	92869494	4894	-1.38776	0.746938	0.000788	0.002821	0.160246	-1	40	26	33	29	71	12	11	40	10	30
ENSMUSG00000020571	chr12	Pdia6	17266545	17266651	3745	0.763614	6.842455	0.00079	0.002827	0.06081	1	1108	1154	1606	1173	2197	2815	3594	1631	4650	4312
ENSMUSG00000057522	chr11	Spop	95414080	95414131	3159	-0.5532	8.181606	0.000791	0.00283	0.032197	-1	4875	5156	6748	5705	6407	5199	5601	4778	6010	5606
ENSMUSG00000098387	chr2	Pet117	1.44E+08	1.44E+08	693	-0.91309	1.751477	0.000791	0.002832	0.071329	-1	61	63	65	83	89	24	66	75	64	43
ENSMUSG00000053038	chr8	Gm6180	42246911	42247411	501	1.088248	1.40638	0.000794	0.002841	0.099864	1	20	16	32	27	42	52	85	37	146	92
ENSMUSG00000023019	chr15	Gpd1	99717515	99717648	2961	-0.72861	9.924278	0.000796	0.002848	0.055879	-1	16542	18903	23080	21259	21336	14749	13073	9979	22329	25676
ENSMUSG00000053985	chr7	Zfp14	30038053	30039416	1506	-1.04429	0.556944	0.000797	0.002849	0.073013	-1	29	23	35	40	31	12	27	30	19	19
ENSMUSG00000059005	chr2	Hnrnpa3	75659261	75659389	5396	0.587136	6.905288	0.000798	0.002854	0.036067	1	1119	1330	1812	1534	2354	2370	3148	2957	4501	4046
ENSMUSG00000034459	chr19	Ifit1	34640871	34640987	2656	1.57611	3.036063	0.0008	0.002858	0.242676	1	40	53	64	92	96	554	146	65	150	373
ENSMUSG00000047030	chr2	Spata2	1.67E+08	1.67E+08	4510	-0.54546	4.590904	0.000801	0.002861	0.029281	-1	390	396	633	422	565	392	465	484	490	437
ENSMUSG00000007682	chr12	Dio2	90724554	90729990	5813	1.043509	2.363204	0.000802	0.002865	0.102464	1	33	38	40	75	93	119	208	70	206	193
ENSMUSG00000037474	chr1	Dtl	1.92E+08	1.92E+08	13709	1.280323	1.195603	0.000806	0.00288	0.142229	1	13	14	23	15	43	55	60	25	124	100
ENSMUSG00000025754	chr7	Agbl1	76318072	76318143	4594	-1.61654	0.816984	0.000808	0.002885	0.23121	-1	44	25	29	59	59	1	18	33	43	9
ENSMUSG00000028933	chr5	Xrcc2	25689812	25692828	5216	-0.88206	2.36449	0.000809	0.002887	0.072191	-1	98	109	139	120	79	44	82	61	135	109
ENSMUSG00000023150	chr1	Ivns1abp	1.51E+08	1.51E+08	5435	-0.58152	6.989866	0.000811	0.002895	0.035497	-1	2321	2113	2820	2341	3189	1730	2477	3069	2548	2065
ENSMUSG00000026393	chr1	Nek7	1.38E+08	1.38E+08	7376	-0.6997	6.717235	0.000814	0.002906	0.05132	-1	1989	1932	2527	2224	2154	1427	1617	2946	1678	1603
ENSMUSG00000041420	chr7	Meis3	16175090	16175184	3173	0.957999	1.333067	0.000815	0.002906	0.071085	1	31	17	23	25	40	40	83	66	94	92
ENSMUSG00000002496	chr17	Tsc2	24595937	24596766	6018	-0.53882	6.03967	0.000819	0.00292	0.030104	-1	1058	1050	1385	1494	1555	1029	1152	1370	1493	1212
ENSMUSG00000022100	chr14	Xpo7	70654246	70666094	15121	-0.54807	5.518913	0.000819	0.002921	0.030822	-1	735	783	1033	927	1092	662	803	1104	960	812
ENSMUSG00000021177	chr12	Tdp1	99884517	99884552	5464	0.849086	2.126078	0.00082	0.002923	0.061679	1	44	51	37	49	71	108	135	84	167	145
ENSMUSG00000028434	chr4	Epb4.1l4b	56991972	56995803	8858	-0.85996	1.930942	0.000821	0.002925	0.063575	-1	93	59	112	69	69	39	67	68	81	60
ENSMUSG00000029054	chr4	Gabrd	1.55E+08	1.55E+08	2875	1.334404	2.000408	0.000826	0.002941	0.166297	1	52	14	49	23	46	137	158	41	221	92

ENSMUSG00000055670	chr11	Zzef1	72796226	72796650	16363	-0.55335	4.686304	0.000826	0.002942	0.030651	-1	436	389	564	560	622	305	487	593	560	509
ENSMUSG00000022574	chr15	Naprt	75890964	75891060	1890	0.735301	2.5966	0.000827	0.002943	0.047241	1	81	67	61	69	90	123	167	148	230	206
ENSMUSG00000091661	chr9	Gm17021	1.24E+08	1.24E+08	462	-0.70799	3.88006	0.000827	0.002944	0.049461	-1	200	272	340	334	391	198	226	402	229	233
ENSMUSG00000029146	chr5	Snx17	31193227	31193465	2791	0.50733	5.647868	0.000828	0.002946	0.026393	1	631	569	765	627	878	1102	1397	1315	1667	1394
ENSMUSG00000019188	chr2	H13	1.53E+08	1.53E+08	8884	0.558751	5.718298	0.000829	0.002948	0.032294	1	532	594	793	635	1056	1091	1384	1311	1915	1679
ENSMUSG00000061207	chr17	Stk19	34823993	34824324	3155	0.62582	2.950659	0.000832	0.002958	0.034337	1	95	79	103	106	117	180	209	223	247	217
ENSMUSG00000004233	chr3	Wars2	99141068	99141188	5946	-0.68831	2.649267	0.000832	0.00296	0.042194	-1	118	113	165	124	118	73	115	122	141	110
ENSMUSG00000063060	chr14	Sox7	63943674	63943993	3298	-0.82964	3.054287	0.000835	0.002968	0.066882	-1	143	188	170	221	147	84	181	111	236	102
ENSMUSG00000034120	chr11	Srsf2	1.17E+08	1.17E+08	2958	0.605667	5.915105	0.000836	0.00297	0.038228	1	644	688	963	633	1117	1268	1572	1318	2287	2144
ENSMUSG00000078794	chr7	Dact3	16875317	16875673	2828	0.76323	2.678682	0.000836	0.00297	0.053737	1	64	45	99	70	120	143	235	188	200	156
ENSMUSG00000001918	chr7	Slc1a5	16781346	16782475	4156	1.40338	5.64676	0.000836	0.002971	0.201042	1	381	223	417	481	865	451	783	878	2712	4101
ENSMUSG00000026111	chr1	Unc50	37430139	37430282	1579	0.543996	4.056332	0.000839	0.002979	0.028303	1	193	203	236	216	277	354	501	523	501	407
ENSMUSG00000048799	chr18	Cep120	53681724	53683464	4553	-0.55012	4.236195	0.00084	0.002984	0.02958	-1	328	313	391	421	410	270	382	419	408	303
ENSMUSG00000074825	chr2	Itpripl1	1.27E+08	1.27E+08	3738	0.829363	2.612686	0.000843	0.002993	0.063481	1	38	63	107	77	81	112	132	192	237	236
ENSMUSG00000020668	chr12	Kif3c	3365132	3367531	6849	-0.69228	4.676065	0.000845	0.002997	0.049035	-1	381	559	704	569	400	326	368	576	485	525
ENSMUSG00000027952	chr3	Pmvk	89459118	89459464	1514	0.697439	3.758632	0.000845	0.002997	0.047629	1	144	157	170	164	222	285	332	263	470	604
ENSMUSG00000012640	chr7	Zfp715	43296197	43296448	5119	-0.8789	3.403921	0.000847	0.003003	0.076613	-1	219	155	267	232	275	103	143	322	128	165
ENSMUSG00000000823	chr2	Znf512b	1.82E+08	1.82E+08	6810	-0.54426	4.40098	0.000848	0.003007	0.029261	-1	382	318	507	363	538	279	393	463	492	390
ENSMUSG00000044792	chr13	Isca1	59755409	59757003	4288	-0.5918	7.439522	0.000849	0.003009	0.037153	-1	2876	3702	3885	3656	3111	2974	3131	3038	3732	3177
ENSMUSG00000021432	chr13	Slc35b3	38932140	38932916	2214	0.831654	1.777002	0.000851	0.003016	0.05534	1	34	43	46	27	48	71	92	89	127	119
ENSMUSG00000027654	chr2	Fam83d	1.59E+08	1.59E+08	3991	-0.78229	2.343173	0.000851	0.003016	0.053946	-1	80	73	125	99	164	69	65	75	116	108
ENSMUSG00000019214	chr17	Chtf18	25718926	25719284	4584	1.246661	0.682569	0.000855	0.003029	0.123214	1	21	6	19	9	18	46	33	26	76	63
ENSMUSG00000045983	chr16	Eif4g1	20668313	20668424	7227	-0.56089	9.242962	0.000857	0.003035	0.033646	-1	10476	10080	13916	12230	13850	8925	10216	14558	11928	11328
ENSMUSG00000027245	chr2	Hypk	1.21E+08	1.21E+08	5278	0.566879	5.534184	0.000864	0.003058	0.033289	1	503	603	644	650	707	1135	1327	947	1532	1491
ENSMUSG00000022898	chr16	Dscr3	94497783	94499082	3670	0.547248	4.48218	0.000866	0.003065	0.029754	1	246	267	325	255	432	423	706	610	725	644
ENSMUSG00000077220	chr1	Gm23436	1.61E+08	1.61E+08	66	1.142961	0.113039	0.000867	0.003066	0.078833	1	11	6	14	7	12	26	31	27	26	43
ENSMUSG00000091337	chr2	Eid1	1.26E+08	1.26E+08	1691	0.531148	5.123015	0.000867	0.003067	0.028703	1	412	444	545	407	570	635	1016	910	1321	992
ENSMUSG00000026471	chr1	Mr1	1.55E+08	1.55E+08	5981	-0.57275	3.71076	0.000869	0.003073	0.031109	-1	230	184	301	296	299	206	213	268	282	251
ENSMUSG00000015750	chr3	Aph1a	95893969	95894283	2863	0.572125	4.807122	0.000872	0.003083	0.033188	1	311	333	397	387	450	512	695	1027	897	790
ENSMUSG00000049672	chr17	Zbtb14	69383050	69383269	4231	-0.65876	2.866144	0.000874	0.00309	0.038853	-1	117	124	181	145	178	98	152	148	126	128
ENSMUSG00000031004	chr7	Mki67	1.36E+08	1.36E+08	10075	0.86553	4.097421	0.000882	0.003116	0.0766	1	148	182	158	184	349	351	519	247	946	584
ENSMUSG00000030122	chr6	Ptms	1.25E+08	1.25E+08	1554	0.656315	6.920577	0.000882	0.003116	0.045837	1	1148	1252	1789	1521	2288	2539	3235	2277	4823	4683
ENSMUSG00000037960	chr13	1110007C09Rik	49202951	49203235	804	0.630842	5.389335	0.000882	0.003117	0.041424	1	392	591	579	664	488	1087	983	1196	1308	1305
ENSMUSG00000043629	chr1	1700019D03Rik	52922324	52925734	4330	-1.17098	0.68641	0.000886	0.00313	0.10716	-1	30	18	41	27	68	20	22	16	17	34
ENSMUSG00000061322	chr4	Dnaic1	41569775	41570018	2782	1.620957	-0.19367	0.000887	0.003131	0.17336	1	5	7	14	3	1	15	46	13	30	29
ENSMUSG00000003528	chr16	Slc25a1	17925211	17925927	2176	2.266211	5.114844	0.000889	0.003137	0.495603	1	104	75	82	363	408	188	380	166	2600	3841
ENSMUSG00000020808	chr11	Fam64a	72042032	72042306	2529	1.123001	1.358222	0.000889	0.003137	0.107186	1	28	29	17	15	37	55	79	42	139	84
ENSMUSG00000032249	chr9	Anp32a	62341293	62341351	3166	0.539888	5.865063	0.00089	0.00314	0.0305	1	664	761	840	801	885	1267	1583	1388	1915	1923
ENSMUSG00000026222	chr1	Sp100	85649988	85650127	7556	0.871727	4.321623	0.00089	0.00314	0.078362	1	172	208	257	265	278	699	444	304	547	925
ENSMUSG00000062078	chr17	Qk	10206471	10209631	9879	-0.6189	7.022621	0.000892	0.003147	0.040888	-1	2127	2073	2666	3472	2839	1608	2495	3019	2964	2000
ENSMUSG00000028691	chr4	Prdx1	1.17E+08	1.17E+08	3043	0.587395	7.941991	0.000894	0.003151	0.036998	1	2779	3277	4155	2911	3225	5608	5898	6088	8547	8445
ENSMUSG00000021501	chr13	Caml	55623005	55623256	1755	0.65908	3.195228	0.000904	0.003187	0.040576	1	96	108	119	121	142	203	237	347	254	243
ENSMUSG00000028086	chr3	Fbxw7	84815268	84815769	7046	-0.56539	4.916034	0.000908	0.0032	0.03283	-1	577	381	624	654	798	460	628	523	670	559
ENSMUSG00000062797	chr7	l7Rn6	89917529	89919007	2933	-0.62233	5.108704	0.000909	0.003202	0.040299	-1	596	727	843	623	674	623	670	445	732	668
ENSMUSG00000027306	chr2	Nusap1	1.2E+08	1.2E+08	4059	1.013415	1.511912	0.000911	0.003207	0.088931	1	24	25	32	18	54	55	89	52	144	96
ENSMUSG00000023572	chr2	Ccndbp1	1.21E+08	1.21E+08	3469	0.645677	4.410115	0.000911	0.003209	0.04245	1	248	233	352	231	320	423	568	893	610	514
ENSMUSG00000032977	chr10	Fam207a	77486656	77488473	2427	0.588898	3.621725	0.000915	0.00322	0.033085	1	132	140	231	142	174	239	333	398	423	331
ENSMUSG00000023284	chr5	Zfp605	1.1E+08	1.1E+08	3497	-0.88281	1.087576	0.000918	0.003231	0.058037	-1	43	27	47	48	60	24	32	37	44	33
ENSMUSG00000032332	chr9	Col12a1	79598991	79601179	15228	-1.30842	6.375052	0.000921	0.003238	0.178996	-1	2546	514	2311	1055	3779	523	2182	852	1495	678
ENSMUSG00000034303	chr9	Ccdc15	37275835	37276565	3525	-1.28469	-0.04897	0.000922	0.003242	0.115975	-1	30	19	25	14	17	3	13	15	22	10
ENSMUSG00000038495	chr3	Otud7b	96104527	96104819	8497	-0.68124	6.13904	0.000925	0.003252	0.049461	-1	1268	1193	1545	1517	1751	886	1115	2025	1182	1081
ENSMUSG00000015143	chr12	Actn1	80167542	80168480	3805	0.709665	4.457038	0.000928	0.003261	0.051949	1	222	201	284	318	377	375	805	384	1044	658
ENSMUSG00000039270	chr4	Megf9	70427065	70433531	8226	-0.66081	3.183584	0.00093	0.003267	0.041592	-1	142	125	189	229	252	108	156	148	231	187
ENSMUSG00000038764	chr4	Ptpn3	57190841	57194362	7238	-1.00049	5.480227	0.00093	0.003268	0.105848	-1	538	1459	984	1340	496	564	671	830	988	443
ENSMUSG00000089703	chr1	Gm15833	44212162	44213118	957	-1.41811	0.979861	0.000932	0.003272	0.179819	-1	34	52	98	23	27	32	20	10	27	30
ENSMUSG00000038233	chr9	Fam198a	1.22E+08	1.22E+08	3622	-1.17367	1.881535	0.000932	0.003273	0.128297	-1	102	43	91	53	138	58	70	59	31	33
ENSMUSG00000061353	chr6	Cxcl12	1.17E+08	1.17E+08	8176	-0.60236	6.370508	0.000933	0.003274	0.038778	-1	1112	1357	1748	2295	1884	1111	1517	1701	1732	1636
ENSMUSG00000021932	chr14	Rnaseh2b	62292589	62292654	6243	0.743119	2.732684	0.000937	0.003289	0.050769	1	87	67	72	82	97	160	184	128	270	219
ENSMUSG00000002346	chr8	Slc25a42	70184340	70185225	5996	-0.66437	5.368828	0.000939	0.003295	0.046678	-1	849	701	928	890	829	493	586	1140	865	667
ENSMUSG00000034906	chr2	Ncaph	1.27E+08	1.27E+08	4307	0.976905	2.169587	0.000941	0.003301	0.089398	1	40	37	61	42	69	93	146	56	229	170
ENSMUSG00000023025	chr15	Larp4	99970074	99970278	6731	-0.7211	5.158533	0.000944	0.003311	0.054966	-1	618	725	728	689	951	363	596	1036	728	454
ENSMUSG00000024862	chr19	Klc2	5107746	5108688	4134	-0.52055	5.981921	0.000946	0.003317	0.028739	-1	999	1068	1411	1323	1446	980	1074	1212	1495	1312
ENSMUSG00000084106	chr1	Gm6136	86908793	86909683	891	0.563763	4.043118	0.000947	0.00332	0.031499	1	160	187	312	192	268	387	490	434	488	470
ENSMUSG00000036777	chr9	Anln	22331214	22333173	5421	0.886455	2.624086	0.00095	0.00333	0.076069	1	49	47	73	58	138	94	175	180	319	179
ENSMUSG00000095597	chrX	Gm6472	1.53E+08	1.53E+08	651	0.58632	3.834442	0.000953	0.003339	0.033731	1	148	179	238	160	225	368	428	375	378	407
ENSMUSG00000006288	chr14	Ttc5	50765415	50766022	1841	0.642851	3.122015	0.000954	0.003341	0.038413	1	79	114	136	104	129	176	279	201	305	272

ENSMUSG00000030374	chr7	Strn4	16815889	16816634	7958	0.559137	4.592679	0.000955	0.003343	0.031858	1	282	246	321	337	452	407	685	766	871	666
ENSMUSG00000028532	chr4	Cachd1	1.01E+08	1.01E+08	6020	-0.70601	2.443942	0.000957	0.003351	0.044371	-1	113	84	112	102	148	60	108	98	115	101
ENSMUSG00000023861	chr17	Mpc1	8282904	8283017	2082	-0.61904	6.688879	0.000958	0.003352	0.041296	-1	1736	2185	2440	2163	1796	1371	1697	2463	2122	1866
ENSMUSG00000055240	chr17	Zfp101	33360507	33361258	7424	-0.76559	1.952986	0.00096	0.00336	0.04933	-1	65	79	100	61	97	50	75	62	77	66
ENSMUSG00000093803	chr9	Ppp2r3d	1.24E+08	1.24E+08	1861	0.619454	2.955104	0.000961	0.003361	0.034601	1	89	86	124	94	111	154	239	196	261	238
ENSMUSG00000078684	chr3	5830417I10Rik	88775216	88775274	6190	-0.61266	3.387432	0.000963	0.003368	0.035949	-1	171	177	248	219	241	119	214	244	204	185
ENSMUSG00000029276	chr5	Glmn	1.08E+08	1.08E+08	2688	-0.70384	2.643771	0.000963	0.003368	0.045283	-1	100	128	179	107	127	92	112	109	138	99
ENSMUSG00000038028	chr6	9630033F20Rik	1.27E+08	1.27E+08	3651	-0.87495	6.174433	0.000966	0.003377	0.082057	-1	1268	1662	2113	1649	1004	1129	827	1858	989	1006
ENSMUSG00000055204	chr5	Ankrd17	90227190	90229341	10053	-0.62044	5.752636	0.000966	0.003377	0.041105	-1	986	773	1132	1242	1358	592	954	1375	1231	873
ENSMUSG00000005949	chr11	Ctns	73183596	73185051	3391	0.599906	3.326082	0.00097	0.003389	0.033595	1	125	107	130	138	158	178	275	310	322	322
ENSMUSG00000041741	chr6	Pde3a	1.41E+08	1.41E+08	10794	-0.69366	2.996366	0.00097	0.003389	0.045668	-1	137	103	198	180	212	97	143	183	172	116
ENSMUSG00000018012	chr11	Rac3	1.21E+08	1.21E+08	1293	1.16339	0.02227	0.000972	0.003391	0.076763	1	7	9	15	6	9	27	33	19	35	30
ENSMUSG00000024921	chr19	Smarca2	26605115	26605233	7854	-0.55324	5.185028	0.000971	0.003391	0.032074	-1	624	552	827	706	937	478	651	884	743	691
ENSMUSG00000042489	chr4	Clspn	1.27E+08	1.27E+08	7186	1.148932	1.25712	0.000971	0.003391	0.115159	1	23	17	22	12	45	65	63	35	114	90
ENSMUSG00000024952	chr19	Rps6ka4	6829085	6829738	3119	0.652533	3.699499	0.000973	0.003395	0.042104	1	156	126	150	187	220	217	335	309	541	480
ENSMUSG00000026925	chr2	Inpp5e	26396249	26397971	4301	-0.58872	3.429048	0.000977	0.003409	0.033102	-1	181	175	244	249	227	156	166	214	280	191
ENSMUSG00000004846	chr5	Plod3	1.37E+08	1.37E+08	4519	0.657604	5.139338	0.000978	0.003412	0.04575	1	389	340	561	384	640	743	1050	597	1509	1214
ENSMUSG00000040865	chr1	Ino80d	62958418	62958632	17713	-0.56102	4.128902	0.00098	0.003418	0.031519	-1	330	255	375	336	452	225	335	398	346	345
ENSMUSG00000026988	chr2	Wdsub1	59852364	59852961	3598	-0.56915	3.615457	0.000982	0.003425	0.031243	-1	182	211	307	216	316	160	273	213	266	242
ENSMUSG00000024145	chr17	Pigf	86997256	86997567	988	0.94884	1.24045	0.000983	0.003425	0.071805	1	19	24	28	24	33	73	59	47	106	59
ENSMUSG00000035274	chr9	Tpbg	85842380	85842592	3828	1.096267	1.153631	0.000988	0.003443	0.102605	1	26	11	20	14	42	39	92	75	81	50
ENSMUSG00000062867	chr9	Impdh2	1.09E+08	1.09E+08	3077	0.5219	5.460207	0.000988	0.003443	0.02875	1	471	498	684	599	794	943	1189	1399	1309	1195
ENSMUSG00000014956	chr5	Ppp1cb	32458974	32459407	7004	-0.68419	8.046877	0.000994	0.003461	0.05107	-1	5122	4807	6332	5203	5670	2953	4239	7661	4922	4010
ENSMUSG00000030474	chr7	Siglece	43651070	43651689	1849	1.427382	-0.13922	0.000994	0.003461	0.142483	1	7	0	8	7	14	20	28	12	41	34
ENSMUSG00000031352	chrX	Hccs	1.69E+08	1.69E+08	5151	-0.59432	4.786117	0.000996	0.003468	0.036953	-1	451	588	619	575	506	435	580	412	703	445
ENSMUSG00000024066	chr17	Xdh	73883908	73884483	4587	0.740848	4.604058	0.000997	0.00347	0.057741	1	316	176	374	325	331	458	458	1027	768	843
ENSMUSG00000026202	chr1	Tuba4a	75214228	75216593	3701	-0.71113	9.350579	0.000997	0.00347	0.055282	-1	10799	13261	15870	13365	14333	11121	12107	5770	14201	14365
ENSMUSG00000021786	chr14	Oxsm	16238656	16241070	4082	-0.53627	4.120695	0.001003	0.003488	0.028635	-1	268	322	379	380	363	266	350	357	365	310
ENSMUSG00000026317	chr8	Cln8	14881335	14881860	7606	0.555064	4.680386	0.00101	0.003513	0.031788	1	298	298	355	343	440	493	769	540	917	874
ENSMUSG00000025737	chr17	Wdr24	25823627	25824686	3432	-0.55793	3.724819	0.001014	0.003526	0.030539	-1	245	208	285	282	289	168	281	208	319	282
ENSMUSG00000093071	chr4	Gm25951	1.41E+08	1.41E+08	64	1.013051	1.143182	0.001016	0.003532	0.085586	1	15	20	33	14	35	45	58	42	101	85
ENSMUSG00000028977	chr4	Casz1	1.49E+08	1.49E+08	12224	-0.63083	5.019282	0.001019	0.003539	0.042183	-1	478	452	783	807	821	415	657	795	611	489
ENSMUSG00000021711	chr13	Trappc13	1.04E+08	1.04E+08	5166	-0.56469	4.932563	0.00102	0.003543	0.033472	-1	484	595	737	532	697	470	667	610	685	438
ENSMUSG00000036644	chr11	Tbc1d9b	50131396	50131556	6429	-0.49939	5.323259	0.001021	0.003546	0.026302	-1	653	634	863	851	933	548	781	808	952	811
ENSMUSG00000031907	chr8	Zfp90	1.06E+08	1.06E+08	2632	0.785801	1.910431	0.001023	0.003551	0.052339	1	32	36	58	39	61	68	128	94	140	115
ENSMUSG00000024798	chr19	Htr7	35958734	35960399	3399	-0.98882	0.56708	0.001024	0.003555	0.066459	-1	26	36	40	26	28	21	21	18	26	24
ENSMUSG00000029625	chr5	Cpsf4	1.45E+08	1.45E+08	3598	0.597206	3.047256	0.001025	0.003557	0.032457	1	99	87	126	108	123	163	224	238	281	248
ENSMUSG00000030861	chr7	Acadsb	1.31E+08	1.31E+08	4474	-0.65809	6.465997	0.001026	0.003558	0.047129	-1	1638	1527	1960	1872	2037	1153	1220	2479	1607	1522
ENSMUSG00000073418	chr17	C4b	34728380	34728627	5695	1.631106	4.936145	0.001026	0.003559	0.276559	1	190	68	136	129	817	477	675	496	1621	2318
ENSMUSG00000029596	chr5	Sdsl	1.2E+08	1.2E+08	1497	1.488249	-0.26091	0.001027	0.003562	0.143995	1	1	6	3	11	10	16	21	12	45	31
ENSMUSG00000022906	chr16	Parp9	35938470	35939060	4872	0.677743	3.710667	0.001028	0.003564	0.046393	1	134	155	185	167	194	391	330	236	414	467
ENSMUSG00000024544	chr18	Ldlrad4	67933257	67933388	2493	-0.7129	2.561386	0.001031	0.003572	0.046318	-1	112	79	147	130	143	86	127	93	127	84
ENSMUSG00000033379	chr4	Atp6v0b	1.18E+08	1.18E+08	2051	0.555742	6.131124	0.001032	0.003577	0.033367	1	877	895	1152	831	955	1667	1810	1704	2321	2213
ENSMUSG00000030107	chr6	Usp18	1.21E+08	1.21E+08	1770	1.54069	2.648893	0.001038	0.003597	0.240404	1	43	41	70	52	59	372	90	44	135	352
ENSMUSG00000032186	chr9	Tmod2	75565621	75574123	10391	-0.85144	3.014519	0.001039	0.003598	0.072666	-1	190	89	198	137	263	92	141	193	152	92
ENSMUSG00000098598	chr15	Pou6f1	1.01E+08	1.01E+08	906	-1.07284	1.223138	0.001039	0.003598	0.101771	-1	44	39	65	48	64	14	32	66	31	29
ENSMUSG00000022237	chr15	Ankrd33b	31291479	31297984	8706	-0.83477	5.273015	0.001039	0.003598	0.075096	-1	840	541	831	877	1070	422	618	1186	599	404
ENSMUSG00000059824	chr7	Dbp	45705088	45705762	2945	-0.92954	5.914208	0.001042	0.003606	0.093609	-1	1880	1265	1568	887	764	924	955	544	1366	1066
ENSMUSG00000050213	chr4	Snip1	1.25E+08	1.25E+08	2428	0.599598	3.086121	0.001043	0.003608	0.032999	1	97	95	130	105	131	178	214	268	288	235
ENSMUSG00000017386	chr11	Traf4	78158499	78160948	3292	0.679174	3.46961	0.001044	0.00361	0.046013	1	75	121	164	145	215	206	337	259	416	382
ENSMUSG00000103212	chr1	AC132393.1	1.2E+08	1.2E+08	1788	0.762999	2.790127	0.001047	0.003622	0.055565	1	67	81	76	75	124	160	218	121	266	241
ENSMUSG00000031939	chr9	Taf1d	15306214	15306283	1361	1.137155	2.880175	0.001048	0.003624	0.131749	1	77	73	83	52	90	121	160	532	172	170
ENSMUSG00000081999	chr2	Gm13461	41987473	41988017	662	0.727671	2.422393	0.00105	0.003628	0.047606	1	46	66	79	54	87	130	151	118	198	168
ENSMUSG00000039601	chr17	Rcan2	43801851	43802096	3744	-0.78171	5.218961	0.001051	0.00363	0.065953	-1	537	904	856	1084	472	536	664	582	920	517
ENSMUSG00000020687	chr11	Cdc27	1.05E+08	1.05E+08	6248	-0.54529	4.828032	0.001055	0.003643	0.031195	-1	474	449	651	547	715	370	545	686	614	490
ENSMUSG00000054079	chr11	Utp18	93859243	93860068	3597	0.666903	3.240293	0.001055	0.003643	0.043	1	117	116	152	86	129	223	292	199	367	264
ENSMUSG00000018537	chr11	Pcgf2	97688823	97690358	3526	0.869642	2.272991	0.001057	0.003648	0.071449	1	48	32	54	46	105	75	171	155	179	143
ENSMUSG00000027540	chr2	Ptpn1	1.68E+08	1.68E+08	5533	0.533665	4.662968	0.001057	0.003648	0.029425	1	304	287	349	358	429	453	658	662	1028	754
ENSMUSG00000035585	chr7	Tsen34	3693375	3693889	2416	0.52344	4.922459	0.001059	0.003655	0.028627	1	336	401	436	435	458	702	858	699	1031	876
ENSMUSG00000071653	chr19	1810009A15Rik	8888853	8888964	1444	0.606082	3.527713	0.001059	0.003655	0.035743	1	127	145	174	144	165	285	339	225	438	327
ENSMUSG00000037533	chr11	Rapgef6	54522847	54523118	12911	-0.57155	3.524718	0.001062	0.003665	0.031922	-1	193	178	264	239	278	127	214	248	266	235
ENSMUSG00000027433	chr2	Xrn2	1.47E+08	1.47E+08	3981	0.538105	4.393003	0.001068	0.003684	0.029677	1	248	199	338	296	359	373	562	645	729	618
ENSMUSG00000046731	chr11	Kctd11	69878261	69881406	3146	0.875409	2.706277	0.001069	0.003686	0.07509	1	71	52	71	66	122	120	254	102	283	230
ENSMUSG00000084843	chr2	B230312C02Rik	1.8E+08	1.8E+08	1703	-1.53828	7.050718	0.001075	0.003707	0.250536	-1	1959	3292	4056	3441	3895	2688	978	158	1302	2306
ENSMUSG00000068551	chr6	Zfp467	48427697	48427879	4255	-0.57213	4.01043	0.001076	0.00371	0.033234	-1	323	312	324	281	347	245	270	287	322	379
ENSMUSG00000026986	chr2	Hnmt	24002910	24003954	1769	-0.91137	1.93022	0.001079	0.003718	0.07709	-1	55	80	95	107	71	35	47	54	78	95

ENSMUSG00000020592	chr12	Sdc1	8771323	8771701	3809	0.804294	3.956847	0.001086	0.003742	0.068225	1	178	95	197	163	329	302	504	265	720	554
ENSMUSG00000003476	chr6	Crhr2	55090049	55091418	5112	-0.57362	4.935357	0.001089	0.003748	0.035096	-1	521	565	710	724	505	409	556	537	732	661
ENSMUSG00000024101	chr17	Wash	66111546	66111649	2986	0.579196	4.434892	0.001089	0.003748	0.034894	1	243	238	340	313	311	444	533	812	604	608
ENSMUSG00000016253	chr2	Nelfcd	1.74E+08	1.74E+08	2883	0.52253	5.017417	0.0011	0.003785	0.028853	1	404	393	515	423	474	781	994	777	1035	840
ENSMUSG00000020277	chr10	Pfkl	77986947	77988357	4395	1.054054	4.353657	0.001101	0.00379	0.119095	1	163	200	211	223	316	327	444	238	1018	1295
ENSMUSG00000005882	chr2	Uqcc1	1.56E+08	1.56E+08	6044	-0.61534	6.94214	0.001103	0.003794	0.041878	-1	2018	2665	2907	2608	2079	2166	2354	1897	2667	2163
ENSMUSG00000039356	chr2	Exosc2	31670715	31670861	2888	0.588764	3.366694	0.001103	0.003794	0.03316	1	116	139	144	117	163	204	289	247	401	309
ENSMUSG00000021254	chr12	Gpatch2l	86241890	86241944	3953	-0.5918	4.022183	0.001115	0.003833	0.035949	-1	257	254	399	350	381	227	289	407	355	232
ENSMUSG00000025364	chr10	Pa2g4	1.29E+08	1.29E+08	2751	0.519436	6.136936	0.001116	0.003835	0.029525	1	766	845	1191	901	1160	1479	1785	2137	2372	1936
ENSMUSG00000036333	chr12	Kidins220	24974932	24975062	7402	-0.53154	5.672048	0.001124	0.003861	0.030741	-1	891	750	1227	1032	1168	646	1148	1068	1161	886
ENSMUSG00000046519	chr3	Golph3l	95588934	95589134	2841	-0.50203	4.054796	0.001125	0.003863	0.025187	-1	288	274	387	316	359	248	316	331	374	334
ENSMUSG00000102101	chr16	2310061J03Rik	55973268	55974617	1350	0.94851	0.975121	0.001125	0.003863	0.066421	1	17	22	22	24	19	42	43	75	69	55
ENSMUSG00000025793	chr11	Hgs	1.2E+08	1.2E+08	2991	0.860244	4.780858	0.001126	0.003866	0.080239	1	242	260	356	368	416	474	583	1637	811	627
ENSMUSG00000034349	chr3	Smc4	69004738	69005090	5210	0.526813	4.031443	0.001127	0.003868	0.027781	1	197	192	238	200	290	315	407	447	638	465
ENSMUSG00000034647	chr17	Ankrd12	65967501	65970337	11508	-0.73484	3.239667	0.001128	0.00387	0.054808	-1	228	153	233	174	182	94	158	234	166	176
ENSMUSG00000047910	chr18	Pcdhb16	37477814	37483038	5225	-1.02338	0.439485	0.001131	0.003881	0.073217	-1	31	14	31	35	34	12	22	17	26	23
ENSMUSG00000053964	chr7	Lgals4	28833854	28834226	2315	1.389572	0.943797	0.001131	0.003881	0.170138	1	16	19	25	10	11	23	38	122	48	73
ENSMUSG00000026853	chr2	Crat	30400471	30402793	5388	-0.61705	8.820516	0.001132	0.003882	0.042618	-1	7128	9098	9579	10827	8767	6756	6400	10752	9042	8543
ENSMUSG00000026339	chr1	Ccdc93	1.21E+08	1.21E+08	11445	-0.57057	4.089067	0.001134	0.003887	0.033566	-1	304	269	341	364	421	211	379	387	360	266
ENSMUSG00000025650	chr9	Col7a1	1.09E+08	1.09E+08	10267	0.850022	3.305264	0.001137	0.003899	0.074767	1	116	69	127	106	172	155	201	461	286	374
ENSMUSG00000022748	chr16	Cmss1	57302199	57302282	930	-0.72584	4.232996	0.001139	0.003903	0.055988	-1	355	372	442	394	373	390	361	179	377	308
ENSMUSG00000061410	chr8	Zcchc14	1.22E+08	1.22E+08	7780	-0.61212	4.798447	0.001142	0.003912	0.04023	-1	436	397	615	583	828	329	536	700	576	441
ENSMUSG00000081453	chr16	Gm6767	51362452	51363832	1381	1.125943	0.416838	0.001142	0.003912	0.085943	1	7	14	10	18	14	24	51	36	59	27
ENSMUSG00000022141	chr15	Nipbl	8291225	8291590	8815	-0.6581	5.079528	0.001143	0.003915	0.04709	-1	640	477	790	698	882	376	571	953	635	537
ENSMUSG00000022300	chr15	Dcaf13	39112865	39113051	1551	0.523614	4.163588	0.001143	0.003915	0.027908	1	184	229	293	210	315	396	497	461	595	509
ENSMUSG00000033739	chr17	Fkbpl	34644764	34644953	1336	0.897758	2.221347	0.001147	0.003925	0.077195	1	40	53	49	46	78	94	97	226	137	134
ENSMUSG00000026356	chr1	Dars	1.28E+08	1.28E+08	4358	-0.52799	6.067622	0.001147	0.003927	0.030654	-1	1046	1314	1514	1302	1425	1066	1282	1378	1458	1207
ENSMUSG00000032766	chr6	Gng11	4003943	4004411	880	0.642048	4.826777	0.001148	0.003927	0.044358	1	259	400	462	382	332	824	773	714	1041	635
ENSMUSG00000048327	chr2	Ckap2l	1.29E+08	1.29E+08	3137	1.116778	1.77556	0.001149	0.003931	0.119345	1	30	28	25	25	68	90	99	44	190	113
ENSMUSG00000065979	chr16	Cpped1	11803721	11805583	5205	-0.52102	5.566152	0.001153	0.003943	0.029537	-1	704	965	1015	926	1041	760	861	950	1081	881
ENSMUSG00000053929	chr15	Cyhr1	76643395	76646574	6210	-0.51732	6.542475	0.001155	0.003948	0.029655	-1	1555	1648	2054	1917	1982	1519	1731	1918	1986	1752
ENSMUSG00000046111	chr9	Cep295	15316915	15317113	11641	-0.79178	3.157782	0.001158	0.003959	0.064173	-1	183	144	200	181	234	93	136	261	162	109
ENSMUSG00000033970	chr5	Rfc3	1.52E+08	1.52E+08	3611	0.877031	2.005455	0.001159	0.00396	0.070982	1	37	42	60	37	54	96	127	61	183	129
ENSMUSG00000029175	chr5	Slc35f6	30647933	30648098	3311	0.514001	4.251538	0.001159	0.00396	0.026903	1	219	240	304	234	310	355	521	483	710	570
ENSMUSG00000036825	chr3	Ssx2ip	1.46E+08	1.46E+08	4195	-0.56065	4.941274	0.001159	0.00396	0.033817	-1	463	612	660	706	596	443	707	507	708	543
ENSMUSG00000002274	chr17	Metrn	25794571	25795291	1434	-0.66972	4.822496	0.001166	0.003981	0.048496	-1	462	509	661	606	671	597	471	309	581	534
ENSMUSG00000000711	chr10	Rab5b	1.29E+08	1.29E+08	3166	-0.56609	6.702374	0.001168	0.003987	0.035721	-1	1982	1765	2261	2043	2304	1433	1742	2602	2143	1887
ENSMUSG00000100725	chr1	Gm28062	1.78E+08	1.78E+08	3030	0.512079	6.895259	0.001169	0.00399	0.029229	1	1351	1378	1736	1700	2080	2387	3137	3615	4023	3276
ENSMUSG00000027323	chr2	Rad51	1.19E+08	1.19E+08	6649	1.156026	1.370495	0.00117	0.003992	0.122164	1	32	20	21	10	44	67	78	40	123	92
ENSMUSG00000044060	chr5	A830010M20Rik	1.07E+08	1.07E+08	9127	-1.07922	3.747488	0.001175	0.004006	0.125251	-1	376	126	348	255	433	142	298	78	387	133
ENSMUSG00000045980	chr11	Tmem104	1.15E+08	1.15E+08	4610	0.70406	3.711362	0.001175	0.004006	0.051679	1	143	93	154	211	236	229	346	305	564	480
ENSMUSG00000032666	chr1	1700025G04Rik	1.52E+08	1.52E+08	11788	-0.54183	6.114303	0.001175	0.004006	0.032456	-1	1208	1138	1608	1499	1400	1220	1249	1344	1518	1199
ENSMUSG00000089837	chr15	Npcd	79789675	79789916	1453	-1.01639	1.824584	0.001175	0.004006	0.100279	-1	91	38	69	66	131	23	66	69	72	45
ENSMUSG00000037029	chr7	Zfp146	30161274	30163228	2071	-0.51499	4.369883	0.001179	0.004019	0.027578	-1	370	320	439	391	518	282	391	448	513	366
ENSMUSG00000021240	chr12	Abcd4	84602531	84603159	2527	0.645376	3.200459	0.00118	0.004021	0.04066	1	102	96	131	145	116	175	257	209	333	335
ENSMUSG00000035069	chr4	Oma1	1.03E+08	1.03E+08	2144	-0.57395	4.512697	0.00118	0.004021	0.034967	-1	379	462	501	502	408	402	409	357	522	435
ENSMUSG00000032609	chr9	Klhdc8b	1.08E+08	1.08E+08	8419	0.711789	2.672166	0.001182	0.004025	0.047827	1	78	51	91	78	101	120	164	227	192	207
ENSMUSG00000074165	chr7	Zfp788	41633203	41633694	4350	-0.68209	2.589233	0.001182	0.004025	0.044044	-1	97	117	164	105	132	64	117	108	141	112
ENSMUSG00000030316	chr6	Tamm41	1.15E+08	1.15E+08	5276	0.642478	2.536207	0.001195	0.004068	0.036405	1	69	66	81	69	85	125	162	164	202	159
ENSMUSG00000031490	chr8	Eif4ebp1	27260327	27260550	981	1.164851	5.777194	0.001196	0.004069	0.149032	1	521	486	580	608	613	803	954	4519	1155	1371
ENSMUSG00000031669	chr8	Gins3	95633559	95633783	2412	1.032325	0.698364	0.0012	0.004083	0.080061	1	9	12	27	17	18	25	45	41	78	52
ENSMUSG00000025616	chr16	Usp16	87454703	87455102	9454	-0.55384	5.240155	0.001205	0.0041	0.033499	-1	572	732	854	823	761	527	689	894	807	660
ENSMUSG00000002486	chr5	Tchp	1.15E+08	1.15E+08	3851	0.830474	1.96335	0.001207	0.004102	0.061156	1	53	39	39	44	49	64	109	134	127	136
ENSMUSG00000068749	chr3	Psma5	1.08E+08	1.08E+08	1321	0.723283	6.127548	0.001207	0.004102	0.058368	1	735	818	1081	799	974	1496	1697	3430	1770	1663
ENSMUSG00000015092	chr2	Edf1	25557847	25558029	1317	0.560225	6.453394	0.00121	0.004113	0.035076	1	822	1202	1343	1248	1303	2226	2539	2037	2808	2496
ENSMUSG00000036526	chr5	Card11	1.41E+08	1.41E+08	4112	1.109338	0.566821	0.001212	0.004119	0.093679	1	13	15	19	12	12	34	52	20	50	61
ENSMUSG00000031792	chr8	Usb1	95332292	95332465	2791	0.721137	2.732433	0.001213	0.00412	0.050047	1	74	71	90	78	99	157	182	118	258	240
ENSMUSG00000039473	chr16	Ubn1	5050068	5050781	6455	-0.51118	5.587299	0.001213	0.00412	0.028697	-1	790	824	1080	963	1070	651	925	1118	1024	922
ENSMUSG00000054115	chr15	Skp2	9111985	9116968	7875	0.981558	1.445943	0.001213	0.00412	0.085438	1	20	27	37	17	47	56	98	48	125	83
ENSMUSG00000021610	chr13	Clptm1l	73604002	73604399	2378	0.537191	5.467896	0.001214	0.004122	0.031652	1	488	488	665	607	792	989	1161	927	1684	1397
ENSMUSG00000038112	chr9	AW551984	39587396	39589125	6082	-1.04074	4.038067	0.001215	0.004122	0.117529	-1	225	212	402	203	909	241	357	140	259	238
ENSMUSG00000068240	chr4	Gm11808	3973092	3973595	504	0.516748	4.777116	0.001216	0.004127	0.028531	1	292	303	495	359	450	623	724	802	831	761
ENSMUSG00000008999	chr2	Bmp7	1.73E+08	1.73E+08	4019	-1.2011	0.164283	0.001224	0.004153	0.107429	-1	22	15	16	21	51	8	11	19	20	17
ENSMUSG00000025997	chr1	Ikzf2	69531214	69539492	11613	-0.70571	2.755352	0.001231	0.004175	0.048301	-1	123	128	155	128	158	95	117	165	115	97
ENSMUSG00000005338	chr1	Cadm3	1.73E+08	1.73E+08	7248	-0.78394	3.633857	0.001232	0.004177	0.06488	-1	208	129	239	257	521	175	235	163	266	224
ENSMUSG00000030591	chr7	Psmd8	29174188	29174747	1540	0.690962	7.571268	0.001232	0.004177	0.053962	1	2260	2051	2994	2322	2512	3829	4721	8991	5326	4455

ENSMUSG00000040167	chr7	Ikzf5	1.31E+08	1.31E+08	4885	-0.85583	3.524208	0.001238	0.004197	0.078072	-1	211	213	257	263	290	94	177	370	171	144
ENSMUSG00000026987	chr2	Baz2b	59899363	59900802	17604	-0.55483	3.881497	0.001239	0.004198	0.031711	-1	271	218	307	313	356	170	299	335	316	281
ENSMUSG00000049421	chr7	Zfp260	30094777	30094882	5790	-0.55174	5.160272	0.001243	0.004209	0.033319	-1	673	588	837	597	864	508	782	799	723	566
ENSMUSG00000031917	chr8	Nip7	1.07E+08	1.07E+08	3031	0.542773	3.82531	0.001246	0.004218	0.029785	1	136	198	226	181	217	305	405	417	454	368
ENSMUSG00000026029	chr1	Casp8	58795374	58795738	2893	0.712378	3.114663	0.001248	0.004224	0.051328	1	82	78	118	130	139	169	272	156	348	315
ENSMUSG00000102252	chr7	Snrpn	59982495	59983277	2159	-0.56113	4.954947	0.001248	0.004226	0.034281	-1	558	542	624	712	627	567	587	460	726	562
ENSMUSG00000021048	chr12	Mthfd1	76255232	76255544	3324	-0.51187	5.282621	0.00125	0.004228	0.028644	-1	579	665	824	843	930	631	795	642	947	734
ENSMUSG00000052135	chr4	Foxo6	1.2E+08	1.2E+08	2615	-0.86627	3.794591	0.00125	0.004228	0.080906	-1	209	233	331	331	412	238	316	81	273	224
ENSMUSG00000044177	chr11	Wfikkn2	94235956	94239118	3827	-0.69517	2.98052	0.00125	0.004228	0.047874	-1	125	149	166	156	218	103	144	194	122	130
ENSMUSG00000018322	chr2	Tomm34	1.64E+08	1.64E+08	3040	0.560134	3.591411	0.001252	0.004234	0.031374	1	142	134	204	138	193	280	308	279	413	384
ENSMUSG00000002307	chr17	Daxx	33909414	33909463	3058	0.547937	3.954823	0.001253	0.004234	0.030859	1	172	178	234	211	255	326	372	543	452	437
ENSMUSG00000044768	chr1	D1Ertd622e	97606318	97646361	41324	-0.76423	3.896024	0.001256	0.004244	0.06273	-1	219	285	319	316	438	264	216	121	338	338
ENSMUSG00000001151	chr10	Pcnt	76351254	76351779	9530	-0.65231	6.09379	0.001263	0.004268	0.047859	-1	1293	1116	1699	1470	1385	883	1052	1906	1198	1136
ENSMUSG00000038204	chr5	Asb10	24532697	24533511	2806	-0.72003	5.649071	0.001273	0.0043	0.058075	-1	827	1167	1183	1111	849	1061	670	682	952	942
ENSMUSG00000051378	chr11	Kif18b	1.03E+08	1.03E+08	3572	1.077533	0.710601	0.001274	0.0043	0.091456	1	14	17	10	12	28	36	41	31	76	59
ENSMUSG00000057561	chr18	Eif1a	46597704	46597800	2879	0.552562	4.266229	0.001274	0.0043	0.032191	1	219	227	323	204	334	382	542	429	764	581
ENSMUSG00000026305	chr1	Lrrfip1	90998737	90998893	6469	-0.57058	7.429158	0.001276	0.004307	0.037048	-1	2605	3056	4175	3132	4429	3108	3532	2423	3668	3312
ENSMUSG00000057841	chr6	Rpl32	1.16E+08	1.16E+08	517	0.513955	7.589957	0.001277	0.004308	0.030088	1	2087	2546	3035	2468	3160	4362	5177	5469	5900	5470
ENSMUSG00000072082	chr17	Ccnf	24223232	24224346	3099	0.99287	1.806648	0.00128	0.004319	0.093146	1	28	39	43	27	52	86	80	53	192	124
ENSMUSG00000098364	chr4	Gm27646	1.38E+08	1.38E+08	110	-0.77807	3.925834	0.001281	0.00432	0.065633	-1	299	269	421	360	236	172	208	441	260	221
ENSMUSG00000030655	chr7	Smg1	1.18E+08	1.18E+08	21225	-0.66358	5.754092	0.001281	0.004321	0.049493	-1	1110	838	1222	1061	1299	558	968	1532	998	850
ENSMUSG00000030208	chr6	Emp1	1.35E+08	1.35E+08	3046	0.785739	7.158621	0.001289	0.004346	0.070098	1	1652	1128	1889	1441	2827	2463	4894	2261	7145	5087
ENSMUSG00000046675	chr12	Tmem251	1.03E+08	1.03E+08	3369	0.686295	2.798873	0.001291	0.004352	0.045235	1	73	92	104	68	100	142	191	246	203	202
ENSMUSG00000024055	chr17	Cyp4f13	32924688	32924954	3330	0.864465	1.569074	0.001294	0.004361	0.06449	1	26	25	50	31	38	56	67	83	106	121
ENSMUSG00000030204	chr6	Ddx47	1.35E+08	1.35E+08	4952	0.499346	5.015513	0.001296	0.004367	0.027081	1	346	402	502	457	536	681	859	989	982	898
ENSMUSG00000036473	chr17	Tbc1d24	24175431	24181395	8053	-0.62837	3.062518	0.001296	0.004367	0.039092	-1	152	118	177	188	212	119	157	118	187	183
ENSMUSG00000041633	chrX	Kctd12b	1.54E+08	1.54E+08	4906	-0.61488	3.245322	0.0013	0.004378	0.03793	-1	152	144	213	252	194	117	170	181	220	190
ENSMUSG00000021962	chr14	Dcp1a	30479565	30479816	5616	-0.56341	3.26491	0.001301	0.004381	0.031056	-1	154	163	196	186	260	130	193	191	218	173
ENSMUSG00000053907	chr6	Mat2a	72432799	72434395	2804	-0.69114	7.645693	0.001302	0.004382	0.05454	-1	2831	3622	5993	3790	4722	3376	4694	2074	4034	3571
ENSMUSG00000064225	chr9	Paqr9	95559657	95568023	8367	-0.86239	3.198547	0.001303	0.004383	0.079205	-1	139	200	195	269	172	91	137	84	215	247
ENSMUSG00000001123	chr11	Lgals9	78962974	78963541	2137	0.783414	4.745679	0.001305	0.00439	0.068239	1	241	268	361	329	466	800	630	378	916	1184
ENSMUSG00000026842	chr2	Abl1	31688376	31689942	11596	-0.59416	5.415748	0.00131	0.004404	0.039479	-1	801	543	902	902	1194	485	789	1028	951	761
ENSMUSG00000030102	chr6	Itpr1	1.08E+08	1.08E+08	9848	-0.56346	4.269251	0.00131	0.004404	0.033959	-1	345	240	398	454	500	242	367	337	478	413
ENSMUSG00000040482	chr17	Dxo	34837019	34837216	1961	0.645954	2.791475	0.001312	0.004411	0.040111	1	64	71	91	95	128	135	187	183	269	209
ENSMUSG00000040521	chr10	Tsfm	1.27E+08	1.27E+08	2904	0.68027	4.192466	0.001313	0.004413	0.050023	1	155	282	285	233	200	478	500	355	703	579
ENSMUSG00000091625	chr6	Lsm5	56701063	56701289	774	0.873927	1.878316	0.001314	0.004414	0.069906	1	43	41	64	24	36	86	115	117	111	105
ENSMUSG00000022836	chr16	Mylk	34745210	34745370	10159	-0.56892	4.762682	0.001319	0.00443	0.035524	-1	525	345	571	627	652	330	592	456	699	514
ENSMUSG00000051748	chr11	Wfdc21	83746940	83747123	434	2.449561	1.217976	0.00132	0.004433	0.573947	1	11	5	0	9	32	12	30	26	104	272
ENSMUSG00000090137	chr8	Uba52	70508263	70508528	1498	0.516145	7.505449	0.001323	0.004443	0.03052	1	1941	2491	2835	2477	2731	4146	4762	5026	5818	5177
ENSMUSG00000031511	chr8	Arhgef7	11728105	11728416	13075	-0.53415	6.081766	0.001325	0.004446	0.032228	-1	1111	1108	1488	1455	1557	1083	1359	974	1726	1349
ENSMUSG00000028696	chr4	Ipp	1.17E+08	1.17E+08	2126	-0.59214	3.273371	0.001329	0.004461	0.034955	-1	184	172	222	168	217	124	181	222	210	162
ENSMUSG00000032340	chr9	Neo1	58874679	58877357	7387	-0.65303	5.882828	0.00133	0.004461	0.048287	-1	1175	742	1203	1032	1988	741	1245	1299	1201	890
ENSMUSG00000036469	chr8	March1	65617900	65618182	7146	1.027573	1.145397	0.001336	0.00448	0.092255	1	25	8	28	23	32	43	94	48	67	76
ENSMUSG00000018068	chr11	Ints2	86210681	86212801	10609	-0.84768	2.540058	0.001342	0.0045	0.073256	-1	97	100	164	123	140	65	133	44	153	96
ENSMUSG00000046185	chr7	Zfp84	29768552	29768695	4113	-0.67467	2.985714	0.001344	0.004504	0.046079	-1	128	140	191	175	176	81	131	198	175	131
ENSMUSG00000005610	chr7	Eif4g2	1.11E+08	1.11E+08	7348	-0.48773	9.340995	0.001344	0.004505	0.027541	-1	10926	10849	14151	12622	14905	9978	12850	13036	15343	12015
ENSMUSG00000032216	chr9	Nedd4	72662346	72662613	10973	-0.573	8.880587	0.001347	0.004513	0.03794	-1	8428	6727	10801	9192	12529	5777	9446	11563	10053	7728
ENSMUSG00000032299	chr9	Commd4	57155041	57155280	824	0.526179	3.93505	0.001347	0.004514	0.028448	1	172	193	241	215	217	330	362	417	492	495
ENSMUSG00000033222	chr3	Ttf2	1.01E+08	1.01E+08	6564	-0.61854	3.207334	0.001349	0.004519	0.038561	-1	146	177	211	164	235	124	190	121	245	177
ENSMUSG00000055320	chr7	Tead1	1.13E+08	1.13E+08	11237	-0.58253	7.019147	0.00135	0.004519	0.03893	-1	2106	1916	2693	3381	2972	1937	2748	2137	3422	1996
ENSMUSG00000001517	chr6	Foxm1	1.28E+08	1.28E+08	5498	1.101922	2.125005	0.001352	0.004527	0.125528	1	19	27	46	41	102	84	157	69	225	157
ENSMUSG00000022765	chr16	Snap29	17406003	17406359	3429	-0.54125	4.605314	0.001359	0.004547	0.031899	-1	353	533	573	440	496	361	441	467	544	501
ENSMUSG00000023118	chr7	Sympk	19024377	19024506	7777	-0.56398	6.479602	0.00136	0.004552	0.036362	-1	1607	1446	1943	1833	2082	1127	1552	2296	1931	1550
ENSMUSG00000029064	chr4	Gnb1	1.55E+08	1.55E+08	4268	0.59	6.431375	0.001362	0.004558	0.039777	1	897	905	1186	1266	1564	1726	2454	1681	3581	2882
ENSMUSG00000026854	chr2	Usp20	30982279	30982398	9017	0.63895	4.763601	0.001365	0.004565	0.045327	1	254	324	402	352	451	493	731	1179	742	704
ENSMUSG00000031756	chr8	Cenpn	1.17E+08	1.17E+08	1768	1.041283	0.547743	0.001365	0.004566	0.077234	1	10	13	15	18	17	35	44	23	69	42
ENSMUSG00000024590	chr18	Lmnb1	56707813	56708474	2962	0.688707	4.000663	0.001368	0.004572	0.051446	1	170	178	202	163	315	319	463	270	751	544
ENSMUSG00000020132	chr10	Rab21	1.15E+08	1.15E+08	1823	-0.50748	5.075706	0.001371	0.004581	0.028479	-1	639	591	735	626	692	486	681	714	775	603
ENSMUSG00000047591	chr15	Mafa	75746843	75747922	1080	-0.69174	4.604389	0.001372	0.004585	0.053106	-1	377	349	647	451	742	428	564	250	488	415
ENSMUSG00000042747	chr3	Krtcap2	89245966	89246515	1522	0.569303	4.787875	0.001374	0.00459	0.035754	1	287	336	370	366	505	737	774	547	969	794
ENSMUSG00000053877	chr7	Srcap	1.28E+08	1.28E+08	18791	-0.51118	5.777334	0.001375	0.004592	0.029499	-1	923	794	1113	1148	1461	781	1048	1003	1390	1106
ENSMUSG00000039206	chr5	Daglb	1.43E+08	1.43E+08	5677	0.546056	4.233488	0.001378	0.004602	0.031753	1	219	212	284	251	310	363	482	408	715	663
ENSMUSG00000044921	chr10	Rassf9	1.03E+08	1.03E+08	2118	-1.4882	0.174576	0.00138	0.004606	0.194361	-1	24	18	26	50	12	4	8	28	11	15
ENSMUSG00000022070	chr14	Bora	99046427	99046680	2673	1.090559	0.909478	0.001385	0.004623	0.105126	1	10	7	27	16	37	41	55	38	76	71
ENSMUSG00000044499	chr10	Hs3st5	36506814	36507615	4340	-1.20241	1.157215	0.001389	0.004633	0.138033	-1	66	45	56	59	20	26	35	14	40	40
ENSMUSG00000016495	chr19	Plgrkt	29348599	29349005	3799	0.576911	3.617098	0.001393	0.004645	0.034208	1	122	163	167	165	199	262	347	259	424	418

ENSMUSG00000022443	chr15	Myh9	77760587	77762016	12928	0.666704	6.670547	0.001396	0.004656	0.051164	1	883	1043	1337	1579	1836	1880	3184	1873	4816	3255
ENSMUSG00000025142	chr11	Aspscr1	1.21E+08	1.21E+08	4770	0.691808	4.829482	0.001398	0.004661	0.05366	1	333	303	429	331	417	569	577	1348	798	780
ENSMUSG00000093445	chr5	Lrch4	1.38E+08	1.38E+08	3925	0.50024	4.598827	0.001398	0.004661	0.026984	1	277	276	367	345	415	480	659	566	896	740
ENSMUSG00000002500	chr17	Rpl3l	24727820	24727886	1643	-0.57697	8.652125	0.001399	0.004664	0.038704	-1	6490	8153	9187	8191	7998	7805	6646	7291	8003	7289
ENSMUSG00000001289	chr15	Pfdn5	1.02E+08	1.02E+08	1394	0.536175	6.281905	0.0014	0.004664	0.032864	1	917	1060	1226	948	1124	1950	1970	2151	2350	2227
ENSMUSG00000075391	chr2	Gm13443	35340409	35340963	555	-0.75676	2.237406	0.0014	0.004664	0.054907	-1	101	97	116	83	85	65	100	72	101	67
ENSMUSG00000026463	chr1	Atp2b4	1.34E+08	1.34E+08	12248	-0.65616	4.802014	0.001404	0.004673	0.048346	-1	473	330	614	692	790	275	642	402	683	582
ENSMUSG00000027978	chr3	Prss12	1.23E+08	1.23E+08	2607	0.982133	1.525288	0.001403	0.004673	0.091363	1	32	16	31	17	62	63	106	83	94	81
ENSMUSG00000021258	chr12	Ccnk	1.08E+08	1.08E+08	2627	-0.5365	5.615583	0.001407	0.00468	0.032595	-1	890	826	1005	1122	972	715	802	1111	1050	991
ENSMUSG00000038602	chr10	Slc35f1	52690533	52691169	4941	-0.99736	0.33669	0.001406	0.00468	0.066442	-1	18	22	32	29	33	12	23	24	21	13
ENSMUSG00000034602	chr10	Mon2	1.23E+08	1.23E+08	9303	-0.61007	5.510914	0.001415	0.004708	0.042316	-1	854	617	1060	852	1281	558	851	1187	939	696
ENSMUSG00000030110	chr6	Ret	1.18E+08	1.18E+08	7341	-1.07185	4.20762	0.001416	0.004708	0.128675	-1	338	246	436	385	746	268	444	65	350	256
ENSMUSG00000021252	chr12	0610007P14Rik	85815448	85816193	4235	0.831922	2.641364	0.001417	0.004713	0.071451	1	54	49	72	56	148	169	169	137	210	224
ENSMUSG00000041372	chr6	B4galnt3	1.2E+08	1.2E+08	3779	-1.07634	0.552469	0.00142	0.004721	0.093871	-1	35	21	22	35	46	14	23	33	22	13
ENSMUSG00000062115	chr11	Rai1	60105013	60105394	9591	-0.57651	4.284731	0.001422	0.004727	0.036334	-1	323	403	364	412	426	229	399	464	427	319
ENSMUSG00000029126	chr5	Nsg1	38137193	38138872	2140	0.75824	2.058333	0.001432	0.004758	0.052509	1	50	42	52	42	65	83	130	93	184	114
ENSMUSG00000021022	chr12	Ppp2r3c	55280814	55281805	2395	-0.58458	4.142354	0.001433	0.00476	0.03696	-1	317	330	397	340	372	281	302	439	321	283
ENSMUSG00000058569	chr13	Tmed9	55593135	55593357	1420	0.562681	6.775928	0.001434	0.004762	0.036642	1	1169	1272	1868	1190	1988	2749	3146	2353	3682	3271
ENSMUSG00000031732	chr8	Phlpp2	1.1E+08	1.1E+08	8449	-0.72264	2.547368	0.001447	0.004805	0.052164	-1	119	79	138	102	171	59	101	128	119	108
ENSMUSG00000036632	chr3	Alg5	54735539	54735649	3537	0.541965	3.813115	0.001448	0.004805	0.03057	1	178	149	242	155	231	262	384	366	498	444
ENSMUSG00000003847	chr8	Nfat5	1.07E+08	1.07E+08	18378	-0.57228	4.773083	0.001449	0.004807	0.036588	-1	565	350	530	544	758	334	535	584	642	497
ENSMUSG00000033486	chr2	Catsper2	1.21E+08	1.21E+08	3695	1.08093	1.163125	0.001449	0.004807	0.105213	1	18	22	26	21	26	38	49	126	56	65
ENSMUSG00000016327	chrX	Atp1b4	38316184	38316329	4201	0.70386	5.142142	0.00145	0.004809	0.056528	1	322	271	445	462	810	716	1080	1419	1066	813
ENSMUSG00000026192	chr1	Atic	71557150	71557274	7985	0.564481	5.052552	0.001454	0.004822	0.035848	1	342	373	512	419	613	759	904	639	1249	1092
ENSMUSG00000027398	chr2	Il1b	1.29E+08	1.29E+08	1907	2.025562	-0.47046	0.001455	0.004823	0.334033	1	0	3	1	10	5	9	21	3	44	38
ENSMUSG00000017146	chr11	Brca1	1.01E+08	1.01E+08	8533	1.27419	0.662643	0.001456	0.004827	0.143796	1	11	10	20	7	24	35	58	18	99	37
ENSMUSG00000035047	chr9	Kri1	21273457	21274248	4182	0.571141	3.43035	0.001457	0.004827	0.033318	1	110	113	164	144	195	226	238	329	392	315
ENSMUSG00000033918	chr16	Parl	20279820	20280085	3892	0.532992	5.081626	0.001458	0.004831	0.031768	1	374	465	487	482	484	817	807	940	1011	1054
ENSMUSG00000061079	chr7	Zfp143	1.1E+08	1.1E+08	3013	-0.57761	3.297501	0.001459	0.004832	0.03392	-1	156	166	194	212	255	130	220	197	190	179
ENSMUSG00000022844	chr16	Pdia5	35397313	35397538	1808	0.732149	2.814668	0.001465	0.004851	0.054851	1	68	64	103	81	125	160	270	126	270	190
ENSMUSG00000040021	chr10	Lats1	7681209	7681450	7300	-0.57994	4.398561	0.001465	0.004851	0.037152	-1	378	352	481	371	536	246	353	551	490	351
ENSMUSG00000003316	chr8	Glg1	1.11E+08	1.11E+08	7090	-0.56147	6.291749	0.001466	0.004853	0.036459	-1	1440	1032	1748	1503	2190	944	1669	1592	1953	1342
ENSMUSG00000032289	chr9	Thsd4	59966931	59972538	13986	-1.00357	1.526899	0.00147	0.004863	0.097928	-1	58	26	75	65	98	29	66	35	63	29
ENSMUSG00000038524	chr18	Fchsd1	37957431	37959654	5473	0.957214	1.27344	0.001476	0.004884	0.081528	1	15	18	20	29	51	45	66	65	94	88
ENSMUSG00000085208	chr11	Brip1os	86201370	86201552	6498	0.645017	3.932257	0.00148	0.004894	0.045363	1	173	141	204	184	300	298	430	280	697	505
ENSMUSG00000042451	chr1	Mybph	1.34E+08	1.34E+08	2329	-0.9964	9.258095	0.001482	0.004902	0.115036	-1	7853	13418	18945	12288	16741	13083	8737	3232	8375	12329
ENSMUSG00000052852	chr6	Reep1	71707561	71708001	3924	-0.56871	7.045038	0.001484	0.004907	0.037732	-1	2461	2002	3106	2210	3534	2380	2761	2086	2876	2201
ENSMUSG00000027808	chr3	Serp1	58521969	58523868	2440	0.658638	5.177898	0.001488	0.004919	0.049586	1	388	334	502	423	738	711	1090	623	1464	1368
ENSMUSG00000018199	chr1	Trove2	1.44E+08	1.44E+08	9541	-0.61609	3.088243	0.001489	0.00492	0.038963	-1	150	140	178	171	219	88	181	156	224	146
ENSMUSG00000020817	chr11	Rabep1	70844778	70845008	6868	-0.5506	5.327506	0.001494	0.004937	0.034529	-1	707	696	894	777	910	519	718	1042	796	731
ENSMUSG00000053560	chr8	Ier2	84661331	84662852	1522	0.754982	3.373491	0.001498	0.004949	0.061341	1	65	100	142	194	144	192	372	231	452	288
ENSMUSG00000022800	chr16	Fyttd1	32877500	32877670	6076	-0.61834	6.146862	0.001501	0.004955	0.044379	-1	1156	1259	1880	1311	1605	891	1426	1862	1318	1026
ENSMUSG00000029319	chr5	Coq2	1.01E+08	1.01E+08	2624	-0.51327	5.659418	0.001503	0.004961	0.030148	-1	924	929	1153	956	961	832	908	981	1079	1034
ENSMUSG00000031985	chr8	Gnpat	1.25E+08	1.25E+08	3587	-0.54004	7.198717	0.001507	0.004975	0.034176	-1	2339	2760	3044	3470	2840	2193	2555	2770	3318	3177
ENSMUSG00000090389	chr14	Gm7236	43121772	43122101	330	-1.21113	-0.05647	0.00151	0.004984	0.103573	-1	18	21	20	20	25	7	24	14	14	4
ENSMUSG00000018672	chr11	Copz2	96849870	96849996	2208	0.589672	4.720984	0.001513	0.004992	0.03913	1	324	259	384	294	513	688	773	507	921	784
ENSMUSG00000020230	chr10	Prmt2	76207222	76207793	3177	0.743445	2.968828	0.001514	0.004994	0.057156	1	84	90	105	95	106	185	275	116	297	261
ENSMUSG00000028149	chr3	Rap1gds1	1.39E+08	1.39E+08	3663	-0.52292	6.208691	0.001525	0.005029	0.03174	-1	1228	1352	1533	1607	1532	1194	1315	1582	1591	1371
ENSMUSG00000020846	chr11	Fam101b	76019194	76022240	3512	-0.63677	5.454907	0.001526	0.005029	0.046772	-1	544	798	999	1176	970	655	977	528	1091	785
ENSMUSG00000035824	chr8	Tk2	1.04E+08	1.04E+08	2400	0.649618	2.705844	0.001531	0.005046	0.041397	1	76	56	99	74	117	128	189	181	210	211
ENSMUSG00000030339	chr6	Ltbr	1.25E+08	1.25E+08	2354	0.496256	5.212639	0.001534	0.005052	0.027772	1	464	417	536	512	644	698	996	990	1405	1040
ENSMUSG00000070343	chr3	Gm10288	1.47E+08	1.47E+08	537	0.62318	3.122399	0.001533	0.005052	0.039339	1	105	99	143	83	137	195	255	260	244	256
ENSMUSG00000009030	chr2	Pdcl	37350074	37352382	3751	-0.51483	3.883817	0.001541	0.005076	0.028136	-1	249	249	295	285	373	177	317	274	366	300
ENSMUSG00000047534	chr12	Mis18bp1	65132734	65133625	7990	1.096819	0.172131	0.001543	0.00508	0.07796	1	12	9	8	9	15	20	36	22	53	32
ENSMUSG00000037395	chr1	Rcor3	1.92E+08	1.92E+08	13622	-0.50804	3.887147	0.001543	0.005081	0.027174	-1	244	257	342	286	318	208	292	330	318	275
ENSMUSG00000026922	chr2	Agpat2	26593057	26593762	2130	1.970066	4.474553	0.00155	0.005102	0.421481	1	93	51	73	267	293	105	243	240	1308	2470
ENSMUSG00000027750	chr3	Postn	54361109	54361267	7833	1.180652	8.1455	0.001556	0.005121	0.161319	1	1847	1502	2457	1835	7767	5340	18429	4696	10162	7926
ENSMUSG00000038025	chr13	Phf2	48801750	48803687	5260	-0.5923	5.54577	0.001562	0.005137	0.040606	-1	801	696	996	1018	1222	591	795	1272	901	791
ENSMUSG00000016637	chr15	Ift27	78159465	78159708	1012	0.591727	4.831223	0.001562	0.005139	0.039844	1	297	324	474	270	557	676	701	970	851	755
ENSMUSG00000071172	chr17	Srsf3	29032673	29032786	5109	0.530046	5.906742	0.001563	0.00514	0.032584	1	653	773	960	670	1069	1292	1722	1366	2101	1836
ENSMUSG00000079469	chr9	Pigb	73007419	73008780	10434	-0.74673	2.280243	0.001576	0.005181	0.055573	-1	79	86	99	109	132	62	84	51	116	110
ENSMUSG00000068614	chr2	Actc1	1.14E+08	1.14E+08	1618	-1.02674	12.54333	0.001577	0.005183	0.123439	-1	73391	135731	166290	114671	192025	120418	94372	24388	109876	97591
ENSMUSG00000059897	chr8	Zfp930	69226343	69226469	1323	-0.89534	1.223471	0.001578	0.005184	0.072147	-1	57	36	50	52	50	17	32	42	50	48
ENSMUSG00000028857	chr4	Tmem222	1.33E+08	1.33E+08	2003	0.496913	4.303476	0.001581	0.005192	0.026766	1	214	253	326	245	330	414	520	567	605	580
ENSMUSG00000048106	chr3	4632415L05Rik	19894886	19895962	1077	-0.90867	0.655331	0.001584	0.005202	0.063329	-1	31	33	39	30	30	17	24	33	25	23
ENSMUSG00000002983	chr7	Relb	19606217	19606941	3885	0.675465	3.099892	0.001585	0.005203	0.0478	1	72	89	157	94	142	212	269	170	323	244

ENSMUSG00000026447	chr1	Pik3c2b	1.33E+08	1.33E+08	9237	-0.5669	4.937572	0.001595	0.005236	0.036558	-1	517	429	725	584	845	563	666	473	622	519
ENSMUSG00000047003	chr15	Zfp41	75616679	75616820	4068	-0.69907	2.184245	0.001598	0.005245	0.046509	-1	86	62	114	88	118	58	87	66	103	88
ENSMUSG00000030180	chr6	Kdm5a	1.2E+08	1.2E+08	14185	-0.69945	4.711949	0.001599	0.005246	0.056332	-1	492	413	619	536	662	241	425	788	537	368
ENSMUSG00000021669	chr13	Col4a3bp	96542618	96542644	5390	-0.55438	5.574621	0.001602	0.005254	0.035674	-1	773	881	1196	894	993	670	782	1214	998	840
ENSMUSG00000029469	chr5	Ift81	1.23E+08	1.23E+08	3453	0.7793	2.343882	0.001602	0.005255	0.06119	1	41	50	62	58	99	100	213	113	180	132
ENSMUSG00000005667	chr6	Mthfd2	83305691	83306809	2722	0.704396	3.142439	0.001603	0.005257	0.052863	1	88	103	134	79	155	195	246	159	364	313
ENSMUSG00000014599	chr3	Csf1	1.08E+08	1.08E+08	5262	1.058887	4.957384	0.001604	0.005257	0.129731	1	299	214	278	292	635	504	651	386	1956	1634
ENSMUSG00000047759	chr11	Hs3st3a1	64435332	64436626	3939	-1.10141	-0.10635	0.001604	0.005257	0.077473	-1	15	10	27	23	24	9	17	15	11	11
ENSMUSG00000032253	chr9	Phip	82866159	82871861	33312	-0.76883	4.249231	0.001613	0.005283	0.067641	-1	387	329	381	386	515	173	271	607	341	259
ENSMUSG00000084347	chr11	Akt2-ps	16514533	16515981	1449	-0.68594	2.065457	0.001613	0.005283	0.043519	-1	72	76	80	89	108	52	78	78	91	72
ENSMUSG00000041653	chr15	Pnpla3	84167816	84168060	4640	1.556698	3.816892	0.001616	0.005293	0.270865	1	110	79	70	140	197	122	184	182	556	1482
ENSMUSG00000028889	chr4	Yrdc	1.25E+08	1.25E+08	1981	0.668979	3.163672	0.00162	0.005303	0.046676	1	98	132	144	87	103	226	243	268	301	223
ENSMUSG00000038146	chr17	Notch3	32120820	32122860	8044	-0.59256	5.223074	0.00162	0.005303	0.040676	-1	527	514	838	994	933	478	779	534	953	784
ENSMUSG00000075033	chr16	Nxpe3	55839953	55844726	6430	1.834911	1.103784	0.001623	0.00531	0.343353	1	25	3	11	17	16	26	34	221	37	45
ENSMUSG00000028795	chr4	Ccdc28b	1.3E+08	1.3E+08	2026	-0.53008	4.761355	0.001626	0.00532	0.03169	-1	444	479	639	514	602	486	490	461	517	599
ENSMUSG00000027397	chr2	Slc20a1	1.29E+08	1.29E+08	5580	0.582551	3.331274	0.001628	0.005326	0.035114	1	126	91	133	139	182	190	272	262	393	298
ENSMUSG00000006403	chr1	Adamts4	1.71E+08	1.71E+08	4810	1.245256	2.212622	0.001637	0.005352	0.169571	1	17	21	32	53	112	103	236	77	228	108
ENSMUSG00000042148	chr11	Cox10	63962627	63964528	3037	-0.56664	5.384333	0.001642	0.005368	0.037321	-1	638	840	1012	912	733	716	768	625	1020	794
ENSMUSG00000086604	chr7	Gm15510	5050730	5050918	548	-1.11405	1.124727	0.001643	0.00537	0.11734	-1	51	47	45	46	51	44	23	41	30	13
ENSMUSG00000053070	chr9	9230110C19Rik	8021672	8022544	1592	1.10042	-0.15674	0.001647	0.005383	0.068455	1	9	6	6	9	11	14	29	26	30	26
ENSMUSG00000022744	chr16	Cldn25	58727910	58728084	2563	-0.61785	5.22702	0.001649	0.005388	0.04443	-1	633	712	930	697	812	507	609	1042	739	543
ENSMUSG00000040282	chr2	BC052040	1.16E+08	1.16E+08	4349	-0.78717	1.949598	0.00165	0.005388	0.058691	-1	67	63	100	71	105	66	79	58	55	61
ENSMUSG00000041815	chr15	Poldip3	83125978	83128055	5679	0.512187	4.557991	0.001654	0.0054	0.029302	1	283	258	301	321	465	455	667	679	768	672
ENSMUSG00000033044	chr11	Dhrs7c	67798187	67798403	1880	-0.60107	7.899522	0.001656	0.005408	0.043205	-1	4430	4444	5438	4436	5202	4920	3908	3522	4492	4800
ENSMUSG00000025151	chrX	Maged1	94535474	94535677	4351	0.713597	6.391973	0.001662	0.005426	0.060423	1	941	662	1073	896	1876	1676	3330	1528	3208	2608
ENSMUSG00000035378	chr6	Shq1	1.01E+08	1.01E+08	2182	0.880847	0.992156	0.001664	0.005429	0.062065	1	18	22	25	15	30	46	48	67	72	50
ENSMUSG00000022119	chr14	Rbm26	1.05E+08	1.05E+08	7649	-0.52884	4.270899	0.001671	0.005451	0.031063	-1	349	288	393	358	528	243	349	436	421	404
ENSMUSG00000008384	chr7	Sertad1	27486910	27487078	1344	0.641996	3.491234	0.001678	0.005472	0.044279	1	106	176	139	140	158	283	298	233	441	334
ENSMUSG00000004267	chr6	Eno2	1.25E+08	1.25E+08	4705	1.185036	0.847044	0.001678	0.005473	0.132481	1	11	7	27	10	33	19	58	49	75	77
ENSMUSG00000055228	chr13	Zfp935	62454323	62455193	1062	-1.19391	0.664734	0.00168	0.005476	0.126151	-1	35	23	46	37	37	21	12	42	12	18
ENSMUSG00000024421	chr18	Lama3	12333819	12334308	10745	-1.1794	1.382433	0.001681	0.005478	0.140872	-1	51	40	61	52	97	15	34	80	33	21
ENSMUSG00000051650	chr11	B3gnt2	22834747	22837195	3350	0.60259	3.295334	0.001687	0.005497	0.038067	1	110	89	160	126	167	174	266	234	366	349
ENSMUSG00000025509	chr7	Pnpla2	1.41E+08	1.41E+08	3020	1.095687	7.938977	0.001688	0.005501	0.141616	1	1865	2347	2355	3696	2780	2883	3107	16370	7992	9367
ENSMUSG00000039911	chr4	Spsb1	1.5E+08	1.5E+08	4396	0.941966	3.848063	0.001689	0.005502	0.101977	1	127	92	166	199	251	231	386	902	351	319
ENSMUSG00000062488	chr19	I830012O16Rik	34607970	34607998	2000	1.591008	2.327411	0.00169	0.005502	0.276595	1	48	29	46	39	41	383	85	47	67	185
ENSMUSG00000058355	chr8	Abce1	79683442	79685277	3813	-0.49207	6.150174	0.001696	0.005523	0.028588	-1	1139	1207	1550	1336	1743	1083	1388	1496	1651	1283
ENSMUSG00000005474	chr5	Myl10	1.37E+08	1.37E+08	822	1.40317	1.781329	0.001699	0.005531	0.208124	1	34	20	48	31	16	30	180	204	106	48
ENSMUSG00000028438	chr4	Kif24	41390745	41392252	8014	1.210405	-0.29536	0.001701	0.005535	0.083784	1	4	6	8	7	10	13	33	15	32	22
ENSMUSG00000033965	chrX	Slc16a2	1.04E+08	1.04E+08	4244	0.706461	3.582234	0.001702	0.005538	0.055456	1	130	84	137	143	279	193	390	341	458	370
ENSMUSG00000092827	chr2	Mir3091	1.8E+08	1.8E+08	76	1.210868	-0.16936	0.001703	0.005538	0.086976	1	5	12	6	8	7	17	23	34	23	28
ENSMUSG00000024048	chr17	Myl12a	70993656	70994784	3201	0.557712	7.800617	0.00171	0.005559	0.037417	1	2538	2776	3113	3511	3044	5128	6709	7353	6479	5121
ENSMUSG00000026255	chr1	Efhd1	87264363	87264754	2125	-0.83216	2.467218	0.001713	0.00557	0.072658	-1	62	99	113	111	217	89	82	71	104	109
ENSMUSG00000078139	chr13	AK157302	21495223	21497146	1924	-0.85616	2.050422	0.001718	0.005583	0.073637	-1	70	103	97	91	72	67	73	84	62	47
ENSMUSG00000063406	chr5	Tmed5	1.08E+08	1.08E+08	7688	-0.57691	4.648552	0.001723	0.0056	0.038447	-1	458	437	573	497	533	249	390	492	666	608
ENSMUSG00000004460	chr16	Dnajb11	22857845	22858109	3236	0.512474	5.840541	0.001724	0.005602	0.030953	1	657	680	894	724	1013	1290	1616	1238	2010	1734
ENSMUSG00000034664	chr11	Itga2b	1.02E+08	1.02E+08	5454	0.977641	1.203574	0.001726	0.005608	0.089586	1	19	15	29	14	49	64	65	59	64	81
ENSMUSG00000041360	chr19	D19Bwg1357e	27388702	27390313	3462	0.52579	4.286472	0.001729	0.005614	0.030812	1	212	225	311	252	341	423	558	394	693	625
ENSMUSG00000030424	chr7	Zfp939	39449518	39449653	2480	-0.91204	0.893486	0.001732	0.005623	0.07077	-1	37	42	39	32	44	15	30	41	30	30
ENSMUSG00000098652	chr16	Gm27671	14128566	14128631	66	-1.34345	-0.26569	0.001732	0.005623	0.13792	-1	19	10	29	17	17	4	9	23	8	6
ENSMUSG00000006715	chr13	Gmnn	24751845	24752230	1465	0.863664	1.950126	0.001734	0.005625	0.071863	1	43	54	37	46	36	95	102	79	172	121
ENSMUSG00000019210	chr6	Atp6v1e1	1.21E+08	1.21E+08	1203	0.503095	6.724033	0.001733	0.005625	0.030253	1	1223	1378	1639	1471	1575	2555	2696	2742	3364	3041
ENSMUSG00000035093	chr2	Secisbp2l	1.26E+08	1.26E+08	8222	-0.52479	4.65644	0.001737	0.005633	0.031423	-1	431	358	510	520	690	315	495	575	572	474
ENSMUSG00000004698	chr12	Hdac9	34371503	34374138	4422	-0.80611	2.123834	0.001738	0.005637	0.067023	-1	67	85	75	104	128	36	95	61	112	71
ENSMUSG00000070392	chr3	Gm20634	96245554	96248509	2956	-0.69551	2.524815	0.001741	0.005645	0.048772	-1	99	86	153	122	133	77	141	85	120	86
ENSMUSG00000006301	chr1	Tmbim1	74288247	74289518	12659	0.576317	6.107609	0.001743	0.005646	0.039556	1	796	773	968	872	1244	1269	1830	2692	1945	1908
ENSMUSG00000024193	chr17	Phf1	26933127	26933534	2429	0.664118	3.691512	0.001742	0.005646	0.048998	1	166	123	180	184	172	239	356	560	341	334
ENSMUSG00000047603	chr7	Zfp235	24134174	24134487	2466	-0.85403	1.479756	0.001743	0.005646	0.068202	-1	66	42	66	57	61	24	48	64	53	40
ENSMUSG00000061878	chr11	Sphk1	1.17E+08	1.17E+08	4774	1.147689	1.289227	0.001748	0.005662	0.132801	1	18	16	28	13	48	36	86	38	145	82
ENSMUSG00000057234	chr2	Mettl15	1.09E+08	1.09E+08	2275	-0.80261	1.881683	0.001753	0.005675	0.063954	-1	75	75	74	89	66	41	57	75	93	47
ENSMUSG00000035299	chrX	Mid1	1.7E+08	1.7E+08	6720	-0.78614	1.865085	0.001754	0.005678	0.058332	-1	68	54	77	76	107	51	64	62	49	77
ENSMUSG00000060743	chr1	H3f3a	1.81E+08	1.81E+08	3504	-0.52982	6.769021	0.001755	0.005681	0.033725	-1	1850	1907	2409	2176	2427	1442	2275	2514	2588	1689
ENSMUSG00000028458	chr4	Tesk1	43441939	43443638	4434	-0.48605	5.82763	0.001761	0.005698	0.027905	-1	923	1010	1217	1165	1211	902	1032	1094	1381	1124
ENSMUSG00000024646	chr18	Cyb5a	84851338	84851607	2143	0.650133	5.044968	0.001763	0.005702	0.049597	1	425	354	468	384	507	616	728	727	1155	1532
ENSMUSG00000033705	chr2	Stard9	1.21E+08	1.21E+08	19408	-0.65639	3.573999	0.001764	0.005706	0.048103	-1	255	139	240	279	305	114	238	257	249	232
ENSMUSG00000001482	chr8	Def8	1.23E+08	1.23E+08	3988	-0.49501	5.653895	0.001765	0.005708	0.028854	-1	811	895	1091	986	1141	839	962	782	1243	1057
ENSMUSG00000001755	chr11	Coasy	1.01E+08	1.01E+08	2867	0.728548	3.922925	0.001766	0.00571	0.060581	1	131	164	211	230	216	209	327	461	517	724

ENSMUSG00000049940	chr3	Pgrmc2	41066326	41068724	3242	0.497719	5.115174	0.001771	0.005723	0.028671	1	373	411	533	517	574	681	963	837	1124	1153
ENSMUSG00000068457	chrY	Uty	1096861	1098573	9791	-2.60745	3.416583	0.001773	0.00573	0.710509	-1	252	246	384	321	340	68	148	0	143	0
ENSMUSG00000035828	chr15	Pim3	88862186	88862752	2419	0.884953	4.541961	0.001775	0.005734	0.091853	1	226	244	308	327	247	338	382	1330	680	812
ENSMUSG00000062373	chr15	Tmem65	58782269	58785010	3747	-0.61988	6.825446	0.001776	0.005737	0.04634	-1	1939	2298	2342	2929	1785	1588	1898	2519	2704	1793
ENSMUSG00000079019	chr8	Insl3	71689214	71689432	623	1.477326	-0.38605	0.001777	0.005737	0.138539	1	8	10	3	4	2	21	15	13	34	28
ENSMUSG00000079737	chr16	3110001I22Rik	13671929	13672078	1722	-0.81801	1.953491	0.001777	0.005738	0.066624	-1	78	52	97	87	95	45	52	98	77	51
ENSMUSG00000027195	chr2	Hsd17b12	94032689	94033661	2407	1.00534	4.250144	0.001779	0.005741	0.118294	1	130	170	215	213	347	300	519	197	997	1053
ENSMUSG00000034974	chr10	Dapk3	81183007	81183096	1766	0.507591	4.104147	0.001785	0.005759	0.028303	1	196	212	280	235	257	429	431	436	589	450
ENSMUSG00000020621	chr12	Rdh14	10390780	10391226	1472	-0.53388	5.089884	0.001791	0.005778	0.033251	-1	570	654	856	630	635	595	631	663	689	632
ENSMUSG00000028057	chr3	Rit1	88716838	88716957	3229	0.663043	4.67181	0.001792	0.005778	0.051283	1	305	292	367	325	345	468	595	1197	690	679
ENSMUSG00000028245	chr4	Nsmaf	6396207	6396817	8368	-0.60682	5.18145	0.001792	0.005778	0.043459	-1	685	640	792	714	813	495	594	1021	636	588
ENSMUSG00000080242	chr6	Gm15487	37806086	37806550	465	0.827885	1.608291	0.001795	0.005785	0.06303	1	34	33	42	30	36	58	70	72	147	100
ENSMUSG00000004070	chr16	Hmox2	4726361	4726471	2217	0.506971	5.209112	0.001805	0.005817	0.029964	1	412	505	537	527	555	873	970	861	1238	1111
ENSMUSG00000051067	chr10	Lingo3	80832807	80836141	3433	-0.82683	4.301679	0.001807	0.005822	0.080115	-1	311	241	414	369	849	284	439	164	449	329
ENSMUSG00000039782	chr5	Cpeb2	43233463	43235088	7122	-0.62224	3.238921	0.001809	0.005826	0.042011	-1	125	182	254	202	192	100	193	180	232	173
ENSMUSG00000018846	chr11	Pank3	35769484	35769947	7376	-0.64809	5.010847	0.001813	0.005839	0.049743	-1	596	419	590	832	875	323	463	684	745	769
ENSMUSG00000019173	chr11	Rab5c	1.01E+08	1.01E+08	2194	0.534272	5.682069	0.001814	0.005839	0.033917	1	567	555	767	750	890	1006	1316	1099	1962	1804
ENSMUSG00000022546	chr15	Gpt	76696764	76697019	1749	0.653557	4.560536	0.001813	0.005839	0.0497	1	244	295	281	366	330	504	421	664	790	989
ENSMUSG00000032329	chr9	Hmg20a	56418644	56418931	3691	-0.4895	4.570733	0.001814	0.005839	0.027135	-1	373	408	471	452	625	369	489	438	510	494
ENSMUSG00000008301	chr18	Phax	56562443	56562723	2223	0.599359	4.29337	0.001817	0.005845	0.041076	1	209	269	299	237	276	465	466	759	543	480
ENSMUSG00000032648	chr19	Pygm	6384399	6384721	3218	-0.60177	12.45578	0.00182	0.005856	0.044309	-1	87317	108958	128445	123383	116898	107442	80924	120811	98367	101841
ENSMUSG00000020974	chr12	Pole2	69201779	69201882	1695	1.189876	0.886649	0.001836	0.005905	0.136531	1	13	9	23	10	35	42	54	22	99	68
ENSMUSG00000025608	chr6	Podxl	31519488	31523219	5488	-0.71019	5.771808	0.001839	0.005913	0.060691	-1	673	979	1118	1861	1032	653	981	763	1227	1278
ENSMUSG00000056900	chr3	Usp13	32817546	32817872	7599	-0.72371	8.137794	0.001841	0.005919	0.063779	-1	4480	5166	7206	6192	6425	3785	3891	8648	4315	3882
ENSMUSG00000002908	chr8	Kcnn1	70842049	70844561	4054	-0.63816	3.875755	0.00185	0.005942	0.046333	-1	241	304	322	329	278	203	205	392	269	260
ENSMUSG00000029614	chr5	Rpl6	1.21E+08	1.21E+08	2433	0.490161	7.673721	0.00185	0.005942	0.029327	1	2186	2413	3140	2770	3840	4347	5548	5265	6853	5957
ENSMUSG00000037594	chr12	BC022687	1.13E+08	1.13E+08	1915	1.331606	-0.22296	0.001849	0.005942	0.131441	1	5	5	18	3	4	20	26	14	29	34
ENSMUSG00000033170	chr15	Card10	78775138	78776830	4952	-0.59632	3.492385	0.001852	0.005947	0.039085	-1	181	183	250	281	232	130	180	264	243	233
ENSMUSG00000034412	chr11	Tbc1d10a	4186789	4187099	2733	0.702352	2.501522	0.001854	0.005955	0.050404	1	57	46	67	78	110	114	153	138	207	198
ENSMUSG00000026249	chr1	Serpine2	79794197	79795042	8287	-0.63066	6.576888	0.001861	0.005976	0.048277	-1	1877	1746	2301	1816	1879	1677	2221	1072	2164	1566
ENSMUSG00000040483	chr11	Xaf1	72301629	72301709	4689	0.970998	2.65646	0.001866	0.005988	0.104727	1	56	61	78	79	75	237	167	79	159	282
ENSMUSG00000029366	chr5	Dck	88764996	88765346	3078	0.77627	2.622787	0.001872	0.006007	0.064462	1	56	64	94	64	98	174	176	92	235	211
ENSMUSG00000040220	chr8	Gas8	1.24E+08	1.24E+08	1679	0.744985	2.222625	0.001872	0.006007	0.055937	1	47	39	67	46	90	91	172	108	155	144
ENSMUSG00000066632	chr12	Pgk1-rs7	10898566	10900296	1731	-0.72751	2.240875	0.001874	0.00601	0.053475	-1	69	100	129	86	103	61	67	104	105	75
ENSMUSG00000016921	chr2	Srsf6	1.63E+08	1.63E+08	4810	0.554577	5.976261	0.001875	0.006013	0.03707	1	743	655	1047	659	1217	1351	1987	1386	2095	1955
ENSMUSG00000050860	chr11	Phospho1	95824499	95824709	2029	-0.50643	7.164085	0.001877	0.006019	0.031286	-1	2388	2433	2982	3140	3113	2423	2410	2824	3309	2823
ENSMUSG00000073609	chr1	D2hgdh	93824909	93825051	4281	-0.48475	4.212064	0.001885	0.00604	0.026121	-1	297	316	385	351	460	307	350	331	414	391
ENSMUSG00000072692	chr5	Rpl37rt	1.15E+08	1.15E+08	682	0.504646	4.841644	0.001886	0.006042	0.029541	1	333	381	415	362	482	675	776	853	808	768
ENSMUSG00000058546	chr11	Rpl23a	78180932	78180997	847	0.505563	7.485701	0.001892	0.006062	0.031288	1	2166	2332	2698	2257	2908	4280	5250	4143	5605	5175
ENSMUSG00000033014	chr3	Trim33	1.03E+08	1.03E+08	8868	-0.62609	3.77988	0.001899	0.006082	0.044478	-1	218	185	329	315	362	155	277	353	277	202
ENSMUSG00000036019	chr10	Tmtc2	1.05E+08	1.05E+08	7779	-0.95483	0.889291	0.001899	0.006082	0.081763	-1	35	20	33	48	64	16	31	28	41	28
ENSMUSG00000026437	chr1	Cdk18	1.32E+08	1.32E+08	4764	0.775595	2.159013	0.0019	0.006082	0.05874	1	54	58	43	59	48	84	121	113	179	153
ENSMUSG00000031371	chrX	Haus7	73437315	73437565	1438	0.517235	3.727625	0.001903	0.006089	0.02904	1	143	160	228	150	230	290	353	339	437	391
ENSMUSG00000042605	chr5	Atxn2	1.22E+08	1.22E+08	7161	-0.50234	5.343589	0.001903	0.006089	0.029926	-1	628	664	821	911	969	640	911	661	976	742
ENSMUSG00000041797	chr11	Abca9	1.1E+08	1.1E+08	8048	-0.73586	4.785866	0.001904	0.00609	0.064654	-1	642	294	594	470	925	277	627	609	540	386
ENSMUSG00000071054	chr17	Safb	56584825	56585350	7268	0.511808	5.584742	0.001905	0.006092	0.03128	1	541	584	679	713	788	1069	1228	1608	1336	1289
ENSMUSG00000026594	chr1	Ralgps2	1.57E+08	1.57E+08	12085	0.856609	2.268524	0.001906	0.006096	0.077811	1	44	29	59	65	88	89	221	144	150	106
ENSMUSG00000044534	chr9	Ackr2	1.22E+08	1.22E+08	2784	-1.09451	0.500169	0.001915	0.006122	0.1027	-1	32	12	26	33	53	16	19	27	25	13
ENSMUSG00000064280	chr5	Ccdc146	21292961	21293495	4366	-0.94466	1.86208	0.001918	0.006129	0.09222	-1	76	71	96	61	89	66	83	33	41	54
ENSMUSG00000021391	chr13	Cenpp	49464027	49464337	1101	1.120528	0.171402	0.00192	0.006134	0.088672	1	12	10	14	8	8	20	44	30	49	20
ENSMUSG00000028466	chr4	Creb3	43562332	43562959	2372	0.5242	5.009022	0.001925	0.006149	0.032434	1	367	348	626	360	526	720	1011	858	978	844
ENSMUSG00000025823	chr6	Pdia4	47796142	47796903	2480	0.78078	5.162203	0.001928	0.006158	0.073462	1	327	346	447	386	737	810	1105	441	1626	1386
ENSMUSG00000048939	chr16	Atp13a5	29231851	29232863	4661	-1.14094	1.465294	0.00193	0.006163	0.135587	-1	89	24	80	59	58	25	58	52	44	19
ENSMUSG00000041235	chr4	Chd7	8690406	8690775	13786	-0.53373	4.36013	0.001938	0.006188	0.03284	-1	354	324	468	420	466	248	378	518	429	393
ENSMUSG00000079003	chr8	Samd1	83997672	83998565	2071	0.551925	3.749504	0.001939	0.006188	0.033808	1	143	148	189	187	245	338	396	273	483	361
ENSMUSG00000018821	chr19	Avpi1	42123273	42123848	1236	0.502913	3.931993	0.00194	0.006192	0.027891	1	177	179	275	180	243	346	417	433	472	401
ENSMUSG00000031461	chr8	Myom2	15057653	15057739	8853	-0.54385	11.05867	0.001942	0.006196	0.036683	-1	30738	38153	52692	42041	49674	38132	34722	45779	40673	40425
ENSMUSG00000025237	chr9	Parp6	59617284	59617408	2714	-0.51038	4.461331	0.001948	0.006213	0.030031	-1	371	423	492	435	421	312	418	491	458	438
ENSMUSG00000032058	chr9	Ppp2r1b	50845301	50845406	6449	0.939931	3.092227	0.001949	0.006213	0.101023	1	78	62	101	120	125	110	198	148	428	459
ENSMUSG00000061244	chr14	Exoc5	49012146	49014349	9932	-0.48496	4.581926	0.001949	0.006213	0.027068	-1	363	421	566	421	575	339	517	475	570	439
ENSMUSG00000063785	chrX	Utp14a	48256862	48256968	4130	0.562427	3.850475	0.001953	0.006224	0.035427	1	145	190	209	188	236	292	327	524	432	418
ENSMUSG00000030539	chr7	Sema4b	80186841	80186991	5434	0.937596	1.980844	0.001953	0.006225	0.092539	1	30	24	56	49	65	73	101	66	181	179
ENSMUSG00000028719	chr4	Cmpk1	1.15E+08	1.15E+08	3420	0.532476	5.096907	0.001957	0.006234	0.03362	1	378	432	561	412	558	675	843	764	1292	1203
ENSMUSG00000034574	chr12	Daam1	71831078	71831331	6004	-0.52717	4.397353	0.001957	0.006234	0.031953	-1	292	350	467	473	511	359	459	343	492	352
ENSMUSG00000030255	chr6	Sspn	1.46E+08	1.46E+08	4996	-0.5103	6.973931	0.001958	0.006235	0.031969	-1	2134	2034	2680	2444	3120	2060	2718	2468	2847	1980
ENSMUSG00000027164	chr2	Traf6	1.02E+08	1.02E+08	7883	-0.54161	4.38911	0.001961	0.006243	0.033898	-1	333	338	473	403	544	295	356	538	421	374

ENSMUSG00000052374	chr13	Actn2	12269426	12269652	3694	0.713682	10.05429	0.001963	0.00625	0.062946	1	8204	13717	13253	20555	11017	23741	30115	38030	40673	22656
ENSMUSG00000023052	chr15	Npff	1.03E+08	1.03E+08	1002	1.205019	-0.24761	0.001964	0.006251	0.089462	1	11	4	7	7	7	20	20	20	22	35
ENSMUSG00000024140	chr17	Epas1	86753907	86754308	5309	-0.61055	6.864874	0.001965	0.006252	0.045839	-1	1846	2036	2372	3235	2223	1504	1775	2859	2656	2056
ENSMUSG00000083844	chr11	2210015D19Rik	5762129	5762240	3102	-0.52558	5.62353	0.001965	0.006252	0.033263	-1	878	879	1072	1018	981	902	821	1035	987	904
ENSMUSG00000040511	chr7	Pvr	19903578	19905192	5408	0.589406	4.165503	0.001973	0.006274	0.040274	1	165	198	269	236	341	376	719	452	517	436
ENSMUSG00000041688	chrX	Amot	1.45E+08	1.45E+08	8402	-0.58475	7.260778	0.001974	0.006275	0.042176	-1	2600	2698	3479	2859	3816	1960	2941	4128	3082	2244
ENSMUSG00000051314	chr7	Ffar2	30818348	30820287	2790	2.256123	0.217451	0.001977	0.006284	0.492922	1	5	4	1	7	12	9	21	2	57	115
ENSMUSG00000026608	chr1	Kctd3	1.89E+08	1.89E+08	8129	-0.48212	4.4691	0.001978	0.006286	0.026586	-1	342	331	496	429	582	323	460	408	524	449
ENSMUSG00000032518	chr9	Rpsa	1.2E+08	1.2E+08	1861	0.50384	9.091775	0.00198	0.006292	0.03156	1	5827	7104	8803	6749	9481	12857	15494	12614	17394	16194
ENSMUSG00000076128	chr14	Mir686	54616677	54616785	109	0.572573	5.842035	0.001984	0.006303	0.039847	1	639	777	927	691	799	1376	1393	1957	1446	1717
ENSMUSG00000067194	chrX	Eif1ax	1.59E+08	1.59E+08	5266	-0.49749	6.615725	0.001985	0.006304	0.030334	-1	1703	1613	2298	1745	2273	1579	1913	2095	2071	1790
ENSMUSG00000097119	chr17	B230354K17Rik	45433852	45434227	4897	-0.54835	3.43945	0.001986	0.006304	0.032514	-1	208	164	271	206	222	147	201	236	233	209
ENSMUSG00000032396	chr9	Dis3l	64306756	64307348	5458	-0.48843	4.807077	0.001991	0.00632	0.027931	-1	466	509	591	565	585	426	486	602	639	565
ENSMUSG00000003575	chr8	Crtc1	70382355	70386335	11182	-0.50631	3.698145	0.001994	0.006328	0.02802	-1	206	207	298	241	327	172	280	242	325	241
ENSMUSG00000021760	chr13	Gpx8	1.13E+08	1.13E+08	1016	0.803438	4.314006	0.001994	0.006328	0.077111	1	233	155	279	180	379	478	748	246	685	787
ENSMUSG00000032468	chr9	Armc8	99478372	99480777	6531	-0.52625	5.657633	0.001998	0.006339	0.033498	-1	898	837	1119	920	1217	789	911	1245	965	878
ENSMUSG00000019254	chr7	Ppp1r12c	4481520	4482158	4981	0.499581	4.836059	0.001999	0.00634	0.029173	1	345	345	450	412	415	527	767	692	1059	907
ENSMUSG00000074361	chr7	C5ar2	16234585	16237974	3561	1.077882	0.022399	0.002005	0.006358	0.07681	1	8	6	15	11	8	19	38	20	35	31
ENSMUSG00000058709	chr7	Egln2	27158658	27159211	2800	-0.49453	6.67656	0.002014	0.006383	0.030076	-1	1647	1819	2331	1992	2217	1754	1804	1953	2305	2050
ENSMUSG00000034573	chr5	Ptpn13	1.03E+08	1.03E+08	8280	-0.96079	2.62705	0.002014	0.006384	0.104907	-1	135	73	157	98	229	66	139	131	108	42
ENSMUSG00000029456	chr5	Acad10	1.22E+08	1.22E+08	6068	0.852205	1.885977	0.002017	0.006391	0.071589	1	34	56	36	39	44	60	99	114	122	148
ENSMUSG00000055980	chr1	Irs1	82233101	82237604	9144	-0.74575	7.021603	0.002017	0.006391	0.068637	-1	1827	2846	2325	1971	4858	2136	3029	1531	2622	1932
ENSMUSG00000035686	chr7	Thrsp	97412938	97413515	1277	1.574129	6.113912	0.002022	0.006403	0.292875	1	320	486	544	887	696	769	739	492	4115	6655
ENSMUSG00000066315	chr4	Gm12918	10848420	10849055	636	0.723791	2.492222	0.00203	0.006426	0.054648	1	56	58	57	70	109	129	148	116	218	196
ENSMUSG00000064354	chrMT	mt-Co2	7013	7696	684	-0.89713	3.688933	0.002034	0.006439	0.095469	-1	200	268	218	515	167	157	146	183	347	237
ENSMUSG00000001833	chr9	Sept7	25252439	25252699	2538	-0.48708	6.466789	0.002035	0.006441	0.029173	-1	1473	1606	1992	1634	1911	1266	1740	1915	2076	1645
ENSMUSG00000025521	chr8	Tmem192	64947185	64947333	1123	0.622196	3.539177	0.002037	0.006446	0.043342	1	112	157	161	172	151	294	237	282	396	415
ENSMUSG00000035596	chr7	Mboat7	3677790	3678849	7716	0.510851	3.928058	0.002041	0.006457	0.029103	1	151	202	251	183	262	289	439	384	561	428
ENSMUSG00000051498	chr5	Tlr6	64953106	64955593	2603	0.982185	1.206485	0.002042	0.006457	0.093259	1	11	26	41	17	29	46	88	44	95	70
ENSMUSG00000096740	chr19	Lbhd1	8883732	8884079	3289	0.562785	3.663996	0.002047	0.006473	0.035179	1	144	168	199	156	177	310	366	249	461	366
ENSMUSG00000080935	chr5	Got2-ps1	1.38E+08	1.38E+08	1293	-0.64532	3.791734	0.002051	0.006484	0.048431	-1	207	292	254	378	259	179	242	308	349	192
ENSMUSG00000027002	chr2	Nckap1	80500512	80501411	4964	-0.48731	5.880171	0.002054	0.006491	0.028953	-1	915	972	1241	1198	1456	803	1253	1240	1363	1103
ENSMUSG00000098923	chr1	Tmem185b	1.2E+08	1.2E+08	2824	0.70777	2.834313	0.002066	0.006529	0.054512	1	70	90	84	78	124	163	223	121	275	242
ENSMUSG00000071660	chr19	Ttc9c	8809075	8811838	3984	-0.47973	4.003064	0.002069	0.006536	0.025696	-1	285	275	346	293	353	238	327	337	355	302
ENSMUSG00000022856	chr16	Tmem41a	21934327	21935045	1359	0.677679	2.630774	0.002072	0.006544	0.049066	1	63	58	101	68	106	177	157	136	204	190
ENSMUSG00000018446	chr11	C1qbp	70977836	70978244	2826	0.522934	6.126187	0.002078	0.006562	0.033619	1	681	948	1106	1033	1018	1745	1786	1908	2263	1846
ENSMUSG00000033949	chr18	Trim36	46165302	46167767	4849	1.261467	-0.0094	0.00208	0.006566	0.12873	1	8	1	8	14	12	17	30	17	35	46
ENSMUSG00000024273	chr18	2700062C07Rik	24470861	24470980	1040	0.798115	1.530657	0.002093	0.006606	0.059443	1	19	32	44	37	38	71	67	74	100	98
ENSMUSG00000028195	chr3	Cyr61	1.46E+08	1.46E+08	2028	1.234021	4.832582	0.002095	0.00661	0.183987	1	201	126	331	513	262	368	588	2333	712	662
ENSMUSG00000086968	chr3	4933431E20Rik	1.08E+08	1.08E+08	6821	-0.73624	2.063843	0.002099	0.006622	0.05436	-1	76	68	89	87	112	65	49	90	82	72
ENSMUSG00000003810	chr4	Mast2	1.16E+08	1.16E+08	7645	-0.51797	6.674742	0.0021	0.006624	0.033324	-1	1846	1690	2190	2146	2152	1401	1777	2458	2325	1897
ENSMUSG00000020882	chr11	Cacnb1	98001508	98003362	4529	-0.53337	7.950119	0.002103	0.006631	0.035634	-1	3731	4289	5343	4939	6355	4788	4372	4187	5121	4771
ENSMUSG00000027680	chr3	Fxr1	34020079	34020163	2323	-0.55234	8.464893	0.002104	0.006631	0.03829	-1	6098	6352	8108	6769	7770	5335	6362	9090	6831	5624
ENSMUSG00000035963	chr10	Odf3l2	79639526	79640379	1248	3.691976	2.12805	0.002103	0.006631	1.286829	1	5	9	16	19	0	7	5	826	5	53
ENSMUSG00000057719	chr18	Sh3rf2	42053667	42054195	5307	-0.95895	4.83008	0.002114	0.006663	0.112341	-1	667	448	476	591	967	241	282	983	387	360
ENSMUSG00000013275	chr1	Slc41a1	1.32E+08	1.32E+08	4912	-0.59114	6.305271	0.00212	0.006679	0.043408	-1	1278	1400	1520	2090	1614	986	1437	1928	1902	1193
ENSMUSG00000040274	chr5	Cdk6	3343893	3343971	3735	1.238309	0.101464	0.002124	0.006691	0.121566	1	10	6	12	6	13	16	30	13	55	46
ENSMUSG00000025484	chr7	Bet1l	1.41E+08	1.41E+08	1552	0.539202	3.888852	0.002143	0.006747	0.033006	1	190	160	216	190	248	277	396	538	442	387
ENSMUSG00000041297	chr13	Cdk13	17715962	17718911	7081	-0.53734	3.992125	0.002143	0.006748	0.033307	-1	285	254	355	309	370	199	301	399	376	249
ENSMUSG00000031826	chr8	Usp10	1.2E+08	1.2E+08	5456	-0.50574	5.148689	0.00215	0.006766	0.030858	-1	495	616	793	667	946	602	681	561	841	729
ENSMUSG00000028850	chr4	Gpatch3	1.34E+08	1.34E+08	2086	0.807712	1.838445	0.002153	0.006775	0.064364	1	29	49	58	26	48	75	97	92	130	123
ENSMUSG00000041355	chr3	Ssr2	88575876	88575980	1864	0.561733	5.835741	0.002155	0.006779	0.039014	1	641	581	879	701	1106	1362	1610	1075	2169	1766
ENSMUSG00000021870	chr14	Slmap	26413168	26414988	8054	-0.60071	5.903504	0.002155	0.006779	0.044745	-1	947	963	1252	1506	1383	720	1159	1601	1155	933
ENSMUSG00000079620	chr16	Muc4	32735886	32736452	11757	-1.06268	0.714694	0.002156	0.006779	0.104995	-1	43	19	26	51	38	14	16	31	27	32
ENSMUSG00000026749	chr2	Nek6	38511643	38511793	4149	0.644799	4.175427	0.002158	0.006784	0.049315	1	155	270	302	215	224	427	451	342	729	631
ENSMUSG00000021768	chr14	Dusp13	21733394	21733851	2744	-0.60816	6.215922	0.002159	0.006785	0.046	-1	1351	1356	1759	1497	1500	1331	1171	1718	1096	1392
ENSMUSG00000027199	chr2	Gatm	1.23E+08	1.23E+08	3001	0.883909	5.381253	0.002159	0.006785	0.096495	1	309	415	619	347	823	998	2257	540	1364	1141
ENSMUSG00000042729	chr19	Wdr74	8735839	8735905	1203	0.51932	3.811554	0.002162	0.006794	0.030466	1	135	158	248	191	237	317	342	354	461	444
ENSMUSG00000040651	chr14	Fam208a	27428847	27429384	7574	-0.58208	3.351298	0.002167	0.006805	0.03789	-1	193	139	218	206	269	110	201	174	258	224
ENSMUSG00000051147	chr8	Nat2	67494867	67494902	1509	1.01112	0.417989	0.002167	0.006805	0.077635	1	8	15	13	16	15	30	47	32	30	49
ENSMUSG00000017724	chr11	Etv4	1.02E+08	1.02E+08	3104	0.686478	2.364681	0.002167	0.006805	0.047979	1	73	45	64	70	68	101	173	133	177	146
ENSMUSG00000021474	chr13	Sfxn1	54071845	54071932	2811	1.224638	3.413753	0.00217	0.006813	0.17905	1	94	52	72	121	200	119	200	162	577	746
ENSMUSG00000068959	chr7	Zfp619	39517766	39517864	5964	-0.94382	0.434396	0.002174	0.006821	0.067496	-1	21	35	29	25	30	15	24	15	28	21
ENSMUSG00000022191	chr15	Drosha	12824815	12824942	5934	-0.47095	5.29002	0.002177	0.006831	0.026852	-1	619	620	803	785	998	591	777	709	1000	775
ENSMUSG00000033055	chr15	Ankrd54	79053094	79054084	4270	0.627603	2.774944	0.002182	0.006845	0.04169	1	80	65	97	80	124	123	183	187	236	236
ENSMUSG00000037001	chr11	Zfp39	58888153	58891546	3890	-0.77075	2.186396	0.002183	0.006847	0.062514	-1	67	67	131	93	124	46	73	114	81	75

ENSMUSG00000025337	chr5	Sbds	1.3E+08	1.3E+08	2033	0.579826	4.741939	0.002192	0.00687	0.040524	1	320	331	373	376	374	553	690	1086	755	630
ENSMUSG00000027222	chr2	Pex16	92374676	92374821	1775	0.630504	4.242156	0.002192	0.00687	0.047383	1	204	204	276	276	277	306	371	697	592	733
ENSMUSG00000073176	chrX	Zfp449	56346400	56346439	3738	-0.66722	2.307375	0.002191	0.00687	0.045111	-1	82	85	116	96	125	67	116	70	110	80
ENSMUSG00000073889	chr4	Il11ra1	41699989	41700116	4471	0.560116	5.823887	0.002193	0.006873	0.038908	1	766	556	874	551	1117	1301	1574	1721	1706	1531
ENSMUSG00000071076	chr8	Jund	70697739	70700616	2878	0.664205	5.491996	0.002201	0.006895	0.054721	1	461	399	536	679	876	1271	1591	758	1653	1121
ENSMUSG00000039396	chr8	Neil3	53586867	53587327	5296	1.327151	-0.0923	0.002205	0.006904	0.145061	1	9	2	8	6	14	21	36	8	45	28
ENSMUSG00000046139	chr19	Patl1	11912399	11912577	4221	-0.51228	4.644266	0.002209	0.006914	0.031273	-1	421	386	485	560	609	375	464	595	532	431
ENSMUSG00000069729	chr17	Arid1b	4994332	4994399	12600	-0.61298	5.187226	0.002209	0.006914	0.046296	-1	611	519	779	851	958	383	622	1014	760	616
ENSMUSG00000026078	chr1	Pdcl3	38985608	38987849	4219	0.491175	5.298171	0.00221	0.006917	0.029394	1	410	496	653	524	663	943	1178	974	1182	1045
ENSMUSG00000028646	chr4	Rragc	1.24E+08	1.24E+08	3341	0.500667	5.049534	0.002212	0.00692	0.030252	1	358	413	459	474	592	584	841	934	1168	1055
ENSMUSG00000044042	chr2	Fmn1	1.13E+08	1.13E+08	15397	1.257926	1.061957	0.002212	0.006921	0.163653	1	26	5	22	7	38	35	64	41	101	89
ENSMUSG00000085148	chr11	Mir22hg	75461539	75461755	1924	0.71507	4.877094	0.002216	0.006931	0.062872	1	369	257	407	331	504	551	683	1481	758	760
ENSMUSG00000028974	chr4	Dffa	1.49E+08	1.49E+08	3540	-0.52335	5.866892	0.002218	0.006935	0.033976	-1	894	1053	1407	1205	1196	1014	1220	922	1442	982
ENSMUSG00000038763	chr7	Alpk3	81057600	81057772	6445	-0.55888	7.350746	0.002219	0.006937	0.03943	-1	2928	2685	3224	3995	3333	2650	3086	3745	3286	2519
ENSMUSG00000031825	chr8	Crispld2	1.2E+08	1.2E+08	4777	-0.63764	4.65506	0.002231	0.006973	0.049543	-1	563	315	514	408	787	338	565	548	464	377
ENSMUSG00000028914	chr4	Casp9	1.42E+08	1.42E+08	5197	0.612557	2.994627	0.002232	0.006973	0.041152	1	84	70	125	99	150	147	222	202	276	275
ENSMUSG00000024301	chr17	Kifc5b	26917091	26917285	2627	1.16365	0.107084	0.002232	0.006974	0.106735	1	7	10	6	11	15	26	24	15	42	48
ENSMUSG00000034898	chr9	Filip1	79815051	79815897	4888	-1.04476	5.501724	0.002239	0.006991	0.135304	-1	863	757	1151	1227	1123	292	515	1704	553	399
ENSMUSG00000085888	chr11	Gm12224	54340369	54340684	1091	-0.7869	4.731619	0.002239	0.006991	0.076145	-1	502	638	746	497	369	593	343	409	419	421
ENSMUSG00000040666	chr16	Sh3bgr	96200470	96200748	1542	-0.6079	9.320692	0.002242	0.006999	0.046974	-1	10906	12559	17162	11142	12624	13408	11382	10280	11379	11118
ENSMUSG00000026492	chr1	Tfb2m	1.8E+08	1.8E+08	2804	-0.58376	4.818349	0.002244	0.007004	0.041572	-1	516	540	613	553	579	392	539	752	520	416
ENSMUSG00000028469	chr4	Npr2	43631935	43632851	4667	-0.56175	5.378474	0.002246	0.007009	0.039025	-1	741	680	850	949	913	513	731	1121	866	707
ENSMUSG00000024044	chr17	Epb4.1l3	69156810	69156910	4109	0.85362	2.380649	0.002248	0.007015	0.080805	1	57	37	58	51	105	106	244	146	170	101
ENSMUSG00000026436	chr1	Elk4	1.32E+08	1.32E+08	6407	0.619953	4.968822	0.002251	0.007022	0.047198	1	352	340	480	455	430	642	758	1358	765	856
ENSMUSG00000036023	chr14	Parp2	50807946	50807987	1788	0.557163	3.334613	0.002264	0.007059	0.033804	1	128	124	160	116	144	179	301	254	354	317
ENSMUSG00000010175	chr1	Prox1	1.9E+08	1.9E+08	8390	-0.80318	2.118981	0.002265	0.00706	0.069471	-1	65	55	132	90	124	42	78	95	102	53
ENSMUSG00000028836	chr4	Slc30a2	1.34E+08	1.34E+08	3564	-1.45691	3.462312	0.002265	0.00706	0.253878	-1	135	465	325	311	56	89	72	309	122	90
ENSMUSG00000032513	chr9	Gorasp1	1.2E+08	1.2E+08	3483	-0.48682	4.062066	0.002268	0.007067	0.02729	-1	286	259	400	294	396	229	317	318	453	323
ENSMUSG00000040850	chr11	Psme4	30771726	30772224	8382	-0.75442	8.105112	0.002274	0.007083	0.072119	-1	4760	5333	6882	5945	5935	3252	3828	8908	3830	3893
ENSMUSG00000064043	chr17	Trerf1	47140875	47140965	9070	0.716479	2.014795	0.002273	0.007083	0.051421	1	45	35	57	39	75	84	112	99	154	126
ENSMUSG00000029703	chr5	Lrwd1	1.36E+08	1.36E+08	6650	0.617418	2.960656	0.002276	0.007087	0.041033	1	90	83	109	108	116	132	251	175	282	262
ENSMUSG00000041075	chr1	Fzd7	59482424	59486955	4532	-0.68281	5.374808	0.002278	0.007093	0.058162	-1	812	521	1047	958	967	437	624	1232	776	668
ENSMUSG00000083992	chr11	Gm11478	86630428	86631026	599	0.629168	2.739051	0.002288	0.007122	0.041524	1	86	82	89	81	88	172	178	162	236	179
ENSMUSG00000003814	chr8	Calr	84841850	84842844	2880	0.658535	8.068881	0.002293	0.007135	0.055187	1	2603	2776	3781	3116	5484	6433	7737	4105	10619	9819
ENSMUSG00000040987	chr7	Mill2	18839966	18840091	1121	-0.97955	0.204705	0.002294	0.007138	0.072354	-1	27	15	20	26	32	10	18	19	17	21
ENSMUSG00000074634	chr13	Gm7120	1.19E+08	1.19E+08	3429	-1.00699	0.353007	0.002295	0.007138	0.084484	-1	22	25	24	20	45	11	12	23	21	27
ENSMUSG00000020485	chr11	Supt4a	87737552	87737668	942	0.602398	4.372554	0.002299	0.007149	0.043734	1	231	258	344	258	273	431	566	846	521	514
ENSMUSG00000021288	chr12	Klc1	1.12E+08	1.12E+08	4070	0.515773	6.174995	0.002307	0.007174	0.033412	1	762	907	1138	1003	1177	1619	2497	1664	2215	1907
ENSMUSG00000031029	chr7	Eif3f	1.09E+08	1.09E+08	2891	0.495041	6.903954	0.002308	0.007174	0.031034	1	1345	1443	1664	1888	1978	2704	3018	3563	3800	3234
ENSMUSG00000052180	chr13	Serpinb6c	33879816	33880332	1391	1.079301	0.096608	0.002313	0.007188	0.08598	1	7	8	16	9	11	14	36	43	35	24
ENSMUSG00000024666	chr19	Tmem138	10570478	10571268	1590	0.835088	0.997581	0.002316	0.007196	0.056523	1	21	19	23	25	24	36	64	47	74	63
ENSMUSG00000027332	chr2	Ivd	1.19E+08	1.19E+08	5505	-0.52546	7.482505	0.002319	0.007204	0.035187	-1	3149	3007	3557	3858	4037	2701	2915	4145	3468	3806
ENSMUSG00000034675	chr13	Dbn1	55473429	55474293	4514	0.762442	4.30558	0.002325	0.007218	0.071683	1	163	132	251	235	488	417	798	366	786	560
ENSMUSG00000038871	chr6	Bpgm	34476207	34476422	3588	-0.58851	6.380487	0.002325	0.007218	0.043794	-1	1580	1697	1984	1502	1488	1547	1297	1756	1570	1458
ENSMUSG00000085213	chr4	Gm13091	1.51E+08	1.51E+08	469	-1.95426	0.465478	0.002325	0.007218	0.406295	-1	18	94	16	21	19	2	7	37	12	8
ENSMUSG00000038422	chr4	Hdhd3	62499008	62500093	1366	1.054395	2.047539	0.00233	0.007233	0.125713	1	27	36	50	30	80	97	140	40	192	172
ENSMUSG00000029661	chr6	Col1a2	4504814	4504865	12136	-1.12256	11.59111	0.002332	0.007236	0.158096	-1	91927	21067	81884	28799	141867	35397	70218	27785	59704	35687
ENSMUSG00000022018	chr14	Rgcc	79288756	79289119	918	0.561206	4.317264	0.002333	0.007237	0.037642	1	274	199	316	250	300	388	399	594	692	712
ENSMUSG00000041390	chr6	Mdfic	15720661	15720963	7427	0.604849	4.196995	0.002341	0.007261	0.044009	1	173	188	313	254	298	294	525	370	822	636
ENSMUSG00000074480	chr3	Mex3a	88532395	88532848	5778	1.107093	1.081322	0.002344	0.007268	0.129038	1	10	8	19	27	45	30	89	50	89	66
ENSMUSG00000097042	chr8	Gm17491	22480291	22482054	2309	1.063577	0.409799	0.002356	0.007305	0.092517	1	17	5	10	14	19	18	40	48	46	41
ENSMUSG00000029309	chr5	Sparcl1	1.04E+08	1.04E+08	3114	-0.53252	7.790773	0.002362	0.00732	0.036338	-1	3213	4182	4886	5437	4072	3183	4714	4012	5208	4149
ENSMUSG00000024018	chr17	Ccdc167	29689378	29690046	4896	-0.80842	2.474473	0.002369	0.00734	0.07387	-1	134	83	153	91	123	77	105	46	126	116
ENSMUSG00000056076	chr5	Eif3b	1.4E+08	1.4E+08	2966	0.505951	6.810383	0.002369	0.00734	0.032586	1	1107	1309	1764	1622	2043	2373	2593	3369	3725	3364
ENSMUSG00000026571	chr1	Dcaf6	1.65E+08	1.65E+08	6424	-0.69733	7.595697	0.002371	0.007342	0.062145	-1	3623	3391	4544	4306	4070	2713	2797	5870	2953	2667
ENSMUSG00000037904	chr12	Ankrd9	1.11E+08	1.11E+08	3160	-0.64573	6.682761	0.00237	0.007342	0.053079	-1	1732	1987	2966	1943	1816	1781	1444	2432	1644	1859
ENSMUSG00000063296	chr15	Tmem117	94629185	94629302	2781	-0.5394	4.650745	0.002379	0.007364	0.035334	-1	432	434	620	447	554	472	534	356	500	491
ENSMUSG00000076372	chr16	Mir568	43640655	43640737	83	-0.94077	0.877163	0.002381	0.007371	0.080897	-1	34	33	52	35	41	24	27	44	19	25
ENSMUSG00000022009	chr14	Nufip1	76110891	76111326	3974	0.665619	3.005625	0.002385	0.007381	0.04987	1	86	96	135	90	104	160	222	324	221	203
ENSMUSG00000031137	chrX	Fgf13	59062145	59063669	4019	-0.48135	4.712428	0.00239	0.007394	0.027963	-1	457	467	554	472	593	413	516	582	574	458
ENSMUSG00000008763	chr3	Man1a2	1.01E+08	1.01E+08	7969	-0.48109	4.337024	0.002396	0.007412	0.027387	-1	340	323	437	364	512	272	401	455	460	388
ENSMUSG00000028708	chr4	Mknk1	1.16E+08	1.16E+08	4502	-0.58257	4.893632	0.002412	0.007459	0.042097	-1	548	594	616	534	658	428	519	801	533	473
ENSMUSG00000074903	chr7	Gm2058	39588931	39589365	560	-1.28874	-0.07628	0.002413	0.007462	0.142554	-1	10	19	26	21	30	5	15	22	16	2
ENSMUSG00000020457	chr11	Drg1	3187360	3187410	3460	0.482111	5.690235	0.002417	0.007472	0.029111	1	554	651	877	711	818	1179	1300	1576	1561	1366
ENSMUSG00000026634	chr1	Angel2	1.91E+08	1.91E+08	5559	-0.49161	4.845864	0.002424	0.00749	0.029545	-1	454	509	654	558	634	391	563	682	608	549
ENSMUSG00000042246	chr7	Tmc7	1.19E+08	1.19E+08	5761	-0.67011	4.19819	0.002425	0.00749	0.054993	-1	316	304	375	451	435	333	397	164	451	299

ENSMUSG00000063160	chr7	Numbl	27258433	27258513	8673	0.747895	3.287363	0.002424	0.00749	0.066178	1	136	57	129	87	204	172	347	290	365	259
ENSMUSG00000071645	chr19	Tut1	8953850	8954021	2747	0.640002	3.305728	0.002428	0.0075	0.047304	1	96	101	156	135	157	191	227	416	325	237
ENSMUSG00000054939	chr16	Zfp174	3847268	3848274	5897	-0.73192	1.760782	0.002429	0.007502	0.05323	-1	61	51	90	81	64	45	56	63	77	52
ENSMUSG00000003062	chr13	Stard3nl	19357677	19358129	1283	0.627093	2.631922	0.002433	0.007511	0.041489	1	69	69	96	70	97	113	203	146	208	201
ENSMUSG00000093315	chr19	Mir5114	44303171	44303231	61	-1.11647	1.841568	0.002433	0.007511	0.142312	-1	52	31	52	88	200	28	63	51	71	51
ENSMUSG00000020377	chr11	Ltc4s	50236469	50236601	736	1.533595	1.431931	0.002439	0.007526	0.265234	1	17	9	12	28	46	29	56	30	124	220
ENSMUSG00000021466	chr13	Ptch1	63508328	63512075	8745	-0.69875	3.806328	0.002442	0.007534	0.059388	-1	203	288	296	286	375	143	183	419	298	211
ENSMUSG00000019823	chr10	Mical1	41476314	41476540	6047	0.637624	3.325375	0.002446	0.007545	0.047337	1	100	79	150	120	216	175	286	244	393	338
ENSMUSG00000022842	chr16	Ece2	20611593	20611820	6547	0.626401	2.68256	0.00245	0.007554	0.041804	1	85	77	94	61	95	136	171	172	239	182
ENSMUSG00000093456	chr9	Gm20662	1.08E+08	1.08E+08	1853	-0.86012	2.689244	0.002452	0.007561	0.086945	-1	126	110	171	125	160	35	111	183	109	102
ENSMUSG00000031227	chrX	Magee1	1.05E+08	1.05E+08	3550	0.877337	1.989061	0.002459	0.007581	0.084359	1	43	24	44	38	82	72	153	77	176	116
ENSMUSG00000081752	chrX	Gm14680	62775585	62776685	1101	-0.56498	3.080064	0.002461	0.007583	0.035149	-1	147	142	225	149	176	127	169	149	194	153
ENSMUSG00000030124	chr6	Lag3	1.25E+08	1.25E+08	2109	1.016035	0.790583	0.002481	0.007645	0.093798	1	18	18	16	13	23	31	56	33	48	84
ENSMUSG00000061032	chr10	Rrp1	78400362	78400984	2008	0.488219	6.076414	0.002485	0.007653	0.030263	1	718	858	1015	1051	1052	1422	1689	1717	2339	2079
ENSMUSG00000021676	chr13	Iqgap2	95627177	95628120	5771	0.684291	2.719186	0.002494	0.007681	0.052407	1	74	50	78	87	132	125	194	151	255	220
ENSMUSG00000034354	chr11	Mtmr3	4480868	4482939	7588	-0.54066	6.220812	0.002496	0.007684	0.037394	-1	1280	1233	1596	1548	1745	1045	1212	1964	1552	1318
ENSMUSG00000025507	chr7	Pidd1	1.41E+08	1.41E+08	4528	1.12295	0.292297	0.002498	0.007687	0.101493	1	11	11	16	11	8	13	39	28	45	55
ENSMUSG00000031696	chr8	Vps35	85260397	85261309	3180	-0.5479	6.165812	0.002497	0.007687	0.038429	-1	1297	1253	1749	1274	1547	844	1353	1814	1699	1182
ENSMUSG00000018965	chr5	Ywhah	33018816	33019154	2274	0.55271	5.521414	0.0025	0.007689	0.038617	1	503	567	679	566	808	1027	1321	805	1866	1424
ENSMUSG00000031513	chr8	Leprotl1	34135572	34137838	2879	0.481446	4.392662	0.0025	0.007689	0.027558	1	245	279	322	287	321	441	591	471	745	617
ENSMUSG00000033256	chr2	Shf	1.22E+08	1.22E+08	2305	0.824136	1.190017	0.0025	0.007689	0.063072	1	14	20	26	34	38	56	69	61	71	64
ENSMUSG00000038156	chr7	Spon1	1.14E+08	1.14E+08	8177	-0.81868	3.564251	0.002501	0.007689	0.082184	-1	292	92	266	195	442	120	252	178	257	204
ENSMUSG00000028538	chr4	St3gal3	1.18E+08	1.18E+08	2768	-0.50591	6.040298	0.002501	0.00769	0.032578	-1	985	1156	1376	1473	1475	1166	1189	1110	1446	1391
ENSMUSG00000025352	chr10	Gdf11	1.29E+08	1.29E+08	4062	-0.69506	3.899059	0.002502	0.007691	0.059123	-1	320	175	418	211	440	204	368	199	351	214
ENSMUSG00000041203	chr8	2310036O22Rik	85026833	85027234	891	0.503589	5.247056	0.002503	0.007692	0.031606	1	425	547	604	506	518	895	938	986	1227	1127
ENSMUSG00000022620	chr15	Arsa	89472476	89473557	3680	0.577134	3.681569	0.002506	0.007697	0.039135	1	139	133	181	168	242	240	363	250	502	455
ENSMUSG00000005686	chr7	Ampd3	1.11E+08	1.11E+08	5605	0.573102	3.663571	0.002507	0.007698	0.03841	1	133	142	179	204	187	268	327	465	424	273
ENSMUSG00000028957	chr4	Per3	1.51E+08	1.51E+08	9608	-0.84476	3.997018	0.002507	0.007698	0.088839	-1	519	257	353	228	309	192	166	435	278	256
ENSMUSG00000048222	chr2	Mfap1b	1.21E+08	1.21E+08	3362	0.512045	3.835631	0.002511	0.007709	0.030398	1	173	174	207	180	243	327	381	461	396	364
ENSMUSG00000002580	chr11	Mien1	98437708	98438145	747	0.564482	4.593879	0.002515	0.007718	0.03918	1	282	334	347	313	330	603	613	483	752	880
ENSMUSG00000038068	chr13	Rnf144b	47122720	47122873	4694	-0.66707	4.271094	0.002515	0.007718	0.055174	-1	311	549	410	341	313	292	275	405	390	368
ENSMUSG00000015354	chr9	Pcolce2	95637601	95637873	4625	-0.83497	3.509191	0.002517	0.007719	0.085389	-1	274	96	275	177	423	119	176	271	184	202
ENSMUSG00000022214	chr14	Dcaf11	55560006	55560121	8070	-0.53724	7.073391	0.002516	0.007719	0.037285	-1	2330	2425	3071	2720	2730	2137	2257	3243	2472	2593
ENSMUSG00000044807	chr11	Zfp354c	50811086	50815993	5596	-0.76945	2.868523	0.002516	0.007719	0.069251	-1	145	95	174	107	259	96	183	91	152	106
ENSMUSG00000103409	chr9	RP23-456B9.23	1.08E+08	1.08E+08	369	-0.63787	3.51394	0.002526	0.007744	0.04805	-1	184	239	293	193	245	220	248	147	210	194
ENSMUSG00000000838	chrX	Fmr1	68678541	68678867	8966	-0.6732	3.262195	0.002531	0.00776	0.054117	-1	181	155	225	160	267	72	168	219	252	173
ENSMUSG00000090187	chr13	AK157302	21495306	21495695	390	-0.83878	1.989374	0.002537	0.007775	0.076118	-1	68	98	94	84	69	64	73	82	56	46
ENSMUSG00000038459	chr7	Abhd17c	84109356	84110801	2415	0.590989	3.126086	0.002544	0.007796	0.038983	1	95	98	116	125	142	178	287	177	309	269
ENSMUSG00000062515	chr3	Fabp4	10204088	10204570	4489	1.113846	8.431578	0.002549	0.007809	0.158338	1	2568	3718	3887	4595	3340	3727	4832	7027	15470	26443
ENSMUSG00000034780	chr2	B3galt1	67565871	67566034	5753	-1.06113	1.906224	0.002563	0.007849	0.130759	-1	104	43	84	99	85	19	57	103	71	36
ENSMUSG00000053656	chr5	Dancr	74093060	74094336	2346	1.044315	0.321333	0.002564	0.007851	0.087768	1	8	18	16	5	14	25	34	29	48	43
ENSMUSG00000029416	chr5	Slc15a4	1.28E+08	1.28E+08	5312	0.678754	4.231683	0.002565	0.007853	0.057106	1	229	206	303	191	272	339	455	910	501	476
ENSMUSG00000005893	chr6	Nr2c2	92091390	92091742	9152	-0.59349	4.814418	0.002571	0.007868	0.044275	-1	492	485	624	580	644	328	519	807	548	422
ENSMUSG00000005968	chr3	Tuft1	94612759	94614191	2564	1.083571	0.134441	0.002571	0.007868	0.092811	1	9	3	16	9	16	14	30	32	44	38
ENSMUSG00000068396	chr6	Rpl34-ps1	71124610	71124963	354	0.861708	1.804976	0.002578	0.007886	0.079004	1	26	46	61	22	46	89	116	105	89	102
ENSMUSG00000018697	chr11	Aatf	84422855	84423019	2869	0.531782	3.45364	0.002585	0.007906	0.032075	1	114	118	168	159	189	214	266	355	343	325
ENSMUSG00000066000	chr4	2610305D13Rik	1.48E+08	1.48E+08	4111	-0.76038	1.543848	0.002587	0.007909	0.057935	-1	52	59	65	53	70	26	46	47	79	55
ENSMUSG00000035049	chr19	Rrp12	41862852	41863312	4319	-0.49635	5.32046	0.002589	0.007915	0.031067	-1	537	697	983	736	1002	579	819	799	1029	674
ENSMUSG00000004451	chr1	Ralb	1.19E+08	1.19E+08	4930	0.584081	4.237202	0.00259	0.007917	0.0418	1	171	238	288	262	303	381	558	326	754	650
ENSMUSG00000079434	chr1	Neu2	87509889	87510215	2590	-0.61889	4.716948	0.002596	0.007934	0.048054	-1	526	393	501	591	644	548	431	312	586	500
ENSMUSG00000041642	chr1	Kif21b	1.36E+08	1.36E+08	12184	1.071866	1.253464	0.002598	0.007936	0.122314	1	11	12	17	36	49	39	82	53	107	84
ENSMUSG00000022634	chr15	Yaf2	93284278	93285622	1873	-0.51139	3.492103	0.002604	0.007953	0.029726	-1	167	211	227	232	263	166	229	228	260	197
ENSMUSG00000022299	chr15	Slc25a32	39094191	39096108	2945	-0.66387	2.623874	0.002609	0.007968	0.049626	-1	122	117	146	121	113	61	99	129	154	119
ENSMUSG00000040564	chr7	Apoc1	19689484	19689636	537	1.885005	2.138938	0.002613	0.007978	0.416019	1	24	12	12	45	61	20	48	49	268	442
ENSMUSG00000033124	chr1	Atg9a	75180860	75181931	5762	-0.5517	7.344236	0.002622	0.008004	0.039723	-1	3014	2552	3468	3219	3937	2522	2713	4212	3083	2727
ENSMUSG00000000686	chr11	Abhd15	77515121	77516052	3035	1.55017	0.350832	0.00263	0.008026	0.249707	1	4	2	5	24	14	13	33	27	45	85
ENSMUSG00000060938	chr11	Rpl26	68901583	68901624	1444	0.483853	7.827237	0.00263	0.008026	0.030648	1	2572	3005	3709	2773	3817	5121	6170	5895	6859	6787
ENSMUSG00000086219	chr5	Srrm4os	1.16E+08	1.16E+08	3655	0.804496	1.922378	0.002633	0.008033	0.070191	1	30	32	51	42	73	110	70	118	123	117
ENSMUSG00000039231	chrX	Suv39h1	8061171	8062983	5270	0.627234	2.776808	0.002635	0.008037	0.042691	1	89	71	90	83	109	117	170	222	259	202
ENSMUSG00000048039	chr3	Isg20l2	87930314	87930611	2893	0.514866	3.686239	0.002642	0.008057	0.030731	1	159	145	174	171	232	293	389	378	378	306
ENSMUSG00000075602	chr15	Ly6a	74994877	74995479	1205	0.679127	6.14689	0.002645	0.008064	0.059788	1	816	849	1034	736	1116	2481	1754	1281	1918	2418
ENSMUSG00000071337	chr6	Tia1	86404219	86404522	12945	-0.47754	3.888668	0.002656	0.008094	0.026675	-1	256	235	320	280	349	206	305	247	365	330
ENSMUSG00000028059	chr3	Arhgef2	88607454	88607580	9496	0.50324	5.299463	0.00266	0.008106	0.032095	1	428	429	537	615	733	736	1316	987	1360	1041
ENSMUSG00000026112	chr1	Coa5	37417084	37420627	5220	-0.57302	7.63073	0.00267	0.008134	0.043068	-1	2903	3869	4728	4046	4296	3693	3928	2430	4488	3910
ENSMUSG00000028229	chr4	Rmdn1	19575162	19575327	1963	-0.65014	4.275626	0.002671	0.008135	0.052898	-1	346	453	446	422	259	354	363	289	408	321
ENSMUSG00000034616	chr19	Ssh3	4261668	4262632	2740	0.809196	2.349148	0.002672	0.008136	0.073964	1	64	36	66	55	83	59	168	196	176	156

ENSMUSG00000036850	chr2	Mrpl41	24974117	24974681	888	0.640453	4.604742	0.002674	0.008139	0.051612	1	257	357	352	332	259	537	615	1009	640	613
ENSMUSG00000064302	chr1	Clasp1	1.18E+08	1.18E+08	19275	-0.49701	5.884339	0.002673	0.008139	0.031794	-1	922	842	1271	1282	1533	852	1315	1021	1495	1086
ENSMUSG00000097467	chr9	Gm26737	44112923	44113235	2138	1.526968	-0.2252	0.002674	0.008139	0.207931	1	5	2	15	2	8	21	39	5	32	30
ENSMUSG00000053173	chr6	Rpl18-ps2	1.28E+08	1.28E+08	604	0.899785	1.322738	0.002685	0.008169	0.08089	1	27	22	44	18	28	65	97	47	83	68
ENSMUSG00000031508	chr8	Ankrd10	11611583	11612947	3950	0.489111	5.029669	0.002705	0.008227	0.030069	1	350	408	511	441	569	648	1079	926	1055	755
ENSMUSG00000043795	chr7	Prr33	1.42E+08	1.42E+08	2348	-0.55392	7.289875	0.002708	0.008234	0.040282	-1	2433	2841	3611	3206	3508	3061	2988	2108	3207	3212
ENSMUSG00000028389	chr4	Zfp37	62189540	62192689	3692	-1.00297	0.356707	0.002709	0.008235	0.088818	-1	25	14	30	27	41	9	21	28	25	12
ENSMUSG00000022246	chr15	Rai14	10568979	10570774	5008	0.69363	2.976404	0.002715	0.008252	0.056299	1	89	68	90	87	169	125	271	192	276	274
ENSMUSG00000027792	chr3	Bche	73635808	73640041	6741	-0.68091	3.219629	0.002716	0.008255	0.055893	-1	167	146	225	187	235	80	114	190	235	233
ENSMUSG00000098955	chr11	Mir6935	1.2E+08	1.2E+08	64	-0.96719	1.593597	0.002719	0.00826	0.102378	-1	54	62	77	43	94	50	53	16	61	52
ENSMUSG00000075254	chr16	Heg1	33684466	33684855	12632	-0.58923	5.670205	0.002719	0.008261	0.044966	-1	743	703	1048	1203	1514	606	1172	674	1237	1136
ENSMUSG00000030188	chr6	Magohb	1.31E+08	1.31E+08	1720	0.752123	1.525669	0.002722	0.008267	0.053781	1	27	36	38	33	37	71	70	67	101	95
ENSMUSG00000074513	chr3	Arfip1	84496093	84497891	2986	0.476159	4.417092	0.002731	0.008293	0.027577	1	276	237	303	270	409	414	610	581	691	611
ENSMUSG00000063358	chr16	Mapk1	16983382	16983739	7110	-0.47724	6.881007	0.002732	0.008295	0.029843	-1	2130	1946	2596	2193	2591	1768	2374	2563	2705	2118
ENSMUSG00000042423	chr7	Fbrs	1.27E+08	1.27E+08	2650	0.495425	4.422121	0.002737	0.008306	0.030113	1	228	239	318	332	375	403	563	716	677	572
ENSMUSG00000030630	chr7	Fah	84585159	84585344	2103	1.392244	2.385442	0.002743	0.008321	0.236284	1	29	30	42	47	93	47	79	64	323	395
ENSMUSG00000061689	chr2	Dlgap4	1.57E+08	1.57E+08	8451	0.563414	6.44634	0.002743	0.008321	0.041557	1	928	798	1381	1264	1612	2079	3131	1738	2897	2280
ENSMUSG00000056579	chr11	Tug1	3639785	3645523	8325	-0.47283	5.455381	0.002744	0.008322	0.028547	-1	721	741	927	844	1038	668	929	970	992	729
ENSMUSG00000084817	chr1	Gm5526	45857332	45857754	423	0.928886	0.899769	0.002746	0.008328	0.078209	1	13	19	25	25	18	42	48	33	73	73
ENSMUSG00000079108	chr12	Srp54b	55155104	55155580	5603	-0.56726	3.761596	0.002748	0.00833	0.038702	-1	206	260	322	212	358	201	248	333	264	218
ENSMUSG00000020680	chr11	Taf15	83473086	83473206	2919	0.557066	4.903217	0.002749	0.008332	0.039442	1	346	314	481	352	548	669	760	583	1015	1136
ENSMUSG00000027875	chr3	Hmgcs2	98280435	98280587	3290	1.793884	0.697209	0.002751	0.008337	0.350863	1	20	6	7	11	9	9	23	162	48	30
ENSMUSG00000103081	chr18	Pcdhgb8	37761801	37764299	4615	0.590561	5.824745	0.002757	0.008354	0.045418	1	697	430	808	652	1282	1207	1820	1405	2016	1549
ENSMUSG00000024740	chr19	Ddb1	10605625	10605766	4155	0.473726	8.025399	0.002758	0.008354	0.029696	1	2953	3058	4052	3647	4667	5336	7279	8097	8023	6687
ENSMUSG00000044749	chr11	Abca6	1.1E+08	1.1E+08	5398	-1.2357	2.476771	0.002762	0.008364	0.186853	-1	201	42	120	116	167	29	58	173	76	53
ENSMUSG00000044405	chr2	Adig	1.59E+08	1.59E+08	810	2.033381	2.699064	0.002768	0.00838	0.491581	1	29	28	9	57	88	21	64	69	342	759
ENSMUSG00000060568	chr1	Fam78b	1.67E+08	1.67E+08	6325	-0.81683	1.763697	0.002782	0.008422	0.072637	-1	65	61	82	76	70	29	62	34	84	80
ENSMUSG00000029513	chr5	Prkab1	1.16E+08	1.16E+08	3066	0.504298	3.626257	0.002791	0.008446	0.029589	1	118	148	178	194	214	271	329	326	393	358
ENSMUSG00000046280	chr3	She	89831370	89832103	5733	-0.6482	3.04715	0.002796	0.008459	0.049795	-1	125	162	169	210	167	104	109	172	231	143
ENSMUSG00000005802	chr2	Slc30a4	1.23E+08	1.23E+08	5482	-0.50533	4.828425	0.002799	0.008466	0.032249	-1	426	502	640	531	702	378	567	698	628	479
ENSMUSG00000021171	chr12	Esyt2	1.16E+08	1.16E+08	5539	-0.50143	5.29222	0.002802	0.008474	0.032278	-1	742	575	833	762	933	502	803	924	916	672
ENSMUSG00000019996	chr10	Map7	20148471	20149080	4351	-0.82764	1.520206	0.00281	0.008497	0.07163	-1	48	57	67	65	62	25	43	75	46	48
ENSMUSG00000064030	chr10	Wibg	1.29E+08	1.29E+08	1285	0.537052	3.390149	0.002813	0.008503	0.033295	1	119	108	193	128	166	233	274	310	302	309
ENSMUSG00000042647	chr5	Acad12	1.22E+08	1.22E+08	5007	-0.5133	3.869518	0.002816	0.00851	0.031501	-1	266	242	325	291	302	239	235	322	288	305
ENSMUSG00000029110	chr5	Rnf4	34336289	34336541	7287	0.506502	5.062368	0.002818	0.008514	0.032624	1	384	393	460	460	617	535	908	1072	1195	936
ENSMUSG00000026627	chr1	Tmem206	1.91E+08	1.91E+08	2246	0.91034	1.892507	0.002819	0.008517	0.093591	1	28	41	37	29	76	57	134	68	168	135
ENSMUSG00000049124	chr17	Gm8186	26098872	26099257	386	0.778894	2.022018	0.002821	0.008521	0.065275	1	40	47	69	46	39	72	132	83	171	135
ENSMUSG00000102440	chr18	PCDHGA9	37736936	37739543	5586	0.587481	5.82724	0.002842	0.008582	0.045226	1	699	431	809	659	1282	1208	1826	1404	2017	1549
ENSMUSG00000026134	chr1	Prim2	33453810	33454304	5938	0.873265	1.397473	0.002844	0.008586	0.078596	1	25	16	40	24	46	52	80	52	130	74
ENSMUSG00000019791	chr10	Hint3	30608141	30608423	990	-0.54322	4.242906	0.002848	0.008596	0.036605	-1	324	348	478	355	359	311	307	442	339	373
ENSMUSG00000035206	chr10	Sppl2b	80855275	80855388	2866	-0.46972	4.288107	0.002848	0.008596	0.0269	-1	279	317	422	406	485	281	415	344	487	396
ENSMUSG00000023036	chr18	Pcdhgc4	37815079	37817983	5596	0.586672	5.828426	0.002853	0.008607	0.045136	1	702	433	813	654	1282	1208	1823	1406	2018	1554
ENSMUSG00000006154	chr7	Eps8l1	4460674	4461024	4953	-1.08491	0.633199	0.002855	0.008611	0.113968	-1	28	22	22	57	40	29	24	15	20	20
ENSMUSG00000038384	chr5	Setd1b	1.23E+08	1.23E+08	10874	-0.71807	3.581308	0.002855	0.008611	0.06453	-1	186	183	258	246	390	81	209	315	265	208
ENSMUSG00000001627	chr12	Ifrd1	40201567	40203451	5858	0.61668	5.26412	0.002856	0.008612	0.049376	1	455	465	584	447	574	930	1014	1618	1022	757
ENSMUSG00000027206	chr2	Cops2	1.26E+08	1.26E+08	3549	-0.5831	6.363807	0.002859	0.008619	0.044863	-1	1393	1507	1997	1538	1825	1036	1482	2326	1604	1257
ENSMUSG00000003581	chr11	Rnf215	4135202	4135563	2232	0.589728	2.721516	0.002867	0.00864	0.03747	1	76	78	97	82	99	130	174	205	199	203
ENSMUSG00000034659	chr19	Tmem109	10870660	10872149	3798	-0.59909	8.421324	0.002867	0.00864	0.047871	-1	6093	5632	8089	6540	8358	6641	6946	3612	8009	6330
ENSMUSG00000033902	chr2	Mapkbp1	1.2E+08	1.2E+08	7584	-0.55368	3.508621	0.002871	0.008648	0.036456	-1	195	183	278	188	292	120	210	236	264	258
ENSMUSG00000033318	chr10	Gstt2	75831845	75832094	1370	1.012304	1.909615	0.002874	0.008656	0.118857	1	33	27	52	48	42	54	65	215	101	134
ENSMUSG00000022389	chr15	Tef	81802421	81802886	7865	-0.69983	8.038894	0.00288	0.00867	0.065177	-1	5824	4803	6410	4400	5529	3374	3603	8058	4295	3909
ENSMUSG00000037621	chr6	Atoh8	72206177	72207155	2355	0.786208	2.438264	0.002879	0.00867	0.071814	1	54	42	61	95	74	109	137	238	181	120
ENSMUSG00000001175	chr12	Calm1	1E+08	1E+08	4698	-0.64153	8.966311	0.002881	0.00867	0.054946	-1	8945	8369	11742	9939	12200	9077	9497	4443	11458	10902
ENSMUSG00000034023	chr6	Fancd2	1.14E+08	1.14E+08	7937	1.153824	0.442011	0.002881	0.008671	0.131543	1	5	7	22	7	25	22	42	23	62	54
ENSMUSG00000034990	chr7	Otoa	1.21E+08	1.21E+08	4284	1.496463	-0.0949	0.00289	0.008691	0.218072	1	6	3	4	6	17	19	57	6	28	30
ENSMUSG00000046572	chr5	Zfp518b	38668484	38674853	6882	-0.64651	2.424068	0.002889	0.008691	0.045822	-1	98	72	123	100	155	70	114	93	123	86
ENSMUSG00000052299	chr16	Ltn1	87376651	87379007	7737	-0.52147	5.065065	0.00289	0.008691	0.034967	-1	599	489	736	620	880	430	629	850	738	577
ENSMUSG00000103897	chr18	PCDHGB6	37725706	37728316	4730	0.58592	5.829343	0.002895	0.008705	0.045158	1	704	434	806	657	1286	1206	1823	1410	2018	1556
ENSMUSG00000037306	chr4	Man1c1	1.35E+08	1.35E+08	5722	0.546931	4.139801	0.0029	0.008718	0.037075	1	243	156	267	208	327	321	613	428	624	475
ENSMUSG00000041117	chr7	Ccdc8	16992708	16997516	4809	0.755114	3.299521	0.002903	0.008725	0.07077	1	122	60	117	95	226	214	382	208	380	256
ENSMUSG00000031930	chr8	Wwp2	1.07E+08	1.07E+08	4280	0.497598	4.259682	0.002908	0.008737	0.030541	1	218	192	291	262	376	345	475	533	688	600
ENSMUSG00000051373	chr2	Ppapdc3	32095528	32096262	2078	-0.54861	6.952075	0.00291	0.008741	0.040006	-1	2102	2090	2853	2514	2757	2435	2540	1680	2494	2396
ENSMUSG00000038002	chr17	Cramp1l	24961228	24964946	7517	-0.54168	3.559911	0.002917	0.00876	0.035209	-1	205	191	274	218	280	129	196	278	281	248
ENSMUSG00000006235	chr9	Epor	21958899	21959670	1829	1.064548	0.152679	0.002919	0.008764	0.09454	1	6	9	11	11	17	23	18	40	29	46
ENSMUSG00000022565	chr15	Plec	76170974	76178385	18113	-0.49747	9.167261	0.002924	0.008778	0.03326	-1	9898	9472	12563	13118	10994	8923	11948	11674	13966	9337
ENSMUSG00000054517	chr11	Trim65	1.16E+08	1.16E+08	5883	-0.54742	2.992709	0.002929	0.008792	0.033308	-1	124	131	190	167	175	121	153	135	187	155

ENSMUSG00000036529	chr15	Sbf1	89288236	89288725	6826	-0.46639	5.689977	0.002931	0.008795	0.028333	-1	814	760	1026	1128	1322	739	1012	1017	1270	1059
ENSMUSG00000031216	chrX	Stard8	99003248	99003511	5499	-0.49149	5.081465	0.002933	0.008797	0.031044	-1	546	452	771	715	865	435	753	620	840	676
ENSMUSG00000084957	chr19	Bbip1	53929677	53931502	2488	-0.52019	4.706353	0.002933	0.008797	0.034378	-1	436	536	580	469	524	483	547	435	560	447
ENSMUSG00000044224	chr15	Dnajc21	10446756	10447226	4777	-0.55779	5.305086	0.002935	0.008802	0.040536	-1	667	699	911	811	839	539	764	1064	672	668
ENSMUSG00000028757	chr4	Ddost	1.38E+08	1.38E+08	2120	0.579012	6.057018	0.002936	0.008802	0.044326	1	771	650	976	749	1391	1541	1970	1211	2568	2086
ENSMUSG00000023104	chr5	Rfc2	1.35E+08	1.35E+08	1518	0.577493	3.756697	0.002936	0.008802	0.040768	1	153	150	182	190	227	325	363	230	506	459
ENSMUSG00000050323	chr4	Ndufaf6	11051045	11051225	1235	-0.58088	3.982831	0.002939	0.008806	0.041975	-1	283	329	370	325	246	294	265	260	320	315
ENSMUSG00000062175	chr2	Tgif2	1.57E+08	1.57E+08	3832	0.894531	1.042187	0.002939	0.008806	0.078212	1	14	17	18	24	42	38	65	44	86	66
ENSMUSG00000102428	chr18	PCDHGA12	37765580	37768540	6664	0.583145	5.834627	0.00294	0.008809	0.044876	1	702	437	817	666	1284	1208	1833	1408	2024	1564
ENSMUSG00000028453	chr4	Fancg	43002343	43003092	3795	0.858926	1.524031	0.00295	0.008834	0.076957	1	29	27	31	38	38	68	99	40	111	99
ENSMUSG00000024515	chr18	Smad4	73639009	73640469	3712	-0.62422	5.208632	0.00295	0.008835	0.051038	-1	686	588	821	759	903	380	612	1107	779	553
ENSMUSG00000032293	chr9	Ireb2	54863755	54863896	5808	-0.49986	5.587268	0.002952	0.008836	0.032648	-1	804	788	1137	886	1113	642	930	1215	1078	805
ENSMUSG00000041695	chr11	Kcnj2	1.11E+08	1.11E+08	5444	-0.66877	5.565027	0.002954	0.008842	0.058983	-1	872	875	887	1136	1046	598	680	1441	937	610
ENSMUSG00000024525	chr18	Impa2	67289253	67289506	1661	0.691652	2.816373	0.002955	0.008843	0.055321	1	59	98	109	107	65	134	203	189	275	212
ENSMUSG00000028041	chr3	Adam15	89338542	89338866	6145	0.599269	5.407157	0.002956	0.008844	0.047032	1	431	494	571	645	683	848	1017	755	1930	1547
ENSMUSG00000026159	chr1	Agfg1	82839483	82839889	8384	-0.45309	5.139082	0.002958	0.008847	0.026314	-1	644	554	728	676	796	520	712	636	924	709
ENSMUSG00000036992	chr2	Nxt1	1.49E+08	1.49E+08	1116	0.647724	2.274187	0.002962	0.008858	0.044822	1	43	61	75	60	69	102	117	134	160	162
ENSMUSG00000057378	chr2	Ryr3	1.13E+08	1.13E+08	17682	0.86965	1.092106	0.002965	0.008863	0.073122	1	14	14	28	30	35	49	75	56	53	68
ENSMUSG00000099703	chr18	Gm28285	35553404	35553469	1264	-0.68188	4.112001	0.002967	0.00887	0.059554	-1	343	281	397	337	419	161	313	528	332	227
ENSMUSG00000055762	chr15	Eef1d	75894796	75895591	5897	0.481373	6.947999	0.002984	0.008918	0.030938	1	1314	1564	1921	1748	2109	2970	3251	3007	3836	3643
ENSMUSG00000013584	chr9	Aldh1a2	71215789	71215963	2264	1.583447	1.577918	0.002992	0.008939	0.295815	1	12	39	12	23	30	92	59	10	176	169
ENSMUSG00000037826	chr6	Ppm1k	57506502	57510849	5560	-0.60613	3.774514	0.002992	0.008939	0.04572	-1	192	261	268	346	307	176	228	368	262	227
ENSMUSG00000048814	chr1	Lonrf2	38793645	38798223	7506	-0.91694	0.821429	0.002998	0.008955	0.079515	-1	28	29	35	30	67	23	38	22	33	21
ENSMUSG00000031242	chrX	2610002M06Rik	1.08E+08	1.08E+08	6337	-0.5565	2.947993	0.002999	0.008956	0.034991	-1	155	117	159	145	185	114	147	140	177	147
ENSMUSG00000041445	chr14	Mmrn2	34375504	34375778	3935	-0.5672	4.32604	0.003004	0.008968	0.041002	-1	282	378	394	560	370	259	330	393	499	424
ENSMUSG00000103144	chr18	Pcdhga1	37661793	37665039	5366	0.581682	5.83628	0.003017	0.009006	0.044894	1	701	438	811	673	1290	1215	1834	1416	2021	1554
ENSMUSG00000017686	chr11	Rhot1	80209019	80209323	7077	-0.46707	5.496461	0.00302	0.009012	0.028462	-1	753	808	1064	841	897	682	904	977	1032	832
ENSMUSG00000049295	chr14	Zfp219	52006077	52007147	3262	0.534424	3.917853	0.003041	0.009072	0.035099	1	183	167	215	198	266	283	363	571	460	403
ENSMUSG00000038235	chr1	F11r	1.71E+08	1.71E+08	2663	0.574609	4.116872	0.003055	0.009111	0.041402	1	180	228	257	296	184	378	389	463	652	545
ENSMUSG00000031176	chrX	Dynlt3	9654267	9656063	2576	-0.46951	5.659617	0.003055	0.009112	0.028966	-1	911	927	1168	833	1039	796	1023	1008	1159	960
ENSMUSG00000032363	chr9	Adamts7	90163069	90163314	6282	0.794415	2.306303	0.003061	0.009125	0.073861	1	42	46	65	59	87	65	232	134	166	131
ENSMUSG00000053931	chr3	Cnn3	1.21E+08	1.21E+08	2003	0.629452	5.979256	0.003073	0.009159	0.052879	1	728	580	910	829	1140	1252	2908	1379	2111	1356
ENSMUSG00000021993	chr14	Mipep	60784566	60784870	2403	-0.50064	5.465679	0.00308	0.009178	0.032905	-1	777	801	984	905	822	821	771	852	953	823
ENSMUSG00000026781	chr2	Acbd5	23068168	23068286	4154	-0.56529	4.764794	0.00308	0.009178	0.041627	-1	471	527	593	499	606	281	468	738	602	501
ENSMUSG00000022568	chr15	Scrib	76047158	76047537	5736	0.615808	4.962239	0.003082	0.009181	0.049712	1	322	350	461	410	524	534	1464	670	930	835
ENSMUSG00000021900	chr14	Btd	31641028	31641135	2353	0.566725	3.587979	0.003085	0.009189	0.039106	1	162	109	159	147	232	244	335	263	411	421
ENSMUSG00000050270	chr11	Tmem220	67025154	67025271	1669	0.844202	0.792648	0.003091	0.009205	0.06029	1	21	14	22	18	21	36	52	41	52	61
ENSMUSG00000042772	chr1	Smg7	1.53E+08	1.53E+08	6341	-0.45375	5.553296	0.003092	0.009205	0.026943	-1	741	701	1087	871	1188	732	959	923	1080	934
ENSMUSG00000029649	chr5	Pomp	1.48E+08	1.48E+08	734	0.545958	6.572748	0.003109	0.009255	0.040049	1	1065	1282	1735	1124	1238	2563	2613	2484	2581	2723
ENSMUSG00000032405	chr9	Pias1	62880077	62882261	3855	-0.52904	3.767721	0.003112	0.009259	0.034271	-1	226	205	267	299	351	179	273	332	280	235
ENSMUSG00000003420	chr7	Fcgrt	45092993	45093355	1738	0.502059	6.24673	0.00312	0.009284	0.033734	1	879	747	1113	1066	1523	1518	1881	2024	2586	2457
ENSMUSG00000103332	chr18	Pcdhga2	37668953	37671525	4689	0.581684	5.832547	0.003123	0.00929	0.045222	1	700	434	813	668	1289	1207	1829	1411	2023	1552
ENSMUSG00000091736	chrX	Yy2	1.58E+08	1.58E+08	2867	-0.84474	1.009919	0.003124	0.009292	0.070117	-1	29	28	54	41	61	18	29	34	55	30
ENSMUSG00000036249	chr2	Rbm43	51924448	51925934	2633	0.73371	1.902126	0.003125	0.009292	0.057336	1	41	38	44	40	65	99	116	72	126	112
ENSMUSG00000057842	chr13	Zfp595	67312998	67314909	5430	-0.85946	0.679087	0.003129	0.009299	0.064957	-1	35	28	41	22	39	15	29	27	31	26
ENSMUSG00000058624	chr19	Gda	21391307	21395258	6135	0.810824	3.966098	0.003129	0.009299	0.085262	1	122	165	222	215	226	231	310	273	765	816
ENSMUSG00000047875	chr4	Gpr157	1.5E+08	1.5E+08	4900	-0.54408	5.947801	0.003138	0.009322	0.039523	-1	836	1210	1330	1432	1307	1167	1155	964	1268	1226
ENSMUSG00000018362	chr11	Kpna2	1.07E+08	1.07E+08	2873	0.498429	4.549481	0.003143	0.009338	0.031603	1	281	303	356	269	409	543	620	492	884	667
ENSMUSG00000019790	chr10	Stxbp5	9755547	9760954	12871	-0.5371	3.586491	0.003147	0.009346	0.035115	-1	221	172	269	228	301	152	185	285	290	238
ENSMUSG00000056209	chr19	Npm3	45747734	45748051	1187	0.617409	3.806624	0.003148	0.009347	0.048229	1	135	166	246	123	260	365	429	259	468	432
ENSMUSG00000020330	chr11	Hmmr	40701395	40702858	5431	1.164468	1.115052	0.003159	0.009379	0.149975	1	17	18	20	12	39	45	62	21	137	75
ENSMUSG00000049090	chr18	Zadh2	84088158	84088373	3321	-0.49169	5.596769	0.00316	0.009379	0.032062	-1	877	877	945	977	1009	704	782	912	1128	1191
ENSMUSG00000021250	chr12	Fos	85473890	85474180	2352	1.221426	3.776942	0.003163	0.009386	0.193666	1	45	104	119	267	156	222	1106	273	344	287
ENSMUSG00000060510	chr9	Zfp266	20495068	20500477	6283	-0.54392	3.969728	0.003191	0.009465	0.037211	-1	284	253	333	274	412	193	338	394	326	239
ENSMUSG00000102543	chr18	PCDHGC5	37819513	37822134	7627	0.583321	5.83221	0.003191	0.009465	0.045688	1	703	433	816	657	1292	1209	1832	1409	2022	1551
ENSMUSG00000020280	chr11	Pus10	23665674	23665748	4325	-0.50583	3.370355	0.003193	0.009467	0.030215	-1	189	182	232	186	215	134	208	197	247	215
ENSMUSG00000030346	chr6	Rad51ap1	1.27E+08	1.27E+08	3969	0.911415	0.961029	0.003193	0.009467	0.07958	1	13	24	19	26	23	36	58	35	83	71
ENSMUSG00000067424	chr17	Zfp563	33089310	33089479	2198	-0.94042	0.588393	0.003197	0.009478	0.078957	-1	29	23	38	34	34	23	25	31	23	11
ENSMUSG00000026199	chr1	Ankzf1	75192151	75194284	5142	0.751105	2.754747	0.003202	0.00949	0.068113	1	78	57	86	88	106	104	191	311	172	196
ENSMUSG00000069379	chr18	Gm4950	51865264	51865881	618	0.927871	0.495018	0.003215	0.009527	0.071777	1	13	13	21	14	13	41	32	42	35	44
ENSMUSG00000043683	chr17	Fem1a	56256793	56263608	6816	-0.53187	8.428871	0.003225	0.009551	0.038712	-1	5642	6359	8141	6830	7022	5598	5423	8649	7166	5836
ENSMUSG00000064342	chrMT	mt-Ti	3706	3774	69	-0.68639	5.481855	0.003225	0.009551	0.063327	-1	845	1039	738	1223	615	598	617	792	1248	810
ENSMUSG00000018500	chr11	Adora2b	62248984	62249436	1845	1.025872	0.607082	0.003227	0.009555	0.10177	1	11	9	26	12	20	19	44	30	74	59
ENSMUSG00000013622	chr5	Atraid	31048312	31048432	2092	0.47623	5.600083	0.003228	0.009556	0.030076	1	604	611	825	603	739	1070	1310	1507	1352	1299
ENSMUSG00000045098	chr19	Suv420h1	3767421	3767730	14116	-0.53764	4.462981	0.003228	0.009556	0.03743	-1	393	359	503	418	510	239	423	587	481	389
ENSMUSG00000015889	chr10	Lta4h	93453396	93453668	2066	0.451017	4.75928	0.003232	0.009562	0.026006	1	316	330	434	376	457	595	736	632	919	769

ENSMUSG00000054589	chr18	Gm9949	62180126	62180603	962	-1.11625	0.142753	0.003231	0.009562	0.117079	-1	22	30	19	19	27	12	5	24	25	11
ENSMUSG00000031143	chrX	Ccdc22	7593809	7594167	3427	0.498481	4.226113	0.003239	0.009579	0.031125	1	252	233	293	222	283	407	481	406	659	606
ENSMUSG00000061778	chrX	Mospd2	1.65E+08	1.65E+08	7914	-0.60078	3.153766	0.003239	0.009579	0.043623	-1	153	139	207	169	230	90	171	222	197	151
ENSMUSG00000025477	chr7	Inpp5a	1.39E+08	1.39E+08	3529	-0.49848	6.180746	0.003241	0.009582	0.033447	-1	1128	1219	1538	1605	1626	1306	1353	1185	1540	1570
ENSMUSG00000018983	chr4	E2f2	1.36E+08	1.36E+08	4882	0.779654	3.354983	0.003243	0.009587	0.077816	1	85	76	139	97	249	220	420	173	404	293
ENSMUSG00000019432	chr17	Ddx39b	35241746	35241852	3783	0.52784	6.245	0.003244	0.009587	0.037623	1	905	830	1091	967	1441	1740	2085	1449	2751	2479
ENSMUSG00000022957	chr16	Itsn1	91729281	91729599	22539	-0.48188	6.057367	0.003247	0.009594	0.031181	-1	1061	995	1408	1347	1746	1040	1458	1109	1462	1416
ENSMUSG00000026421	chr1	Csrp1	1.36E+08	1.36E+08	1956	0.525741	5.390122	0.003256	0.009618	0.036712	1	465	459	552	743	651	814	1275	909	1709	1163
ENSMUSG00000083307	chrX	AA414768	12936872	12938128	1257	1.23209	0.724601	0.003262	0.009636	0.164912	1	17	9	25	3	23	41	75	20	68	47
ENSMUSG00000044501	chr17	Zfp758	22361453	22361707	2974	-0.77722	2.472057	0.003271	0.00966	0.072051	-1	88	103	140	107	146	62	85	163	98	64
ENSMUSG00000017493	chr11	Igfbp4	99041244	99041845	4416	0.636168	6.621976	0.003273	0.009662	0.055082	1	1111	783	1263	1190	2261	2153	3334	1798	3556	3258
ENSMUSG00000038722	chr5	Bud31	1.45E+08	1.45E+08	1609	0.511461	5.318992	0.003274	0.009663	0.03468	1	458	571	672	444	589	1000	1090	994	1133	1190
ENSMUSG00000021546	chr13	Hnrnpk	58391142	58392476	5634	0.454073	7.424361	0.003276	0.009669	0.028169	1	2006	2069	2765	2257	3107	3519	4686	4771	5688	4634
ENSMUSG00000033066	chr11	Gas7	67455437	67455774	11342	0.862924	4.571903	0.003278	0.00967	0.099373	1	200	121	244	281	624	468	768	393	1059	959
ENSMUSG00000039463	chr2	Slc9a8	1.67E+08	1.67E+08	9095	-0.46277	5.056544	0.003278	0.00967	0.02796	-1	531	550	708	635	813	523	605	754	745	631
ENSMUSG00000014856	chr8	Tmem208	1.05E+08	1.05E+08	1511	0.548749	4.31374	0.003283	0.009682	0.038718	1	224	251	320	240	309	492	602	339	682	626
ENSMUSG00000015305	chr10	Sash1	8722219	8725760	7183	-0.56003	5.009986	0.003284	0.009682	0.04157	-1	500	378	735	653	1026	378	604	696	714	678
ENSMUSG00000020910	chr11	Adprm	67037905	67038445	1977	0.762203	2.65135	0.003288	0.009693	0.070029	1	78	61	90	74	77	125	141	305	171	159
ENSMUSG00000024767	chr19	Otub1	7198202	7199239	2545	0.455296	5.162832	0.003289	0.009693	0.027123	1	398	452	572	533	569	789	883	892	1223	1053
ENSMUSG00000040026	chr7	Saa3	46711998	46712264	531	2.100031	0.35596	0.003296	0.009713	0.49666	1	2	1	1	21	11	17	34	4	75	93
ENSMUSG00000019916	chr10	P4ha1	59323296	59323476	4114	-0.64991	5.873371	0.003311	0.009753	0.057207	-1	1265	775	1489	897	1622	959	1403	626	1209	1103
ENSMUSG00000022982	chr16	Sod1	90220742	90220929	646	0.585186	7.224112	0.003324	0.009789	0.046909	1	1522	1883	2464	1942	2213	3032	3181	6034	3979	4626
ENSMUSG00000030557	chr7	Mef2a	67231163	67235228	6283	-0.54561	6.704994	0.003329	0.009802	0.040673	-1	1813	1840	2187	2036	2473	1225	2249	2703	2213	1592
ENSMUSG00000102222	chr18	Pcdhga10	37746993	37749605	4732	0.576104	5.835672	0.003331	0.009806	0.044964	1	700	447	811	660	1303	1206	1835	1412	2021	1553
ENSMUSG00000015961	chr1	Adss	1.78E+08	1.78E+08	4531	0.517587	3.761826	0.00334	0.00983	0.032832	1	165	160	194	175	233	214	347	378	543	411
ENSMUSG00000078877	chr2	Gm14295	1.77E+08	1.77E+08	3527	-0.87493	1.81247	0.00334	0.00983	0.08835	-1	58	42	106	46	134	43	55	70	74	43
ENSMUSG00000070423	chr7	Olfr558	1.03E+08	1.03E+08	2915	-0.65707	2.476889	0.003341	0.00983	0.049489	-1	95	79	110	136	147	89	117	74	118	99
ENSMUSG00000033020	chr15	Polr2f	79141351	79141434	543	0.560381	4.401544	0.003343	0.009833	0.040768	1	224	304	286	292	303	628	573	434	656	586
ENSMUSG00000030610	chr7	Det1	78822962	78823260	2877	-0.49785	3.5047	0.00335	0.009852	0.029706	-1	213	172	267	223	228	175	220	216	263	220
ENSMUSG00000020888	chr11	Dvl2	70000595	70001026	6298	0.739593	2.847283	0.003354	0.009862	0.066777	1	74	70	78	107	115	99	179	183	395	222
ENSMUSG00000022386	chr15	Trmu	85879312	85879458	3974	0.537426	3.295577	0.003357	0.00987	0.033897	1	120	139	145	126	124	191	281	270	342	269
ENSMUSG00000074577	chr2	Fam65c	1.68E+08	1.68E+08	4244	1.186122	0.903439	0.003366	0.009892	0.155663	1	21	4	19	10	37	31	75	78	67	34
ENSMUSG00000031959	chr8	Wdr59	1.11E+08	1.11E+08	5222	-0.45759	3.890754	0.003377	0.009922	0.025605	-1	225	264	309	296	337	213	296	300	358	295
ENSMUSG00000023940	chr17	Sgol1	53674786	53676711	3810	1.083796	0.15493	0.003381	0.00993	0.099131	1	13	8	10	4	18	23	35	20	53	29
ENSMUSG00000025130	chr11	P4hb	1.21E+08	1.21E+08	2861	0.504633	8.180333	0.003381	0.00993	0.035189	1	3205	3201	4383	3519	6076	6413	8115	6441	10137	8830
ENSMUSG00000025950	chr1	Idh1	65158616	65159555	2771	0.579367	5.704951	0.003381	0.00993	0.045499	1	569	519	663	690	1107	946	1089	1547	1739	2045
ENSMUSG00000060373	chr14	Hnrnpc	52073380	52075160	2869	0.516386	6.408501	0.003384	0.009935	0.03639	1	930	1052	1418	1072	1399	2038	2620	1618	2930	2465
ENSMUSG00000026163	chr1	Sphkap	83254139	83257270	9602	-1.07116	0.080958	0.003386	0.009939	0.101399	-1	24	14	26	14	35	15	16	5	21	17
ENSMUSG00000039298	chr4	Cdk5rap2	70216856	70223114	13012	-0.54719	3.189217	0.003391	0.009951	0.035977	-1	166	154	203	162	215	109	212	152	235	165
ENSMUSG00000044367	chr11	Slc16a13	70216789	70217921	2601	0.991444	0.536591	0.003392	0.009953	0.084897	1	10	22	9	15	17	34	33	33	61	47
ENSMUSG00000020908	chr11	Myh3	67078300	67078324	6057	2.270475	8.324233	0.003395	0.00996	0.63759	1	2583	66	53	4069	2343	5339	26394	5150	15789	11219
ENSMUSG00000020866	chr11	Cacna1g	94408391	94409876	10137	-1.00497	3.218296	0.003405	0.009986	0.132021	-1	231	59	236	122	425	110	218	101	178	115
ENSMUSG00000028370	chr4	Pappa	65124174	65124947	11027	-1.30501	0.503311	0.003406	0.009986	0.192009	-1	46	16	32	19	49	5	15	43	17	12
ENSMUSG00000053453	chr14	Thoc7	13949014	13949327	883	-0.521	5.949975	0.003407	0.009986	0.036861	-1	1053	1243	1520	1046	1182	1073	1188	1271	1211	1113
ENSMUSG00000078963	chr18	Hsbp1l1	80229758	80230561	1251	-0.87318	1.761031	0.003407	0.009986	0.086734	-1	51	83	85	73	65	68	67	45	47	39
ENSMUSG00000062203	chr16	Gspt1	11219292	11220879	4297	-0.46376	6.165011	0.003408	0.009988	0.029216	-1	1136	1123	1594	1409	1747	1044	1377	1587	1729	1341
ENSMUSG00000038683	chr13	Pak1ip1	41001023	41001413	4049	0.456374	5.183628	0.003412	0.009996	0.02749	1	429	465	569	505	587	752	888	1109	1109	1041
ENSMUSG00000061536	chr9	Sec22c	1.22E+08	1.22E+08	6301	-0.49397	3.567517	0.003426	0.010034	0.029621	-1	194	192	287	241	241	165	258	200	283	246
ENSMUSG00000028066	chr3	Pmf1	88394143	88394570	1351	0.525517	3.712454	0.003427	0.010036	0.034355	1	135	164	192	177	227	362	337	289	429	356
ENSMUSG00000103677	chr18	Pcdhga4	37685210	37687817	4727	0.578504	5.833304	0.003429	0.010041	0.045628	1	711	434	817	657	1291	1207	1831	1413	2017	1550
ENSMUSG00000056174	chr4	Col8a2	1.26E+08	1.26E+08	4489	-1.18942	3.767198	0.003431	0.010042	0.187398	-1	457	107	358	162	517	133	406	167	193	68
ENSMUSG00000033047	chr15	Eif3l	79075223	79075292	1893	0.479835	5.989651	0.003438	0.010063	0.031261	1	661	780	906	944	1174	1277	1524	1899	2140	1845
ENSMUSG00000040857	chr7	Erf	25242561	25245531	3607	0.582617	3.370059	0.003444	0.010074	0.041622	1	113	123	116	133	203	173	271	314	434	272
ENSMUSG00000104063	chr18	Pcdhgb7	37751600	37754193	4713	0.576036	5.834773	0.003443	0.010074	0.045275	1	708	438	816	662	1294	1206	1828	1411	2022	1555
ENSMUSG00000024866	chr19	Acy3	3986661	3987305	1505	0.77883	2.092766	0.003445	0.010075	0.069907	1	34	47	53	59	63	77	83	109	164	188
ENSMUSG00000006019	chr7	Dhx34	16197147	16197422	4596	0.646787	2.706441	0.003447	0.010077	0.049127	1	87	56	89	80	107	121	188	142	232	242
ENSMUSG00000036775	chr17	Decr2	26081211	26082261	2288	0.669564	2.695968	0.003446	0.010077	0.053488	1	69	60	117	72	97	145	222	115	242	195
ENSMUSG00000026596	chr1	Abl2	1.57E+08	1.57E+08	10800	-0.44441	4.680451	0.003448	0.010078	0.025492	-1	411	402	537	512	618	396	493	530	578	535
ENSMUSG00000035476	chrX	Tab3	85574022	85574165	6639	-0.63201	2.728656	0.003452	0.010088	0.047957	-1	128	124	151	114	147	60	136	134	142	139
ENSMUSG00000078695	chr11	Cisd3	97685826	97685864	833	0.503161	5.42223	0.003454	0.010088	0.034048	1	427	578	643	648	664	1128	1044	977	1436	1233
ENSMUSG00000098597	chr5	Mir6418	1.38E+08	1.38E+08	115	0.475491	4.130016	0.003453	0.010088	0.028431	1	202	187	260	263	315	313	481	445	613	544
ENSMUSG00000026072	chr1	Il1r1	40225080	40225306	6363	0.617223	3.569573	0.00346	0.010106	0.048159	1	144	136	187	106	207	213	279	291	592	338
ENSMUSG00000046667	chr4	Rbm12b1	12140264	12140605	3122	0.777895	1.219387	0.003461	0.010107	0.059254	1	21	21	27	29	39	62	51	72	73	65
ENSMUSG00000030452	chr7	Nipa2	55931287	55933547	5386	-0.444	4.991107	0.003469	0.010128	0.025946	-1	537	551	721	587	658	473	629	619	760	675
ENSMUSG00000071855	chr18	Ccdc112	46282151	46283286	2801	1.065791	-0.16242	0.003472	0.010135	0.078452	1	7	7	8	5	15	18	33	24	30	18
ENSMUSG00000028098	chr3	Rnf115	96727611	96727910	2265	-0.54672	6.345724	0.003474	0.010136	0.041042	-1	1277	1453	2055	1694	1593	1260	1462	2039	1758	1168

ENSMUSG00000063531	chr5	Sema3e	14025276	14026024	7581	-1.29372	0.43598	0.003475	0.010139	0.184926	-1	30	8	31	16	74	8	21	17	32	11
ENSMUSG00000083716	chr2	Gm13436	36807826	36808392	567	0.674621	2.586217	0.003488	0.010172	0.053042	1	60	82	63	94	75	121	143	153	245	195
ENSMUSG00000103472	chr18	Pcdhga7	37714764	37717374	5217	0.577626	5.839693	0.00349	0.010178	0.045666	1	714	436	822	660	1297	1212	1836	1419	2027	1558
ENSMUSG00000031591	chr8	Asah1	41340197	41341685	3390	0.510568	5.05879	0.003498	0.0102	0.034814	1	441	328	516	401	627	581	1121	799	1177	952
ENSMUSG00000036769	chrX	Wdr44	23693051	23693539	8353	-0.61748	3.866111	0.003501	0.010206	0.049633	-1	247	272	339	290	320	162	279	422	291	192
ENSMUSG00000061838	chr6	Suclg2	95474134	95475164	2279	-0.50192	5.849899	0.003505	0.010213	0.034325	-1	870	1087	1308	1270	1089	934	1035	1254	1171	1140
ENSMUSG00000019979	chr10	Apaf1	90989311	90991596	9028	0.583445	3.099031	0.003509	0.010223	0.040678	1	108	82	131	111	136	173	264	171	340	253
ENSMUSG00000103793	chr18	Pcdhga6	37707039	37709652	4733	0.574882	5.8399	0.003511	0.010227	0.045285	1	713	440	818	665	1297	1215	1839	1418	2021	1552
ENSMUSG00000031974	chr8	Abcb10	1.24E+08	1.24E+08	4306	-0.45643	4.764755	0.00352	0.010252	0.027257	-1	474	478	579	525	554	456	560	527	602	514
ENSMUSG00000034040	chr5	Wbscr17	1.31E+08	1.31E+08	8989	0.500453	4.056355	0.003523	0.010258	0.031662	1	233	188	235	217	267	392	474	356	625	424
ENSMUSG00000049349	chr3	Gm5105	1.38E+08	1.38E+08	1665	-0.89146	0.852074	0.003523	0.010258	0.075761	-1	37	30	36	35	51	34	33	18	27	27
ENSMUSG00000031781	chr8	Ciapin1	94819818	94823207	5691	0.489413	5.222115	0.003539	0.0103	0.032056	1	413	554	554	519	527	871	1009	861	1288	1053
ENSMUSG00000031075	chr7	Ano1	1.45E+08	1.45E+08	5206	-0.6579	2.382813	0.003551	0.010334	0.050469	-1	102	68	113	105	144	54	96	83	134	109
ENSMUSG00000027778	chr3	Ift80	68892499	68894181	12428	-0.76401	2.239576	0.003554	0.010341	0.070106	-1	118	69	98	79	125	49	125	64	89	80
ENSMUSG00000031197	chrX	Vbp1	75514299	75514428	2132	-0.53501	5.220712	0.003561	0.010357	0.038748	-1	666	742	904	596	751	546	832	846	750	567
ENSMUSG00000037852	chr8	Cpe	64592558	64593221	2087	-0.57801	7.898834	0.003563	0.010363	0.046579	-1	3940	4343	5770	4910	4910	5168	3968	3512	4331	4762
ENSMUSG00000060862	chr4	Zbtb40	1.37E+08	1.37E+08	10710	-0.57174	3.312047	0.003573	0.010389	0.040075	-1	130	178	203	205	282	169	193	150	195	212
ENSMUSG00000026181	chr16	Ppm1f	16896469	16896624	4922	-0.5004	4.635019	0.003578	0.010402	0.033158	-1	373	440	560	536	522	357	557	358	696	464
ENSMUSG00000041120	chr4	Nbl1	1.39E+08	1.39E+08	2033	0.62347	5.437665	0.003587	0.010425	0.053261	1	569	302	578	552	897	750	1527	1510	1209	1156
ENSMUSG00000097080	chr18	1700086O06Rik	38238405	38239189	1931	0.937198	0.311906	0.003588	0.010426	0.067867	1	8	13	16	16	11	27	28	36	38	43
ENSMUSG00000025898	chr9	Cwf19l2	3404085	3404190	3953	-0.8408	4.139114	0.003593	0.010438	0.095341	-1	374	322	433	358	387	150	251	627	258	187
ENSMUSG00000024395	chr18	Lims2	31931507	31931550	1688	-0.60579	4.569695	0.003598	0.010451	0.049364	-1	347	426	545	684	373	283	368	508	527	531
ENSMUSG00000068329	chr6	Htra2	83051266	83051634	2764	0.462271	4.449921	0.0036	0.010453	0.027476	1	277	283	327	284	354	428	577	514	774	681
ENSMUSG00000069662	chr10	Marcks	37133375	37136935	4048	0.556813	6.657016	0.003601	0.010456	0.043067	1	1161	974	1423	1223	2170	2453	3169	1938	3561	2912
ENSMUSG00000103037	chr18	Pcdhgb1	37680233	37682839	5776	0.575283	5.833599	0.003603	0.01046	0.045605	1	709	434	820	660	1294	1206	1827	1411	2018	1551
ENSMUSG00000038880	chr17	Mrps34	24895116	24895488	2064	0.481548	5.587934	0.003604	0.01046	0.031524	1	489	684	810	660	703	1141	1262	1376	1421	1285
ENSMUSG00000026484	chr1	Rnf2	1.51E+08	1.51E+08	4127	-0.50239	3.908795	0.00361	0.010473	0.032138	-1	227	275	304	287	379	178	322	352	334	273
ENSMUSG00000003752	chr7	Itpkc	27207172	27208444	3644	0.729124	2.637579	0.003621	0.010502	0.064815	1	68	52	81	91	94	129	147	283	164	160
ENSMUSG00000102742	chr18	PCDHGB6	37755731	37758367	4756	0.576933	5.836301	0.003621	0.010502	0.045919	1	714	434	818	658	1297	1207	1835	1414	2021	1555
ENSMUSG00000104346	chr18	PCDHGB6	37674307	37676907	4720	0.57468	5.837779	0.003622	0.010503	0.045564	1	704	438	822	663	1304	1211	1830	1415	2027	1552
ENSMUSG00000038518	chr13	Jarid2	44729474	44729777	9715	-0.49671	5.129123	0.003626	0.010513	0.033278	-1	516	612	749	639	937	538	737	487	905	745
ENSMUSG00000073468	chr17	Sft2d1	8311102	8311285	3580	0.688173	2.941097	0.003628	0.010517	0.058384	1	94	85	114	79	111	143	239	126	301	300
ENSMUSG00000058594	chr2	Fbxo18	11742573	11742808	5115	-0.45836	5.379856	0.003637	0.010538	0.028399	-1	613	702	890	814	1038	622	927	694	993	877
ENSMUSG00000026171	chr1	Rnf25	74593748	74594402	2181	0.493173	4.06147	0.00364	0.010545	0.031095	1	207	175	271	235	269	361	436	555	447	451
ENSMUSG00000020287	chr11	Mpg	32226505	32226717	3752	0.620256	3.024967	0.003645	0.010558	0.046632	1	95	115	133	65	118	171	219	232	270	247
ENSMUSG00000001604	chr4	Tcea3	1.36E+08	1.36E+08	1400	-0.5035	6.899324	0.003653	0.01058	0.035334	-1	1951	2183	2517	2556	2441	2222	1980	2252	2448	2474
ENSMUSG00000009013	chr5	Dynll1	1.15E+08	1.15E+08	2926	0.671363	5.652281	0.00366	0.010596	0.062229	1	480	672	772	543	778	1363	1962	680	1676	1475
ENSMUSG00000040229	chrX	Gpr34	13632089	13632197	2090	0.938484	1.631387	0.003679	0.010648	0.102111	1	45	19	41	17	49	60	123	114	96	64
ENSMUSG00000103183	chr4	RP23-118E21.11	1.56E+08	1.56E+08	4105	0.906277	1.250221	0.003679	0.010648	0.087422	1	37	12	34	17	31	48	61	79	74	82
ENSMUSG00000028127	chr3	Abcd3	1.22E+08	1.22E+08	3399	-0.4697	5.908702	0.003681	0.01065	0.030377	-1	951	1120	1317	1251	1159	878	1122	1261	1453	1198
ENSMUSG00000027015	chr2	Cybrd1	71117923	71118312	5339	-1.41447	1.998392	0.003715	0.010747	0.257094	-1	127	21	137	44	165	29	87	76	46	13
ENSMUSG00000034059	chr2	Ypel4	84734058	84734293	2614	1.316541	-0.02498	0.003717	0.010752	0.161645	1	12	8	3	7	10	13	24	58	20	28
ENSMUSG00000060149	chr17	BC002059	16951539	16951708	1964	-0.75429	1.36828	0.003726	0.010775	0.059715	-1	55	51	52	48	55	31	36	58	51	43
ENSMUSG00000035529	chr10	Prdm4	85891970	85893439	3917	-0.49164	4.486946	0.003735	0.0108	0.031913	-1	385	364	479	439	523	319	420	568	432	425
ENSMUSG00000103749	chr18	Pcdhgb5	37731009	37733559	6733	0.573773	5.838244	0.003739	0.010809	0.045738	1	705	435	819	669	1306	1208	1829	1417	2024	1558
ENSMUSG00000018923	chr11	Med11	70451919	70452063	1046	0.680778	2.533273	0.003743	0.010816	0.054433	1	75	76	78	64	65	133	176	110	217	184
ENSMUSG00000002017	chr17	Fam98a	75537086	75538861	3479	-0.45595	5.417634	0.003749	0.010832	0.028295	-1	656	787	971	747	978	731	842	778	1048	801
ENSMUSG00000027566	chr2	Psma7	1.8E+08	1.8E+08	3072	0.630365	6.530602	0.003751	0.010835	0.055602	1	1034	1155	1383	1109	1370	1911	2129	4358	2319	2276
ENSMUSG00000071796	chr8	6820431F20Rik	20262613	20262670	5006	-0.95824	0.536857	0.003755	0.010842	0.088756	-1	35	25	38	21	33	14	24	36	18	17
ENSMUSG00000102748	chr18	Pcdhgb2	37689828	37692369	4882	0.570913	5.838312	0.003754	0.010842	0.045316	1	712	438	822	667	1297	1213	1825	1411	2027	1553
ENSMUSG00000054720	chr5	Lrrc8c	1.06E+08	1.06E+08	7654	-0.48902	3.980226	0.003757	0.010846	0.03084	-1	276	234	348	341	339	183	347	323	412	289
ENSMUSG00000048000	chr1	Gigyf2	87326998	87327092	14216	-0.50752	5.193394	0.003774	0.010892	0.035172	-1	661	560	729	697	959	490	678	940	737	682
ENSMUSG00000022855	chr16	Senp2	22009484	22009742	4499	-0.46086	5.105877	0.003775	0.010894	0.028648	-1	555	587	817	596	790	597	716	582	786	684
ENSMUSG00000014769	chr17	Psmb1	15475721	15476205	1036	0.563368	6.960073	0.003778	0.0109	0.044609	1	1476	1632	2023	1540	1676	2887	3000	4784	3123	3314
ENSMUSG00000103585	chr18	Pcdhgb4	37720369	37722917	5812	0.574533	5.836641	0.003782	0.01091	0.045974	1	707	435	814	664	1308	1209	1827	1412	2021	1559
ENSMUSG00000046314	chr12	Stxbp6	44852488	44855877	4855	-0.78568	2.944808	0.003784	0.010913	0.079822	-1	160	83	163	151	268	66	148	196	159	96
ENSMUSG00000030839	chr7	Sergef	46443168	46443535	2368	0.819528	1.898424	0.003791	0.010932	0.077854	1	34	34	54	48	49	92	122	50	171	109
ENSMUSG00000003119	chr11	Cdk12	98203059	98204410	11730	-0.57398	3.527872	0.003794	0.010934	0.042478	-1	215	164	239	253	281	118	216	289	287	186
ENSMUSG00000034687	chr5	Fras1	96373955	96374885	15848	-0.84985	3.447183	0.003794	0.010934	0.096578	-1	292	129	234	154	369	140	309	105	227	129
ENSMUSG00000052253	chr15	Zfp622	25984366	25985183	2803	0.481642	4.487619	0.003795	0.010935	0.030589	1	251	291	370	311	334	516	550	725	662	566
ENSMUSG00000067365	chr5	Tmem128	38260185	38260492	1942	0.547648	3.272042	0.003803	0.010955	0.036755	1	102	131	176	113	125	202	277	278	287	279
ENSMUSG00000026074	chr1	Map4k4	39900913	39901286	9579	0.533477	5.753627	0.00381	0.010974	0.039543	1	513	532	740	864	1102	868	1580	1554	1934	1641
ENSMUSG00000022797	chr16	Tfrc	32608920	32609036	6185	-0.65566	8.610881	0.003813	0.01098	0.060839	-1	5627	9553	8651	8909	6632	7322	7768	4332	9269	6501
ENSMUSG00000034709	chr17	Ppp1r21	88530118	88530318	4255	0.542395	3.282891	0.00382	0.010997	0.036207	1	116	91	158	113	186	181	299	235	341	292
ENSMUSG00000054931	chr13	Zkscan4	21478907	21479509	2400	1.063531	0.028346	0.003821	0.010997	0.095822	1	7	3	17	14	8	23	23	22	39	36
ENSMUSG00000058603	chr1	Rpl28-ps1	1.28E+08	1.28E+08	414	0.658893	2.279105	0.003821	0.010997	0.049321	1	53	54	52	72	75	122	109	131	188	128

ENSMUSG00000018167	chr11	Stard3	98358368	98358508	3557	0.489793	3.937331	0.003825	0.011007	0.030391	1	215	186	244	196	208	293	397	478	479	437
ENSMUSG00000028167	chr3	Bdh2	1.35E+08	1.35E+08	1202	0.94626	0.920956	0.003827	0.011008	0.09273	1	13	11	29	22	28	33	45	87	50	57
ENSMUSG00000036046	chr15	5031439G07Rik	84943936	84949278	9604	-0.56311	7.196486	0.003832	0.011021	0.044787	-1	2149	2961	3772	2997	2700	2704	2372	2125	3194	3297
ENSMUSG00000095123	chr10	Gm21781	4391587	4396424	4838	1.104304	0.824996	0.003835	0.011028	0.131046	1	23	11	17	9	27	21	49	48	52	96
ENSMUSG00000031103	chrX	Elf4	48411046	48415446	6148	0.729811	3.303862	0.003855	0.011083	0.070057	1	103	77	108	102	240	191	337	176	389	352
ENSMUSG00000022940	chr16	Pigp	94358763	94359174	1888	-0.50711	5.685062	0.003857	0.011086	0.035673	-1	1012	925	1149	881	1033	897	980	1144	965	904
ENSMUSG00000028517	chr4	Ppap2b	1.05E+08	1.05E+08	3159	-0.51831	6.489248	0.003859	0.011091	0.037774	-1	1502	1282	1937	1770	2470	1252	1559	2283	2069	1497
ENSMUSG00000021243	chr12	Fcf1	84970897	84970965	1117	0.481607	3.650466	0.003866	0.011104	0.028665	1	145	170	200	156	196	257	340	330	378	391
ENSMUSG00000070923	chr4	Klhl9	88718292	88722465	4174	-0.49095	5.71446	0.003865	0.011104	0.033486	-1	876	943	1075	1004	1224	691	1077	1306	1207	847
ENSMUSG00000021589	chr13	Rhobtb3	75869537	75872461	5684	-0.46611	4.403195	0.003868	0.011106	0.028428	-1	343	319	487	396	520	369	427	433	447	376
ENSMUSG00000022223	chr14	Sdr39u1	55897286	55898012	1226	-0.5072	5.812832	0.003867	0.011106	0.035798	-1	870	1092	1249	1172	1101	1060	959	907	1303	1142
ENSMUSG00000034032	chr2	Rpap1	1.2E+08	1.2E+08	6636	-0.45334	4.375712	0.003873	0.011119	0.026923	-1	339	328	431	429	480	306	368	381	530	472
ENSMUSG00000058706	chr6	0610030E20Rik	72347317	72347515	4632	-0.47214	4.338658	0.003875	0.011123	0.029361	-1	351	346	358	386	520	273	415	448	466	384
ENSMUSG00000039840	chr18	Epg5	77938467	77938559	9672	-0.63873	5.065648	0.003889	0.01116	0.056564	-1	622	564	775	652	797	385	544	1055	535	526
ENSMUSG00000048142	chr5	Nat8l	33995984	33997210	6529	2.370915	2.508833	0.003905	0.011204	0.694823	1	11	10	8	77	46	12	33	32	381	696
ENSMUSG00000000440	chr6	Pparg	1.15E+08	1.15E+08	1984	1.240067	3.015156	0.003906	0.011204	0.205087	1	68	53	57	119	97	79	100	129	502	570
ENSMUSG00000046404	chr1	Yod1	1.31E+08	1.31E+08	6128	-0.59431	2.261914	0.003916	0.011228	0.039115	-1	78	87	101	95	115	69	88	93	109	82
ENSMUSG00000050447	chr2	Lypd6	50066429	50066584	3729	-0.84803	1.265946	0.003916	0.011228	0.078232	-1	45	42	58	54	52	32	61	24	53	26
ENSMUSG00000067608	chr19	Pcna-ps2	9283238	9284494	1257	0.960545	0.627912	0.003922	0.011242	0.08835	1	9	21	14	10	27	42	48	30	56	43
ENSMUSG00000029056	chr4	Pank4	1.55E+08	1.55E+08	3487	-0.4789	4.690807	0.003926	0.011251	0.03089	-1	461	476	497	531	519	392	502	601	540	472
ENSMUSG00000029070	chr4	Mxra8	1.56E+08	1.56E+08	2918	0.583345	6.286845	0.003928	0.011255	0.048032	1	940	657	1066	946	1721	1421	2772	2563	2212	1994
ENSMUSG00000039410	chr4	Prdm16	1.54E+08	1.54E+08	9321	-0.86056	1.973543	0.003938	0.011281	0.091888	-1	87	67	57	128	70	31	69	61	78	88
ENSMUSG00000015542	chr11	Nat9	1.15E+08	1.15E+08	2066	0.573956	3.356427	0.003941	0.011289	0.041861	1	102	131	165	112	175	195	227	375	316	307
ENSMUSG00000026283	chr1	Ing5	93803965	93804039	4729	0.590778	2.644668	0.003946	0.011301	0.040834	1	66	75	81	78	111	110	167	198	209	186
ENSMUSG00000064068	chr3	Mtx1	89209081	89209421	3584	0.492052	3.949316	0.003951	0.011313	0.031082	1	175	215	227	218	224	362	409	337	493	488
ENSMUSG00000066643	chr12	Wdr35	8973892	8974179	7273	-0.58125	3.590771	0.003958	0.011328	0.043955	-1	247	172	270	206	312	190	301	153	273	205
ENSMUSG00000039774	chr4	Galnt12	47091909	47092328	2288	1.504898	-0.10466	0.003965	0.011346	0.235194	1	6	0	7	3	20	11	35	13	51	33
ENSMUSG00000074158	chr7	9830147E19Rik	42609526	42614223	4995	-1.14854	0.07172	0.003968	0.011354	0.130982	-1	23	27	18	24	19	6	18	4	20	25
ENSMUSG00000020122	chr11	Egfr	16752203	16752570	11326	-0.61799	4.765909	0.003972	0.011364	0.052816	-1	557	342	714	429	746	326	515	670	687	339
ENSMUSG00000006941	chr9	Eif1b	1.2E+08	1.2E+08	917	0.470698	4.784873	0.003977	0.011374	0.029889	1	308	376	452	377	407	673	741	707	785	784
ENSMUSG00000061780	chr10	Cfd	79890853	79890980	923	1.971378	8.003045	0.00399	0.011411	0.511214	1	1425	688	382	2696	3797	804	2918	2337	15740	29293
ENSMUSG00000041559	chr1	Fmod	1.34E+08	1.34E+08	3306	-1.24582	8.503731	0.003993	0.011416	0.215842	-1	11346	2666	9488	4250	16123	2921	7604	8870	4321	1394
ENSMUSG00000051726	chr12	Kcnf1	17172100	17176888	4789	-1.00067	2.918652	0.003995	0.011418	0.133009	-1	81	229	153	156	217	190	112	65	90	93
ENSMUSG00000031864	chr8	Ints10	68793929	68794148	6706	-0.4815	4.075757	0.004	0.01143	0.03025	-1	279	321	380	322	324	291	343	271	398	330
ENSMUSG00000063904	chr19	Dpp3	4907229	4907797	2683	0.445682	5.315598	0.004	0.01143	0.027251	1	435	535	657	546	645	785	1019	1108	1321	1153
ENSMUSG00000039715	chr2	Wdr34	30031546	30031972	2359	0.653202	2.321292	0.004017	0.011476	0.050176	1	42	57	75	64	82	95	126	185	148	144
ENSMUSG00000103567	chr18	Pcdhga5	37694380	37696924	4664	0.570109	5.837201	0.004018	0.011476	0.04587	1	715	436	810	669	1304	1207	1832	1409	2022	1552
ENSMUSG00000074247	chr8	Dda1	71469199	71469325	2846	0.454999	4.889057	0.004021	0.011481	0.028077	1	346	355	472	396	526	664	733	906	906	765
ENSMUSG00000028111	chr3	Ctsk	95499286	95499336	1482	0.727782	5.021608	0.004024	0.011489	0.07426	1	405	216	446	234	803	715	1269	844	1022	866
ENSMUSG00000037613	chr7	Tnfrsf23	1.44E+08	1.44E+08	3353	0.55411	3.355242	0.004027	0.011495	0.038988	1	116	86	143	150	201	232	327	228	340	281
ENSMUSG00000103515	chr8	AL591003.1	1.22E+08	1.22E+08	1990	0.894332	0.508248	0.004032	0.011505	0.069743	1	11	14	14	18	19	21	40	52	40	46
ENSMUSG00000026289	chr1	Atg16l1	87755870	87756085	9628	-0.44667	4.641478	0.004033	0.011506	0.026718	-1	396	460	579	463	497	392	481	505	582	503
ENSMUSG00000021224	chr12	Numb	83794034	83796154	3823	-0.48172	3.852034	0.004036	0.011509	0.029948	-1	254	192	313	320	330	187	285	292	371	284
ENSMUSG00000027303	chr2	Ptpra	1.3E+08	1.3E+08	3335	0.482449	4.808136	0.004035	0.011509	0.031705	1	315	285	406	398	572	528	780	672	1042	833
ENSMUSG00000054641	chr6	Mmrn1	60924976	60925042	5868	-1.05601	2.705735	0.004036	0.011509	0.147895	-1	100	106	216	136	189	86	53	217	79	44
ENSMUSG00000006362	chr8	Cbfa2t3	1.23E+08	1.23E+08	4775	-0.57601	4.150008	0.004044	0.011528	0.044782	-1	244	257	504	409	383	239	466	246	396	324
ENSMUSG00000008730	chr3	Hipk1	1.04E+08	1.04E+08	8591	-0.55824	5.738721	0.004047	0.011534	0.04396	-1	889	832	1288	1046	1306	574	928	1518	1158	919
ENSMUSG00000023755	chr15	Rhebl1	98877778	98878297	1940	1.103636	0.761285	0.00405	0.011539	0.134756	1	20	8	24	17	14	30	39	95	34	50
ENSMUSG00000001034	chr11	Mapk7	61488812	61489270	4394	0.687074	3.118432	0.004076	0.011612	0.061731	1	79	74	119	112	177	164	281	143	367	305
ENSMUSG00000025938	chr1	Slco5a1	12866549	12872328	13137	-0.61723	5.368302	0.004081	0.011623	0.053549	-1	603	854	866	1003	823	852	831	462	884	706
ENSMUSG00000051721	chr12	BC068281	4843303	4843451	3131	-0.66754	1.688809	0.004091	0.01165	0.046621	-1	59	54	73	62	76	41	58	68	64	54
ENSMUSG00000031144	chrX	Syp	7638471	7638728	5211	0.822255	1.050788	0.004099	0.011672	0.064773	1	25	20	21	22	29	41	54	42	85	73
ENSMUSG00000001424	chr6	Snd1	28475139	28475207	9757	0.483774	5.975671	0.004109	0.011698	0.033064	1	725	723	921	850	1201	1393	1644	1328	2305	1948
ENSMUSG00000020357	chr11	Flt4	49609263	49609827	8232	-0.60114	2.969799	0.004125	0.01174	0.045417	-1	116	103	182	196	197	123	119	160	191	129
ENSMUSG00000029171	chr5	Pgm1	64092936	64093088	2608	0.708548	2.246113	0.004158	0.011832	0.060062	1	38	56	55	66	80	79	129	106	218	156
ENSMUSG00000048271	chr5	Rbm33	28317121	28317410	10592	-0.50294	4.745008	0.004162	0.011839	0.034784	-1	492	426	599	531	572	357	471	696	520	541
ENSMUSG00000035105	chr12	Egln3	54178981	54180655	2662	1.427747	5.544793	0.004176	0.011878	0.281762	1	355	303	402	510	556	501	782	5269	771	555
ENSMUSG00000097799	chr2	Gm26899	1.21E+08	1.21E+08	3328	-2.70578	0.415643	0.004182	0.011891	0.87594	-1	14	15	8	124	26	0	0	1	39	6
ENSMUSG00000030168	chr6	Adipor2	1.19E+08	1.19E+08	5979	-0.48039	7.132837	0.004186	0.011901	0.033228	-1	2330	2343	3108	2766	3150	1798	2282	2988	3534	3268
ENSMUSG00000026615	chr1	Eprs	1.85E+08	1.85E+08	18102	-0.50336	7.700088	0.004189	0.011906	0.036595	-1	3114	3510	4743	4275	4890	3176	3634	5304	4133	3732
ENSMUSG00000071074	chr17	Yipf3	46248080	46248328	2693	0.452797	5.223464	0.0042	0.011937	0.028425	1	431	426	526	621	635	827	978	953	1225	1051
ENSMUSG00000017692	chr11	Rhbdl3	80300912	80301271	4734	-0.57604	3.71813	0.00421	0.011963	0.043924	-1	150	260	292	298	321	251	227	193	306	240
ENSMUSG00000041219	chr2	Arhgap11a	1.14E+08	1.14E+08	5332	0.698289	2.290532	0.004227	0.012008	0.058628	1	54	53	62	47	90	80	139	114	235	142
ENSMUSG00000062760	chr15	1810041L15Rik	84379203	84384392	6551	0.841031	3.152607	0.004229	0.012011	0.096445	1	52	74	102	79	243	200	375	180	333	235
ENSMUSG00000026349	chr1	Ccnt2	1.28E+08	1.28E+08	12345	-0.45503	4.748621	0.004237	0.012028	0.028348	-1	486	507	564	441	578	377	560	560	624	536
ENSMUSG00000037570	chr15	Mcrs1	99242818	99243220	1915	0.433604	4.681986	0.004236	0.012028	0.02534	1	297	318	428	365	416	555	689	707	834	650

ENSMUSG00000061286	chr7	Exosc5	25659153	25659383	1030	0.506744	3.691615	0.004242	0.012039	0.033085	1	158	153	171	190	211	293	263	363	436	402
ENSMUSG00000054612	chr7	Mgmt	1.37E+08	1.37E+08	818	0.747486	1.827287	0.004242	0.012039	0.063426	1	40	38	51	40	44	99	95	61	125	119
ENSMUSG00000038250	chr8	Usp38	80980734	80981980	4684	-0.61332	4.677219	0.004253	0.012067	0.052626	-1	407	447	634	524	582	327	392	791	480	362
ENSMUSG00000020372	chr11	Gnb2l1	48800332	48803968	5119	0.439334	8.462804	0.004259	0.01208	0.028073	1	4216	4472	5478	4608	6374	7425	9746	9281	11215	9869
ENSMUSG00000040760	chr14	Appl1	26918988	26923871	8719	-0.4549	5.014586	0.00429	0.012164	0.028639	-1	572	507	699	584	768	523	758	560	741	595
ENSMUSG00000055553	chr8	Kxd1	70508272	70508528	3176	0.462891	7.844795	0.00429	0.012164	0.031125	1	2522	3190	3610	3355	3434	5239	5793	6294	7208	6499
ENSMUSG00000029434	chr5	Vps33a	1.24E+08	1.24E+08	4107	-0.48348	5.411601	0.004296	0.012179	0.033001	-1	699	784	969	818	860	573	801	1073	916	791
ENSMUSG00000090516	chr9	Rps11-ps1	59471759	59472233	475	0.98621	0.001493	0.0043	0.012188	0.072145	1	9	11	8	8	13	19	30	20	44	26
ENSMUSG00000040111	chr9	Gramd1b	40293233	40298079	9721	-0.51957	4.622046	0.004319	0.01224	0.037236	-1	345	339	563	432	808	376	451	489	538	503
ENSMUSG00000027411	chr2	Vps16	1.3E+08	1.3E+08	3727	0.473185	3.941547	0.00432	0.01224	0.029198	1	172	197	244	191	269	291	368	401	520	511
ENSMUSG00000021326	chr13	Trim27	21179445	21179556	4702	0.450352	4.540309	0.004327	0.012251	0.027424	1	256	285	367	351	384	533	576	545	786	687
ENSMUSG00000023075	chr4	Akirin1	1.24E+08	1.24E+08	3450	-0.48549	5.326478	0.004326	0.012251	0.033202	-1	578	749	1000	679	928	663	904	624	953	756
ENSMUSG00000025730	chr17	Rab40c	25882114	25883908	3094	0.499558	3.269225	0.004326	0.012251	0.030649	1	123	106	148	129	155	175	254	277	341	272
ENSMUSG00000100410	chr13	2310020H05Rik	99076526	99076800	720	0.797311	1.745104	0.004334	0.012269	0.07556	1	25	34	47	51	41	83	132	104	94	61
ENSMUSG00000032841	chr2	Prr5l	1.02E+08	1.02E+08	4967	1.08835	0.479523	0.004351	0.012313	0.123041	1	6	14	15	8	26	33	38	17	62	54
ENSMUSG00000038347	chr17	Tcte2	13482553	13483004	8560	-1.02982	0.072943	0.004358	0.012331	0.090645	-1	12	22	21	23	33	16	20	7	14	17
ENSMUSG00000068823	chr3	Csde1	1.03E+08	1.03E+08	4201	-0.4913	9.258202	0.00436	0.012335	0.035349	-1	10760	10970	13826	11341	12716	10179	10830	14597	11711	11510
ENSMUSG00000029778	chr6	Adcyap1r1	55451978	55452368	6601	0.691708	3.039317	0.004364	0.012345	0.063743	1	73	48	113	108	195	166	231	249	273	256
ENSMUSG00000041685	chr13	Fcho2	98723407	98725776	5229	-0.63284	4.345646	0.004377	0.012378	0.056084	-1	385	315	471	448	442	200	355	628	390	299
ENSMUSG00000025583	chr11	Rptor	1.2E+08	1.2E+08	13471	-0.46437	5.216991	0.004384	0.012395	0.030337	-1	590	579	842	727	892	477	846	804	921	640
ENSMUSG00000025420	chr18	Katnal2	76977148	76977525	4061	1.512121	-0.2037	0.004388	0.012402	0.230816	1	7	3	9	5	8	3	21	61	21	24
ENSMUSG00000031386	chrX	Hcfc1	73942792	73944477	8360	-0.47372	6.231113	0.004387	0.012402	0.032297	-1	1338	1015	1559	1487	1973	1102	1580	1588	1752	1347
ENSMUSG00000028949	chr5	Smarcd3	24590818	24593118	4545	-0.57412	6.825059	0.00439	0.012406	0.047865	-1	1810	2269	2688	2367	2130	2216	2115	1343	2469	2357
ENSMUSG00000037977	chr9	6430571L13Rik	1.07E+08	1.07E+08	2912	-0.74639	5.963415	0.004396	0.012418	0.080337	-1	982	1272	1431	1167	1720	1278	1313	419	1372	965
ENSMUSG00000045128	chr8	Rpl18a	70894722	70895507	1291	0.447915	8.171857	0.004402	0.012434	0.029363	1	3431	3601	4549	3899	4987	6306	7488	8606	8581	7763
ENSMUSG00000074899	chr2	Sptbn5	1.2E+08	1.2E+08	10292	-1.08282	-0.11438	0.004404	0.012436	0.105157	-1	19	13	17	22	26	4	18	22	12	8
ENSMUSG00000025404	chr10	R3hdm2	1.27E+08	1.27E+08	5987	-0.46987	6.555508	0.004407	0.012442	0.031952	-1	1550	1466	2003	2144	1975	1427	1695	2103	2332	1692
ENSMUSG00000020018	chr10	Snrpf	93583029	93583530	861	0.603609	4.626354	0.004409	0.012443	0.05123	1	274	311	462	233	357	712	750	417	814	731
ENSMUSG00000079164	chr1	Tlr5	1.83E+08	1.83E+08	4790	-0.95625	2.034087	0.004409	0.012443	0.117821	-1	28	87	168	82	91	42	84	55	97	48
ENSMUSG00000079491	chr17	H2-T10	36115876	36117734	3419	1.142885	0.546872	0.004419	0.012468	0.137209	1	13	20	20	6	9	37	21	35	54	68
ENSMUSG00000029638	chr6	Glcci1	8509600	8510319	7756	-0.63646	2.428763	0.004425	0.012484	0.049837	-1	105	81	114	99	145	54	97	125	122	95
ENSMUSG00000014361	chr2	Mertk	1.29E+08	1.29E+08	4336	0.686252	2.928414	0.004434	0.012506	0.060938	1	110	53	129	84	106	107	218	232	294	254
ENSMUSG00000031375	chrX	Bgn	73483602	73483762	6099	0.838831	8.438249	0.00445	0.012546	0.102355	1	4242	1820	3982	2959	8532	7356	16314	5968	13748	9290
ENSMUSG00000032915	chr17	Emr4	55749984	55750092	3491	1.377215	-0.19261	0.004449	0.012546	0.1878	1	4	7	11	4	9	19	52	5	27	24
ENSMUSG00000028496	chr4	Mllt3	87769925	87774146	12004	-0.57822	6.201816	0.004461	0.012575	0.048472	-1	1380	1160	2008	1421	1398	1105	1175	1988	1261	1289
ENSMUSG00000097052	chr2	Snhg7	26637177	26637633	2465	0.908193	1.320308	0.004464	0.012582	0.093549	1	30	27	30	14	36	38	60	94	70	102
ENSMUSG00000020654	chr12	Adcy3	4133103	4133778	6246	0.726295	2.793429	0.004471	0.012598	0.069199	1	85	39	78	86	150	138	207	153	262	244
ENSMUSG00000047554	chr7	Tmem41b	1.1E+08	1.1E+08	5316	-0.45441	4.035331	0.004476	0.01261	0.02725	-1	289	232	357	309	403	252	364	312	391	295
ENSMUSG00000030862	chr7	Cpxm2	1.32E+08	1.32E+08	4450	-1.21875	5.156577	0.004487	0.012634	0.210928	-1	1325	200	993	370	1337	307	981	575	415	220
ENSMUSG00000030921	chr7	Trim30a	1.04E+08	1.04E+08	4419	0.934586	3.173502	0.004487	0.012634	0.120834	1	69	73	117	117	145	328	204	98	234	459
ENSMUSG00000072407	chr10	Gm6419	74862988	74863419	432	-1.09448	0.213511	0.004488	0.012634	0.117678	-1	16	29	20	36	22	21	20	10	21	8
ENSMUSG00000003526	chr16	Prodh	18060357	18060757	3461	1.038584	2.641161	0.004502	0.012673	0.145715	1	71	55	59	79	65	76	76	399	214	210
ENSMUSG00000054792	chr9	Klhl18	1.1E+08	1.1E+08	4526	-0.48123	3.702699	0.00451	0.012693	0.030159	-1	200	204	279	291	294	211	271	206	334	246
ENSMUSG00000026153	chr1	Fam135a	24011093	24012497	7773	-0.71992	3.827262	0.00452	0.012718	0.072382	-1	286	218	295	307	368	159	203	472	240	171
ENSMUSG00000032199	chr9	Polr2m	71478437	71479540	2424	-0.49088	7.438194	0.004522	0.012722	0.035361	-1	2864	3215	3817	3495	3466	3115	3595	2595	4353	3146
ENSMUSG00000039450	chr11	Dcxr	1.21E+08	1.21E+08	1144	0.734838	2.71417	0.004533	0.012749	0.070501	1	80	56	93	64	115	97	149	265	185	252
ENSMUSG00000029090	chr5	Gpr125	49959951	49961514	4475	-0.50407	4.44613	0.004537	0.012757	0.035143	-1	365	299	441	404	658	290	482	483	452	399
ENSMUSG00000041236	chr13	Vps41	18717292	18717336	3195	-0.44862	5.862613	0.004542	0.012768	0.028943	-1	999	1040	1204	1114	1227	935	1097	1197	1268	1229
ENSMUSG00000038252	chr6	Ncapd2	1.25E+08	1.25E+08	6267	0.510156	4.090016	0.004543	0.012769	0.035276	1	181	194	257	243	302	317	441	355	751	513
ENSMUSG00000020840	chr11	Blmh	76924809	76924877	5891	0.437027	5.594749	0.004559	0.012808	0.027257	1	535	591	816	654	859	1033	1379	1123	1556	1405
ENSMUSG00000061024	chr1	Rrs1	9545408	9547455	2048	0.549065	4.206308	0.004558	0.012808	0.041602	1	229	195	240	257	329	342	440	747	604	428
ENSMUSG00000020447	chr11	Npc1l1	6211013	6211660	4467	-0.863	0.620312	0.004572	0.012844	0.070598	-1	31	22	39	28	39	19	33	29	18	21
ENSMUSG00000027322	chr2	Siglec1	1.31E+08	1.31E+08	7143	1.102257	3.114814	0.004577	0.012855	0.169543	1	58	31	114	50	231	277	221	118	318	411
ENSMUSG00000032902	chr3	Slc16a1	1.05E+08	1.05E+08	4426	0.493599	5.533725	0.004578	0.012855	0.034859	1	534	690	665	688	589	930	1225	1166	1858	1228
ENSMUSG00000040774	chr3	Cept1	1.07E+08	1.07E+08	3116	-0.47078	4.513677	0.00459	0.012886	0.030682	-1	366	431	466	417	530	330	511	344	546	515
ENSMUSG00000001687	chr5	Ubl3	1.49E+08	1.49E+08	2668	-0.55057	5.971842	0.004613	0.012949	0.044178	-1	1193	1007	1370	1212	1449	731	1101	1798	1309	1045
ENSMUSG00000020334	chr11	Slc22a4	53983123	53983685	2553	0.728916	2.522633	0.004617	0.012957	0.067592	1	61	67	100	58	67	91	122	238	185	192
ENSMUSG00000001313	chr11	Rnd2	1.01E+08	1.01E+08	1990	0.706131	1.61256	0.004625	0.012977	0.054972	1	31	22	53	38	45	62	86	73	116	93
ENSMUSG00000026709	chr1	Dars2	1.61E+08	1.61E+08	5195	-0.57585	3.546863	0.004634	0.012999	0.04476	-1	189	229	290	256	189	185	217	149	278	264
ENSMUSG00000037455	chr10	Slc18b1	23796986	23797183	3258	-0.71668	2.555358	0.004637	0.013002	0.066888	-1	114	100	135	100	158	72	120	50	139	140
ENSMUSG00000070305	chr9	Mpzl3	45055186	45055318	6987	-0.7593	1.274689	0.004637	0.013002	0.061407	-1	37	36	73	48	56	31	52	31	46	44
ENSMUSG00000030091	chr6	Nup210	91013068	91014496	8163	-0.45624	5.276678	0.004649	0.013032	0.02964	-1	638	699	876	698	828	661	871	653	862	748
ENSMUSG00000043313	chr18	Pcdhb19	37496991	37504128	7138	-1.05575	0.133745	0.004659	0.013058	0.107273	-1	22	12	21	19	44	9	21	13	27	9
ENSMUSG00000066979	chr7	Bub3	1.32E+08	1.32E+08	2055	0.426738	5.266841	0.004685	0.013128	0.025773	1	489	473	587	518	677	806	1029	983	1304	1047
ENSMUSG00000020430	chr11	Pes1	3963975	3964060	3024	0.448179	4.98771	0.004699	0.013165	0.028313	1	374	367	516	448	545	625	768	1015	978	889
ENSMUSG00000036733	chr7	Rbm42	30640994	30641220	2193	0.44503	5.122791	0.0047	0.013166	0.028047	1	365	453	605	485	565	716	926	1039	1141	873

ENSMUSG00000027502	chr2	Rtfdc1	1.72E+08	1.72E+08	2644	0.434492	5.617904	0.004708	0.013184	0.027119	1	563	625	825	698	782	1054	1182	1272	1607	1481
ENSMUSG00000071708	chrX	Sms	1.57E+08	1.57E+08	6010	-0.47475	6.854328	0.004711	0.01319	0.033208	-1	1966	1917	2958	1932	2525	1961	2278	2314	2307	2345
ENSMUSG00000005534	chr8	Insr	3150922	3156023	9633	-0.65257	6.130793	0.004713	0.013193	0.062547	-1	1291	1068	1550	1645	1620	824	1098	2241	1197	986
ENSMUSG00000030281	chr6	Il17rc	1.13E+08	1.13E+08	2671	0.674295	2.491756	0.004723	0.013219	0.058043	1	57	45	84	63	113	110	178	108	211	194
ENSMUSG00000025792	chr11	Slc25a10	1.2E+08	1.2E+08	3455	1.220525	3.998956	0.004727	0.013229	0.212158	1	112	75	95	213	328	182	314	193	797	1222
ENSMUSG00000004264	chr6	Phb2	1.25E+08	1.25E+08	3718	0.487657	6.828069	0.004732	0.013237	0.035062	1	1185	1620	1748	1769	1530	2470	2695	3239	3710	3389
ENSMUSG00000041684	chr1	Bivm	44118957	44119195	4206	-0.59394	2.819345	0.004734	0.013243	0.04521	-1	136	111	164	148	142	88	139	172	132	120
ENSMUSG00000030970	chr7	Ctbp2	1.33E+08	1.33E+08	6220	-0.51034	3.502865	0.004747	0.013275	0.034134	-1	157	192	277	234	256	191	175	199	286	236
ENSMUSG00000001555	chr11	Fkbp10	1E+08	1E+08	2935	0.760017	5.036226	0.004755	0.013295	0.084134	1	411	195	444	247	801	695	1136	592	1418	1046
ENSMUSG00000036381	chr3	P2ry14	59114626	59116061	1797	0.863874	0.988916	0.004763	0.013314	0.077904	1	25	12	21	28	24	46	43	77	65	49
ENSMUSG00000031987	chr8	Egln1	1.25E+08	1.25E+08	3515	-0.53402	7.39046	0.004772	0.013337	0.042347	-1	2766	3255	3757	3803	2830	3154	2767	3154	3267	3406
ENSMUSG00000024942	chr19	Capn1	5988546	5989387	3190	-0.44564	6.470944	0.004783	0.013364	0.029205	-1	1452	1417	2123	1589	2022	1432	1849	1623	2265	1633
ENSMUSG00000025224	chr19	Gbf1	46152509	46152792	9062	-0.45252	6.176126	0.004801	0.013414	0.030001	-1	1185	1023	1584	1384	1894	1153	1473	1406	1724	1380
ENSMUSG00000021918	chr14	Nek4	30951486	30951718	2754	-0.66945	1.882695	0.004813	0.013443	0.053165	-1	61	68	83	80	79	41	60	86	87	56
ENSMUSG00000022032	chr14	Scara5	65666403	65666746	6093	-0.92365	4.911474	0.004818	0.013456	0.1242	-1	659	392	648	621	1020	296	296	1115	353	338
ENSMUSG00000032328	chr9	Tmem30a	79768943	79771479	5646	-0.49424	6.428434	0.004831	0.013488	0.036099	-1	1499	1493	2032	1480	1924	1114	1634	2213	1891	1544
ENSMUSG00000034656	chr8	Cacna1a	84388440	84388522	11418	-0.69681	1.998595	0.004834	0.013493	0.058379	-1	70	46	82	105	108	54	77	58	90	73
ENSMUSG00000079508	chrX	Apoo	94367117	94367162	1255	-0.55972	6.224466	0.004837	0.013501	0.046263	-1	1362	1630	1658	1372	1295	1332	1403	1682	1381	1141
ENSMUSG00000002769	chr17	Gnmt	46725664	46725971	1206	2.140382	0.701338	0.00484	0.013505	0.567402	1	16	8	1	5	14	21	11	207	21	18
ENSMUSG00000022253	chr15	Nadk2	9071260	9071765	4345	-0.75402	4.690511	0.004852	0.013536	0.082732	-1	501	489	578	599	512	256	348	904	391	339
ENSMUSG00000025213	chr19	Kazald1	45075241	45075518	1681	-0.76697	2.982616	0.004853	0.013536	0.079844	-1	198	99	202	97	238	136	182	114	124	109
ENSMUSG00000047098	chr14	Rnf31	55591708	55592072	4838	0.463522	3.674259	0.004857	0.013542	0.027898	1	155	152	193	190	199	244	316	388	415	361
ENSMUSG00000082044	chr2	Gm14284	1.31E+08	1.31E+08	279	0.802539	0.752819	0.004857	0.013542	0.058359	1	14	16	29	15	22	37	47	47	57	45
ENSMUSG00000026670	chr1	Uap1	1.7E+08	1.7E+08	4011	-0.42602	5.388735	0.004864	0.013558	0.026096	-1	722	678	912	768	936	640	871	886	961	818
ENSMUSG00000067017	chr1	Gm3608	1.05E+08	1.05E+08	2858	-0.92719	0.044805	0.004874	0.013583	0.07696	-1	27	17	16	19	25	8	15	18	22	15
ENSMUSG00000031835	chr8	Mbtps1	1.2E+08	1.2E+08	4370	-0.49665	5.63773	0.004891	0.01363	0.036093	-1	849	612	1088	987	1419	646	1094	1077	1181	867
ENSMUSG00000025178	chr19	Pi4k2a	42090435	42090936	3771	0.512155	4.745121	0.004898	0.013644	0.03745	1	324	284	420	373	451	492	532	972	927	781
ENSMUSG00000022849	chr16	Hspbap1	35770386	35770539	4590	0.651207	1.893661	0.004901	0.01365	0.048105	1	43	37	56	47	51	84	103	120	103	100
ENSMUSG00000016481	chr1	Cr1l	1.95E+08	1.95E+08	10349	-0.42676	5.375245	0.004917	0.013691	0.026283	-1	736	704	890	738	897	624	851	775	1042	865
ENSMUSG00000020919	chr11	Stat5b	1.01E+08	1.01E+08	5539	-0.67118	7.402815	0.004918	0.013691	0.067254	-1	3238	2377	3478	3940	4461	2055	2284	5348	2583	2874
ENSMUSG00000025026	chr19	Add3	53140445	53140714	4938	-0.50717	5.129489	0.004919	0.013693	0.037258	-1	561	431	710	686	1123	472	708	677	873	678
ENSMUSG00000017843	chr12	Ppp2r5c	1.1E+08	1.1E+08	4224	-0.44355	6.139944	0.004923	0.0137	0.028965	-1	1095	1236	1555	1403	1506	1116	1485	1455	1562	1346
ENSMUSG00000032372	chr9	Plscr2	92275602	92276018	3180	1.090177	-0.07282	0.004927	0.013708	0.105923	1	7	9	11	11	6	36	24	15	34	21
ENSMUSG00000028261	chr4	Ndufaf4	24898083	24898302	3902	-0.57231	5.149403	0.004931	0.013718	0.047783	-1	529	791	873	657	666	666	810	491	811	519
ENSMUSG00000025613	chr16	Cct8	87483326	87484065	3088	0.467151	7.348031	0.004932	0.013719	0.032628	1	1865	2160	2780	2081	2557	3922	4645	3648	5159	4606
ENSMUSG00000030512	chr7	Snrpa1	66060299	66060585	3082	0.470803	3.907438	0.004936	0.013725	0.029797	1	165	208	248	179	245	353	381	348	500	437
ENSMUSG00000029648	chr5	Flt1	1.48E+08	1.48E+08	11583	-0.52533	5.27327	0.004938	0.013728	0.040292	-1	592	687	762	1052	688	540	662	856	830	819
ENSMUSG00000000359	chr2	Rem1	1.53E+08	1.53E+08	2156	0.679294	1.757924	0.004962	0.013793	0.052077	1	36	34	39	47	54	68	113	74	127	92
ENSMUSG00000070319	chr9	Eif3g	20894352	20894442	1075	0.449686	5.856593	0.004974	0.013823	0.029707	1	666	672	1024	741	1027	1246	1435	1712	1804	1601
ENSMUSG00000081519	chr2	Gm13331	23508860	23509307	448	-0.98138	-0.20933	0.004976	0.013827	0.074032	-1	17	16	23	19	12	9	16	11	15	11
ENSMUSG00000005716	chr15	Pvalb	78191114	78191694	1041	-0.57445	13.97363	0.004983	0.013843	0.049809	-1	321054	269063	416644	233901	371620	339194	295896	264937	272714	293822
ENSMUSG00000055912	chr6	Tmem150a	72355447	72355544	1546	-0.56703	4.097877	0.004984	0.013843	0.045451	-1	298	335	365	357	332	285	380	182	382	374
ENSMUSG00000036568	chr17	Gltscr1l	46798116	46801829	6579	-0.56534	3.514235	0.004992	0.013864	0.043794	-1	202	154	257	241	291	130	189	308	264	191
ENSMUSG00000071652	chr19	Ints5	8888926	8888964	3889	0.44069	4.6876	0.005007	0.013902	0.027361	1	276	324	423	360	450	563	667	587	914	740
ENSMUSG00000020181	chr10	Nav3	1.1E+08	1.1E+08	13806	-0.80397	1.916644	0.00501	0.013903	0.082422	-1	88	50	97	54	109	34	76	91	67	50
ENSMUSG00000025935	chr1	Tram1	13564698	13566396	3162	0.522872	4.982774	0.005011	0.013903	0.03968	1	404	306	454	365	664	625	906	640	1265	977
ENSMUSG00000028329	chr4	Xpa	46155347	46155826	1894	0.820153	2.270905	0.005011	0.013903	0.087882	1	52	56	50	69	53	101	97	247	129	122
ENSMUSG00000032528	chr9	Vipr1	1.22E+08	1.22E+08	5564	-0.85275	0.742313	0.005012	0.013903	0.074059	-1	34	26	50	35	27	18	29	35	25	26
ENSMUSG00000019261	chr8	Map1s	70905974	70906127	3271	0.567341	3.646917	0.005028	0.013947	0.044363	1	120	147	158	163	259	277	339	234	546	362
ENSMUSG00000040428	chr7	Plekha4	45526330	45526441	4187	0.628098	2.377566	0.005036	0.013964	0.04933	1	65	44	75	57	96	106	177	123	158	158
ENSMUSG00000087993	chr10	Mir1982	80828797	80828870	74	0.8721	0.892514	0.005044	0.013984	0.079257	1	22	21	21	19	18	61	43	56	57	40
ENSMUSG00000058997	chr14	Vwa8	78849178	78849443	6928	-0.52461	6.720651	0.00505	0.013996	0.041228	-1	1617	1869	2192	2596	2093	1602	1664	2675	2323	1818
ENSMUSG00000079065	chr5	BC005561	1.05E+08	1.05E+08	5181	-0.96072	1.76501	0.005049	0.013996	0.121877	-1	87	49	91	75	64	23	39	105	44	55
ENSMUSG00000033790	chr7	Tubgcp5	55794148	55794340	3681	-0.55181	3.137862	0.005062	0.014027	0.040196	-1	166	133	213	137	226	115	193	166	224	139
ENSMUSG00000028830	chr4	AU040320	1.27E+08	1.27E+08	6259	-0.42891	5.12048	0.005068	0.01404	0.026439	-1	549	563	743	708	780	566	659	746	820	664
ENSMUSG00000004151	chr12	Etv1	38779380	38779479	5889	-0.84611	1.284424	0.005077	0.014059	0.085898	-1	51	25	70	48	64	24	37	57	55	27
ENSMUSG00000062300	chr7	Pvrl2	19716644	19717787	3440	0.660181	2.85437	0.005077	0.014059	0.057974	1	51	79	100	115	122	118	209	157	299	259
ENSMUSG00000030399	chr7	Ckm	19411094	19411146	1415	-0.52617	14.5023	0.005082	0.014069	0.042037	-1	342149	424822	513611	474158	546125	469027	339905	464549	433615	464591
ENSMUSG00000039156	chr5	Stim2	53998417	53999034	5215	-0.44703	4.988858	0.005083	0.01407	0.028741	-1	476	570	671	593	759	497	722	513	762	649
ENSMUSG00000041650	chr14	Pcca	1.23E+08	1.23E+08	5210	-0.46135	5.319785	0.005087	0.014078	0.0311	-1	708	644	754	868	877	586	733	679	971	978
ENSMUSG00000045374	chr11	Wdr81	75440944	75442089	7038	0.476123	3.888505	0.005097	0.014102	0.030696	1	170	168	223	210	264	243	358	420	570	447
ENSMUSG00000066442	chr9	Mthfs	89210676	89210821	7498	0.78412	1.610313	0.005107	0.014129	0.071942	1	27	34	49	42	27	73	66	66	116	114
ENSMUSG00000063884	chr6	Ptcd3	71880648	71881231	2585	-0.49187	5.997585	0.005116	0.014149	0.036011	-1	1012	1308	1408	1276	1175	1074	1355	1113	1604	1056
ENSMUSG00000000708	chr17	Kat2b	53566861	53566915	4867	-0.61111	6.026626	0.005137	0.014205	0.055857	-1	1196	1070	1489	1301	1542	906	990	2001	999	1053
ENSMUSG00000041028	chr14	Ghitm	37120444	37122226	3081	-0.51185	8.701725	0.005146	0.014228	0.039786	-1	7019	8291	9704	8088	7418	6699	7478	10116	8280	7199
ENSMUSG00000026520	chr1	Pycr2	1.81E+08	1.81E+08	2958	0.47381	4.200487	0.005151	0.014239	0.031102	1	207	258	276	258	274	400	457	397	686	562

ENSMUSG00000005161	chr8	Prdx2	84969587	84969762	3050	0.495486	7.368497	0.005159	0.014256	0.037099	1	1817	2367	2895	2202	2108	4171	4358	4282	5160	4418
ENSMUSG00000039230	chr11	Tbcd	1.21E+08	1.21E+08	8096	0.461259	4.111244	0.005159	0.014256	0.029294	1	191	188	265	268	307	295	462	497	633	475
ENSMUSG00000032181	chr9	Scg3	75643264	75643944	2249	-0.98479	0.800883	0.005177	0.014302	0.110661	-1	38	15	35	27	76	19	33	28	30	21
ENSMUSG00000028668	chr4	Tceb3	1.36E+08	1.36E+08	4708	-0.51037	6.067303	0.005183	0.014316	0.038952	-1	1039	1132	1541	1369	1537	927	1176	1836	1355	1156
ENSMUSG00000028470	chr4	Hint2	43654227	43654411	1540	0.51475	4.240081	0.005185	0.014319	0.037293	1	214	278	284	287	211	437	456	497	584	598
ENSMUSG00000057895	chr9	Zfp105	1.23E+08	1.23E+08	2130	0.787475	1.087368	0.005188	0.014325	0.065491	1	29	17	24	17	36	43	60	63	81	52
ENSMUSG00000002210	chr7	Smg9	24399619	24399891	3702	0.446776	4.091635	0.005193	0.014332	0.027255	1	208	204	245	247	297	342	398	481	558	515
ENSMUSG00000036599	chr5	Chst12	1.41E+08	1.41E+08	2362	0.611996	3.696294	0.005193	0.014332	0.05291	1	171	88	165	163	278	263	305	307	490	471
ENSMUSG00000024352	chr18	Spata24	35656690	35656844	967	0.917304	0.751805	0.005198	0.014342	0.086557	1	14	19	13	28	15	42	33	58	52	52
ENSMUSG00000071856	chr18	Mcc	44425061	44430067	8426	-0.61633	2.304975	0.005203	0.014352	0.046142	-1	64	91	125	102	115	76	98	94	90	88
ENSMUSG00000000976	chr11	Heatr6	83753696	83753941	6419	-0.49511	3.541607	0.005208	0.014365	0.032992	-1	231	165	242	231	263	153	229	269	250	226
ENSMUSG00000033149	chr16	Phldb2	45746243	45747931	7577	-0.50402	3.925942	0.00521	0.014366	0.035455	-1	309	211	337	287	341	184	377	315	336	263
ENSMUSG00000031958	chr8	Ldhd	1.12E+08	1.12E+08	5328	-0.56467	5.677326	0.005217	0.014382	0.047617	-1	812	1131	1161	1186	716	866	858	1063	1080	911
ENSMUSG00000036257	chr12	Pnpla8	44221370	44221460	3947	-0.75872	6.44019	0.005221	0.014392	0.086651	-1	1585	1729	2285	1807	1656	836	1034	3024	1354	1292
ENSMUSG00000012535	chr6	Tnpo3	29540827	29541866	10246	-0.42729	5.702127	0.005224	0.014392	0.026944	-1	850	855	1102	990	1206	832	1019	1153	1228	949
ENSMUSG00000030036	chr6	Mogs	83115496	83115926	2892	0.556717	3.904402	0.005225	0.014392	0.043748	1	173	149	238	166	295	317	411	261	578	525
ENSMUSG00000074676	chr2	Foxs1	1.53E+08	1.53E+08	1311	0.887287	1.55563	0.005225	0.014392	0.096682	1	21	30	28	47	39	64	127	41	115	84
ENSMUSG00000103088	chr18	Pcdhgb6	37742094	37744658	4684	0.548626	5.854965	0.005223	0.014392	0.045087	1	727	448	845	676	1323	1213	1837	1432	2028	1562
ENSMUSG00000006219	chr4	Fblim1	1.42E+08	1.42E+08	4457	0.817707	1.775281	0.005229	0.014399	0.083003	1	35	37	36	46	44	66	121	48	167	102
ENSMUSG00000027947	chr3	Il6ra	89869324	89871386	3343	1.247033	2.701379	0.005246	0.014444	0.220782	1	66	42	52	71	84	57	118	592	148	137
ENSMUSG00000002324	chr14	Rec8	55618037	55618353	2748	1.186527	-0.10768	0.005261	0.014481	0.137742	1	4	4	8	7	19	20	19	13	54	28
ENSMUSG00000025724	chr7	Sec11a	80904889	80905051	4614	0.454357	4.710533	0.005266	0.014493	0.029594	1	325	326	428	286	485	579	768	636	838	701
ENSMUSG00000062093	chr14	Gm10110	89896223	89896981	2169	-0.47513	3.595712	0.005283	0.014535	0.030088	-1	178	229	259	240	262	207	242	228	250	239
ENSMUSG00000064341	chrMT	mt-Nd1	2751	3707	957	-0.55481	12.84523	0.005283	0.014535	0.047114	-1	111873	144908	186746	177850	103142	121284	133770	127518	160848	150198
ENSMUSG00000022358	chr15	Fbxo32	58175879	58181555	6936	2.36432	7.747129	0.005294	0.014558	0.753549	1	694	1003	1155	2026	939	737	809	37626	1110	1298
ENSMUSG00000041298	chr5	Katnal1	1.49E+08	1.49E+08	11881	-0.59541	2.726419	0.005294	0.014558	0.04635	-1	140	106	155	123	131	80	115	156	154	110
ENSMUSG00000028991	chr4	Mtor	1.48E+08	1.48E+08	10109	-0.50353	5.109479	0.005298	0.014566	0.037422	-1	561	557	750	779	737	398	720	895	756	593
ENSMUSG00000017776	chr11	Crk	75679259	75679664	4730	-0.45847	5.812817	0.005307	0.014589	0.031393	-1	965	1027	1042	1014	1376	789	1168	1241	1402	971
ENSMUSG00000012114	chr16	Med15	17651221	17652263	3383	0.539765	4.443256	0.005323	0.014626	0.04219	1	255	204	306	336	388	366	507	859	692	599
ENSMUSG00000026960	chr2	Arl6ip6	53191726	53191880	2703	-0.54768	2.858923	0.005323	0.014626	0.03883	-1	140	129	152	145	141	103	152	132	183	117
ENSMUSG00000041328	chr7	Pcf11	92643712	92644777	6412	-0.54698	3.837708	0.005327	0.014633	0.042159	-1	294	220	276	258	364	210	237	380	311	211
ENSMUSG00000099913	chr1	Gm28551	53325507	53326457	3142	-0.46297	6.101572	0.005333	0.014649	0.032199	-1	1259	1282	1442	1259	1340	1161	1304	1445	1527	1267
ENSMUSG00000044092	chr5	C130050O18Rik	1.39E+08	1.39E+08	3180	1.214062	0.09512	0.005337	0.014656	0.155762	1	9	5	8	7	19	17	55	10	36	38
ENSMUSG00000046807	chr10	Lrrc75b	75550125	75554120	4601	-1.38406	0.208912	0.005349	0.014685	0.229285	-1	37	6	27	11	54	6	26	19	9	10
ENSMUSG00000025503	chr7	Taldo1	1.41E+08	1.41E+08	1998	0.599946	6.612317	0.005354	0.014697	0.05461	1	1041	1195	1533	1330	1400	1996	2141	1712	3832	4293
ENSMUSG00000015852	chr3	Fcrls	87250758	87251396	2334	1.118048	3.519441	0.005364	0.01472	0.18178	1	103	66	146	108	190	377	538	49	558	293
ENSMUSG00000056870	chr1	Gulp1	44551511	44551872	3758	-0.75656	1.945808	0.005365	0.01472	0.073915	-1	76	44	73	83	128	31	69	72	97	68
ENSMUSG00000070730	chr2	Rmdn3	1.19E+08	1.19E+08	3537	0.744055	3.027421	0.005366	0.01472	0.077151	1	90	73	102	113	126	154	214	110	362	363
ENSMUSG00000027997	chr3	Casp6	1.3E+08	1.3E+08	1676	0.652927	2.066851	0.005378	0.014749	0.050928	1	34	49	62	59	62	68	116	117	162	129
ENSMUSG00000101111	chr1	Gm28437	24613189	24613971	783	-0.62241	3.785355	0.005378	0.014749	0.05556	-1	195	302	352	339	186	231	214	269	334	212
ENSMUSG00000051790	chr11	Nlgn2	69823122	69826079	5785	0.556421	3.454172	0.00539	0.014778	0.042866	1	141	85	161	130	230	202	362	294	349	313
ENSMUSG00000002997	chr12	Prkar2b	31958476	31960522	3652	1.809666	3.941592	0.005409	0.014827	0.463517	1	82	36	48	223	187	69	151	109	1054	1583
ENSMUSG00000032238	chr9	Rora	68653786	68653972	13071	-0.8493	6.086375	0.00541	0.014828	0.109011	-1	1396	1263	1526	1249	1874	656	737	2546	824	855
ENSMUSG00000043257	chr4	Pigv	1.34E+08	1.34E+08	4180	-0.49126	3.800406	0.005417	0.014844	0.033168	-1	236	238	353	241	288	264	261	246	282	275
ENSMUSG00000021643	chr13	Serf1	1E+08	1E+08	1315	0.686272	2.254437	0.005432	0.014879	0.05995	1	49	49	73	42	89	105	171	97	138	158
ENSMUSG00000036561	chr15	Ppp6r2	89253035	89253261	2887	-0.50829	5.24941	0.005432	0.014879	0.038422	-1	652	666	830	768	803	617	607	1009	742	652
ENSMUSG00000034247	chr11	Plekhm1	1.03E+08	1.03E+08	5968	0.550104	4.638322	0.005435	0.014883	0.044452	1	254	236	343	424	447	415	514	700	982	905
ENSMUSG00000016018	chr13	Skiv2l2	1.13E+08	1.13E+08	3309	-0.42742	5.298896	0.005445	0.014909	0.026926	-1	695	642	882	707	842	603	794	848	920	758
ENSMUSG00000002393	chr8	Nr2f6	71374123	71374421	2983	0.465329	4.383205	0.005447	0.01491	0.03084	1	244	262	351	277	326	512	607	425	682	576
ENSMUSG00000025931	chr1	Paqr8	20890606	20890686	5488	0.832946	0.997334	0.005454	0.014927	0.074435	1	16	23	26	18	30	36	84	53	69	41
ENSMUSG00000032515	chr9	Csrnp1	1.2E+08	1.2E+08	2870	0.761354	2.02754	0.005458	0.014935	0.074036	1	30	45	49	78	42	76	92	117	164	141
ENSMUSG00000024853	chr19	Sf3b2	5273923	5274527	3231	0.433315	6.715135	0.005473	0.014973	0.028556	1	1215	1298	1640	1544	1801	2149	2636	3054	3346	2947
ENSMUSG00000022721	chr16	Trmt2a	18248679	18250033	4952	0.486559	3.636762	0.005478	0.014984	0.032082	1	158	135	173	159	239	210	347	322	468	364
ENSMUSG00000022550	chr15	Adck5	76576358	76576494	3452	0.662932	2.093245	0.005481	0.014988	0.052685	1	53	46	49	62	56	69	112	130	149	142
ENSMUSG00000028189	chr3	Ctbs	1.46E+08	1.46E+08	2892	-0.54968	2.544961	0.005488	0.015004	0.037087	-1	100	87	130	113	147	85	111	102	130	120
ENSMUSG00000042215	chr1	Bag2	33745484	33747016	3059	-0.5765	4.67873	0.005507	0.015055	0.049235	-1	412	520	570	496	548	430	694	289	562	412
ENSMUSG00000022723	chr16	Crybg3	59490775	59493685	7488	-0.54394	5.061089	0.005514	0.015069	0.044173	-1	448	709	671	713	758	457	607	903	672	525
ENSMUSG00000050428	chr7	Fbxo46	19119859	19119936	3025	0.671526	1.735543	0.005529	0.015108	0.05383	1	26	30	58	39	58	77	85	92	112	95
ENSMUSG00000038398	chr8	Upf3a	13785615	13785884	1402	0.478176	3.536015	0.005546	0.015151	0.030566	1	146	140	166	163	186	250	259	294	395	370
ENSMUSG00000033386	chr3	Frrs1	1.17E+08	1.17E+08	2396	0.878933	1.682902	0.005559	0.015183	0.098195	1	23	42	42	32	42	47	79	56	175	128
ENSMUSG00000100783	chr5	2310047D07Rik	1.49E+08	1.49E+08	823	-0.76584	2.284485	0.00557	0.015211	0.078859	-1	94	103	118	92	94	90	77	42	84	116
ENSMUSG00000045210	chr1	Vcpip1	9718622	9725350	9749	-0.48044	4.1505	0.005573	0.015216	0.032968	-1	306	258	408	339	426	218	333	437	454	307
ENSMUSG00000036893	chr2	Ehmt1	24790769	24792130	7136	-0.44753	4.569749	0.005576	0.015223	0.028937	-1	411	351	536	416	590	321	498	537	575	429
ENSMUSG00000005698	chr8	Ctcf	1.06E+08	1.06E+08	4860	-0.43848	5.013283	0.005582	0.015235	0.028306	-1	570	467	669	643	767	436	659	729	779	621
ENSMUSG00000019943	chr10	Atp2b1	98915152	98915371	7130	-0.46881	6.070775	0.005589	0.015251	0.033441	-1	1268	960	1521	1297	1491	804	1305	1300	1834	1471
ENSMUSG00000032806	chrX	Slc10a3	74369217	74371011	2023	0.617546	2.434516	0.005592	0.015256	0.049107	1	55	50	88	71	89	140	182	118	167	135

ENSMUSG00000057596	chr7	Trim30d	1.04E+08	1.04E+08	3758	1.023663	1.632705	0.005604	0.015287	0.142682	1	21	16	46	37	49	115	78	35	83	141
ENSMUSG00000039239	chr1	Tgfb2	1.87E+08	1.87E+08	5791	-0.47346	4.499573	0.005605	0.015287	0.032399	-1	363	291	522	429	628	370	500	402	529	404
ENSMUSG00000055093	chr6	Gm8430	1.22E+08	1.22E+08	471	0.648437	2.448004	0.005608	0.015291	0.054052	1	59	78	55	68	84	148	138	138	157	170
ENSMUSG00000005625	chr3	Psmd4	95032694	95032984	2808	0.661308	7.184279	0.00561	0.015294	0.067281	1	1421	1634	2328	1899	2207	2960	3050	7457	3520	3616
ENSMUSG00000092595	chr17	Gm20427	34026034	34026225	3703	0.458991	6.612533	0.005613	0.015298	0.032263	1	1081	1071	1486	1379	1967	2096	2536	2272	3442	2959
ENSMUSG00000027087	chr2	Itgav	83724397	83724919	10744	-0.44501	5.325504	0.00562	0.015315	0.029573	-1	626	686	892	729	947	570	910	641	1086	806
ENSMUSG00000022010	chr14	Tsc22d1	76414961	76415717	8994	0.451746	6.954044	0.005631	0.015341	0.031365	1	1581	1307	1856	1922	2123	2755	3677	3412	3699	3118
ENSMUSG00000053617	chr19	Sh3pxd2a	47260174	47268936	10464	-0.50695	6.781145	0.005633	0.015345	0.039523	-1	1603	1543	2296	2348	3213	1218	2473	2192	2567	2329
ENSMUSG00000069899	chr11	Gm12166	46051354	46052311	968	0.831173	0.624862	0.00564	0.015361	0.064091	1	16	16	18	17	18	41	35	31	61	45
ENSMUSG00000028159	chr3	Dapp1	1.38E+08	1.38E+08	3284	0.690546	1.888342	0.005644	0.015367	0.05785	1	42	37	42	50	58	81	119	67	127	125
ENSMUSG00000025907	chr1	Rb1cc1	6206197	6206270	14690	-0.69713	6.26673	0.00565	0.015377	0.074522	-1	1531	1385	1732	1629	1626	854	1162	2611	1258	957
ENSMUSG00000030747	chr7	Dgat2	99153663	99154700	2251	1.404713	5.829092	0.00565	0.015377	0.292605	1	392	425	268	974	507	289	595	1238	3098	4986
ENSMUSG00000022614	chr15	Lmf2	89351004	89351887	2906	0.498233	4.335634	0.005664	0.015414	0.036055	1	233	186	276	305	413	408	555	440	813	573
ENSMUSG00000020246	chr10	Hcfc2	82696160	82696207	5485	-0.43649	4.544094	0.005678	0.015447	0.027494	-1	402	380	499	391	575	347	544	434	544	449
ENSMUSG00000084910	chr4	C630043F03Rik	72201348	72202270	2581	-0.80411	1.212923	0.005683	0.015458	0.07202	-1	35	50	50	47	57	46	39	37	39	26
ENSMUSG00000059412	chr9	Fxyd2	45403138	45403300	632	0.830107	0.753306	0.005698	0.015496	0.068484	1	19	12	19	23	21	37	32	46	60	60
ENSMUSG00000067235	chr17	H2-Q10	35470089	35470179	4348	2.142618	1.596498	0.005699	0.015496	0.620527	1	6	4	5	40	36	17	21	15	183	339
ENSMUSG00000018076	chr5	Med13l	1.19E+08	1.19E+08	9293	-0.57948	4.614197	0.0057	0.015496	0.050133	-1	480	324	546	497	618	271	424	725	448	428
ENSMUSG00000037926	chr11	Ssh2	77216287	77216515	18519	-0.65885	6.024283	0.005703	0.015502	0.066594	-1	1032	869	1555	1684	1611	702	998	2066	1117	1017
ENSMUSG00000025858	chr5	Get4	1.39E+08	1.39E+08	2431	0.467577	5.21806	0.005723	0.01555	0.032655	1	471	504	585	467	563	810	878	1225	1072	1023
ENSMUSG00000031157	chrX	Pqbp1	7894519	7894867	1636	0.47823	4.350876	0.005723	0.01555	0.03304	1	231	263	275	299	350	509	559	404	667	609
ENSMUSG00000022571	chr15	Pycrl	75916463	75917079	1353	0.508972	3.336659	0.005734	0.015577	0.034594	1	123	132	175	116	141	206	266	236	354	319
ENSMUSG00000011263	chr7	Exoc3l2	19489056	19489174	2201	0.833952	0.799373	0.005738	0.015585	0.072705	1	13	18	14	20	33	41	56	45	64	37
ENSMUSG00000044968	chr5	Napepld	21662901	21665362	3956	-0.50345	3.950723	0.005743	0.015594	0.036049	-1	228	265	377	292	359	233	245	400	298	303
ENSMUSG00000014550	chr6	Zfyve20	92186712	92190458	5757	-0.42347	4.58397	0.005745	0.015598	0.025831	-1	365	392	519	475	552	389	502	496	555	442
ENSMUSG00000036138	chr9	Acaa1a	1.19E+08	1.19E+08	4414	0.473467	5.662324	0.005748	0.015601	0.033974	1	526	724	807	714	760	1147	1269	1122	1611	1712
ENSMUSG00000027714	chr3	Exosc9	36552606	36552751	4711	0.42809	4.469535	0.005754	0.015611	0.026164	1	268	300	347	304	348	481	632	532	715	598
ENSMUSG00000094365	chr7	Gm21982	30641001	30641220	3821	0.43272	5.243636	0.005753	0.015611	0.027896	1	407	492	670	524	609	762	1009	1090	1262	975
ENSMUSG00000048154	chr15	Kmt2d	98831669	98834592	19887	-0.47892	5.572534	0.005755	0.015612	0.034768	-1	797	693	1013	908	1269	659	892	1239	1024	833
ENSMUSG00000039483	chr2	Asb6	30823097	30824504	5439	0.553305	3.381424	0.005775	0.015663	0.042637	1	104	127	170	126	177	218	235	401	333	245
ENSMUSG00000004667	chr10	Polr2e	80035949	80036301	2670	0.431773	5.120342	0.005785	0.015687	0.027666	1	389	448	594	502	541	705	890	1047	1069	949
ENSMUSG00000015214	chrX	Mtmr1	71364760	71365072	5859	-0.60394	4.808789	0.005788	0.015693	0.055112	-1	546	465	630	550	623	293	495	876	498	441
ENSMUSG00000019362	chr8	D8Ertd738e	84246237	84246693	659	0.467988	6.317756	0.005792	0.015701	0.033624	1	975	1139	1172	1100	1151	1970	1968	2241	2367	2154
ENSMUSG00000040842	chr4	Szrd1	1.41E+08	1.41E+08	3327	-0.47453	7.161943	0.005796	0.015707	0.034925	-1	2238	2554	3443	2683	3030	2583	2848	2132	3395	2976
ENSMUSG00000059263	chr7	Usp47	1.12E+08	1.12E+08	5540	-0.47688	7.982182	0.005802	0.01572	0.035447	-1	4132	3874	5573	5379	5782	4050	4355	6297	5253	4591
ENSMUSG00000060803	chr19	Gstp1	4035407	4035661	757	0.478812	6.017507	0.005811	0.015742	0.03513	1	738	856	1016	851	1061	1653	1559	1906	1682	1856
ENSMUSG00000074793	chr2	Hspa12b	1.31E+08	1.31E+08	3685	-0.54118	3.754148	0.005829	0.015789	0.04204	-1	185	250	281	364	245	213	240	211	370	254
ENSMUSG00000020608	chr12	Smc6	11265886	11266288	5603	-0.43627	5.315549	0.005836	0.015803	0.028575	-1	612	708	786	749	981	645	829	827	966	683
ENSMUSG00000020272	chr11	Stk10	32533305	32533559	5187	0.606282	2.77248	0.005842	0.015812	0.049145	1	72	65	88	110	113	128	223	137	239	231
ENSMUSG00000033161	chr3	Atp1a1	1.02E+08	1.02E+08	4487	0.540035	7.046838	0.005843	0.015812	0.045318	1	1272	1643	1935	1795	2454	2722	3815	2248	5421	4397
ENSMUSG00000057335	chr1	Cep170	1.77E+08	1.77E+08	18049	-0.49604	4.004123	0.005841	0.015812	0.035401	-1	311	204	333	289	443	199	378	289	386	316
ENSMUSG00000028847	chr4	Trappc3	1.26E+08	1.26E+08	1737	0.456423	4.383087	0.00585	0.01583	0.030043	1	220	296	370	286	288	435	593	519	662	603
ENSMUSG00000038900	chr2	Rpl12	32961559	32961839	3598	0.460712	7.552238	0.005853	0.015834	0.033084	1	2205	2413	3294	2043	3339	4152	5146	5056	5602	5356
ENSMUSG00000051235	chr12	Gen1	11240926	11242576	3283	-0.98223	0.552687	0.00586	0.015851	0.112047	-1	31	28	22	36	37	14	27	6	35	30
ENSMUSG00000028330	chr4	Ncbp1	46138613	46138886	3386	0.432116	4.802598	0.005887	0.015918	0.027466	1	299	370	446	388	485	605	808	641	921	765
ENSMUSG00000069910	chr11	Spdl1	34809190	34809842	3460	0.930848	0.405241	0.005886	0.015918	0.083063	1	12	11	12	16	18	24	36	20	59	49
ENSMUSG00000020926	chr11	Adam11	1.03E+08	1.03E+08	5669	0.87701	0.301121	0.005895	0.015935	0.068095	1	11	8	16	14	17	28	29	29	35	47
ENSMUSG00000046916	chr10	Myct1	5593728	5593901	2775	-0.62432	3.36192	0.005907	0.015966	0.056035	-1	144	237	225	264	150	128	175	236	229	178
ENSMUSG00000030768	chr1	Disp1	1.83E+08	1.83E+08	5224	-0.60881	2.82765	0.00591	0.015971	0.05063	-1	113	90	171	158	190	100	158	94	194	113
ENSMUSG00000024797	chr19	Vps51	6067842	6068375	4748	0.452193	4.05053	0.005916	0.015982	0.028944	1	164	217	272	239	277	319	415	515	509	472
ENSMUSG00000058126	chr14	Tpm3-rs7	1.13E+08	1.13E+08	2106	0.83783	1.408357	0.005919	0.015984	0.085753	1	19	24	21	43	46	63	52	69	125	75
ENSMUSG00000070814	chr7	6330408A02Rik	13258967	13261640	11662	-0.4952	3.532649	0.005918	0.015984	0.034041	-1	200	197	257	239	228	193	239	160	286	239
ENSMUSG00000040557	chr5	Wbscr27	1.35E+08	1.35E+08	3342	1.036667	1.463495	0.005928	0.016005	0.142237	1	24	18	24	43	35	29	67	166	96	62
ENSMUSG00000009079	chr11	Ewsr1	5069689	5070103	5907	0.439716	6.3646	0.005934	0.016018	0.029848	1	1024	957	1331	1084	1482	1565	2031	2305	2688	2566
ENSMUSG00000023938	chr17	Aars2	45506841	45507081	3348	-0.50595	4.432219	0.005953	0.016067	0.0379	-1	280	412	493	464	471	344	435	281	553	477
ENSMUSG00000023030	chr15	Slc11a2	1E+08	1E+08	6354	-0.4653	5.131044	0.005969	0.016106	0.032655	-1	531	647	869	576	784	591	727	526	865	727
ENSMUSG00000021838	chr14	Samd4	46882854	46883168	8529	-0.6073	5.632413	0.005978	0.016129	0.056951	-1	862	815	1075	1181	1065	611	864	1555	864	679
ENSMUSG00000074063	chr8	Osgin1	1.19E+08	1.19E+08	2674	-0.71876	4.100527	0.005981	0.016132	0.077659	-1	395	326	349	276	413	290	243	504	262	175
ENSMUSG00000066148	chr4	Prpf4	62408797	62408901	5671	-0.45725	4.942145	0.005987	0.016145	0.031272	-1	472	533	680	602	690	487	533	752	627	604
ENSMUSG00000032596	chr9	Uba7	1.08E+08	1.08E+08	6692	0.83572	2.911784	0.006002	0.016184	0.101474	1	78	54	105	87	128	199	215	92	198	392
ENSMUSG00000020333	chr11	Acsl6	54303798	54303922	9914	-0.50319	4.345053	0.006008	0.016197	0.037338	-1	357	361	394	435	426	322	388	523	382	324
ENSMUSG00000043421	chr6	Hilpda	29272488	29272608	1103	0.675685	2.159056	0.006029	0.016249	0.058471	1	47	48	66	57	62	107	128	73	159	159
ENSMUSG00000020182	chr11	Ddc	11814101	11814517	4461	0.976263	2.504358	0.00604	0.016276	0.138586	1	17	58	61	58	131	162	266	95	153	169
ENSMUSG00000026926	chr2	Pmpca	26389339	26389432	4282	-0.46419	7.612095	0.006047	0.016293	0.033857	-1	3022	3594	4332	4008	3966	3370	3679	4357	4002	3610
ENSMUSG00000031706	chr8	Rfx1	84066836	84067048	4172	0.588323	2.789636	0.006054	0.016304	0.045374	1	105	86	78	83	94	148	211	180	225	191
ENSMUSG00000033916	chr7	Chmp2a	13032006	13032202	927	0.439039	5.887861	0.006053	0.016304	0.029628	1	704	765	926	869	926	1355	1402	1654	1811	1693

ENSMUSG00000063362	chr8	Alg11	22060721	22060770	4960	-0.54013	3.006982	0.006069	0.016342	0.03939	-1	136	124	179	157	199	104	147	199	182	131
ENSMUSG00000015846	chr2	Rxra	27676440	27676515	5462	-0.53264	6.984985	0.006097	0.016414	0.044526	-1	2005	2058	2619	2822	3088	1750	1980	3601	2483	2249
ENSMUSG00000004508	chr7	Gab2	97081751	97081906	5997	0.496972	3.687944	0.006101	0.016423	0.034892	1	157	124	177	199	236	219	374	419	431	324
ENSMUSG00000021488	chr13	Nsd1	55209782	55209875	12784	-0.44959	6.322218	0.006111	0.016443	0.031449	-1	1296	1254	1801	1458	1978	1122	1654	1892	1746	1504
ENSMUSG00000042029	chr12	Ncapg2	1.16E+08	1.16E+08	6604	0.771625	2.306964	0.00611	0.016443	0.0826	1	49	41	77	36	102	79	158	92	218	183
ENSMUSG00000027165	chr2	B230118H07Rik	1.02E+08	1.02E+08	4289	-0.50893	5.518403	0.006114	0.016448	0.039851	-1	815	856	1070	834	890	943	872	711	866	926
ENSMUSG00000038302	chr10	Lace1	42312585	42313616	2705	-0.69133	4.254279	0.006131	0.016489	0.072606	-1	259	458	496	426	305	336	364	158	470	370
ENSMUSG00000010651	chr9	Acaa1b	1.19E+08	1.19E+08	1962	2.522833	0.382475	0.006145	0.016524	0.819334	1	3	0	0	5	22	5	11	6	70	147
ENSMUSG00000028936	chr4	Rpl22	1.52E+08	1.52E+08	2911	0.450161	6.712182	0.006149	0.016532	0.031711	1	1325	1393	1770	1284	1611	2348	2796	3051	3002	2853
ENSMUSG00000035311	chr10	Gnptab	88379132	88379296	5883	-0.56516	4.577589	0.00618	0.016612	0.04862	-1	381	392	555	456	616	297	407	266	700	629
ENSMUSG00000099875	chr1	Gm15453	1.5E+08	1.5E+08	465	1.091394	0.876758	0.006184	0.016619	0.143776	1	23	23	17	13	12	26	35	99	48	65
ENSMUSG00000024645	chr18	Timm21	84947294	84947745	1315	-0.51541	4.082544	0.006197	0.01665	0.039187	-1	300	362	379	332	257	287	333	316	387	293
ENSMUSG00000034422	chr16	Parp14	35832874	35834935	9306	0.716783	4.38586	0.006219	0.016708	0.078707	1	194	220	291	306	313	762	486	280	583	812
ENSMUSG00000051166	chr12	Eml5	98786604	98790386	10136	-0.70807	1.870282	0.00623	0.016732	0.064128	-1	75	44	79	60	120	46	55	59	92	70
ENSMUSG00000020641	chr12	Rsad2	26442753	26445570	4328	1.278138	3.837548	0.006256	0.016795	0.246521	1	67	113	162	278	69	770	206	211	221	767
ENSMUSG00000044408	chr12	Sptssa	54645374	54646535	1363	0.42828	4.631792	0.006255	0.016795	0.027085	1	284	309	449	337	388	466	625	689	824	733
ENSMUSG00000029814	chr6	Igf2bp3	49085221	49087440	4344	1.037685	0.528108	0.006269	0.016824	0.119606	1	16	11	12	8	25	15	41	29	69	60
ENSMUSG00000036845	chr7	Lin37	30555441	30555608	1388	0.568022	2.647553	0.006269	0.016824	0.042052	1	69	83	98	73	90	119	164	207	187	183
ENSMUSG00000029407	chr5	Uso1	92137938	92138163	3897	-0.43281	6.750188	0.006275	0.016838	0.02946	-1	1755	1717	2431	1872	2644	1692	2352	2140	2351	2147
ENSMUSG00000041828	chr11	Abca8a	1.1E+08	1.1E+08	6272	-0.59475	6.029475	0.006285	0.016861	0.05555	-1	1564	750	1278	1278	1707	761	1359	1669	1339	987
ENSMUSG00000026496	chr1	Parp1	1.81E+08	1.81E+08	5293	-0.42328	6.023058	0.006288	0.016867	0.027866	-1	1056	1076	1340	1234	1539	1068	1281	1178	1681	1300
ENSMUSG00000033557	chr1	Fam20b	1.57E+08	1.57E+08	8770	-0.42226	5.967115	0.00629	0.016869	0.027694	-1	1040	1067	1329	1203	1339	1045	1244	1202	1480	1261
ENSMUSG00000033106	chr8	Slc7a6os	1.06E+08	1.06E+08	1525	0.542708	2.997573	0.006292	0.016871	0.039809	1	79	114	125	103	113	179	203	194	249	264
ENSMUSG00000030805	chr7	Stx4a	1.28E+08	1.28E+08	2364	0.449885	5.659879	0.006302	0.016894	0.031282	1	655	651	898	596	759	1097	1427	1153	1569	1562
ENSMUSG00000079884	chr9	Gm10698	33728247	33728850	604	-0.59981	2.247797	0.006304	0.016894	0.046519	-1	94	78	89	96	113	52	92	92	123	83
ENSMUSG00000026088	chr1	Mitd1	37874801	37875125	2770	0.780387	1.617064	0.006316	0.016921	0.078492	1	27	33	44	28	51	95	90	46	113	87
ENSMUSG00000072893	chr11	4933439C10Rik	59505662	59506886	5616	0.80432	1.219209	0.006315	0.016921	0.074746	1	25	23	38	22	26	35	55	94	74	73
ENSMUSG00000026721	chr1	Rabgap1l	1.6E+08	1.6E+08	23232	-0.56574	3.129154	0.006331	0.016957	0.045364	-1	178	134	198	145	213	86	169	202	194	179
ENSMUSG00000026003	chr1	Acadl	66830839	66831527	2005	0.709447	8.286875	0.006337	0.01697	0.079808	1	3042	4318	3863	5203	3019	5614	6413	15833	9614	7972
ENSMUSG00000033417	chr19	Cacul1	60524696	60529087	5790	-0.44496	5.314517	0.006345	0.01699	0.030424	-1	651	626	888	779	905	566	710	988	942	744
ENSMUSG00000006010	chr1	BC003331	1.5E+08	1.5E+08	4100	-0.49062	4.537621	0.006354	0.017011	0.036288	-1	414	373	560	384	542	297	463	610	460	424
ENSMUSG00000034353	chr1	Ramp1	91179822	91180140	3022	-0.54245	5.039378	0.006373	0.017057	0.045577	-1	678	605	681	739	483	459	676	752	750	497
ENSMUSG00000040562	chr3	Gstm2	1.08E+08	1.08E+08	1679	0.569341	5.998994	0.006385	0.017086	0.05108	1	750	581	873	832	1338	1724	1335	2123	1534	2003
ENSMUSG00000071657	chr19	Bscl2	8837467	8837864	5897	0.769181	4.364682	0.00639	0.017096	0.091265	1	218	187	256	241	381	302	454	301	968	1103
ENSMUSG00000033294	chr5	Noc4l	1.11E+08	1.11E+08	2505	0.448557	4.246863	0.006403	0.017129	0.029363	1	234	249	273	262	313	446	401	519	646	530
ENSMUSG00000058402	chr7	Zfp420	29859979	29860093	4238	-0.70857	1.057542	0.006408	0.017138	0.053617	-1	31	44	45	41	47	28	37	33	40	40
ENSMUSG00000059475	chr9	Zfp426	20468549	20471248	4888	-0.50937	3.233688	0.006425	0.017177	0.035706	-1	153	134	222	180	239	130	228	180	203	162
ENSMUSG00000068264	chr2	Ap5s1	1.31E+08	1.31E+08	1660	0.454351	3.855277	0.006425	0.017177	0.029262	1	175	198	243	188	204	341	392	349	469	383
ENSMUSG00000020925	chr11	Ccdc43	1.03E+08	1.03E+08	3341	-0.4691	6.133424	0.006429	0.017183	0.034581	-1	1022	1358	1684	1254	1502	1265	1490	1258	1446	1340
ENSMUSG00000028076	chr3	Cd1d1	86995834	86996601	2570	1.468936	2.351561	0.006442	0.017215	0.316209	1	45	17	24	54	83	33	71	61	274	457
ENSMUSG00000032397	chr9	Tipin	64281607	64281652	1211	0.526638	3.207742	0.006443	0.017215	0.03865	1	87	132	146	103	160	204	270	204	306	277
ENSMUSG00000071723	chrX	Gspt2	94636069	94638559	3781	1.146036	-0.08006	0.006445	0.017217	0.129389	1	10	7	7	1	18	14	35	22	29	34
ENSMUSG00000097978	chr5	Gm5864	32420003	32420972	970	1.100083	0.276828	0.00646	0.017254	0.132725	1	6	12	8	23	8	36	36	24	57	21
ENSMUSG00000020067	chr10	Mypn	63115795	63117026	5246	-0.485	8.419489	0.006465	0.017264	0.037686	-1	5511	5185	7637	7110	8237	5544	5743	8856	6846	6064
ENSMUSG00000018547	chr11	Pip4k2b	97715157	97718939	5204	-0.42902	6.285438	0.006473	0.017281	0.028989	-1	1290	1214	1764	1566	1668	1180	1548	1737	1834	1482
ENSMUSG00000038533	chr2	Cbfa2t2	1.54E+08	1.54E+08	8650	-0.4563	4.23699	0.006477	0.01729	0.030584	-1	295	249	411	383	508	304	354	411	446	335
ENSMUSG00000029068	chr4	Ccnl2	1.56E+08	1.56E+08	5278	0.514327	5.124974	0.006492	0.017326	0.040895	1	488	447	569	342	536	583	999	1108	962	1157
ENSMUSG00000033596	chr8	Rfwd3	1.11E+08	1.11E+08	4443	0.503316	3.298416	0.006509	0.017368	0.03493	1	115	119	154	127	159	177	269	212	370	326
ENSMUSG00000025993	chr1	Slc40a1	45908068	45909719	9000	-0.74992	4.474704	0.006518	0.017387	0.087399	-1	297	485	484	663	374	270	317	683	268	368
ENSMUSG00000033319	chr18	Fem1c	46501746	46506389	5726	-0.45051	4.43506	0.006536	0.017432	0.030255	-1	350	352	417	433	539	349	512	433	479	350
ENSMUSG00000054364	chr12	Rhob	8497763	8499985	2223	0.545377	5.906788	0.006539	0.017436	0.04702	1	519	557	892	1203	961	1006	1656	1753	2165	1865
ENSMUSG00000020681	chr11	Ace	1.06E+08	1.06E+08	5287	-0.46994	6.525366	0.006555	0.017476	0.03506	-1	1696	1122	2087	1829	2310	1580	1890	1775	2046	1676
ENSMUSG00000097767	chr5	Miat	1.12E+08	1.12E+08	9293	-1.08686	0.437131	0.006557	0.01748	0.139478	-1	33	15	44	11	46	12	28	25	13	17
ENSMUSG00000040549	chr2	Ckap5	91526762	91526850	9462	-0.43061	5.506113	0.006576	0.017527	0.028804	-1	733	708	991	925	1019	731	963	1014	1014	782
ENSMUSG00000031538	chr8	Plat	22757744	22757828	2531	0.642683	4.001898	0.0066	0.017588	0.063233	1	161	125	206	230	341	329	726	292	548	387
ENSMUSG00000030282	chr6	Cmas	1.43E+08	1.43E+08	2783	0.441545	4.852719	0.006602	0.017589	0.029595	1	367	386	472	336	478	582	815	660	962	880
ENSMUSG00000029053	chr4	Prkcz	1.55E+08	1.55E+08	6318	-0.73777	1.03668	0.00661	0.017607	0.060023	-1	43	27	50	37	51	22	42	38	38	34
ENSMUSG00000031290	chrX	Lrch2	1.47E+08	1.47E+08	6420	-0.90244	0.58778	0.006612	0.017609	0.092455	-1	26	14	32	29	59	11	27	26	31	23
ENSMUSG00000054434	chr5	Tmem120b	1.23E+08	1.23E+08	2852	0.679083	3.749928	0.006619	0.017624	0.069605	1	102	221	163	199	160	215	343	283	535	588
ENSMUSG00000020783	chr11	1200014J11Rik	73047783	73048082	8140	0.460261	3.573419	0.006669	0.017752	0.029918	1	125	136	192	155	233	252	314	297	435	310
ENSMUSG00000023048	chr15	Prr13	1.02E+08	1.02E+08	1562	0.507178	4.648811	0.006671	0.017752	0.039401	1	295	316	411	329	372	531	592	465	951	925
ENSMUSG00000025586	chr7	Cpeb1	81347026	81348439	4192	-0.47521	4.199269	0.006671	0.017752	0.033509	-1	312	292	470	325	388	336	390	360	336	339
ENSMUSG00000032096	chr9	Arcn1	44741564	44744016	6084	-0.43509	6.658032	0.006672	0.017753	0.030205	-1	1764	1548	2184	1869	2380	1528	2150	2258	2242	1850
ENSMUSG00000041231	chr11	Ublcp1	44454571	44455615	2542	-0.44594	4.03055	0.006692	0.017802	0.029059	-1	275	317	366	271	331	275	339	300	390	303
ENSMUSG00000031805	chr8	Jak3	71676296	71676583	5352	0.696101	2.767511	0.006694	0.017803	0.069274	1	78	76	83	81	108	101	167	128	308	293
ENSMUSG00000026142	chr1	Rhbdd1	82316452	82316648	6966	-0.45149	3.573161	0.006701	0.017819	0.028581	-1	186	180	265	215	310	173	258	237	280	225

ENSMUSG00000061080	chr16	Lsamp	39984361	39984727	17213	-0.98865	1.528645	0.006717	0.017858	0.13234	-1	69	32	57	42	121	63	34	44	36	34
ENSMUSG00000073633	chr1	Fbxo36	84839841	84839968	2148	0.78855	0.65333	0.006723	0.01787	0.059491	1	16	14	24	18	17	33	44	53	48	37
ENSMUSG00000022150	chr15	Dab2	6299788	6299899	7342	0.666209	5.438753	0.00673	0.017885	0.070505	1	470	305	608	507	993	762	1124	769	2222	1544
ENSMUSG00000020152	chr11	Actr2	20062304	20064859	5204	0.472115	5.993846	0.00674	0.017907	0.035368	1	731	762	993	826	1182	1120	1707	1384	2495	2111
ENSMUSG00000098140	chr5	Gm26938	1.4E+08	1.4E+08	744	0.561375	2.582689	0.006741	0.017908	0.041811	1	73	64	87	73	101	157	162	135	200	159
ENSMUSG00000002797	chr6	Ggct	54982580	54986001	4437	-0.65848	2.932115	0.006747	0.01792	0.062926	-1	118	185	187	124	154	136	155	80	181	131
ENSMUSG00000087141	chr16	Plcxd2	45959263	45965174	7140	-0.89408	0.189614	0.00676	0.01795	0.077267	-1	12	23	20	27	35	9	17	18	23	21
ENSMUSG00000040429	chr5	Mterf1a	3890581	3891897	2442	1.053979	-0.13045	0.006769	0.017972	0.103444	1	5	7	16	11	4	18	34	15	30	29
ENSMUSG00000087117	chr11	Gm11523	96862997	96863571	1095	0.99212	0.13106	0.006782	0.018003	0.099817	1	10	8	14	6	17	32	40	20	41	18
ENSMUSG00000028629	chr4	Exo5	1.21E+08	1.21E+08	2008	0.762954	1.545516	0.006793	0.018029	0.073669	1	34	25	34	33	48	66	101	43	116	89
ENSMUSG00000030704	chr7	Rab6a	1.01E+08	1.01E+08	3728	-0.4586	6.182975	0.006802	0.01805	0.03355	-1	1258	1153	1711	1283	1653	1079	1678	1614	1587	1187
ENSMUSG00000038323	chr1	1700066M21Rik	57377620	57377946	3235	-0.66585	1.815681	0.006826	0.01811	0.056878	-1	46	67	84	71	89	36	56	57	93	76
ENSMUSG00000039345	chr16	Mettl22	8470788	8470865	2665	-0.48059	6.196015	0.006831	0.018118	0.03691	-1	1284	1359	1573	1378	1495	1459	1466	1155	1589	1372
ENSMUSG00000020614	chr11	Fam20a	1.1E+08	1.1E+08	3634	0.683756	1.762017	0.006839	0.018138	0.059058	1	38	29	51	36	58	58	129	80	117	93
ENSMUSG00000030247	chr6	Kcnj8	1.43E+08	1.43E+08	2188	-0.53054	4.044115	0.006853	0.01817	0.042672	-1	226	316	347	428	298	228	289	413	331	308
ENSMUSG00000022247	chr15	Brix1	10474779	10476596	2731	0.433157	4.17503	0.006862	0.01819	0.027709	1	191	238	305	233	319	410	450	487	586	474
ENSMUSG00000032243	chr9	Itga11	62677826	62677996	5131	-0.75705	3.602606	0.006869	0.018205	0.088083	-1	273	91	215	253	471	135	267	251	196	201
ENSMUSG00000034903	chr2	Cobll1	65088339	65089557	8342	-0.58733	2.451758	0.006883	0.018238	0.04708	-1	93	84	116	132	118	58	117	92	142	105
ENSMUSG00000082454	chr11	Gm12183	48751867	48753714	1848	-0.70987	2.078242	0.006886	0.018244	0.069058	-1	80	63	94	92	104	36	90	102	97	50
ENSMUSG00000054659	chr4	Pm20d2	33174230	33174480	1834	-1.27038	3.047617	0.006893	0.018259	0.247101	-1	187	131	147	293	209	29	82	334	68	52
ENSMUSG00000020376	chr11	Rnf130	50025346	50025647	1558	0.44029	5.121716	0.006896	0.018261	0.030112	1	469	427	562	452	546	769	811	937	1013	1121
ENSMUSG00000032456	chr9	Nmnat3	98287435	98287576	5004	-0.45993	3.932249	0.006896	0.018261	0.031128	-1	289	280	316	273	298	270	286	249	362	322
ENSMUSG00000023044	chr15	Csad	1.02E+08	1.02E+08	2265	0.871892	3.19327	0.006902	0.018273	0.116214	1	103	58	86	82	218	122	219	204	328	523
ENSMUSG00000030089	chr6	Slc41a3	90604725	90605008	2812	-0.67893	6.699218	0.006915	0.018304	0.074388	-1	1859	1453	2283	2374	2848	1917	2052	721	2393	2185
ENSMUSG00000028161	chr3	Ppp3ca	1.37E+08	1.37E+08	5512	-0.45896	7.654786	0.006938	0.018357	0.034234	-1	3765	3059	4334	3582	4823	3333	3501	4719	4159	3966
ENSMUSG00000050761	chr16	Gp1bb	18620319	18621332	1881	0.883389	1.419437	0.006938	0.018357	0.103778	1	27	20	18	21	67	53	98	62	92	84
ENSMUSG00000022131	chr14	Gpr180	1.18E+08	1.18E+08	2877	-0.44033	4.779792	0.006947	0.018378	0.029802	-1	510	470	559	483	604	503	502	490	618	582
ENSMUSG00000020458	chr11	Rtn4	29692947	29693693	6991	-0.45278	9.835577	0.006964	0.018408	0.03356	-1	16652	15578	20889	15061	20009	15485	19451	19671	18530	16186
ENSMUSG00000028164	chr3	Manba	1.35E+08	1.35E+08	6971	0.485254	3.669786	0.006963	0.018408	0.034073	1	189	126	180	187	193	284	369	274	431	365
ENSMUSG00000029833	chr6	Trim24	37870811	37871474	8521	-0.53976	5.181797	0.006963	0.018408	0.046198	-1	532	760	848	740	689	490	609	1015	655	667
ENSMUSG00000031953	chr8	Tmem170	1.12E+08	1.12E+08	1943	-0.84059	0.363315	0.006963	0.018408	0.070989	-1	29	19	25	24	33	19	16	14	33	20
ENSMUSG00000027500	chr3	Stmn2	8509360	8509630	5602	-0.83432	1.307645	0.006969	0.018417	0.088478	-1	34	35	65	84	41	31	50	39	53	30
ENSMUSG00000029777	chr6	Gars	55038001	55038233	2390	0.420495	6.233778	0.006972	0.018417	0.028298	1	835	960	1186	1120	1298	1502	2014	1941	2451	2200
ENSMUSG00000032565	chr9	Nudt16	1.05E+08	1.05E+08	2573	0.763841	2.901343	0.006973	0.018417	0.085987	1	102	87	98	97	60	136	159	372	235	182
ENSMUSG00000076435	chr11	Acsf2	94557102	94558357	3432	0.85181	2.772586	0.006972	0.018417	0.108595	1	50	58	74	88	139	90	128	144	334	351
ENSMUSG00000037638	chr12	Zbtb42	1.13E+08	1.13E+08	3490	0.670209	1.867714	0.007002	0.018487	0.05726	1	33	42	36	49	69	73	94	87	145	114
ENSMUSG00000087679	chr2	C330006A16Rik	26136814	26138913	2483	0.475148	4.573351	0.007002	0.018487	0.034767	1	240	274	307	438	407	543	622	545	834	685
ENSMUSG00000070871	chr1	Ccnyl1	64690455	64690676	3456	-0.45411	4.160331	0.007004	0.018488	0.03083	-1	280	300	408	349	390	272	320	446	377	336
ENSMUSG00000091277	chr12	Gm1818	48554182	48556344	2399	-0.74812	1.365417	0.007008	0.018493	0.069324	-1	58	49	63	48	41	32	45	58	44	39
ENSMUSG00000100934	chr2	FMN1	1.13E+08	1.13E+08	3615	1.293446	-0.55136	0.007008	0.018493	0.159095	1	9	1	3	4	10	11	20	7	27	30
ENSMUSG00000023942	chr17	Slc29a1	45585200	45585782	4008	0.47271	5.863364	0.007017	0.018512	0.03582	1	660	568	872	752	1305	1175	1729	1618	1928	1484
ENSMUSG00000026974	chr2	Zmynd19	24949792	24950047	4168	-0.41138	4.323364	0.007023	0.018526	0.025185	-1	334	343	407	369	450	318	404	427	464	387
ENSMUSG00000016382	chrX	Pls3	75785654	75786899	4238	-0.44144	5.21141	0.007038	0.018562	0.030628	-1	617	550	788	785	838	543	916	689	890	647
ENSMUSG00000027524	chr2	Edn3	1.75E+08	1.75E+08	4113	-0.89917	1.475703	0.007057	0.018603	0.109486	-1	39	47	48	52	117	44	61	21	57	37
ENSMUSG00000032452	chr9	Clstn2	97444395	97445713	5691	-0.92978	0.571231	0.007058	0.018603	0.100472	-1	30	13	42	21	53	18	29	20	32	15
ENSMUSG00000041625	chr14	Ggact	1.23E+08	1.23E+08	1988	-0.57475	2.887485	0.007056	0.018603	0.046112	-1	137	135	168	150	137	141	110	148	153	126
ENSMUSG00000022682	chr16	Rrn3	13780699	13780839	3597	-0.4262	5.328831	0.007061	0.018607	0.028532	-1	587	690	945	757	890	687	861	806	886	738
ENSMUSG00000027298	chr2	Tyro3	1.2E+08	1.2E+08	6198	0.791951	1.549245	0.007072	0.018632	0.080481	1	38	28	23	30	52	53	94	115	92	63
ENSMUSG00000036667	chr6	Fam115a	42668002	42670323	9622	0.528501	4.275096	0.007078	0.018645	0.04323	1	230	170	292	232	421	412	702	389	655	512
ENSMUSG00000002524	chr15	Puf60	76070184	76070627	1912	0.419347	6.021409	0.007088	0.018668	0.028151	1	759	816	1025	887	1179	1390	1822	1577	2180	1733
ENSMUSG00000074656	chr2	Eif2s2	1.55E+08	1.55E+08	6755	-0.47905	7.178855	0.007092	0.018675	0.037398	-1	2628	2592	3369	2398	3071	2457	2675	3424	2731	2677
ENSMUSG00000001436	chr10	Slc19a1	77032241	77032290	4644	0.641983	3.082145	0.007094	0.018676	0.060522	1	87	89	116	115	142	136	181	180	344	377
ENSMUSG00000027203	chr2	Dut	1.25E+08	1.25E+08	2410	0.52149	3.180802	0.007099	0.018683	0.038154	1	101	115	152	119	127	201	240	183	340	278
ENSMUSG00000033377	chr3	Palmd	1.17E+08	1.17E+08	3812	-0.48106	4.804173	0.007099	0.018683	0.036248	-1	373	577	581	661	503	420	526	549	670	564
ENSMUSG00000000184	chr6	Ccnd2	1.27E+08	1.27E+08	5701	-0.70863	4.682277	0.007116	0.018725	0.08006	-1	501	259	474	457	1051	296	527	269	614	607
ENSMUSG00000011831	chr5	Evi5	1.08E+08	1.08E+08	8060	-0.49812	3.909676	0.007119	0.018729	0.037197	-1	248	191	348	312	387	205	311	378	297	257
ENSMUSG00000056537	chrX	Rlim	1.04E+08	1.04E+08	8917	0.44289	4.806614	0.007121	0.018731	0.030413	1	350	304	456	363	521	522	672	894	953	746
ENSMUSG00000004896	chr3	Rrnad1	87922601	87923912	6342	0.548477	2.623414	0.007138	0.018771	0.039852	1	81	73	91	64	101	118	166	165	212	185
ENSMUSG00000040124	chr1	Gorab	1.63E+08	1.63E+08	2855	-0.6555	1.918009	0.007171	0.018855	0.056516	-1	67	71	86	55	102	44	75	79	89	53
ENSMUSG00000030410	chr7	Dmwd	19076249	19076701	2534	0.499541	5.056942	0.007184	0.018886	0.039496	1	417	351	426	545	562	577	1018	1194	953	819
ENSMUSG00000042010	chr5	Acacb	1.14E+08	1.14E+08	9632	-0.66295	7.684653	0.007187	0.018888	0.07191	-1	3401	3966	4234	5060	4293	2337	2288	6609	3678	3710
ENSMUSG00000032589	chr9	Bsn	1.08E+08	1.08E+08	15938	1.232892	-0.02153	0.007194	0.018901	0.173232	1	8	1	7	7	21	20	14	19	51	40
ENSMUSG00000033147	chr3	Slc22a15	1.02E+08	1.02E+08	11085	0.886397	0.452969	0.007194	0.018901	0.08029	1	15	9	13	19	17	26	41	23	47	54
ENSMUSG00000030061	chr6	Uba3	97183670	97184865	2589	-0.47698	5.440367	0.007201	0.018917	0.036416	-1	682	772	1003	858	906	566	1080	958	1035	635
ENSMUSG00000026223	chr1	Itm2c	85894281	85894789	2491	0.464997	5.866283	0.007215	0.018949	0.034854	1	660	644	908	773	1162	1229	1717	1162	2022	1816
ENSMUSG00000028156	chr3	Eif4e	1.39E+08	1.39E+08	2882	-0.48623	6.430639	0.007216	0.018949	0.038463	-1	1430	1848	1903	1549	1575	1556	1701	1366	2015	1704

ENSMUSG00000036932	chrX	Aifm1	48474944	48475188	4006	-0.44684	5.585641	0.007228	0.018977	0.031978	-1	753	970	997	1006	847	762	988	907	1127	962
ENSMUSG00000032925	chr14	Itgbl1	1.24E+08	1.24E+08	4229	-0.83795	4.805605	0.007233	0.018984	0.112711	-1	832	222	717	348	915	318	677	585	478	283
ENSMUSG00000024235	chr18	Map3k8	4331327	4332436	4504	0.863534	1.005629	0.007267	0.01907	0.094214	1	25	7	33	22	26	39	67	74	57	47
ENSMUSG00000020707	chr11	Rnf135	80183851	80184255	2140	0.641207	2.014497	0.007295	0.019133	0.053797	1	45	42	48	59	62	113	102	92	120	124
ENSMUSG00000026039	chr1	Sgol2	57995971	57996312	7007	0.922307	0.963621	0.007293	0.019133	0.107035	1	15	20	22	10	40	41	47	33	89	74
ENSMUSG00000030621	chr7	Me3	89632392	89632569	14624	-0.50192	6.156587	0.007295	0.019133	0.040953	-1	1195	1351	1543	1530	1303	1323	1217	1611	1302	1313
ENSMUSG00000038155	chr19	Gstp2	4040285	4040539	770	0.598665	3.751393	0.007297	0.019133	0.055116	1	113	192	226	177	180	359	272	516	353	343
ENSMUSG00000051184	chr7	Zfp524	5015501	5015560	1110	0.522779	3.004144	0.007298	0.019133	0.038128	1	88	108	123	110	111	186	193	249	235	219
ENSMUSG00000059430	chr6	Actg2	83512905	83513128	1562	1.299014	-0.13236	0.007304	0.019147	0.198803	1	1	6	13	14	4	19	34	8	50	23
ENSMUSG00000093565	chr17	Rab26os	24528248	24528436	497	1.143662	-0.23063	0.007306	0.019148	0.122207	1	6	15	4	4	8	21	18	16	39	25
ENSMUSG00000020086	chr10	H2afy2	61738665	61739462	2175	0.791521	1.374895	0.007309	0.019152	0.079836	1	23	24	29	21	57	50	100	54	96	70
ENSMUSG00000102976	chr1	Zc3h11a	1.34E+08	1.34E+08	6031	-0.43487	7.118877	0.007311	0.019154	0.031007	-1	2258	2164	3042	2500	3515	2215	3088	2908	2961	2583
ENSMUSG00000032010	chr9	Usp2	44067021	44067220	4807	-0.55463	7.360786	0.00733	0.0192	0.05062	-1	3634	3054	3984	3019	2308	2854	3075	3429	3267	2740
ENSMUSG00000024948	chr19	Map4k2	6341135	6341345	6646	-0.57344	3.302654	0.007359	0.019272	0.049532	-1	143	187	246	220	183	93	176	205	210	251
ENSMUSG00000039187	chr7	Fanci	79391929	79392265	5766	1.248437	-0.09633	0.007371	0.019299	0.181529	1	2	6	12	5	16	17	23	8	60	30
ENSMUSG00000024327	chr17	Slc39a7	34028267	34029068	2594	0.476582	6.226084	0.007376	0.01931	0.037071	1	816	750	1128	1014	1627	1537	2029	1649	2786	2276
ENSMUSG00000006818	chr17	Sod2	13007839	13008068	3824	-0.49261	7.831579	0.007378	0.019312	0.040092	-1	3624	4648	4817	5109	3761	4103	4025	4190	5207	4423
ENSMUSG00000042275	chr13	Pelo	1.15E+08	1.15E+08	1600	0.52298	3.84123	0.007384	0.019324	0.041497	1	146	198	200	214	214	334	351	535	401	318
ENSMUSG00000029430	chr5	Ran	1.29E+08	1.29E+08	2646	0.457125	6.652141	0.007386	0.019324	0.034223	1	1132	1314	1723	1282	1658	2340	2536	2086	3580	3081
ENSMUSG00000021983	chr14	Atp8a2	59647531	59647924	6419	-0.70987	1.928596	0.007389	0.019328	0.068108	-1	75	42	84	70	124	58	69	78	74	50
ENSMUSG00000031657	chr8	Heatr3	88137855	88138157	4497	-0.44894	5.459319	0.007397	0.019347	0.03227	-1	744	712	1025	760	1020	789	834	1005	905	756
ENSMUSG00000027936	chr3	Crtc2	90254163	90254558	4094	0.507447	4.279277	0.007404	0.019359	0.03983	1	247	243	261	252	326	336	429	748	575	574
ENSMUSG00000032280	chr9	Tle3	61372366	61373461	11653	0.582762	4.158726	0.007453	0.019485	0.0534	1	248	125	196	248	388	324	619	435	593	542
ENSMUSG00000024807	chr19	Syvn1	6046576	6047128	4772	0.433319	4.866388	0.007456	0.019488	0.029535	1	342	299	442	427	586	584	709	822	974	836
ENSMUSG00000034731	chr14	Dgkh	78569609	78570157	3967	-0.85322	0.262193	0.007457	0.019489	0.068908	-1	15	20	33	28	26	15	16	18	18	26
ENSMUSG00000030685	chr7	Kctd13	1.27E+08	1.27E+08	2487	0.710139	1.493958	0.007473	0.019526	0.061393	1	30	33	37	34	36	51	64	64	110	108
ENSMUSG00000056938	chr11	Acbd4	1.03E+08	1.03E+08	2937	0.57009	4.040349	0.007485	0.019554	0.050756	1	180	168	233	214	319	267	307	518	530	689
ENSMUSG00000020424	chr11	Gatsl3	4218225	4218426	1574	0.62226	2.063659	0.007501	0.019583	0.050306	1	46	40	75	51	57	83	94	135	145	122
ENSMUSG00000020923	chr11	Ubtf	1.02E+08	1.02E+08	6552	0.436774	5.870999	0.007499	0.019583	0.030923	1	683	748	905	845	976	1132	1452	1928	1893	1486
ENSMUSG00000029924	chr6	Slc37a3	39334770	39337284	4065	-0.4603	4.147822	0.0075	0.019583	0.032303	-1	306	239	381	296	515	266	386	317	415	359
ENSMUSG00000040289	chr3	Hey1	8663359	8665064	3265	0.553021	2.446048	0.007512	0.01961	0.040358	1	62	58	92	69	82	114	157	166	161	142
ENSMUSG00000033623	chr5	Pcgf3	1.08E+08	1.08E+08	9544	-0.48941	5.603845	0.007524	0.019637	0.038876	-1	700	798	996	1108	1176	704	889	1315	935	856
ENSMUSG00000018593	chr11	Sparc	55394500	55395613	3367	-0.66358	10.86842	0.007526	0.019639	0.073108	-1	45996	18241	42689	25399	62891	26072	45378	26469	40939	30982
ENSMUSG00000020818	chr11	Mfsd11	1.17E+08	1.17E+08	7076	0.43487	4.870784	0.00754	0.019668	0.029692	1	332	407	484	415	428	583	683	877	959	832
ENSMUSG00000030541	chr7	Idh2	80094846	80095203	2588	0.627278	7.134469	0.00754	0.019668	0.065054	1	1366	1698	1549	2676	1874	2748	2906	6221	4805	3339
ENSMUSG00000014791	chr8	Elmo3	1.05E+08	1.05E+08	3060	0.848381	0.841612	0.007554	0.019702	0.082073	1	18	26	15	16	23	27	52	39	72	66
ENSMUSG00000097971	chr17	Gm26917	39843013	39846341	3329	0.613837	5.320786	0.007556	0.019702	0.061321	1	384	672	593	341	627	1048	826	969	1154	1570
ENSMUSG00000005656	chr12	Snx6	54746349	54747059	1928	0.437114	4.915899	0.007577	0.019752	0.030229	1	391	340	484	372	565	642	905	702	870	917
ENSMUSG00000021646	chr13	Mccc2	99948533	99948956	2123	-0.42531	4.984362	0.007584	0.019763	0.028686	-1	543	541	635	646	648	489	585	567	761	760
ENSMUSG00000086742	chr7	Gm16201	1.4E+08	1.4E+08	2917	0.977459	0.031543	0.007584	0.019763	0.099101	1	6	5	19	6	16	21	24	24	29	42
ENSMUSG00000061013	chr18	Mkx	6910459	6910633	3925	-1.39212	2.097988	0.007591	0.019779	0.295778	-1	173	27	152	38	125	24	104	89	43	14
ENSMUSG00000034601	chr12	2700049A03Rik	71136848	71138038	5879	-0.53698	2.507821	0.007608	0.019819	0.038903	-1	100	95	109	114	138	85	120	92	126	113
ENSMUSG00000020085	chr10	Aifm2	61715263	61715352	4121	0.714205	4.293162	0.007619	0.019842	0.081755	1	212	229	230	275	281	275	380	381	794	1085
ENSMUSG00000026483	chr1	Fam129a	1.52E+08	1.52E+08	7380	-0.49008	4.867271	0.00762	0.019842	0.03842	-1	526	328	667	661	696	409	676	553	742	477
ENSMUSG00000051705	chr9	Senp8	59734259	59737868	3792	-0.62247	2.726141	0.007629	0.019862	0.055874	-1	121	120	152	136	131	114	163	76	123	120
ENSMUSG00000029408	chr5	Abcb9	1.24E+08	1.24E+08	5817	-0.52878	3.28579	0.007632	0.019867	0.041199	-1	141	170	248	204	197	170	218	131	233	172
ENSMUSG00000002266	chr7	Zim1	6675443	6678262	3641	-1.36691	2.704607	0.007658	0.019928	0.291799	-1	153	62	143	112	340	20	63	251	44	44
ENSMUSG00000035493	chr13	Tgfbi	56609603	56609780	2678	0.76948	6.092658	0.007658	0.019928	0.097612	1	908	321	746	561	1834	1294	2415	1727	2748	2026
ENSMUSG00000023571	chr4	Fam132a	1.56E+08	1.56E+08	1366	0.512925	3.586023	0.007661	0.019931	0.039263	1	144	150	164	169	190	214	266	327	369	471
ENSMUSG00000023272	chr15	Creld2	88819646	88819834	1364	0.663822	3.605831	0.007666	0.019941	0.069192	1	127	111	167	129	263	290	361	158	461	468
ENSMUSG00000096696	chr17	Zfp960	17064113	17064206	2667	-1.12307	0.790432	0.007669	0.019944	0.173769	-1	36	33	38	44	39	12	17	63	19	11
ENSMUSG00000064370	chrMT	mt-Cytb	14145	15288	1144	-0.55148	13.43086	0.007683	0.019977	0.050964	-1	154457	213557	295965	275718	150459	179111	203623	200919	233725	224324
ENSMUSG00000023977	chr17	Ubr2	46928292	46930500	7747	-0.57286	6.321288	0.007703	0.020025	0.054334	-1	1430	1421	1766	1540	1824	989	1274	2532	1491	1214
ENSMUSG00000048497	chr11	Mmgt2	62648664	62648816	4898	0.662813	2.32702	0.007706	0.02003	0.06183	1	55	56	74	41	94	115	181	92	172	143
ENSMUSG00000079487	chrX	Med12	1.01E+08	1.01E+08	7704	-0.53637	4.342111	0.007747	0.020132	0.045854	-1	386	274	440	406	509	195	393	557	459	355
ENSMUSG00000035713	chr7	Usp35	97309380	97310496	5285	0.808067	1.237417	0.007758	0.020157	0.083162	1	15	22	24	31	46	37	76	55	72	96
ENSMUSG00000040007	chr2	Bahd1	1.19E+08	1.19E+08	4664	0.535583	3.540987	0.007784	0.02022	0.043573	1	147	107	156	150	236	215	272	432	406	283
ENSMUSG00000075225	chr10	Ccdc162	41538846	41539304	5572	0.893487	0.428534	0.007794	0.020243	0.08356	1	13	14	10	17	17	22	58	40	38	29
ENSMUSG00000025239	chr9	Limd1	1.23E+08	1.23E+08	4849	-0.48839	6.264035	0.007798	0.020248	0.039513	-1	1300	1336	1805	1446	1607	1042	1325	2126	1607	1376
ENSMUSG00000042590	chr13	Ipo11	1.07E+08	1.07E+08	7878	-0.41142	4.207399	0.0078	0.020251	0.025681	-1	297	311	408	343	400	298	413	356	431	347
ENSMUSG00000033282	chr8	Rpgrip1l	91217030	91220289	9855	-0.65441	2.007837	0.007804	0.020254	0.058282	-1	56	82	112	68	88	62	84	51	91	71
ENSMUSG00000061028	chr7	Clasrp	19581044	19581158	2153	0.586271	2.991545	0.007803	0.020254	0.050078	1	121	85	119	86	108	128	208	275	243	255
ENSMUSG00000021143	chr12	Pacs2	1.13E+08	1.13E+08	5480	-0.41372	6.081708	0.00781	0.020265	0.02812	-1	1059	1066	1430	1354	1595	1064	1499	1253	1610	1369
ENSMUSG00000093076	chr17	Mir3082	25831365	25831428	64	0.459089	3.899718	0.007817	0.020278	0.031839	1	178	194	251	198	220	377	372	319	478	445
ENSMUSG00000020224	chr10	Llph	1.2E+08	1.2E+08	1517	0.527166	3.268279	0.007819	0.02028	0.041605	1	105	100	162	115	179	245	216	316	263	255
ENSMUSG00000024238	chr18	Zeb1	5591860	5591967	10112	-0.46969	5.369443	0.007841	0.020335	0.035965	-1	653	603	842	866	1090	535	866	1054	926	688

ENSMUSG00000015653	chr5	Steap2	5664831	5673696	12142	0.856451	1.123721	0.007877	0.020423	0.096049	1	23	12	29	15	46	39	76	45	99	57
ENSMUSG00000071711	chr15	Mpst	78406712	78406744	1509	-0.43358	5.401471	0.007884	0.020437	0.0305	-1	653	676	1009	861	873	717	769	960	894	824
ENSMUSG00000099689	chr7	Unspecified	29908223	29908651	3208	-0.67693	2.682226	0.007891	0.020452	0.068971	-1	133	104	134	127	154	48	130	176	130	97
ENSMUSG00000100801	chr5	Gm15459	5781615	5783555	1941	-0.45891	5.441582	0.007893	0.020452	0.034365	-1	678	776	851	797	1117	788	922	613	1069	865
ENSMUSG00000032228	chr9	Tcf12	71842688	71846560	15529	-0.48815	5.144938	0.007896	0.020458	0.038815	-1	616	490	747	677	959	410	797	886	795	583
ENSMUSG00000034109	chr3	Golim4	75875084	75878177	11072	-0.54276	4.707824	0.007904	0.020474	0.047758	-1	475	306	565	455	842	303	636	400	699	493
ENSMUSG00000032492	chr9	Pth1r	1.11E+08	1.11E+08	2484	1.04424	2.43698	0.007926	0.020528	0.16966	1	39	26	38	51	148	65	119	135	218	318
ENSMUSG00000031438	chrX	Rnf128	1.4E+08	1.4E+08	3464	-0.49899	4.473369	0.00793	0.020535	0.039884	-1	390	438	492	438	384	339	329	354	650	501
ENSMUSG00000037991	chr16	Rmi2	10835059	10835390	4495	-1.29397	2.303468	0.007937	0.020549	0.260091	-1	80	119	132	110	143	86	93	2	79	63
ENSMUSG00000021458	chr13	2010111I01Rik	63014934	63015963	6349	0.448756	4.80579	0.007947	0.020569	0.032185	1	302	363	468	387	458	650	826	550	960	776
ENSMUSG00000028580	chr4	Pum1	1.31E+08	1.31E+08	6008	-0.44062	5.115798	0.007948	0.020569	0.031393	-1	552	531	686	711	878	474	712	849	799	615
ENSMUSG00000041737	chr9	Tmem45b	31426199	31426956	1572	2.82102	2.462982	0.007953	0.020578	1.108738	1	16	5	1	69	17	4	18	6	517	644
ENSMUSG00000048856	chr12	Slc25a47	1.09E+08	1.09E+08	1579	-0.68173	1.543684	0.007958	0.020586	0.058894	-1	48	45	74	67	60	43	36	63	57	55
ENSMUSG00000015013	chr8	Trappc2l	1.23E+08	1.23E+08	607	0.469963	4.669525	0.007961	0.020592	0.03526	1	294	367	406	294	411	668	609	596	742	780
ENSMUSG00000056687	chr11	Gm11696	1.09E+08	1.09E+08	4250	0.996063	-0.1927	0.007981	0.020638	0.089579	1	8	6	8	11	9	16	20	39	26	17
ENSMUSG00000025060	chr19	Slk	47579678	47580343	8284	-0.42528	5.719081	0.00799	0.020658	0.029752	-1	864	907	1152	1005	1111	716	1150	1201	1294	932
ENSMUSG00000023336	chr8	Wfdc1	1.2E+08	1.2E+08	1213	-0.55791	6.184819	0.007999	0.020678	0.05191	-1	1204	1374	1689	1510	1427	1511	1441	784	1592	1428
ENSMUSG00000062960	chr5	Kdr	75932827	75934618	7278	-0.54909	5.760554	0.00801	0.020703	0.050137	-1	712	946	1073	1647	987	710	916	899	1468	1231
ENSMUSG00000029038	chr4	Ssu72	1.56E+08	1.56E+08	2689	0.461217	4.941332	0.008019	0.020721	0.034255	1	361	436	454	416	475	603	713	1071	889	867
ENSMUSG00000045333	chr8	Zfp423	87661810	87662507	5608	-0.48398	3.267599	0.008025	0.020734	0.034045	-1	159	139	200	205	236	118	210	186	210	215
ENSMUSG00000017756	chr13	Slc12a7	73763697	73763890	5131	0.550175	3.596323	0.008076	0.020862	0.046715	1	137	121	137	204	218	246	274	249	497	424
ENSMUSG00000045624	chr2	Esf1	1.4E+08	1.4E+08	4471	-0.48466	4.244256	0.00808	0.020869	0.037145	-1	325	343	468	309	395	271	401	479	402	285
ENSMUSG00000024357	chr18	Sil1	35266400	35266909	1695	0.443212	4.099547	0.008084	0.020873	0.030395	1	192	193	247	235	355	368	449	425	510	539
ENSMUSG00000026196	chr1	Bard1	71027498	71030852	5659	1.341977	0.14636	0.008096	0.0209	0.234141	1	9	6	9	2	21	24	35	5	54	49
ENSMUSG00000037138	chr1	Aff3	38177326	38179570	6579	-0.85741	2.084911	0.008098	0.020902	0.109238	-1	55	38	101	79	200	49	93	75	71	58
ENSMUSG00000071656	chr19	Lrrn4cl	8850785	8851112	2583	-0.60871	3.577818	0.008106	0.020921	0.058213	-1	243	139	229	216	392	150	210	321	209	206
ENSMUSG00000031729	chr8	Ist1	1.1E+08	1.1E+08	2341	0.421251	5.30693	0.00812	0.020948	0.028826	1	531	503	608	532	638	787	993	1195	1153	1155
ENSMUSG00000037295	chr4	Ldlrap1	1.35E+08	1.35E+08	3829	0.506132	3.353569	0.00812	0.020948	0.037944	1	127	110	135	132	199	184	235	267	361	357
ENSMUSG00000098148	chr8	Gm20204	1.17E+08	1.17E+08	5220	0.600827	2.759266	0.008122	0.02095	0.052784	1	75	61	78	93	141	133	243	157	249	165
ENSMUSG00000036880	chr18	Acaa2	74779197	74779265	1515	0.55176	7.536888	0.008127	0.020959	0.051418	1	1967	2863	2421	3160	1913	3667	4153	5724	7141	5429
ENSMUSG00000037278	chr11	Tmem97	78541817	78542796	1375	0.835589	2.6231	0.008129	0.02096	0.108215	1	52	49	56	59	158	147	179	81	291	220
ENSMUSG00000043881	chr14	Kbtbd7	79426511	79431039	4529	-0.56649	3.133442	0.008136	0.020973	0.048685	-1	154	140	180	182	216	93	156	242	200	139
ENSMUSG00000026565	chr1	Pou2f1	1.66E+08	1.66E+08	16597	-0.51816	3.198904	0.008142	0.020986	0.039696	-1	156	128	176	190	257	114	168	216	192	190
ENSMUSG00000047592	chr5	Nxpe5	1.38E+08	1.38E+08	4473	0.958617	1.275283	0.00818	0.021079	0.127862	1	23	13	36	26	34	47	75	23	115	102
ENSMUSG00000004035	chr3	Gstm7	1.08E+08	1.08E+08	1601	0.75419	1.744609	0.008224	0.021189	0.078231	1	29	41	22	60	47	75	85	110	108	95
ENSMUSG00000000127	chr17	Fer	63896018	63896283	3473	-0.45461	3.269348	0.008234	0.021211	0.030204	-1	168	155	206	171	228	128	200	179	246	201
ENSMUSG00000024424	chr18	Ttc39c	12599926	12600003	5197	0.660902	1.548471	0.008242	0.021226	0.05518	1	31	31	43	28	50	62	68	88	85	98
ENSMUSG00000021702	chr13	Thbs4	92751590	92751812	3289	0.774605	9.028647	0.008244	0.021227	0.101424	1	6954	3092	8515	3714	10852	9701	26568	13632	18612	9449
ENSMUSG00000047669	chr10	Msl3l2	56106917	56107029	2140	0.909887	0.253808	0.008261	0.021268	0.082822	1	10	9	16	17	10	22	31	20	48	45
ENSMUSG00000026575	chr1	Nme7	1.64E+08	1.64E+08	5876	0.751405	1.398455	0.008277	0.021306	0.071791	1	20	38	32	29	37	55	78	46	112	83
ENSMUSG00000072940	chr6	Gm10443	86334031	86334240	210	0.748606	1.305084	0.0083	0.021361	0.068478	1	31	33	28	17	36	60	70	62	94	59
ENSMUSG00000022390	chr15	Zc3h7b	81744848	81745346	5958	-0.40789	5.544521	0.008303	0.021362	0.027394	-1	729	675	938	963	1185	723	937	915	1155	971
ENSMUSG00000062743	chr17	Zfp677	21383748	21384020	2917	-0.83129	0.267321	0.008304	0.021362	0.072097	-1	21	21	27	24	28	8	14	27	24	23
ENSMUSG00000045464	chr2	2810002D19Rik	94406151	94406966	2040	-0.6873	1.886685	0.008311	0.021377	0.064992	-1	71	63	83	77	79	70	77	38	70	65
ENSMUSG00000046413	chr8	Irx3os	91800415	91800538	3687	-1.84385	-0.04507	0.008314	0.021379	0.477036	-1	2	37	52	24	4	10	12	1	21	3
ENSMUSG00000068798	chr3	Rap1a	1.06E+08	1.06E+08	2401	-0.43241	5.774513	0.008316	0.021382	0.031137	-1	827	976	1252	1069	1132	751	1077	1313	1335	1004
ENSMUSG00000034164	chr11	Emid1	5106265	5106969	2890	-0.73197	2.713529	0.008319	0.021384	0.081401	-1	95	153	171	137	117	142	97	67	111	137
ENSMUSG00000020523	chr11	Fam114a2	57482993	57484140	3075	-0.43585	5.960988	0.008331	0.021412	0.031723	-1	1045	1115	1329	1160	1315	1083	1236	1383	1296	1124
ENSMUSG00000032410	chr9	Xrn1	95954760	95954943	18585	-0.5555	4.010939	0.008343	0.02144	0.049572	-1	292	213	369	317	426	168	253	474	348	293
ENSMUSG00000020610	chr11	Amz2	1.09E+08	1.09E+08	5584	-0.4367	6.157907	0.008347	0.021445	0.031966	-1	1202	1245	1544	1378	1471	1305	1391	1452	1448	1398
ENSMUSG00000042677	chr4	Zc3h12a	1.25E+08	1.25E+08	2882	0.623293	2.097799	0.008359	0.021473	0.052215	1	34	60	62	56	62	77	135	120	157	108
ENSMUSG00000026662	chr2	Sephs1	4881564	4881860	5925	-0.40352	4.584234	0.008362	0.021477	0.025804	-1	413	383	520	417	551	380	492	430	627	491
ENSMUSG00000097989	chr15	Gm4335	93196595	93197598	1004	-1.20696	0.250441	0.008366	0.021482	0.196746	-1	23	39	11	43	10	10	8	19	22	22
ENSMUSG00000034789	chr13	Rab24	55319223	55320214	1865	0.437711	4.933379	0.008369	0.021487	0.031037	1	414	416	485	382	447	704	752	839	864	903
ENSMUSG00000026470	chr1	Stx6	1.55E+08	1.55E+08	10637	0.446581	3.869477	0.008405	0.021574	0.030378	1	181	168	203	231	244	275	387	326	528	464
ENSMUSG00000025271	chrX	Pfkfb1	1.51E+08	1.51E+08	4017	-0.63688	5.010155	0.008409	0.021578	0.067719	-1	529	828	670	758	393	508	429	707	607	664
ENSMUSG00000069495	chr2	Epc2	49451486	49451958	4697	-0.56933	3.782523	0.008408	0.021578	0.051785	-1	242	222	290	269	352	142	248	421	278	210
ENSMUSG00000071647	chr19	Eml3	8929694	8929952	3161	0.52816	3.329225	0.008432	0.02163	0.042607	1	113	91	148	122	220	179	248	259	362	343
ENSMUSG00000098543	chr19	Gm27533	5844286	5844437	152	0.644356	4.605739	0.008434	0.02163	0.068666	1	280	276	455	217	363	298	610	639	823	1170
ENSMUSG00000101939	chr1	Gm28438	24612775	24613119	345	-0.82386	2.014041	0.008434	0.02163	0.102174	-1	69	81	100	129	38	43	56	71	102	70
ENSMUSG00000002550	chr2	Uck1	32255002	32256211	2751	0.720744	4.187543	0.008441	0.021642	0.085442	1	218	168	222	234	306	286	353	291	820	968
ENSMUSG00000005575	chr7	Ube2m	13035120	13035754	2287	0.441495	6.571149	0.008458	0.021684	0.032986	1	1046	1326	1435	1479	1423	2259	2292	2298	3123	2777
ENSMUSG00000005469	chr8	Prkaca	83972978	83973232	2293	0.409796	7.486598	0.008464	0.02169	0.028652	1	2113	2246	2728	2752	3065	3975	4970	4560	5768	4618
ENSMUSG00000057098	chr11	Ebf1	44617317	44618312	9756	-0.52597	3.844746	0.008463	0.02169	0.043995	-1	234	166	333	299	409	157	253	245	404	344
ENSMUSG00000016763	chr15	Scube1	83602583	83607477	8346	-1.05151	-0.04027	0.008466	0.021691	0.12248	-1	12	12	15	31	33	8	10	8	29	15
ENSMUSG00000040520	chr4	Manea	26324506	26328308	4867	-0.52029	2.661334	0.008484	0.021734	0.037713	-1	107	95	124	125	170	92	115	120	157	120

ENSMUSG00000025159	chr19	Mms19	41941086	41944580	10415	0.486036	4.17098	0.008492	0.021749	0.037516	1	231	209	267	249	290	314	415	691	538	495
ENSMUSG00000018347	chr11	Zkscan6	65807175	65807261	2371	0.610749	1.895118	0.008511	0.021794	0.048048	1	45	39	50	41	64	76	91	101	118	124
ENSMUSG00000087153	chr8	Gm6483	19682268	19682655	6290	-0.90542	0.335058	0.008519	0.02181	0.093297	-1	30	14	22	28	36	13	29	24	16	14
ENSMUSG00000029634	chr5	Rnf6	1.46E+08	1.46E+08	4022	-0.53519	5.391473	0.008521	0.021812	0.048041	-1	685	720	1001	859	889	535	814	1250	808	590
ENSMUSG00000029050	chr4	Ski	1.55E+08	1.55E+08	5562	-0.47656	6.248341	0.00853	0.02183	0.038467	-1	1331	989	1416	1497	2270	1063	1695	1603	1790	1317
ENSMUSG00000044250	chr15	Pced1b	97247107	97247164	2198	0.84163	0.78759	0.008531	0.02183	0.082704	1	14	15	26	25	16	33	32	44	62	72
ENSMUSG00000045268	chr4	Zfp691	1.19E+08	1.19E+08	2399	-0.46171	3.872494	0.008535	0.021835	0.033165	-1	230	276	337	295	266	228	279	346	327	250
ENSMUSG00000004285	chr6	Atp6v1f	29467718	29467974	1063	0.42829	5.545	0.008561	0.021891	0.030548	1	545	607	839	610	727	1125	1082	1234	1404	1353
ENSMUSG00000011256	chr11	Adam19	46055992	46056210	7115	0.590036	4.744666	0.008562	0.021891	0.058031	1	288	183	351	375	640	479	1059	659	852	735
ENSMUSG00000034285	chr11	Nipsnap1	4873951	4874103	2649	0.925012	0.531559	0.00856	0.021891	0.103871	1	11	8	25	9	25	21	36	30	60	60
ENSMUSG00000028282	chr4	Casp8ap2	32615451	32615492	6826	-0.56287	2.84122	0.008571	0.021911	0.046953	-1	126	115	143	146	180	84	131	183	174	105
ENSMUSG00000017210	chr11	Med24	98704591	98705016	6528	-0.39464	5.586374	0.00861	0.022004	0.02588	-1	755	781	1020	951	1064	775	1001	862	1216	1008
ENSMUSG00000040296	chr4	Ddx58	40203773	40204065	7050	0.716985	3.248003	0.00861	0.022004	0.0826	1	73	101	130	130	169	331	246	129	263	355
ENSMUSG00000075701	chr7	Vimp	66079649	66079789	1198	0.430139	4.908142	0.008616	0.022013	0.030258	1	396	317	511	369	558	605	823	796	859	930
ENSMUSG00000032366	chr9	Tpm1	67022590	67023441	6485	-0.54348	14.41899	0.00869	0.022199	0.051091	-1	321325	439209	552218	406506	454540	475288	338687	388569	359310	455326
ENSMUSG00000027829	chr3	Ccnl1	65946151	65946948	5997	0.464807	3.780657	0.008692	0.022199	0.033352	1	171	169	203	159	260	237	362	363	429	474
ENSMUSG00000042369	chr2	Rbm45	76369984	76370428	1898	0.454429	3.503492	0.008709	0.022238	0.030987	1	132	137	201	159	164	270	311	271	343	313
ENSMUSG00000103627	chr6	IFFO1	1.25E+08	1.25E+08	1680	0.524442	3.986619	0.008717	0.022256	0.044408	1	162	147	270	196	330	271	626	421	471	398
ENSMUSG00000035051	chr17	Dhx57	80238304	80238930	5077	-0.45083	3.541383	0.008725	0.022272	0.03081	-1	227	163	229	217	284	160	230	244	276	240
ENSMUSG00000059159	chr6	Gm8129	52346730	52346942	213	0.785737	1.10054	0.008731	0.022282	0.07757	1	16	28	23	27	30	69	65	54	53	51
ENSMUSG00000021270	chr12	Hsp90aa1	1.11E+08	1.11E+08	3931	0.514907	6.08457	0.008737	0.022295	0.045172	1	589	905	1127	868	1235	1373	2243	1204	2536	2078
ENSMUSG00000018263	chr5	Tbx5	1.2E+08	1.2E+08	3941	-1.00519	0.466346	0.008747	0.022314	0.130053	-1	20	16	16	37	61	15	11	21	27	28
ENSMUSG00000020513	chr11	Tubd1	86544991	86545336	2070	-0.59636	2.877365	0.008748	0.022314	0.05439	-1	160	139	165	118	141	108	155	84	186	150
ENSMUSG00000015312	chr10	Gadd45b	80930091	80930359	1266	0.71487	4.588345	0.008753	0.02232	0.085584	1	240	286	462	346	167	469	506	1088	580	811
ENSMUSG00000019817	chr10	Plagl1	13060504	13060859	7819	0.725049	4.377163	0.008752	0.02232	0.088114	1	211	134	225	190	599	354	807	449	858	609
ENSMUSG00000017376	chr11	Nlk	78567168	78568975	5447	-0.47972	3.378462	0.008759	0.022329	0.035065	-1	194	194	241	175	193	144	232	178	247	214
ENSMUSG00000021823	chr14	Vcl	20929433	20929688	5229	-0.4354	7.025399	0.008794	0.022416	0.032583	-1	1958	2160	2936	2504	3052	2031	3188	2265	3206	2298
ENSMUSG00000085218	chr2	BB218582	1.07E+08	1.07E+08	1311	-0.91332	1.723696	0.008808	0.022447	0.124534	-1	60	89	79	68	51	70	56	19	65	47
ENSMUSG00000032898	chr5	Fbxo21	1.18E+08	1.18E+08	3909	0.635941	3.745087	0.00881	0.022449	0.065709	1	154	120	182	202	218	164	258	566	515	436
ENSMUSG00000038372	chr13	Gmds	31819579	31819978	3323	0.915088	1.169357	0.008833	0.022502	0.118347	1	22	13	31	15	45	50	72	27	93	86
ENSMUSG00000024500	chr18	Ppp2r2b	42637432	42637927	3985	-1.05427	-0.10563	0.008839	0.022511	0.118183	-1	17	8	21	15	38	11	20	14	13	6
ENSMUSG00000036513	chr3	Commd2	57642904	57646876	4757	0.475442	3.638544	0.00884	0.022511	0.034832	1	172	154	205	143	185	325	339	288	364	341
ENSMUSG00000025277	chr14	Abhd6	8002902	8002963	2157	-0.70544	2.059138	0.008851	0.022536	0.072787	-1	59	92	107	95	69	60	52	72	72	106
ENSMUSG00000053716	chr9	Dusp7	1.06E+08	1.06E+08	3356	-0.49407	4.196241	0.008891	0.022632	0.039688	-1	429	278	389	303	367	273	323	445	399	330
ENSMUSG00000044155	chr6	Lsm8	18848579	18848763	4108	0.510384	3.286277	0.00892	0.0227	0.039816	1	113	109	199	111	137	229	267	225	290	306
ENSMUSG00000097354	chr6	2310001H17Rik	1.29E+08	1.29E+08	5694	-0.578	3.90763	0.008921	0.0227	0.05431	-1	271	337	378	252	233	308	253	288	252	262
ENSMUSG00000021947	chr14	Cryl1	57275034	57275562	1410	0.610986	2.221544	0.008923	0.022701	0.051587	1	61	49	55	58	77	102	107	101	184	154
ENSMUSG00000037406	chr8	Htra4	25025451	25025734	1795	-1.24365	0.791794	0.008924	0.022701	0.22711	-1	56	8	62	19	55	14	29	43	14	14
ENSMUSG00000040661	chr9	Rad54l2	1.07E+08	1.07E+08	11828	-0.46636	3.723373	0.008928	0.022706	0.034086	-1	198	193	273	254	377	156	258	253	362	285
ENSMUSG00000031808	chr8	Slc27a1	71568927	71569023	2795	0.879764	5.880212	0.008944	0.022744	0.13206	1	615	633	550	914	705	666	777	3740	1920	1959
ENSMUSG00000026580	chr1	Selp	1.64E+08	1.64E+08	4413	0.771814	1.440811	0.008957	0.022771	0.081197	1	18	28	33	43	39	53	46	79	130	82
ENSMUSG00000020335	chr11	Zfp354b	50921823	50923840	2888	-0.82643	1.290356	0.008964	0.022785	0.094835	-1	47	42	66	43	57	24	33	74	45	25
ENSMUSG00000040464	chr5	Gtpbp10	5537454	5539451	4744	-0.45496	3.520581	0.008967	0.022788	0.031549	-1	184	193	276	242	205	187	218	210	279	231
ENSMUSG00000031250	chrX	Tnmd	1.34E+08	1.34E+08	1353	-1.09986	5.913937	0.008974	0.022803	0.204833	-1	1899	524	1702	572	2307	626	1870	888	816	263
ENSMUSG00000041957	chr16	Pkp2	16213318	16213595	5360	0.803075	1.029087	0.008986	0.02283	0.082379	1	12	19	34	30	23	51	79	44	66	44
ENSMUSG00000039103	chr3	Nexn	1.52E+08	1.52E+08	2562	-0.49857	8.54406	0.008993	0.022842	0.043288	-1	6238	6392	8268	7567	8085	7598	8263	4764	8068	6880
ENSMUSG00000025024	chr19	Smndc1	53379214	53380601	2125	0.432549	4.394143	0.008995	0.022843	0.030199	1	228	256	344	318	351	442	524	697	612	524
ENSMUSG00000020722	chr11	Cacng1	1.08E+08	1.08E+08	1249	0.507896	7.989649	0.009029	0.02292	0.044912	1	2740	2772	3815	3760	4656	6270	5603	9640	6544	6234
ENSMUSG00000032040	chr9	Dcps	35124408	35124844	1451	0.518685	2.887305	0.009027	0.02292	0.038904	1	88	98	114	93	105	168	207	154	252	223
ENSMUSG00000034472	chr8	Rasd2	75213944	75214078	3176	-1.18286	2.130058	0.009034	0.022929	0.222552	-1	62	142	147	119	19	74	51	56	33	83
ENSMUSG00000052139	chr5	Bre	31697684	31698077	4781	0.435875	4.529909	0.009038	0.022935	0.031005	1	237	283	379	346	403	543	537	512	785	712
ENSMUSG00000024248	chr17	Cox7a2l	83501919	83502737	1147	0.468701	6.876625	0.009053	0.022962	0.038	1	1366	1679	1942	1733	1430	2780	3269	3452	3374	2911
ENSMUSG00000029715	chr5	Pop7	1.38E+08	1.38E+08	1081	0.623124	2.896033	0.009051	0.022962	0.059533	1	80	89	108	95	110	212	210	107	260	241
ENSMUSG00000049960	chr14	Mrps16	20391231	20391460	566	0.49666	5.12469	0.009052	0.022962	0.041526	1	411	512	570	457	435	971	925	693	1181	939
ENSMUSG00000087119	chr3	Atg4a-ps	1.04E+08	1.04E+08	1185	-0.88255	0.629779	0.009097	0.023069	0.097088	-1	31	21	41	47	19	20	20	33	29	19
ENSMUSG00000027951	chr3	Adar	89715022	89715150	6786	0.629216	3.423048	0.009106	0.023084	0.06411	1	107	94	134	163	210	273	259	166	368	437
ENSMUSG00000028070	chr3	Apoa1bp	88056520	88056776	908	0.4268	4.783068	0.009107	0.023084	0.03002	1	281	353	439	436	457	597	708	606	950	831
ENSMUSG00000079509	chrX	Zfx	94074631	94079979	7755	-0.53036	4.149014	0.009126	0.02313	0.046384	-1	300	275	360	345	482	186	355	510	376	280
ENSMUSG00000036940	chr4	Kdm1a	1.37E+08	1.37E+08	5179	0.415396	4.911681	0.009147	0.023179	0.028535	1	329	382	457	458	534	576	843	921	941	742
ENSMUSG00000050621	chr9	Rps27rt	1.15E+08	1.15E+08	370	0.55156	3.265023	0.009184	0.023268	0.046783	1	140	125	139	115	114	211	289	328	249	230
ENSMUSG00000037426	chr5	Depdc5	32863701	32863743	11767	-0.53231	3.251408	0.009206	0.02332	0.044296	-1	169	148	194	216	207	130	185	116	281	208
ENSMUSG00000048647	chr2	Exd1	1.2E+08	1.2E+08	6042	-0.97219	1.063148	0.009215	0.023338	0.137668	-1	43	50	53	38	37	20	34	8	45	56
ENSMUSG00000027439	chr2	Gzf1	1.49E+08	1.49E+08	4472	-0.45124	4.656638	0.009226	0.02336	0.033776	-1	416	412	588	543	465	373	502	623	577	411
ENSMUSG00000031928	chr9	Mre11a	14784654	14784757	5902	-0.51377	3.639157	0.009237	0.023381	0.042007	-1	234	161	320	218	298	214	255	156	315	254
ENSMUSG00000038429	chr6	Usp5	1.25E+08	1.25E+08	4621	0.415908	6.267351	0.009236	0.023381	0.029793	1	927	938	1187	1100	1386	1488	1916	2409	2530	1995
ENSMUSG00000028559	chr4	Osbpl9	1.09E+08	1.09E+08	7006	-0.44868	6.415806	0.009256	0.023425	0.034875	-1	1506	1408	1886	1566	1867	1245	1521	2219	1811	1627

ENSMUSG00000004568	chr8	Arhgef18	3393006	3393102	8395	-0.43506	3.54599	0.009264	0.02344	0.028917	-1	205	174	218	243	278	165	250	231	277	237
ENSMUSG00000101970	chr7	RP23-32A8.1	73544036	73544410	3778	0.600917	2.761777	0.009266	0.02344	0.054137	1	88	95	72	94	85	122	185	246	204	185
ENSMUSG00000066441	chr12	Rdh11	79174337	79176250	3455	0.58878	2.399275	0.009272	0.023451	0.050215	1	61	55	73	54	105	93	130	136	217	162
ENSMUSG00000055322	chr1	Tns1	73910231	73914674	16010	-0.46547	8.192575	0.009275	0.023454	0.038031	-1	4534	4638	6043	6712	6555	3662	4827	7428	6928	6166
ENSMUSG00000027599	chr3	Armc1	19131402	19134223	3673	-0.41941	4.906352	0.009279	0.02346	0.029341	-1	489	579	652	524	602	463	592	649	758	542
ENSMUSG00000070348	chr7	Ccnd1	1.45E+08	1.45E+08	3835	0.544246	4.792525	0.009305	0.023523	0.05013	1	319	330	366	365	505	659	764	402	1227	826
ENSMUSG00000055633	chr7	Zfp580	5051532	5051714	1101	0.697274	1.422406	0.009328	0.023576	0.062483	1	27	26	24	46	40	67	70	68	84	79
ENSMUSG00000103480	chr3	Bdh2	1.35E+08	1.35E+08	768	0.881113	0.800385	0.009349	0.023624	0.101088	1	12	11	26	21	27	25	40	81	44	56
ENSMUSG00000034485	chr9	Uaca	60794548	60794692	4428	-0.466	6.761646	0.009353	0.023631	0.037884	-1	1783	1532	2326	2526	2414	1568	1889	2801	2485	1924
ENSMUSG00000024474	chr18	Ik	36744656	36744788	1996	0.412434	6.147504	0.009364	0.023655	0.029345	1	743	925	1154	1090	1192	1436	1969	1960	2211	1893
ENSMUSG00000050315	chr3	Synpo2	1.23E+08	1.23E+08	9403	-0.47289	9.258136	0.00937	0.023664	0.03944	-1	9576	9930	12570	13865	13752	12172	12432	8583	14827	11321
ENSMUSG00000004996	chr8	Mri1	84249906	84251711	3273	0.464794	3.530468	0.009377	0.023678	0.033264	1	165	123	175	147	194	211	281	361	355	351
ENSMUSG00000028986	chr5	Klhl7	24100590	24100874	3419	-0.73319	5.085555	0.00939	0.023703	0.092712	-1	682	602	639	714	893	308	453	1255	570	402
ENSMUSG00000032905	chr18	Atg12	46732417	46734509	2492	-0.4367	5.062899	0.00939	0.023703	0.032182	-1	605	624	779	538	637	543	729	677	730	621
ENSMUSG00000020755	chr11	Sap30bp	1.16E+08	1.16E+08	3708	0.40905	4.206875	0.009399	0.023721	0.026694	1	233	215	318	234	327	357	478	547	582	494
ENSMUSG00000026643	chr2	Nmt2	3284212	3284406	6556	-0.4184	3.938752	0.009419	0.023762	0.027593	-1	235	259	334	288	350	227	285	275	369	379
ENSMUSG00000051185	chr1	Fam174a	95313623	95314250	4814	-0.427	5.427248	0.009417	0.023762	0.031069	-1	695	823	957	787	833	730	744	939	973	876
ENSMUSG00000025192	chr19	Entpd7	43689672	43689904	8963	0.86278	1.455995	0.009444	0.023813	0.107978	1	28	23	34	15	58	46	81	46	127	105
ENSMUSG00000033953	chr11	Ppp3r1	17159263	17159542	3228	-0.41453	7.525398	0.009442	0.023813	0.030186	-1	3080	2883	4153	3184	4421	3168	3756	3743	4382	3343
ENSMUSG00000099858	chr1	Gm6652	1.54E+08	1.54E+08	1070	-0.81064	0.470245	0.009443	0.023813	0.071143	-1	22	21	38	34	25	18	20	28	18	26
ENSMUSG00000063800	chr4	Prpf38a	1.09E+08	1.09E+08	5298	0.45264	3.75769	0.009458	0.023844	0.031868	1	183	190	210	176	176	267	392	342	412	403
ENSMUSG00000053838	chr11	Nudcd3	6105691	6108355	6496	-0.41209	6.833034	0.009493	0.023927	0.029685	-1	1840	1803	2384	2144	2779	1969	2160	2423	2558	2250
ENSMUSG00000023009	chr15	Nckap5l	99422035	99422908	5002	0.617985	2.940219	0.009503	0.023949	0.060565	1	76	59	100	86	193	142	241	187	297	219
ENSMUSG00000051586	chr6	Mical3	1.21E+08	1.21E+08	7398	-0.4622	4.968398	0.00953	0.024012	0.036165	-1	398	457	740	567	944	451	563	646	721	703
ENSMUSG00000017548	chr11	Suz12	79993106	79993599	4945	-0.40288	4.35076	0.009539	0.02403	0.026332	-1	329	332	431	375	477	282	435	460	495	389
ENSMUSG00000054920	chr5	Klhl5	65107568	65107861	4866	0.487494	3.534855	0.009541	0.024031	0.037324	1	141	115	180	170	199	165	328	363	386	351
ENSMUSG00000074457	chr3	S100a16	90537254	90537417	1617	0.442959	5.910748	0.009559	0.024072	0.033979	1	668	776	939	914	965	1386	1662	1188	1982	1869
ENSMUSG00000038168	chr16	Leprel1	25959288	25960450	3721	-0.73251	2.490211	0.009613	0.024203	0.084535	-1	130	41	147	100	174	64	107	115	124	82
ENSMUSG00000020929	chr11	Eftud2	1.03E+08	1.03E+08	8395	0.418362	4.964818	0.009644	0.024276	0.02953	1	344	359	514	424	617	639	817	700	1149	898
ENSMUSG00000031253	chrX	Srpx2	1.34E+08	1.34E+08	2922	0.6238	3.864135	0.009691	0.024388	0.06552	1	174	102	175	164	362	269	587	322	536	362
ENSMUSG00000079243	chr9	Xirp1	1.2E+08	1.2E+08	5839	-0.59897	7.167004	0.009691	0.024388	0.063359	-1	1827	2370	2250	3764	4489	2457	3226	2312	3642	1704
ENSMUSG00000078234	chr4	Klhdc7a	1.4E+08	1.4E+08	7807	2.239529	2.213683	0.009711	0.024432	0.774168	1	17	8	6	57	44	7	28	11	307	568
ENSMUSG00000063801	chr7	Ap3s2	79875332	79880612	5797	-0.40183	5.413055	0.009746	0.024517	0.027663	-1	719	719	955	796	851	656	880	950	988	813
ENSMUSG00000078813	chr7	Leng1	3660098	3661360	2222	0.470746	3.214656	0.009785	0.024609	0.033593	1	94	117	134	138	163	181	225	286	315	246
ENSMUSG00000075486	chr14	Commd6	1.02E+08	1.02E+08	1322	0.487502	2.835571	0.009812	0.024673	0.034345	1	88	82	115	90	115	155	199	169	242	196
ENSMUSG00000020131	chr10	Pcsk4	80321283	80321951	2958	1.030217	0.010424	0.009825	0.024701	0.113331	1	11	11	11	5	10	16	14	41	30	39
ENSMUSG00000095687	chr17	Rnaset2a	8128610	8128886	1259	0.616211	2.326434	0.009832	0.024715	0.055109	1	51	75	71	66	56	132	142	109	181	126
ENSMUSG00000033581	chr16	Igf2bp2	22059009	22060885	7131	0.746253	2.770909	0.009859	0.024778	0.091351	1	49	48	100	66	174	102	238	141	277	248
ENSMUSG00000035877	chr2	Zhx3	1.61E+08	1.61E+08	13259	-0.43585	4.925302	0.009864	0.024786	0.032233	-1	443	403	699	584	847	483	611	633	755	537
ENSMUSG00000024911	chr19	Fibp	5460607	5460778	1240	0.428085	4.249369	0.009875	0.024809	0.029943	1	237	232	309	282	286	438	465	406	621	603
ENSMUSG00000041488	chr19	Stx3	11775119	11776588	4979	0.82082	1.9087	0.00989	0.024844	0.102905	1	28	44	53	63	29	56	72	105	151	170
ENSMUSG00000044931	chr10	Apba3	81268172	81268319	2106	-0.451	5.62736	0.0099	0.024863	0.035422	-1	801	861	1161	1009	921	768	896	1274	1050	866
ENSMUSG00000027162	chr2	Lin7c	1.1E+08	1.1E+08	4521	-0.41861	4.535203	0.009933	0.024936	0.029348	-1	367	379	485	449	541	275	464	533	596	480
ENSMUSG00000054309	chr12	Cpsf3	21286297	21286544	2560	0.424393	4.480456	0.009934	0.024936	0.029995	1	242	271	353	332	400	515	575	472	712	696
ENSMUSG00000071072	chr10	Ptges3	1.28E+08	1.28E+08	2217	0.424104	5.832454	0.009932	0.024936	0.031362	1	633	790	906	740	1005	1118	1428	1774	1691	1616
ENSMUSG00000023094	chr2	Msrb2	19371440	19371543	1377	-0.55252	4.018327	0.009952	0.024976	0.051492	-1	243	408	362	335	221	270	290	264	372	329
ENSMUSG00000037262	chr2	Kin	10080593	10080744	1705	0.577324	2.55876	0.009963	0.024998	0.049419	1	76	80	73	62	93	115	172	201	160	158
ENSMUSG00000003545	chr7	Fosb	19302721	19305302	3751	1.826704	1.151781	0.009972	0.025009	0.524364	1	9	3	10	18	40	11	279	35	37	20
ENSMUSG00000004069	chr16	Dnaja3	4639989	4640148	3912	-0.44306	6.818324	0.009973	0.025009	0.034833	-1	1738	2232	2465	2250	2101	2063	2193	2062	2710	2078
ENSMUSG00000031996	chr9	Aplp2	31149557	31150972	3694	-0.42264	7.91414	0.009972	0.025009	0.031937	-1	3843	4093	5272	4576	5370	3328	4506	4197	6617	5799
ENSMUSG00000037885	chr2	Stk35	1.3E+08	1.3E+08	6195	-0.52058	3.191201	0.009974	0.025009	0.0432	-1	201	141	181	174	188	99	172	201	245	170
ENSMUSG00000031938	chr9	4931406C07Rik	15283337	15284991	2981	0.75164	3.995719	0.009984	0.025029	0.097065	1	142	150	203	234	270	257	346	201	736	858
ENSMUSG00000097375	chr13	6720427I07Rik	48535523	48537822	2300	0.799871	0.718657	0.009986	0.025029	0.073435	1	13	25	21	15	18	24	53	47	60	46
ENSMUSG00000031986	chr8	Sprtn	1.25E+08	1.25E+08	2116	-0.66665	2.134514	0.009996	0.025049	0.067478	-1	82	65	123	87	88	44	79	120	85	65
ENSMUSG00000040734	chr7	Ppp1r13l	19359749	19359798	3604	0.624749	1.784515	0.010011	0.025083	0.053877	1	31	29	57	49	56	66	110	104	111	83
ENSMUSG00000060733	chr10	Ipmk	71347763	71348090	7093	-0.42075	4.317201	0.010016	0.025092	0.029154	-1	326	339	463	377	394	349	340	437	461	387
ENSMUSG00000008845	chr6	Cd163	1.24E+08	1.24E+08	4492	-0.6592	3.956355	0.010028	0.025117	0.074215	-1	306	177	414	240	482	165	207	445	240	343
ENSMUSG00000022110	chr14	Sucla2	73525319	73525546	3988	-0.47055	9.188973	0.010057	0.025186	0.039796	-1	9284	11933	12859	11801	10172	10240	10337	13471	12081	10419
ENSMUSG00000034936	chr11	Arl4d	1.02E+08	1.02E+08	1382	0.770487	2.678086	0.010061	0.02519	0.096879	1	63	70	77	89	88	111	153	362	127	163
ENSMUSG00000055991	chr5	Zkscan5	1.45E+08	1.45E+08	4114	-0.55306	3.421614	0.010071	0.025209	0.050019	-1	186	166	231	260	214	126	200	307	200	177
ENSMUSG00000047181	chr11	Samd14	95009879	95010576	3379	0.812998	1.714377	0.010074	0.025214	0.101059	1	38	12	39	33	75	65	109	87	139	77
ENSMUSG00000038279	chr6	Nop2	1.25E+08	1.25E+08	2623	0.40008	4.487861	0.010081	0.025225	0.026394	1	256	307	339	332	375	464	584	618	761	555
ENSMUSG00000033499	chr13	Larp4b	9093881	9094180	8464	-0.43513	6.645416	0.010125	0.025332	0.033664	-1	1391	1930	2230	1995	2069	1731	2113	1650	2438	1994
ENSMUSG00000083863	chr2	Gm13341	22587291	22587962	672	-0.80383	0.746144	0.010148	0.025386	0.085145	-1	24	45	36	38	25	18	24	22	43	32
ENSMUSG00000052825	chr8	Gm9892	52196065	52197056	992	-0.5488	3.241626	0.010186	0.025476	0.04881	-1	209	181	184	162	180	124	190	240	181	155
ENSMUSG00000019437	chr11	Tlcd1	78176711	78176887	5009	0.994348	2.446047	0.010194	0.025492	0.164281	1	36	35	45	87	100	61	89	113	416	205

ENSMUSG00000005774	chr3	Rfx5	94954075	94954192	5497	-0.49157	3.18299	0.0102	0.025501	0.037651	-1	149	122	197	182	242	137	190	134	235	186
ENSMUSG00000001942	chr9	Siae	37613847	37613926	3433	-0.47953	3.190497	0.010204	0.025505	0.035792	-1	157	138	198	178	215	150	185	130	213	206
ENSMUSG00000049882	chr12	Vcpkmt	69577628	69577940	1027	0.67821	1.302857	0.010228	0.025563	0.059255	1	27	29	42	20	33	61	62	64	85	65
ENSMUSG00000039372	chr1	March4	72427112	72429009	4553	-0.88751	0.145628	0.010247	0.025605	0.079656	-1	19	13	27	26	28	21	11	13	19	19
ENSMUSG00000031402	chrX	Mpp1	75109733	75110843	5343	0.500077	5.205368	0.010261	0.025635	0.04377	1	465	415	551	405	736	797	861	689	1449	1300
ENSMUSG00000030607	chr7	Acan	79053483	79053608	7355	-2.26497	2.054327	0.010289	0.025701	0.803744	-1	90	11	58	11	454	20	80	4	64	2
ENSMUSG00000018845	chr11	Unc45b	82910550	82911253	4493	-0.4114	8.057151	0.010314	0.025758	0.030536	-1	4241	4328	6447	4801	5733	4652	5635	5240	5757	5227
ENSMUSG00000062234	chr5	Gak	1.09E+08	1.09E+08	5938	0.451362	4.5347	0.010335	0.025806	0.034639	1	287	227	362	313	463	382	573	591	891	742
ENSMUSG00000001729	chr12	Akt1	1.13E+08	1.13E+08	4098	0.445774	6.499413	0.010358	0.025858	0.035517	1	926	1092	1249	1300	1922	1617	2688	2612	3140	2272
ENSMUSG00000022485	chr15	Hoxc5	1.03E+08	1.03E+08	3089	-0.46734	3.942957	0.010367	0.025876	0.035882	-1	250	249	370	307	312	313	272	258	298	332
ENSMUSG00000031489	chr8	Adrb3	27225776	27226528	2893	2.520774	2.551027	0.010369	0.025876	0.977107	1	13	13	1	32	90	4	40	13	323	819
ENSMUSG00000026377	chr1	Nifk	1.18E+08	1.18E+08	1965	0.429203	4.514987	0.010382	0.025905	0.031179	1	218	319	417	306	372	515	641	583	663	634
ENSMUSG00000001783	chr10	Rtcb	85938637	85939119	2615	0.394844	6.022694	0.010394	0.025922	0.027546	1	788	839	1083	888	1103	1389	1682	1774	2022	1747
ENSMUSG00000030609	chr7	Aen	78895854	78896014	5687	-0.46757	4.846777	0.010395	0.025922	0.0379	-1	474	577	709	529	468	471	556	646	650	482
ENSMUSG00000042737	chr3	Dpm3	89259358	89259591	919	0.50543	2.907956	0.010394	0.025922	0.038697	1	77	100	98	102	135	142	196	193	240	249
ENSMUSG00000027547	chr2	Sall4	1.69E+08	1.69E+08	5536	-0.76719	0.714303	0.010414	0.025967	0.071012	-1	31	22	39	42	31	29	27	19	31	28
ENSMUSG00000070424	chr7	Art5	1.02E+08	1.02E+08	1806	0.989778	4.397467	0.010425	0.025987	0.171456	1	286	178	206	285	191	298	420	1697	395	423
ENSMUSG00000004994	chr8	Ccdc130	84257795	84258926	2694	0.560123	2.228679	0.010427	0.025988	0.044614	1	60	46	73	55	76	99	136	146	138	116
ENSMUSG00000020284	chr10	1810043G02Rik	77978524	77978781	6627	0.626107	2.452352	0.010433	0.025999	0.059911	1	58	82	83	59	66	99	122	202	164	175
ENSMUSG00000028136	chr3	Snx27	94497550	94502065	6241	-0.39814	5.487876	0.010438	0.026002	0.027747	-1	696	710	986	852	1046	642	869	810	1216	1037
ENSMUSG00000078201	chr2	Tmem203	25255439	25256292	854	0.600227	2.646956	0.010437	0.026002	0.055847	1	72	59	90	94	95	144	116	228	174	196
ENSMUSG00000020087	chr10	Tysnd1	61695514	61696742	2286	0.500673	3.708772	0.010451	0.026029	0.041237	1	120	189	198	186	205	268	259	325	476	463
ENSMUSG00000045538	chr8	Ddx28	1.06E+08	1.06E+08	2262	0.461359	3.73382	0.010474	0.026081	0.034595	1	147	175	211	188	207	294	311	462	398	312
ENSMUSG00000026977	chr2	March7	60209887	60210084	10391	-0.56051	4.47079	0.010491	0.02612	0.054766	-1	412	342	538	400	522	227	381	702	456	341
ENSMUSG00000031389	chrX	Arhgap4	73891442	73894963	8105	0.433505	4.491578	0.0105	0.026138	0.031832	1	245	308	331	319	392	529	576	460	741	696
ENSMUSG00000030314	chr6	Atg7	1.15E+08	1.15E+08	5273	0.491485	3.294328	0.010504	0.026139	0.038224	1	105	121	145	131	176	175	222	230	388	334
ENSMUSG00000098798	chr8	Gm27288	19493189	19493268	80	0.573011	2.529907	0.010502	0.026139	0.049338	1	57	81	89	59	95	108	201	167	183	136
ENSMUSG00000032035	chr9	Ets1	32636221	32636314	8476	-0.49864	4.81695	0.010508	0.026143	0.043511	-1	367	463	600	791	539	351	602	465	792	568
ENSMUSG00000020390	chr11	Ube2b	51985497	51986810	2126	-0.5362	8.212283	0.010515	0.026156	0.052135	-1	5202	5717	6994	5946	5196	5023	4786	8171	5018	4782
ENSMUSG00000020831	chr11	0610010K14Rik	70235206	70235464	1896	0.436891	3.941029	0.01052	0.026164	0.031126	1	155	227	214	232	253	322	417	347	510	462
ENSMUSG00000040599	chr11	Mis12	71019611	71020189	3003	0.488511	3.160518	0.010528	0.02618	0.036689	1	118	114	118	120	140	194	276	189	314	237
ENSMUSG00000048040	chrX	Arxes2	1.36E+08	1.36E+08	1532	1.972469	0.899178	0.010543	0.026212	0.603556	1	12	5	2	14	25	3	15	13	114	193
ENSMUSG00000031200	chrX	Mtcp1	75410444	75411131	4478	-0.72331	1.233351	0.010547	0.026216	0.070761	-1	42	48	69	39	38	26	46	44	38	47
ENSMUSG00000032288	chr9	Imp3	56937475	56938398	924	0.441126	4.731494	0.010575	0.026279	0.033377	1	329	398	434	333	363	622	629	744	772	766
ENSMUSG00000079037	chr2	Prnp	1.32E+08	1.32E+08	2343	-0.41531	6.960937	0.010576	0.026279	0.031099	-1	1840	1886	2958	2328	3047	2074	2659	2147	3037	2561
ENSMUSG00000028034	chr3	Fubp1	1.52E+08	1.52E+08	6491	0.407528	4.719345	0.010585	0.026297	0.028318	1	329	304	384	346	540	500	699	726	903	700
ENSMUSG00000024777	chr19	Ppp2r5b	6227765	6228531	2895	-0.39255	5.026507	0.010598	0.02632	0.026569	-1	523	545	704	645	668	547	700	595	782	660
ENSMUSG00000038047	chr4	Haus6	86578855	86582018	6459	-0.49526	2.68986	0.010598	0.02632	0.036557	-1	106	111	126	138	142	99	113	121	160	128
ENSMUSG00000008575	chr4	Nfib	82290173	82296811	14957	-0.41861	6.725216	0.01063	0.026395	0.031562	-1	1771	1621	2196	1972	2624	1897	2191	1741	2453	2238
ENSMUSG00000058396	chr10	Gpr182	1.28E+08	1.28E+08	3954	1.073278	0.479329	0.010641	0.026418	0.153839	1	9	10	16	23	10	23	16	77	44	42
ENSMUSG00000026857	chr2	Ntmt1	30807826	30808083	2798	0.46527	3.879842	0.010663	0.026468	0.035917	1	141	221	266	174	226	363	411	387	445	357
ENSMUSG00000047714	chr16	Ppp1r2	31251537	31254733	4440	-0.43757	6.502005	0.010713	0.026587	0.034531	-1	1617	1527	2009	1724	1798	1435	1699	2256	2024	1551
ENSMUSG00000035632	chr7	Cnot3	3645290	3645584	4340	0.408313	4.34603	0.010719	0.026596	0.027802	1	276	237	300	270	374	356	527	565	701	581
ENSMUSG00000038369	chr2	Ncoa6	1.55E+08	1.55E+08	9744	-0.41049	4.474005	0.010731	0.026621	0.028676	-1	376	385	436	436	473	310	450	506	592	388
ENSMUSG00000020251	chr10	Glt8d2	82650433	82651518	5773	-0.67152	1.999132	0.010759	0.026682	0.06719	-1	75	53	98	56	129	70	75	69	81	55
ENSMUSG00000052707	chr7	Tnrc6a	1.23E+08	1.23E+08	8471	-0.43305	4.936129	0.010758	0.026682	0.032768	-1	600	406	635	583	720	397	620	713	771	571
ENSMUSG00000020184	chr10	Mdm2	1.18E+08	1.18E+08	5070	-0.47239	5.68307	0.010762	0.026683	0.039875	-1	787	891	1204	1034	1083	764	910	1437	953	922
ENSMUSG00000017405	chr11	Nek8	78166106	78166777	5222	0.73894	0.880148	0.010768	0.026687	0.066746	1	20	13	25	19	32	39	66	42	50	54
ENSMUSG00000027079	chr2	Clp1	84722104	84722752	2672	0.565906	2.24139	0.010769	0.026687	0.045523	1	49	66	71	54	70	98	113	134	148	151
ENSMUSG00000036036	chr17	Zfp57	37001163	37001340	3786	1.012049	-0.12061	0.010769	0.026687	0.106868	1	10	8	11	5	10	14	33	14	24	41
ENSMUSG00000082127	chr2	Gm13577	64474745	64474957	213	0.740142	1.381258	0.010778	0.026705	0.077388	1	27	27	44	16	43	56	53	88	104	65
ENSMUSG00000008435	chr7	Rdh13	4424770	4425638	6595	-0.42816	4.321325	0.010792	0.026735	0.031027	-1	298	392	445	353	419	350	414	336	529	358
ENSMUSG00000041570	chr1	Camsap2	1.36E+08	1.36E+08	9195	-0.50245	3.937074	0.010797	0.026743	0.042982	-1	240	196	319	311	459	156	299	363	409	280
ENSMUSG00000038208	chr11	Pgap3	98388677	98390101	3248	0.611825	1.696081	0.010811	0.026773	0.051397	1	28	36	44	53	46	72	77	91	112	90
ENSMUSG00000103436	chrX	RP23-135F22.6	7558602	7560883	5727	0.41596	4.350608	0.010844	0.026849	0.029027	1	282	259	336	253	318	424	507	471	690	633
ENSMUSG00000028383	chr4	Hsdl2	59581563	59581775	2795	-0.58468	5.755549	0.010857	0.026878	0.061742	-1	866	1208	1128	1297	811	628	757	1517	1291	914
ENSMUSG00000027291	chr2	Vps39	1.2E+08	1.2E+08	8605	-0.38609	4.889595	0.01086	0.02688	0.02571	-1	514	454	604	571	662	462	604	566	753	626
ENSMUSG00000024937	chr19	Ehbp1l1	5707376	5708425	6440	-0.43069	9.238456	0.010869	0.026896	0.034069	-1	8657	9688	14714	11400	14209	10705	13052	9220	14593	12384
ENSMUSG00000003644	chr4	Rps6ka1	1.34E+08	1.34E+08	4258	0.444406	3.603253	0.010878	0.026915	0.031632	1	156	131	192	175	202	190	345	315	435	367
ENSMUSG00000021485	chr13	Mxd3	55325168	55325898	2081	1.104955	0.586876	0.010908	0.026973	0.178015	1	7	18	12	11	25	28	46	10	91	52
ENSMUSG00000041225	chr18	Arhgap12	6024427	6026730	8016	-0.42429	4.408427	0.010907	0.026973	0.030657	-1	369	322	430	426	485	340	441	333	472	525
ENSMUSG00000051768	chr7	Xrcc1	24547150	24547359	2155	0.414437	4.045399	0.010907	0.026973	0.02833	1	187	197	256	277	261	335	394	466	498	499
ENSMUSG00000048200	chr7	Cracr2b	1.41E+08	1.41E+08	2764	0.542725	2.725831	0.010929	0.027021	0.045034	1	81	79	105	102	71	129	168	198	210	199
ENSMUSG00000037242	chr4	Clic4	1.35E+08	1.35E+08	6572	0.453497	6.193822	0.01094	0.027044	0.037187	1	796	821	1021	1039	1560	1316	2075	1634	2836	2198
ENSMUSG00000011382	chr7	Dhdh	45472956	45475375	3678	-0.49515	4.838115	0.010944	0.027049	0.04331	-1	537	379	581	550	771	381	377	656	667	708
ENSMUSG00000020427	chr11	Igfbp3	7206086	7207506	3130	1.003284	5.776724	0.010948	0.027054	0.180527	1	553	281	523	549	1247	841	1065	4290	1021	1236

ENSMUSG00000049929	chrX	Lpar4	1.07E+08	1.07E+08	4238	-0.65917	1.934685	0.010974	0.027113	0.065142	-1	47	60	89	74	123	39	58	87	92	69
ENSMUSG00000031458	chr8	Coprs	13884788	13885201	802	0.657309	2.703885	0.010982	0.027127	0.0707	1	53	77	127	82	79	181	230	104	198	191
ENSMUSG00000027304	chr2	Rtf1	1.2E+08	1.2E+08	5731	-0.40716	5.293865	0.010989	0.027141	0.029293	-1	658	641	806	775	852	595	695	948	901	799
ENSMUSG00000037075	chr15	Rnf139	58889229	58889494	4348	-0.45285	5.452435	0.010992	0.027142	0.036642	-1	809	775	989	819	794	686	854	1104	844	792
ENSMUSG00000033327	chr17	Tnxb	34670535	34670904	12209	-0.58894	7.0189	0.011017	0.0272	0.063404	-1	2735	1171	2798	2101	4569	1749	2746	2173	3305	2273
ENSMUSG00000025780	chr2	Itih5	10153571	10153755	7900	-0.6192	6.443175	0.011036	0.027241	0.069867	-1	1682	768	1767	1548	3338	1125	1839	1926	1824	1330
ENSMUSG00000030096	chr6	Slc6a6	91684067	91684308	6169	-0.50055	6.63619	0.011043	0.027253	0.045765	-1	1664	1615	2111	2381	1940	995	1833	2614	2253	2083
ENSMUSG00000026031	chr1	Cflar	58711508	58711592	12669	-0.41478	5.051039	0.011068	0.027311	0.030288	-1	615	461	667	640	790	476	615	627	824	799
ENSMUSG00000087658	chr6	Hotairm1	52156902	52156982	1025	0.873489	0.028836	0.011071	0.027313	0.071571	1	10	8	13	13	9	19	29	34	23	31
ENSMUSG00000021494	chr13	Ddx41	55530410	55530731	2205	0.436826	3.646191	0.011114	0.027415	0.030814	1	166	141	217	158	202	243	326	279	467	374
ENSMUSG00000090877	chr17	Hspa1b	34956436	34959238	2803	0.771811	1.136272	0.011119	0.027422	0.07964	1	24	18	18	35	33	40	84	71	65	47
ENSMUSG00000043719	chr9	Col6a6	1.06E+08	1.06E+08	9166	-0.66294	5.123846	0.01113	0.027443	0.079173	-1	577	351	714	584	1492	650	717	400	733	608
ENSMUSG00000038102	chr8	Trappc11	47490115	47490918	6482	-0.44254	4.864972	0.011136	0.027453	0.034517	-1	521	464	654	500	669	368	575	770	636	548
ENSMUSG00000058571	chr14	Gpc6	1.17E+08	1.17E+08	9428	-0.6733	3.022557	0.011146	0.027473	0.076621	-1	156	69	150	165	313	102	170	132	203	128
ENSMUSG00000034111	chr12	Tmed8	87166242	87172631	7179	-0.5783	2.619557	0.011167	0.02752	0.053053	-1	129	76	151	105	152	83	128	81	163	122
ENSMUSG00000070604	chr7	Vsig10l	43463151	43463272	3730	0.77681	0.699925	0.011175	0.027537	0.070116	1	19	13	21	15	25	27	35	61	54	47
ENSMUSG00000039427	chr16	Alg1	5233621	5233857	2682	0.41501	3.815823	0.011202	0.027596	0.028025	1	174	175	192	202	260	296	327	373	468	408
ENSMUSG00000025911	chr1	Adhfe1	9547948	9548151	3780	-0.64439	5.066141	0.011207	0.027605	0.075083	-1	798	460	656	676	803	337	352	824	608	955
ENSMUSG00000029022	chr4	Miip	1.48E+08	1.48E+08	3354	0.688202	2.838896	0.011251	0.027709	0.078545	1	108	69	113	64	93	110	151	333	239	193
ENSMUSG00000040822	chr14	1700123O20Rik	54686171	54687120	1889	0.440392	3.400848	0.011267	0.027743	0.0306	1	127	137	144	153	179	239	258	252	356	302
ENSMUSG00000026387	chr1	Sctr	1.2E+08	1.2E+08	2012	0.641731	2.516336	0.011295	0.027804	0.066039	1	46	82	84	89	62	160	120	132	184	193
ENSMUSG00000080875	chr5	Gm7332	9260945	9261388	444	0.690768	1.947186	0.011296	0.027804	0.073451	1	28	52	79	44	36	81	102	102	122	133
ENSMUSG00000025175	chr11	Fn3k	1.21E+08	1.21E+08	4399	0.517148	3.772681	0.011307	0.027826	0.045432	1	150	193	230	179	174	345	432	231	499	357
ENSMUSG00000032743	chr7	D430042O09Rik	1.26E+08	1.26E+08	7191	-0.5534	2.627296	0.011323	0.027861	0.048554	-1	116	95	120	127	150	62	133	146	137	108
ENSMUSG00000072772	chr6	Grcc10	1.25E+08	1.25E+08	1988	0.466212	5.876384	0.011342	0.027902	0.039504	1	628	911	952	789	804	1560	1482	1578	1607	1589
ENSMUSG00000041444	chr9	Arhgap32	32116136	32116251	17179	-0.63555	2.648738	0.01135	0.027917	0.066316	-1	119	64	143	106	215	63	137	116	146	115
ENSMUSG00000023018	chr15	Smarcd1	99702287	99702498	3153	0.46528	3.468023	0.011374	0.027972	0.035133	1	113	141	169	175	173	188	265	287	405	364
ENSMUSG00000030551	chr7	Nr2f2	70351946	70354931	4863	-0.47794	3.835986	0.011397	0.028022	0.038797	-1	273	177	284	302	356	211	244	356	350	232
ENSMUSG00000030309	chr6	Caprin2	1.49E+08	1.49E+08	7656	-0.68932	2.673997	0.011414	0.028051	0.079189	-1	129	89	124	80	243	82	159	88	149	92
ENSMUSG00000030614	chr7	Tmem126b	90468194	90469161	3984	-0.46065	4.57237	0.011411	0.028051	0.03726	-1	424	471	534	409	433	473	438	385	534	473
ENSMUSG00000091345	chr9	Col6a5	1.06E+08	1.06E+08	9405	-0.96394	1.321733	0.011414	0.028051	0.146794	-1	43	26	59	25	128	30	40	22	64	39
ENSMUSG00000000326	chr16	Comt	18406886	18408040	2532	0.40319	5.595256	0.011419	0.028053	0.029214	1	590	596	742	695	863	918	1144	1184	1629	1606
ENSMUSG00000032252	chr9	Glce	62057248	62061035	6828	-0.46176	3.797743	0.01142	0.028053	0.035852	-1	217	173	327	278	370	178	285	334	303	268
ENSMUSG00000044328	chr11	Trp53i13	77508099	77508377	2157	0.605679	2.767053	0.011428	0.028069	0.060377	1	79	56	81	87	148	147	224	127	213	234
ENSMUSG00000047686	chrX	Zcchc5	1.07E+08	1.07E+08	2948	0.713459	2.631432	0.011464	0.028152	0.085422	1	58	63	77	44	153	168	239	124	195	147
ENSMUSG00000058905	chr5	Gm10051	1.33E+08	1.33E+08	414	0.897814	-0.01857	0.011466	0.028153	0.075897	1	9	11	7	14	9	17	23	27	30	36
ENSMUSG00000054519	chr11	Zfp867	59461197	59464286	3412	-0.58462	2.234008	0.011472	0.028163	0.051476	-1	64	84	121	83	118	63	116	87	91	76
ENSMUSG00000042426	chr13	Dhx29	1.13E+08	1.13E+08	4405	-0.40179	4.365775	0.01151	0.02825	0.027591	-1	290	340	520	374	449	321	420	405	494	434
ENSMUSG00000058163	chr11	Gm5431	48887422	48889715	3800	0.977317	0.943067	0.011515	0.028259	0.141807	1	14	26	15	17	29	67	71	21	43	69
ENSMUSG00000025776	chr1	Crispld1	17727045	17727134	4515	-0.87477	2.548563	0.011529	0.028286	0.130538	-1	130	42	118	78	284	70	130	109	89	76
ENSMUSG00000028411	chr4	Aptx	40682382	40686713	5886	-0.42767	4.141912	0.011532	0.028291	0.031101	-1	307	287	407	323	361	313	365	290	364	405
ENSMUSG00000006782	chr11	Cnp	1.01E+08	1.01E+08	3639	0.415868	4.234781	0.01154	0.028304	0.029416	1	265	189	267	291	332	384	513	459	681	485
ENSMUSG00000070572	chr4	Trmt112-ps2	1.49E+08	1.49E+08	378	0.960083	0.026591	0.01156	0.028348	0.094922	1	16	8	9	10	7	31	26	30	30	20
ENSMUSG00000014349	chr11	Ube2z	96047432	96050414	3997	0.379727	5.675328	0.011567	0.02836	0.025972	1	612	675	838	691	902	1066	1335	1371	1661	1324
ENSMUSG00000050029	chrX	Rap2c	51003912	51006750	3545	-0.38508	5.021543	0.011573	0.02837	0.02617	-1	506	520	703	597	763	498	672	717	794	615
ENSMUSG00000062190	chr6	Lancl2	57702601	57703263	2958	-0.50516	3.21651	0.011577	0.028376	0.042022	-1	129	172	248	151	213	105	195	212	223	168
ENSMUSG00000025027	chr19	Xpnpep1	52943417	52943656	7120	0.384982	5.339937	0.011601	0.028429	0.026509	1	468	491	634	585	777	855	1131	1045	1299	1026
ENSMUSG00000026097	chr1	Ormdl1	53297095	53297188	4711	-0.5572	3.088705	0.011624	0.02848	0.051717	-1	153	160	211	140	173	123	206	95	220	162
ENSMUSG00000048349	chr14	Pou4f1	1.04E+08	1.04E+08	4672	-0.83453	1.638229	0.011665	0.028575	0.109562	-1	34	74	78	75	66	73	30	41	48	54
ENSMUSG00000001016	chr3	Ilf2	90476201	90476245	1973	0.387693	5.091295	0.011675	0.028594	0.026652	1	429	441	558	463	572	767	859	911	1011	932
ENSMUSG00000053559	chr15	Smagp	1.01E+08	1.01E+08	1142	0.702609	1.95067	0.011711	0.028679	0.075975	1	44	33	53	73	33	83	81	108	160	116
ENSMUSG00000030265	chr6	Kras	1.45E+08	1.45E+08	5347	-0.3955	4.553344	0.011719	0.028693	0.027247	-1	348	367	500	461	568	323	465	439	657	514
ENSMUSG00000051695	chr6	Pcbp1	86524492	86526321	1830	0.399711	6.843614	0.011722	0.028695	0.02961	1	1268	1393	1824	1752	2109	2594	3125	3002	3614	2881
ENSMUSG00000032702	chr19	Kank1	25236975	25237317	6166	-0.54622	4.459343	0.011733	0.028716	0.053461	-1	329	287	544	453	611	246	376	670	421	379
ENSMUSG00000015217	chrX	Hmgb3	71555918	71556008	2234	0.490529	3.201356	0.011736	0.028719	0.039002	1	103	102	164	123	144	177	258	179	355	290
ENSMUSG00000039084	chr11	Chad	94565047	94565868	1680	-0.94386	4.783114	0.011743	0.028732	0.162257	-1	718	223	507	349	1329	329	735	485	483	162
ENSMUSG00000059851	chr7	Suv420h2	4740115	4740181	4001	0.489212	3.639186	0.011756	0.028759	0.040351	1	148	137	202	186	188	212	380	232	453	438
ENSMUSG00000036968	chr5	Cnpy4	1.38E+08	1.38E+08	2399	0.662138	2.980369	0.011777	0.028798	0.075072	1	97	68	93	81	172	215	238	110	317	234
ENSMUSG00000051579	chrX	Tceal8	1.36E+08	1.36E+08	2563	0.442966	4.625592	0.011775	0.028798	0.034709	1	312	289	391	284	480	494	810	488	870	679
ENSMUSG00000030960	chr7	Mettl10	1.33E+08	1.33E+08	1764	0.582402	2.238521	0.011797	0.028842	0.051382	1	59	42	68	61	80	105	155	89	162	136
ENSMUSG00000101304	chr9	Plet1os	50488795	50489487	1245	-0.53508	3.293682	0.011815	0.028881	0.048123	-1	190	200	157	215	182	166	161	199	174	217
ENSMUSG00000038400	chr2	Pmepa1	1.73E+08	1.73E+08	4913	0.624283	4.754985	0.011831	0.028916	0.07112	1	275	216	401	401	514	589	1252	379	832	765
ENSMUSG00000028760	chr4	Eif4g3	1.38E+08	1.38E+08	11063	-0.61057	7.398305	0.011902	0.029084	0.069703	-1	3020	2493	3701	3715	4234	1961	2489	5773	2787	2536
ENSMUSG00000020271	chr11	Fbxw11	32642724	32642935	4327	-0.40971	6.045062	0.011909	0.02909	0.030898	-1	1090	1132	1440	1173	1464	1087	1200	1550	1432	1318
ENSMUSG00000030256	chr6	Bhlhe41	1.46E+08	1.46E+08	6262	-0.49635	5.320447	0.011908	0.02909	0.045123	-1	692	623	938	982	646	700	710	533	1078	858
ENSMUSG00000043518	chrX	Rai2	1.62E+08	1.62E+08	2403	-0.40392	4.314889	0.011919	0.029111	0.028111	-1	331	318	359	406	477	344	402	344	471	429

ENSMUSG00000021901	chr14	Bap1	31251450	31251654	4682	-0.4217	5.84674	0.011931	0.02913	0.032669	-1	941	956	1231	1143	1235	928	1078	1440	1236	1031
ENSMUSG00000030868	chr7	Dctn5	1.22E+08	1.22E+08	2649	0.412794	4.65359	0.011931	0.02913	0.03002	1	283	343	396	346	433	572	666	512	848	751
ENSMUSG00000032067	chr9	Pts	50521618	50522336	1035	0.48711	3.046775	0.011993	0.029269	0.037831	1	93	123	123	106	118	178	205	196	286	251
ENSMUSG00000050737	chr2	Ptges	30889471	30892826	3931	0.94552	2.954994	0.011992	0.029269	0.158966	1	56	30	58	106	207	124	172	162	302	438
ENSMUSG00000026398	chr1	Nr5a2	1.37E+08	1.37E+08	5899	-0.91957	-0.05529	0.012005	0.029289	0.096553	-1	18	21	15	22	20	4	14	23	20	12
ENSMUSG00000041598	chr11	Cdc42ep4	1.14E+08	1.14E+08	3643	0.511039	3.973645	0.012003	0.029289	0.046047	1	150	129	225	263	335	253	379	463	571	515
ENSMUSG00000083649	chr7	Rasl2-9	5124938	5125950	1013	-0.8161	0.457218	0.012015	0.029308	0.080267	-1	21	39	23	30	23	18	24	19	26	23
ENSMUSG00000020261	chr11	Slc36a1	55204350	55204488	5626	0.527503	3.175623	0.012025	0.029322	0.046067	1	114	98	127	121	152	152	299	166	363	278
ENSMUSG00000054196	chr15	Cthrc1	39076932	39077159	1480	1.289135	3.346728	0.012025	0.029322	0.295916	1	139	15	124	26	200	192	654	93	368	380
ENSMUSG00000020573	chr12	Pik3cg	32173473	32173969	6786	0.743443	1.727477	0.012029	0.029327	0.085477	1	43	25	51	28	54	76	103	46	140	107
ENSMUSG00000096145	chr7	Vkorc1	1.28E+08	1.28E+08	767	0.555544	4.169351	0.012033	0.029332	0.055246	1	211	191	242	211	370	429	653	254	659	501
ENSMUSG00000030682	chr7	Cdipt	1.27E+08	1.27E+08	1876	0.4367	5.314438	0.012038	0.029339	0.034698	1	494	516	682	496	632	856	1075	749	1497	1208
ENSMUSG00000036155	chr1	Mgat5	1.27E+08	1.27E+08	10291	0.681572	2.758707	0.012065	0.0294	0.079135	1	63	59	103	72	140	114	180	106	327	260
ENSMUSG00000021051	chr12	Ppp2r5e	75450883	75453813	4808	-0.40908	5.118881	0.012084	0.029439	0.030229	-1	607	555	716	641	792	522	691	863	806	604
ENSMUSG00000026659	chr1	Dusp12	1.71E+08	1.71E+08	2743	0.544773	2.340959	0.012098	0.029469	0.04525	1	63	59	80	47	89	99	156	125	170	141
ENSMUSG00000091228	chr11	Gm20390	93949819	93950046	991	0.449959	8.406458	0.01211	0.029493	0.038234	1	3731	5284	5865	4556	4311	8313	8800	8742	10523	9062
ENSMUSG00000025218	chr19	Poll	45552275	45553170	2324	-0.43082	4.167104	0.012115	0.0295	0.032205	-1	288	369	373	286	392	324	330	327	416	373
ENSMUSG00000018830	chr16	Myh11	14194527	14195184	6632	-0.58401	4.860683	0.012132	0.02953	0.062815	-1	449	428	538	897	597	330	467	412	1042	565
ENSMUSG00000025887	chr9	Casp12	5345430	5345525	3840	-0.64836	3.214872	0.01213	0.02953	0.073715	-1	104	280	240	144	160	129	194	180	194	143
ENSMUSG00000037525	chr15	Bcdin3d	99470084	99471079	1271	0.571444	2.015776	0.012135	0.029534	0.047694	1	39	51	59	50	66	90	96	126	117	117
ENSMUSG00000012848	chr7	Rps5	12922290	12922388	1734	0.398408	8.204369	0.012146	0.029555	0.029984	1	3598	4098	4580	3936	5033	6779	7802	7720	8827	7844
ENSMUSG00000079215	chr5	Zfp664	1.25E+08	1.25E+08	5729	-0.40573	4.894628	0.012157	0.029576	0.02959	-1	494	489	565	638	635	408	657	660	751	535
ENSMUSG00000022452	chr15	Smdt1	82338959	82339085	1077	0.449634	6.292757	0.012173	0.029611	0.0377	1	856	1143	1365	1032	1120	2082	2102	1809	2265	2155
ENSMUSG00000036748	chr19	Cuedc2	46329812	46330834	1941	0.402096	5.543649	0.012175	0.029611	0.029531	1	532	697	679	661	768	1045	1138	1184	1500	1318
ENSMUSG00000024844	chr19	Banf1	5364641	5365158	820	0.439675	6.261234	0.012184	0.029626	0.036011	1	965	1026	1296	1042	1076	2054	1964	1729	2329	2096
ENSMUSG00000028821	chr4	Syf2	1.35E+08	1.35E+08	2043	0.481608	5.274283	0.012191	0.029638	0.04259	1	455	484	658	540	553	757	914	1551	995	1011
ENSMUSG00000059208	chr17	Hnrnpm	33646233	33646659	4701	0.439662	6.382166	0.012203	0.029662	0.036095	1	1027	984	1388	1074	1477	1706	2428	1564	2899	2708
ENSMUSG00000036678	chr15	Aaas	1.02E+08	1.02E+08	1816	0.528829	2.932252	0.012216	0.029688	0.045046	1	101	97	115	94	103	166	174	161	321	229
ENSMUSG00000070697	chr5	Utp3	88554483	88556083	1601	0.442902	4.968507	0.012228	0.029713	0.035633	1	305	421	549	410	546	669	803	1059	820	818
ENSMUSG00000021226	chr12	Acot2	83987861	83988481	2196	1.055005	2.770433	0.012239	0.029732	0.196597	1	51	66	99	79	69	73	101	574	173	140
ENSMUSG00000065126	chr11	Snord104	1.07E+08	1.07E+08	70	0.891451	0.065603	0.01224	0.029732	0.085056	1	7	16	10	7	14	31	25	23	36	25
ENSMUSG00000032431	chr9	Crtap	1.14E+08	1.14E+08	1772	0.580047	4.83635	0.01226	0.029775	0.061954	1	379	207	394	325	644	616	914	458	1157	894
ENSMUSG00000041329	chr11	Atp1b2	69599736	69601412	4085	-0.47784	9.003136	0.012266	0.029785	0.04332	-1	7825	7501	11847	9491	14163	10727	10048	7052	11764	9752
ENSMUSG00000037824	chr14	Tspan14	40906445	40908129	2475	0.512915	4.82598	0.012288	0.029828	0.04796	1	266	467	381	336	490	570	925	506	1090	845
ENSMUSG00000039680	chr16	Mrps6	92058270	92058480	1053	0.473771	3.775029	0.012288	0.029828	0.03848	1	169	188	222	173	192	326	377	245	464	432
ENSMUSG00000039771	chr5	Polr2j	1.36E+08	1.36E+08	1106	0.429422	4.385595	0.012301	0.029853	0.032549	1	239	280	336	304	320	554	565	486	565	573
ENSMUSG00000059343	chr4	Aldoart1	72850583	72852632	2052	-0.77477	2.039224	0.012319	0.029892	0.099614	-1	85	106	62	101	59	61	54	104	75	52
ENSMUSG00000001911	chr8	Nfix	84699876	84700219	7351	-0.41385	8.071576	0.012342	0.029941	0.032486	-1	4289	3774	5216	5988	6655	4666	5240	4996	6909	5146
ENSMUSG00000041238	chr18	Rbbp8	11633276	11633524	3867	0.573006	2.091618	0.012347	0.029948	0.049196	1	45	42	58	60	76	80	119	92	152	143
ENSMUSG00000047557	chr3	Lxn	67457998	67458327	1508	0.634834	1.994988	0.012363	0.029981	0.060448	1	42	49	49	62	49	83	101	83	185	108
ENSMUSG00000039662	chr4	Icmt	1.52E+08	1.52E+08	5287	-0.38596	5.113318	0.012375	0.030007	0.026998	-1	606	551	739	651	721	485	692	761	839	748
ENSMUSG00000021756	chr13	Il6st	1.12E+08	1.12E+08	11099	-0.43665	7.427659	0.012399	0.030059	0.036109	-1	2890	2414	3715	3303	4418	2338	3214	4469	4001	3168
ENSMUSG00000037892	chr3	Pcdh18	49743296	49745274	5366	-0.59325	2.769365	0.012437	0.030146	0.05935	-1	128	72	138	124	232	86	147	119	169	115
ENSMUSG00000070372	chr3	Capza1	1.05E+08	1.05E+08	3532	-0.42479	4.620554	0.012442	0.030153	0.03245	-1	394	384	517	480	591	308	635	402	632	508
ENSMUSG00000021576	chr13	Pdcd6	74303121	74304048	1524	0.41152	4.317719	0.012459	0.030178	0.029449	1	275	243	274	289	337	348	484	529	717	607
ENSMUSG00000043557	chr17	Mdga1	29827956	29832399	9395	-0.63784	5.397833	0.012458	0.030178	0.076087	-1	896	571	868	758	1229	632	1073	356	1283	575
ENSMUSG00000078931	chr8	Pdf	1.07E+08	1.07E+08	1704	-0.44834	5.510492	0.012456	0.030178	0.037221	-1	792	903	956	800	897	913	938	705	1030	854
ENSMUSG00000018428	chr11	Akap1	88830792	88831829	4390	-0.43483	6.157383	0.012473	0.030206	0.035457	-1	979	1242	1378	1756	1504	1022	1574	1354	1884	1328
ENSMUSG00000042320	chr12	Prox2	85086385	85087554	3335	-0.80521	0.299603	0.012477	0.030212	0.076763	-1	19	17	27	29	32	11	16	13	32	28
ENSMUSG00000004637	chr8	Wwox	1.14E+08	1.14E+08	10173	-0.48094	3.040343	0.012546	0.030372	0.037639	-1	139	144	169	175	163	147	140	172	183	147
ENSMUSG00000030045	chr6	Mrpl19	81957851	81962162	5450	-0.44789	4.614302	0.012566	0.030415	0.036291	-1	386	480	539	472	463	446	467	350	681	475
ENSMUSG00000079427	chr9	Mthfsl	88688602	88688985	4728	0.590726	1.89675	0.012577	0.030438	0.050096	1	48	41	53	49	48	88	90	84	125	119
ENSMUSG00000030730	chr7	Atp2a1	1.26E+08	1.26E+08	3483	-0.47208	14.76943	0.012617	0.030529	0.042738	-1	485417	409753	576091	565729	695694	457668	426835	764668	572704	488666
ENSMUSG00000003531	chr16	Dgcr6	18052860	18053121	2985	0.418791	4.626605	0.012631	0.030557	0.031313	1	290	375	372	363	341	544	583	663	768	724
ENSMUSG00000007029	chr17	Vars	35000987	35001232	5608	0.440561	5.3598	0.012653	0.030605	0.035979	1	431	456	645	624	790	702	940	1414	1451	1080
ENSMUSG00000040929	chr19	Rfx3	27761721	27768693	11034	-0.70513	1.637257	0.012698	0.030709	0.07678	-1	73	37	88	59	58	31	75	59	57	50
ENSMUSG00000024953	chr19	Prdx5	6906697	6907127	2139	0.481266	7.196711	0.012706	0.030723	0.044085	1	1665	2269	2031	2402	1676	3402	3305	4193	4775	4237
ENSMUSG00000036596	chr5	Cpz	35502215	35502681	2248	-0.98188	2.921354	0.012716	0.030742	0.172642	-1	169	71	178	73	380	174	93	54	123	121
ENSMUSG00000045867	chr10	Cradd	95174746	95175978	1650	-0.49974	2.721849	0.012738	0.030791	0.039628	-1	96	118	126	139	162	104	121	144	139	121
ENSMUSG00000031370	chrX	Zrsr2	1.64E+08	1.64E+08	7194	0.459813	3.81139	0.012753	0.03082	0.036625	1	189	165	200	181	245	268	307	513	430	371
ENSMUSG00000036707	chr1	Cab39	85793441	85793821	7077	-0.44585	7.272068	0.01276	0.030823	0.037932	-1	2641	2862	3592	2929	2756	2398	2827	3873	3532	2641
ENSMUSG00000041654	chr11	Slc39a11	1.13E+08	1.13E+08	3359	0.651449	2.574602	0.01276	0.030823	0.070558	1	80	78	71	50	97	109	173	100	251	218
ENSMUSG00000042408	chr4	Zmym6	1.27E+08	1.27E+08	7692	-0.52219	3.026468	0.012763	0.030823	0.046214	-1	157	118	196	163	162	78	173	178	187	172
ENSMUSG00000079442	chr2	St6galnac4	32587095	32587227	6482	0.489775	5.209954	0.012762	0.030823	0.044752	1	309	420	528	590	771	834	1198	689	1261	1070
ENSMUSG00000029621	chr5	Arpc1a	1.45E+08	1.45E+08	2567	0.392678	5.082349	0.012797	0.030899	0.028099	1	418	446	548	449	584	725	876	743	1175	985
ENSMUSG00000020248	chr10	Nfyb	82748701	82750447	5068	-0.39461	4.401079	0.012819	0.030947	0.027573	-1	385	373	404	387	434	351	404	448	499	420

ENSMUSG00000049687	chr15	Fam109b	82338942	82339085	3311	0.859965	1.358285	0.012835	0.030982	0.118482	1	21	18	28	21	61	52	89	33	121	80
ENSMUSG00000000787	chrX	Ddx3x	13280970	13281157	5277	-0.56944	7.130886	0.012846	0.031003	0.061962	-1	2445	2375	2990	2834	3384	1251	2223	4518	2832	2538
ENSMUSG00000040225	chr1	Prrc2c	1.63E+08	1.63E+08	16092	-0.40666	5.730292	0.012857	0.031023	0.03095	-1	910	736	1123	1007	1325	720	1095	1248	1301	1010
ENSMUSG00000008153	chr6	Clstn3	1.24E+08	1.24E+08	4968	1.694754	1.932424	0.012885	0.031084	0.496218	1	15	11	16	47	60	19	35	17	244	380
ENSMUSG00000024404	chr18	Riok3	12128850	12128973	3661	-0.48959	7.114058	0.012889	0.031084	0.045836	-1	2523	2269	3135	2563	3030	1959	2294	4103	2637	2404
ENSMUSG00000032267	chr9	Usp28	48985385	48985537	4220	-0.4035	6.153499	0.012887	0.031084	0.03071	-1	1158	1100	1584	1372	1593	1105	1511	1656	1635	1248
ENSMUSG00000053091	chr7	Lins	66689889	66690023	5886	-0.57137	2.647518	0.012902	0.03111	0.05385	-1	114	99	158	107	144	117	129	73	157	104
ENSMUSG00000068917	chr3	Clk2	89164795	89165106	5299	0.446763	3.842264	0.012904	0.03111	0.034546	1	192	185	185	170	274	262	372	453	406	430
ENSMUSG00000034723	chr2	Tmx4	1.35E+08	1.35E+08	10907	-0.48919	3.980344	0.012914	0.031129	0.042904	-1	274	220	379	323	349	172	290	451	355	277
ENSMUSG00000020463	chr11	Smek2	29172890	29173447	5694	-0.45311	4.522716	0.013002	0.031329	0.037514	-1	380	394	481	436	526	271	399	646	528	439
ENSMUSG00000030731	chr7	Syt3	44384102	44384176	3118	-0.95706	0.412172	0.013002	0.031329	0.132506	-1	19	35	24	37	22	19	18	5	32	27
ENSMUSG00000032220	chr9	Myo1e	70207350	70207703	4944	0.437436	4.291912	0.013027	0.031385	0.034323	1	207	218	279	278	424	337	571	498	766	498
ENSMUSG00000036890	chr2	Gtdc1	44564412	44565534	7928	-0.50951	3.826071	0.013031	0.031389	0.046408	-1	232	252	320	282	299	181	234	428	253	261
ENSMUSG00000034248	chr14	Slc25a37	69241848	69245354	6021	-0.40428	4.527347	0.013056	0.031443	0.029341	-1	369	400	495	398	533	407	449	366	563	523
ENSMUSG00000044700	chr4	Tmem201	1.5E+08	1.5E+08	8944	-0.40194	5.421151	0.013071	0.031473	0.030086	-1	654	716	764	926	1020	713	788	946	1004	846
ENSMUSG00000024483	chr18	Ankhd1	36559987	36560101	9845	-0.4349	5.069959	0.013087	0.031507	0.03511	-1	574	543	736	653	717	473	618	921	717	603
ENSMUSG00000018474	chr11	Chd3	69343273	69344478	8443	0.600211	4.49802	0.013108	0.031551	0.067298	1	225	174	292	302	548	370	946	416	814	680
ENSMUSG00000024743	chr19	Syt7	10389090	10389513	6966	-0.7058	1.146316	0.013149	0.031644	0.071328	-1	36	24	66	44	56	28	46	30	56	32
ENSMUSG00000033762	chr15	Recql4	76703553	76703865	3922	0.901512	0.1071	0.013205	0.031775	0.093779	1	6	10	10	15	15	21	24	18	36	48
ENSMUSG00000042190	chr5	Cmklr1	1.14E+08	1.14E+08	3408	0.576683	3.950388	0.013208	0.031775	0.060939	1	213	94	173	232	335	297	466	321	568	523
ENSMUSG00000028657	chr4	Ppt1	1.23E+08	1.23E+08	3674	0.42082	5.048114	0.01322	0.0318	0.032756	1	438	390	485	423	632	623	998	681	1220	953
ENSMUSG00000064061	chr16	Dzip3	48924232	48926102	9081	-0.6214	2.06881	0.013231	0.03182	0.06212	-1	76	55	96	69	129	40	98	71	103	75
ENSMUSG00000019822	chr10	Smpd2	41485642	41486609	4468	0.456801	3.398501	0.013239	0.031834	0.035152	1	124	135	200	114	165	219	304	241	332	318
ENSMUSG00000025979	chr1	Mob4	55131231	55131359	4855	-0.4036	5.544355	0.013248	0.031849	0.030536	-1	723	820	1122	810	972	864	953	922	1072	838
ENSMUSG00000049288	chr3	Lix1l	96601133	96601473	2509	0.482268	4.081841	0.013271	0.031899	0.042333	1	182	138	281	219	387	333	578	430	533	428
ENSMUSG00000031725	chr8	Ces1f	93256236	93256600	3285	2.049174	1.725395	0.013286	0.03193	0.717082	1	17	8	2	24	54	3	21	33	181	388
ENSMUSG00000012705	chr8	Retn	3655770	3655843	1579	1.900573	4.293742	0.013295	0.031947	0.637727	1	109	43	25	213	322	47	188	85	1100	2401
ENSMUSG00000030079	chr6	Ruvbl1	88465409	88465668	1899	0.380786	4.358367	0.013453	0.032321	0.025761	1	241	257	324	298	369	445	513	539	609	584
ENSMUSG00000037373	chr5	Ctbp1	33247724	33248686	2288	-0.38238	7.200817	0.01347	0.032355	0.028271	-1	2280	2424	3044	2877	3340	2381	2952	3024	3504	3065
ENSMUSG00000075307	chr2	Klhl41	69670120	69671306	2529	0.425506	8.965452	0.013484	0.032383	0.035326	1	5715	6353	8373	7501	7795	11515	13689	16115	13043	11808
ENSMUSG00000025609	chr6	Mkln1	31398735	31398954	22296	-0.43364	6.23791	0.013488	0.032387	0.036062	-1	1234	1276	1765	1399	1581	1245	1357	1928	1504	1395
ENSMUSG00000098457	chr15	Mir8097	36240046	36240164	119	0.986133	0.407756	0.013496	0.032401	0.132979	1	7	20	7	16	17	46	42	42	31	21
ENSMUSG00000025102	chr7	3110040N11Rik	81782182	81782581	1231	0.449682	3.388527	0.013513	0.032437	0.034097	1	139	128	163	136	164	270	283	229	332	272
ENSMUSG00000001506	chr11	Col1a1	94936224	94936444	6563	-0.99263	11.46468	0.013516	0.032439	0.188511	-1	77822	16625	70184	25066	138173	31723	68695	20078	67506	37447
ENSMUSG00000040653	chr10	Ppp1r14c	3366150	3366969	2524	-0.43468	7.247183	0.013519	0.03244	0.036629	-1	2783	2182	3171	2701	3860	2817	3453	2397	3596	2729
ENSMUSG00000031373	chrX	Car5b	1.64E+08	1.64E+08	6354	1.495987	3.058612	0.013538	0.032479	0.406382	1	56	23	36	101	154	40	99	69	504	791
ENSMUSG00000038615	chr11	Nfe2l1	96817414	96820516	5441	-0.421	8.952783	0.013545	0.032492	0.034628	-1	7755	8054	11079	10799	9768	7754	9238	12309	10440	9566
ENSMUSG00000029003	chr4	Mad2l2	1.48E+08	1.48E+08	2622	0.479948	2.932702	0.013551	0.032499	0.037901	1	84	102	117	106	115	184	176	222	224	209
ENSMUSG00000022201	chr15	Zfr	12117831	12117947	5911	-0.469	5.671082	0.013609	0.032633	0.042093	-1	809	797	1195	984	1197	581	1074	1444	1119	817
ENSMUSG00000062542	chr7	Syt9	1.07E+08	1.07E+08	3979	-1.1333	-0.12555	0.013667	0.032767	0.182995	-1	29	14	22	4	28	12	20	12	13	4
ENSMUSG00000032352	chr9	Lrrc1	77430823	77432280	8247	0.800397	1.151752	0.013724	0.032897	0.098316	1	24	12	29	18	48	34	95	56	69	61
ENSMUSG00000030278	chr6	Cidec	1.13E+08	1.13E+08	1856	1.689074	4.767954	0.01374	0.032929	0.51934	1	186	83	67	357	401	54	249	268	1549	3043
ENSMUSG00000020328	chr11	Nudcd2	40733667	40734154	2054	0.387367	3.821115	0.013747	0.032941	0.025545	1	182	181	223	195	234	287	408	355	443	369
ENSMUSG00000027637	chr2	1110008F13Rik	1.57E+08	1.57E+08	2871	0.407895	5.540639	0.01375	0.032942	0.031538	1	563	678	801	605	671	1054	1120	1318	1358	1302
ENSMUSG00000030157	chr6	Clec2d	1.29E+08	1.29E+08	1213	0.550368	5.474902	0.013762	0.032965	0.058086	1	597	653	589	475	650	1051	908	1788	983	1318
ENSMUSG00000020023	chr10	Tmcc3	94311949	94312202	7153	-0.42298	5.17656	0.013797	0.033038	0.033759	-1	534	514	818	816	810	501	625	863	801	828
ENSMUSG00000020264	chr11	Slc36a2	55158470	55159615	3255	1.653623	2.848806	0.013797	0.033038	0.494025	1	39	24	22	88	119	24	70	42	502	705
ENSMUSG00000022564	chr15	Grina	76246807	76246900	1693	0.418605	6.790049	0.013849	0.033156	0.034067	1	1316	1366	1568	1702	1983	2256	2362	3313	3385	3484
ENSMUSG00000030498	chr7	Gas2	51862015	51862444	4993	-0.70477	2.294146	0.013859	0.033171	0.084876	-1	86	56	147	78	147	54	120	117	79	59
ENSMUSG00000046516	chr16	Cox17	38346991	38347207	5773	0.486336	5.788181	0.01386	0.033171	0.045543	1	637	861	924	685	687	1593	1498	1249	1527	1498
ENSMUSG00000057672	chr8	Pkn1	83669762	83670368	7386	-0.40853	4.93318	0.013885	0.033227	0.031326	-1	424	517	657	638	689	384	581	590	898	672
ENSMUSG00000074766	chr2	Ism1	1.4E+08	1.4E+08	2965	-1.24287	0.785506	0.0139	0.033255	0.254658	-1	52	4	59	14	73	20	37	19	20	17
ENSMUSG00000070808	chr7	Gltscr1	15971262	15972889	5360	-0.45561	3.258749	0.013905	0.033261	0.035364	-1	131	144	195	214	246	126	182	179	262	201
ENSMUSG00000042331	chr11	Specc1	61956779	61956889	13276	0.69101	2.473805	0.013938	0.033336	0.082777	1	60	43	70	83	95	89	165	81	276	200
ENSMUSG00000078878	chr2	Gm14305	1.77E+08	1.77E+08	2500	-0.82782	1.436747	0.013975	0.033418	0.113372	-1	31	32	92	39	100	21	42	62	63	38
ENSMUSG00000097666	chr18	A330094K24Rik	77729681	77730478	1027	-0.74214	1.467482	0.013979	0.033422	0.087223	-1	29	58	54	77	65	49	29	39	62	55
ENSMUSG00000021577	chr13	Sdha	74322254	74323173	3883	-0.43958	9.927432	0.013985	0.03343	0.038152	-1	15504	19197	19830	21351	16676	15649	17284	22812	22469	18200
ENSMUSG00000005370	chr17	Msh6	87975050	87975405	4254	0.537105	3.050488	0.014004	0.033469	0.050053	1	99	76	106	103	182	157	226	169	320	276
ENSMUSG00000022801	chr16	Lrch3	32914100	32914403	6610	-0.42247	4.4297	0.014008	0.033474	0.032847	-1	394	315	404	417	533	319	378	548	507	398
ENSMUSG00000052539	chr3	Magi3	1.04E+08	1.04E+08	6773	-0.53951	2.666729	0.014034	0.033529	0.048601	-1	113	77	126	135	179	79	151	119	144	110
ENSMUSG00000038587	chr10	Akap12	4266329	4266668	6244	-0.48752	4.359482	0.014039	0.033537	0.044283	-1	309	224	377	513	618	282	432	414	457	415
ENSMUSG00000087128	chr4	Gm12655	94460931	94461355	961	-0.72656	1.012077	0.014055	0.033569	0.074946	-1	34	39	51	32	47	35	39	20	51	26
ENSMUSG00000036402	chr6	Gng12	66896397	66896527	4694	-0.38266	4.938044	0.014059	0.033571	0.027339	-1	475	441	667	612	728	429	625	613	846	631
ENSMUSG00000015461	chr17	Atf6b	34647146	34647316	2757	0.38807	3.97886	0.014083	0.033624	0.026433	1	180	190	247	219	309	299	431	383	536	445
ENSMUSG00000002320	chr14	Tm9sf1	55635965	55636612	3880	0.389043	4.792175	0.0141	0.033659	0.028143	1	318	319	451	379	557	568	790	637	889	788
ENSMUSG00000024668	chr19	Sdhaf2	10500513	10503129	3096	-0.40666	5.335943	0.014113	0.033684	0.031527	-1	642	776	824	847	714	676	838	747	1015	780

ENSMUSG00000046056	chr7	Sbsn	30734739	30734768	3802	0.802473	1.48623	0.014147	0.033758	0.104884	1	26	21	20	31	69	70	52	95	81	96
ENSMUSG00000069094	chr3	Pde7a	19223108	19227841	7748	-0.63133	5.255733	0.01416	0.033784	0.077197	-1	542	867	1079	798	553	510	544	1193	634	587
ENSMUSG00000020176	chr11	Grb10	11930508	11933609	9089	0.495251	7.393783	0.014177	0.033818	0.048318	1	1831	1533	2328	2284	3991	3744	6145	3865	5034	4128
ENSMUSG00000028990	chr4	Lzic	1.49E+08	1.49E+08	1866	0.45506	3.657492	0.0142	0.033867	0.036707	1	140	162	230	143	213	237	451	281	406	328
ENSMUSG00000020803	chr11	Txndc17	72207547	72207768	1324	0.41223	5.273472	0.014207	0.033879	0.032293	1	483	547	699	478	546	845	1010	902	1207	1181
ENSMUSG00000025059	chrX	Gyk	85701937	85704396	7743	0.929335	1.400376	0.014221	0.033907	0.140834	1	28	34	26	33	19	38	45	47	163	110
ENSMUSG00000019577	chr6	Pdk4	5483351	5485592	3511	1.469534	8.401924	0.014226	0.033913	0.405803	1	1940	4525	4962	2369	751	1865	3878	37253	10901	5338
ENSMUSG00000036737	chr9	Oxsr1	1.19E+08	1.19E+08	5350	-0.38953	6.257927	0.014246	0.033954	0.029496	-1	1260	1277	1667	1490	1546	1271	1464	1679	1716	1577
ENSMUSG00000024592	chr18	C330018D20Rik	56955833	56957921	3233	-0.52172	3.199345	0.014284	0.034034	0.048479	-1	151	180	238	165	159	148	186	111	243	192
ENSMUSG00000060594	chr9	Layn	51056780	51057656	1786	0.76409	1.032398	0.014283	0.034034	0.082796	1	26	17	35	18	23	37	76	35	84	56
ENSMUSG00000020205	chr10	Phlda1	1.12E+08	1.12E+08	2205	0.510276	2.791289	0.014294	0.034051	0.0431	1	79	77	91	98	127	138	230	183	246	145
ENSMUSG00000047459	chr2	Dynlrb1	1.55E+08	1.55E+08	1009	0.405755	5.753382	0.01431	0.034083	0.031741	1	715	667	824	857	786	1246	1470	1162	1698	1575
ENSMUSG00000046070	chr17	Igfals	24878770	24878824	2111	-0.74536	2.086987	0.014346	0.034163	0.096406	-1	53	79	64	67	187	53	53	69	97	96
ENSMUSG00000038888	chr7	Ctu1	43672016	43672075	2475	0.560894	1.689824	0.014359	0.034188	0.044118	1	37	33	49	40	52	69	89	87	106	83
ENSMUSG00000026135	chr1	Zfp142	74565127	74567347	11355	-0.43033	3.462494	0.014379	0.034231	0.032222	-1	175	196	202	221	256	158	236	241	282	181
ENSMUSG00000040054	chr10	Baz2a	1.28E+08	1.28E+08	8372	-0.39612	4.870727	0.014383	0.034234	0.029541	-1	496	406	621	574	698	375	598	658	704	641
ENSMUSG00000029463	chr5	Fam216a	1.22E+08	1.22E+08	1388	0.58701	2.255262	0.014389	0.034243	0.054311	1	63	67	73	52	51	96	133	151	162	114
ENSMUSG00000060450	chr18	Rnf14	38296635	38296798	3515	-0.39621	6.428638	0.014393	0.034246	0.030695	-1	1495	1404	1846	1534	1903	1493	1728	1917	1872	1611
ENSMUSG00000044037	chr9	Als2cl	1.11E+08	1.11E+08	5848	-0.7135	2.780558	0.014399	0.034253	0.093185	-1	110	154	137	179	116	49	89	179	120	175
ENSMUSG00000056941	chr2	Commd7	1.54E+08	1.54E+08	5493	0.482409	3.976078	0.014401	0.034253	0.042795	1	177	194	243	225	253	362	489	237	540	506
ENSMUSG00000026923	chr2	Notch1	26457903	26460976	14232	-0.44374	4.360828	0.014448	0.034359	0.036875	-1	330	271	404	475	514	242	421	370	628	418
ENSMUSG00000037351	chr1	Actr1b	36698114	36700178	4274	-0.38378	7.263867	0.014453	0.034365	0.029088	-1	2454	2491	3384	2904	3358	2628	3097	3286	3609	2905
ENSMUSG00000038648	chr6	Creb3l2	37327255	37332500	7283	-0.42365	4.927834	0.014513	0.034501	0.034115	-1	553	421	602	513	852	473	718	501	769	587
ENSMUSG00000028950	chr4	Tas1r1	1.52E+08	1.52E+08	4776	0.695707	1.963767	0.014591	0.034682	0.081214	1	43	28	74	43	57	115	143	67	111	101
ENSMUSG00000069601	chr10	Ank3	69533772	69534284	33152	-0.65571	6.476564	0.014598	0.034691	0.084881	-1	1682	1344	1890	2040	2176	968	1194	3270	1405	1212
ENSMUSG00000028600	chr4	Podn	1.08E+08	1.08E+08	4270	0.541227	4.079386	0.014629	0.034761	0.055378	1	219	124	182	273	362	361	615	364	491	492
ENSMUSG00000036002	chr4	Fam214b	43032414	43033688	4129	0.44822	5.275353	0.014644	0.03479	0.03877	1	483	477	611	581	571	683	952	1489	1088	1009
ENSMUSG00000036986	chr9	Pml	58218076	58220569	5571	0.569266	3.341911	0.014689	0.034891	0.059635	1	117	81	137	137	216	288	288	188	259	349
ENSMUSG00000002395	chr8	Use1	71366848	71367078	2203	0.40665	5.596227	0.014699	0.034907	0.032042	1	530	682	784	747	718	1005	1224	1552	1372	1255
ENSMUSG00000050663	chr10	Trhde	1.14E+08	1.14E+08	8065	-0.94349	0.207151	0.014703	0.034912	0.118338	-1	31	11	15	19	44	12	16	17	16	25
ENSMUSG00000020829	chr11	Slc46a1	78465697	78466005	3080	0.828658	1.279777	0.014722	0.034952	0.111653	1	21	19	27	28	46	54	67	27	88	111
ENSMUSG00000028033	chr1	Kcnq5	21398403	21403125	7689	-0.65049	3.168646	0.014735	0.034969	0.078463	-1	195	136	177	234	158	94	175	264	188	98
ENSMUSG00000029173	chr5	Sepsecs	52640087	52644107	5347	-0.4238	3.399624	0.014735	0.034969	0.031035	-1	156	171	230	201	254	140	222	243	252	197
ENSMUSG00000058704	chr17	Memo1	74200706	74201325	1513	-0.40831	5.654228	0.014752	0.035003	0.032438	-1	763	1015	1144	886	959	904	1034	951	1187	947
ENSMUSG00000050912	chr9	Tmem123	7764041	7764312	3109	-0.40088	5.121086	0.014757	0.035009	0.030805	-1	491	544	769	739	791	506	811	567	945	711
ENSMUSG00000020598	chr12	Nrcam	44328885	44329096	7581	0.797239	1.35305	0.014761	0.035012	0.103339	1	29	11	38	31	42	54	36	76	115	85
ENSMUSG00000096370	chr19	Gm21992	4742913	4744867	5780	0.386227	3.771059	0.014795	0.035087	0.025935	1	174	173	209	183	244	279	361	356	416	383
ENSMUSG00000043716	chr1	Rpl7	16101295	16101359	2687	0.385665	8.435013	0.014802	0.035099	0.029785	1	4153	4684	6021	4432	5859	7470	9769	9032	10059	9328
ENSMUSG00000034312	chr6	Iqsec1	90659598	90661025	7412	-0.41573	5.478243	0.01487	0.035253	0.033663	-1	740	620	922	997	998	652	939	681	1301	953
ENSMUSG00000020937	chr11	Plcd3	1.03E+08	1.03E+08	3393	0.864157	2.234578	0.014875	0.03526	0.134676	1	64	29	52	48	80	54	110	285	114	132
ENSMUSG00000005505	chr2	Kbtbd4	90904740	90904812	3139	-0.37709	3.929197	0.0149	0.035314	0.025194	-1	228	240	334	309	328	231	331	302	379	306
ENSMUSG00000047216	chr1	Cdh19	1.11E+08	1.11E+08	4280	-0.96732	-0.04147	0.014908	0.035325	0.124785	-1	16	17	17	18	32	6	10	27	23	6
ENSMUSG00000031119	chrX	Gpc4	52053021	52053726	2651	0.399414	4.864467	0.014942	0.0354	0.030314	1	355	326	411	450	567	518	788	897	923	763
ENSMUSG00000020847	chr11	Rph3al	75830999	75832214	3814	-0.6521	2.631614	0.014945	0.0354	0.075794	-1	131	101	129	147	111	93	95	182	91	87
ENSMUSG00000032285	chr9	Dnaja4	54698873	54699413	3589	-0.4201	6.382045	0.014964	0.03544	0.034961	-1	1346	1388	1799	1699	1744	1483	2008	1403	2058	1355
ENSMUSG00000003549	chr7	Ercc1	19344778	19345196	3111	0.408017	3.760604	0.014987	0.035487	0.029611	1	157	178	224	171	240	313	397	300	417	358
ENSMUSG00000043587	chr9	Pxylp1	96823336	96825622	6148	0.940679	1.79415	0.014989	0.035487	0.159619	1	31	13	27	30	99	70	153	55	143	99
ENSMUSG00000057440	chr18	Mpp7	7347962	7351144	4975	-0.67879	1.568584	0.015027	0.035571	0.073488	-1	67	29	68	55	82	32	49	68	62	51
ENSMUSG00000020605	chr12	Hs1bp3	8313433	8313497	2958	0.455392	3.309844	0.015033	0.035579	0.036171	1	119	97	153	156	172	168	230	289	369	291
ENSMUSG00000001656	chr15	Hoxc11	1.03E+08	1.03E+08	2021	0.600097	2.288188	0.015044	0.035599	0.061158	1	52	59	61	64	81	150	87	136	148	137
ENSMUSG00000019843	chr10	Fyn	39368855	39369065	4363	0.429988	4.136166	0.015089	0.035699	0.034336	1	210	167	267	277	340	313	591	424	603	442
ENSMUSG00000098234	chr1	Snhg6	9941959	9942155	1146	0.588086	3.354741	0.015098	0.035714	0.063852	1	135	137	151	111	133	207	249	468	236	244
ENSMUSG00000042453	chr5	Reln	21884454	21885569	19834	-0.6388	2.819503	0.015102	0.035717	0.074195	-1	121	109	176	145	166	100	111	216	138	70
ENSMUSG00000033022	chr18	Cdo1	46713205	46713961	1530	1.820754	5.183346	0.015113	0.035738	0.613878	1	221	66	52	459	582	73	269	334	2240	4150
ENSMUSG00000029028	chr4	Lrrc47	1.54E+08	1.54E+08	3510	0.474868	5.008299	0.015131	0.035774	0.043875	1	325	377	479	537	542	552	706	1292	1018	825
ENSMUSG00000035575	chr11	Utp6	79932321	79932714	4517	-0.39264	5.53127	0.015161	0.035838	0.030038	-1	808	684	1089	760	1072	843	904	836	1087	969
ENSMUSG00000033577	chr9	Myo6	80165031	80165229	12078	-0.45324	3.376776	0.01522	0.035972	0.036094	-1	175	143	211	216	260	143	186	248	211	230
ENSMUSG00000028312	chr4	Smc2	52439243	52439334	5478	0.687398	2.48299	0.015271	0.036087	0.084865	1	58	64	65	43	125	103	175	91	276	166
ENSMUSG00000020674	chr12	Pxdn	29938036	29938324	9517	-0.50393	6.084894	0.015292	0.036118	0.050689	-1	1041	912	1501	1430	1890	890	1716	776	1914	1389
ENSMUSG00000025925	chr1	Terf1	15805646	15805957	4608	0.572098	1.932732	0.015292	0.036118	0.04976	1	49	38	48	57	56	82	91	108	113	122
ENSMUSG00000044783	chr1	Hjurp	88262471	88266658	8331	0.478922	4.733984	0.01529	0.036118	0.044446	1	371	262	358	302	579	523	799	496	987	849
ENSMUSG00000058756	chr11	Thra	98740638	98740687	4614	-0.41391	6.211754	0.015307	0.036148	0.034069	-1	1270	1035	1363	1545	1914	1198	1371	1727	1695	1413
ENSMUSG00000020935	chr11	Dcakd	1.03E+08	1.03E+08	2556	0.506327	4.296275	0.015314	0.036157	0.049008	1	228	251	242	332	286	513	564	302	745	555
ENSMUSG00000060771	chr1	Tsga10	37754776	37755521	10662	-0.56681	1.955442	0.015326	0.036179	0.05094	-1	70	71	85	66	87	58	74	53	108	69
ENSMUSG00000020128	chr11	Vps54	21239281	21239371	7515	-0.46201	4.568677	0.015334	0.03619	0.041105	-1	384	405	494	503	504	315	409	700	479	423
ENSMUSG00000024393	chr17	Prrc2a	35149076	35149401	7631	-0.41856	7.433757	0.015336	0.03619	0.035304	-1	2658	2496	3549	3631	4390	2755	3563	2555	4749	3820

ENSMUSG00000028525	chr4	Pde4b	1.02E+08	1.02E+08	10560	-0.56023	5.682008	0.01534	0.036194	0.062481	-1	829	715	823	942	1928	845	873	895	1622	669
ENSMUSG00000022974	chr16	Paxbp1	91014037	91015178	5508	0.439038	3.483857	0.015352	0.036216	0.034131	1	134	133	195	138	191	183	334	273	348	369
ENSMUSG00000028621	chr4	Cyb5rl	1.07E+08	1.07E+08	7430	-0.50606	3.406687	0.015358	0.036225	0.046567	-1	154	179	224	228	255	202	190	131	218	264
ENSMUSG00000028706	chr4	Nsun4	1.16E+08	1.16E+08	5993	-0.44791	4.923206	0.015375	0.036253	0.038993	-1	432	623	659	599	592	547	698	422	710	601
ENSMUSG00000069972	chr7	Rps13-ps2	88530446	88530898	453	0.642441	2.059309	0.015374	0.036253	0.068093	1	55	59	40	37	70	100	95	97	175	114
ENSMUSG00000039041	chr2	Adrm1	1.8E+08	1.8E+08	4457	0.488092	6.08847	0.015397	0.036298	0.04761	1	672	860	1181	926	1132	1411	1449	2807	1870	1678
ENSMUSG00000042644	chr17	Itpr3	27057304	27057674	8990	-0.53082	2.659401	0.015404	0.036307	0.048634	-1	120	84	108	146	161	80	121	128	126	144
ENSMUSG00000058922	chr9	Gm10052	1.24E+08	1.24E+08	960	0.704339	2.185345	0.015406	0.036307	0.08628	1	42	59	65	50	65	49	134	208	153	110
ENSMUSG00000038213	chr6	Tapbpl	1.25E+08	1.25E+08	2352	0.559458	2.418528	0.015442	0.036382	0.053716	1	58	45	89	71	96	121	145	98	187	180
ENSMUSG00000039167	chr3	Eltd1	1.51E+08	1.51E+08	4343	-0.58913	4.661983	0.015445	0.036382	0.068302	-1	334	497	643	702	341	294	404	714	536	425
ENSMUSG00000040354	chr10	Mars	1.27E+08	1.27E+08	3423	-0.37275	5.700441	0.015446	0.036382	0.02732	-1	885	845	1059	941	1173	805	948	1159	1237	1151
ENSMUSG00000062075	chr10	Lmnb2	80901203	80902900	4286	0.564426	3.888503	0.015506	0.036518	0.061284	1	121	152	229	180	338	332	515	216	578	428
ENSMUSG00000028322	chr4	Exosc3	45316613	45317028	1324	0.437197	3.294019	0.015514	0.036529	0.033238	1	136	99	161	150	142	220	243	262	305	270
ENSMUSG00000027455	chr2	Nsfl1c	1.51E+08	1.51E+08	3967	0.438358	6.095934	0.015522	0.036543	0.038397	1	739	866	1155	998	1116	1482	1584	2489	1874	1686
ENSMUSG00000028773	chr4	Fabp3	1.3E+08	1.3E+08	823	0.619902	8.528427	0.015541	0.036582	0.077779	1	3418	5881	5336	6048	3128	8299	8612	16086	11113	7816
ENSMUSG00000040537	chr5	Adam22	8072352	8078706	12231	-0.69988	1.454673	0.015556	0.036603	0.077548	-1	61	29	66	42	82	42	45	55	61	34
ENSMUSG00000098905	chr13	Zfp953	67339307	67343657	4676	-0.76729	0.705949	0.015556	0.036603	0.084993	-1	21	40	33	36	33	22	33	35	29	15
ENSMUSG00000046324	chr19	Ermp1	29608214	29612679	9338	-0.43676	4.089063	0.015561	0.03661	0.035936	-1	258	307	402	302	365	244	344	231	488	402
ENSMUSG00000056947	chr3	Mab21l1	55782510	55785285	2776	-0.75383	0.979086	0.015573	0.036632	0.083225	-1	26	26	45	40	67	37	25	25	34	41
ENSMUSG00000035376	chr16	Ptplb	35022421	35022635	3603	0.852037	2.818131	0.015594	0.036675	0.137164	1	68	45	84	88	137	93	147	94	319	426
ENSMUSG00000042903	chrX	Foxo4	1.01E+08	1.01E+08	3485	-0.48329	6.776974	0.015601	0.036684	0.047146	-1	2028	1790	2481	2122	2230	1613	1797	3242	1973	1968
ENSMUSG00000049728	chr7	Zfp668	1.28E+08	1.28E+08	4655	0.563369	1.98182	0.015614	0.036709	0.049752	1	45	44	55	52	63	96	79	115	129	113
ENSMUSG00000000001	chr3	Gnai3	1.08E+08	1.08E+08	3262	0.405828	4.823936	0.015659	0.036802	0.031767	1	373	305	407	366	600	518	777	699	1030	787
ENSMUSG00000001964	chrX	Emd	74254687	74255033	2517	0.389951	4.651169	0.015656	0.036802	0.028923	1	335	324	438	307	405	590	633	692	765	615
ENSMUSG00000002409	chr7	Dyrk1b	28179469	28179640	2695	-0.4376	5.994976	0.015674	0.036819	0.038301	-1	923	860	1213	1354	1902	953	1088	1438	1612	1271
ENSMUSG00000019564	chr10	Arid3a	79927043	79927256	5562	0.645775	2.161078	0.015673	0.036819	0.070764	1	56	39	57	63	69	51	126	170	148	138
ENSMUSG00000026655	chr2	Fam107b	3613758	3613938	3762	0.571874	2.791932	0.015671	0.036819	0.058624	1	75	64	83	94	149	116	220	132	271	232
ENSMUSG00000022668	chr16	Gtpbp8	44736768	44739368	3527	-0.44407	3.416065	0.015681	0.036829	0.035393	-1	171	221	240	192	187	173	215	213	241	205
ENSMUSG00000075229	chr16	Ccdc58	36071660	36072137	1225	0.532128	3.644124	0.015709	0.03689	0.053203	1	119	205	212	155	147	362	379	289	323	320
ENSMUSG00000037896	chr12	Rcor1	1.11E+08	1.11E+08	5684	-0.4227	4.106666	0.015715	0.036897	0.033578	-1	275	241	359	312	481	218	362	368	492	304
ENSMUSG00000032295	chr9	Man2c1	57130690	57130889	7052	0.421869	4.25063	0.015734	0.036935	0.033412	1	268	212	268	249	359	298	471	576	667	564
ENSMUSG00000043964	chr7	Orai3	1.28E+08	1.28E+08	2141	0.376872	3.996462	0.015748	0.036961	0.025619	1	192	201	258	235	270	291	426	456	482	449
ENSMUSG00000062822	chr13	4833420G17Rik	1.19E+08	1.19E+08	2574	0.454432	3.698733	0.015752	0.036966	0.037905	1	177	157	225	152	195	263	305	449	340	373
ENSMUSG00000034066	chr1	Farp2	93512079	93512184	5235	-0.51631	3.123085	0.01576	0.036977	0.047863	-1	134	108	219	151	259	116	157	215	185	160
ENSMUSG00000004043	chr11	Stat5a	1.01E+08	1.01E+08	7133	0.422905	4.175608	0.01578	0.037017	0.033699	1	219	182	258	260	382	324	473	434	603	598
ENSMUSG00000026466	chr1	Tor1aip1	1.56E+08	1.56E+08	5406	-0.51169	6.664365	0.01579	0.037036	0.053017	-1	1785	1584	2186	2175	2246	1402	1502	3182	1832	1789
ENSMUSG00000038784	chr6	Cnot4	35022066	35023432	7185	-0.38763	4.355768	0.015798	0.037048	0.02817	-1	325	344	429	403	432	339	376	480	444	416
ENSMUSG00000010110	chr19	Stx5a	8741413	8741575	5808	0.416902	4.519968	0.015818	0.037089	0.033232	1	317	265	380	257	424	410	635	747	695	581
ENSMUSG00000039016	chr9	Timm8b	50603901	50604039	527	-0.44519	5.886809	0.015839	0.037131	0.039718	-1	979	1223	1350	1057	1020	1127	1204	1137	1180	1110
ENSMUSG00000026867	chr2	Gapvd1	34676184	34678177	8287	-0.39071	5.303758	0.015862	0.037178	0.030027	-1	669	609	832	678	977	556	783	967	918	782
ENSMUSG00000026577	chr1	Blzf1	1.64E+08	1.64E+08	5336	-0.43571	4.241509	0.015924	0.037317	0.036163	-1	295	310	432	392	386	269	396	509	395	301
ENSMUSG00000042271	chrX	Nxt2	1.42E+08	1.42E+08	3176	-0.64374	1.559096	0.015928	0.037321	0.065985	-1	71	43	62	45	71	38	52	52	83	41
ENSMUSG00000051671	chr8	Coa6	1.26E+08	1.26E+08	762	-0.49852	3.370076	0.015947	0.03736	0.04552	-1	187	185	266	181	180	198	230	148	204	200
ENSMUSG00000042073	chr9	Abhd14b	1.06E+08	1.06E+08	1820	0.542201	2.68676	0.015954	0.037369	0.051033	1	93	74	81	72	108	109	173	180	181	238
ENSMUSG00000074918	chr2	Inafm2	1.19E+08	1.19E+08	3053	0.525497	2.675816	0.015969	0.037399	0.04676	1	81	77	93	84	93	112	171	130	242	225
ENSMUSG00000028233	chr4	Tgs1	3574875	3575129	5314	-0.39972	3.756258	0.015977	0.037411	0.028954	-1	213	236	267	270	290	224	310	246	340	236
ENSMUSG00000036826	chr7	Igflr1	30565427	30565466	1270	0.873252	0.679022	0.015998	0.037453	0.111446	1	24	17	19	7	19	31	48	37	36	71
ENSMUSG00000068606	chr18	Gm4841	60268301	60271039	2838	-0.74848	4.376821	0.016037	0.037539	0.11152	-1	240	720	539	288	334	361	365	166	520	395
ENSMUSG00000071281	chr13	Zfp65	67705306	67708929	4124	-0.56215	2.137815	0.016047	0.037555	0.052096	-1	79	81	112	66	93	64	71	101	87	84
ENSMUSG00000062526	chr18	Mppe1	67225530	67225884	2007	0.601536	2.26903	0.016053	0.037556	0.061515	1	67	55	69	44	76	104	127	85	207	149
ENSMUSG00000086534	chr17	Gm16758	29890084	29890577	3848	-0.91366	0.491343	0.016051	0.037556	0.128967	-1	39	20	33	28	24	18	38	8	31	14
ENSMUSG00000059149	chr1	Mfsd4	1.32E+08	1.32E+08	7187	-0.85752	2.098689	0.016074	0.037598	0.136505	-1	60	112	86	136	50	28	62	124	84	60
ENSMUSG00000007777	chr11	0610009B22Rik	51685386	51686092	998	-0.44853	4.00934	0.016116	0.03769	0.037993	-1	282	307	395	245	309	296	350	280	298	337
ENSMUSG00000015085	chr2	Entpd2	25395874	25396089	2128	0.470121	4.421533	0.016118	0.03769	0.043122	1	310	182	306	259	457	498	531	686	569	578
ENSMUSG00000039163	chr9	Cmc1	1.18E+08	1.18E+08	1181	0.492783	3.453438	0.016134	0.037721	0.044826	1	113	179	181	117	158	269	229	304	339	329
ENSMUSG00000028838	chr4	Extl1	1.34E+08	1.34E+08	4333	-0.41668	5.739798	0.016164	0.037784	0.034822	-1	775	901	1128	1170	1142	885	952	1353	1126	988
ENSMUSG00000027618	chr2	Nfs1	1.56E+08	1.56E+08	3612	-0.42638	6.620156	0.016201	0.037863	0.037009	-1	1595	1845	2119	1819	2004	1672	1676	2495	2065	1808
ENSMUSG00000020420	chr7	Zfp607	27862557	27862589	2061	-0.83394	0.209491	0.016205	0.037867	0.092166	-1	27	13	34	11	32	13	19	19	24	16
ENSMUSG00000029490	chr5	Mfsd7a	1.08E+08	1.08E+08	2508	0.705504	1.462696	0.016208	0.037867	0.081463	1	16	41	34	33	44	58	68	61	81	114
ENSMUSG00000005150	chr8	Wdr83	85075035	85075343	2818	0.421717	4.442229	0.016232	0.037918	0.034129	1	248	325	398	281	284	513	556	505	715	598
ENSMUSG00000024976	chr19	Shoc2	53944306	53944402	4203	-0.39644	4.573789	0.016258	0.037972	0.030321	-1	400	346	536	425	568	328	519	564	598	407
ENSMUSG00000021400	chr13	Wrnip1	32802038	32803044	2633	0.413494	3.409625	0.016268	0.03799	0.030186	1	118	116	170	154	205	222	309	260	344	273
ENSMUSG00000036315	chr17	Znrd1	36954356	36954552	819	0.447687	3.683903	0.016275	0.037999	0.036941	1	157	189	211	161	175	325	368	266	387	356
ENSMUSG00000029482	chr5	Aacs	1.25E+08	1.25E+08	3668	1.000142	3.848652	0.016325	0.038109	0.198513	1	92	98	79	194	363	163	240	229	751	947
ENSMUSG00000016831	chr14	Tox4	52279146	52279232	6940	-0.40633	5.986476	0.016345	0.038142	0.033369	-1	985	1028	1505	1219	1325	965	1199	1613	1393	1187
ENSMUSG00000063015	chr5	Ccni	93181933	93183420	3303	0.484698	5.82956	0.016342	0.038142	0.047614	1	634	631	828	888	1005	852	1341	2362	1765	1509

ENSMUSG00000006699	chr4	Cdc42	1.37E+08	1.37E+08	2966	0.37898	7.979397	0.016364	0.038181	0.029583	1	3170	3302	4240	3454	4183	5551	6609	5805	8163	7228
ENSMUSG00000019970	chr10	Sgk1	21882184	21882707	4903	-0.51099	7.163721	0.016375	0.038194	0.053626	-1	2075	2707	2956	3943	2257	2208	2293	2892	2675	3656
ENSMUSG00000032840	chr5	2410131K14Rik	1.18E+08	1.18E+08	5649	-0.39568	3.874456	0.016375	0.038194	0.028822	-1	216	231	308	327	309	217	285	339	337	298
ENSMUSG00000007670	chr17	Khsrp	57021058	57022970	3990	0.40161	4.76629	0.016406	0.038253	0.031437	1	356	301	392	363	558	466	676	762	953	801
ENSMUSG00000028689	chr4	Ccdc163	1.17E+08	1.17E+08	2519	0.65093	1.404752	0.016405	0.038253	0.064425	1	29	26	39	39	31	38	93	60	97	80
ENSMUSG00000001285	chr15	Myg1	1.02E+08	1.02E+08	2823	0.421847	3.533864	0.016435	0.038314	0.031963	1	151	152	190	145	179	258	316	238	390	336
ENSMUSG00000055994	chr8	Nod2	88647315	88647409	5014	0.683662	1.007956	0.016445	0.038331	0.067112	1	25	14	25	26	32	43	70	49	49	60
ENSMUSG00000038174	chr1	Fam126b	58522806	58530259	12041	-0.6574	2.847737	0.016452	0.038342	0.082387	-1	137	117	138	144	196	50	79	141	207	194
ENSMUSG00000035161	chr14	Ints6	62676330	62678167	4993	-0.56866	2.805401	0.01648	0.0384	0.058965	-1	129	93	147	128	203	77	135	195	140	108
ENSMUSG00000020652	chr12	Cenpo	4196004	4197106	7263	0.673736	1.193001	0.016511	0.038459	0.065956	1	18	28	24	24	47	47	53	68	72	72
ENSMUSG00000045482	chr5	Trrap	1.45E+08	1.45E+08	15185	-0.39573	4.954336	0.016511	0.038459	0.030837	-1	516	386	715	583	783	444	695	603	809	602
ENSMUSG00000076240	chr5	Mir702	1.37E+08	1.37E+08	109	0.609846	1.698862	0.016535	0.038508	0.058814	1	38	33	52	34	51	64	90	63	144	89
ENSMUSG00000030980	chr7	Knop1	1.19E+08	1.19E+08	5871	-0.36453	4.912796	0.016568	0.038579	0.025906	-1	454	515	637	551	681	492	583	634	762	606
ENSMUSG00000039917	chr5	Rhbdd2	1.36E+08	1.36E+08	7478	0.467058	2.971678	0.016577	0.038594	0.037925	1	100	89	118	108	128	165	189	167	287	249
ENSMUSG00000003660	chr2	Snrnp200	1.27E+08	1.27E+08	7819	-0.40947	5.830392	0.016602	0.038634	0.034	-1	902	855	1193	1197	1308	752	1086	1482	1356	1074
ENSMUSG00000032737	chr7	Inppl1	1.02E+08	1.02E+08	4981	-0.39168	7.282831	0.0166	0.038634	0.031622	-1	2353	2514	3352	3339	3253	2453	3755	2776	3787	3014
ENSMUSG00000086316	chrX	2210013O21Rik	1.54E+08	1.54E+08	1880	0.461832	3.253535	0.016603	0.038634	0.037932	1	126	127	149	136	117	227	271	224	328	224
ENSMUSG00000097295	chr10	Hmgb1-ps8	22262742	22263367	626	-1.01261	0.734968	0.016608	0.03864	0.173752	-1	37	20	33	53	35	5	19	46	17	38
ENSMUSG00000024792	chr19	Zfpl1	6080762	6081214	1798	0.435149	3.215661	0.016665	0.038765	0.033817	1	111	86	158	147	157	198	233	248	293	262
ENSMUSG00000038264	chr9	Sema7a	57940113	57940328	3296	0.472373	4.414434	0.016693	0.038825	0.043655	1	254	257	342	348	278	342	701	398	869	645
ENSMUSG00000003072	chr10	Atp5d	80138632	80138855	1928	0.448308	8.550723	0.016702	0.038831	0.04174	1	3818	5598	5829	6293	4741	9745	9175	9236	12373	9625
ENSMUSG00000014503	chr18	Pkd2l2	34409423	34409497	2666	-0.73589	0.810119	0.016701	0.038831	0.080218	-1	31	39	42	37	24	33	28	23	31	30
ENSMUSG00000034108	chr19	Ccs	4825366	4825664	1057	0.403386	4.173756	0.016748	0.038933	0.031169	1	189	196	295	271	361	387	409	528	542	517
ENSMUSG00000039983	chr2	Ccdc32	1.19E+08	1.19E+08	2214	0.478529	2.915513	0.016755	0.038943	0.040777	1	93	77	143	86	125	171	211	221	211	190
ENSMUSG00000000126	chr11	Wnt9a	59306928	59307067	3329	-0.44848	4.070826	0.016765	0.03896	0.03875	-1	306	279	415	301	307	255	393	405	325	266
ENSMUSG00000037035	chr1	Inhbb	1.19E+08	1.19E+08	4255	1.126547	0.54385	0.016773	0.038971	0.210401	1	23	6	8	11	21	16	21	93	38	47
ENSMUSG00000090698	chr6	Apold1	1.35E+08	1.35E+08	3284	-0.89332	2.001396	0.016825	0.039086	0.149365	-1	32	55	71	204	69	49	66	59	83	67
ENSMUSG00000074272	chr7	Ceacam1	25461702	25463900	3736	-0.61085	2.628108	0.016874	0.039193	0.069819	-1	95	106	123	193	95	63	105	108	156	145
ENSMUSG00000004455	chr5	Ppp1cc	1.22E+08	1.22E+08	3424	-0.39717	6.023191	0.016905	0.039253	0.032239	-1	1006	1258	1416	1168	1298	1000	1286	1537	1495	1238
ENSMUSG00000021178	chr12	Psmc1	1E+08	1E+08	1518	0.431046	7.260164	0.016906	0.039253	0.038532	1	1845	1960	2592	2051	2481	3247	3571	5619	4163	3818
ENSMUSG00000078862	chr2	Gm14326	1.78E+08	1.78E+08	2863	-0.67378	2.573877	0.016909	0.039254	0.083942	-1	69	68	214	84	197	73	114	118	110	115
ENSMUSG00000031818	chr8	Cox4i1	1.21E+08	1.21E+08	1550	0.440315	9.428203	0.016928	0.039292	0.040505	1	7111	10583	10919	10944	8866	17267	16045	19013	20773	18654
ENSMUSG00000026924	chr2	Sec16a	26409431	26410953	9189	-0.46183	5.479218	0.01695	0.039335	0.043424	-1	789	540	884	886	1285	579	863	1206	968	782
ENSMUSG00000023143	chr16	Nagpa	5195289	5196058	2370	0.537294	3.192858	0.016995	0.039434	0.053597	1	117	98	123	132	145	184	210	153	399	328
ENSMUSG00000020268	chr11	Lyrm7	54826866	54827065	3597	-0.50807	3.88998	0.017016	0.039476	0.050506	-1	280	286	289	308	263	262	304	154	406	303
ENSMUSG00000071141	chr6	Rpl36a-ps3	1.36E+08	1.36E+08	321	0.678237	2.206256	0.017031	0.039503	0.082741	1	50	65	77	46	48	150	131	107	93	144
ENSMUSG00000024639	chr19	Gnaq	16132831	16133461	6185	-0.40131	4.395829	0.017037	0.039512	0.031367	-1	279	337	425	428	554	270	442	404	597	438
ENSMUSG00000008540	chr6	Mgst1	1.38E+08	1.38E+08	2013	0.826317	4.727993	0.01705	0.039535	0.138956	1	231	283	224	376	488	253	419	552	1211	1687
ENSMUSG00000087231	chr6	E230016M11Rik	67036599	67036935	3353	0.828733	0.088086	0.017054	0.039537	0.078765	1	11	9	14	9	14	21	19	41	27	33
ENSMUSG00000099060	chr5	Mir7025	75176831	75176904	74	-1.03684	0.038544	0.017093	0.039622	0.164948	-1	29	7	22	19	31	6	9	30	21	8
ENSMUSG00000027459	chr2	Fam110a	1.52E+08	1.52E+08	2207	0.623725	2.014131	0.017158	0.039766	0.06717	1	25	50	65	64	56	90	105	82	169	116
ENSMUSG00000020900	chr11	Myh10	68691559	68691842	10458	-0.43745	4.843869	0.017161	0.039766	0.038336	-1	381	375	574	696	783	393	688	542	702	545
ENSMUSG00000026017	chr1	Carf	60098247	60098307	14557	-0.56743	1.624842	0.01717	0.039781	0.049784	-1	60	53	65	55	66	46	50	63	59	64
ENSMUSG00000002658	chr17	Gtf2f1	57003405	57003631	1717	0.431269	4.698017	0.01719	0.03982	0.037058	1	241	345	459	376	436	581	693	483	948	785
ENSMUSG00000025782	chr2	Taf3	9914552	9916466	6389	-0.44253	3.272135	0.017242	0.039925	0.035293	-1	141	152	216	192	231	136	185	241	229	163
ENSMUSG00000073079	chr12	Srp54a	55089202	55089279	1515	-0.6786	1.009923	0.01724	0.039925	0.070298	-1	40	42	44	29	43	27	25	46	47	30
ENSMUSG00000097919	chr8	Gm27021	1.21E+08	1.21E+08	758	0.676246	1.667988	0.017252	0.039942	0.075289	1	33	34	48	37	45	43	85	62	127	134
ENSMUSG00000019763	chr10	Rmnd1	4401915	4403501	5894	-0.46491	4.70461	0.017278	0.039977	0.043487	-1	434	535	579	533	402	455	533	354	622	584
ENSMUSG00000020593	chr12	Lpin1	16535669	16538572	5725	-0.57055	7.694331	0.017274	0.039977	0.068045	-1	3337	4455	5194	4187	3262	2812	2781	6490	3778	3506
ENSMUSG00000028085	chr3	Gatb	85574119	85574319	4299	-0.40123	4.336426	0.017273	0.039977	0.031298	-1	321	387	435	394	362	350	352	431	470	415
ENSMUSG00000062070	chrX	Pgk1	1.06E+08	1.06E+08	2244	-0.41249	10.07446	0.017278	0.039977	0.03582	-1	16721	21356	23743	18920	21692	20862	18885	21574	24032	21413
ENSMUSG00000022407	chr15	Adsl	80948490	80948700	4398	-0.42313	6.684501	0.017298	0.040012	0.03721	-1	1594	1846	2202	2188	1976	1880	1642	2376	2341	1930
ENSMUSG00000097318	chr16	1700007L15Rik	33379855	33380379	737	0.945512	0.06132	0.017299	0.040012	0.120088	1	6	17	12	10	7	33	14	33	30	30
ENSMUSG00000047153	chr14	Khnyn	55884969	55885142	3876	-0.54932	3.206323	0.017313	0.040038	0.05788	-1	173	133	198	174	238	78	183	259	176	184
ENSMUSG00000025738	chr17	Fbxl16	25809085	25809386	3478	-0.50693	2.266837	0.017318	0.040042	0.042342	-1	79	73	97	98	121	64	110	93	110	83
ENSMUSG00000024539	chr18	Ptpn2	67665511	67665874	3125	0.406891	3.854199	0.017333	0.040071	0.031096	1	164	215	234	166	253	316	392	398	408	388
ENSMUSG00000036298	chr15	Slc2a13	91267696	91272380	8367	-0.77488	1.155029	0.017336	0.040072	0.100805	-1	54	23	58	24	72	22	43	36	56	32
ENSMUSG00000030199	chr6	Etv6	1.34E+08	1.34E+08	5983	0.467374	3.845483	0.017352	0.040101	0.042428	1	115	179	222	203	301	301	452	278	531	391
ENSMUSG00000020232	chr10	Hmg20b	81346048	81346477	3149	0.416782	3.79661	0.017367	0.040123	0.032401	1	174	177	234	201	198	227	429	321	466	426
ENSMUSG00000047514	chr10	Tspyl1	34282190	34285275	3086	-0.40153	6.040406	0.017366	0.040123	0.033238	-1	1094	1185	1413	1167	1379	1026	1306	1651	1401	1213
ENSMUSG00000029769	chr6	Ccdc136	29396309	29396335	4298	0.546732	2.959315	0.017377	0.040139	0.055701	1	85	68	112	111	153	150	210	312	199	187
ENSMUSG00000053477	chr18	Tcf4	69344146	69345025	12250	-0.38803	5.888198	0.017428	0.04025	0.030961	-1	855	882	1201	1321	1400	824	1290	1231	1539	1170
ENSMUSG00000019864	chr10	Rtn4ip1	43901807	43902536	3135	-0.56284	5.024609	0.017483	0.040364	0.065089	-1	505	715	730	719	524	601	644	292	860	667
ENSMUSG00000074024	chr7	4632427E13Rik	92734166	92739264	7303	0.975551	-0.33178	0.017481	0.040364	0.106267	1	8	6	11	4	9	10	11	24	31	31
ENSMUSG00000033059	chr2	Pygb	1.51E+08	1.51E+08	4809	0.583544	4.228471	0.017495	0.040385	0.068867	1	216	134	238	249	443	275	461	397	763	790
ENSMUSG00000090262	chr5	Mpv17	31140660	31141850	3208	-0.38196	5.162703	0.017531	0.040461	0.029401	-1	613	605	760	674	717	641	819	669	838	641

ENSMUSG00000021958	chr14	Pinx1	63860312	63860447	1351	0.63118	1.947699	0.017559	0.040519	0.069685	1	26	47	73	35	69	93	114	79	141	105
ENSMUSG00000038368	chr4	Focad	88094629	88094675	11311	-0.44096	3.775676	0.017591	0.040584	0.03714	-1	202	178	293	289	373	222	279	194	370	295
ENSMUSG00000044339	chr5	Alkbh2	1.14E+08	1.14E+08	1115	0.87642	0.360482	0.017606	0.040614	0.111204	1	8	9	13	23	16	26	51	18	33	48
ENSMUSG00000036334	chr3	Igsf10	59316735	59320374	10150	-0.6827	4.498314	0.017617	0.040631	0.095375	-1	425	174	516	331	981	374	534	295	488	319
ENSMUSG00000037211	chr3	Spry1	37639947	37640064	2906	0.413233	4.872062	0.01762	0.040633	0.034303	1	381	311	497	479	426	537	862	954	842	709
ENSMUSG00000063383	chr17	Zfp947	22144359	22146534	2872	-0.85881	0.285905	0.01765	0.040693	0.108886	-1	20	31	38	18	15	12	14	14	32	25
ENSMUSG00000030088	chr6	Aldh1l1	90486427	90486531	4512	1.053684	3.60343	0.017657	0.040701	0.224867	1	78	56	88	191	266	130	152	206	571	918
ENSMUSG00000031660	chr8	Brd7	88331039	88331442	5244	-0.38945	6.224439	0.017659	0.040701	0.031449	-1	1072	1250	1633	1519	1647	1381	1449	1548	1644	1461
ENSMUSG00000023805	chr17	Synj2	5941280	5941577	8342	0.563103	4.680898	0.017692	0.040764	0.06477	1	379	217	411	366	347	409	724	1143	862	462
ENSMUSG00000026888	chr2	Grb14	64912476	64912853	7185	-0.65648	3.670618	0.017695	0.040764	0.086643	-1	195	257	294	368	163	234	183	122	400	220
ENSMUSG00000027887	chr3	Sypl2	1.08E+08	1.08E+08	4377	-0.48205	10.20115	0.017693	0.040764	0.049209	-1	17231	19008	26271	21352	32647	23970	23949	13470	29826	22567
ENSMUSG00000019659	chr9	Ccdc12	1.11E+08	1.11E+08	818	0.405772	5.045023	0.017701	0.04077	0.033296	1	337	490	547	478	513	788	852	712	1082	936
ENSMUSG00000027387	chr2	Zc3h8	1.29E+08	1.29E+08	1624	-0.53995	3.125605	0.01775	0.040877	0.055346	-1	132	184	207	149	183	168	195	104	163	181
ENSMUSG00000027427	chr2	Polr3f	1.45E+08	1.45E+08	7710	-0.45388	3.46657	0.01779	0.040956	0.039046	-1	181	196	244	207	232	138	208	305	230	206
ENSMUSG00000031393	chrX	Mecp2	74026592	74036494	10592	-0.4957	5.17537	0.01779	0.040956	0.050659	-1	610	564	779	728	867	468	586	1161	729	554
ENSMUSG00000016758	chr15	Bik	83526862	83526936	943	0.886757	0.338548	0.017827	0.041035	0.106965	1	6	22	12	14	12	22	48	23	39	43
ENSMUSG00000048186	chr2	Bend7	4717831	4718292	4194	-0.86303	0.838166	0.017834	0.041044	0.127251	-1	26	28	46	52	34	13	17	58	28	27
ENSMUSG00000027466	chr2	Rbck1	1.52E+08	1.52E+08	4601	0.389699	5.236127	0.017859	0.04109	0.030893	1	380	520	560	612	658	760	919	922	1275	1139
ENSMUSG00000052566	chr8	Hook2	84990595	84990752	2617	0.550243	1.846205	0.01786	0.04109	0.047204	1	39	45	53	51	47	74	84	107	122	98
ENSMUSG00000038644	chr7	Pold1	44532746	44532894	4860	0.544717	2.778317	0.017877	0.041121	0.054701	1	79	65	111	93	115	156	164	115	292	220
ENSMUSG00000021811	chr14	Dnajc9	20384638	20385478	1631	0.390355	4.087594	0.017882	0.041126	0.029155	1	231	224	289	202	273	391	448	429	558	409
ENSMUSG00000050122	chr1	Vwa3b	37026596	37026645	5386	-0.83432	0.855431	0.017886	0.041129	0.112039	-1	30	42	39	51	21	36	24	34	25	23
ENSMUSG00000089774	chr16	Slc5a3	92058322	92058480	10913	0.479632	3.30894	0.017925	0.041212	0.043643	1	121	96	154	109	216	181	270	339	286	261
ENSMUSG00000042046	chr1	Dstyk	1.32E+08	1.32E+08	9345	-0.37584	4.548091	0.017929	0.041214	0.027848	-1	397	362	500	418	533	345	485	551	495	495
ENSMUSG00000060397	chr7	Zfp128	12881177	12881360	4087	-0.62338	1.27484	0.017967	0.041294	0.061451	-1	39	36	67	51	46	25	54	40	60	40
ENSMUSG00000027663	chr3	Zmat3	32334792	32341695	11435	-0.38915	4.067946	0.017996	0.041352	0.029139	-1	262	257	358	280	445	251	387	289	426	349
ENSMUSG00000050505	chr14	Pcdh20	88464743	88469730	5492	-0.83865	0.890635	0.017998	0.041352	0.115383	-1	29	12	41	40	76	20	27	23	45	36
ENSMUSG00000020848	chr11	Doc2b	75768966	75772068	4361	1.593773	0.241618	0.01804	0.041443	0.45787	1	6	2	10	9	18	4	26	122	26	7
ENSMUSG00000020003	chr10	Pex7	19859929	19860994	2351	-0.40947	4.186246	0.01808	0.041527	0.032751	-1	291	316	438	342	339	343	344	327	377	407
ENSMUSG00000044629	chr11	Cnrip1	17051586	17051824	4003	0.522911	2.453913	0.018087	0.041536	0.04747	1	61	55	83	78	94	80	167	173	186	145
ENSMUSG00000034610	chr4	Zcchc11	1.08E+08	1.08E+08	8684	-0.52018	3.739845	0.018114	0.04159	0.053812	-1	249	192	277	270	327	137	237	418	265	229
ENSMUSG00000063439	chr7	B9d2	25681158	25681474	1021	0.536225	2.805394	0.018121	0.0416	0.052527	1	70	111	118	80	86	189	191	169	213	177
ENSMUSG00000002332	chr14	Dhrs1	55739020	55739420	2760	0.393544	5.282699	0.018142	0.041642	0.031692	1	433	586	610	586	573	891	985	898	1250	1118
ENSMUSG00000020456	chr11	Ogdh	6291633	6291693	5456	-0.41122	9.72209	0.018158	0.041671	0.036143	-1	12628	14585	16309	20400	16366	14511	14113	17327	22026	16822
ENSMUSG00000029636	chr5	Wasf3	1.46E+08	1.46E+08	3996	-0.84035	0.090183	0.0182	0.041761	0.094321	-1	11	15	17	27	38	8	19	14	26	17
ENSMUSG00000049630	chr2	C1ql3	13003457	13004444	2535	-1.00327	0.197732	0.018216	0.041791	0.156711	-1	18	8	42	24	31	7	21	29	21	6
ENSMUSG00000046794	chr8	Ppp1r3b	35375741	35375805	4206	1.394079	2.414395	0.01829	0.041952	0.38304	1	24	31	36	77	75	47	61	20	327	474
ENSMUSG00000030161	chr6	Gabarapl1	1.3E+08	1.3E+08	1765	0.804705	5.462232	0.018331	0.04204	0.135712	1	489	471	626	560	514	521	798	3225	1113	917
ENSMUSG00000021708	chr13	Rasgrf2	91880400	91884524	8810	-0.54847	1.984162	0.018354	0.04208	0.051257	-1	61	70	83	96	74	61	61	79	95	73
ENSMUSG00000038521	chr6	C1s1	1.25E+08	1.25E+08	3129	0.427298	6.281842	0.018352	0.04208	0.038537	1	1109	718	1198	939	1654	1661	2300	1980	2234	2212
ENSMUSG00000068196	chr16	Col8a1	57624258	57628817	5108	0.771054	4.986339	0.018368	0.042104	0.124397	1	452	153	373	352	660	555	1748	408	1271	773
ENSMUSG00000033767	chr3	D930015E06Rik	83897655	83898613	10572	0.464933	3.564278	0.018448	0.04228	0.041938	1	91	144	195	219	182	266	292	321	419	294
ENSMUSG00000035356	chr16	Nfkbiz	55811375	55812783	5018	0.698553	1.005298	0.018489	0.042367	0.076266	1	16	17	38	23	28	29	70	48	58	71
ENSMUSG00000078485	chr4	Plekhn1	1.56E+08	1.56E+08	2210	0.905814	0.297303	0.018498	0.04238	0.118925	1	18	9	10	7	20	21	25	21	50	55
ENSMUSG00000064262	chr6	Gimap8	48647234	48647285	3654	-0.62234	2.121579	0.018528	0.042444	0.071708	-1	58	89	115	103	67	49	60	72	119	102
ENSMUSG00000055041	chr15	Commd5	76899910	76899992	1060	0.45747	2.914562	0.018533	0.042448	0.037455	1	102	89	122	87	123	180	197	192	216	211
ENSMUSG00000021824	chr14	Ap3m1	21031442	21036703	7015	-0.36211	4.921799	0.018547	0.042473	0.02656	-1	469	472	657	551	717	446	670	553	791	661
ENSMUSG00000031990	chr9	Jam3	27097385	27098401	2539	0.448523	3.757067	0.01857	0.04251	0.039251	1	156	147	209	196	249	244	519	296	464	307
ENSMUSG00000039308	chr14	Ndst2	20723739	20724360	3305	0.448733	3.323493	0.018567	0.04251	0.037499	1	135	109	126	150	180	198	241	228	337	341
ENSMUSG00000058729	chr1	Lin9	1.81E+08	1.81E+08	7244	-0.50444	2.415332	0.018581	0.04253	0.044135	-1	110	82	102	102	117	85	115	100	104	101
ENSMUSG00000032554	chr9	Trf	1.03E+08	1.03E+08	3320	0.727774	6.060407	0.018613	0.042595	0.11228	1	708	386	577	917	1756	1246	1864	1012	2497	3261
ENSMUSG00000063698	chr19	Sfxn4	60837277	60839050	2975	0.765847	0.621858	0.018631	0.04263	0.082738	1	18	16	16	19	18	29	69	28	47	37
ENSMUSG00000074570	chr2	Cass4	1.72E+08	1.72E+08	5334	0.855051	0.13073	0.018674	0.042722	0.099868	1	7	9	18	7	18	19	27	17	40	46
ENSMUSG00000030086	chr6	Chchd6	89383146	89383348	1126	0.62491	2.034582	0.018678	0.042723	0.068589	1	46	51	61	50	52	88	100	69	139	171
ENSMUSG00000006423	chrX	C330007P06Rik	36823737	36824169	7424	-0.41761	3.968161	0.018707	0.042783	0.034433	-1	263	211	329	310	392	173	297	359	392	364
ENSMUSG00000001700	chr18	Gramd3	56432132	56432357	2605	-0.38872	3.886036	0.018721	0.042795	0.02897	-1	238	243	345	266	305	263	328	245	368	282
ENSMUSG00000047409	chr9	Ctdspl	1.19E+08	1.19E+08	5190	0.503261	3.517008	0.018722	0.042795	0.049515	1	156	109	163	154	206	138	323	349	373	404
ENSMUSG00000056476	chr3	Med12l	59006978	59007100	10408	-1.01444	0.371364	0.018717	0.042795	0.175775	-1	23	8	38	15	58	9	25	9	37	17
ENSMUSG00000058407	chr1	Txndc9	37985189	37987779	9102	0.373181	5.084968	0.0188	0.042967	0.02856	1	386	458	628	481	516	741	888	891	1000	927
ENSMUSG00000025869	chr13	Nop16	54584185	54585424	1845	0.39357	4.343236	0.018815	0.042995	0.030837	1	237	284	368	244	328	468	541	449	623	588
ENSMUSG00000036181	chr13	Hist1h1c	23738808	23740367	1560	0.50729	7.126009	0.01882	0.042997	0.055171	1	1562	1648	2596	1946	1919	2453	2714	6118	4426	3562
ENSMUSG00000060166	chr16	Zdhhc8	18220754	18223377	4867	-0.35979	5.128071	0.018845	0.043049	0.026538	-1	533	576	685	682	816	594	713	640	928	708
ENSMUSG00000035407	chr4	Kank4	98754898	98756585	4795	-0.74439	1.097156	0.018862	0.043079	0.092822	-1	51	33	26	53	51	24	44	49	39	25
ENSMUSG00000020389	chr11	Cdkl3	52004221	52004417	5360	0.673576	1.049805	0.018877	0.043092	0.065946	1	29	25	16	23	31	39	60	58	68	57
ENSMUSG00000026803	chr2	Ttf1	29060262	29060303	6023	-0.48018	2.849952	0.018875	0.043092	0.042353	-1	142	122	151	134	140	106	148	164	130	144
ENSMUSG00000050954	chr13	Zfp169	48487647	48489318	8017	-0.86631	0.003035	0.018874	0.043092	0.105745	-1	22	17	26	11	24	5	15	24	13	20

ENSMUSG00000007411	chr12	Mark3	1.12E+08	1.12E+08	3388	-0.38911	5.771285	0.018894	0.043118	0.031838	-1	837	922	1245	1005	1182	883	1024	1375	1200	1015
ENSMUSG00000027506	chr3	Tpd52	8925593	8931174	7487	0.440406	5.051008	0.018892	0.043118	0.040303	1	351	456	577	467	495	708	790	605	1267	1125
ENSMUSG00000036442	chr8	Thap11	1.06E+08	1.06E+08	1848	0.380674	4.570148	0.018915	0.043158	0.029125	1	270	319	376	372	380	520	598	723	698	572
ENSMUSG00000071041	chr8	Gm15210	1E+08	1E+08	1545	0.511288	2.198615	0.018928	0.04318	0.044694	1	57	42	75	59	78	103	119	119	132	139
ENSMUSG00000048388	chr2	Fam171b	83812636	83812977	5744	-0.64656	2.433938	0.018966	0.043261	0.079414	-1	109	52	125	78	195	87	119	74	111	92
ENSMUSG00000028214	chr4	Gem	11704457	11704566	2104	0.623099	2.136304	0.018974	0.04327	0.071959	1	42	24	70	68	85	88	139	139	149	94
ENSMUSG00000021725	chr13	Parp8	1.17E+08	1.17E+08	3088	-0.3842	3.677057	0.018995	0.043306	0.027947	-1	207	235	261	229	267	205	280	263	308	234
ENSMUSG00000027077	chr2	Smtnl1	84811176	84811539	1761	0.867994	5.265953	0.018993	0.043306	0.159136	1	220	494	284	950	272	531	901	2089	1426	954
ENSMUSG00000035413	chr11	Tmem98	80810175	80810459	1633	0.596075	1.892504	0.019003	0.043316	0.062347	1	35	38	57	41	72	81	89	68	147	126
ENSMUSG00000028318	chr4	Polr1e	45018583	45018792	3897	0.56068	2.132558	0.019006	0.043316	0.055731	1	59	33	68	55	76	115	115	98	134	127
ENSMUSG00000027314	chr2	Dll4	1.19E+08	1.19E+08	3852	-0.49621	3.12197	0.019028	0.043358	0.047719	-1	141	153	144	216	186	105	139	158	242	209
ENSMUSG00000032244	chr9	Fem1b	62791832	62797728	6488	-0.3745	5.058978	0.019038	0.043374	0.028909	-1	466	522	731	605	860	487	661	632	915	730
ENSMUSG00000062456	chr19	Rpl9-ps6	32465885	32466575	691	0.531085	2.23916	0.019045	0.043383	0.04764	1	59	61	61	72	58	108	126	114	173	117
ENSMUSG00000031822	chr8	Gse1	1.2E+08	1.2E+08	8098	-0.4002	5.021322	0.019073	0.043441	0.033111	-1	541	410	825	664	673	516	687	725	691	634
ENSMUSG00000020108	chr10	Ddit4	59949675	59951029	1685	1.184354	4.907099	0.019105	0.043505	0.292365	1	204	154	416	517	257	366	394	3061	354	608
ENSMUSG00000079036	chr12	Alkbh1	87425840	87429437	6574	0.475887	2.80458	0.019183	0.043675	0.040887	1	87	95	92	77	129	144	204	161	242	189
ENSMUSG00000003929	chr17	Zfp81	33329342	33335653	6639	-0.58939	1.793029	0.019257	0.043837	0.059584	-1	63	45	75	56	107	42	74	73	73	56
ENSMUSG00000030598	chr7	Fbxo17	28716804	28717038	2497	0.549151	2.849475	0.019301	0.04393	0.058298	1	74	65	105	77	173	148	265	181	228	165
ENSMUSG00000070461	chr2	9230112E08Rik	1.81E+08	1.81E+08	3352	-0.46449	3.110939	0.019362	0.044063	0.040361	-1	150	120	218	162	186	142	199	180	167	146
ENSMUSG00000038914	chr2	Dido1	1.81E+08	1.81E+08	13307	-0.5337	4.405129	0.019378	0.044091	0.059536	-1	410	252	449	430	572	212	376	662	410	373
ENSMUSG00000019373	chr11	Cops3	59817795	59818108	3454	-0.37098	5.992373	0.019395	0.044122	0.029256	-1	1024	1071	1365	1200	1336	1102	1370	1340	1451	1185
ENSMUSG00000023707	chr5	Ogfod2	1.24E+08	1.24E+08	2260	0.441099	3.539551	0.01942	0.044173	0.037656	1	131	168	215	129	173	261	275	275	355	380
ENSMUSG00000019579	chr17	D17Wsu104e	56175744	56177003	2222	0.475152	4.861117	0.01943	0.044187	0.047382	1	335	391	476	320	511	696	856	433	1038	922
ENSMUSG00000029475	chr5	Kdm2b	1.23E+08	1.23E+08	11818	-0.40347	3.342008	0.019438	0.0442	0.030487	-1	168	142	206	207	242	152	201	194	276	199
ENSMUSG00000026361	chr1	Cdc73	1.44E+08	1.44E+08	17538	-0.3879	4.844307	0.019445	0.044208	0.031052	-1	433	453	639	563	646	416	631	717	626	513
ENSMUSG00000019088	chrX	Dnase1l1	74273217	74273691	2121	-0.43687	6.658884	0.019468	0.044242	0.041193	-1	1834	1850	2184	1771	1994	1803	1772	2547	1819	1919
ENSMUSG00000021185	chr12	9030617O03Rik	1.01E+08	1.01E+08	4434	-0.4763	3.893254	0.01947	0.044242	0.045902	-1	217	252	238	437	285	238	294	319	305	281
ENSMUSG00000036214	chr17	Znrd1as	36958592	36958702	1360	-0.42039	3.275082	0.019468	0.044242	0.033199	-1	167	168	225	169	187	165	189	161	240	205
ENSMUSG00000063889	chr18	Crem	3266048	3267732	5895	-0.45943	3.470382	0.019475	0.044247	0.041042	-1	129	201	267	214	268	197	240	161	284	201
ENSMUSG00000037872	chr1	Ackr1	1.73E+08	1.73E+08	1405	0.601813	2.467722	0.01951	0.044318	0.06948	1	54	42	70	61	144	114	138	143	176	194
ENSMUSG00000021936	chr14	Mapk8	33377898	33382324	9255	-0.42626	5.051446	0.019517	0.044322	0.038147	-1	572	578	733	617	659	508	649	910	631	577
ENSMUSG00000022894	chr16	Adamts5	85858170	85863177	8091	-0.42679	4.445094	0.019518	0.044322	0.037412	-1	382	253	485	394	605	305	351	459	590	486
ENSMUSG00000033184	chr18	Tmed7	46560235	46561072	8839	-0.40453	5.197249	0.019529	0.044341	0.034504	-1	660	557	767	630	889	434	738	901	996	680
ENSMUSG00000024350	chr18	Dnajc18	35671103	35675243	5169	-0.3815	5.107567	0.019533	0.044341	0.030318	-1	600	529	797	606	730	560	737	812	732	633
ENSMUSG00000030643	chr7	Rab30	92741603	92741842	2116	-0.61644	1.900501	0.019567	0.044412	0.06759	-1	62	85	71	67	82	59	83	38	84	74
ENSMUSG00000028268	chr3	Gbp3	1.43E+08	1.43E+08	3239	0.680721	3.159263	0.019576	0.044425	0.094463	1	79	90	117	148	137	341	207	114	247	314
ENSMUSG00000082241	chr16	Gm15776	22295027	22295231	205	-0.68272	0.93954	0.019593	0.044457	0.071418	-1	30	49	42	29	38	22	36	26	43	40
ENSMUSG00000030020	chr6	Prickle2	92370892	92376820	8637	-0.56491	2.220392	0.019646	0.044569	0.058903	-1	70	73	102	100	117	36	95	102	117	93
ENSMUSG00000005483	chr8	Dnajb1	83608175	83608542	2263	0.427906	3.425647	0.019656	0.044584	0.034877	1	136	126	142	143	215	232	310	221	376	294
ENSMUSG00000097245	chr10	Gm5421	22343439	22345792	2354	-0.69618	1.868104	0.019683	0.044637	0.09037	-1	65	81	57	110	48	61	53	64	87	54
ENSMUSG00000022554	chr15	Hgh1	76368898	76369569	1959	0.589649	1.621	0.019702	0.044669	0.056591	1	39	29	39	31	61	62	85	69	118	86
ENSMUSG00000041961	chr11	Znrf3	5276324	5279761	7893	-0.6168	2.181111	0.019703	0.044669	0.070816	-1	60	66	84	84	170	56	70	110	101	77
ENSMUSG00000038375	chr2	Trp53inp2	1.55E+08	1.55E+08	5257	-0.42997	9.311796	0.01976	0.044791	0.040555	-1	9550	11837	13779	14302	11099	11867	12915	9386	16452	12479
ENSMUSG00000006169	chr11	Clint1	45852051	45852192	6946	-0.42203	5.36081	0.019806	0.044881	0.0379	-1	589	606	895	780	1126	505	867	1060	1033	685
ENSMUSG00000021456	chr13	Fbp2	62836884	62837280	1325	0.728728	5.642602	0.019804	0.044881	0.114423	1	518	660	600	657	671	1217	772	3065	904	1107
ENSMUSG00000021483	chr13	Cdk20	64432553	64432670	1826	0.539924	2.400686	0.019885	0.045052	0.052818	1	58	54	76	78	88	75	141	124	215	179
ENSMUSG00000033576	chr15	Apol6	77044729	77045171	4499	0.734841	3.809108	0.01989	0.045056	0.113081	1	149	162	102	327	107	308	337	234	623	562
ENSMUSG00000031703	chr8	Itfg1	85717557	85718927	3355	-0.3708	5.736307	0.019903	0.045079	0.029346	-1	939	889	1242	889	1048	870	1176	1046	1290	1048
ENSMUSG00000031988	chr9	Vps26b	27004503	27010037	6872	-0.35397	5.452017	0.019913	0.045094	0.026463	-1	724	700	944	821	913	673	849	990	1096	895
ENSMUSG00000033454	chr12	Zbtb1	76370266	76370730	12190	-0.39668	3.766617	0.019923	0.045101	0.030852	-1	210	193	286	270	342	177	274	318	359	255
ENSMUSG00000092981	chr17	Mir5125	23823291	23823369	79	0.81928	0.976511	0.019923	0.045101	0.110342	1	26	20	27	10	28	23	61	65	48	81
ENSMUSG00000046351	chr13	Zfp322a	23353103	23357713	5197	-0.38616	4.065614	0.019953	0.045162	0.029813	-1	270	291	382	302	332	239	426	325	389	318
ENSMUSG00000028763	chr4	Hspg2	1.37E+08	1.37E+08	14307	-0.46368	8.435447	0.019989	0.045236	0.047238	-1	6046	3838	7992	6534	9867	4792	9045	5238	9142	6241
ENSMUSG00000030007	chr6	Cct7	85451505	85452127	2452	0.375344	7.048517	0.020026	0.045312	0.030741	1	1522	1714	2280	1837	2336	3046	3490	2993	4097	3771
ENSMUSG00000025381	chr10	Cnpy2	1.28E+08	1.28E+08	1017	0.395028	4.909119	0.020066	0.045396	0.032652	1	420	351	553	338	508	618	879	656	957	879
ENSMUSG00000040711	chr11	Sh3pxd2b	32347820	32347968	9709	0.647171	4.789785	0.020074	0.045405	0.090129	1	277	150	351	318	784	527	997	487	1149	847
ENSMUSG00000040164	chr2	Kcns1	1.64E+08	1.64E+08	2712	-1.26191	0.432968	0.020097	0.04545	0.291169	-1	28	12	29	17	71	8	39	1	20	21
ENSMUSG00000020962	chr12	Gtf2a1	91555916	91559851	5587	0.448479	4.126751	0.020116	0.045485	0.041181	1	211	218	261	224	318	273	419	685	523	462
ENSMUSG00000022817	chr16	Itgb5	33829665	33830030	3362	0.426885	6.116804	0.020123	0.045495	0.0395	1	944	702	1068	1026	1229	1237	1817	2557	2029	1681
ENSMUSG00000019054	chr5	Fis1	1.37E+08	1.37E+08	1714	0.399066	6.467009	0.020145	0.045529	0.034626	1	1088	1234	1464	1212	1348	2222	2049	2385	2402	2520
ENSMUSG00000051675	chr4	Trim32	65604986	65605069	3229	-0.38681	3.599805	0.020144	0.045529	0.028749	-1	198	196	250	210	293	192	263	225	332	217
ENSMUSG00000021468	chr13	Sptlc1	53332716	53333977	2606	0.368682	4.069605	0.020211	0.045672	0.026798	1	214	206	257	251	291	327	395	464	512	506
ENSMUSG00000038619	chr3	Ensa	95624980	95625176	2947	-0.40552	7.379165	0.020273	0.045803	0.036138	-1	2896	2829	3679	2912	3513	2848	3210	4174	3352	2973
ENSMUSG00000043671	chr7	Dpy19l3	35685165	35690942	11173	0.584673	2.932076	0.020298	0.045853	0.068517	1	72	63	97	88	199	180	272	151	249	200
ENSMUSG00000026632	chr1	Tatdn3	1.91E+08	1.91E+08	2786	-0.43053	3.249136	0.020304	0.045858	0.035346	-1	150	191	213	166	179	159	198	184	204	189
ENSMUSG00000060950	chr12	Trmt61a	1.12E+08	1.12E+08	2433	0.498425	2.495245	0.020328	0.045906	0.044554	1	61	74	91	57	102	131	135	140	200	151

ENSMUSG00000039068	chr3	Zzz3	1.52E+08	1.52E+08	8401	-0.37467	4.571049	0.020336	0.045917	0.029029	-1	392	412	469	394	574	318	500	559	577	478
ENSMUSG00000087497	chr11	2810001G20Rik	64079484	64079777	1057	0.740156	1.510727	0.020363	0.04597	0.095296	1	36	46	37	24	23	75	65	106	84	64
ENSMUSG00000004099	chr9	Dnmt1	20907206	20907561	6304	0.46898	4.134232	0.02038	0.046	0.04565	1	192	187	265	248	349	329	513	286	776	521
ENSMUSG00000030435	chr7	U2af2	5062143	5062336	2266	0.37931	5.73666	0.02042	0.046083	0.031004	1	640	595	875	771	1031	1126	1327	1145	1978	1521
ENSMUSG00000040112	chr6	Mrps35	1.47E+08	1.47E+08	5543	0.420607	4.489064	0.020505	0.046267	0.03694	1	232	325	389	321	329	609	507	537	657	634
ENSMUSG00000049580	chr7	Tsku	98350668	98353130	2859	0.73974	2.273717	0.020538	0.046334	0.109784	1	42	28	60	50	127	86	175	72	214	158
ENSMUSG00000039176	chr7	Polg	79448791	79450037	6843	-0.36187	5.171661	0.020544	0.046339	0.027798	-1	613	621	711	697	721	505	761	768	853	816
ENSMUSG00000041638	chr5	Gcn1l1	1.16E+08	1.16E+08	15903	-0.40317	5.223107	0.020552	0.046343	0.03478	-1	575	495	742	821	964	502	753	917	933	682
ENSMUSG00000093470	chr11	Gm20645	23736847	23740357	3511	0.505531	2.230285	0.020549	0.046343	0.043891	1	53	56	60	71	76	103	139	101	157	129
ENSMUSG00000005615	chr16	Pcyt1a	32430921	32431031	5751	-0.44465	7.070696	0.020641	0.046537	0.043655	-1	2303	2180	2840	2771	2846	2060	2137	3910	2761	2360
ENSMUSG00000092329	chr8	Gm20388	1.2E+08	1.2E+08	3953	-0.36778	6.06148	0.020652	0.046553	0.02941	-1	1051	952	1459	1278	1613	958	1510	1267	1673	1459
ENSMUSG00000020794	chr11	Ube2g1	72607283	72607635	4579	-0.52017	6.592391	0.02066	0.046558	0.059612	-1	1717	1733	2283	1745	1994	1382	1450	3159	1714	1471
ENSMUSG00000041378	chr16	Cldn5	18776847	18778260	1414	0.501072	3.991761	0.020658	0.046558	0.052286	1	113	234	227	286	235	279	338	474	547	552
ENSMUSG00000023259	chr9	Slc26a6	1.09E+08	1.09E+08	5411	-0.43579	3.299124	0.020665	0.046561	0.036769	-1	141	198	234	176	187	173	210	172	222	188
ENSMUSG00000002871	chr6	Tpra1	88902251	88902530	3026	0.420888	4.529769	0.020699	0.046629	0.037099	1	277	308	383	322	350	568	645	396	771	687
ENSMUSG00000041498	chr1	Kif14	1.36E+08	1.36E+08	10211	0.927156	0.271535	0.020724	0.046679	0.133921	1	10	5	14	9	26	20	37	14	62	38
ENSMUSG00000028980	chr4	H6pd	1.5E+08	1.5E+08	5236	-0.40272	5.948156	0.020786	0.046809	0.035413	-1	894	1017	1457	1145	1410	840	995	1553	1566	1314
ENSMUSG00000019297	chr14	Nop9	55745693	55746020	3694	0.377649	4.0669	0.020795	0.046823	0.028629	1	185	230	317	214	270	341	413	452	525	473
ENSMUSG00000022257	chr15	Laptm4b	34238026	34238422	1897	-0.42666	4.917149	0.020816	0.04686	0.038879	-1	433	555	732	516	669	535	660	387	775	650
ENSMUSG00000048707	chr2	Tprn	25262618	25264553	2932	0.606031	1.569768	0.020818	0.04686	0.062185	1	27	28	40	44	52	57	59	72	126	95
ENSMUSG00000075600	chr15	Zc3h3	75754432	75754950	3360	0.543047	2.271152	0.020826	0.04687	0.053805	1	53	40	74	64	95	81	137	167	143	129
ENSMUSG00000040158	chr11	Tax1bp3	73177083	73177342	2989	0.463423	3.027334	0.020857	0.046931	0.040932	1	86	107	114	114	146	158	259	159	278	245
ENSMUSG00000005699	chr8	Pard6a	1.06E+08	1.06E+08	1430	0.508533	2.431493	0.02089	0.046992	0.047208	1	53	78	80	74	78	130	141	161	170	118
ENSMUSG00000020211	chr10	Sf3a2	80798198	80798805	2658	0.377133	4.596198	0.020891	0.046992	0.029681	1	266	296	369	383	451	557	519	643	808	649
ENSMUSG00000030629	chr7	Zfand6	84615054	84615968	1668	-0.38714	6.254222	0.020915	0.04704	0.032899	-1	1397	1432	1583	1284	1448	1337	1530	1534	1742	1538
ENSMUSG00000024924	chr19	Vldlr	27216484	27216948	10068	-0.54528	6.901162	0.020925	0.047054	0.0659	-1	2038	2018	2537	2847	2366	1599	1574	3992	2313	1837
ENSMUSG00000027698	chr3	Nceh1	27182965	27183215	5253	0.510786	4.676498	0.020929	0.047055	0.055856	1	234	416	415	404	262	437	603	608	1149	796
ENSMUSG00000032870	chr4	Smap2	1.21E+08	1.21E+08	3160	0.411839	4.588987	0.020941	0.047075	0.03574	1	264	282	356	381	451	526	607	453	977	673
ENSMUSG00000037762	chr10	Slc16a9	70245100	70245378	3869	-0.61832	2.849073	0.020981	0.047157	0.07667	-1	77	114	189	158	202	109	94	210	114	121
ENSMUSG00000028959	chr5	Fastk	24438440	24439918	4372	-0.39291	7.179356	0.020988	0.047165	0.034265	-1	2378	2759	3005	2828	2647	2691	2838	2659	3467	2889
ENSMUSG00000027828	chr3	Ssr3	65379655	65382034	4172	-0.36354	7.803186	0.021006	0.047199	0.029441	-1	3794	3520	4933	3763	5083	3512	4490	4900	5144	4784
ENSMUSG00000031403	chrX	Dkc1	75095854	75096127	4121	-0.35587	4.668129	0.021034	0.047253	0.026377	-1	372	431	572	460	556	401	526	458	678	554
ENSMUSG00000033788	chr6	Dysf	84008590	84009002	8333	-0.39994	6.512509	0.021055	0.047292	0.035301	-1	1300	1399	2079	1774	2240	1593	2051	1344	2180	2007
ENSMUSG00000070056	chr8	Mfhas1	35587798	35591358	6666	0.439843	3.39056	0.021098	0.047383	0.038032	1	119	116	142	170	194	236	274	215	421	263
ENSMUSG00000040706	chr4	Agmat	1.42E+08	1.42E+08	1407	0.802809	-0.10536	0.021105	0.047389	0.081098	1	4	11	12	8	15	23	29	19	32	18
ENSMUSG00000031482	chr8	Slc25a15	22375554	22377981	3451	-0.39714	4.148746	0.021117	0.047409	0.032331	-1	281	319	412	295	372	330	386	275	432	350
ENSMUSG00000097574	chr9	C920006O11Rik	78175914	78176035	1444	0.936004	-0.21901	0.021127	0.047424	0.115052	1	4	6	16	8	9	9	20	28	21	37
ENSMUSG00000037816	chr13	Fbxw17	50417864	50417987	3818	0.620795	2.016781	0.02114	0.047445	0.070985	1	48	47	48	37	80	97	120	64	141	135
ENSMUSG00000044854	chr1	1700056E22Rik	1.84E+08	1.84E+08	1272	0.978209	0.142275	0.021186	0.04754	0.140533	1	7	14	12	17	4	27	16	30	59	23
ENSMUSG00000036565	chr5	Ttyh3	1.41E+08	1.41E+08	4650	0.517769	4.546713	0.021217	0.047602	0.057954	1	220	212	318	310	590	388	715	438	1009	739
ENSMUSG00000042541	chr6	Shfm1	6557294	6558491	1472	0.410499	6.32276	0.021228	0.047619	0.037238	1	917	1162	1447	1046	1149	1999	2055	1890	2188	2394
ENSMUSG00000087365	chrX	C430049B03Rik	53055046	53055490	1610	0.951403	0.443922	0.021239	0.047636	0.149327	1	10	12	9	14	26	17	78	19	45	35
ENSMUSG00000047819	chr3	Tigd4	84593574	84597032	3459	-0.65669	3.837549	0.021249	0.047652	0.092609	-1	330	192	411	183	350	159	325	386	322	112
ENSMUSG00000002881	chr1	Nab1	52457294	52459306	4100	-0.42981	4.03842	0.021259	0.047666	0.038591	-1	224	286	290	366	413	173	367	308	443	375
ENSMUSG00000020650	chr12	Bcap29	31595354	31596377	2008	-0.46131	4.822955	0.021268	0.047679	0.045965	-1	500	517	623	496	585	410	467	860	565	462
ENSMUSG00000037364	chr5	Srrt	1.37E+08	1.37E+08	3024	0.382854	5.164543	0.021309	0.047756	0.031602	1	370	439	595	524	702	762	941	749	1191	1107
ENSMUSG00000054978	chr9	Kbtbd13	65388684	65391652	2969	-0.53514	4.280537	0.02131	0.047756	0.061408	-1	312	357	395	517	313	403	441	219	457	303
ENSMUSG00000064289	chr2	Tank	61578585	61578693	6096	-0.40109	3.763657	0.021313	0.047756	0.032423	-1	207	248	320	227	285	181	262	335	309	281
ENSMUSG00000060019	chr8	Gm10073	1.07E+08	1.07E+08	496	0.4941	2.610478	0.02139	0.047921	0.04468	1	78	83	73	90	87	145	159	136	195	181
ENSMUSG00000035024	chr9	Ncapd3	27030175	27030499	5499	-0.46538	3.015759	0.021405	0.047947	0.042359	-1	145	114	172	167	182	84	157	189	206	165
ENSMUSG00000025872	chr13	Thoc3	54458837	54460237	2428	0.363617	4.034936	0.021418	0.047967	0.026414	1	190	218	266	232	289	290	408	429	565	476
ENSMUSG00000039994	chr10	Timeless	1.28E+08	1.28E+08	6115	0.592817	2.556609	0.021421	0.047967	0.068839	1	54	69	93	91	78	133	154	82	244	207
ENSMUSG00000021770	chr14	Samd8	21750531	21750780	7638	-0.38238	5.51324	0.02144	0.048003	0.031835	-1	814	778	1040	717	957	807	1057	886	972	866
ENSMUSG00000040928	chr4	S100pbp	1.29E+08	1.29E+08	9448	0.429335	3.205517	0.021445	0.048005	0.035448	1	119	91	138	131	176	170	223	268	283	285
ENSMUSG00000008822	chr12	Acyp1	85272398	85272827	1380	-0.51849	3.901202	0.021464	0.048041	0.056728	-1	234	307	412	231	276	253	220	419	256	257
ENSMUSG00000041763	chr1	Tpp2	43933647	43933873	10078	-0.46173	5.575603	0.021521	0.04816	0.047021	-1	717	908	1046	925	1012	639	944	1437	976	685
ENSMUSG00000021428	chr13	Riok1	38036989	38037531	2744	0.424216	3.055118	0.021547	0.048211	0.033938	1	94	98	123	116	159	160	224	247	257	214
ENSMUSG00000026701	chr1	Prdx6	1.61E+08	1.61E+08	4804	0.398708	6.280323	0.021562	0.048228	0.035243	1	855	1085	1267	1300	1064	1725	1792	1909	2531	2363
ENSMUSG00000048922	chr14	Cdca2	67676331	67678022	5715	0.77137	0.993964	0.021562	0.048228	0.105339	1	13	22	19	15	49	45	45	41	95	54
ENSMUSG00000018171	chr11	Vmp1	86583865	86585451	3862	-0.41466	5.971127	0.021588	0.048264	0.038094	-1	1034	1206	1442	1088	1176	852	1189	1650	1356	1249
ENSMUSG00000026357	chr1	Rgs18	1.45E+08	1.45E+08	2031	0.748587	0.210979	0.021589	0.048264	0.069483	1	12	10	13	13	17	27	18	32	42	34
ENSMUSG00000029673	chr5	Auts2	1.31E+08	1.31E+08	16200	-0.5905	4.390684	0.021585	0.048264	0.075633	-1	247	216	358	508	864	364	434	325	481	335
ENSMUSG00000005982	chr16	Naa60	3872375	3872581	3815	-0.35917	5.091096	0.0216	0.048266	0.027703	-1	569	585	686	651	691	586	699	621	927	661
ENSMUSG00000026999	chr2	Nup35	80617236	80617284	3366	-0.4708	3.443798	0.0216	0.048266	0.044778	-1	163	216	253	178	240	211	247	139	251	201
ENSMUSG00000029455	chr5	Aldh2	1.22E+08	1.22E+08	4704	0.45187	7.19717	0.021597	0.048266	0.045797	1	1833	1384	2013	2516	2701	2475	3021	4623	4832	5097
ENSMUSG00000024190	chr17	Dusp1	26505590	26506650	2697	-0.54285	5.456858	0.021608	0.048277	0.06513	-1	481	873	1208	1126	662	877	968	725	859	659

ENSMUSG00000023235	chr8	Ccl25	4325210	4325288	2668	-0.70121	1.728548	0.021619	0.048285	0.092136	-1	43	69	114	59	52	69	59	44	61	49
ENSMUSG00000054091	chr3	1810037I17Rik	1.23E+08	1.23E+08	1131	0.455236	4.587876	0.021617	0.048285	0.044486	1	284	364	411	276	341	642	656	420	764	722
ENSMUSG00000029404	chr5	Arl6ip4	1.24E+08	1.24E+08	1438	0.374871	4.866358	0.02164	0.048325	0.029977	1	351	373	559	403	434	623	687	818	860	837
ENSMUSG00000030659	chr7	Nucb2	1.17E+08	1.17E+08	2301	0.580313	3.340644	0.021651	0.04834	0.070596	1	104	108	137	84	255	222	331	162	357	339
ENSMUSG00000080848	chr9	Gm9385	1.16E+08	1.16E+08	472	0.392064	4.084952	0.021659	0.04835	0.031559	1	195	238	274	258	249	415	405	482	482	427
ENSMUSG00000070737	chr4	Gm12942	1.27E+08	1.27E+08	1910	0.548961	2.067858	0.021671	0.04837	0.05377	1	49	41	58	60	70	88	114	80	135	151
ENSMUSG00000100215	chr1	Gm8292	55335401	55335796	396	0.740631	0.332237	0.021677	0.048375	0.078609	1	14	8	24	12	14	31	39	33	28	34
ENSMUSG00000057069	chr13	Ero1lb	12565883	12566178	4237	0.58489	1.955744	0.021691	0.048399	0.06152	1	33	42	61	49	70	59	105	85	171	122
ENSMUSG00000026457	chr1	Adipor1	1.34E+08	1.34E+08	5025	-0.39401	7.982829	0.021731	0.048481	0.03501	-1	4030	4149	5490	5105	5264	4300	4705	6349	5130	4814
ENSMUSG00000071644	chr19	Eef1g	8967041	8967225	2600	0.373479	9.021719	0.021806	0.048639	0.031603	1	5805	6824	8786	7809	8810	12745	13945	11695	16639	13117
ENSMUSG00000039481	chr17	Nrtn	56751325	56751830	1023	0.877905	0.836841	0.021861	0.048751	0.131914	1	27	12	20	27	10	51	29	70	43	54
ENSMUSG00000090157	chr2	Gm16534	32050086	32051219	1711	-0.8471	1.605794	0.021863	0.048751	0.140774	-1	65	55	57	62	80	54	92	23	56	20
ENSMUSG00000054280	chr5	Prr14l	32789218	32793832	11004	-0.4444	3.263082	0.021919	0.048869	0.03907	-1	178	113	202	171	267	126	200	198	233	195
ENSMUSG00000083282	chr19	Ctsf	4855129	4855486	1975	0.432431	4.942253	0.021926	0.048877	0.040699	1	371	420	454	406	526	666	671	1172	808	757
ENSMUSG00000013236	chr17	Ptprs	56412431	56413393	6970	-0.55248	5.445999	0.021938	0.048896	0.067866	-1	692	719	1192	750	1022	779	1158	351	991	825
ENSMUSG00000020528	chr11	Prpsap2	61729650	61730302	1962	0.489937	2.43205	0.021966	0.04895	0.044324	1	66	51	93	74	86	101	153	120	176	177
ENSMUSG00000033237	chr15	Arid2	96287518	96287786	10737	-0.43169	4.408541	0.022046	0.049121	0.039989	-1	397	307	413	393	530	259	427	599	465	370
ENSMUSG00000039828	chr15	Wdr70	7873055	7873253	2151	-0.37174	4.174754	0.022072	0.049171	0.028381	-1	264	304	377	345	414	343	347	360	429	339
ENSMUSG00000026116	chr1	Tmem131	36792191	36793205	9413	-0.40289	5.170068	0.022113	0.049252	0.035602	-1	555	544	725	800	815	463	639	961	906	687
ENSMUSG00000039989	chr11	Cbx4	1.19E+08	1.19E+08	5210	0.587078	2.491124	0.022116	0.049252	0.068108	1	54	57	87	78	96	99	125	97	277	198
ENSMUSG00000033060	chr14	Lmo7	1.02E+08	1.02E+08	11951	-0.38862	6.391856	0.022132	0.049281	0.033854	-1	1234	1531	1889	1574	1730	1245	2040	1869	1904	1450
ENSMUSG00000006587	chr8	Snai3	1.22E+08	1.22E+08	1589	0.795897	2.493505	0.022184	0.049382	0.131721	1	53	55	70	108	47	124	78	317	145	143
ENSMUSG00000031520	chr8	Vegfc	54077532	54077925	1881	-0.57872	1.573489	0.022185	0.049382	0.056296	-1	53	45	65	62	66	44	56	57	44	68
ENSMUSG00000025216	chr19	Lbx1	45232684	45234257	2484	-0.42862	5.362288	0.022193	0.049384	0.040527	-1	567	786	941	826	818	894	753	655	952	766
ENSMUSG00000039942	chr15	Ptger4	5206661	5209784	6648	0.781207	1.44216	0.022191	0.049384	0.113605	1	18	27	30	55	29	44	93	39	112	104
ENSMUSG00000018286	chr11	Psmb6	70525367	70525495	1872	0.390621	7.429743	0.022214	0.049423	0.034566	1	2114	2319	3041	2282	2710	4108	3990	5153	4673	4650
ENSMUSG00000051048	chr7	P4ha3	1E+08	1E+08	3043	1.116292	0.95086	0.022239	0.049469	0.245051	1	22	6	14	9	47	40	105	14	80	53
ENSMUSG00000044172	chr17	Ptx4	25120760	25120991	1582	-1.05486	2.296288	0.022269	0.04953	0.235736	-1	141	23	136	47	220	30	142	71	101	34
ENSMUSG00000038827	chr4	Fam206a	56802345	56803647	5574	0.574011	2.137989	0.022277	0.049538	0.062622	1	58	37	68	45	83	94	127	79	183	124
ENSMUSG00000060904	chr10	Arl1	88730858	88730985	2369	-0.36086	6.451474	0.022281	0.04954	0.029223	-1	1471	1531	1896	1414	1901	1349	1885	1845	2125	1774
ENSMUSG00000020111	chr10	Micu1	59702477	59702687	9234	0.362403	6.331217	0.022287	0.049545	0.029388	1	938	1072	1172	1280	1429	1715	2123	2147	2586	2011
ENSMUSG00000028468	chr4	Rgp1	43578715	43579003	6199	-0.36885	5.462219	0.022298	0.049562	0.029973	-1	650	734	990	870	918	604	877	1087	1049	903
ENSMUSG00000027102	chr2	Hoxd8	74704615	74704724	2744	-0.78253	3.728751	0.022308	0.049576	0.133554	-1	113	362	390	316	209	292	136	148	167	344
ENSMUSG00000086119	chr9	Gm2415	1.19E+08	1.19E+08	3735	0.602461	1.182327	0.022339	0.049637	0.054346	1	26	27	30	30	29	37	62	63	71	73
ENSMUSG00000052534	chr1	Pbx1	1.68E+08	1.68E+08	13844	-0.36626	4.310535	0.022353	0.049653	0.028116	-1	318	312	398	358	487	269	400	479	493	395
ENSMUSG00000063049	chr8	Ing2	47667178	47669336	3019	0.469939	3.608457	0.022352	0.049653	0.045933	1	141	152	189	164	203	259	245	491	319	312
ENSMUSG00000040327	chr17	Cul9	46500572	46501071	12198	-0.38334	4.016099	0.022361	0.049661	0.030402	-1	280	219	344	319	372	215	323	400	374	332
ENSMUSG00000040356	chr17	Skiv2l	34839228	34839831	4977	0.373645	4.958163	0.022403	0.049747	0.030221	1	388	396	479	434	566	575	710	962	909	944
ENSMUSG00000042675	chr7	Ypel3	1.27E+08	1.27E+08	1848	0.619531	5.720441	0.02242	0.049777	0.086256	1	710	587	725	732	678	909	1080	2988	1148	1269
ENSMUSG00000023156	chr14	Rpp14	8080367	8080512	2401	-0.41373	4.803952	0.022441	0.049815	0.037234	-1	501	530	648	447	510	529	580	564	536	538
ENSMUSG00000035095	chr14	Fam167a	63436394	63436632	4274	-1.04676	1.073757	0.022524	0.049985	0.215508	-1	61	12	42	44	74	18	71	11	28	28
ENSMUSG00000050390	chr4	C77080	1.29E+08	1.29E+08	5770	0.59123	1.959912	0.022521	0.049985	0.064202	1	47	33	48	51	75	60	141	104	148	87
ENSMUSG00000020917	chr11	Acly	1E+08	1E+08	5279	1.348717	6.367642	0.022549	0.050031	0.396981	0	415	323	457	1403	1433	539	832	559	4790	8018
ENSMUSG00000038515	chr8	Grtp1	13176869	13177142	1310	-0.70859	1.704205	0.022618	0.050176	0.097125	0	42	81	64	67	75	44	72	22	86	63
ENSMUSG00000056692	chr17	D17Wsu92e	27751232	27753995	4250	-0.37748	7.971275	0.022624	0.050183	0.032567	0	3774	4484	5419	5206	4742	4443	4582	5090	5965	5315
ENSMUSG00000028973	chr5	Abcb8	24393663	24393702	4739	-0.37553	5.318912	0.022653	0.050238	0.031201	0	598	723	814	859	749	600	828	694	1114	864
ENSMUSG00000093930	chr13	Hmgcs1	1.2E+08	1.2E+08	3233	-0.47437	5.539505	0.02267	0.050268	0.050541	0	657	638	852	941	1539	578	837	688	1276	1256
ENSMUSG00000027894	chr3	Slc6a17	1.07E+08	1.07E+08	10283	-0.72181	0.238527	0.022772	0.050485	0.073542	0	16	19	27	30	23	12	22	12	25	27
ENSMUSG00000007080	chr5	Pole	1.1E+08	1.1E+08	11160	0.676055	1.745798	0.022805	0.050542	0.087015	0	37	23	49	30	74	52	77	124	144	78
ENSMUSG00000036111	chr7	Lmo1	1.09E+08	1.09E+08	1071	0.589273	1.318748	0.022802	0.050542	0.053785	0	27	30	32	35	34	54	55	76	89	61
ENSMUSG00000053830	chr10	Gm9923	72309225	72311848	2624	-0.89702	0.315908	0.022822	0.050572	0.138213	0	22	16	27	41	21	5	31	18	34	11
ENSMUSG00000028755	chr4	Cda	1.38E+08	1.38E+08	1035	0.799581	0.033584	0.022831	0.050583	0.085651	0	6	9	18	9	14	25	31	14	36	29
ENSMUSG00000037010	chrX	Apln	48025146	48027707	3149	-0.72966	3.041591	0.022848	0.05061	0.113961	0	105	138	193	203	227	155	189	40	221	112
ENSMUSG00000049303	chr19	Syt12	4445908	4447860	5539	0.58399	2.59352	0.02285	0.05061	0.067994	0	51	102	86	73	80	88	133	172	230	225
ENSMUSG00000023286	chr4	Ube2j2	1.56E+08	1.56E+08	4409	0.400954	5.271625	0.022877	0.050662	0.035638	0	486	512	630	572	562	861	829	1311	1085	997
ENSMUSG00000031169	chrX	Porcn	8193848	8194277	3000	0.561974	2.43527	0.022903	0.05071	0.062053	0	55	62	90	65	88	77	205	187	151	124
ENSMUSG00000004665	chr10	Cnn2	79988584	79988740	2460	0.54913	4.249594	0.022933	0.05077	0.066454	0	219	169	237	302	373	379	769	255	763	503
ENSMUSG00000006763	chr7	Saal1	46686108	46689455	8108	0.505045	2.392094	0.022942	0.050775	0.047387	0	59	61	66	62	110	100	129	139	207	139
ENSMUSG00000010492	chr2	Uckl1os	1.82E+08	1.82E+08	2522	-0.6215	5.230408	0.022943	0.050775	0.087158	0	737	609	968	816	644	464	418	1352	600	591
ENSMUSG00000028790	chr4	Khdrbs1	1.3E+08	1.3E+08	6419	0.366857	5.255161	0.022964	0.050815	0.029714	0	439	463	641	533	735	755	1073	804	1371	1065
ENSMUSG00000018378	chr11	Cuedc1	88098058	88098128	5779	-0.38248	6.571333	0.022972	0.050823	0.033258	0	1695	1595	1949	1940	1735	1704	1832	1805	2096	2132
ENSMUSG00000019927	chr10	Ube2d1	71254980	71255874	4371	-0.40878	7.566226	0.022976	0.050824	0.038315	0	3207	3247	4561	2989	4102	3428	3672	4529	3618	3492
ENSMUSG00000040717	chr14	Il17rd	27039001	27039229	8220	-0.5014	3.034146	0.022981	0.050828	0.051709	0	173	102	188	149	186	88	183	204	179	140
ENSMUSG00000001416	chr3	Cct3	88297116	88297266	6370	0.382085	7.013265	0.023014	0.050884	0.033363	0	1493	1710	2503	1513	2225	2809	3689	3250	4013	3293
ENSMUSG00000030386	chr7	Zfp606	12478293	12478706	7680	-0.45702	2.919167	0.023014	0.050884	0.040684	0	128	149	144	136	162	121	153	176	154	129
ENSMUSG00000027001	chr2	Dusp19	80617045	80617606	2992	-0.45039	3.063849	0.023061	0.050979	0.040068	0	143	148	195	155	155	163	164	149	187	146

ENSMUSG00000002102	chr2	Psmc3	91054009	91054331	2607	0.400494	7.792479	0.023114	0.051077	0.036903	0	2599	2935	3609	3085	3785	4794	5432	7723	5752	5496
ENSMUSG00000021759	chr13	Ppap2a	1.13E+08	1.13E+08	1635	0.375972	5.751953	0.023116	0.051077	0.031731	0	674	709	1010	716	804	1225	1618	1290	1624	1311
ENSMUSG00000024534	chr18	Sncaip	52767709	52767950	4522	-0.63959	2.303041	0.023113	0.051077	0.082346	0	66	96	109	144	77	69	63	130	117	67
ENSMUSG00000029422	chr5	Rsrc2	1.24E+08	1.24E+08	8172	-0.3737	5.299788	0.023223	0.051297	0.031074	0	662	679	823	678	865	579	794	1007	870	755
ENSMUSG00000040183	chr4	Ankrd6	32804035	32806642	5477	-0.59801	1.041299	0.023221	0.051297	0.053946	0	36	30	52	41	41	31	40	31	44	38
ENSMUSG00000083678	chr4	Gm12989	1.36E+08	1.36E+08	731	0.882126	-0.16661	0.023238	0.051321	0.098848	0	13	7	10	6	9	15	21	38	19	24
ENSMUSG00000023224	chr2	Serping1	84765387	84765827	2325	0.413879	6.689235	0.023245	0.051328	0.039237	0	1422	938	1456	1377	2316	2289	2860	2707	3062	2794
ENSMUSG00000035239	chr7	Neu3	99811439	99814307	3341	-0.54158	2.148324	0.023282	0.051403	0.055717	0	72	69	116	101	74	66	97	67	116	72
ENSMUSG00000063268	chr15	Parp10	76231174	76231378	4275	0.600823	3.263989	0.023371	0.051591	0.077574	0	101	104	108	163	155	254	216	122	350	393
ENSMUSG00000042742	chr6	B630005N14Rik	13625677	13629100	4139	-0.60387	3.366431	0.023388	0.051621	0.079016	0	174	160	245	197	268	96	122	360	222	162
ENSMUSG00000000320	chr11	Alox12	70241457	70242564	4085	-0.78695	0.655597	0.023409	0.051659	0.10698	0	24	38	17	41	37	11	20	34	32	34
ENSMUSG00000040811	chr7	Eml2	19176421	19176761	3540	0.389728	3.869183	0.023441	0.05172	0.031392	0	187	189	223	195	256	247	384	486	460	362
ENSMUSG00000040383	chr2	Aqr	1.14E+08	1.14E+08	11805	-0.36058	4.290717	0.023479	0.051787	0.027613	0	299	305	382	367	495	269	446	378	478	442
ENSMUSG00000041439	chr1	Mfsd6	52656286	52658545	8231	-0.40689	3.42308	0.023476	0.051787	0.033544	0	186	162	201	222	245	167	227	162	276	245
ENSMUSG00000068854	chr3	Hist2h2be	96221119	96223738	2620	-0.42324	3.238851	0.023487	0.051798	0.035717	0	179	151	184	151	232	159	169	195	198	208
ENSMUSG00000024294	chr18	Mib1	10725548	10726533	10369	-0.46238	5.149367	0.02362	0.052082	0.048313	0	648	449	801	645	934	385	691	1044	789	612
ENSMUSG00000029147	chr5	Ppm1g	31202668	31203284	2165	0.356691	5.366134	0.023693	0.052234	0.028418	0	451	536	694	613	745	770	979	1214	1386	1097
ENSMUSG00000037022	chr8	Mmaa	79266424	79268215	2843	-0.49878	3.899149	0.023703	0.052248	0.054155	0	191	316	346	320	275	292	302	164	335	330
ENSMUSG00000019774	chr10	Mtrf1l	5811887	5813406	3261	-0.46301	2.635815	0.023721	0.052279	0.040872	0	121	97	140	109	126	106	106	109	154	128
ENSMUSG00000022074	chr14	Tnfrsf10b	69767472	69767791	3171	0.590389	1.389856	0.023788	0.05242	0.058001	0	27	31	42	32	35	50	89	58	101	58
ENSMUSG00000038902	chr3	Pogz	94837567	94837740	9218	-0.35324	4.29992	0.023831	0.052505	0.026498	0	327	308	388	345	481	300	456	401	450	410
ENSMUSG00000034327	chr14	Kctd9	67715937	67716181	4746	-0.52273	5.378081	0.023853	0.052545	0.062435	0	808	784	1012	755	680	586	773	1303	692	589
ENSMUSG00000028447	chr4	Dctn3	41714798	41715238	1042	0.364996	4.519721	0.023861	0.052555	0.028832	0	261	303	405	326	380	502	555	510	729	709
ENSMUSG00000071650	chr19	Ganab	8898090	8898159	3862	0.412349	5.615712	0.023888	0.052606	0.038694	0	663	498	759	609	1025	907	1435	949	1838	1508
ENSMUSG00000073233	chr12	Gm9144	7859827	7860076	1265	-0.69701	0.690694	0.023896	0.052614	0.07574	0	24	22	46	32	37	21	20	41	34	21
ENSMUSG00000049106	chr12	Dcaf5	80335847	80340276	5707	-0.42371	5.560271	0.023902	0.052621	0.040831	0	715	688	1151	933	1079	724	821	1359	975	800
ENSMUSG00000032872	chr9	Cyb5r4	87022014	87022253	6736	-0.34947	5.349564	0.023913	0.052635	0.027341	0	621	718	860	761	851	687	897	723	1040	844
ENSMUSG00000048706	chr4	Lurap1l	80910646	80911645	3066	-0.55872	2.131687	0.023929	0.052663	0.060405	0	74	74	76	92	114	60	106	49	114	83
ENSMUSG00000002107	chr2	Celf2	6539694	6545675	25884	-0.37072	5.904907	0.024001	0.052813	0.031408	0	1007	890	1213	1171	1387	771	1177	1412	1483	1327
ENSMUSG00000038712	chr3	Fam63a	95281345	95281611	6458	0.535437	5.125222	0.02407	0.052956	0.065456	0	370	386	503	520	617	543	654	1722	986	933
ENSMUSG00000021408	chr13	Ripk1	34002363	34002706	6138	0.452589	3.371545	0.024143	0.0531	0.042787	0	117	114	143	121	240	168	273	268	412	292
ENSMUSG00000049832	chr17	Gm9840	35935624	35935950	327	0.672605	0.562089	0.02414	0.0531	0.062016	0	16	20	22	12	17	35	38	36	48	38
ENSMUSG00000029449	chr5	Rhof	1.23E+08	1.23E+08	4602	1.25615	-0.42615	0.024173	0.053158	0.252826	0	9	1	6	2	13	13	25	3	26	37
ENSMUSG00000073791	chr4	Efcab7	99829198	99829454	2252	0.793014	0.196355	0.024235	0.053285	0.092935	0	16	5	15	12	15	25	43	17	38	30
ENSMUSG00000026817	chr2	Ak1	32621758	32621877	2593	-0.43089	10.85024	0.024281	0.053378	0.043658	0	28872	35008	41793	33692	37351	40410	33960	26508	40884	38419
ENSMUSG00000007888	chr8	Crlf1	70493158	70493400	1644	0.724509	1.556835	0.024299	0.0534	0.102877	0	27	21	52	51	28	84	81	41	96	105
ENSMUSG00000020486	chr11	Sept4	87568903	87568958	3563	0.402959	3.861487	0.024297	0.0534	0.034556	0	139	179	231	244	255	294	342	348	439	501
ENSMUSG00000081683	chr5	Fzd10	1.29E+08	1.29E+08	3250	0.793547	1.584819	0.024304	0.053403	0.124852	0	44	20	23	45	42	56	136	71	130	41
ENSMUSG00000016194	chr1	Hsd11b1	1.93E+08	1.93E+08	4251	0.645915	2.447645	0.024348	0.053492	0.085291	0	72	65	71	80	53	87	93	146	195	253
ENSMUSG00000028641	chr4	Lepre1	1.19E+08	1.19E+08	3846	0.447984	4.936603	0.02436	0.053509	0.045534	0	399	296	465	346	691	667	908	543	1185	855
ENSMUSG00000002885	chr8	Cd97	83723251	83723902	3757	0.432084	5.468717	0.024424	0.053641	0.042768	0	471	526	624	693	862	737	1664	855	1464	1299
ENSMUSG00000092137	chr9	Gcom1	71479325	71479540	1726	-0.38083	5.813748	0.024441	0.053669	0.03327	0	896	967	1241	1059	1146	1055	1269	902	1431	1024
ENSMUSG00000015668	chrX	Pdzd11	1.01E+08	1.01E+08	2127	0.374332	4.107518	0.024491	0.053772	0.029789	0	209	247	277	229	282	378	476	356	588	469
ENSMUSG00000033111	chr14	3830406C13Rik	12284209	12284257	2477	-0.39427	3.495102	0.02453	0.053841	0.032135	0	182	215	246	204	209	171	220	211	263	269
ENSMUSG00000039952	chr9	Dag1	1.08E+08	1.08E+08	6357	-0.38768	8.412507	0.024531	0.053841	0.035365	0	5035	4625	7466	6636	9114	5171	7947	7724	7923	5788
ENSMUSG00000024925	chr19	Rnaseh2c	5601873	5602080	1455	0.402815	3.516816	0.024541	0.053856	0.033344	0	158	147	206	140	161	260	293	323	329	293
ENSMUSG00000046079	chr5	Lrrc8d	1.06E+08	1.06E+08	12573	0.617757	2.953525	0.024611	0.054	0.082577	0	67	62	101	107	181	98	182	178	336	322
ENSMUSG00000058317	chr14	Ube2e2	18573575	18574391	4671	0.4784	2.53787	0.024624	0.05402	0.043919	0	76	62	83	75	103	104	170	124	194	191
ENSMUSG00000027883	chr3	Gpsm2	1.09E+08	1.09E+08	3909	0.485514	3.304632	0.02473	0.054245	0.0505	0	141	77	132	113	229	199	302	242	353	247
ENSMUSG00000070733	chr5	Fryl	73020322	73022297	14668	-0.39072	4.44466	0.024744	0.054267	0.033709	0	347	270	430	480	559	289	451	508	500	462
ENSMUSG00000015806	chr5	Qdpr	45434032	45434678	1914	-0.39279	6.270836	0.024755	0.054281	0.035857	0	1308	1218	1800	1229	1816	1401	1463	1196	1845	1859
ENSMUSG00000067038	chr19	Rps12-ps3	59322290	59322783	494	0.706626	0.354629	0.024771	0.054308	0.06833	0	10	17	15	10	22	20	36	38	40	36
ENSMUSG00000083669	chr7	Gm10169	29965218	29965565	348	0.664625	0.673028	0.024782	0.054324	0.065481	0	14	17	19	20	26	44	34	33	57	43
ENSMUSG00000022456	chr15	Sept3	82274935	82275053	4971	0.804793	-0.09058	0.024823	0.054404	0.077951	0	10	7	15	10	8	26	25	21	33	17
ENSMUSG00000009905	chr1	Kdsr	1.07E+08	1.07E+08	8147	0.530356	2.543108	0.024857	0.054472	0.056109	0	63	77	88	81	80	89	132	227	182	167
ENSMUSG00000032336	chr9	Nptn	58582240	58582526	6168	-0.36954	6.621223	0.024923	0.054607	0.031947	0	1762	1599	2207	1606	2093	1557	2169	1642	2674	2072
ENSMUSG00000034771	chr10	Tle2	81574561	81575691	6221	-0.62658	2.083974	0.024927	0.054607	0.079421	0	104	65	104	53	95	50	83	68	67	115
ENSMUSG00000028718	chr4	Stil	1.15E+08	1.15E+08	5795	0.958412	-0.23047	0.025002	0.054759	0.130463	0	7	7	5	4	19	10	24	14	34	34
ENSMUSG00000035900	chr15	Gramd4	86057695	86057831	5567	-0.43651	3.96509	0.025004	0.054759	0.041811	0	242	174	375	344	388	186	277	361	353	383
ENSMUSG00000028911	chr4	Srsf4	1.32E+08	1.32E+08	3561	0.348796	4.804786	0.02508	0.054917	0.027108	0	336	338	456	399	536	620	719	644	913	751
ENSMUSG00000005034	chr3	Prkacb	1.47E+08	1.47E+08	5451	-0.35398	5.428501	0.02514	0.055039	0.028708	0	670	635	958	810	997	567	867	943	1210	896
ENSMUSG00000034889	chr10	Cactin	81321103	81321446	2724	0.364957	3.78819	0.025152	0.055057	0.027774	0	169	165	219	198	257	271	347	314	463	422
ENSMUSG00000054723	chr17	Vmac	56713932	56715817	2276	0.57559	2.18735	0.025164	0.055074	0.065533	0	61	33	89	50	68	64	133	135	165	136
ENSMUSG00000014771	chr17	Pdcd2	15519208	15520364	2582	0.470202	3.169632	0.025173	0.055085	0.046324	0	102	117	165	111	128	212	190	318	250	223
ENSMUSG00000037251	chr8	Pomk	25980604	25983644	3601	-0.46079	3.856473	0.025183	0.055098	0.046809	0	266	242	323	229	337	259	303	153	402	306
ENSMUSG00000081534	chr15	Slc48a1	97784355	97784616	2690	0.407681	5.857828	0.02519	0.055106	0.038679	0	694	665	898	928	996	1108	1130	2023	1787	1692

ENSMUSG00000028180	chr3	Zranb2	1.58E+08	1.58E+08	4301	-0.41783	5.566036	0.025215	0.055151	0.040525	0	824	842	1094	826	916	627	911	1357	945	895
ENSMUSG00000031980	chr8	Agt	1.25E+08	1.25E+08	1891	0.43081	3.901444	0.025264	0.055248	0.040853	0	133	180	239	232	288	338	292	450	411	484
ENSMUSG00000058093	chr13	AA987161	67589443	67593915	4861	-0.57986	1.869338	0.025268	0.055248	0.064176	0	72	47	67	74	101	44	65	96	72	59
ENSMUSG00000050164	chr15	Mchr1	81235499	81235855	2188	-0.91641	2.20329	0.025299	0.055308	0.185106	0	43	159	81	138	62	78	81	22	127	63
ENSMUSG00000034471	chr11	Caskin2	1.16E+08	1.16E+08	5177	-0.36395	4.428056	0.025371	0.055458	0.029316	0	302	339	434	475	481	288	441	463	600	433
ENSMUSG00000039217	chr9	Il18	50575273	50575348	714	0.945163	0.352915	0.025394	0.055498	0.160779	0	9	15	16	5	22	47	32	11	38	46
ENSMUSG00000031028	chr7	Tub	1.09E+08	1.09E+08	6919	-0.74216	0.293946	0.025424	0.055556	0.083681	0	18	14	36	25	29	21	21	10	29	19
ENSMUSG00000054716	chr7	Zfp771	1.27E+08	1.27E+08	1371	0.528529	3.42596	0.025437	0.055576	0.061592	0	112	115	197	147	164	210	234	497	263	252
ENSMUSG00000017747	chr11	Ghdc	1.01E+08	1.01E+08	2692	0.394534	3.615437	0.02547	0.055639	0.032326	0	166	174	198	153	179	216	329	372	380	326
ENSMUSG00000067276	chrX	Capn6	1.44E+08	1.44E+08	7795	0.622883	4.795271	0.025496	0.055686	0.090402	0	320	205	384	283	686	526	1453	521	890	559
ENSMUSG00000029189	chr5	Sel1l3	53107084	53108174	4511	-0.42163	6.2732	0.025512	0.055712	0.041821	0	1343	1085	1541	1409	2102	1472	1820	1094	1962	1335
ENSMUSG00000019470	chr8	Xab2	3608421	3610219	4685	0.384078	3.978951	0.025516	0.055714	0.031758	0	191	190	251	232	277	255	397	535	492	414
ENSMUSG00000030127	chr6	Cops7a	1.25E+08	1.25E+08	2711	-0.35139	6.382627	0.025534	0.055726	0.028977	0	1319	1425	1683	1575	1811	1443	1525	1682	2145	1770
ENSMUSG00000059363	chr19	Fxn	24261453	24262053	2053	-0.38351	3.943631	0.025533	0.055726	0.031656	0	223	290	316	325	287	287	292	295	352	314
ENSMUSG00000097471	chr7	5830432E09Rik	1.36E+08	1.36E+08	4527	1.123544	-0.70497	0.02553	0.055726	0.172449	0	4	2	12	5	3	4	21	7	25	25
ENSMUSG00000007570	chr17	Fance	28313530	28313882	3183	0.472329	2.969723	0.025573	0.055802	0.046157	0	89	99	119	102	133	132	204	299	225	193
ENSMUSG00000022369	chr15	Mtbp	55557408	55557737	5481	0.631876	1.349332	0.02562	0.055888	0.069993	0	36	24	35	24	40	35	76	58	106	79
ENSMUSG00000085342	chr11	Gm12254	58508791	58509261	471	0.410007	3.47982	0.02562	0.055888	0.035098	0	126	153	161	190	158	255	244	298	383	293
ENSMUSG00000005718	chr16	Tfap4	4544661	4545747	2113	0.726494	1.781925	0.025626	0.055892	0.106638	0	49	30	43	41	44	44	79	183	94	87
ENSMUSG00000028413	chr4	B4galt1	40804602	40807317	4234	0.383324	6.211345	0.025639	0.055911	0.034557	0	751	1038	1094	983	1561	1628	1781	1881	2452	2059
ENSMUSG00000021279	chr12	Cdc42bpb	1.11E+08	1.11E+08	6718	-0.40094	5.034611	0.02571	0.056057	0.037052	0	485	447	620	713	894	377	692	713	929	655
ENSMUSG00000019699	chr1	Akt3	1.77E+08	1.77E+08	4980	-0.58461	3.51636	0.02573	0.056091	0.077106	0	214	190	215	266	250	102	192	399	227	155
ENSMUSG00000050174	chr3	Nudt6	37404910	37405494	1635	-0.49461	3.573032	0.025779	0.056188	0.054064	0	179	274	276	252	154	214	218	244	242	216
ENSMUSG00000066800	chr1	Rnasel	1.54E+08	1.54E+08	6641	0.568521	2.568281	0.025786	0.056195	0.067616	0	81	43	98	52	125	93	177	194	183	173
ENSMUSG00000024471	chr18	Myot	44334074	44334156	2209	-0.45531	9.650296	0.025794	0.056205	0.049707	0	14379	15465	15657	18434	12287	13163	13585	21294	17408	13248
ENSMUSG00000062981	chr10	Mrpl42	95480806	95480977	666	-0.43908	7.520203	0.025809	0.056228	0.046011	0	3002	3576	4152	3604	3146	3807	3828	2543	3997	3734
ENSMUSG00000002031	chr9	Ift46	44767908	44767927	5658	0.361213	3.758916	0.025835	0.056277	0.027154	0	193	169	212	185	220	276	347	354	405	383
ENSMUSG00000021388	chr13	Aspn	49544443	49544717	2346	-0.55952	5.293443	0.025855	0.05631	0.073659	0	671	544	912	673	1175	336	1223	884	861	468
ENSMUSG00000037580	chr14	Gch1	47153895	47155924	2775	0.655901	2.055097	0.025862	0.056313	0.088363	0	33	55	70	54	50	112	100	55	193	122
ENSMUSG00000090641	chr13	Zfp712	67038594	67042232	3970	-0.75915	0.389376	0.025864	0.056313	0.094445	0	32	12	25	36	24	13	26	24	19	25
ENSMUSG00000049321	chr11	Zfp2	50898712	50901291	4019	-0.52975	1.959507	0.025886	0.056351	0.054125	0	74	73	83	71	72	48	74	86	71	86
ENSMUSG00000036560	chr7	Lgi4	31059342	31060190	4584	-0.57779	2.969819	0.025921	0.056418	0.072985	0	151	79	153	133	281	111	202	109	190	121
ENSMUSG00000045629	chr18	Sh3tc2	61953075	61953167	4536	-0.67209	1.059013	0.025946	0.056465	0.080133	0	24	38	42	66	36	26	36	31	52	38
ENSMUSG00000022677	chr16	Fopnl	14299244	14300209	1465	-0.40599	5.744253	0.025984	0.056538	0.038681	0	940	1009	1257	895	954	1081	1105	903	1152	1058
ENSMUSG00000037730	chr3	Mynn	30602065	30602695	6764	-0.49141	3.430238	0.026025	0.056618	0.052872	0	170	190	233	206	250	134	179	344	207	176
ENSMUSG00000034329	chr11	Brip1	86058138	86062045	7454	0.916401	0.006345	0.026046	0.056656	0.135163	0	3	7	14	15	13	19	40	9	38	31
ENSMUSG00000021066	chr12	Atl1	69893105	69893344	2818	-0.65784	0.494896	0.026063	0.056665	0.064054	0	21	21	36	30	29	21	28	15	34	23
ENSMUSG00000026473	chr1	Glul	1.54E+08	1.54E+08	3323	0.748097	8.056658	0.02606	0.056665	0.13313	0	4615	2127	3425	2779	3421	2796	4625	16666	7285	8171
ENSMUSG00000030782	chr7	Tgfb1i1	1.28E+08	1.28E+08	3598	0.539607	3.574192	0.026062	0.056665	0.06551	0	130	101	159	168	263	242	447	167	474	328
ENSMUSG00000033632	chr18	AW554918	25168999	25169086	7014	-0.5594	2.203287	0.026096	0.056729	0.063891	0	101	47	98	102	105	47	101	93	103	90
ENSMUSG00000025272	chrX	Tro	1.51E+08	1.51E+08	7296	0.923799	0.429775	0.026114	0.056758	0.155095	0	11	8	15	12	26	24	76	15	51	24
ENSMUSG00000001249	chr7	Hpn	31098725	31099073	4101	-0.50338	2.574881	0.02613	0.056776	0.051549	0	120	89	131	130	102	90	102	143	111	119
ENSMUSG00000021282	chr12	Eif5	1.12E+08	1.12E+08	4061	-0.40854	7.266859	0.026128	0.056776	0.039951	0	2511	2604	3760	2436	3445	2234	2874	4253	3195	2876
ENSMUSG00000038718	chr2	Pbx3	34171457	34172973	6109	0.526237	2.232519	0.026159	0.05683	0.054034	0	67	48	71	65	61	104	144	149	138	94
ENSMUSG00000026478	chr1	Lamc1	1.53E+08	1.53E+08	8272	-0.4028	7.836043	0.026181	0.056869	0.03897	0	3606	2883	4659	4310	6746	3472	5547	3990	5946	4217
ENSMUSG00000029650	chr5	Slc46a3	1.48E+08	1.48E+08	2458	-0.4359	3.020334	0.026193	0.056885	0.039766	0	143	149	150	161	163	106	175	179	215	133
ENSMUSG00000021771	chr14	Vdac2	21831269	21831667	4658	0.390894	8.082231	0.026198	0.056888	0.036741	0	2980	4132	4343	4076	3946	6987	6592	6843	8258	6832
ENSMUSG00000074886	chr13	Grk6	55445334	55445560	3241	0.35675	4.300105	0.026214	0.056914	0.027873	0	253	260	313	256	357	340	483	521	668	592
ENSMUSG00000010358	chr11	Ifi35	1.01E+08	1.01E+08	1727	0.574232	3.965312	0.02623	0.056939	0.075759	0	145	227	308	154	210	443	435	212	435	608
ENSMUSG00000031562	chr8	Dctd	48099092	48099141	3409	0.77497	0.845063	0.026255	0.056985	0.111076	0	14	10	21	22	39	41	46	23	84	57
ENSMUSG00000028834	chr4	Trim63	1.34E+08	1.34E+08	2842	1.271917	8.019221	0.026295	0.057063	0.374318	0	1736	2007	3019	3265	2793	2734	2339	31359	2617	3193
ENSMUSG00000032586	chr9	Traip	1.08E+08	1.08E+08	6281	0.858886	0.478767	0.026306	0.057077	0.121672	0	10	24	16	12	12	30	24	22	63	56
ENSMUSG00000038301	chr6	Snx10	51523901	51524034	4912	0.459034	3.414812	0.026327	0.057114	0.045391	0	120	138	167	134	187	156	212	310	421	364
ENSMUSG00000024597	chr18	Slc12a2	57878678	57879544	6520	-0.63212	5.893638	0.026336	0.057125	0.095122	0	884	1296	1302	1301	1213	683	770	2256	807	875
ENSMUSG00000025958	chr1	Creb1	64532645	64532904	13742	-0.3571	4.33172	0.026387	0.057225	0.028421	0	330	337	364	364	492	280	455	363	538	445
ENSMUSG00000011148	chr12	Adssl1	1.13E+08	1.13E+08	1861	-0.3975	9.096702	0.026431	0.057313	0.03822	0	9691	8967	11227	11859	9869	9902	9083	13157	11894	10610
ENSMUSG00000034152	chr13	Exoc3	74169805	74172244	4596	-0.35371	5.563466	0.026459	0.057365	0.029233	0	731	754	1103	858	1006	789	1074	778	1153	1056
ENSMUSG00000021096	chr12	Ppm1a	72761211	72761631	2789	-0.44655	6.994423	0.026501	0.057447	0.047921	0	2167	2216	2730	2527	2608	1791	2110	3945	2570	2157
ENSMUSG00000028709	chr4	Mob3c	1.16E+08	1.16E+08	2975	0.512645	2.34465	0.026532	0.057504	0.05279	0	53	48	86	62	99	104	138	94	186	167
ENSMUSG00000041974	chr16	Spidr	15889227	15889785	3279	0.65299	1.713105	0.026539	0.057507	0.084784	0	48	21	40	34	64	50	83	70	141	119
ENSMUSG00000089704	chr8	Galnt2	1.24E+08	1.24E+08	4282	-0.35225	6.041034	0.026542	0.057507	0.029361	0	1039	935	1430	1253	1574	948	1504	1252	1659	1449
ENSMUSG00000038975	chr3	Rabggtb	1.54E+08	1.54E+08	1509	0.447305	5.949674	0.026558	0.057534	0.047652	0	656	849	1082	798	996	1270	1385	2526	1608	1467
ENSMUSG00000013698	chr1	Pea15a	1.72E+08	1.72E+08	3861	0.42665	5.954221	0.026574	0.057551	0.043293	0	788	675	897	982	1091	1343	2036	1014	2344	1639
ENSMUSG00000045875	chr14	Adra1a	66635251	66635603	8144	-0.94233	0.782081	0.026573	0.057551	0.178605	0	25	17	22	59	62	13	17	15	33	56
ENSMUSG00000036862	chr7	Dchs1	1.06E+08	1.06E+08	11070	-0.44844	3.764576	0.026589	0.057574	0.044845	0	237	156	269	292	369	188	364	210	356	234
ENSMUSG00000028093	chr3	Acp6	97158777	97159365	4592	-0.37868	3.957187	0.026614	0.057619	0.031458	0	250	296	286	324	289	274	305	274	369	343

ENSMUSG00000036112	chr10	Metap2	93858489	93861602	7588	-0.3736	7.471138	0.02664	0.057661	0.033658	0	2744	3070	3909	3144	3918	2825	3421	4551	4013	3206
ENSMUSG00000046733	chr6	Gprc5a	1.35E+08	1.35E+08	2083	1.063669	-0.40023	0.026642	0.057661	0.165927	0	5	5	2	6	17	14	34	7	25	22
ENSMUSG00000079415	chr19	Cntf	12763660	12764380	1073	0.72151	0.873072	0.026656	0.057683	0.089435	0	20	17	20	24	27	27	51	82	40	49
ENSMUSG00000031758	chr8	Cdyl2	1.17E+08	1.17E+08	8087	0.472446	2.493795	0.026662	0.057687	0.044823	0	59	55	82	84	112	103	181	134	176	161
ENSMUSG00000034254	chr17	Agpat1	34604262	34604490	3001	-0.37492	5.846523	0.026705	0.057763	0.033301	0	937	907	1170	1145	1279	982	1125	860	1526	1378
ENSMUSG00000044252	chr18	Osbpl1a	12755314	12756307	7392	-0.39929	5.719393	0.026705	0.057763	0.037809	0	864	957	1028	986	1151	754	887	1487	1198	988
ENSMUSG00000091780	chr15	Sco2	89371639	89372465	1143	0.424205	3.398347	0.02672	0.057786	0.038456	0	109	149	181	159	145	259	256	268	380	232
ENSMUSG00000022490	chr15	Ppp1r1a	1.04E+08	1.04E+08	1295	-0.60609	5.488886	0.026746	0.057833	0.087712	0	818	749	947	1027	972	405	461	1595	794	933
ENSMUSG00000019960	chr10	Dusp6	99263231	99264091	2796	0.386202	4.671116	0.026759	0.057852	0.03412	0	309	271	507	413	348	433	715	642	909	714
ENSMUSG00000020564	chr12	Atxn7l1	33147693	33147915	12523	-0.39009	3.885183	0.026807	0.057947	0.033487	0	231	284	282	280	309	250	283	229	350	374
ENSMUSG00000027668	chr3	Mfn1	32529465	32529695	6114	-0.41781	7.22836	0.026863	0.058059	0.042194	0	2343	3080	3033	3213	2453	2742	2759	3363	3267	2705
ENSMUSG00000045100	chr6	Slc25a26	94500314	94500457	1915	-0.41685	4.277261	0.026879	0.058084	0.039463	0	343	370	430	368	310	394	376	360	389	379
ENSMUSG00000053226	chr8	Dand5	84815405	84816533	1584	-0.4172	3.223672	0.026933	0.058191	0.036627	0	167	146	166	215	186	165	189	182	214	172
ENSMUSG00000022757	chr16	Tfg	56690332	56691153	2292	-0.35337	5.842192	0.026941	0.058195	0.029568	0	919	978	1200	1010	1273	1042	1148	1011	1475	1194
ENSMUSG00000023960	chr17	Enpp5	44078813	44078898	4858	-0.4305	3.525423	0.026943	0.058195	0.040865	0	211	169	206	244	268	143	190	201	313	312
ENSMUSG00000067150	chr17	Xpo5	46202855	46203025	3709	-0.40941	3.705984	0.026982	0.05827	0.036986	0	212	192	289	223	336	149	265	332	342	236
ENSMUSG00000024614	chr18	Tmx3	90510154	90510377	4611	-0.37197	4.517662	0.02702	0.058343	0.031525	0	373	316	574	387	530	326	545	427	635	423
ENSMUSG00000025757	chr3	Hspa4l	40744495	40744785	11792	-0.48193	3.474877	0.02703	0.058352	0.052132	0	187	179	299	198	217	123	326	159	297	195
ENSMUSG00000049907	chr5	Rasl11b	74195288	74195590	1941	0.604706	2.503998	0.027033	0.058352	0.079036	0	71	39	61	70	135	108	209	189	154	122
ENSMUSG00000008035	chrX	Mid1ip1	10715013	10715067	2128	0.539915	4.515136	0.027047	0.058373	0.068059	0	303	337	274	403	184	452	514	504	1050	703
ENSMUSG00000029020	chr4	Mfn2	1.48E+08	1.48E+08	5194	-0.38672	8.919717	0.027112	0.058505	0.036493	0	7225	9004	9622	10596	9137	8877	7988	10525	11434	9877
ENSMUSG00000038510	chr10	Rpf2	40223246	40223920	1924	0.407059	3.724953	0.027129	0.058533	0.036227	0	171	185	232	165	183	336	379	290	377	344
ENSMUSG00000039196	chr4	Orm1	63344560	63344714	775	2.183893	1.867805	0.027134	0.058534	1.001623	0	16	5	5	38	43	7	19	0	228	456
ENSMUSG00000041426	chr1	Hibch	52844929	52848693	6059	-0.37617	5.475383	0.027154	0.058568	0.033484	0	640	854	994	908	773	686	836	983	1010	1005
ENSMUSG00000030701	chr7	Plekhb1	1.01E+08	1.01E+08	3554	-0.41962	5.379717	0.027158	0.058568	0.041744	0	721	715	968	790	762	706	662	1108	759	865
ENSMUSG00000030423	chr7	Pop4	38262820	38263309	1214	0.404512	3.44656	0.027198	0.058645	0.034743	0	143	145	199	140	145	255	285	244	367	284
ENSMUSG00000001521	chr6	Tulp3	1.28E+08	1.28E+08	6704	0.386004	3.59712	0.027221	0.058667	0.032298	0	117	144	198	170	255	244	341	335	360	309
ENSMUSG00000015247	chr4	Nipsnap3b	53011880	53012047	1687	0.607793	1.962286	0.027213	0.058667	0.07499	0	37	36	62	56	62	65	87	69	179	148
ENSMUSG00000026104	chr1	Stat1	52119440	52119623	7105	0.57327	4.821735	0.027221	0.058667	0.078158	0	310	320	421	412	436	943	695	310	889	1011
ENSMUSG00000026315	chr1	Serpinb8	1.08E+08	1.08E+08	4795	0.623906	1.798508	0.027272	0.058768	0.078343	0	47	23	43	46	64	76	81	60	136	128
ENSMUSG00000097184	chr16	4632428C04Rik	30008667	30008730	2430	-0.78672	1.046851	0.027334	0.058893	0.12327	0	27	56	43	56	25	20	32	58	36	26
ENSMUSG00000058881	chr18	Zfp516	82910879	82910992	7817	-0.38818	4.468438	0.02734	0.058897	0.034463	0	348	309	414	412	640	346	457	524	542	369
ENSMUSG00000027656	chr2	Wisp2	1.64E+08	1.64E+08	1924	0.751583	2.282258	0.027359	0.058929	0.123602	0	73	44	73	44	58	85	101	56	277	204
ENSMUSG00000039615	chr17	Stub1	25830636	25831010	1672	0.384974	6.356805	0.027369	0.058941	0.035721	0	1004	1136	1431	1082	1272	2069	2000	1705	2570	2405
ENSMUSG00000006517	chr8	Mvd	1.22E+08	1.22E+08	1761	0.451457	2.85481	0.027374	0.058941	0.042632	0	80	72	97	102	160	138	198	186	222	222
ENSMUSG00000061787	chr7	Rps17	81342732	81342849	1274	0.370657	7.614834	0.027383	0.058952	0.033481	0	2423	2669	3607	2472	3129	4613	5159	4957	5346	5483
ENSMUSG00000048058	chr2	Ldlrad3	1.02E+08	1.02E+08	6023	0.555455	3.64857	0.027482	0.059156	0.071032	0	140	125	158	179	249	174	369	598	361	242
ENSMUSG00000044006	chr8	Cilp2	69880369	69883208	4314	-0.87058	5.570485	0.02759	0.059376	0.18192	0	1255	350	1139	478	2086	574	1295	960	842	245
ENSMUSG00000057777	chr3	Mab21l2	86545581	86548283	3049	-0.83131	0.365281	0.027593	0.059376	0.111446	0	18	22	36	19	37	27	14	18	11	28
ENSMUSG00000020393	chr11	Kremen1	5191552	5195121	7722	-0.47396	5.82017	0.027622	0.059423	0.05429	0	653	1106	1078	1598	1028	725	967	1435	1268	1164
ENSMUSG00000042410	chr2	Agps	75832177	75832511	9421	-0.34333	4.943227	0.027623	0.059423	0.027377	0	485	487	642	558	713	471	681	527	862	655
ENSMUSG00000017801	chr11	Mlx	1.01E+08	1.01E+08	1999	0.354843	3.891627	0.027692	0.059563	0.027226	0	193	174	228	227	262	255	381	408	475	433
ENSMUSG00000031906	chr8	Smpd3	1.06E+08	1.06E+08	5148	-1.19587	2.257055	0.027727	0.059628	0.328069	0	43	30	56	56	418	33	56	36	81	134
ENSMUSG00000024043	chr17	Arhgap28	67842713	67845817	5377	0.506767	2.734559	0.027744	0.059647	0.054489	0	69	78	103	90	115	116	280	151	208	150
ENSMUSG00000026383	chr1	Epb4.1l5	1.2E+08	1.2E+08	14758	-0.63147	1.614069	0.027744	0.059647	0.080187	0	64	47	73	61	57	29	38	80	56	73
ENSMUSG00000024758	chr19	Rtn3	7425901	7427875	5030	0.356587	6.051496	0.027768	0.05968	0.030562	0	850	797	1065	971	1194	1209	1627	1585	2223	2144
ENSMUSG00000026399	chr1	Cd55	1.3E+08	1.3E+08	4853	-0.50368	5.596068	0.027767	0.05968	0.06129	0	578	1244	1201	923	724	924	866	720	1278	863
ENSMUSG00000041997	chr2	Tlk1	70712407	70714165	6474	-0.38091	5.342183	0.027789	0.059714	0.03446	0	593	621	897	851	897	616	828	1082	864	710
ENSMUSG00000036390	chr6	Gadd45a	67035096	67035772	1764	0.608788	5.291154	0.027827	0.059788	0.089616	0	295	452	788	422	693	801	824	1993	722	1075
ENSMUSG00000026770	chr2	Il2ra	11642807	11643064	5711	-0.65814	0.421528	0.02786	0.059848	0.064086	0	30	15	28	27	29	18	25	22	25	24
ENSMUSG00000038280	chr10	Ostm1	42583822	42583866	7211	-0.40357	5.053969	0.027881	0.059885	0.038653	0	560	642	736	583	606	594	730	451	866	696
ENSMUSG00000027694	chr3	Gm8325	60877014	60877046	464	-0.71999	0.641934	0.027897	0.059904	0.088921	0	24	22	37	42	30	13	17	38	28	36
ENSMUSG00000093769	chr3	Hist2h3c1	96246685	96248504	1820	-0.50094	2.335614	0.027898	0.059904	0.05115	0	83	73	130	102	102	71	135	81	113	83
ENSMUSG00000070709	chr7	1700049G17Rik	27907392	27912261	7518	-0.56701	1.362274	0.027948	0.06	0.057462	0	37	37	57	55	66	26	57	42	66	48
ENSMUSG00000039783	chr1	Kmo	1.76E+08	1.76E+08	4724	0.846832	0.037484	0.027959	0.060015	0.123226	0	7	2	14	13	20	27	30	16	25	37
ENSMUSG00000089810	chr9	Gm16536	45856769	45858357	1589	0.454399	2.938614	0.027979	0.060048	0.043355	0	86	98	112	124	111	151	193	271	220	184
ENSMUSG00000009470	chr13	Tnpo1	98839019	98844620	8579	-0.37161	5.754637	0.028058	0.060209	0.03324	0	899	774	1142	936	1390	734	1047	1380	1314	1062
ENSMUSG00000024246	chr17	Thumpd2	81026327	81026970	1856	0.585997	1.280765	0.028102	0.060293	0.059505	0	26	27	33	30	39	49	64	82	55	72
ENSMUSG00000029474	chr5	Rnf34	1.23E+08	1.23E+08	1954	-0.38793	4.54842	0.028119	0.06032	0.034893	0	347	414	510	470	468	403	470	594	448	418
ENSMUSG00000010376	chr14	Nedd8	55662265	55662400	604	0.384816	6.113643	0.028155	0.060369	0.035925	0	853	1028	1148	897	1058	1811	1798	1613	2018	1786
ENSMUSG00000026667	chr1	Uhmk1	1.7E+08	1.7E+08	8101	-0.34835	5.012243	0.02815	0.060369	0.028556	0	536	479	712	612	688	465	632	583	952	731
ENSMUSG00000028953	chr5	Abcf2	24565341	24566003	2573	-0.37588	7.05394	0.028151	0.060369	0.034636	0	2135	2211	2911	2358	2966	2243	2360	3395	2805	2602
ENSMUSG00000020834	chr11	Dhrs13	78032280	78032498	1967	0.637954	0.978574	0.028165	0.060381	0.068689	0	15	25	31	28	22	40	47	39	79	62
ENSMUSG00000004270	chr6	Lpcat3	1.25E+08	1.25E+08	3268	0.367197	4.562785	0.028192	0.060412	0.031235	0	224	308	370	364	474	438	584	679	759	660
ENSMUSG00000070939	chr1	Tgfbrap1	43047200	43049835	10972	-0.38009	4.368933	0.028191	0.060412	0.033209	0	320	320	432	405	482	308	347	558	463	415
ENSMUSG00000103316	chr11	Coil	88973949	88974202	1722	-0.54396	1.539305	0.028192	0.060412	0.053299	0	46	58	52	47	78	38	55	57	62	58

ENSMUSG00000006463	chr19	Zdhhc24	4878668	4878736	2916	0.532638	2.532608	0.02822	0.060453	0.059992	0	84	61	104	61	76	105	158	222	156	142
ENSMUSG00000054057	chr2	A930004D18Rik	18025193	18028238	3378	-0.78934	-0.0711	0.028219	0.060453	0.097841	0	16	15	21	16	25	4	20	8	27	18
ENSMUSG00000034205	chr14	Loxl2	69609068	69609294	5405	-0.56936	5.949497	0.028292	0.060599	0.079204	0	1268	603	1422	849	2205	904	1643	713	1541	1058
ENSMUSG00000004947	chr5	Dtx2	1.36E+08	1.36E+08	7032	0.43629	3.244259	0.028301	0.060608	0.041378	0	128	89	134	141	178	156	220	246	336	321
ENSMUSG00000058258	chr13	Idi1	8885501	8885996	3505	-0.70462	1.929885	0.028306	0.06061	0.108305	0	68	51	69	76	130	38	67	27	109	101
ENSMUSG00000037992	chr11	Rara	98927818	98927910	4365	0.351978	3.992326	0.028332	0.060655	0.027417	0	188	189	233	242	319	321	435	365	544	421
ENSMUSG00000052951	chr2	C130021I20Rik	33641193	33641344	4140	-1.01934	0.22116	0.028338	0.060659	0.200153	0	32	11	19	9	54	13	31	9	11	19
ENSMUSG00000024935	chr19	Slc1a1	28835049	28835332	6170	-0.68	1.491374	0.028354	0.060683	0.092885	0	48	37	69	69	61	41	33	84	54	32
ENSMUSG00000017132	chr11	Cyth1	1.18E+08	1.18E+08	3905	-0.34432	5.279369	0.028361	0.06069	0.028197	0	612	644	808	785	771	601	764	706	1066	892
ENSMUSG00000074582	chr2	Arfgef2	1.67E+08	1.67E+08	8770	-0.42787	5.211599	0.028391	0.060745	0.04407	0	554	556	795	838	830	449	623	1101	809	729
ENSMUSG00000075376	chr2	Rc3h2	37370069	37375428	11688	-0.34079	5.220273	0.028414	0.060784	0.027434	0	556	616	814	648	865	628	779	790	824	799
ENSMUSG00000000759	chr8	Tubgcp3	12614277	12615296	8568	-0.38426	3.303461	0.028419	0.060786	0.031164	0	160	138	230	192	214	150	188	221	230	206
ENSMUSG00000026556	chr1	Vangl2	1.72E+08	1.72E+08	6990	0.592668	1.460142	0.028449	0.060841	0.06409	0	26	36	31	40	42	45	85	63	79	101
ENSMUSG00000023832	chr17	Acat2	12942890	12944032	2544	0.836705	2.958608	0.028497	0.060934	0.164221	0	55	65	78	105	168	103	147	84	378	480
ENSMUSG00000020653	chr12	Klf11	24651371	24651566	4228	0.645397	2.640429	0.028524	0.060983	0.094583	0	32	49	149	88	95	86	173	214	205	208
ENSMUSG00000037343	chr15	Taf2	55015129	55016601	5033	-0.36582	3.989149	0.028538	0.061002	0.029961	0	240	231	364	325	339	249	396	274	409	295
ENSMUSG00000029062	chr4	Cdk11b	1.56E+08	1.56E+08	3752	0.339559	5.70547	0.02855	0.061019	0.02773	0	606	691	841	801	918	1072	1230	1450	1532	1509
ENSMUSG00000000276	chr11	Dgke	89035179	89040911	8387	-0.52444	2.679137	0.02857	0.061052	0.060188	0	80	93	151	186	119	75	106	128	162	145
ENSMUSG00000015290	chrX	Ubl4	74365718	74367586	3142	-0.37277	6.172144	0.028588	0.06108	0.033905	0	1172	1333	1609	1279	1365	1380	1473	1385	1725	1312
ENSMUSG00000043015	chr1	Tmem194b	52630703	52630851	7078	0.646715	0.625554	0.02867	0.061246	0.067494	0	12	12	16	26	28	31	43	34	54	43
ENSMUSG00000048371	chr8	Pdp2	1.05E+08	1.05E+08	3485	-0.67968	1.839415	0.028702	0.061305	0.098693	0	38	40	92	102	99	45	39	94	66	70
ENSMUSG00000031502	chr8	Col4a1	11198423	11199882	6818	-0.38674	9.410341	0.028732	0.061359	0.037297	0	8944	10062	15414	15813	15001	9907	14805	11610	20678	13125
ENSMUSG00000095432	chr13	Zfp748	67538641	67542910	4970	-0.57957	1.590734	0.028751	0.06139	0.064632	0	40	57	70	58	71	27	55	77	67	53
ENSMUSG00000024026	chr17	Glo1	30592866	30593074	1935	-0.38224	6.415943	0.028819	0.061526	0.035897	0	1456	1530	1993	1477	1569	1660	1814	1519	1878	1680
ENSMUSG00000069045	chrY	Ddx3y	1260771	1263367	5199	-2.15768	5.217365	0.028824	0.061529	1.022653	0	824	751	1231	1106	1224	305	521	1	833	0
ENSMUSG00000033542	chr6	Arhgef5	43265582	43265743	9977	-0.44401	3.138708	0.02889	0.06166	0.043243	0	157	146	182	163	192	111	168	245	194	151
ENSMUSG00000057342	chr7	Sphk2	45709467	45711811	4159	0.408874	4.324514	0.028917	0.061707	0.039278	0	172	223	319	339	407	346	471	607	622	634
ENSMUSG00000035530	chr11	Eif1	1E+08	1E+08	2098	0.440131	8.562538	0.028927	0.06172	0.048305	0	4672	4983	6111	5245	5720	7872	8004	15500	9295	9681
ENSMUSG00000023963	chr17	Cyp39a1	43667425	43667794	3053	-0.49299	2.550637	0.028967	0.061795	0.051243	0	95	98	148	112	113	86	132	141	121	80
ENSMUSG00000022031	chr14	Elp3	65530446	65531600	2891	-0.35318	5.886581	0.028991	0.061837	0.030343	0	996	966	1291	1032	1259	1112	1163	1240	1348	1144
ENSMUSG00000090778	chr8	Gm3235	91621448	91622006	695	-1.01134	0.183572	0.029015	0.06188	0.201664	0	34	21	14	28	19	11	7	41	13	10
ENSMUSG00000027184	chr2	Caprin1	1.04E+08	1.04E+08	10219	-0.34905	6.585858	0.029024	0.061889	0.03003	0	1429	1466	1946	1781	2474	1443	2024	1814	2678	2020
ENSMUSG00000045896	chr6	Paip2b	83805401	83808892	6157	-0.55695	6.595476	0.029119	0.062082	0.076923	0	1872	1754	2133	1965	1790	1216	1477	3472	1535	1368
ENSMUSG00000030016	chr6	Zfml	83914353	83914479	6470	-0.41923	5.091174	0.029185	0.062212	0.04255	0	622	524	724	569	828	465	677	999	739	527
ENSMUSG00000030447	chr7	Cyfip1	55841745	55842066	8925	0.401732	5.231576	0.029351	0.062556	0.039054	0	501	427	589	534	656	584	1010	756	1564	1212
ENSMUSG00000081895	chr7	Rpl17-ps10	72648757	72649311	555	0.471964	2.601902	0.029372	0.062591	0.046753	0	82	71	114	63	87	148	172	150	177	155
ENSMUSG00000098812	chr2	Mir7578	27450549	27450630	82	-0.6618	0.423746	0.029397	0.062635	0.062902	0	21	19	26	23	42	19	27	21	27	20
ENSMUSG00000003808	chr8	Farsa	84856989	84857181	4538	0.344278	4.793734	0.029407	0.062646	0.02794	0	325	385	461	373	498	642	709	644	863	740
ENSMUSG00000028885	chr4	Smpdl3b	1.33E+08	1.33E+08	2006	0.670786	1.956721	0.029487	0.062808	0.095917	0	59	39	34	32	78	89	164	79	129	79
ENSMUSG00000081111	chr8	Gm5913	97427712	97429110	1399	-0.51127	1.65959	0.029528	0.062886	0.046787	0	47	47	71	61	80	48	58	65	64	61
ENSMUSG00000052192	chr16	Gm5963	35573321	35573556	236	0.871498	-0.01992	0.029564	0.062953	0.113853	0	12	16	7	7	8	34	25	19	28	23
ENSMUSG00000006464	chr19	Bbs1	4886898	4890758	5581	-0.54416	1.540981	0.029596	0.063012	0.055774	0	51	37	70	68	56	43	48	48	74	58
ENSMUSG00000024220	chr17	Zfp523	28177207	28177415	3991	-0.38323	3.675653	0.029611	0.063025	0.032866	0	202	196	277	239	296	172	238	323	264	294
ENSMUSG00000097589	chr14	Dleu2	61602839	61603806	11334	0.526392	2.58446	0.02961	0.063025	0.061229	0	51	61	118	72	110	144	170	107	176	210
ENSMUSG00000022878	chr16	Adipoq	23146536	23146641	1381	1.522843	5.283346	0.029617	0.063027	0.546921	0	328	87	70	464	783	97	391	357	2247	4106
ENSMUSG00000027832	chr3	Ptx3	66219910	66220191	2682	0.648235	4.077547	0.029636	0.063058	0.101721	0	196	195	265	205	228	377	414	134	814	708
ENSMUSG00000057778	chr11	Cyb5d2	72777232	72778952	5143	-0.40201	3.997076	0.029648	0.063073	0.037426	0	271	315	371	264	276	293	366	250	364	316
ENSMUSG00000024427	chr18	Spry4	38586268	38590755	4587	-0.43159	3.182538	0.029657	0.063082	0.041292	0	141	123	171	232	202	135	190	151	254	176
ENSMUSG00000042595	chrX	Fam199x	1.37E+08	1.37E+08	8299	-0.60268	2.680409	0.029661	0.063082	0.08306	0	110	124	168	83	157	71	98	211	117	92
ENSMUSG00000024810	chr19	Il33	29925114	29925161	2886	0.646243	3.031584	0.029703	0.06316	0.096861	0	109	63	68	117	172	111	173	169	414	329
ENSMUSG00000028433	chr4	Ubap2	41194313	41195246	4802	-0.35178	6.371044	0.029707	0.06316	0.030666	0	1257	1159	1611	1761	2047	1297	1660	1774	2144	1662
ENSMUSG00000098808	chr3	Mir7009	36475461	36475524	64	0.955723	-0.27455	0.029723	0.063185	0.13359	0	7	11	3	12	6	10	26	13	42	22
ENSMUSG00000047022	chr12	Mipol1	57230427	57230611	9342	-0.69269	1.54924	0.029739	0.063209	0.100983	0	50	52	75	58	60	20	50	94	59	36
ENSMUSG00000003226	chr10	Ranbp2	58446852	58447051	9477	-0.50616	6.542791	0.029745	0.063211	0.064018	0	1504	1500	2125	1834	2249	1093	1616	3241	1706	1341
ENSMUSG00000093264	chr11	Gm23419	1.2E+08	1.2E+08	84	0.463393	5.544662	0.029852	0.06343	0.053128	0	456	528	775	658	914	859	1357	680	2039	1535
ENSMUSG00000062694	chr6	Cav3	1.12E+08	1.12E+08	1160	0.432887	6.778416	0.029889	0.063497	0.046941	0	1174	1618	1915	1323	1785	2873	3798	2059	3219	2594
ENSMUSG00000027770	chr3	Dhx36	62468013	62470747	10217	-0.36118	4.873158	0.029897	0.063505	0.031338	0	504	480	689	446	636	403	723	550	741	605
ENSMUSG00000053317	chr4	Sec61b	47474658	47474753	1271	0.469284	4.51262	0.029915	0.063534	0.053272	0	251	294	442	258	358	531	622	318	872	762
ENSMUSG00000005225	chr6	Plekha8	54595111	54595471	7005	-0.42805	2.555411	0.029976	0.063654	0.036769	0	88	98	121	113	139	97	120	106	134	120
ENSMUSG00000029314	chr5	Agpat9	1.01E+08	1.01E+08	3502	0.672716	2.513385	0.029985	0.063663	0.104415	0	54	45	63	81	125	87	117	108	198	308
ENSMUSG00000038206	chr8	Fbxo8	56551090	56551376	3740	-0.37674	3.85287	0.030005	0.063696	0.032373	0	224	255	330	287	256	213	302	354	319	274
ENSMUSG00000057315	chr5	Arhgap24	1.02E+08	1.02E+08	8791	0.367794	3.963957	0.030029	0.063738	0.0306	0	216	176	223	252	263	262	494	386	508	415
ENSMUSG00000061723	chr7	Tnnt3	1.42E+08	1.42E+08	1391	-0.38747	14.25644	0.030094	0.063864	0.038146	0	298198	340340	429425	378021	410802	395970	334047	436735	379693	394835
ENSMUSG00000072872	chr6	Rybp	1E+08	1E+08	4458	-0.59594	1.769834	0.030116	0.063903	0.072774	0	61	49	57	54	120	38	71	71	59	72
ENSMUSG00000050052	chr8	Tdrp	13952009	13954135	4694	-0.53493	2.871675	0.030164	0.063994	0.06506	0	79	166	175	162	133	121	93	163	154	156
ENSMUSG00000028766	chr4	Alpl	1.38E+08	1.38E+08	4033	-0.69721	2.853319	0.030212	0.064087	0.114306	0	113	130	148	202	145	122	124	33	190	173

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ENSMUSG00000092416	chr7	Zfp141	42473386	42476683	4665	-0.53456	2.079201	0.030247	0.06415	0.059066	0	77	69	97	61	109	57	65	112	93	70
ENSMUSG00000026034	chr1	Clk1	58410189	58412340	8132	0.492041	4.692834	0.030327	0.064311	0.059178	0	350	362	418	287	352	447	520	1063	598	879
ENSMUSG00000000296	chr10	Tpd52l1	31332380	31332969	1267	-0.4089	3.923872	0.030341	0.06433	0.039106	0	244	302	319	280	282	235	269	413	353	245
ENSMUSG00000024387	chr17	Csnk2b	35116196	35116425	2067	0.356991	6.350922	0.030364	0.064369	0.03185	0	951	1082	1308	1267	1379	1993	1840	2086	2490	2202
ENSMUSG00000006058	chr11	Snf8	96034885	96035067	2677	0.427902	4.410754	0.030377	0.06438	0.044061	0	236	264	344	302	372	492	538	333	700	776
ENSMUSG00000032606	chr9	Nicn1	1.08E+08	1.08E+08	2835	-0.38	3.57774	0.030379	0.06438	0.032337	0	181	237	248	218	230	204	264	205	280	249
ENSMUSG00000029169	chr5	Dhx15	52150209	52150778	3009	-0.34511	5.532391	0.030436	0.064491	0.029288	0	758	729	964	819	1072	650	1012	1133	1140	856
ENSMUSG00000016496	chr19	Cd274	29367455	29367506	3622	0.804669	2.018254	0.03045	0.064511	0.147876	0	37	42	55	72	30	94	61	54	158	222
ENSMUSG00000062031	chr7	Athl1	1.41E+08	1.41E+08	3346	0.490367	3.196959	0.030469	0.064542	0.055738	0	121	70	123	110	219	189	254	197	284	316
ENSMUSG00000032548	chr9	Slco2a1	1.03E+08	1.03E+08	13545	0.618129	2.312259	0.030502	0.064591	0.084315	0	53	56	46	66	100	64	94	166	244	143
ENSMUSG00000039997	chr1	Ifi203	1.74E+08	1.74E+08	6706	0.538517	3.817795	0.0305	0.064591	0.069841	0	131	179	219	228	198	437	354	202	356	538
ENSMUSG00000021662	chr13	Arhgef28	97898595	97899816	6259	-0.72414	1.821824	0.030603	0.064796	0.117887	0	45	71	75	87	84	15	42	80	91	89
ENSMUSG00000032860	chr7	P2ry2	1.01E+08	1.01E+08	3000	-0.36398	5.455801	0.030665	0.064917	0.03267	0	645	679	868	981	969	790	890	763	1272	781
ENSMUSG00000020604	chr11	Arsg	1.09E+08	1.09E+08	3906	0.60443	1.740701	0.030714	0.06501	0.075822	0	36	35	36	31	79	51	97	118	103	90
ENSMUSG00000069727	chr7	Gm5595	42660105	42662996	3148	-0.54182	1.617354	0.030728	0.06503	0.057862	0	62	55	61	53	63	42	61	75	59	47
ENSMUSG00000037020	chr7	Wdr62	30240138	30240484	5743	0.690155	1.877325	0.030821	0.065218	0.101942	0	49	41	43	38	54	40	62	161	142	121
ENSMUSG00000040997	chr14	Abhd4	54254129	54254471	2749	0.479237	4.85813	0.03084	0.065247	0.056731	0	387	316	455	406	454	446	657	1351	845	661
ENSMUSG00000081058	chr3	Hist2h3c2	96238108	96239127	1020	0.644961	1.245388	0.030945	0.06546	0.081561	0	20	25	42	31	30	72	69	36	69	70
ENSMUSG00000037376	chr2	Trmt6	1.33E+08	1.33E+08	5384	0.363659	3.416092	0.030958	0.065478	0.028588	0	143	134	185	140	170	212	279	275	342	287
ENSMUSG00000097855	chr19	A930007I19Rik	29486355	29487671	4341	0.849153	-0.36205	0.031034	0.065628	0.077928	0	8	10	7	6	8	11	22	16	26	26
ENSMUSG00000025228	chr19	Actr1a	46376814	46378469	2742	0.33404	6.637264	0.031068	0.065659	0.028167	0	1212	1293	1576	1538	1755	2102	2443	2577	3241	2626
ENSMUSG00000028062	chr3	Lamtor2	88549819	88550004	1218	0.40638	5.084499	0.031061	0.065659	0.040765	0	402	483	593	476	464	903	847	630	1050	1026
ENSMUSG00000028398	chr4	Tmem261	75277354	75277769	741	0.375817	4.968636	0.031065	0.065659	0.034511	0	383	442	536	474	419	798	793	720	890	865
ENSMUSG00000063972	chr2	Nr6a1	38723370	38727915	7488	-0.6504	1.189201	0.031056	0.065659	0.080647	0	45	25	67	45	45	35	27	55	44	38
ENSMUSG00000043822	chr10	Adamtsl5	80339110	80339143	4722	0.403769	4.998966	0.031076	0.065662	0.040094	0	402	376	527	557	422	744	959	620	1221	721
ENSMUSG00000071335	chr10	G630090E17Rik	39946907	39948123	1787	-0.5797	1.411703	0.031078	0.065662	0.065591	0	49	44	72	50	43	25	54	44	68	56
ENSMUSG00000001472	chr8	Tcf25	1.23E+08	1.23E+08	3765	-0.34124	7.38746	0.031096	0.065689	0.029655	0	2516	2857	3709	2954	3664	2814	3233	3257	4099	3858
ENSMUSG00000031691	chr8	Tnpo2	85036915	85036977	4990	-0.38076	5.373187	0.031117	0.065724	0.035996	0	653	705	980	691	899	588	767	1145	877	824
ENSMUSG00000015016	chr8	Acsf3	1.23E+08	1.23E+08	2206	0.38777	4.006246	0.031129	0.065738	0.035123	0	160	223	264	267	243	322	346	368	597	505
ENSMUSG00000015291	chrX	Gdi1	74304998	74305441	4296	0.345513	5.545719	0.031149	0.065772	0.029506	0	668	570	754	650	784	817	1151	1410	1439	1326
ENSMUSG00000027104	chr2	Atf2	73816509	73819148	8187	-0.40942	3.944463	0.031184	0.065825	0.039922	0	259	272	260	330	331	177	284	421	382	295
ENSMUSG00000039661	chr8	Dusp26	31089471	31089895	2305	0.679636	5.454287	0.03118	0.065825	0.116311	0	600	508	521	587	548	715	952	2869	888	813
ENSMUSG00000024283	chr18	Wac	7868832	7869091	5962	-0.35842	5.006084	0.031194	0.065835	0.031456	0	548	484	574	646	766	457	693	802	754	592
ENSMUSG00000022484	chr15	Hoxc10	1.03E+08	1.03E+08	1909	-0.37925	5.964217	0.031214	0.065867	0.036115	0	1064	1012	1369	1240	1190	1294	1205	1193	1274	1248
ENSMUSG00000031963	chr9	Bmper	23223076	23223773	3793	0.433865	3.275014	0.03123	0.065888	0.042514	0	132	82	182	117	177	174	269	214	358	290
ENSMUSG00000049047	chrX	Armcx3	1.35E+08	1.35E+08	3540	-0.43932	4.73095	0.031233	0.065888	0.047549	0	445	355	646	458	684	414	782	354	650	439
ENSMUSG00000018669	chr11	Cdk5rap3	96907426	96908122	3812	0.337969	4.703311	0.031239	0.065888	0.02737	0	345	310	413	353	507	536	613	658	817	769
ENSMUSG00000054321	chr18	Taf4b	14783245	14783934	5149	-0.58872	1.633871	0.031242	0.065888	0.070811	0	48	82	63	45	62	47	60	56	78	43
ENSMUSG00000034832	chr6	Tet3	83362373	83369825	11999	-0.39239	5.184519	0.031256	0.065906	0.038168	0	592	415	753	798	942	496	650	899	909	747
ENSMUSG00000048486	chr2	Fitm2	1.63E+08	1.63E+08	3967	-0.36733	6.880142	0.031286	0.065952	0.034345	0	1831	2147	2459	2331	2264	1920	2085	2911	2824	2265
ENSMUSG00000069565	chr10	Dazap1	80261486	80261575	2944	0.3239	4.97924	0.031287	0.065952	0.025314	0	403	385	540	462	555	591	805	815	1036	871
ENSMUSG00000097960	chr8	A330074K22Rik	1.2E+08	1.2E+08	2489	-0.60179	0.907157	0.031326	0.066025	0.063396	0	32	26	36	50	37	29	37	34	37	29
ENSMUSG00000000738	chr8	Spg7	1.23E+08	1.23E+08	4188	-0.37359	6.567702	0.031421	0.066215	0.035464	0	1424	1744	2061	1918	1756	1653	1662	2238	2057	1965
ENSMUSG00000021193	chr13	Pitrm1	6548157	6548229	3524	-0.36967	5.358973	0.031449	0.066264	0.03402	0	693	649	803	836	876	584	794	1124	927	758
ENSMUSG00000073422	chr17	H2-Ke6	34026033	34026225	1533	0.359882	4.612566	0.031473	0.066304	0.031181	0	294	335	385	397	364	576	544	649	690	711
ENSMUSG00000090015	chr5	Gm15446	1.1E+08	1.1E+08	3780	-0.55549	2.103179	0.03149	0.06633	0.066597	0	71	87	97	69	95	64	57	120	76	79
ENSMUSG00000004934	chr10	Pias4	81153266	81154372	4582	0.423313	4.101785	0.031505	0.066342	0.043127	0	166	210	286	274	294	315	406	677	467	417
ENSMUSG00000007036	chr17	Abhd16a	35089263	35089456	3220	-0.34215	5.746384	0.031506	0.066342	0.029268	0	887	908	1140	933	1139	898	1021	1249	1187	1145
ENSMUSG00000080904	chr11	Gm11966	5818497	5818583	87	-0.73593	1.710136	0.031538	0.0664	0.121464	0	55	91	43	90	45	59	50	53	87	32
ENSMUSG00000037286	chr9	Stag1	1.01E+08	1.01E+08	11781	-0.39806	4.775106	0.031563	0.066443	0.039014	0	479	380	562	496	703	346	527	778	617	504
ENSMUSG00000039686	chr2	Zer1	30097283	30098843	9784	-0.34662	5.164645	0.031612	0.066526	0.02964	0	584	556	777	670	774	523	705	918	872	682
ENSMUSG00000045667	chr11	Smtnl2	72389164	72391413	3815	-0.44559	7.707255	0.03161	0.066526	0.051017	0	2879	3729	5291	4802	3419	3626	3312	5170	3685	4560
ENSMUSG00000050211	chr2	Pla2g4e	1.2E+08	1.2E+08	6960	-0.3598	5.169852	0.031627	0.066547	0.031896	0	539	509	808	645	927	673	604	729	881	769
ENSMUSG00000025217	chr19	Btrc	45363734	45363886	6323	-0.3301	4.626639	0.031632	0.066548	0.026092	0	374	404	495	490	535	398	524	439	642	560
ENSMUSG00000027338	chr2	Prnd	1.32E+08	1.32E+08	3211	-0.95045	3.021159	0.031676	0.06663	0.222346	0	80	224	161	269	143	118	194	23	262	62
ENSMUSG00000009647	chr10	Mcu	59446984	59448858	6936	0.352999	5.563489	0.031682	0.066633	0.031128	0	570	616	770	729	783	1081	1454	964	1478	1192
ENSMUSG00000074890	chr2	Lcmt2	1.21E+08	1.21E+08	3350	0.433197	2.670643	0.031689	0.066638	0.039583	0	69	83	110	79	106	120	200	173	186	163
ENSMUSG00000033544	chr1	Angptl1	1.57E+08	1.57E+08	2841	-0.65846	5.241763	0.031704	0.066647	0.109833	0	936	339	767	509	1401	409	1275	542	740	493
ENSMUSG00000046985	chr5	Tapt1	44175164	44177182	3487	-0.3874	5.782512	0.031699	0.066647	0.037855	0	938	911	1271	956	1133	894	1061	1491	1048	1018
ENSMUSG00000025245	chr9	Lztfl1	1.24E+08	1.24E+08	9249	-0.43595	3.706929	0.031725	0.066682	0.04522	0	224	230	269	244	277	147	261	391	261	237
ENSMUSG00000058665	chr1	En1	1.21E+08	1.21E+08	2624	0.569919	2.494978	0.031748	0.06672	0.073745	0	44	81	60	106	78	141	191	130	200	107
ENSMUSG00000032217	chr9	Rnf111	70425429	70427107	5003	-0.40267	3.70096	0.031828	0.066875	0.038278	0	238	214	226	244	305	143	259	333	333	255
ENSMUSG00000033276	chr1	Stk36	74601445	74601613	6437	0.81702	0.313458	0.031831	0.066875	0.125358	0	5	10	25	8	22	21	52	19	39	38
ENSMUSG00000024371	chr17	C2	34862604	34863031	3872	0.601909	2.810963	0.031842	0.066888	0.086228	0	67	53	71	92	190	122	164	177	218	300
ENSMUSG00000085566	chr2	A730017L22Rik	1.31E+08	1.31E+08	6012	-0.55806	1.358436	0.031894	0.066986	0.058387	0	39	37	50	56	68	39	47	32	62	56
ENSMUSG00000001844	chr5	Zdhhc4	1.43E+08	1.43E+08	2864	0.344244	4.224099	0.031903	0.066995	0.027778	0	218	253	272	295	332	374	425	539	603	497

ENSMUSG00000024986	chr19	Hhex	37434810	37435233	1918	0.724172	1.658547	0.031917	0.067014	0.114517	0	23	39	38	61	28	52	73	51	143	135
ENSMUSG00000024456	chr18	Diap1	37843601	37845498	6339	-0.40215	6.470465	0.031949	0.067073	0.041407	0	1159	1706	2165	1955	1415	1393	1751	1531	2431	1893
ENSMUSG00000063412	chr8	Gm10131	34111143	34111736	594	0.557572	1.30465	0.03199	0.067148	0.055691	0	28	28	31	34	38	44	67	52	83	85
ENSMUSG00000086863	chr6	Gm15543	1.45E+08	1.45E+08	361	-0.76528	2.740284	0.032074	0.067314	0.141917	0	99	206	124	184	57	124	99	74	199	80
ENSMUSG00000067870	chr15	Rpl31-ps8	90764279	90764656	378	0.364931	4.87788	0.032122	0.067404	0.032862	0	347	390	580	320	522	611	780	770	837	848
ENSMUSG00000095325	chr17	Zfp870	32879228	32884165	5126	-0.44136	2.858968	0.032147	0.067446	0.042732	0	99	131	185	142	136	101	158	163	150	140
ENSMUSG00000021572	chr13	Cep72	74036495	74038328	3632	0.881775	-0.45457	0.032161	0.067454	0.092688	0	8	6	10	3	9	8	20	15	26	26
ENSMUSG00000029464	chr5	Gpn3	1.22E+08	1.22E+08	2508	-0.3983	3.633545	0.032157	0.067454	0.036975	0	236	209	295	181	247	186	259	304	261	231
ENSMUSG00000047496	chr1	Rnf152	1.05E+08	1.05E+08	8532	-0.57358	1.365604	0.032201	0.067528	0.064564	0	38	47	58	56	51	26	46	35	71	62
ENSMUSG00000004610	chr7	Etfb	43444108	43444204	1139	0.39839	7.529599	0.032238	0.067596	0.04103	0	2169	2722	2663	3149	2458	3861	3755	5298	5855	5813
ENSMUSG00000031388	chrX	Naa10	73916873	73917195	4132	0.352087	5.070221	0.032247	0.067606	0.030728	0	381	470	529	478	609	818	816	737	1073	921
ENSMUSG00000020993	chr12	Trappc6b	59043093	59043676	1254	-0.34031	4.449964	0.032299	0.067693	0.027831	0	381	371	485	359	431	363	468	392	551	477
ENSMUSG00000062825	chr11	Actg1	1.2E+08	1.2E+08	2658	0.474158	7.641312	0.032297	0.067693	0.058222	0	1920	2317	3190	2822	3960	3857	5618	2786	8788	6728
ENSMUSG00000068039	chr17	Tcp1	12915701	12915871	5030	0.339801	7.601755	0.032311	0.067708	0.029875	0	2202	2633	3275	2814	3481	4097	4885	5533	5803	4985
ENSMUSG00000021215	chr13	Net1	3882565	3884473	3734	0.543486	5.55706	0.032367	0.067815	0.07554	0	615	378	714	648	886	575	1027	2235	1783	1055
ENSMUSG00000044456	chr12	Rin3	1.02E+08	1.02E+08	6835	0.492781	3.414531	0.032403	0.06788	0.058109	0	118	104	143	190	183	233	395	160	402	264
ENSMUSG00000092074	chr17	Dynlt1a	6310547	6310943	742	0.61655	1.075445	0.032431	0.067928	0.069005	0	28	21	30	22	30	37	61	43	59	83
ENSMUSG00000029158	chr5	Yipf7	69516675	69517198	1214	-0.43642	6.40731	0.032523	0.068102	0.049049	0	1662	1440	1828	1468	1692	1905	1885	1160	1796	1484
ENSMUSG00000035296	chr14	Sgcg	61221059	61221776	1878	-0.39885	7.199967	0.03252	0.068102	0.041207	0	2585	2115	3064	2762	3533	2260	3230	3961	3035	2259
ENSMUSG00000089979	chr16	Gm15954	18069214	18069335	466	0.421236	3.228432	0.032545	0.068138	0.03974	0	113	143	131	142	124	221	212	256	279	262
ENSMUSG00000021810	chr14	Ecd	20319859	20320951	3125	-0.33357	5.204363	0.032603	0.068247	0.027647	0	551	583	823	705	786	661	751	745	942	699
ENSMUSG00000028270	chr3	Gbp2	1.43E+08	1.43E+08	2516	0.529116	3.56708	0.032649	0.068333	0.068359	0	118	127	172	225	163	371	271	169	416	370
ENSMUSG00000068245	chr14	Phf11d	59347407	59349051	4498	0.790712	2.241537	0.032682	0.068393	0.148538	0	28	64	75	59	58	205	111	59	90	181
ENSMUSG00000049285	chr5	Mblac1	1.38E+08	1.38E+08	1308	0.673987	0.640622	0.032694	0.068407	0.078433	0	15	15	21	12	31	31	31	31	63	54
ENSMUSG00000032116	chr9	Stt3a	36729344	36732962	8948	0.412242	5.585286	0.032706	0.068422	0.043363	0	634	514	719	575	1039	948	1372	823	1864	1486
ENSMUSG00000030942	chr7	Thumpd1	1.2E+08	1.2E+08	2653	0.351391	4.846869	0.032812	0.068633	0.030591	0	313	374	536	403	498	598	698	847	772	823
ENSMUSG00000067058	chr5	Rps15a-ps5	1.06E+08	1.06E+08	393	0.511259	2.256842	0.032817	0.068633	0.056611	0	41	59	94	45	88	106	146	112	142	133
ENSMUSG00000024661	chr19	Fth1	9982703	9982983	866	0.372069	10.37347	0.032869	0.068732	0.036316	0	14293	17396	21150	21988	22222	29310	26787	35570	40132	42614
ENSMUSG00000019861	chr10	Gopc	52337024	52339853	4317	-0.34174	4.14505	0.032923	0.068829	0.027655	0	304	259	370	312	409	279	428	349	434	331
ENSMUSG00000026319	chr1	2310035C23Rik	1.06E+08	1.06E+08	9500	-0.42719	3.233488	0.032925	0.068829	0.042488	0	168	118	213	165	242	104	193	219	256	176
ENSMUSG00000024118	chr17	1600002H07Rik	24215054	24216005	2551	0.509921	1.804785	0.032985	0.068944	0.050192	0	49	37	42	48	56	75	87	83	130	92
ENSMUSG00000018209	chr2	Stk4	1.64E+08	1.64E+08	5860	0.346833	4.380952	0.033045	0.069058	0.029141	0	241	239	332	301	433	412	534	465	694	627
ENSMUSG00000048787	chr7	Dcun1d3	1.2E+08	1.2E+08	6203	-0.35996	3.941267	0.033096	0.069155	0.030829	0	230	307	291	256	348	213	334	287	383	362
ENSMUSG00000020493	chr11	Prr11	87089153	87091865	3824	0.682677	1.182866	0.033115	0.069184	0.09469	0	18	22	32	25	43	33	56	37	119	76
ENSMUSG00000041482	chr18	Piezo2	63010213	63011800	14566	-0.73773	1.852652	0.033125	0.069195	0.1251	0	77	30	54	55	166	33	74	74	68	64
ENSMUSG00000028729	chr4	Ebna1bp2	1.19E+08	1.19E+08	3553	0.344121	4.950382	0.033141	0.069217	0.029423	0	385	426	482	407	574	686	815	655	966	902
ENSMUSG00000067942	chr17	Zfp160	21008941	21008986	3791	-0.49153	2.332998	0.033149	0.069222	0.052921	0	117	66	110	89	100	68	83	110	118	106
ENSMUSG00000042642	chr3	Flad1	89401004	89402312	4087	-0.33737	5.151157	0.033179	0.069276	0.0285	0	562	638	695	676	723	644	728	632	871	774
ENSMUSG00000036061	chr15	Smug1	1.03E+08	1.03E+08	3281	-0.37863	3.595435	0.033231	0.069373	0.033357	0	201	223	275	190	242	187	281	270	262	218
ENSMUSG00000073680	chr4	Tmem88b	1.56E+08	1.56E+08	3471	0.587885	1.07752	0.033278	0.069461	0.062489	0	24	15	30	26	40	42	61	60	53	63
ENSMUSG00000032549	chr9	Rab6b	1.03E+08	1.03E+08	5031	-0.50178	2.904267	0.033295	0.069479	0.059151	0	168	91	173	124	172	76	126	195	182	150
ENSMUSG00000063334	chr10	Krr1	1.12E+08	1.12E+08	5958	-0.33934	4.827305	0.033297	0.069479	0.028469	0	449	441	627	551	583	473	594	669	658	519
ENSMUSG00000022297	chr15	Fzd6	39006280	39006432	4134	-0.46635	2.761187	0.033328	0.069513	0.049366	0	97	106	175	160	114	88	117	148	158	152
ENSMUSG00000027131	chr2	Emc4	1.12E+08	1.12E+08	1052	-0.34955	5.308762	0.033326	0.069513	0.0309	0	631	698	891	674	809	654	841	951	901	705
ENSMUSG00000037275	chr11	Gemin5	58120002	58121784	6618	-0.35953	4.448667	0.03332	0.069513	0.03144	0	317	312	543	381	523	379	426	513	475	419
ENSMUSG00000041264	chr5	Uspl1	1.49E+08	1.49E+08	6648	-0.33259	4.885637	0.033424	0.069704	0.027433	0	434	525	658	546	584	505	608	589	733	614
ENSMUSG00000104357	chr3	TTC14	33800279	33800436	2145	-0.44389	2.736017	0.033471	0.069791	0.043629	0	129	113	148	90	154	94	150	123	152	136
ENSMUSG00000021891	chr14	Mettl6	31478320	31479810	2436	0.417225	3.21893	0.033514	0.069869	0.039799	0	105	129	157	106	164	185	221	310	249	260
ENSMUSG00000026966	chr2	Ssna1	25271039	25271581	1276	0.371721	4.31755	0.033519	0.069869	0.033724	0	230	300	368	244	300	475	491	433	651	556
ENSMUSG00000007207	chr5	Stx1a	1.35E+08	1.35E+08	2666	0.696797	0.250431	0.033584	0.069994	0.072791	0	13	15	9	12	19	24	34	22	47	30
ENSMUSG00000003273	chr7	Car11	45699843	45700339	1926	-0.61345	1.100182	0.0336	0.070006	0.071836	0	40	38	41	50	38	29	28	45	35	53
ENSMUSG00000028920	chr4	Fbxo42	1.41E+08	1.41E+08	5934	-0.33622	4.065386	0.033599	0.070006	0.026761	0	283	265	318	284	410	267	336	366	431	328
ENSMUSG00000052337	chr6	Immt	71831331	71831515	4964	-0.37428	8.31315	0.033626	0.070051	0.036938	0	4623	6240	6318	6828	5738	5381	5756	7457	7675	6026
ENSMUSG00000045917	chr4	6330416G13Rik	63558781	63558957	3974	-0.36448	4.030663	0.033635	0.070059	0.03183	0	258	275	345	287	370	289	305	249	406	412
ENSMUSG00000026544	chr1	Dusp23	1.73E+08	1.73E+08	1410	-0.38794	5.282628	0.033674	0.070129	0.038453	0	685	748	827	744	622	775	742	763	858	740
ENSMUSG00000022228	chr13	Zscan26	21442175	21445829	4371	-0.4257	3.911676	0.03369	0.070151	0.044619	0	259	227	311	294	350	150	294	443	354	276
ENSMUSG00000025208	chr19	Mrpl43	45005014	45005940	1213	0.378161	5.299629	0.033748	0.070263	0.036471	0	424	629	701	555	526	918	1010	1093	1145	981
ENSMUSG00000056429	chr6	Tgoln1	72608432	72612110	5013	-0.36085	5.857111	0.033793	0.070345	0.033704	0	1005	846	1204	1010	1414	715	1091	1209	1619	1404
ENSMUSG00000037443	chr4	Cep85	1.34E+08	1.34E+08	5269	-0.37135	5.411198	0.033836	0.070425	0.035342	0	706	720	797	978	769	713	808	1010	871	893
ENSMUSG00000042446	chr4	Zmym4	1.27E+08	1.27E+08	8139	-0.34086	4.012419	0.033874	0.070493	0.027672	0	265	230	328	313	374	210	363	336	396	369
ENSMUSG00000000223	chrX	Drp2	1.34E+08	1.34E+08	8553	0.466376	3.593381	0.033948	0.070636	0.053068	0	165	104	142	176	262	214	462	279	420	267
ENSMUSG00000031204	chrX	Asb12	95470201	95470466	1258	-0.36437	5.322009	0.033988	0.070709	0.033883	0	645	591	826	847	861	720	705	1004	841	765
ENSMUSG00000024766	chr19	Lipo1	33517740	33517777	3431	-0.49153	2.165367	0.034046	0.070818	0.051968	0	68	54	114	93	109	54	85	95	122	79
ENSMUSG00000003534	chr17	Ddr1	35681567	35682518	4774	0.352848	4.636689	0.034069	0.070841	0.030894	0	289	335	370	361	471	455	759	715	815	529
ENSMUSG00000032712	chr6	2810474O19Rik	1.49E+08	1.49E+08	6802	0.412666	4.098235	0.034069	0.070841	0.04188	0	191	250	203	225	354	288	610	417	572	414
ENSMUSG00000087298	chr7	Gm9392	46820864	46821417	554	-0.5562	1.289934	0.034072	0.070841	0.058149	0	34	35	56	56	57	31	43	58	55	38

ENSMUSG00000041958	chr11	Pigs	78328415	78328508	2501	0.35716	4.817185	0.034102	0.070882	0.03212	0	336	308	487	401	555	590	730	561	973	857
ENSMUSG00000095159	chr5	Tubb4b-ps1	7179365	7180699	1335	-0.77516	0.529146	0.034098	0.070882	0.118942	0	21	34	47	27	14	16	35	16	22	29
ENSMUSG00000061897	chr2	Gm14292	1.79E+08	1.79E+08	456	-0.56399	0.992994	0.034109	0.070886	0.057064	0	32	32	39	36	53	21	42	32	51	37
ENSMUSG00000072568	chr15	Fam84b	60818994	60823991	5926	-0.54369	2.479221	0.034132	0.070923	0.069133	0	100	82	111	154	95	62	72	109	172	122
ENSMUSG00000033669	chr15	Zfp7	76879259	76879353	2769	0.726702	0.323015	0.034172	0.070995	0.08207	0	13	14	12	13	19	15	36	24	56	39
ENSMUSG00000032845	chr18	Alpk2	65265529	65266290	7782	-0.50042	5.743869	0.034187	0.071017	0.065543	0	964	880	896	1202	1286	658	917	1682	1388	599
ENSMUSG00000084929	chr4	Foxo6os	1.2E+08	1.2E+08	2291	-0.67148	5.025094	0.034237	0.071109	0.11727	0	520	567	788	625	875	632	819	138	885	449
ENSMUSG00000071350	chr14	Setdb2	59402009	59402416	4047	-0.48481	1.972226	0.034254	0.071133	0.047739	0	58	56	91	81	93	66	84	64	92	68
ENSMUSG00000017929	chr2	B4galt5	1.67E+08	1.67E+08	4308	0.435686	4.481194	0.034306	0.07121	0.048047	0	201	349	368	236	440	396	625	429	897	703
ENSMUSG00000021234	chr12	Fam161b	84345309	84346409	4656	-0.75013	0.229353	0.034305	0.07121	0.099171	0	24	19	37	12	23	8	28	17	26	18
ENSMUSG00000087249	chr11	Gm16062	59810080	59810261	771	-0.68947	2.825462	0.034301	0.07121	0.116619	0	136	151	231	115	82	164	147	61	125	111
ENSMUSG00000022012	chr14	Enox1	77156763	77157042	3495	0.675732	0.697614	0.034347	0.071283	0.086648	0	12	9	23	24	31	26	64	38	48	42
ENSMUSG00000045114	chr7	Prrt2	1.27E+08	1.27E+08	3272	0.439477	2.736224	0.034406	0.071396	0.0434	0	74	63	115	88	133	118	173	182	199	215
ENSMUSG00000039201	chrX	Tbc1d25	8154472	8156066	2794	0.51411	1.980747	0.034436	0.071437	0.057002	0	48	32	51	64	71	87	106	125	120	87
ENSMUSG00000083610	chr3	Oaz2-ps	1.36E+08	1.36E+08	537	-0.48627	1.786352	0.034434	0.071437	0.046332	0	57	52	80	69	72	50	60	76	80	63
ENSMUSG00000031232	chrX	Magt1	1.06E+08	1.06E+08	4672	-0.37121	5.275296	0.034462	0.07148	0.03543	0	626	617	810	685	928	679	879	518	1028	846
ENSMUSG00000031740	chr8	Mmp2	92827328	92827777	3038	0.523188	7.568155	0.034474	0.071495	0.072607	0	2592	1315	2619	2015	4853	3766	5718	7249	4806	4450
ENSMUSG00000035236	chr2	Scai	39066214	39075156	11668	-0.57943	1.676104	0.034576	0.071685	0.071092	0	76	44	82	49	60	38	56	80	68	52
ENSMUSG00000041440	chr9	Gk5	96119362	96119612	8493	-0.59554	1.308164	0.034575	0.071685	0.072086	0	46	24	62	43	71	27	49	52	60	38
ENSMUSG00000005371	chr17	Fbxo11	87990859	87992175	4144	-0.34204	5.310373	0.034619	0.071763	0.03002	0	669	634	809	716	877	588	852	1000	919	732
ENSMUSG00000010025	chr11	Aldh3a2	61223417	61224686	5619	-0.34487	3.998561	0.034665	0.071848	0.028709	0	244	238	358	287	376	200	344	318	453	353
ENSMUSG00000033629	chr9	Ptplad1	64986985	64988529	2731	0.345288	4.103895	0.034716	0.071942	0.028864	0	231	185	295	223	337	337	470	401	536	501
ENSMUSG00000013787	chr17	Ehmt2	34898469	34898540	5489	0.33294	5.318954	0.034738	0.071977	0.02833	0	549	453	647	615	689	723	961	1141	1356	1061
ENSMUSG00000003421	chr7	Nosip	45062429	45062531	2920	0.331901	4.943354	0.034752	0.071995	0.027769	0	343	437	506	471	515	637	733	840	925	857
ENSMUSG00000017765	chr8	Slc12a4	1.06E+08	1.06E+08	4297	0.438169	4.218289	0.034768	0.072018	0.048438	0	269	158	243	242	420	321	592	378	745	506
ENSMUSG00000052942	chr19	Glis3	28258851	28263115	8842	0.649443	0.729898	0.034794	0.072061	0.074947	0	17	16	18	18	32	22	35	47	66	55
ENSMUSG00000001380	chr18	Hars	36766530	36766953	1987	0.321459	5.361371	0.0348	0.072062	0.026421	0	491	555	665	590	759	829	1058	971	1309	1178
ENSMUSG00000039956	chr16	Mrap	90738324	90738669	1464	1.613459	2.194211	0.03482	0.072092	0.631559	0	22	11	8	64	83	15	33	17	301	467
ENSMUSG00000049323	chr11	Smcr8	60777524	60781067	8078	-0.42456	4.943829	0.034851	0.072139	0.046555	0	504	431	592	652	791	387	591	941	592	555
ENSMUSG00000071451	chr13	Psmg4	34162964	34163249	554	0.453749	2.709497	0.034853	0.072139	0.045973	0	67	94	115	84	93	141	161	141	205	221
ENSMUSG00000006932	chr9	Ctnnb1	1.21E+08	1.21E+08	5099	-0.32223	8.022918	0.034917	0.072262	0.027729	0	4017	4128	5470	5036	5586	4018	5603	5666	6361	5461
ENSMUSG00000015568	chr8	Lpl	68880491	68880840	6810	0.580102	9.052334	0.034999	0.072421	0.0898	0	5681	7650	6065	9220	6335	6781	8166	15286	21580	24974
ENSMUSG00000023495	chr9	Pcbp4	1.06E+08	1.06E+08	4242	0.34628	5.530033	0.03503	0.072473	0.031013	0	588	616	800	703	674	827	1434	1297	1445	1073
ENSMUSG00000042712	chrX	Wbp5	1.36E+08	1.36E+08	1037	0.409935	4.874797	0.03505	0.072505	0.043279	0	394	324	510	351	536	610	970	483	1138	747
ENSMUSG00000050786	chr6	Ccdc126	49319274	49319480	2421	-0.53332	1.347782	0.035076	0.072546	0.053308	0	40	40	65	41	60	43	46	50	53	42
ENSMUSG00000030934	chr7	Oat	1.33E+08	1.33E+08	2155	-0.414	7.728509	0.035106	0.072599	0.045843	0	3735	3360	4260	3959	4971	3130	3537	6492	4285	3708
ENSMUSG00000000581	chr11	C1d	17257579	17257658	3995	-0.33578	4.818087	0.035118	0.072611	0.028584	0	469	512	602	502	520	436	557	620	726	583
ENSMUSG00000029726	chr5	Mepce	1.38E+08	1.38E+08	3292	0.345049	4.436516	0.035128	0.072622	0.029445	0	317	252	347	319	347	433	510	666	629	577
ENSMUSG00000041025	chr4	Iffo2	1.4E+08	1.4E+08	6216	0.552621	3.038374	0.035133	0.072622	0.075509	0	64	80	89	138	191	148	269	135	317	277
ENSMUSG00000020491	chr11	2810021J22Rik	58867216	58867309	3928	-0.56114	0.994323	0.035145	0.072635	0.055283	0	31	36	45	43	35	30	34	34	47	36
ENSMUSG00000026172	chr1	Bcs1l	74588289	74588393	2192	-0.4539	4.142586	0.035165	0.072666	0.052332	0	280	315	384	383	330	310	415	171	461	382
ENSMUSG00000029250	chr5	Polr2b	77310147	77310630	4667	-0.31862	5.576288	0.035231	0.072791	0.02629	0	755	763	1008	904	997	754	1000	1097	1178	938
ENSMUSG00000031134	chrX	Rbmx	57383530	57384561	4330	0.360145	4.06645	0.035464	0.073262	0.031594	0	173	237	258	265	289	272	457	402	600	495
ENSMUSG00000085653	chr1	Gm15179	75368212	75368431	867	-0.46987	3.196959	0.035502	0.073329	0.05335	0	185	173	187	169	154	189	185	127	174	199
ENSMUSG00000014763	chr17	Fam120b	15396246	15396560	4518	-0.35917	4.091918	0.035615	0.07354	0.031785	0	267	246	402	340	350	242	351	436	410	308
ENSMUSG00000032342	chr9	Mto1	78448208	78448510	4078	-0.33894	4.503779	0.035614	0.07354	0.02878	0	352	388	518	440	407	377	443	502	570	443
ENSMUSG00000005621	chr7	Zfp592	80993681	80993762	7412	-0.3419	4.452719	0.035629	0.073559	0.029201	0	365	298	435	432	525	334	420	531	556	419
ENSMUSG00000022360	chr15	Atad2	58094047	58095571	5683	0.505269	2.400001	0.035654	0.073599	0.058305	0	63	53	69	64	112	100	136	109	247	133
ENSMUSG00000018648	chr11	Dusp14	84048041	84049310	1945	0.494674	2.979174	0.035668	0.073618	0.059228	0	80	101	134	108	118	229	253	122	254	190
ENSMUSG00000028651	chr4	Ppie	1.23E+08	1.23E+08	1719	0.388742	3.8377	0.035684	0.073618	0.036968	0	156	224	232	192	218	369	385	289	443	376
ENSMUSG00000040943	chr3	Tet2	1.33E+08	1.33E+08	9179	-0.45301	4.145726	0.035681	0.073618	0.052455	0	363	273	281	322	459	231	366	526	339	275
ENSMUSG00000044122	chr11	Proca1	78193392	78193766	2088	0.968364	0.935102	0.035679	0.073618	0.213512	0	22	17	15	16	30	24	36	14	89	123
ENSMUSG00000021361	chr13	Tmem14c	41016250	41016398	945	0.3934	5.879714	0.035732	0.073694	0.04096	0	733	834	1080	766	812	1448	1561	1069	1937	1755
ENSMUSG00000024833	chr19	Pola2	5940543	5941017	2872	0.383888	3.997526	0.03573	0.073694	0.036221	0	192	235	281	223	211	340	419	309	529	510
ENSMUSG00000024480	chr18	Ap3s1	46741917	46742081	1479	0.48035	3.791971	0.035747	0.073715	0.058001	0	166	165	216	193	220	189	321	253	594	577
ENSMUSG00000025646	chr9	Atrip	1.09E+08	1.09E+08	6725	0.371261	4.691776	0.035771	0.073752	0.035301	0	286	348	392	391	466	587	533	853	702	684
ENSMUSG00000042111	chr1	Ccdc115	34436670	34437610	2543	0.34149	4.090975	0.035832	0.073869	0.028393	0	217	232	308	209	284	351	420	463	490	484
ENSMUSG00000033732	chr8	Sf3b3	1.11E+08	1.11E+08	4299	0.366375	5.512867	0.035848	0.073879	0.035302	0	540	465	686	681	1016	900	1273	953	1664	1277
ENSMUSG00000081113	chr6	Gm7308	1.27E+08	1.27E+08	447	-0.82728	-0.23855	0.035845	0.073879	0.117193	0	18	14	8	25	16	10	10	8	26	12
ENSMUSG00000047379	chr19	B3gnt1	5038826	5040032	2035	0.327994	4.814064	0.035883	0.07394	0.027324	0	367	348	436	407	527	627	704	773	823	699
ENSMUSG00000063275	chr2	Ptpla	13850282	13851259	2118	-0.42538	7.32318	0.035901	0.073965	0.048703	0	2448	2818	3752	2710	3703	3512	3593	2010	3425	3103
ENSMUSG00000001120	chr10	Pcbp3	76761857	76762526	2933	0.530617	1.658522	0.035914	0.073981	0.057916	0	39	26	51	40	54	52	86	107	88	89
ENSMUSG00000039405	chr7	Prss23	89507785	89510870	3226	-0.45878	6.707324	0.035921	0.073985	0.056508	0	1397	2023	2372	2232	2083	1985	2301	1043	2664	2253
ENSMUSG00000095440	chr15	Fignl2	1.01E+08	1.01E+08	4206	0.717285	1.030971	0.035955	0.074045	0.109092	0	18	9	24	34	39	27	46	47	94	74
ENSMUSG00000022053	chr14	Ebf2	67233292	67233956	6928	-0.46013	3.211148	0.036015	0.074157	0.051507	0	177	103	162	181	279	108	177	205	206	217
ENSMUSG00000036057	chr9	Ptpn23	1.1E+08	1.1E+08	5336	0.350497	3.986807	0.036041	0.0742	0.029844	0	192	186	248	235	306	253	425	383	593	451

ENSMUSG00000031283	chrX	Chrdl1	1.43E+08	1.43E+08	6755	-0.65408	2.819054	0.036059	0.074225	0.106975	0	189	51	147	89	252	78	170	113	159	123
ENSMUSG00000049299	chr11	Trappc1	69323980	69324066	1112	0.367926	5.169606	0.03612	0.074339	0.035252	0	459	552	628	441	517	905	907	831	1127	915
ENSMUSG00000021112	chr12	Mpp5	78748947	78749106	5512	-0.46949	4.585428	0.036187	0.074468	0.057738	0	418	491	566	409	412	280	431	772	459	410
ENSMUSG00000075467	chr2	Dnlz	26348121	26350558	2916	-0.35673	5.04623	0.036199	0.074481	0.033032	0	505	611	733	648	578	615	639	587	787	730
ENSMUSG00000022217	chr14	Emc9	55581516	55581743	2465	0.356355	4.066307	0.036233	0.074538	0.031197	0	225	232	278	218	261	393	382	373	525	502
ENSMUSG00000024052	chr17	Lpin2	71182560	71183257	12233	0.457786	2.749247	0.036284	0.074626	0.048393	0	69	99	109	66	125	128	162	215	207	185
ENSMUSG00000026511	chr1	Srp9	1.82E+08	1.82E+08	5541	0.336783	5.556548	0.036286	0.074626	0.029775	0	595	659	808	665	731	1082	1173	1227	1268	1316
ENSMUSG00000040048	chr17	Ndufb10	24722060	24722520	1217	0.413704	7.985533	0.036297	0.074638	0.046404	0	2696	4029	3788	4158	3270	7030	6250	5328	8037	6724
ENSMUSG00000003200	chr17	Sh3gl1	56016753	56017736	2072	0.423068	4.300263	0.036342	0.074718	0.045982	0	270	196	272	220	463	322	664	424	706	555
ENSMUSG00000034271	chr12	Jdp2	85599105	85599227	1881	0.546623	2.988271	0.036381	0.074788	0.073554	0	119	81	95	86	150	175	357	138	231	181
ENSMUSG00000068882	chr2	Ssb	69861562	69861739	2160	0.337756	5.90922	0.03639	0.074795	0.030243	0	812	796	1077	732	1016	1284	1668	1498	1803	1562
ENSMUSG00000057506	chr19	Bloc1s2	44139266	44139713	878	0.412189	3.283194	0.036427	0.074861	0.040138	0	117	153	161	116	137	237	261	206	301	271
ENSMUSG00000038354	chr3	Ankrd35	96670131	96670449	3688	0.617481	1.407833	0.036484	0.074967	0.083006	0	17	23	32	37	63	53	68	91	67	78
ENSMUSG00000043059	chr5	Zfp513	31198981	31200147	2476	0.42708	3.030537	0.036497	0.07497	0.042666	0	104	84	165	96	131	155	207	186	268	273
ENSMUSG00000058291	chr5	Zfp68	1.39E+08	1.39E+08	3834	-0.41209	4.436675	0.036495	0.07497	0.04383	0	391	302	440	444	489	306	433	648	433	338
ENSMUSG00000020708	chr11	Psmc5	1.06E+08	1.06E+08	1394	0.369726	7.473662	0.036526	0.075019	0.037069	0	2194	2478	3172	2319	2779	4070	4080	5717	4652	4615
ENSMUSG00000026309	chr1	Ilkap	91373861	91375538	5556	0.337848	5.14234	0.036577	0.075112	0.02969	0	415	475	671	502	543	708	1035	965	964	911
ENSMUSG00000037936	chr5	Scarb1	1.25E+08	1.25E+08	6291	0.377759	5.490705	0.036585	0.075117	0.037801	0	425	572	721	825	742	813	1030	1071	1635	1466
ENSMUSG00000037519	chr7	Ppfia1	1.44E+08	1.44E+08	10105	-0.35299	4.676232	0.03665	0.07524	0.032149	0	439	420	494	512	514	332	511	659	581	551
ENSMUSG00000063952	chr17	Brpf3	28801090	28801361	7194	-0.44784	3.980774	0.036659	0.075248	0.051404	0	251	211	346	280	457	165	254	469	346	338
ENSMUSG00000025421	chr18	Hdhd2	76930126	76930216	4822	-0.36317	5.778852	0.036677	0.075273	0.035127	0	821	1016	1173	1095	1028	1032	1277	899	1332	1032
ENSMUSG00000070729	chr4	Gm12966	1.3E+08	1.3E+08	810	0.668228	0.605888	0.036694	0.075286	0.080323	0	15	13	25	21	17	39	33	24	49	56
ENSMUSG00000078570	chr4	1110065P20Rik	1.25E+08	1.25E+08	2069	0.369662	3.622833	0.036689	0.075286	0.032731	0	146	179	219	177	164	277	346	295	364	319
ENSMUSG00000008136	chr1	Fhl2	43123074	43123665	1897	0.782474	1.878719	0.036709	0.075306	0.147164	0	10	65	41	43	60	82	152	52	144	100
ENSMUSG00000041319	chr17	Thoc6	23668614	23668886	2026	0.395848	3.573871	0.036756	0.07539	0.03815	0	143	155	210	162	182	274	349	204	419	325
ENSMUSG00000022335	chr15	Zfat	68083766	68084561	7321	-0.51818	1.716139	0.036762	0.075391	0.056405	0	57	46	59	62	95	46	68	45	83	69
ENSMUSG00000034274	chr11	Thoc5	4895320	4895378	2861	0.354977	4.051232	0.036981	0.075811	0.031489	0	183	197	287	226	332	371	451	335	598	416
ENSMUSG00000035212	chr4	Leprot	1.02E+08	1.02E+08	1898	0.3474	4.694958	0.036983	0.075811	0.030996	0	351	291	459	348	461	463	796	580	960	631
ENSMUSG00000066151	chr4	Fkbp15	62300342	62300990	7515	0.333066	4.362026	0.036982	0.075811	0.027852	0	231	251	372	302	373	378	490	508	734	590
ENSMUSG00000026150	chr1	Mff	82724890	82725084	9757	-0.36716	6.695724	0.037023	0.075882	0.036526	0	1714	1889	2257	1883	1950	1848	2054	2549	2146	1858
ENSMUSG00000056749	chr13	Nfil3	52967209	52969021	2026	-0.41745	4.380738	0.037053	0.075932	0.045215	0	226	450	452	448	406	361	439	427	537	312
ENSMUSG00000010362	chr11	Rdm1	1.02E+08	1.02E+08	1575	-0.38627	3.804731	0.037092	0.07599	0.036877	0	240	239	328	233	273	270	231	316	273	295
ENSMUSG00000032002	chr9	Dcun1d5	7184566	7184882	1201	-0.36466	5.354324	0.037101	0.07599	0.035232	0	646	791	946	704	728	742	807	936	846	793
ENSMUSG00000036299	chr18	BC031181	75005900	75006114	1047	0.409213	4.743732	0.037094	0.07599	0.043972	0	269	373	460	394	427	656	717	426	865	881
ENSMUSG00000038418	chr18	Egr1	34859823	34861786	4484	0.814287	4.286055	0.037114	0.07599	0.176562	0	103	97	179	544	278	306	1156	501	612	349
ENSMUSG00000085241	chr4	Snhg3	1.32E+08	1.32E+08	986	0.577376	2.891497	0.037112	0.07599	0.082387	0	72	119	127	81	86	142	152	351	189	182
ENSMUSG00000101645	chr2	Gm28635	84601439	84602903	4734	-0.35127	6.001954	0.037113	0.07599	0.033144	0	971	929	1286	1219	1672	917	1537	1170	1834	1213
ENSMUSG00000015757	chr10	Ppil4	7792891	7793020	6450	-0.35012	3.781692	0.037128	0.076008	0.030018	0	247	202	271	242	323	180	333	284	341	282
ENSMUSG00000030317	chr6	Timp4	1.15E+08	1.15E+08	1416	-0.52716	4.343489	0.037183	0.076106	0.073567	0	389	382	509	485	186	313	328	508	441	341
ENSMUSG00000033852	chr2	Gm28042	1.2E+08	1.2E+08	5188	0.464543	2.459883	0.037187	0.076106	0.048201	0	66	84	92	54	80	114	145	141	165	165
ENSMUSG00000001663	chr10	Gstt1	75783813	75784233	1528	0.510956	2.663496	0.037203	0.076128	0.063106	0	90	49	78	69	150	153	153	181	178	181
ENSMUSG00000040752	chr14	Myh6	54941921	54942001	6407	0.746397	1.505286	0.03721	0.076131	0.127283	0	33	24	29	55	26	39	93	117	119	39
ENSMUSG00000029163	chr5	Emilin1	30913402	30914044	4938	0.573218	5.225175	0.03725	0.076195	0.088616	0	416	252	496	436	1001	752	1388	497	1593	1086
ENSMUSG00000029208	chr5	Guf1	69556924	69557165	9114	-0.3526	4.503814	0.037253	0.076195	0.031906	0	355	436	506	420	384	394	479	472	515	449
ENSMUSG00000032221	chr9	Mns1	72438011	72438114	2537	0.777619	0.291513	0.037304	0.076288	0.114963	0	9	8	6	21	25	30	34	19	47	34
ENSMUSG00000020857	chr11	Nme2	93949814	93950046	1171	0.37609	8.216275	0.037332	0.076335	0.038807	0	3387	4770	5268	4129	3867	7141	7541	7676	8892	7679
ENSMUSG00000027300	chr2	Ubox5	1.31E+08	1.31E+08	5585	-0.37324	3.637021	0.03737	0.076401	0.034087	0	207	185	288	255	232	194	234	313	305	215
ENSMUSG00000024290	chr18	Rock1	10064401	10066051	6187	-0.3645	4.194764	0.037391	0.076422	0.033945	0	307	266	370	347	437	206	428	430	496	339
ENSMUSG00000034435	chr12	Tmem30b	73543114	73546395	3282	0.718605	0.713006	0.037391	0.076422	0.105835	0	16	10	28	16	28	34	78	38	41	29
ENSMUSG00000034006	chr18	Pqlc1	80253292	80253393	6100	0.353244	4.551396	0.037398	0.076425	0.032132	0	283	312	304	319	506	523	539	612	758	625
ENSMUSG00000021701	chr13	Plk2	1.1E+08	1.1E+08	2802	0.41135	3.960092	0.037464	0.07654	0.042862	0	145	220	240	276	227	262	445	305	621	475
ENSMUSG00000091144	chr14	Phf11c	59380833	59381147	3459	0.767861	0.026162	0.037466	0.07654	0.099413	0	7	12	11	12	14	31	18	24	19	38
ENSMUSG00000024194	chr17	Cuta	26937973	26938176	649	0.368033	5.426611	0.037483	0.076565	0.036142	0	537	574	689	624	703	1161	1014	847	1310	1244
ENSMUSG00000093593	chr17	Gm20683	25834465	25835197	2790	-0.41462	6.379996	0.037543	0.076676	0.046812	0	1226	1796	1866	1671	1279	1614	1440	1354	2197	1695
ENSMUSG00000050855	chr7	Zfp940	29833620	29835803	6090	-0.77059	-0.22577	0.03758	0.076741	0.099013	0	16	15	23	17	10	9	18	8	24	9
ENSMUSG00000020150	chr10	Gamt	80258151	80258457	1444	0.455726	5.833455	0.037614	0.076798	0.056432	0	482	728	1017	747	1116	1619	1626	866	1807	1673
ENSMUSG00000026740	chr2	Dnajc1	18195654	18195921	11651	-0.34964	4.190211	0.037713	0.076989	0.031033	0	359	276	354	300	409	261	382	440	441	354
ENSMUSG00000005506	chr2	Celf1	90940382	90940641	8446	-0.32902	6.383156	0.037748	0.077048	0.029352	0	1191	1383	1769	1437	2059	1347	1777	1680	1987	1857
ENSMUSG00000030166	chr6	Rad52	1.2E+08	1.2E+08	3371	0.452243	2.643776	0.03776	0.077051	0.047175	0	63	89	104	84	93	127	172	212	177	138
ENSMUSG00000079418	chrX	Atg4a	1.41E+08	1.41E+08	2661	-0.35592	4.593462	0.037759	0.077051	0.032861	0	409	435	561	423	413	407	506	556	508	473
ENSMUSG00000041837	chr9	Pdcd7	65346068	65347008	2454	0.378675	3.561959	0.037884	0.077291	0.03511	0	134	147	208	187	176	262	275	384	342	273
ENSMUSG00000013701	chr14	Timm23	32180162	32180670	1786	-0.36221	6.702842	0.037905	0.077323	0.035887	0	1699	2003	2123	2021	1831	1896	2035	2343	2364	1919
ENSMUSG00000021281	chr12	Tnfaip2	1.11E+08	1.11E+08	4984	-0.56135	6.962652	0.037914	0.077331	0.086472	0	1690	1991	2707	2208	4146	1975	2909	839	3682	2538
ENSMUSG00000020611	chr11	Gna13	1.09E+08	1.09E+08	6421	0.363135	5.190567	0.037971	0.077435	0.035048	0	425	489	522	545	691	599	851	1247	1183	963
ENSMUSG00000029066	chr4	Mrpl20	1.56E+08	1.56E+08	1664	0.360299	5.119653	0.037978	0.077439	0.034368	0	447	538	596	436	496	786	804	950	977	1003
ENSMUSG00000017485	chr14	Top2b	16365179	16365726	6355	-0.39069	5.79613	0.038	0.07746	0.041389	0	887	859	1139	964	1471	734	1208	1577	1187	923

ENSMUSG00000027635	chr2	Dsn1	1.57E+08	1.57E+08	3354	0.535459	1.109092	0.037999	0.07746	0.052424	0	22	19	34	28	38	42	60	60	63	58
ENSMUSG00000046962	chr16	Zbtb21	97947435	97950869	6010	-0.45989	2.374377	0.038061	0.077574	0.04839	0	80	79	107	108	124	64	135	77	128	105
ENSMUSG00000029161	chr5	Cgref1	30933146	30933988	1328	0.675861	2.947157	0.038068	0.077576	0.11801	0	126	43	117	38	175	177	308	201	200	195
ENSMUSG00000026675	chr1	Hsd17b7	1.7E+08	1.7E+08	5104	-0.48873	2.357195	0.038081	0.077592	0.05532	0	71	74	91	110	155	61	81	113	140	104
ENSMUSG00000057858	chr19	Fam204a	60198586	60199487	2035	-0.36048	3.568361	0.038285	0.077985	0.031758	0	205	171	274	230	229	168	238	288	289	230
ENSMUSG00000099200	chr4	Mir7019	1.38E+08	1.38E+08	69	-0.53558	2.736646	0.03828	0.077985	0.07079	0	124	102	161	138	126	96	98	210	102	115
ENSMUSG00000021109	chr12	Hif1a	73901375	73901498	5896	-0.39604	4.801903	0.038313	0.078029	0.041809	0	410	372	514	527	879	322	610	528	816	599
ENSMUSG00000020038	chr10	Cry1	85131702	85132307	3014	-0.4286	3.299398	0.038365	0.078113	0.04531	0	164	149	191	196	242	141	164	289	222	158
ENSMUSG00000051323	chrX	Pcdh19	1.34E+08	1.34E+08	10464	-0.4756	2.742091	0.038362	0.078113	0.05534	0	96	89	147	158	162	77	158	103	212	114
ENSMUSG00000003518	chr11	Dusp3	1.02E+08	1.02E+08	4682	-0.39501	7.507768	0.038378	0.078127	0.04316	0	2688	3116	4167	3443	3945	3601	4168	2280	4538	3651
ENSMUSG00000024561	chr18	Mbd1	74268272	74268433	2689	-0.3568	3.741286	0.038387	0.078135	0.03151	0	214	215	285	249	288	187	280	349	297	253
ENSMUSG00000022672	chr16	Prkdc	15637866	15638042	13187	-0.39209	3.235337	0.038521	0.078397	0.036953	0	160	146	228	142	216	156	203	154	209	220
ENSMUSG00000051615	chr14	Rap2a	1.2E+08	1.2E+08	4174	0.402357	3.917947	0.038553	0.078448	0.04134	0	184	174	231	207	294	222	447	288	604	491
ENSMUSG00000030802	chr7	Bckdk	1.28E+08	1.28E+08	3063	-0.36476	7.193101	0.038559	0.078451	0.036791	0	2304	2587	3118	3080	2585	2702	2626	3377	3256	2832
ENSMUSG00000026198	chr1	Abcb6	75171717	75171988	5315	-0.32942	5.059051	0.038573	0.078468	0.028683	0	521	552	739	624	661	580	626	760	760	701
ENSMUSG00000022091	chr14	Sorbs3	70180468	70181231	2914	0.582413	5.182943	0.038728	0.07877	0.092573	0	562	341	431	586	471	527	766	2022	1011	779
ENSMUSG00000053870	chr3	Fpgt	1.55E+08	1.55E+08	6282	-0.44577	2.431972	0.038769	0.078842	0.045331	0	83	79	101	117	137	72	101	128	137	93
ENSMUSG00000073702	chr1	Rpl31	39367842	39367934	1662	0.338452	7.236663	0.038841	0.078978	0.031742	0	1900	2172	2600	1946	2490	3463	4045	3501	4482	4072
ENSMUSG00000066607	chr9	6030419C18Rik	58488603	58489239	2139	-0.37887	3.40371	0.038869	0.079023	0.035008	0	174	156	212	225	228	164	238	255	237	172
ENSMUSG00000021550	chr13	2210016F16Rik	58380046	58382009	2822	0.420668	4.272137	0.038929	0.079132	0.046559	0	223	272	318	261	296	467	446	295	736	638
ENSMUSG00000073910	chr4	Mob3b	34949074	34954047	6200	0.686218	1.018661	0.038988	0.07924	0.098802	0	31	11	17	28	35	30	53	43	81	74
ENSMUSG00000050552	chr5	Lamtor4	1.38E+08	1.38E+08	1176	0.381667	5.449462	0.039061	0.079377	0.039578	0	541	681	775	513	630	1132	1121	928	1250	1257
ENSMUSG00000044139	chr7	Prss53	1.28E+08	1.28E+08	2134	-0.68924	1.095243	0.039218	0.079685	0.105411	0	50	27	58	34	44	30	39	17	37	61
ENSMUSG00000036377	chr5	C530008M17Rik	76656512	76658355	12305	-0.68006	1.149946	0.039232	0.079703	0.103845	0	48	31	43	56	41	16	31	68	41	39
ENSMUSG00000018900	chr11	Slc22a5	53864542	53865896	3071	-0.37156	3.436511	0.039256	0.079728	0.034121	0	152	174	227	227	240	126	219	247	276	244
ENSMUSG00000060989	chr4	Gm11847	12232833	12233951	1119	1.234411	-0.24242	0.039256	0.079728	0.300704	0	17	3	3	6	5	10	7	45	49	12
ENSMUSG00000020061	chr10	Mybpc1	88518279	88518569	4527	0.51487	10.81581	0.039268	0.079739	0.07423	0	26953	17179	24984	26584	27955	27889	50527	85405	57423	29151
ENSMUSG00000021785	chr14	Ngly1	16249280	16249497	5274	-0.42203	5.550303	0.03928	0.079741	0.048882	0	732	799	1061	883	1018	615	810	1513	860	862
ENSMUSG00000035783	chr19	Acta2	34241090	34241810	1781	0.650026	7.46927	0.039276	0.079741	0.117472	0	1152	1777	2194	2486	4335	3880	8643	1757	6597	4659
ENSMUSG00000094568	chr8	Gm1815	41657593	41658669	1077	0.625146	0.842016	0.039293	0.079755	0.076435	0	11	28	21	24	26	38	50	59	44	45
ENSMUSG00000030752	chr7	Kdm8	1.25E+08	1.25E+08	2385	-0.42432	2.847067	0.039307	0.079773	0.042542	0	93	126	168	139	161	138	155	123	152	134
ENSMUSG00000027204	chr2	Fbn1	1.25E+08	1.25E+08	12128	-0.56699	7.646419	0.03933	0.079794	0.089671	0	3410	2014	3883	3559	7861	2754	5302	1831	5550	3762
ENSMUSG00000036854	chr7	Hspb6	30552178	30553062	2299	0.397631	9.369847	0.039335	0.079794	0.044397	0	8410	7923	11004	11282	8911	16143	19367	11850	25502	15365
ENSMUSG00000053819	chr3	Camk2d	1.27E+08	1.27E+08	15928	-0.34167	6.283158	0.039329	0.079794	0.032155	0	1120	1285	1769	1346	1817	1438	1613	1303	1910	1724
ENSMUSG00000073987	chr4	Ggh	20042052	20042282	1965	0.42763	3.203671	0.039403	0.079921	0.045329	0	109	119	168	101	155	185	282	157	333	276
ENSMUSG00000031447	chr8	Lamp1	13159135	13159434	2255	0.320697	9.026191	0.039553	0.080213	0.028945	0	7026	6771	8851	7659	8371	10724	12128	14131	16311	14485
ENSMUSG00000031790	chr8	Mmp15	95352268	95353018	4348	-0.39711	5.282634	0.039574	0.080243	0.04311	0	525	664	759	899	859	614	1023	523	1095	705
ENSMUSG00000010914	chr2	Pdhx	1.03E+08	1.03E+08	3930	-0.37946	6.707399	0.039639	0.080356	0.040148	0	1501	2204	2194	2177	1664	1804	1995	2215	2466	2090
ENSMUSG00000032735	chr18	Ablim3	61799395	61801408	4560	0.443286	4.866061	0.039641	0.080356	0.053282	0	309	402	437	571	315	480	1112	726	894	743
ENSMUSG00000073639	chr18	Rab18	6765205	6765332	2257	-0.37401	6.500903	0.039685	0.080433	0.038931	0	1605	1507	1928	1525	1963	1315	1767	2569	1976	1584
ENSMUSG00000046410	chr7	Kcnk6	29221928	29225259	4089	0.552704	2.562212	0.039783	0.08062	0.07605	0	75	46	81	70	127	114	158	87	266	198
ENSMUSG00000028049	chr3	Scamp3	89177473	89177657	2270	0.337832	5.213348	0.039828	0.0807	0.030831	0	449	489	621	527	656	811	914	750	1215	1147
ENSMUSG00000078622	chr11	Ccdc47	1.06E+08	1.06E+08	6414	-0.41373	6.89043	0.039846	0.080724	0.047919	0	1966	1994	2660	2081	2653	1721	2167	3703	2241	1978
ENSMUSG00000034640	chr3	Tiparp	65528410	65528632	4358	-0.34873	3.820616	0.039865	0.080751	0.030732	0	261	205	338	245	266	206	274	315	342	315
ENSMUSG00000023034	chr15	Nr4a1	1.01E+08	1.01E+08	2474	-0.51977	6.531447	0.039874	0.080758	0.0755	0	1201	1825	2216	2478	1313	2017	1876	994	1927	1871
ENSMUSG00000000561	chr3	Wdr77	1.06E+08	1.06E+08	6644	0.335753	5.354712	0.03989	0.080778	0.03063	0	459	579	731	554	706	909	993	1210	1149	1023
ENSMUSG00000022558	chr15	Mroh1	76380261	76380342	16533	0.378733	4.219161	0.039896	0.080778	0.037346	0	210	279	277	297	273	306	407	616	598	546
ENSMUSG00000038576	chr1	Susd4	1.83E+08	1.83E+08	3858	-0.7547	-0.02739	0.039931	0.080827	0.086776	0	11	14	25	21	25	21	13	16	12	14
ENSMUSG00000099632	chr2	2900093K20Rik	1.63E+08	1.63E+08	567	0.865495	0.23657	0.039932	0.080827	0.148981	0	9	16	11	15	11	28	24	65	22	18
ENSMUSG00000029432	chr5	Gbas	1.3E+08	1.3E+08	2750	-0.37972	8.971478	0.039952	0.080857	0.040731	0	8145	9313	10270	10289	8980	8783	8961	13272	10886	8609
ENSMUSG00000030315	chr6	Vgll4	1.15E+08	1.15E+08	4133	-0.38999	3.751203	0.03998	0.080888	0.039383	0	214	192	223	291	361	150	290	272	396	279
ENSMUSG00000038612	chr3	Mcl1	95658721	95659487	3485	0.341184	7.621157	0.039985	0.080888	0.032724	0	2425	2710	3324	3136	2851	4342	4639	5526	5715	5350
ENSMUSG00000076060	chr6	Mir704	47803576	47803652	77	0.728858	1.128581	0.039978	0.080888	0.119077	0	19	25	28	13	47	50	72	24	88	70
ENSMUSG00000054555	chr7	Adam12	1.34E+08	1.34E+08	8273	0.880721	3.145942	0.039998	0.080902	0.209141	0	83	42	134	56	224	144	363	50	394	409
ENSMUSG00000012429	chr13	Mplkip	17695413	17695820	2672	0.510403	2.028546	0.040016	0.080926	0.058898	0	48	45	51	65	64	67	119	150	110	100
ENSMUSG00000020115	chr10	Tbk1	1.22E+08	1.22E+08	3031	0.450403	3.937808	0.040096	0.081077	0.053544	0	206	196	236	196	235	252	390	682	414	319
ENSMUSG00000042705	chr18	Commd10	46958862	46958928	1561	0.485362	2.871895	0.040113	0.081098	0.058938	0	76	71	118	118	125	162	208	105	289	229
ENSMUSG00000024472	chr18	Dcp2	44380500	44380686	8643	-0.35723	4.129561	0.04012	0.081101	0.033003	0	264	274	344	344	421	316	326	269	431	440
ENSMUSG00000017679	chr2	Ttpal	1.64E+08	1.64E+08	5951	0.378763	3.277631	0.040127	0.081104	0.034695	0	128	102	172	125	176	170	282	215	331	285
ENSMUSG00000052748	chr1	Swt1	1.51E+08	1.51E+08	12865	-0.43052	2.335073	0.040246	0.081332	0.042138	0	94	79	102	92	109	62	94	112	132	101
ENSMUSG00000030103	chr6	Bhlhe40	1.09E+08	1.09E+08	3272	-0.44488	6.543971	0.040252	0.081333	0.055552	0	1741	1435	1424	2610	1649	1658	1600	1346	2356	2264
ENSMUSG00000030649	chr7	Anapc15	1.02E+08	1.02E+08	4737	0.382063	3.642295	0.04026	0.081337	0.03686	0	139	185	212	176	183	295	318	236	418	368
ENSMUSG00000020024	chr10	Cep83	94688790	94689046	2986	-0.41492	3.593089	0.040285	0.081375	0.044692	0	171	227	276	252	216	130	239	326	267	253
ENSMUSG00000051730	chr2	Mettl5	69871198	69871316	2437	-0.41586	3.2305	0.040291	0.081375	0.043017	0	165	179	196	169	171	186	178	136	218	205
ENSMUSG00000055694	chr8	Gdf1	70329817	70330276	1349	-0.41886	3.860678	0.040361	0.081505	0.045824	0	237	215	339	276	325	295	312	160	356	310
ENSMUSG00000041135	chr4	Ripk2	16122733	16123891	2816	0.513026	1.944539	0.04042	0.081612	0.059301	0	59	42	57	44	53	81	91	75	146	125

ENSMUSG00000018678	chr11	Sp2	96953340	96954570	3415	-0.35842	3.629008	0.040435	0.081619	0.032186	0	189	152	273	273	282	180	241	261	335	255
ENSMUSG00000056673	chrY	Kdm5d	897788	898115	15164	-1.71227	3.257588	0.040431	0.081619	0.759227	0	246	182	265	235	296	103	209	1	219	1
ENSMUSG00000005125	chr15	Ndrg1	66929321	66931108	6593	0.392926	4.855778	0.040478	0.081692	0.041942	0	366	317	433	518	452	472	677	1082	950	690
ENSMUSG00000051098	chr13	Mblac2	81711417	81711982	3881	-0.61353	0.635212	0.040483	0.081692	0.070528	0	26	19	39	27	40	12	24	29	41	33
ENSMUSG00000025479	chr7	Cyp2e1	1.41E+08	1.41E+08	1827	1.227409	4.866287	0.040682	0.082082	0.408999	0	354	123	104	317	572	42	367	659	1904	2159
ENSMUSG00000020053	chr10	Igf1	87858265	87859013	9904	-0.48019	6.183195	0.040718	0.082142	0.064844	0	948	1019	1541	1110	2708	1035	1836	871	1935	1502
ENSMUSG00000035245	chr6	Eogt	97110024	97112206	4900	-0.4194	2.915825	0.040735	0.082165	0.043126	0	133	108	175	161	137	103	193	130	189	139
ENSMUSG00000022099	chr14	Dmtn	70602184	70604854	4629	0.868342	1.416121	0.040742	0.082168	0.18487	0	30	21	24	34	41	33	58	25	102	177
ENSMUSG00000025156	chr11	Gps1	1.21E+08	1.21E+08	2879	-0.31469	5.393124	0.040751	0.082172	0.027003	0	666	646	942	771	878	745	906	782	1075	859
ENSMUSG00000034586	chr11	Hid1	1.15E+08	1.15E+08	4595	0.553841	1.494607	0.040768	0.082196	0.064817	0	26	29	36	55	37	49	75	93	88	73
ENSMUSG00000007987	chr5	Ift22	1.37E+08	1.37E+08	911	0.469389	2.030353	0.040787	0.082221	0.047903	0	44	53	69	50	63	66	122	98	143	118
ENSMUSG00000028344	chr4	Invs	48279760	48279975	11431	-0.57869	1.704814	0.040818	0.082268	0.078026	0	76	46	59	48	90	56	75	35	70	61
ENSMUSG00000050010	chr5	Shisa3	67607883	67608684	4753	-0.65037	1.362317	0.040822	0.082268	0.0998	0	56	55	62	35	43	38	52	55	63	20
ENSMUSG00000033033	chr19	Calhm2	47105353	47107208	4361	0.528267	2.220809	0.040859	0.082331	0.068368	0	62	31	62	58	104	117	139	99	164	107
ENSMUSG00000021763	chr13	BC067074	1.13E+08	1.13E+08	8410	0.637251	1.993492	0.040893	0.082375	0.099196	0	63	25	39	46	81	52	133	154	123	95
ENSMUSG00000092686	chr10	Gm25745	86705316	86705448	133	-0.52885	2.849842	0.040891	0.082375	0.071573	0	84	98	176	117	255	74	190	112	186	135
ENSMUSG00000026526	chr1	Fh1	1.76E+08	1.76E+08	3392	-0.37086	8.050741	0.040973	0.082523	0.039156	0	3955	5418	5242	5496	4573	4971	4804	5780	6089	5120
ENSMUSG00000090952	chr17	Gm17251	33759992	33760587	925	0.719966	2.345498	0.040989	0.082544	0.133993	0	55	59	71	54	74	89	78	328	107	112
ENSMUSG00000028082	chr3	Sh3d19	85971109	85971424	8888	-0.39523	4.340176	0.041012	0.082579	0.041877	0	382	218	450	336	564	301	435	493	444	364
ENSMUSG00000074874	chr13	Ctla2b	60895351	60896143	1147	0.655848	1.372571	0.041027	0.082597	0.099163	0	17	38	54	24	28	70	74	45	72	88
ENSMUSG00000058135	chr3	Gstm1	1.08E+08	1.08E+08	1394	0.433644	6.987686	0.041041	0.082613	0.053335	0	1689	1238	1739	1984	2442	2528	2356	4987	3301	3765
ENSMUSG00000005763	chr1	Cd247	1.66E+08	1.66E+08	5329	-0.81448	0.468293	0.041111	0.082742	0.143119	0	13	41	29	39	15	13	16	21	24	38
ENSMUSG00000017615	chr11	Tnfaip1	78522850	78525541	3781	-0.336	6.032733	0.041145	0.082792	0.031563	0	1016	1106	1265	1308	1401	1188	1445	1084	1734	1305
ENSMUSG00000022913	chr16	Psmg1	95979933	95980111	1344	0.446856	3.153858	0.041148	0.082792	0.051074	0	99	125	160	102	136	230	232	156	257	297
ENSMUSG00000082922	chr7	Gm6939	1.27E+08	1.27E+08	864	0.622386	0.727444	0.041193	0.082872	0.071377	0	22	20	24	10	25	39	36	42	55	46
ENSMUSG00000046556	chr8	Zfp319	95326137	95329812	4106	-0.44217	2.781656	0.041328	0.08313	0.048248	0	90	96	154	150	176	75	170	136	172	132
ENSMUSG00000045671	chr11	Spred2	19924375	19924956	4619	-0.35829	3.637625	0.04134	0.083143	0.032551	0	178	167	247	269	317	181	254	249	362	238
ENSMUSG00000028636	chr4	Ppcs	1.19E+08	1.19E+08	1605	0.421496	2.503054	0.041367	0.083185	0.040125	0	79	67	81	88	79	119	149	139	184	154
ENSMUSG00000063902	chr7	Gm7964	83755904	83756233	1392	0.344902	3.70363	0.041399	0.083237	0.029927	0	182	139	205	191	239	238	373	376	383	326
ENSMUSG00000089781	chr6	Gm15756	90596685	90597034	682	-0.86385	1.927497	0.041426	0.083279	0.192682	0	73	73	97	77	83	83	72	6	85	58
ENSMUSG00000025153	chr11	Fasn	1.21E+08	1.21E+08	9849	1.723077	8.044117	0.041438	0.08329	0.78071	0	848	478	546	4483	4422	501	1358	650	19065	29808
ENSMUSG00000071984	chr17	Fndc1	7738569	7739330	9903	-0.62536	6.459993	0.04146	0.083323	0.110858	0	2027	671	1889	1255	3354	1227	2557	840	2023	1503
ENSMUSG00000032657	chr3	Fam189b	89183143	89183494	3649	-0.32921	3.967642	0.041505	0.083402	0.027645	0	248	235	376	260	341	265	342	279	383	344
ENSMUSG00000024505	chr18	Dtwd2	49696145	49698500	3520	-0.49345	1.987854	0.041583	0.083546	0.055277	0	64	73	86	82	73	81	67	73	79	71
ENSMUSG00000039629	chr6	Strip2	29917013	29917230	8328	-0.72434	0.658838	0.041596	0.083561	0.114031	0	33	18	37	34	35	6	22	43	37	28
ENSMUSG00000086158	chr9	Ccpg1os	72979722	72980196	2404	-0.50353	2.104843	0.04163	0.083616	0.058451	0	72	69	96	91	86	82	86	97	78	58
ENSMUSG00000020638	chr12	Cmpk2	26469204	26470026	3198	0.808166	2.936794	0.041672	0.083688	0.177426	0	61	80	98	116	107	405	129	77	143	284
ENSMUSG00000002948	chr8	Map2k7	4238740	4239033	5359	-0.37278	6.197235	0.04172	0.083772	0.039325	0	1214	1249	1583	1435	1407	1130	1278	2067	1561	1403
ENSMUSG00000032407	chr9	U2surp	95456898	95461543	14642	-0.33763	4.712013	0.04175	0.083822	0.030961	0	482	367	571	466	558	333	564	624	648	560
ENSMUSG00000030615	chr7	Tmem126a	90450700	90450935	1018	-0.40149	5.738909	0.041768	0.083844	0.045404	0	914	1088	1152	921	931	1137	1113	752	1242	1046
ENSMUSG00000005362	chr6	Crbn	1.07E+08	1.07E+08	5179	-0.58389	4.746454	0.041871	0.084039	0.095762	0	546	452	626	533	506	277	362	1071	457	338
ENSMUSG00000022092	chr14	Ppp3cc	70217898	70218277	1948	-0.47106	3.603836	0.041885	0.084055	0.059427	0	210	231	270	272	173	183	193	365	227	206
ENSMUSG00000056144	chr7	Trim34a	1.04E+08	1.04E+08	4255	0.638952	2.064748	0.041891	0.084055	0.103387	0	42	40	73	51	63	133	82	60	103	186
ENSMUSG00000037470	chr1	Uggt1	36140027	36144251	12853	-0.36733	5.956919	0.041906	0.084072	0.038122	0	1099	858	1312	1120	1498	810	1203	1726	1464	1178
ENSMUSG00000007613	chr4	Tgfbr1	47353222	47353396	6534	-0.39721	5.043965	0.04194	0.084128	0.043977	0	568	520	703	535	822	387	689	969	782	530
ENSMUSG00000024795	chr19	Kif20b	34922358	34922433	5563	0.734114	0.913006	0.041945	0.084128	0.117006	0	24	11	29	20	27	25	54	32	114	44
ENSMUSG00000043505	chr6	Gimap5	48746197	48746430	2353	-0.59642	1.046339	0.041971	0.084167	0.075686	0	27	37	48	52	36	18	33	34	54	50
ENSMUSG00000057982	chr9	Zfp809	22225714	22225832	1325	-0.50111	1.399607	0.041981	0.084175	0.051887	0	49	43	45	59	53	40	48	47	61	52
ENSMUSG00000027274	chr2	Mkks	1.37E+08	1.37E+08	3227	-0.41645	5.466781	0.042045	0.084289	0.048804	0	709	948	1051	746	710	943	906	664	918	902
ENSMUSG00000033287	chr15	Kctd17	78428564	78428867	2134	0.441088	3.999768	0.04205	0.084289	0.052719	0	175	159	206	285	315	320	444	241	636	532
ENSMUSG00000072889	chr5	Nfxl1	72513301	72514331	4919	0.445403	2.720337	0.042088	0.084352	0.04812	0	103	69	89	76	121	109	161	200	238	178
ENSMUSG00000031016	chr7	Wee1	1.1E+08	1.1E+08	1941	-0.5167	1.70725	0.042148	0.08445	0.060177	0	58	52	89	42	75	48	51	54	86	70
ENSMUSG00000046818	chr3	Ddit4l	1.38E+08	1.38E+08	2916	-0.48	7.867787	0.042149	0.08445	0.066256	0	4625	3869	3704	4678	5721	3201	3494	7620	3651	4599
ENSMUSG00000031774	chr8	Fam192a	94574943	94575857	1797	0.321143	4.711877	0.042217	0.084574	0.027875	0	306	346	448	387	462	600	587	700	784	698
ENSMUSG00000002428	chr3	Hltf	20057811	20058007	5931	-0.43165	3.040177	0.04225	0.084604	0.047463	0	160	124	203	137	157	120	178	108	220	194
ENSMUSG00000020902	chr11	Ntn1	68209364	68213334	6277	-0.457	4.096086	0.04225	0.084604	0.057123	0	324	157	322	297	591	221	331	391	434	320
ENSMUSG00000027603	chr2	Ggt7	1.55E+08	1.55E+08	3264	0.59233	0.609233	0.042249	0.084604	0.059874	0	17	17	19	17	24	24	40	33	53	51
ENSMUSG00000017221	chr11	Psmd3	98682554	98682937	4967	0.39366	6.836235	0.042288	0.084668	0.044412	0	1312	1464	1867	1798	1823	2255	2524	4530	3110	2668
ENSMUSG00000006717	chr13	Acot13	24817948	24818191	721	-0.3957	5.876133	0.04231	0.0847	0.044409	0	930	1170	1268	1202	928	1253	1113	993	1344	1120
ENSMUSG00000018666	chr11	Cbx1	96789127	96789353	4273	-0.3181	5.041822	0.042336	0.08474	0.027754	0	556	559	708	528	694	537	720	701	754	702
ENSMUSG00000030095	chr6	Tmem43	91473703	91473898	3741	0.343102	5.577979	0.042438	0.084931	0.033034	0	688	542	847	564	894	850	1146	1453	1451	1370
ENSMUSG00000035248	chr13	Zcchc6	59771879	59772859	5551	-0.32497	5.182569	0.042562	0.085167	0.029266	0	613	559	755	666	781	545	689	928	867	742
ENSMUSG00000030603	chr7	Psmc4	28041707	28041920	2169	0.402118	6.667524	0.042585	0.085201	0.046428	0	1225	1285	1736	1455	1628	2072	2182	4120	2616	2416
ENSMUSG00000027706	chr3	Sec62	30792875	30793383	4343	-0.40767	5.947364	0.042673	0.085352	0.047443	0	1014	956	1260	1139	1551	745	1200	1933	1274	1068
ENSMUSG00000034160	chrX	Ogt	1.02E+08	1.02E+08	8045	-0.37109	6.39382	0.042673	0.085352	0.039452	0	1718	1256	1947	1235	1745	1123	1868	1925	1769	1912
ENSMUSG00000026799	chr2	Med27	29346819	29347047	3310	0.348187	3.368982	0.042695	0.085384	0.029607	0	123	141	150	166	170	211	273	270	309	275

ENSMUSG00000061288	chr5	Taok3	1.17E+08	1.17E+08	10952	0.446907	3.269046	0.042726	0.085434	0.05237	0	130	82	134	152	182	165	273	174	343	351
ENSMUSG00000041560	chr7	Gltscr2	15937838	15937889	1555	0.374372	5.949513	0.042794	0.085557	0.039914	0	640	833	1013	1014	1008	1056	1461	2253	1853	1569
ENSMUSG00000049241	chr5	Hcar1	1.24E+08	1.24E+08	3285	1.731398	1.619526	0.042826	0.085608	0.778288	0	16	3	2	36	60	8	29	7	243	278
ENSMUSG00000026095	chr1	Asnsd1	53344617	53344979	3528	-0.34458	6.296183	0.04284	0.085612	0.033937	0	1413	1434	1566	1384	1462	1462	1553	1702	1782	1511
ENSMUSG00000040631	chr8	Dok4	94863828	94865247	2604	-0.43946	3.526181	0.042835	0.085612	0.05176	0	152	230	208	290	213	174	250	149	354	227
ENSMUSG00000050856	chr5	Atp5k	1.08E+08	1.08E+08	616	0.417688	8.003641	0.042858	0.085636	0.050569	0	2642	4272	4347	3766	3119	7408	6440	6482	6962	6210
ENSMUSG00000019433	chr8	Gipc1	83652678	83652737	1615	0.340381	4.395107	0.042892	0.085691	0.03116	0	231	265	345	368	341	446	561	435	766	547
ENSMUSG00000074743	chr2	Thbd	1.48E+08	1.48E+08	3723	-0.39589	4.996393	0.042925	0.085744	0.043932	0	447	434	600	622	991	511	769	460	931	579
ENSMUSG00000092569	chr18	Gm20544	75365332	75365862	690	-0.65179	0.098136	0.042995	0.085873	0.06513	0	22	13	21	23	22	12	16	22	20	20
ENSMUSG00000020739	chr11	Nup85	1.16E+08	1.16E+08	3385	0.329004	4.576144	0.043012	0.085893	0.029273	0	321	304	441	295	403	504	567	539	826	671
ENSMUSG00000036167	chr15	Pphln1	93398350	93398461	4264	-0.31916	3.892131	0.043054	0.085965	0.026157	0	220	231	315	266	350	226	345	288	389	299
ENSMUSG00000085965	chr1	2310016D23Rik	60778843	60778916	388	-0.79947	2.272594	0.043194	0.086232	0.170265	0	68	129	117	93	95	126	57	23	62	118
ENSMUSG00000007655	chr6	Cav1	17306335	17306479	3444	-0.40127	7.572613	0.043211	0.086254	0.046805	0	2765	3473	3935	4662	3123	2341	3735	3171	5400	4937
ENSMUSG00000056966	chr5	Gjc3	1.38E+08	1.38E+08	3515	-0.76836	1.003455	0.043253	0.086324	0.139912	0	36	16	47	53	55	9	41	57	38	25
ENSMUSG00000052560	chr15	Cpne8	90487482	90489175	4164	0.520822	1.875623	0.043292	0.086391	0.062457	0	36	46	52	55	55	48	82	108	146	118
ENSMUSG00000021981	chr14	Cab39l	59440981	59441018	3037	-0.35038	4.244536	0.043315	0.086423	0.033101	0	308	294	464	344	363	310	436	283	460	455
ENSMUSG00000025235	chr9	Bbs4	59321966	59322982	2542	-0.4314	2.641154	0.043361	0.086502	0.045907	0	108	105	143	112	122	95	120	163	125	107
ENSMUSG00000024772	chr19	Ehd1	6276725	6277378	3705	0.359071	5.519921	0.043395	0.086545	0.036617	0	477	547	752	733	889	874	1286	845	1643	1444
ENSMUSG00000026778	chr2	Prkcq	11172108	11172460	7081	-0.37433	5.924082	0.043392	0.086545	0.040118	0	1020	964	1101	1293	1337	1061	1113	1649	1222	1055
ENSMUSG00000027495	chr2	Fam210b	1.72E+08	1.72E+08	3617	-0.33653	3.485988	0.043402	0.086549	0.028364	0	167	193	231	215	232	190	212	235	286	227
ENSMUSG00000028274	chr4	Rngtt	33310311	33310524	7094	-0.43671	3.50351	0.043414	0.086558	0.050781	0	169	187	215	257	258	220	255	121	296	223
ENSMUSG00000027163	chr2	Commd9	1.02E+08	1.02E+08	1602	0.330797	4.696322	0.043432	0.086582	0.029944	0	338	358	477	339	395	591	617	676	730	722
ENSMUSG00000034591	chr10	Slc41a2	83230848	83233750	5349	0.667542	2.018045	0.043555	0.086815	0.116108	0	48	24	66	38	84	60	168	52	171	128
ENSMUSG00000031379	chrX	Pir	1.64E+08	1.64E+08	5553	0.776275	1.938062	0.043576	0.086845	0.158558	0	51	42	53	34	46	69	68	258	80	66
ENSMUSG00000039050	chr2	Osbpl2	1.8E+08	1.8E+08	4187	-0.33015	4.510432	0.043664	0.087007	0.029819	0	405	383	434	426	452	324	494	562	539	444
ENSMUSG00000029096	chr5	Htra3	35652041	35653122	3860	0.408775	6.189583	0.043691	0.087049	0.048321	0	1088	632	1007	938	1644	1381	1779	2402	1957	2188
ENSMUSG00000022812	chr16	Gsk3b	38089001	38090613	9831	-0.48115	5.951321	0.043795	0.087244	0.067014	0	1073	990	1228	1347	1381	693	971	2210	1266	922
ENSMUSG00000001910	chr8	Nacc1	84670483	84673304	4300	-0.33576	5.473672	0.04383	0.087275	0.031949	0	569	690	966	875	1099	741	955	773	1301	854
ENSMUSG00000032000	chr9	Birc3	7848699	7849456	5009	0.416336	2.806349	0.043828	0.087275	0.042497	0	88	79	91	109	127	123	199	152	225	230
ENSMUSG00000039246	chr1	Lyplal1	1.86E+08	1.86E+08	1578	0.593337	1.119076	0.043822	0.087275	0.075358	0	23	16	28	28	44	28	74	49	78	66
ENSMUSG00000048482	chr2	Bdnf	1.1E+08	1.1E+08	6217	0.863734	0.277656	0.043839	0.08728	0.167151	0	5	11	8	13	29	16	24	47	66	17
ENSMUSG00000034343	chr1	Ube2f	91250304	91250437	8842	-0.33317	6.136141	0.04385	0.087291	0.031883	0	1045	1207	1643	1186	1496	1334	1492	1306	1681	1401
ENSMUSG00000005803	chr2	Sqrdl	1.23E+08	1.23E+08	4084	-0.38559	4.952025	0.043901	0.087379	0.042005	0	481	588	726	581	528	528	452	599	700	839
ENSMUSG00000099143	chr7	Gm27483	1.43E+08	1.43E+08	71	1.27722	1.133112	0.043908	0.087381	0.423689	0	5	24	13	35	21	17	20	18	267	56
ENSMUSG00000028194	chr3	Ddah1	1.46E+08	1.46E+08	3983	0.455612	3.597685	0.044014	0.087579	0.056179	0	149	143	138	219	192	300	404	192	461	268
ENSMUSG00000041408	chr14	Wapal	34673928	34674360	6623	-0.42777	5.646463	0.04405	0.087638	0.052783	0	828	823	1037	962	1160	637	826	1692	996	836
ENSMUSG00000017176	chr11	Nt5c3b	1E+08	1E+08	3420	0.359255	3.200139	0.044069	0.087662	0.031672	0	123	118	136	134	152	182	258	203	312	246
ENSMUSG00000036751	chr7	Cox6b1	30616974	30617162	505	0.381925	8.728082	0.044079	0.08767	0.042865	0	4874	6855	6788	6665	5139	10709	10240	11544	12444	10446
ENSMUSG00000055148	chr8	Klf2	72319033	72319149	1847	0.470863	3.980864	0.044149	0.087797	0.061815	0	144	135	198	399	231	328	434	425	460	479
ENSMUSG00000027284	chr2	Cdan1	1.21E+08	1.21E+08	11421	-0.35127	3.463543	0.044166	0.087819	0.03144	0	195	147	227	198	267	172	234	249	272	201
ENSMUSG00000040867	chr12	Begain	1.09E+08	1.09E+08	3751	0.827988	0.063558	0.044207	0.087888	0.133711	0	10	7	10	14	15	25	37	6	43	29
ENSMUSG00000061330	chr13	Gm11361	28257636	28258094	459	0.683751	0.090077	0.044214	0.087889	0.077722	0	8	12	8	15	18	20	39	23	28	27
ENSMUSG00000048782	chr7	Insc	1.15E+08	1.15E+08	3717	-0.82115	1.147776	0.044285	0.088016	0.166313	0	70	18	45	28	69	32	64	19	45	21
ENSMUSG00000030275	chr6	Etnk1	1.43E+08	1.43E+08	6429	-0.31835	5.23647	0.044354	0.088142	0.028519	0	646	525	803	712	820	656	757	721	878	889
ENSMUSG00000025577	chr11	Cbx2	1.19E+08	1.19E+08	4257	0.784994	1.30725	0.044396	0.088212	0.157299	0	22	10	29	37	50	18	63	119	90	67
ENSMUSG00000022021	chr14	Diap3	86655367	86656582	4584	0.704159	0.699831	0.044467	0.08834	0.107887	0	12	8	32	20	26	24	47	28	82	44
ENSMUSG00000028882	chr4	Ppp1r8	1.33E+08	1.33E+08	2924	0.330878	4.371485	0.044495	0.088384	0.029786	0	228	303	384	267	348	446	484	520	646	584
ENSMUSG00000039254	chr2	Pomt1	32236590	32236741	6442	-0.36198	3.978082	0.044503	0.088386	0.035307	0	224	244	347	284	394	251	275	244	420	426
ENSMUSG00000032667	chr6	Pon2	5264147	5265479	4655	0.323727	5.776438	0.044513	0.088395	0.030019	0	719	738	979	814	795	1126	1405	1563	1585	1415
ENSMUSG00000038550	chr3	Ciart	95878503	95879149	2261	-0.96014	0.690568	0.04456	0.088475	0.232908	0	72	41	22	15	10	19	22	26	25	32
ENSMUSG00000041740	chr5	Rnf10	1.15E+08	1.15E+08	4447	-0.32019	8.102204	0.044605	0.088551	0.03022	0	3969	4280	5615	5703	6096	4524	5140	6200	6609	6080
ENSMUSG00000021087	chr12	Rtn1	72211752	72212577	4003	0.679227	0.241322	0.044646	0.088616	0.071896	0	11	13	10	20	14	20	39	30	40	26
ENSMUSG00000031916	chr8	Cog8	1.07E+08	1.07E+08	4637	-0.34295	5.977673	0.044663	0.088616	0.034024	0	1068	1171	1281	1095	1219	1240	1326	1135	1500	1222
ENSMUSG00000032782	chr11	Cntrob	69299487	69299990	6660	0.535665	1.811978	0.04466	0.088616	0.068878	0	43	27	62	41	62	63	131	64	120	97
ENSMUSG00000038607	chr4	Gng10	59035088	59035318	1314	0.393932	3.248884	0.044654	0.088616	0.040309	0	103	104	142	139	201	174	273	187	325	303
ENSMUSG00000043079	chr18	Synpo	60593973	60596488	9533	-0.35623	6.804085	0.044672	0.08862	0.037171	0	2055	1462	2493	2373	2098	1745	2302	2630	2931	1899
ENSMUSG00000029119	chr5	Man2b2	36806921	36807210	3528	0.495818	3.653954	0.044821	0.088903	0.068504	0	156	98	140	158	336	226	325	238	532	424
ENSMUSG00000040624	chr10	Plekhg1	3740364	3740540	8739	-0.42864	3.143835	0.044892	0.089032	0.048117	0	105	116	191	231	212	111	165	188	223	197
ENSMUSG00000031918	chr9	Mtmr2	13748410	13749400	4913	-0.30832	4.461975	0.044985	0.08919	0.025969	0	341	386	434	418	446	352	431	450	592	482
ENSMUSG00000079677	chr9	Fdx1l	21067520	21067925	782	0.383447	4.559933	0.044978	0.08919	0.041274	0	268	367	433	324	297	627	578	494	737	635
ENSMUSG00000002455	chr2	Prpf6	1.82E+08	1.82E+08	3859	0.364626	5.282915	0.045006	0.089206	0.038163	0	460	465	664	576	695	733	853	1463	1119	941
ENSMUSG00000021645	chr13	Smn1	1E+08	1E+08	2592	0.36606	3.246288	0.045002	0.089206	0.03383	0	127	120	160	127	150	187	209	293	301	248
ENSMUSG00000046691	chr8	Chtf8	1.07E+08	1.07E+08	3036	0.352862	5.032771	0.045078	0.089336	0.035335	0	442	399	476	471	612	655	964	581	1104	1008
ENSMUSG00000032557	chr9	Uba5	1.04E+08	1.04E+08	5243	0.363798	4.464699	0.045138	0.089442	0.036859	0	301	302	318	249	437	489	631	422	675	669
ENSMUSG00000029798	chr6	Herc6	57580992	57581232	5279	0.704678	1.598682	0.045161	0.089475	0.127322	0	34	23	38	41	51	100	67	32	78	134
ENSMUSG00000040385	chr19	Ppp1ca	4192158	4192271	1379	0.315357	7.649157	0.045219	0.089577	0.029407	0	2475	2695	3204	2899	3726	4276	4634	5043	6433	5648

ENSMUSG00000024773	chr19	Atg2a	6241668	6241966	7693	-0.37158	4.685862	0.045308	0.08974	0.039124	0	396	386	492	575	582	337	452	746	600	497
ENSMUSG00000073435	chr17	Nme3	24896500	24896559	876	0.467775	2.227079	0.045321	0.089755	0.051639	0	58	64	83	50	64	88	147	107	132	147
ENSMUSG00000032842	chr17	Abcc10	46303221	46303652	6856	0.554253	1.855852	0.045338	0.089775	0.073744	0	51	34	47	46	59	56	109	149	98	77
ENSMUSG00000032598	chr9	Nckipsd	1.09E+08	1.09E+08	4656	0.400695	2.96259	0.045406	0.089896	0.040608	0	95	89	115	107	152	131	183	185	309	235
ENSMUSG00000028736	chr4	Pax7	1.4E+08	1.4E+08	5860	0.451223	2.580359	0.045425	0.089921	0.051333	0	74	58	73	98	114	112	215	143	183	143
ENSMUSG00000004562	chr14	Arhgef40	51984719	51984991	10366	0.40021	4.476171	0.045437	0.089932	0.0453	0	319	182	330	324	463	330	753	545	800	580
ENSMUSG00000004473	chr7	Clec11a	44303770	44304986	1952	-0.9092	3.468475	0.045572	0.090174	0.236174	0	346	69	260	86	471	144	332	47	244	135
ENSMUSG00000047166	chr15	Tigd5	75909760	75910466	2387	0.593283	0.987955	0.045572	0.090174	0.072381	0	21	30	20	24	28	37	48	74	60	44
ENSMUSG00000027115	chr2	Kif18a	1.09E+08	1.09E+08	9832	-0.73294	0.08702	0.045627	0.09027	0.103058	0	16	12	35	19	22	4	24	18	23	19
ENSMUSG00000042626	chr3	Shc1	89418443	89418709	5645	0.324424	5.315463	0.045709	0.090418	0.030217	0	497	463	676	532	817	747	1123	1161	1238	918
ENSMUSG00000043510	chr5	Hscb	1.11E+08	1.11E+08	905	0.448392	2.438389	0.045718	0.090424	0.048116	0	69	81	88	70	62	119	135	150	174	137
ENSMUSG00000027210	chr2	Meis2	1.16E+08	1.16E+08	12043	0.697314	0.597885	0.045725	0.090425	0.103272	0	17	4	21	18	31	27	36	34	69	40
ENSMUSG00000027544	chr2	Nfatc2	1.68E+08	1.68E+08	10578	0.457092	3.595354	0.045772	0.090505	0.05848	0	134	78	188	156	319	234	379	300	395	322
ENSMUSG00000030393	chr7	Zik1	10487229	10491008	4199	-0.58682	0.573215	0.045809	0.090564	0.065587	0	22	31	27	27	34	12	31	26	38	27
ENSMUSG00000006276	chr8	Eps15l1	72341001	72341524	3141	-0.31627	4.34784	0.045845	0.090623	0.027395	0	322	281	444	376	477	289	398	464	525	455
ENSMUSG00000097388	chr7	Gm3200	1.01E+08	1.01E+08	1002	-0.73229	0.078425	0.045889	0.090697	0.108847	0	22	32	14	15	16	13	19	15	27	13
ENSMUSG00000020455	chr11	Trim11	58978093	58978644	3580	0.3238	3.677297	0.045912	0.090716	0.027369	0	150	154	220	193	232	277	351	324	356	332
ENSMUSG00000076012	chr6	Mir705	85336292	85336373	82	0.614167	1.221691	0.045907	0.090716	0.088786	0	15	18	32	36	49	34	60	90	78	55
ENSMUSG00000022199	chr14	Slc22a17	54906727	54907359	2294	0.495437	2.20037	0.045922	0.090724	0.060123	0	68	42	61	54	87	62	137	124	153	148
ENSMUSG00000033031	chr16	C330027C09Rik	48994185	48994379	5688	0.592408	1.528487	0.045994	0.090852	0.085998	0	18	39	33	28	70	50	85	72	118	71
ENSMUSG00000027253	chr2	Lrp4	91457511	91457752	10504	-0.3847	3.741378	0.046076	0.091002	0.040443	0	194	190	214	333	338	184	310	292	343	232
ENSMUSG00000020262	chr10	Adarb1	77290726	77294961	11272	-0.52799	3.849041	0.046089	0.091014	0.079634	0	275	226	342	302	264	158	204	539	268	206
ENSMUSG00000013858	chr10	Tmem259	79974948	79977853	4663	0.316883	6.295919	0.046103	0.09103	0.029493	0	978	1030	1365	1229	1240	1533	1971	2296	2427	1977
ENSMUSG00000028741	chr4	Mrto4	1.39E+08	1.39E+08	2611	0.320084	4.559222	0.04612	0.091049	0.028438	0	292	323	419	316	398	502	627	495	813	624
ENSMUSG00000023439	chr6	Gnb3	1.25E+08	1.25E+08	2632	0.573838	1.247717	0.046128	0.091053	0.077024	0	19	25	28	26	57	63	57	60	60	71
ENSMUSG00000041540	chr6	Sox5	1.44E+08	1.44E+08	14376	-0.77655	0.220944	0.04618	0.091143	0.133495	0	20	17	10	25	44	11	12	13	27	32
ENSMUSG00000027452	chr2	Acss1	1.51E+08	1.51E+08	4128	1.054072	5.30263	0.0462	0.091156	0.32177	0	421	355	353	555	426	323	413	4298	537	602
ENSMUSG00000028133	chr3	Rwdd3	1.21E+08	1.21E+08	5063	0.655274	0.360201	0.046195	0.091156	0.081846	0	12	10	27	9	19	27	33	26	36	45
ENSMUSG00000002010	chrX	Idh3g	73778963	73779171	2701	-0.3699	8.268157	0.046216	0.091174	0.040985	0	4514	5962	6220	6730	5355	5378	5255	7683	6997	5905
ENSMUSG00000027805	chr3	Pfn2	57841895	57843314	3017	-0.39722	7.154977	0.046242	0.0912	0.047052	0	2569	2528	3110	2548	2671	2420	2358	4144	2724	2540
ENSMUSG00000074682	chr2	Zcchc3	1.52E+08	1.52E+08	3073	0.54081	1.497865	0.046238	0.0912	0.065723	0	23	24	42	51	47	47	86	68	111	70
ENSMUSG00000024277	chr18	Mapre2	23752333	23752420	10202	-0.30928	5.323307	0.046258	0.091219	0.027525	0	652	619	839	799	786	640	744	853	1102	862
ENSMUSG00000019899	chr10	Lama2	26980036	26984513	16338	-0.46657	6.598224	0.046268	0.091224	0.064748	0	1967	943	2059	1580	3048	1331	2215	2525	2114	1336
ENSMUSG00000100164	chr6	2610306M01Rik	86848399	86849440	1042	0.450836	2.265438	0.046338	0.09135	0.049975	0	41	63	91	68	71	107	135	138	136	114
ENSMUSG00000020235	chr10	Fzr1	81366222	81367550	4488	0.327522	4.361205	0.046356	0.091359	0.029618	0	269	240	362	311	339	422	572	405	700	578
ENSMUSG00000091971	chr17	Hspa1a	34969190	34972156	2967	0.658463	1.649125	0.046353	0.091359	0.110065	0	25	31	26	73	40	68	101	117	88	55
ENSMUSG00000009097	chr16	Tbx1	18581713	18582456	1777	0.42846	4.414204	0.046378	0.091378	0.052665	0	233	239	331	390	324	484	429	870	575	453
ENSMUSG00000038467	chr2	Chmp4b	1.55E+08	1.55E+08	2027	0.323026	6.994767	0.046379	0.091378	0.031024	0	1611	1814	2094	1858	2055	2740	2910	3272	3875	3733
ENSMUSG00000020135	chr10	Apc2	80295977	80296053	11281	-0.74853	0.393521	0.04639	0.091387	0.117584	0	14	17	21	38	42	12	28	34	16	17
ENSMUSG00000027710	chr3	Acad9	36066000	36066270	3913	-0.32124	5.318647	0.046452	0.091495	0.029824	0	626	761	776	756	746	698	853	773	980	827
ENSMUSG00000037820	chr2	Tgm2	1.58E+08	1.58E+08	4608	0.33657	6.798128	0.046524	0.091613	0.03372	0	1314	1218	1826	1818	2140	2148	2703	2435	3912	3467
ENSMUSG00000066568	chr7	Lsm14a	34344646	34345958	3104	-0.32	6.003834	0.04652	0.091613	0.030077	0	962	1130	1391	1145	1324	1062	1341	1496	1483	1265
ENSMUSG00000030822	chr7	Prr14	1.27E+08	1.27E+08	3456	0.339253	4.3081	0.046564	0.091675	0.031972	0	242	239	314	307	360	366	474	681	583	474
ENSMUSG00000047037	chr7	Nipa1	55977567	55979903	3183	-0.49581	1.926261	0.046569	0.091675	0.061387	0	52	67	86	72	90	39	81	58	125	69
ENSMUSG00000007739	chr11	Cct4	22990519	22990880	4201	0.31981	6.800039	0.046596	0.091714	0.030418	0	1342	1558	1988	1511	1900	2310	3016	3115	3137	2822
ENSMUSG00000020745	chr11	Pafah1b1	74673949	74679614	9620	-0.34048	7.261769	0.046619	0.091746	0.034666	0	2569	2418	3373	2658	3354	2460	2993	4076	3333	2893
ENSMUSG00000021973	chr14	Micu2	57916280	57917375	2310	0.312126	5.669094	0.046646	0.091788	0.028356	0	587	751	898	726	824	1060	1408	1212	1556	1341
ENSMUSG00000024958	chr19	Gpr137	6938069	6938529	2768	0.386486	3.226795	0.046661	0.091804	0.038745	0	134	119	136	140	135	201	258	177	311	282
ENSMUSG00000051343	chr6	Rab11fip5	85334963	85337226	4104	0.347684	5.288388	0.046747	0.091959	0.035166	0	436	444	539	693	786	710	952	1176	1390	935
ENSMUSG00000031972	chr8	Acta1	1.24E+08	1.24E+08	1433	-0.32629	15.2534	0.046788	0.092027	0.032227	0	555209	594454	794696	755198	977481	743329	722573	815845	942327	795538
ENSMUSG00000032673	chr11	Prorsd1	29511757	29513676	2128	-0.38029	3.766196	0.04689	0.092214	0.039663	0	247	261	306	202	250	260	307	269	299	223
ENSMUSG00000078153	chr11	Psme2b	48945354	48946190	837	0.554664	1.551502	0.046898	0.092217	0.070413	0	38	37	43	32	39	58	64	51	116	108
ENSMUSG00000017667	chr2	Zfp334	1.65E+08	1.65E+08	8205	-0.45714	2.221358	0.046956	0.092318	0.050024	0	82	61	95	93	116	74	103	101	107	66
ENSMUSG00000034211	chr5	Mrps17	1.3E+08	1.3E+08	2330	0.343129	5.04677	0.04703	0.092451	0.033995	0	393	486	571	506	456	819	841	851	929	812
ENSMUSG00000002250	chr17	Ppard	28232754	28232864	4631	-0.35387	4.964598	0.047038	0.092453	0.036121	0	464	397	670	640	800	494	561	826	733	580
ENSMUSG00000000881	chrX	Dlg3	1.01E+08	1.01E+08	5844	0.516892	1.904132	0.047053	0.09247	0.065951	0	50	28	52	51	71	55	135	95	112	108
ENSMUSG00000030055	chr6	Rab43	87788853	87792840	5526	0.339829	3.988096	0.047072	0.092494	0.031594	0	226	172	251	191	334	292	458	435	485	399
ENSMUSG00000034345	chr17	Gtf2h5	6079786	6079911	3855	0.344261	5.356943	0.047095	0.092527	0.034603	0	519	592	755	532	600	1042	1067	964	1124	1070
ENSMUSG00000029111	chr5	Nelfa	33896936	33898909	4927	0.349993	3.393638	0.047151	0.092609	0.031411	0	144	121	155	155	191	199	283	270	385	241
ENSMUSG00000062127	chr3	Cttnbp2nl	1.05E+08	1.05E+08	5000	0.382306	3.52435	0.04715	0.092609	0.039664	0	115	115	183	210	217	209	330	238	427	327
ENSMUSG00000028789	chr4	Azin2	1.29E+08	1.29E+08	4024	0.530717	2.004229	0.047213	0.092717	0.069016	0	59	41	47	52	66	60	83	153	126	122
ENSMUSG00000021843	chr14	Ktn1	47648448	47648577	9582	-0.3912	7.385047	0.047271	0.092819	0.046131	0	2842	2719	3611	3091	3596	2299	3148	5215	3416	2801
ENSMUSG00000049807	chr11	Arhgap23	97415533	97415667	6637	0.433582	4.042993	0.047278	0.09282	0.054005	0	184	111	276	238	394	255	511	510	524	428
ENSMUSG00000044134	chr5	Fam109a	1.22E+08	1.22E+08	2335	0.394203	3.138705	0.047289	0.092828	0.039997	0	100	135	138	122	129	163	209	288	279	221
ENSMUSG00000094130	chr14	Rpp14	8090078	8090554	477	-0.39745	3.540931	0.047331	0.092897	0.043081	0	196	238	270	174	210	216	256	237	208	230
ENSMUSG00000000266	chrX	Mid2	1.41E+08	1.41E+08	8114	-0.38586	2.967208	0.047344	0.09291	0.038243	0	117	125	166	154	175	108	153	200	189	139

ENSMUSG00000026554	chr1	Dcaf8	1.72E+08	1.72E+08	12996	-0.39096	7.969433	0.047387	0.092968	0.046223	0	4372	4085	5179	4905	5157	4082	4067	7519	4766	4629
ENSMUSG00000036275	chr11	9530068E07Rik	52396428	52396603	3296	0.342011	6.535007	0.047381	0.092968	0.035003	0	1245	1109	1517	1219	1783	1855	2359	3090	2484	2262
ENSMUSG00000005973	chr2	Rcn1	1.05E+08	1.05E+08	3196	0.490261	4.981092	0.047398	0.092976	0.071168	0	409	280	515	304	732	690	1194	424	1108	909
ENSMUSG00000039740	chr4	Alg2	47465067	47465418	3450	-0.40434	4.051866	0.047458	0.09308	0.046473	0	279	259	349	261	439	251	398	183	464	386
ENSMUSG00000004071	chr16	Cdip1	4750348	4750601	5746	-0.31549	6.599005	0.047475	0.093101	0.029752	0	1601	1617	1905	1723	2126	1747	1960	2048	2162	2095
ENSMUSG00000029403	chr5	Cdkl2	92006074	92008134	4967	-0.39922	2.721586	0.04749	0.093117	0.040197	0	94	125	132	133	134	102	126	147	138	142
ENSMUSG00000035704	chr7	Alg8	97371606	97371732	2794	0.545927	2.465233	0.047567	0.093254	0.081111	0	57	51	84	72	110	135	136	68	195	217
ENSMUSG00000025010	chr19	Ccnj	40831279	40831442	4355	-0.4577	2.345067	0.047578	0.093263	0.053091	0	82	85	120	99	98	86	123	62	131	92
ENSMUSG00000024150	chr17	Mcfd2	87254658	87256057	2612	0.359864	5.441601	0.047695	0.093479	0.038166	0	507	598	778	608	687	852	1105	775	1543	1487
ENSMUSG00000104139	chr14	AC102815.1	1.03E+08	1.03E+08	3805	-0.46668	4.145027	0.047779	0.09363	0.063256	0	329	168	335	311	612	193	451	314	497	315
ENSMUSG00000052911	chr9	Lamb2	1.08E+08	1.08E+08	6082	-0.32744	7.350862	0.047788	0.093634	0.032401	0	2657	2027	3427	3182	4105	2755	3450	3311	4127	3288
ENSMUSG00000030224	chr6	Strap	1.38E+08	1.38E+08	3090	-0.33271	6.6792	0.048138	0.094308	0.033385	0	1701	1780	2258	1806	1958	1721	1931	2531	2304	2058
ENSMUSG00000031446	chr8	Cul4a	13105621	13105903	6408	-0.34233	6.715502	0.048274	0.094546	0.03541	0	1629	1714	2317	1925	2268	1664	2100	2845	2235	1931
ENSMUSG00000035172	chr11	Plekhh3	1.01E+08	1.01E+08	3582	-0.33398	4.448515	0.048268	0.094546	0.031746	0	325	408	383	435	468	391	453	354	557	493
ENSMUSG00000036983	chr17	Tfb1m	3519263	3519795	1327	-0.40652	2.803317	0.04829	0.094565	0.042891	0	125	136	123	125	141	127	152	118	158	134
ENSMUSG00000066406	chr7	Akap13	75455534	75455748	15203	-0.35627	6.185054	0.04836	0.094688	0.038198	0	1223	878	1581	1383	1862	963	1506	1865	1802	1387
ENSMUSG00000045106	chr2	Ccdc73	1.05E+08	1.05E+08	4351	0.709947	0.204137	0.048383	0.094707	0.098874	0	13	14	18	12	8	30	19	36	24	39
ENSMUSG00000070544	chr2	Top1	1.61E+08	1.61E+08	10426	-0.3623	5.490805	0.048383	0.094707	0.039056	0	531	925	894	795	1098	717	1160	778	1080	866
ENSMUSG00000049939	chr6	Lrrc4	28661831	28662211	3996	0.731665	0.115197	0.04849	0.094902	0.098928	0	19	9	7	8	17	20	40	25	34	23
ENSMUSG00000030986	chr7	Dhx32	1.34E+08	1.34E+08	4173	-0.40218	5.069228	0.048553	0.095	0.04799	0	462	509	701	751	800	455	631	1049	712	528
ENSMUSG00000038816	chr4	Ctnnal1	56810935	56812388	7661	-0.37387	3.176057	0.04855	0.095	0.037062	0	144	134	186	175	212	142	229	140	237	170
ENSMUSG00000003746	chr10	Man1a	53904788	53907563	9058	-0.40632	4.377001	0.048696	0.095265	0.048176	0	383	232	387	342	670	242	392	450	550	485
ENSMUSG00000026672	chr2	Optn	5020642	5021228	3753	-0.41328	5.495619	0.048761	0.095379	0.051346	0	760	803	1117	891	694	599	722	1360	926	913
ENSMUSG00000002228	chr3	Ppm1j	1.05E+08	1.05E+08	1721	-0.3679	5.312769	0.048792	0.095427	0.040283	0	667	763	917	701	647	805	759	631	974	840
ENSMUSG00000023010	chr15	Tmbim6	99392882	99393040	3806	0.309755	7.780358	0.048832	0.09549	0.029342	0	2836	2784	3494	3280	4073	4479	5131	5612	6777	6484
ENSMUSG00000021102	chr12	Glrx5	1.05E+08	1.05E+08	930	0.363967	5.895283	0.048855	0.095522	0.039829	0	718	905	921	954	794	1545	1502	1239	1868	1583
ENSMUSG00000010122	chr11	Slc47a1	61343401	61344528	3383	-0.50951	4.925785	0.048891	0.095579	0.077749	0	374	723	711	744	376	664	527	380	680	618
ENSMUSG00000054469	chr17	Lclat1	73107985	73108145	4689	-0.3231	3.916725	0.048952	0.095686	0.028707	0	245	216	321	311	307	233	372	274	398	294
ENSMUSG00000009614	chr2	Sardh	27188393	27189644	5432	0.566006	2.37294	0.048968	0.095696	0.087604	0	51	40	73	57	131	95	165	75	198	185
ENSMUSG00000061576	chr5	Dpp6	26817203	26818118	10030	-0.54884	1.245401	0.048971	0.095696	0.067112	0	32	27	47	57	69	35	45	47	57	34
ENSMUSG00000027075	chr2	Slc43a1	84838850	84839681	5716	0.890947	4.243872	0.048987	0.095713	0.236266	0	207	149	285	179	298	173	219	1741	343	381
ENSMUSG00000098188	chr10	Sowahc	59221953	59226434	4482	0.667542	1.696346	0.049035	0.09578	0.117573	0	28	29	37	49	61	29	77	75	115	165
ENSMUSG00000103578	chr10	Septin10	59221953	59222224	4477	0.667542	1.696346	0.049033	0.09578	0.11757	0	28	29	37	49	61	29	77	75	115	165
ENSMUSG00000037239	chr7	Spred3	29158829	29162194	5997	0.635473	0.642798	0.049077	0.095849	0.080757	0	17	19	17	18	23	16	39	42	53	60
ENSMUSG00000020196	chr10	Cabin1	75646110	75646687	7460	0.350533	4.282282	0.049103	0.095885	0.035042	0	278	193	287	271	407	306	502	540	711	525
ENSMUSG00000061666	chr11	Gdpd1	87033867	87035295	2336	0.436296	2.541867	0.049172	0.095994	0.048556	0	52	88	94	88	83	124	182	147	186	129
ENSMUSG00000103458	chr18	PCDHA4	36952741	36955150	2856	-0.44191	3.395646	0.049173	0.095994	0.055188	0	178	109	235	172	340	120	252	237	256	185
ENSMUSG00000050188	chr4	Lsm10	1.26E+08	1.26E+08	943	0.430671	2.471763	0.049284	0.096198	0.046921	0	49	65	101	95	80	106	139	138	193	160
ENSMUSG00000039953	chr4	Clstn1	1.5E+08	1.5E+08	4662	-0.32082	5.491676	0.049296	0.096208	0.030634	0	703	588	891	865	1185	679	1006	1008	1131	870
ENSMUSG00000036620	chr11	Mgat4b	50210890	50211030	2719	0.343903	5.14875	0.049308	0.096219	0.034964	0	439	451	591	597	522	652	712	1081	1104	1103
ENSMUSG00000031731	chr8	Ap1g1	1.1E+08	1.1E+08	7681	-0.31241	5.820574	0.049375	0.096336	0.029264	0	907	789	1227	1066	1282	885	1205	1332	1303	1161
ENSMUSG00000040297	chr1	Suco	1.62E+08	1.62E+08	8928	-0.34678	3.590362	0.049387	0.096344	0.032775	0	179	176	270	225	282	151	270	296	273	251
ENSMUSG00000031545	chr8	Agpat6	23172946	23174660	3944	0.343359	5.851836	0.049434	0.09641	0.035521	0	666	785	961	877	968	1038	1310	1243	2146	1927
ENSMUSG00000074358	chr7	Ccdc61	18890883	18891173	2122	0.454409	2.18209	0.049432	0.09641	0.050277	0	52	62	75	58	64	91	148	87	148	127
ENSMUSG00000039985	chr6	Fam60a	1.49E+08	1.49E+08	3851	0.60854	1.073868	0.049504	0.096518	0.084278	0	16	28	19	29	40	34	64	37	89	63
ENSMUSG00000092060	chr5	Bend4	67392147	67398450	7935	0.815056	0.019693	0.0495	0.096518	0.131697	0	16	3	7	12	16	13	32	15	42	35
ENSMUSG00000030268	chr6	Bcat1	1.45E+08	1.45E+08	9322	0.792038	2.617426	0.049515	0.096526	0.181771	0	72	26	80	40	166	146	233	47	253	220
ENSMUSG00000022178	chr14	Ajuba	54567469	54569056	3503	0.391867	2.827789	0.049524	0.096532	0.039991	0	92	69	119	95	136	138	182	154	248	214
ENSMUSG00000055401	chr4	Fbxo6	1.48E+08	1.48E+08	2207	0.381754	4.490041	0.049535	0.096539	0.042542	0	288	314	415	292	305	443	476	841	631	558
ENSMUSG00000063455	chr6	D630045J12Rik	38123174	38128575	13450	-0.68458	0.795432	0.049566	0.096585	0.110357	0	42	21	29	24	56	19	36	14	50	33
ENSMUSG00000094530	chr8	Gm21399	1.29E+08	1.29E+08	600	0.614766	0.351474	0.049583	0.096605	0.065948	0	15	13	13	21	14	26	26	34	43	36
ENSMUSG00000074212	chr3	Dnajb14	1.38E+08	1.38E+08	12553	-0.33073	4.665214	0.049623	0.09667	0.031731	0	333	372	538	508	642	427	488	426	702	592
ENSMUSG00000043061	chr12	Tmem18	30584443	30584562	2952	-0.33292	3.436318	0.049687	0.096781	0.029574	0	196	163	234	179	230	165	243	209	283	219
ENSMUSG00000038543	chr3	BC028528	95883954	95884237	1402	0.512449	2.235777	0.049716	0.096823	0.068032	0	39	75	81	69	50	106	117	90	181	142
ENSMUSG00000046470	chr2	Sox18	1.82E+08	1.82E+08	1620	0.408272	3.87996	0.049723	0.096823	0.047356	0	160	242	215	242	174	289	405	278	608	402
ENSMUSG00000066894	chr5	Vsig10	1.17E+08	1.17E+08	5122	0.545254	2.701795	0.049741	0.096844	0.083413	0	69	61	116	89	105	88	171	317	147	165
ENSMUSG00000026494	chr1	Kif26b	1.79E+08	1.79E+08	14696	-0.55631	1.788993	0.049758	0.096864	0.079097	0	46	45	120	50	84	50	84	48	82	57
ENSMUSG00000000732	chr10	Icosl	78069360	78069535	2756	0.551525	1.453981	0.049794	0.096906	0.068977	0	43	39	25	30	37	61	70	81	81	70
ENSMUSG00000019948	chr10	Actr6	89711973	89712560	1703	-0.44366	2.710745	0.049793	0.096906	0.052771	0	92	139	170	116	102	110	137	106	155	132
ENSMUSG00000000441	chr6	Raf1	1.16E+08	1.16E+08	6363	-0.36507	7.251686	0.049881	0.097063	0.041061	0	2552	2432	3139	3011	3195	2502	2707	4308	2831	3039
ENSMUSG00000081788	chr7	Gm5898	63542479	63544549	2071	-0.57343	2.223523	0.049904	0.097094	0.090808	0	77	61	89	110	128	47	63	158	103	65
ENSMUSG00000041341	chr12	Atg2b	1.06E+08	1.06E+08	10173	-0.37419	4.820823	0.050014	0.097295	0.041626	0	470	390	603	552	668	385	535	854	623	479
ENSMUSG00000038696	chr2	Mapkap1	34406771	34406848	4059	-0.33308	5.174728	0.050036	0.097324	0.03306	0	504	642	756	725	734	640	798	543	970	786
ENSMUSG00000028793	chr4	Rnf19b	1.29E+08	1.29E+08	2872	0.307412	4.959799	0.050068	0.097371	0.027694	0	349	439	525	441	576	594	770	898	964	800
ENSMUSG00000020532	chr11	Acaca	84129672	84130130	15155	1.200387	5.612277	0.050093	0.097402	0.428152	0	245	229	269	884	938	248	451	289	2936	4587
ENSMUSG00000031904	chr8	Slc7a6	1.06E+08	1.06E+08	3730	0.369402	3.451606	0.050098	0.097402	0.037363	0	153	116	178	132	218	182	274	356	348	281

ENSMUSG00000022270	chr15	Fam134b	25843264	25843612	3346	1.177366	6.880997	0.050126	0.097444	0.413321	0	1015	1021	1119	1548	1311	1008	917	14535	1261	1150
ENSMUSG00000021714	chr13	Cenpk	1.04E+08	1.04E+08	1830	0.669538	0.116381	0.05015	0.097465	0.080287	0	10	8	24	11	10	23	30	21	38	28
ENSMUSG00000040097	chr17	Flywch1	23755423	23755944	2977	-0.47589	4.343739	0.050151	0.097465	0.067671	0	325	339	439	445	420	233	319	741	374	312
ENSMUSG00000021338	chr13	Lrrc16a	24012344	24013460	8977	0.645118	0.884865	0.050187	0.097521	0.09931	0	25	8	23	18	41	40	52	62	57	35
ENSMUSG00000014195	chr11	Dnajc7	1.01E+08	1.01E+08	4863	0.341116	6.886851	0.050213	0.097557	0.035855	0	1405	1556	2291	1616	1893	2893	3072	3300	3023	2915
ENSMUSG00000016664	chr15	Pacsin2	83375607	83377730	3885	-0.3089	5.977919	0.050278	0.097657	0.028968	0	882	1041	1350	1235	1345	949	1445	1288	1671	1275
ENSMUSG00000038502	chr7	Ptov1	44863068	44863444	4212	0.328982	6.351379	0.050271	0.097657	0.033137	0	912	1063	1247	1308	1555	1708	1919	2511	2252	2170
ENSMUSG00000028042	chr3	Zbtb7b	89377644	89379994	5591	-0.31253	5.056078	0.050295	0.097677	0.028842	0	470	516	701	578	849	514	660	687	808	805
ENSMUSG00000028809	chr4	Srrm1	1.35E+08	1.35E+08	7299	0.330618	5.60134	0.050388	0.097843	0.033045	0	624	541	781	709	970	880	1075	1603	1546	1247
ENSMUSG00000042532	chr19	Golga7b	42247574	42247636	2988	-0.42114	3.320421	0.050402	0.097856	0.049378	0	196	145	189	172	248	202	154	156	203	260
ENSMUSG00000049751	chr12	Rpl36al	69182731	69183165	1353	0.340367	6.385728	0.05044	0.097917	0.035579	0	941	1203	1505	1080	1459	2103	2041	1974	2288	2349
ENSMUSG00000025171	chr19	Ubtd1	41981763	41982008	1527	0.317109	4.275962	0.050455	0.097931	0.028731	0	245	244	301	257	398	433	528	517	552	452
ENSMUSG00000044876	chr7	Zfp444	6172226	6172399	3421	0.403282	2.73751	0.050503	0.098012	0.041766	0	90	85	122	88	84	150	178	159	211	173
ENSMUSG00000031668	chr6	Eif2ak3	70844515	70845021	5428	-0.40317	3.436846	0.050596	0.098177	0.045842	0	191	135	203	175	338	147	240	170	315	229
ENSMUSG00000010529	chr12	Gm266	1.11E+08	1.11E+08	1213	0.706462	0.563483	0.05072	0.098404	0.113571	0	11	13	12	19	33	44	40	17	54	41
ENSMUSG00000019143	chr18	Hars2	36783008	36783494	4279	-0.32366	4.378181	0.050733	0.098417	0.030261	0	306	389	479	363	382	346	477	386	496	445
ENSMUSG00000095464	chr16	Gm21987	38347040	38347207	456	0.380578	5.890064	0.050747	0.09843	0.044386	0	726	925	1052	764	790	1652	1603	1283	1583	1543
ENSMUSG00000024218	chr17	Taf11	27901122	27901789	2290	0.323508	4.282948	0.050826	0.098569	0.030064	0	244	251	375	266	305	467	526	469	576	456
ENSMUSG00000020776	chr11	Fbf1	1.16E+08	1.16E+08	7751	-0.35566	3.483874	0.05086	0.098621	0.034978	0	187	165	210	219	266	159	237	175	288	292
ENSMUSG00000002108	chr2	Nr1h3	91184061	91184482	2515	0.455306	3.719194	0.050876	0.098637	0.060052	0	172	173	196	195	175	215	248	261	498	581
ENSMUSG00000020544	chr11	Cox11	90638173	90638552	1423	-0.36107	4.316403	0.050934	0.098738	0.038057	0	309	407	433	343	355	418	395	345	464	380
ENSMUSG00000022451	chr15	Twf1	94577951	94579990	3054	0.371444	4.167418	0.05096	0.098773	0.040203	0	265	163	274	231	385	325	471	380	701	521
ENSMUSG00000002104	chr2	Rapsn	91035620	91035988	1802	0.341984	4.733871	0.050968	0.098774	0.034594	0	380	334	433	370	430	622	880	555	774	607
ENSMUSG00000020089	chr10	Ppa1	61648552	61648791	2902	0.348683	5.484739	0.050977	0.098779	0.036908	0	513	599	725	671	790	891	1101	808	1578	1533
ENSMUSG00000033752	chr3	Mnd1	84087933	84088174	875	0.703656	0.790186	0.051	0.09881	0.109123	0	14	32	12	22	20	26	47	46	45	71
ENSMUSG00000078812	chr11	Eif5a	69916714	69917341	2377	0.323771	8.852004	0.051105	0.098998	0.032851	0	5248	6646	7617	6736	8137	10846	10390	10776	14210	13486
ENSMUSG00000028187	chr3	Rpf1	1.47E+08	1.47E+08	1263	0.336038	3.686171	0.051161	0.099093	0.031158	0	149	178	246	173	199	250	349	384	366	315
ENSMUSG00000032064	chr9	Dixdc1	50662752	50666275	9971	-0.60018	1.964447	0.051198	0.099151	0.097652	0	93	50	68	73	101	44	42	124	77	70
ENSMUSG00000063019	chr2	Manbal	1.57E+08	1.57E+08	1107	0.312128	4.083289	0.051223	0.099186	0.027648	0	195	212	294	227	343	372	436	431	495	438
ENSMUSG00000025417	chr10	Pip4k2c	1.27E+08	1.27E+08	3374	0.353591	4.024283	0.051235	0.099195	0.035775	0	236	161	299	232	264	256	382	423	562	533
ENSMUSG00000025209	chr19	Peo1	45006558	45008375	3488	-0.32399	4.663284	0.051249	0.099209	0.030858	0	399	410	546	537	447	451	512	573	559	507
ENSMUSG00000053080	chr19	2700081O15Rik	7417625	7417917	7032	-0.37285	3.848323	0.051263	0.099209	0.039989	0	246	156	347	241	390	179	312	280	397	317
ENSMUSG00000096393	chr9	Gm590	1.11E+08	1.11E+08	499	0.859402	0.44889	0.051264	0.099209	0.174807	0	13	6	15	24	16	11	42	74	45	19
ENSMUSG00000031843	chr8	Mphosph6	1.18E+08	1.18E+08	1054	0.508428	2.375323	0.051317	0.099299	0.069103	0	48	69	104	53	79	110	160	77	200	157
ENSMUSG00000063605	chr8	Ccdc102a	94902869	94903391	2504	0.502486	2.759098	0.051371	0.099388	0.071913	0	57	57	106	96	159	167	199	104	260	185
ENSMUSG00000003380	chr7	Rabac1	24969750	24970009	875	0.342497	6.327853	0.051418	0.099465	0.036265	0	1113	1074	1328	1049	1331	1707	1710	2664	2273	2074
ENSMUSG00000032085	chr9	Tagln	45929628	45930515	1586	0.410667	5.140879	0.051426	0.099467	0.051381	0	405	435	568	677	424	765	1065	561	1410	949
ENSMUSG00000019647	chr18	Sema6a	47235598	47235928	8778	-0.38669	3.677258	0.051509	0.09961	0.043014	0	180	193	298	301	238	149	267	349	293	243
ENSMUSG00000031467	chr8	Agpat5	18846277	18846778	10783	-0.31562	5.363931	0.051514	0.09961	0.030078	0	657	657	851	721	940	760	933	663	1008	900
ENSMUSG00000030849	chr7	Fgfr2	1.3E+08	1.3E+08	7240	-0.63758	1.129944	0.051561	0.099687	0.101753	0	26	28	51	34	83	16	38	33	58	53
ENSMUSG00000033396	chr2	Spg11	1.22E+08	1.22E+08	8042	-0.36773	3.212889	0.051597	0.099742	0.037299	0	155	124	186	186	222	108	180	202	258	208
ENSMUSG00000058298	chr10	Mcm9	53536329	53538767	4868	0.60321	1.174621	0.051637	0.099806	0.087809	0	15	28	30	33	37	39	32	71	93	72
ENSMUSG00000097743	chr14	Gm16973	56696280	56698038	2421	0.614556	0.615225	0.05166	0.099837	0.074936	0	22	20	21	14	15	30	30	52	50	39
ENSMUSG00000035878	chr9	Hykk	54917283	54917858	8936	-0.56115	0.986254	0.051736	0.099969	0.070362	0	41	28	39	39	42	29	37	21	43	50
ENSMUSG00000039813	chr4	Tbc1d2	46604390	46605968	5425	0.813035	0.85928	0.051768	0.100018	0.169957	0	9	20	16	36	21	29	22	31	91	87
ENSMUSG00000055850	chr6	Rnf181	72359714	72360642	2070	0.385517	5.434971	0.051822	0.100109	0.045607	0	555	617	724	566	647	811	1017	1731	1051	1070
ENSMUSG00000022604	chr16	Cep97	55899888	55905869	9163	-0.49418	2.573438	0.051857	0.10016	0.067836	0	105	83	152	96	145	62	93	184	117	118
ENSMUSG00000047368	chr19	Abhd17b	21653309	21653593	2475	-0.3939	4.067194	0.051931	0.10029	0.045711	0	268	297	336	265	425	248	310	514	334	271
ENSMUSG00000025742	chrX	Prps2	1.67E+08	1.67E+08	3873	0.458614	2.153048	0.051941	0.100296	0.053255	0	54	44	70	65	74	88	114	81	184	129
ENSMUSG00000024969	chr19	Mark2	7275396	7277450	7942	-0.29403	5.163267	0.05201	0.100407	0.025898	0	522	554	758	661	825	567	750	713	915	828
ENSMUSG00000031298	chrX	Gpr64	1.6E+08	1.6E+08	5278	-1.00415	1.148533	0.052013	0.100407	0.28388	0	71	15	47	13	99	7	47	61	25	29
ENSMUSG00000022466	chr15	Rpap3	97675105	97675379	2260	-0.32994	3.908173	0.052149	0.100654	0.030911	0	212	290	310	291	280	257	294	342	345	302
ENSMUSG00000059995	chr11	Atxn7l3	1.02E+08	1.02E+08	4121	0.340985	4.821196	0.052199	0.100737	0.035046	0	341	288	447	435	600	502	682	932	870	716
ENSMUSG00000005397	chr13	Nid1	13437602	13437926	6046	-0.393	7.982716	0.052257	0.100836	0.048744	0	4184	2712	4776	4843	8104	3541	5543	6130	5994	4492
ENSMUSG00000024181	chr17	Mrpl28	26123520	26123849	1274	0.367609	5.761089	0.052301	0.100906	0.041857	0	545	842	895	884	766	1440	1332	1116	1677	1478
ENSMUSG00000039221	chr3	Rpl22l1	28805436	28805543	1989	0.3607	5.859267	0.052376	0.101036	0.040299	0	905	846	933	612	890	1359	1626	1522	1561	1463
ENSMUSG00000048307	chr15	Ankrd46	36477668	36479473	2480	-0.3055	4.759659	0.052397	0.101064	0.027636	0	454	430	558	420	645	459	574	575	627	581
ENSMUSG00000042766	chr3	Trim46	89234177	89235292	3792	0.972173	-0.18922	0.052429	0.101112	0.217438	0	9	4	5	3	23	25	30	5	31	26
ENSMUSG00000040043	chr10	Rbms2	1.28E+08	1.28E+08	5609	-0.32534	5.916748	0.052483	0.101202	0.032797	0	966	942	1169	1232	1308	1025	1304	928	1657	1381
ENSMUSG00000068391	chr15	Chrac1	73090392	73090583	2353	-0.32127	5.216992	0.052497	0.101213	0.031353	0	624	662	740	641	761	693	744	860	836	686
ENSMUSG00000042447	chr6	Mios	8209222	8209411	6552	-0.40705	4.044115	0.052714	0.101618	0.049509	0	298	250	363	311	343	196	289	540	345	288
ENSMUSG00000023915	chr17	Tnfrsf21	43016555	43017092	3626	-0.29833	5.257899	0.052759	0.10169	0.026944	0	585	539	833	749	845	659	813	763	1005	770
ENSMUSG00000051977	chr17	Prdm9	15543079	15545360	4308	-0.51375	1.509378	0.052813	0.101782	0.064223	0	49	46	50	61	66	51	49	32	69	65
ENSMUSG00000070526	chr7	Peg12	62461871	62464510	2640	0.673805	0.637137	0.052842	0.101823	0.103099	0	14	10	15	23	32	28	34	23	69	57
ENSMUSG00000031156	chrX	Slc35a2	7884041	7884433	3081	0.328794	3.74025	0.052872	0.101865	0.030356	0	158	178	226	183	242	280	399	269	436	347
ENSMUSG00000004500	chr7	Zfp324	12965838	12966299	4776	-0.45393	1.92577	0.052894	0.101893	0.051021	0	61	54	83	64	102	61	81	63	103	61

ENSMUSG00000026274	chr1	Pask	93308770	93310249	9060	0.830164	0.232015	0.052937	0.101964	0.160539	0	15	7	7	7	28	17	31	14	60	41
ENSMUSG00000022146	chr15	Osmr	6813577	6815928	12113	0.402067	3.21954	0.052979	0.10203	0.044976	0	134	113	125	139	147	147	203	328	329	236
ENSMUSG00000022841	chr16	Ap2m1	20535478	20535601	4172	0.301885	6.644458	0.053027	0.102094	0.028583	0	1263	1396	1724	1352	1759	2006	2508	2470	3201	2767
ENSMUSG00000024384	chr18	Iws1	32067734	32068039	9623	-0.29474	4.846302	0.053026	0.102094	0.025955	0	464	432	566	529	664	440	620	620	779	577
ENSMUSG00000035372	chr19	1810055G02Rik	3708333	3708436	1882	-0.54391	3.557982	0.053099	0.102218	0.089147	0	186	140	250	197	424	189	308	94	356	181
ENSMUSG00000030884	chr7	Uqcrc2	1.21E+08	1.21E+08	2506	-0.3637	9.101163	0.05317	0.10234	0.0422	0	8340	11277	11675	11045	8596	9542	10468	13337	12734	9735
ENSMUSG00000079588	chr1	Tmem182	40805601	40805887	2716	-0.37183	7.920581	0.053182	0.10235	0.043975	0	4214	3926	5006	4850	4749	3850	4331	7187	4777	4331
ENSMUSG00000023022	chr15	Lima1	99778470	99781290	7167	0.408822	5.038154	0.053203	0.102376	0.051844	0	433	266	503	390	823	603	1166	758	1098	786
ENSMUSG00000021592	chr13	Arsk	76060422	76062602	5681	-0.45305	2.33734	0.053254	0.10246	0.054554	0	100	55	101	87	144	69	106	102	133	86
ENSMUSG00000092781	chr10	Mir3057	81271597	81271687	91	-0.4418	2.623999	0.053359	0.102647	0.052272	0	92	92	152	129	125	115	103	156	120	100
ENSMUSG00000020964	chr12	Sel1l	91806043	91810053	8555	-0.30417	6.086659	0.053421	0.102745	0.028905	0	1161	940	1412	1257	1537	1034	1485	1465	1794	1376
ENSMUSG00000021287	chr12	Xrcc3	1.12E+08	1.12E+08	2750	0.741072	0.496765	0.053425	0.102745	0.130962	0	9	7	17	20	30	19	29	24	53	68
ENSMUSG00000025981	chr1	Coq10b	55052770	55052990	4805	-0.35437	4.226501	0.053439	0.102758	0.037516	0	330	404	365	291	327	329	403	344	491	346
ENSMUSG00000074211	chr7	Sdhaf1	30321406	30323895	2490	0.386388	3.930722	0.053453	0.10277	0.043804	0	179	265	221	226	185	382	337	403	428	429
ENSMUSG00000044556	chr4	Tex38	1.16E+08	1.16E+08	802	-0.76712	0.526749	0.053464	0.102778	0.141582	0	22	45	27	30	16	30	25	10	32	20
ENSMUSG00000002413	chr6	Braf	39603237	39610404	13862	-0.37997	3.359818	0.053486	0.102806	0.041019	0	188	137	200	191	253	116	224	266	246	196
ENSMUSG00000049624	chr9	Slc17a5	78536488	78538299	3356	0.44307	2.891478	0.053498	0.102814	0.054747	0	93	67	131	102	131	101	174	259	224	240
ENSMUSG00000020811	chr11	Wscd1	71749920	71750100	4287	-0.50743	1.757708	0.053516	0.102835	0.065666	0	47	54	79	90	54	55	56	78	71	57
ENSMUSG00000042520	chr3	Ubap2l	89999589	90000253	5446	-0.30881	6.232654	0.053611	0.103004	0.029924	0	1143	1056	1475	1460	1898	1163	1603	1552	2049	1543
ENSMUSG00000003458	chr1	Ncstn	1.72E+08	1.72E+08	3975	0.31078	5.756058	0.053636	0.103036	0.030067	0	714	587	872	768	1134	1029	1382	1452	1603	1537
ENSMUSG00000022124	chr14	Fbxl3	1.03E+08	1.03E+08	5103	-0.40187	5.327652	0.053725	0.103193	0.0505	0	717	639	801	756	899	504	694	1336	828	684
ENSMUSG00000037166	chr7	Ppp1r14a	29289320	29289535	531	0.626317	0.830425	0.053737	0.103202	0.087071	0	22	17	21	30	18	37	57	24	66	54
ENSMUSG00000028126	chr3	Pip5k1a	95058530	95060085	4383	-0.317	4.881707	0.05376	0.103224	0.030459	0	429	499	561	589	654	478	611	741	674	549
ENSMUSG00000065990	chr4	Aurkaip1	1.56E+08	1.56E+08	1766	0.321558	5.845367	0.053764	0.103224	0.032292	0	617	850	976	907	914	1282	1330	1445	1782	1593
ENSMUSG00000020422	chr11	Tns3	8431652	8434638	11182	0.429269	4.744598	0.053818	0.103314	0.057136	0	388	195	403	310	651	406	875	643	1018	723
ENSMUSG00000000739	chr8	Sult5a1	1.23E+08	1.23E+08	1764	0.532736	1.930016	0.053927	0.103509	0.074774	0	46	34	50	51	74	57	87	144	91	133
ENSMUSG00000041592	chr11	Sdk2	1.14E+08	1.14E+08	15469	-0.95108	1.327047	0.053984	0.103605	0.262225	0	61	8	58	25	129	14	71	26	59	30
ENSMUSG00000030876	chr7	Mettl9	1.21E+08	1.21E+08	1822	0.305129	4.277396	0.054013	0.103647	0.027072	0	245	245	360	265	335	333	522	471	673	528
ENSMUSG00000023411	chr14	Nfatc4	55824795	55825136	4019	0.474404	3.034657	0.054039	0.103659	0.065547	0	112	52	130	92	194	143	273	242	239	207
ENSMUSG00000050332	chrX	Amer1	95420318	95428598	8496	-0.38858	3.713075	0.054028	0.103659	0.044077	0	153	157	289	325	341	197	302	254	275	291
ENSMUSG00000075296	chr19	Aldh3b2	3972328	3972613	2141	1.439933	0.703332	0.054042	0.103659	0.583078	0	9	4	4	16	36	3	22	6	94	144
ENSMUSG00000086845	chr4	Gm13010	1.37E+08	1.37E+08	828	0.787579	0.05732	0.054071	0.103699	0.124641	0	6	18	20	7	5	26	34	21	29	26
ENSMUSG00000047248	chr7	C2cd3	1E+08	1E+08	11706	-0.35931	3.543742	0.054078	0.103699	0.037091	0	208	162	245	220	257	144	257	312	264	218
ENSMUSG00000028919	chr4	Arhgef19	1.41E+08	1.41E+08	4242	0.708441	0.774322	0.054117	0.103759	0.121304	0	21	13	15	17	36	34	86	28	48	35
ENSMUSG00000025161	chr11	Slc16a3	1.21E+08	1.21E+08	5318	-0.3549	8.352497	0.054164	0.103806	0.04044	0	4406	5753	8424	5982	6257	6375	5414	6572	7005	7699
ENSMUSG00000029060	chr4	Mib2	1.56E+08	1.56E+08	4724	-0.30437	4.177631	0.05415	0.103806	0.02707	0	297	302	393	321	347	268	363	415	465	386
ENSMUSG00000029229	chr5	Chic2	75001026	75006763	6712	0.365204	3.471384	0.054158	0.103806	0.037737	0	147	141	183	159	170	206	293	392	307	246
ENSMUSG00000024846	chr19	Cst6	5344705	5348049	3951	0.441183	3.424325	0.054194	0.103838	0.056975	0	138	158	188	150	107	316	241	284	270	282
ENSMUSG00000100594	chr1	2810414N06Rik	1.52E+08	1.52E+08	1381	-0.6058	0.719791	0.054196	0.103838	0.086101	0	27	42	30	25	32	13	28	25	44	39
ENSMUSG00000018554	chr11	Ybx2	69935796	69936248	1885	-0.63011	1.406137	0.054214	0.103859	0.105405	0	38	44	55	84	39	34	36	35	50	82
ENSMUSG00000039367	chr14	Sec24c	20674321	20674388	4446	-0.29993	6.271002	0.054255	0.103924	0.028383	0	1201	1246	1440	1477	1771	1263	1598	1481	2092	1697
ENSMUSG00000021594	chr13	Srd5a1	69573449	69575196	2881	0.596808	0.520055	0.054288	0.103971	0.074942	0	11	14	19	17	28	32	45	22	54	34
ENSMUSG00000031246	chrX	Sh3bgrl	1.09E+08	1.09E+08	3298	0.431041	4.930855	0.05434	0.104058	0.057947	0	365	330	492	414	589	389	738	578	1522	1038
ENSMUSG00000102828	chr18	RP23-407E2.30	37823879	37824425	1530	-0.41148	3.866359	0.05455	0.104444	0.050879	0	249	148	314	240	472	179	350	317	374	256
ENSMUSG00000027661	chr2	Slc2a10	1.66E+08	1.66E+08	3570	-0.55827	2.056697	0.054558	0.104446	0.086574	0	91	50	74	52	146	64	93	53	111	68
ENSMUSG00000015647	chr2	Lama5	1.8E+08	1.8E+08	11388	-0.34997	4.56006	0.054572	0.104457	0.037531	0	388	383	443	547	426	294	462	620	586	482
ENSMUSG00000030847	chr7	Bag3	1.29E+08	1.29E+08	2591	0.349003	6.930449	0.054596	0.104489	0.038978	0	1296	1681	1889	2166	1929	2937	2763	3702	3611	2785
ENSMUSG00000047656	chr19	Trpt1	6996131	6996524	1142	0.358555	3.580508	0.054607	0.104496	0.036934	0	173	139	205	172	176	287	297	365	300	284
ENSMUSG00000090115	chr17	Usp49	47630690	47630915	8581	-0.38587	2.61721	0.054631	0.104527	0.03981	0	103	97	117	107	152	77	133	134	143	132
ENSMUSG00000021047	chr12	Nova1	46694517	46700973	7000	-0.4756	2.356328	0.054642	0.104535	0.062397	0	107	51	96	91	152	64	92	115	124	103
ENSMUSG00000010406	chr14	Mrpl52	54426909	54426960	412	0.35143	4.771043	0.054662	0.104558	0.037911	0	342	387	532	366	361	656	747	553	777	799
ENSMUSG00000032966	chr2	Fkbp1a	1.52E+08	1.52E+08	3857	0.33935	7.155426	0.054763	0.104737	0.036942	0	1605	2069	2306	2166	2364	3345	3733	2661	4796	4054
ENSMUSG00000074746	chr19	Pdzd8	59296084	59301708	7076	-0.3471	3.97497	0.054791	0.104777	0.035594	0	243	205	306	340	387	204	359	405	356	296
ENSMUSG00000026918	chr2	Brd3	27445579	27448580	7336	-0.29553	5.218129	0.054811	0.104786	0.026862	0	544	566	790	668	889	601	857	767	932	752
ENSMUSG00000027655	chr2	Dhx35	1.59E+08	1.59E+08	5170	-0.33615	3.238143	0.05481	0.104786	0.030896	0	135	158	203	168	214	138	200	186	228	220
ENSMUSG00000018169	chr15	Mfng	78755882	78756644	2839	0.628925	2.268181	0.054921	0.104967	0.112417	0	51	56	45	87	66	50	105	98	199	239
ENSMUSG00000079168	chr8	Cd209g	4134733	4134787	1088	-0.88584	0.092966	0.054917	0.104967	0.193582	0	21	11	30	11	37	11	8	12	9	40
ENSMUSG00000028019	chr3	Pdgfc	81036416	81037554	5089	0.564281	1.556082	0.05501	0.105122	0.08444	0	32	17	33	37	77	62	79	77	85	90
ENSMUSG00000061062	chr17	Gm10093	78491565	78493541	1977	0.576483	0.692995	0.055061	0.105204	0.067952	0	18	13	19	18	34	28	47	34	51	52
ENSMUSG00000022941	chr16	Ripply3	94328420	94328597	1531	0.643907	0.566058	0.055094	0.105244	0.096191	0	13	5	18	27	28	35	36	36	39	47
ENSMUSG00000064264	chr7	Zfp428	24507006	24507436	1308	0.505743	1.754507	0.055097	0.105244	0.063454	0	38	43	57	46	40	83	87	56	126	96
ENSMUSG00000031099	chrX	Smarca1	47809368	47810120	6118	-0.56547	1.831511	0.055113	0.105261	0.08682	0	66	56	100	41	88	67	90	42	78	48
ENSMUSG00000049044	chr2	Rapgef4	71981240	71981351	6677	-0.6371	0.597804	0.055129	0.105276	0.095038	0	25	23	31	36	31	8	29	42	35	20
ENSMUSG00000029253	chr5	Cenpc1	86012043	86012327	3173	-0.43432	2.613681	0.055212	0.10542	0.051402	0	71	98	168	115	138	115	124	101	154	104
ENSMUSG00000004880	chr1	Lbr	1.82E+08	1.82E+08	4761	-0.30787	4.271711	0.055281	0.105517	0.027946	0	321	279	396	313	486	328	377	438	466	397
ENSMUSG00000070394	chr11	Tmem256	69838514	69838573	1105	0.369307	5.259567	0.055285	0.105517	0.042861	0	501	597	722	444	492	991	947	993	1004	1010

ENSMUSG00000093485	chr11	Gm20708	1.18E+08	1.18E+08	1780	-0.33462	3.967595	0.055273	0.105517	0.03287	0	253	251	326	267	360	263	291	416	372	262
ENSMUSG00000078656	chr11	Vps25	1.01E+08	1.01E+08	1642	0.296797	5.357271	0.055294	0.105519	0.027325	0	542	558	691	591	680	879	1003	937	1275	1174
ENSMUSG00000096751	chr12	Gm21971	1.03E+08	1.03E+08	2724	-0.84104	-0.1664	0.055302	0.10552	0.162624	0	10	21	18	17	21	3	4	26	24	13
ENSMUSG00000053253	chr14	Ndfip2	1.05E+08	1.05E+08	11553	-0.30649	4.00229	0.05536	0.105616	0.027424	0	292	246	321	268	345	227	367	354	395	335
ENSMUSG00000042502	chr7	Cd2bp2	1.27E+08	1.27E+08	3379	0.299932	5.336466	0.055504	0.105876	0.027984	0	495	573	683	570	701	794	1071	1172	1124	1029
ENSMUSG00000021065	chr12	Fut8	77238104	77238199	3543	-0.30247	4.021603	0.055611	0.106052	0.026694	0	245	245	335	339	333	235	377	324	437	336
ENSMUSG00000022043	chr14	Trim35	66297031	66297549	4045	-0.33504	8.094115	0.055608	0.106052	0.036441	0	4283	3750	6592	4828	6368	4936	6599	4195	6839	5615
ENSMUSG00000047804	chr11	Akap10	61871307	61873021	6451	-0.32475	3.475121	0.055632	0.106076	0.029825	0	187	162	230	225	223	151	235	234	282	255
ENSMUSG00000026761	chr2	Orc4	48902824	48905599	7458	-0.32462	3.92445	0.055697	0.106156	0.030657	0	243	225	366	260	319	256	336	363	326	277
ENSMUSG00000048550	chr2	Thnsl1	21205724	21205845	4043	-0.41701	2.443597	0.055697	0.106156	0.046472	0	101	95	100	110	101	77	127	117	129	89
ENSMUSG00000061877	chr7	BC048679	81494275	81494378	640	0.783853	1.058033	0.055683	0.106156	0.160507	0	28	19	24	38	8	38	34	103	58	57
ENSMUSG00000019558	chrX	Slc6a8	73673150	73674050	5210	-0.32782	6.877363	0.055749	0.10624	0.034671	0	1724	2116	2366	2431	2252	2028	2562	2736	2780	2024
ENSMUSG00000032839	chr9	Trpc1	95705082	95706967	8030	-0.67313	0.111337	0.055852	0.106423	0.084454	0	22	10	23	17	32	10	17	24	17	22
ENSMUSG00000054894	chr12	Atp5s	69724962	69725014	1485	-0.37951	3.210532	0.055874	0.10645	0.040877	0	163	176	206	161	151	163	189	208	202	163
ENSMUSG00000027086	chr2	Fastkd1	69686815	69687140	5853	-0.32654	3.816155	0.055914	0.106496	0.031257	0	220	278	299	243	251	214	287	308	333	314
ENSMUSG00000032740	chr11	Ccdc88a	29373658	29374410	10891	-0.47074	2.809735	0.055912	0.106496	0.064412	0	124	80	139	124	220	80	188	134	190	100
ENSMUSG00000015468	chr17	Notch4	34564268	34564509	8061	-0.37539	3.954093	0.055996	0.106639	0.042908	0	231	276	302	402	228	222	293	293	444	339
ENSMUSG00000021684	chr13	Pde8b	95024454	95026229	5879	-0.58075	1.237985	0.056043	0.106714	0.082985	0	29	37	70	58	36	35	34	37	46	61
ENSMUSG00000044857	chr17	Lemd2	27189601	27190790	2595	0.3495	5.081721	0.056074	0.106758	0.038321	0	479	446	595	434	516	687	815	1199	858	829
ENSMUSG00000031967	chr8	Afg3l1	1.23E+08	1.23E+08	4757	-0.30535	5.824661	0.05614	0.106869	0.029634	0	801	1032	1169	1064	1161	1001	1111	1124	1434	1241
ENSMUSG00000031628	chr8	Casp3	46617449	46617496	1455	0.453152	2.104877	0.056216	0.106998	0.053494	0	39	53	66	58	83	77	145	100	155	96
ENSMUSG00000024174	chr17	Pot1b	55652025	55653518	3499	0.555656	1.477536	0.056249	0.107046	0.079913	0	38	18	54	28	45	54	107	59	81	71
ENSMUSG00000048878	chr11	Hexim1	1.03E+08	1.03E+08	3495	0.303868	4.965131	0.056302	0.107133	0.028647	0	366	364	496	479	655	572	802	790	959	924
ENSMUSG00000069682	chr10	Gm10275	29698746	29699380	635	0.292261	4.65568	0.056336	0.107182	0.025964	0	301	335	414	353	497	520	663	663	729	649
ENSMUSG00000024053	chr17	Emilin2	71252176	71253093	3910	0.575963	4.653414	0.056455	0.107394	0.106184	0	263	157	303	317	712	440	601	341	1184	1049
ENSMUSG00000018565	chr11	Elp5	69968222	69968540	2294	0.318765	5.186366	0.056521	0.107506	0.03188	0	411	551	608	556	566	846	1007	794	1153	893
ENSMUSG00000037499	chr1	Nenf	1.91E+08	1.91E+08	742	0.313716	5.373059	0.056577	0.107597	0.031123	0	520	537	790	569	676	1026	1039	959	1196	1075
ENSMUSG00000055900	chr4	Tmem69	1.17E+08	1.17E+08	2069	-0.34366	4.252219	0.056593	0.107613	0.035918	0	284	365	450	340	325	372	418	320	452	376
ENSMUSG00000051043	chr11	Gprc5c	1.15E+08	1.15E+08	5245	-0.49974	6.574646	0.056647	0.1077	0.081229	0	928	2106	2051	1369	3062	1511	2700	1044	2422	1599
ENSMUSG00000061477	chr12	Rps7	28630847	28631193	961	0.307487	7.579867	0.056662	0.107714	0.030864	0	2400	2694	3465	2582	3150	3960	5187	5210	5293	4979
ENSMUSG00000020467	chr11	Efemp1	28853204	28853324	2037	-0.52295	3.395899	0.056682	0.107723	0.08395	0	191	97	191	161	427	130	146	258	229	246
ENSMUSG00000022175	chr14	Lrp10	54464164	54464611	4201	0.299613	5.752339	0.056676	0.107723	0.028594	0	615	664	914	870	1007	1105	1400	1221	1871	1390
ENSMUSG00000023952	chr17	Gtpbp2	46161032	46161326	5305	-0.31575	5.810003	0.056703	0.107731	0.031927	0	908	983	1163	1014	1104	827	1113	1440	1275	1190
ENSMUSG00000026102	chr1	Inpp1	52785427	52790217	6460	-0.38698	2.683602	0.05671	0.107731	0.040674	0	99	84	148	136	140	99	125	110	181	134
ENSMUSG00000045799	chr14	Gm9800	8799589	8800294	914	0.505536	1.838503	0.0567	0.107731	0.067557	0	51	35	49	31	75	69	101	71	144	97
ENSMUSG00000001248	chr7	Gramd1a	31130127	31130584	5103	0.315688	4.768636	0.056752	0.107797	0.030777	0	330	404	411	336	547	542	714	617	875	789
ENSMUSG00000004929	chr10	Thop1	81070035	81070278	5059	0.319276	4.787349	0.056775	0.107806	0.031685	0	320	299	420	476	557	516	844	674	906	659
ENSMUSG00000022560	chr15	Slc52a2	76538943	76539195	2700	0.461707	2.269349	0.056781	0.107806	0.056474	0	63	61	71	57	78	69	131	99	187	167
ENSMUSG00000098496	chr7	1810026B05Rik	73539801	73544382	5140	0.413314	2.84522	0.056773	0.107806	0.047228	0	101	105	86	98	110	116	201	231	210	193
ENSMUSG00000063821	chr14	Dupd1	21676582	21677160	1093	-0.49248	6.148705	0.056804	0.107835	0.078704	0	1014	1295	2185	1120	1370	1675	1349	675	1379	1605
ENSMUSG00000038773	chr18	Kdm3b	34777008	34777325	7112	-0.34251	4.836959	0.056896	0.107984	0.0368	0	448	413	613	530	687	383	563	822	677	511
ENSMUSG00000073771	chr4	Btbd19	1.17E+08	1.17E+08	3883	0.549984	1.206706	0.056898	0.107984	0.072764	0	24	21	35	25	46	49	54	38	84	82
ENSMUSG00000009378	chr19	Slc16a12	34668403	34670893	4051	-0.68255	0.508723	0.056916	0.108003	0.109656	0	18	15	26	48	33	18	22	12	37	33
ENSMUSG00000001143	chr1	Lman2l	36419871	36420035	7359	-0.38679	4.964907	0.056957	0.108067	0.047554	0	527	469	714	535	728	527	817	335	832	662
ENSMUSG00000098004	chr2	Gm27027	93956817	93957105	547	0.364552	3.422676	0.057035	0.108201	0.03863	0	125	145	175	178	149	272	236	294	287	286
ENSMUSG00000024259	chr18	Slc25a46	31580168	31583769	4371	-0.33829	5.782198	0.05705	0.108215	0.036833	0	904	1025	1213	954	994	882	1044	1469	1231	1029
ENSMUSG00000028431	chr4	Ikbkap	56749680	56751719	7399	-0.28695	5.034291	0.057059	0.108216	0.025554	0	482	499	670	614	763	533	705	692	850	675
ENSMUSG00000029657	chr5	Hsph1	1.5E+08	1.5E+08	7042	-0.47763	6.418629	0.05707	0.108221	0.074383	0	1282	1486	2704	1171	1773	1551	2343	817	2073	1541
ENSMUSG00000042198	chr4	Chchd7	3938888	3938962	4060	0.366842	3.807414	0.05714	0.108339	0.04005	0	193	216	217	208	161	343	338	366	393	367
ENSMUSG00000022680	chr16	Pdxdc1	13833148	13834846	7973	-0.3084	5.802304	0.057153	0.10835	0.030538	0	927	907	1115	998	1206	799	1215	1400	1388	1056
ENSMUSG00000058966	chr7	Fam57b	1.27E+08	1.27E+08	2804	-0.39972	5.106569	0.057276	0.108568	0.051239	0	536	669	567	790	670	682	520	535	1137	610
ENSMUSG00000020400	chr11	Tnip1	54910785	54911571	3539	-0.29302	5.670268	0.057299	0.108597	0.027428	0	791	818	1091	1007	970	794	999	1059	1362	1166
ENSMUSG00000017264	chr4	Exosc10	1.49E+08	1.49E+08	3594	0.315779	4.422898	0.057455	0.108878	0.03033	0	293	275	334	329	354	380	511	692	615	578
ENSMUSG00000022773	chr16	Ypel1	17069696	17070363	4635	0.71923	0.182637	0.057484	0.108918	0.105275	0	8	16	11	12	17	9	28	42	34	38
ENSMUSG00000073725	chr1	Lmbrd1	24678630	24678816	5960	-0.31945	5.414957	0.057506	0.108944	0.032584	0	679	677	967	789	847	626	874	1148	949	835
ENSMUSG00000028952	chr4	Zbtb48	1.52E+08	1.52E+08	3199	0.564483	1.351949	0.057523	0.108962	0.082513	0	30	23	28	25	61	60	60	51	73	94
ENSMUSG00000016946	chr17	Kctd5	24047734	24049444	2751	0.314507	4.137551	0.057612	0.109101	0.029631	0	215	245	314	249	280	386	517	371	554	437
ENSMUSG00000028988	chr4	Ctnnbip1	1.5E+08	1.5E+08	2792	-0.32408	5.406428	0.057605	0.109101	0.033478	0	617	748	803	784	993	827	781	826	882	1018
ENSMUSG00000053801	chr7	Grwd1	45825227	45826093	2053	0.313652	4.065081	0.057669	0.109194	0.029474	0	181	233	277	240	317	383	404	365	548	452
ENSMUSG00000039285	chr9	Azi2	1.18E+08	1.18E+08	6439	-0.28578	5.007424	0.05768	0.109199	0.025479	0	502	514	632	611	692	510	669	728	779	700
ENSMUSG00000039128	chr2	Cdc123	5794294	5794880	3463	0.29856	5.233699	0.057749	0.109315	0.028217	0	482	479	700	491	679	798	947	991	1055	1026
ENSMUSG00000047139	chr10	Cd24a	43579169	43579322	1813	0.449745	6.812226	0.057766	0.109317	0.066408	0	1758	1520	2178	1471	812	2186	3109	3336	3359	3197
ENSMUSG00000095832	chr3	Supt20	54692823	54692859	2112	0.407841	2.740117	0.057762	0.109317	0.045894	0	96	62	116	105	93	125	184	154	202	215
ENSMUSG00000020982	chr12	Nemf	69311544	69312080	3721	-0.33016	4.436283	0.057815	0.109395	0.033811	0	345	329	435	401	511	273	494	581	514	392
ENSMUSG00000026856	chr2	Dolpp1	30392254	30392512	3233	0.369888	3.122477	0.057824	0.109396	0.038816	0	104	112	156	104	155	160	233	180	292	280
ENSMUSG00000040128	chr4	Pnrc1	33245423	33246507	2095	0.598543	5.347392	0.05784	0.109413	0.116634	0	410	464	597	652	583	671	660	2620	795	911

ENSMUSG00000031834	chr8	Pik3r2	70768176	70768897	4176	0.322541	4.738858	0.057856	0.109427	0.032648	0	314	276	420	419	581	459	736	790	827	672
ENSMUSG00000029203	chr5	Ube2k	65537233	65537546	5173	0.303165	5.72215	0.057906	0.109507	0.029546	0	671	735	851	759	925	1209	1211	1460	1539	1333
ENSMUSG00000053769	chr3	Lysmd1	95134088	95134996	2394	0.444099	2.005408	0.057915	0.10951	0.049742	0	49	59	53	45	69	79	94	119	126	109
ENSMUSG00000030982	chr7	9030624J02Rik	1.19E+08	1.19E+08	8969	0.309876	4.665954	0.058004	0.109647	0.02988	0	325	282	414	373	514	517	667	519	842	745
ENSMUSG00000031842	chr8	Pde4c	70723720	70723783	5545	-0.55627	1.182474	0.058002	0.109647	0.079437	0	39	40	55	45	38	18	47	55	37	52
ENSMUSG00000015405	chrX	Ace2	1.64E+08	1.64E+08	3762	-0.72065	0.090067	0.058216	0.110034	0.111811	0	19	6	34	25	20	13	24	20	15	14
ENSMUSG00000025092	chr19	Hspa12a	58795751	58799998	5733	-0.46066	3.18775	0.058255	0.110091	0.06464	0	159	101	175	230	218	122	214	97	258	214
ENSMUSG00000036864	chr7	Proser3	30539134	30539578	3512	-0.50041	1.717005	0.058378	0.11031	0.067115	0	59	47	50	88	69	36	77	60	86	57
ENSMUSG00000044148	chrX	1810030O07Rik	12654879	12656486	2699	0.322044	3.921782	0.058468	0.110465	0.031091	0	226	162	274	204	255	362	368	362	450	397
ENSMUSG00000068874	chr3	Selenbp1	94933056	94933162	2273	0.554671	4.288474	0.058483	0.110478	0.099096	0	271	160	225	279	392	223	313	975	560	672
ENSMUSG00000079480	chrX	Pin4	1.02E+08	1.02E+08	651	0.338797	3.699658	0.05854	0.11057	0.034315	0	150	164	246	187	209	326	354	274	352	354
ENSMUSG00000061751	chr16	Kalrn	33974258	33976079	18660	-0.33852	3.876573	0.058552	0.110578	0.034757	0	250	246	273	298	288	226	288	385	380	235
ENSMUSG00000039713	chr4	Plekhg5	1.52E+08	1.52E+08	4945	0.335494	3.687823	0.058609	0.11067	0.033499	0	135	145	211	218	248	230	413	332	407	298
ENSMUSG00000048701	chr10	Ccdc6	70097121	70097581	6385	-0.35798	6.264089	0.05862	0.110675	0.042097	0	1367	1163	1429	1458	1801	1309	1344	2194	1504	1424
ENSMUSG00000031148	chrX	Gpkow	7697131	7697395	3737	-0.35268	4.262587	0.058661	0.110738	0.03885	0	307	299	416	330	453	228	383	566	431	371
ENSMUSG00000017721	chr2	Pigt	1.64E+08	1.64E+08	3856	0.308997	5.647375	0.058807	0.110999	0.030919	0	616	597	750	808	994	1055	1138	1105	1793	1426
ENSMUSG00000101892	chr15	9130401M01Rik	58022259	58022563	2666	0.323249	3.60382	0.05884	0.111046	0.030587	0	154	133	234	161	223	228	293	301	384	370
ENSMUSG00000040154	chr2	Wfdc5	1.64E+08	1.64E+08	2322	-1.19361	-0.47173	0.05888	0.111106	0.379394	0	16	8	33	4	15	3	25	0	16	3
ENSMUSG00000025150	chr11	Cbr2	1.21E+08	1.21E+08	1327	0.376736	4.701318	0.058915	0.111157	0.045501	0	353	264	413	315	567	613	607	441	972	804
ENSMUSG00000008450	chr8	Nutf2	1.06E+08	1.06E+08	1966	-0.31988	5.279616	0.058945	0.111196	0.032861	0	608	671	854	695	765	782	844	639	954	775
ENSMUSG00000030032	chr6	Wdr54	83149361	83152897	6562	0.682899	0.176516	0.058952	0.111196	0.09909	0	13	15	18	3	16	29	29	24	39	25
ENSMUSG00000041966	chr2	Dcaf17	71055328	71055496	9806	-0.40525	2.439422	0.05898	0.111234	0.044454	0	95	80	130	86	121	86	85	109	135	124
ENSMUSG00000023795	chr17	Pisd-ps2	3076578	3076782	2108	-0.59952	0.626011	0.05905	0.111351	0.082414	0	29	17	43	25	35	16	18	30	32	41
ENSMUSG00000031154	chrX	Otud5	7841364	7841400	5200	0.305569	4.404717	0.059086	0.111394	0.028685	0	265	248	381	318	376	331	562	555	709	610
ENSMUSG00000049755	chr11	Zfp672	58315114	58317534	6674	-0.30676	4.836804	0.059089	0.111394	0.029686	0	434	521	569	505	599	524	650	568	713	511
ENSMUSG00000022404	chr15	Slc25a17	81318921	81319776	1667	0.333795	3.742595	0.059172	0.111535	0.033109	0	155	177	248	189	217	207	335	402	405	401
ENSMUSG00000056383	chr7	AI987944	41372923	41375374	2671	-0.3785	3.286947	0.05918	0.111536	0.042126	0	161	150	219	186	201	135	189	284	212	165
ENSMUSG00000074802	chr10	Gas2l3	89408823	89414492	6748	0.567242	1.380218	0.059277	0.111702	0.082705	0	25	26	35	36	47	43	71	37	123	83
ENSMUSG00000020166	chr10	Cnot2	1.16E+08	1.16E+08	3711	-0.29213	4.792658	0.059291	0.111715	0.026714	0	420	422	571	527	618	449	569	655	636	591
ENSMUSG00000015120	chr17	Ube2i	25261916	25262491	5474	0.30019	4.545989	0.059329	0.111772	0.027886	0	283	314	343	377	428	416	587	682	703	629
ENSMUSG00000100455	chr1	Gm29170	1.44E+08	1.44E+08	3666	-0.50001	1.760081	0.059351	0.111798	0.066088	0	51	60	76	70	67	51	58	97	57	54
ENSMUSG00000041040	chr1	Fam117b	59913006	59913752	7290	0.38812	3.137126	0.05936	0.111799	0.043725	0	119	107	136	134	130	143	190	304	264	259
ENSMUSG00000000131	chr7	Xpo6	1.26E+08	1.26E+08	9692	0.331746	4.343115	0.059398	0.111835	0.034261	0	287	229	339	237	416	332	551	479	659	645
ENSMUSG00000006005	chr1	Tpr	1.5E+08	1.5E+08	10496	-0.31067	6.478103	0.059404	0.111835	0.031899	0	1378	1287	1940	1734	1970	1298	1710	2282	2245	1819
ENSMUSG00000032311	chr9	Nrg4	55220222	55221408	6075	1.586342	0.516038	0.059393	0.111835	0.720444	0	5	3	6	24	16	7	6	1	104	123
ENSMUSG00000041361	chr9	Myzap	71504347	71505229	5635	0.425169	2.61639	0.059523	0.112045	0.050686	0	66	79	91	95	99	116	227	140	207	123
ENSMUSG00000028035	chr3	Dnajb4	1.52E+08	1.52E+08	4318	-0.38338	5.690889	0.059551	0.112067	0.048429	0	734	1057	951	1216	857	849	1102	1321	1197	745
ENSMUSG00000031311	chrX	Nono	1.01E+08	1.01E+08	4375	0.293482	6.210516	0.059551	0.112067	0.028315	0	916	935	1259	1041	1453	1407	1976	1929	2409	1865
ENSMUSG00000024258	chr18	Polr2d	31789159	31789244	956	0.351776	3.495751	0.059598	0.112139	0.036567	0	128	168	199	156	167	255	334	219	365	290
ENSMUSG00000019849	chr10	Prep	45067206	45067375	2729	0.284852	4.989375	0.059629	0.112183	0.025612	0	396	414	516	515	549	627	861	778	1022	796
ENSMUSG00000090222	chr1	Gm16340	1.74E+08	1.74E+08	2164	-0.7472	0.174207	0.059637	0.112183	0.135884	0	17	23	26	28	15	16	23	3	24	26
ENSMUSG00000039899	chr5	Fgl2	21372642	21373308	3788	0.415758	4.907047	0.059667	0.112224	0.056549	0	344	290	510	323	735	746	1050	624	989	563
ENSMUSG00000028271	chr3	Gtf2b	1.43E+08	1.43E+08	1271	0.341291	3.75619	0.059807	0.112461	0.035026	0	156	205	258	159	210	255	354	413	421	315
ENSMUSG00000038437	chr11	Mllt6	97663414	97663680	7451	-0.32266	6.087825	0.059816	0.112461	0.034389	0	1158	1074	1357	1390	1305	1015	1279	1779	1530	1459
ENSMUSG00000060090	chrX	Rp2h	20364481	20364828	5141	-0.44502	2.679612	0.059817	0.112461	0.058815	0	117	82	117	118	183	59	156	134	175	118
ENSMUSG00000020936	chr11	Nmt1	1.03E+08	1.03E+08	5017	0.335834	6.05704	0.06	0.112789	0.037271	0	886	842	1045	1020	1114	1202	1521	2399	1874	1687
ENSMUSG00000044730	chr4	9930104L06Rik	1.25E+08	1.25E+08	5592	-0.37058	3.299952	0.060031	0.112817	0.040833	0	170	172	239	147	191	142	196	256	199	201
ENSMUSG00000051319	chr2	1500011K16Rik	1.28E+08	1.28E+08	800	-0.34492	5.269859	0.060029	0.112817	0.038716	0	671	688	844	691	674	808	733	834	754	751
ENSMUSG00000031865	chr6	Dctn1	83165920	83165994	6509	-0.30738	7.017012	0.060067	0.112859	0.03157	0	1813	2140	2614	2553	2917	2039	2377	3094	3430	2658
ENSMUSG00000049922	chr2	Slc35c1	92452764	92454774	3275	0.344891	3.327703	0.06007	0.112859	0.034664	0	141	103	152	147	193	181	269	286	350	227
ENSMUSG00000027255	chr2	Arfgap2	91264974	91265404	4129	-0.3716	7.509978	0.060137	0.112969	0.04639	0	3004	3426	4145	3139	3349	3221	2697	4880	3532	3990
ENSMUSG00000038527	chr6	C1rl	1.24E+08	1.24E+08	3010	0.655728	1.074819	0.060144	0.112969	0.114681	0	24	12	30	26	39	34	47	28	89	93
ENSMUSG00000062762	chr9	Ei24	36779159	36780269	3459	-0.30172	6.494999	0.06022	0.113096	0.030242	0	1405	1556	1851	1667	1822	1671	1898	1702	2100	2001
ENSMUSG00000003038	chr4	Hmgn2	1.34E+08	1.34E+08	3060	0.407964	3.550946	0.06027	0.113158	0.051822	0	132	98	162	184	278	214	388	239	460	274
ENSMUSG00000031149	chrX	Praf2	7728439	7728762	1339	0.5841	2.96404	0.06027	0.113158	0.107793	0	71	73	141	72	173	171	261	70	318	272
ENSMUSG00000037110	chr2	Ralgapa2	1.46E+08	1.46E+08	18352	-0.51628	3.785894	0.060391	0.11336	0.086343	0	256	211	264	284	337	126	182	158	392	506
ENSMUSG00000079225	chr9	Gm9531	81677598	81677859	1080	0.44822	2.082636	0.060394	0.11336	0.053196	0	53	51	44	71	71	86	93	109	151	121
ENSMUSG00000079260	chr9	Tmppe	1.14E+08	1.14E+08	6855	0.476582	2.445949	0.060469	0.113486	0.06588	0	61	55	92	67	103	85	139	92	222	206
ENSMUSG00000065987	chr8	Cd209b	3917655	3918827	2115	-1.101	-0.49809	0.060492	0.113513	0.307958	0	17	7	10	9	30	4	1	4	9	29
ENSMUSG00000036835	chr7	Psenen	30561868	30562134	648	0.314578	5.171539	0.060526	0.113563	0.031988	0	527	511	623	459	533	817	872	975	1028	929
ENSMUSG00000030588	chr7	Yif1b	29238329	29238436	1378	0.31791	4.739977	0.060548	0.113587	0.032347	0	309	315	451	406	523	583	708	508	988	691
ENSMUSG00000038539	chr7	Atf5	44812257	44813520	1992	0.349562	5.561829	0.060583	0.113638	0.040403	0	555	468	698	797	1004	973	1030	1074	1425	1680
ENSMUSG00000020801	chr11	Med31	72211724	72212077	1730	0.420705	2.507186	0.060605	0.113664	0.049528	0	56	90	99	78	73	136	143	148	163	149
ENSMUSG00000019189	chr11	Rnf145	44518964	44519274	7786	0.306026	4.11334	0.060644	0.113722	0.028735	0	229	193	263	242	373	332	454	424	557	470
ENSMUSG00000043290	chr7	Zfp784	5034439	5036479	2153	0.451629	1.61259	0.060697	0.113806	0.050122	0	27	38	50	40	55	63	79	89	95	72
ENSMUSG00000022521	chr16	Crebbp	4081328	4086198	12920	-0.34012	4.604744	0.060834	0.114047	0.037124	0	439	328	430	480	598	353	476	676	553	448

ENSMUSG00000025626	chrX	Phf6	52912266	52912436	6946	-0.40177	2.534865	0.060906	0.114167	0.045917	0	87	90	107	124	139	66	140	102	155	123
ENSMUSG00000067786	chr2	Nnat	1.58E+08	1.58E+08	1829	1.731525	2.147233	0.060915	0.114168	0.910559	0	67	5	6	35	47	4	28	8	152	612
ENSMUSG00000031585	chr8	Gtf2e2	33731833	33731988	2348	0.338651	3.580985	0.060999	0.114311	0.03458	0	140	161	223	149	207	288	350	249	360	290
ENSMUSG00000023345	chr9	Poc1a	1.06E+08	1.06E+08	2995	0.51187	1.339316	0.061104	0.114477	0.062224	0	26	37	33	36	33	53	57	52	104	70
ENSMUSG00000063172	chr4	Hspb11	1.07E+08	1.07E+08	2071	0.456001	1.889687	0.061101	0.114477	0.055367	0	37	55	60	37	65	85	104	87	100	106
ENSMUSG00000032602	chr9	Slc25a20	1.09E+08	1.09E+08	4844	0.413462	6.086948	0.061129	0.114507	0.057275	0	784	1038	1019	1140	813	1232	1218	2685	2142	1833
ENSMUSG00000071035	chr17	Gm5499	87078271	87079155	885	-0.64761	0.022614	0.061235	0.114691	0.077525	0	21	18	22	12	22	14	23	10	20	18
ENSMUSG00000048379	chr14	Socs4	47276931	47277221	6873	-0.34792	3.260133	0.061278	0.114756	0.036097	0	170	119	202	181	225	125	225	177	263	202
ENSMUSG00000043183	chr13	Simc1	54503779	54504004	5675	-0.47157	1.658317	0.061422	0.115009	0.058152	0	66	36	63	53	83	43	60	65	67	67
ENSMUSG00000039089	chr10	L3mbtl3	26274468	26276263	4651	-0.34698	3.128353	0.061445	0.115021	0.034703	0	141	139	160	149	227	126	172	193	216	190
ENSMUSG00000041263	chr3	Rusc1	89083981	89084650	3840	0.348415	3.9844	0.061442	0.115021	0.038021	0	192	194	280	239	255	319	381	583	422	341
ENSMUSG00000021731	chr13	Mrps30	1.18E+08	1.18E+08	1590	0.334202	4.929718	0.061492	0.115094	0.036298	0	341	467	494	513	412	696	678	889	902	767
ENSMUSG00000043872	chr4	Zmym1	1.27E+08	1.27E+08	4164	-0.44005	1.703795	0.061554	0.115179	0.049876	0	61	45	73	62	65	40	67	61	76	74
ENSMUSG00000059237	chr9	Ppp1r2-ps4	66805306	66805938	633	-0.66728	0.150481	0.061552	0.115179	0.088995	0	19	18	25	18	26	11	18	28	10	25
ENSMUSG00000039683	chr5	Sdk1	1.41E+08	1.41E+08	11087	-0.68385	1.514546	0.061631	0.115306	0.138449	0	60	14	48	62	111	33	58	33	78	52
ENSMUSG00000098050	chr8	Gm5345	40853828	40854040	1014	-0.81149	-0.00585	0.061664	0.115353	0.154205	0	21	18	21	10	28	10	8	36	12	11
ENSMUSG00000040435	chr7	Ppp1r15a	45522916	45523273	2937	0.67744	4.562068	0.061688	0.115383	0.152835	0	211	258	380	343	332	372	444	1737	444	345
ENSMUSG00000037375	chr1	Hhat	1.92E+08	1.92E+08	9150	0.603936	0.720782	0.061782	0.115543	0.089804	0	11	15	23	18	37	29	57	25	60	48
ENSMUSG00000026563	chr1	Tada1	1.66E+08	1.66E+08	4110	0.389734	3.082416	0.061804	0.115569	0.044666	0	93	122	112	104	177	152	237	176	331	232
ENSMUSG00000068735	chr2	Trp53i11	93187548	93187747	3690	0.477087	4.029401	0.062081	0.116056	0.074454	0	111	166	234	397	239	271	397	346	728	527
ENSMUSG00000073436	chr17	Eme2	24888486	24892944	6000	-0.33854	3.255311	0.062081	0.116056	0.033647	0	136	158	208	154	237	129	188	218	256	198
ENSMUSG00000010607	chr9	Pigyl	22156846	22156913	777	0.342089	3.746453	0.062132	0.116103	0.035995	0	152	209	236	181	199	307	393	321	332	366
ENSMUSG00000030772	chr7	Dkk3	1.12E+08	1.12E+08	3357	-0.73737	3.000068	0.062126	0.116103	0.176479	0	232	56	194	73	291	61	180	247	123	89
ENSMUSG00000092341	chr19	Malat1	5795690	5802672	6983	-0.55844	7.507566	0.062117	0.116103	0.10614	0	5557	2119	3337	2652	4162	1421	3143	3047	3666	6319
ENSMUSG00000097616	chr6	1110019D14Rik	13871526	13871627	1722	-0.47624	1.607467	0.06241	0.116607	0.05874	0	52	61	57	49	68	54	67	41	63	63
ENSMUSG00000086324	chr16	Gm15564	35966752	35966870	821	-0.53847	3.963832	0.062477	0.116716	0.095552	0	284	449	281	170	312	307	184	305	229	416
ENSMUSG00000027895	chr3	Kcnc4	1.07E+08	1.07E+08	3013	-0.34433	6.970987	0.062597	0.116926	0.040412	0	2164	1773	2440	2122	3347	2409	2779	2901	2564	2060
ENSMUSG00000036395	chr9	Glb1l2	26763044	26764823	5031	-0.77299	2.935853	0.062648	0.117001	0.196108	0	204	127	114	158	183	19	68	163	157	275
ENSMUSG00000103653	chr1	WI1-1003N17.1	1.92E+08	1.92E+08	631	0.396631	2.514842	0.062654	0.117001	0.043966	0	76	69	88	77	94	127	116	160	161	176
ENSMUSG00000048387	chr12	Osr1	9574442	9574742	2010	0.493944	1.689982	0.062785	0.117228	0.066153	0	43	20	46	47	63	63	78	72	112	104
ENSMUSG00000038503	chr7	Mesdc2	83884466	83884655	5081	0.297035	4.85896	0.062794	0.117229	0.028696	0	350	353	518	400	573	607	804	614	939	774
ENSMUSG00000046879	chr11	Irgm1	48861968	48865209	5810	0.387098	4.42118	0.062828	0.117277	0.049283	0	229	293	333	323	371	683	468	416	551	620
ENSMUSG00000062683	chr15	Atp5g2	1.03E+08	1.03E+08	1675	0.320297	6.856501	0.062842	0.117288	0.034988	0	1432	1665	1940	1789	1738	2891	2780	3098	3203	2843
ENSMUSG00000087260	chr3	Lamtor5	1.07E+08	1.07E+08	881	0.318313	5.061013	0.062865	0.117314	0.03323	0	455	526	543	449	470	735	833	879	930	911
ENSMUSG00000017188	chr11	Coa3	1.01E+08	1.01E+08	886	0.352176	5.619126	0.062925	0.117412	0.041738	0	609	687	889	692	712	1329	1247	850	1529	1395
ENSMUSG00000090266	chr11	Mettl23	1.17E+08	1.17E+08	2697	-0.32241	4.970118	0.063026	0.117583	0.034221	0	536	595	642	513	589	626	659	540	746	644
ENSMUSG00000032547	chr9	Ryk	1.03E+08	1.03E+08	4534	-0.29063	6.126808	0.063045	0.117602	0.028473	0	1083	1126	1442	1254	1537	1182	1496	1587	1633	1421
ENSMUSG00000001211	chr10	Agpat3	78269178	78273775	7577	0.322462	6.941619	0.063113	0.117715	0.035569	0	1461	1503	2064	2027	2120	2067	3169	4145	3526	3138
ENSMUSG00000058443	chr9	Rpl10-ps3	50344240	50344981	742	0.657779	0.553919	0.063165	0.117795	0.101003	0	15	18	5	22	27	28	42	32	58	36
ENSMUSG00000029684	chr6	Wasl	24613805	24616346	4923	-0.35196	4.279331	0.06318	0.117807	0.040275	0	362	295	392	336	426	234	420	561	463	328
ENSMUSG00000052373	chr11	Mpp3	1.02E+08	1.02E+08	9385	-0.33294	4.176579	0.063192	0.117814	0.03522	0	307	301	336	284	454	324	314	446	369	389
ENSMUSG00000025578	chr11	Cbx8	1.19E+08	1.19E+08	3675	0.489572	1.705628	0.063431	0.118228	0.064624	0	41	24	52	57	46	70	88	67	94	110
ENSMUSG00000030407	chr7	Qpctl	19140217	19141299	2100	0.43405	2.030978	0.063428	0.118228	0.051638	0	48	38	64	58	78	66	119	89	148	121
ENSMUSG00000020009	chr10	Ifngr1	19591949	19592197	2847	0.301792	5.399885	0.063448	0.118243	0.030247	0	600	543	709	601	692	714	1143	1295	1227	1091
ENSMUSG00000027508	chr3	Pag1	9687479	9694129	9580	-0.46251	2.713058	0.063468	0.118265	0.064813	0	85	80	113	125	245	101	126	123	135	150
ENSMUSG00000029084	chr5	Cd38	43868809	43869120	3014	-0.32519	3.459983	0.0636	0.118494	0.031807	0	155	168	228	250	218	170	227	217	264	259
ENSMUSG00000044030	chr7	Irf2bp1	19004065	19006761	2697	0.287138	4.355394	0.063617	0.118494	0.026113	0	252	256	340	310	385	460	509	496	609	530
ENSMUSG00000081051	chr1	Gm15427	95498621	95499151	531	0.304828	3.98686	0.063614	0.118494	0.028927	0	212	190	254	234	292	350	356	467	437	409
ENSMUSG00000026389	chr1	Steap3	1.2E+08	1.2E+08	5715	-0.35706	5.791816	0.06367	0.118576	0.043293	0	908	761	964	1109	1509	1011	1256	723	1516	1175
ENSMUSG00000058013	chr5	Sept11	93093457	93093597	5008	0.290945	6.043461	0.063683	0.118584	0.028631	0	900	760	1054	1010	1256	1218	1707	1761	2032	1803
ENSMUSG00000000168	chr9	Dlat	50634633	50636554	4886	-0.33518	7.904093	0.063718	0.118634	0.038868	0	3568	4761	4838	4996	3886	4346	4625	4387	6487	4918
ENSMUSG00000047414	chr12	Flrt2	95692226	95692615	7721	-0.35319	3.516996	0.063769	0.118714	0.038785	0	176	169	172	232	328	158	233	226	326	241
ENSMUSG00000055184	chr1	Fam72a	1.32E+08	1.32E+08	2191	0.695883	-0.28854	0.063885	0.118914	0.096266	0	5	5	17	5	14	13	27	15	25	23
ENSMUSG00000024451	chr18	Arap3	37972624	37973651	5224	-0.34296	4.18158	0.063922	0.118966	0.038382	0	291	316	332	415	319	220	366	332	523	460
ENSMUSG00000050240	chr16	Hic2	17233572	17233730	6354	-0.57758	1.046979	0.06398	0.119058	0.090311	0	50	27	42	34	45	12	43	44	48	44
ENSMUSG00000017831	chr17	Rab5a	53479234	53479608	2357	-0.42429	4.9694	0.064014	0.119101	0.060941	0	524	513	745	585	630	329	614	1085	642	474
ENSMUSG00000046598	chr16	Bdh1	31422280	31422512	3800	-1.21366	3.030582	0.06402	0.119101	0.483446	0	36	325	66	458	15	77	42	87	257	137
ENSMUSG00000056999	chr19	Ide	37268743	37270837	5823	-0.34238	6.736512	0.064043	0.119127	0.040346	0	1665	1731	2201	2104	2276	1830	1806	3044	2379	1843
ENSMUSG00000028756	chr4	Pink1	1.38E+08	1.38E+08	2673	-0.4103	9.02457	0.064082	0.119168	0.0585	0	8803	8665	11688	10659	9671	8085	7689	17057	8809	9943
ENSMUSG00000091460	chr9	Gm7808	19927896	19928282	387	-0.69627	0.743665	0.064076	0.119168	0.133805	0	36	26	11	51	39	23	19	35	44	23
ENSMUSG00000047171	chr8	Helt	46292050	46292729	1530	-0.84332	-0.1949	0.064149	0.119273	0.184433	0	12	29	16	17	9	5	22	4	15	22
ENSMUSG00000098986	chr19	Gm28006	5844916	5845037	122	0.445201	4.493668	0.064156	0.119273	0.06625	0	283	268	425	302	309	241	617	547	663	1025
ENSMUSG00000028445	chr4	Enho	41638144	41639001	1269	0.366162	4.943485	0.064227	0.119389	0.044905	0	458	390	579	297	515	663	1023	611	1073	686
ENSMUSG00000034263	chr9	Vwa9	64960832	64960938	3208	-0.27871	4.637573	0.064326	0.119558	0.024949	0	368	376	541	472	531	422	533	515	636	518
ENSMUSG00000020219	chr10	Timm13	80899450	80900259	1225	0.341311	5.844519	0.064382	0.119645	0.039739	0	690	859	1091	770	800	1435	1434	1164	1711	1677
ENSMUSG00000029664	chr6	Tfpi2	3962589	3963447	1637	0.750094	0.615403	0.064399	0.11966	0.154204	0	23	8	11	17	29	20	79	24	60	29

ENSMUSG00000025602	chr9	Zfp202	40192316	40192437	3877	-0.42511	1.791077	0.064431	0.119704	0.048057	0	52	65	74	58	75	53	70	60	96	61
ENSMUSG00000037652	chr3	Phc3	30899371	30907490	17485	-0.44673	4.257262	0.064499	0.119814	0.0667	0	364	223	422	364	485	209	346	661	329	341
ENSMUSG00000037740	chr2	Mrps26	1.31E+08	1.31E+08	4358	0.30619	4.750892	0.064547	0.119888	0.030632	0	333	431	446	387	388	591	690	668	809	696
ENSMUSG00000014075	chr16	Tctex1d2	32419702	32419927	2385	0.409787	2.116442	0.064609	0.119986	0.045346	0	60	50	73	53	67	95	117	94	149	110
ENSMUSG00000031969	chr9	Acad8	26974135	26975760	4143	-0.31797	5.415496	0.064688	0.120118	0.034166	0	677	838	923	730	744	780	847	953	940	872
ENSMUSG00000003546	chr17	Klc4	46630631	46631073	2322	0.289461	4.248161	0.064722	0.120165	0.026425	0	227	258	299	326	310	391	497	485	560	494
ENSMUSG00000020612	chr11	Prkar1a	1.1E+08	1.1E+08	4321	0.28591	7.872958	0.064735	0.120173	0.028454	0	2957	3024	3924	3628	4184	4530	6602	6190	6871	5955
ENSMUSG00000016409	chrX	Nkap	37126795	37127375	4326	-0.32578	3.416124	0.064797	0.120272	0.032131	0	169	156	231	184	254	157	185	257	278	230
ENSMUSG00000021895	chr14	Arhgef3	27238039	27238153	3585	-0.30835	3.869877	0.064828	0.120313	0.029788	0	223	200	297	301	336	194	317	338	399	291
ENSMUSG00000024378	chr18	Stard4	33199355	33203815	5586	-0.47531	3.152785	0.064883	0.120382	0.072491	0	102	120	143	194	325	125	155	120	242	232
ENSMUSG00000025162	chr11	Csnk1d	1.21E+08	1.21E+08	5022	0.305012	6.166965	0.064881	0.120382	0.031929	0	942	809	1165	1065	1438	1373	1738	2213	2128	1835
ENSMUSG00000063286	chr7	Gm8995	1.07E+08	1.07E+08	7280	0.436717	2.902117	0.065013	0.120609	0.059007	0	92	76	113	129	114	165	185	116	242	284
ENSMUSG00000000439	chr6	Mkrn2	1.16E+08	1.16E+08	2240	-0.35439	5.368141	0.065117	0.120778	0.04279	0	696	681	919	800	755	652	705	1232	804	802
ENSMUSG00000044609	chr7	Gm9294	42953600	42954388	789	0.574231	0.785444	0.065131	0.120778	0.074763	0	22	20	16	24	25	31	31	40	65	61
ENSMUSG00000073616	chr1	Myeov2	92637145	92637403	1499	0.342568	5.574467	0.065128	0.120778	0.040052	0	580	760	897	602	635	1228	1244	1125	1293	1225
ENSMUSG00000034127	chr10	Tspan8	1.16E+08	1.16E+08	1522	-0.41841	5.570396	0.065161	0.120817	0.060187	0	984	827	1153	719	797	904	877	1279	677	881
ENSMUSG00000019124	chr6	Scrn1	54505890	54509362	8371	-0.48706	2.855572	0.065338	0.12113	0.074699	0	70	130	148	139	228	110	211	90	168	120
ENSMUSG00000020167	chr10	Tcf3	80409514	80410274	4039	0.301622	4.338298	0.06544	0.121295	0.029421	0	212	251	329	333	400	352	528	579	658	506
ENSMUSG00000032679	chr2	Cd59a	1.04E+08	1.04E+08	1811	-0.34388	5.744209	0.065445	0.121295	0.040626	0	788	1161	1202	847	957	1019	965	1134	1164	1167
ENSMUSG00000020828	chr11	Pld2	70540064	70540208	6252	-0.32021	3.887141	0.065487	0.12134	0.032561	0	254	235	320	272	281	245	324	223	369	373
ENSMUSG00000051396	chr2	Hspa14	3488850	3489069	8083	0.298807	4.10843	0.065479	0.12134	0.028175	0	229	224	318	242	272	360	447	370	584	460
ENSMUSG00000006736	chr10	Tspan31	1.27E+08	1.27E+08	1516	0.345252	5.46478	0.065536	0.121416	0.040826	0	544	526	725	602	881	1054	1170	703	1462	1365
ENSMUSG00000022537	chr16	Tmem44	30511855	30514822	8822	-0.47482	2.289719	0.06555	0.121425	0.067505	0	57	81	102	140	89	64	94	125	91	96
ENSMUSG00000078815	chr7	Cacng6	3424195	3424992	1977	-0.31816	7.157622	0.065589	0.121481	0.035315	0	2398	2325	3000	2589	2904	2929	3033	2737	2882	2995
ENSMUSG00000022995	chr1	Enah	1.82E+08	1.82E+08	21452	0.330539	5.758899	0.065934	0.122104	0.037632	0	569	691	841	971	956	1100	1795	1112	1851	1228
ENSMUSG00000018906	chr11	P4ha2	54100095	54100168	6239	0.310533	4.868581	0.065943	0.122105	0.032367	0	343	356	506	400	595	654	864	574	887	778
ENSMUSG00000063108	chr9	Zfp26	20432972	20438660	9631	-0.42117	3.149236	0.066057	0.122299	0.056364	0	154	121	208	138	232	89	178	256	222	149
ENSMUSG00000015671	chr13	Psma2	14613242	14613315	944	0.351783	6.56667	0.066197	0.122542	0.043234	0	1221	1315	1685	1270	1441	1878	2207	3578	2388	2272
ENSMUSG00000032802	chr2	Srxn1	1.52E+08	1.52E+08	2820	0.522763	5.066886	0.066279	0.122677	0.094541	0	331	490	498	489	472	508	607	1931	821	736
ENSMUSG00000028207	chr4	Asph	9448069	9448275	16102	-0.31047	8.469325	0.066336	0.122766	0.034045	0	5482	5133	8296	5979	8301	6934	6814	7333	7543	7843
ENSMUSG00000026767	chr2	Fam188a	12347263	12348203	6294	-0.33838	3.181325	0.066381	0.122833	0.035008	0	122	160	215	158	189	124	182	190	249	195
ENSMUSG00000100621	chr19	Gm28374	6076945	6077478	728	0.411016	2.348826	0.06639	0.122833	0.049094	0	45	57	97	82	81	86	156	146	156	126
ENSMUSG00000046201	chr17	Scaf8	3114972	3115418	4869	-0.34028	4.583897	0.066433	0.122897	0.038848	0	415	319	497	458	560	328	436	703	588	427
ENSMUSG00000035392	chr2	Dennd1a	37798991	37801250	5740	-0.30395	4.474577	0.066471	0.122949	0.03041	0	371	295	427	431	539	336	398	452	596	556
ENSMUSG00000002265	chr7	Peg3	6703892	6711731	13314	0.62323	6.870605	0.066556	0.123074	0.136165	0	1725	530	1662	963	3097	1688	4016	5653	3231	2102
ENSMUSG00000028848	chr4	Gpn2	1.34E+08	1.34E+08	1482	0.381129	2.812774	0.066554	0.123074	0.043876	0	63	93	126	111	113	135	201	152	210	220
ENSMUSG00000040033	chr10	Stat2	1.28E+08	1.28E+08	4397	0.499328	3.625868	0.066568	0.123081	0.083765	0	123	165	171	144	253	382	310	131	376	444
ENSMUSG00000033904	chr7	Ccp110	1.19E+08	1.19E+08	8256	-0.42609	1.957752	0.066641	0.123183	0.051792	0	77	59	86	68	73	44	79	76	98	88
ENSMUSG00000072653	chr6	Zfp783	47943171	47943377	6848	-0.45733	1.829528	0.066641	0.123183	0.057844	0	67	48	89	50	85	49	89	63	75	67
ENSMUSG00000032475	chr9	Nck1	1E+08	1E+08	4792	-0.29272	4.569401	0.066785	0.123417	0.028276	0	364	421	491	457	433	402	551	485	567	477
ENSMUSG00000049641	chr10	Vgll2	52022502	52022803	1650	0.426483	5.225243	0.066786	0.123417	0.062956	0	432	472	410	838	473	873	981	1175	1313	650
ENSMUSG00000043162	chr6	Pyurf	57686576	57689878	3573	-0.37532	5.414309	0.066821	0.123465	0.048728	0	627	880	874	836	760	973	888	590	1014	786
ENSMUSG00000060600	chr11	Eno3	70657202	70657267	1739	-0.3434	12.67899	0.066878	0.123554	0.041982	0	98481	124105	147753	114550	126189	146339	114191	113879	148885	139165
ENSMUSG00000030590	chr7	Fam98c	29152511	29152847	2712	0.335996	3.597836	0.066942	0.123656	0.035461	0	131	191	204	185	170	285	284	312	352	319
ENSMUSG00000021038	chr12	Vipas39	87238875	87239836	2701	0.307054	3.735043	0.067152	0.124027	0.029213	0	183	157	222	216	208	235	316	341	445	389
ENSMUSG00000034154	chr2	Ino80	1.19E+08	1.19E+08	6803	-0.32585	4.422994	0.067215	0.124127	0.035296	0	374	343	463	363	442	355	402	593	430	418
ENSMUSG00000041607	chr18	Mbp	82475146	82475394	8403	0.354342	4.937937	0.067256	0.124187	0.042886	0	399	325	404	622	488	550	826	862	1204	634
ENSMUSG00000026890	chr2	Lhx6	36081953	36084075	4805	-0.54646	1.423471	0.067394	0.124407	0.085172	0	28	53	57	75	45	43	37	54	76	39
ENSMUSG00000027099	chr2	Mtx2	74825803	74826043	3675	0.336399	4.672817	0.06739	0.124407	0.038014	0	298	435	371	414	327	539	646	727	774	621
ENSMUSG00000028550	chr4	Atg4c	99193934	99194452	3351	-0.34258	3.042895	0.067552	0.124666	0.035684	0	132	107	156	172	203	121	175	169	203	178
ENSMUSG00000033096	chr2	Apmap	1.51E+08	1.51E+08	2428	0.377131	5.026631	0.067547	0.124666	0.049023	0	428	414	523	444	554	562	640	644	1134	1381
ENSMUSG00000028967	chr4	Errfi1	1.51E+08	1.51E+08	3582	0.403009	5.011171	0.067657	0.124844	0.056381	0	354	315	483	645	538	588	724	1356	939	675
ENSMUSG00000032959	chr5	Pebp1	1.17E+08	1.17E+08	1771	0.309654	7.535667	0.067769	0.125034	0.034099	0	2216	2671	3428	2668	2848	4360	4330	5111	5220	4728
ENSMUSG00000019737	chr7	Syne4	30314807	30315086	2946	0.746921	0.006382	0.067857	0.12518	0.131864	0	7	14	5	7	23	24	34	29	16	25
ENSMUSG00000022752	chr16	Tomm70a	57121714	57122194	3778	-0.31049	6.314829	0.067885	0.125214	0.03393	0	1157	1471	1698	1450	1568	1298	1604	2023	1896	1468
ENSMUSG00000022248	chr15	Rad1	10486018	10486264	7400	0.389158	2.436962	0.067939	0.125297	0.043219	0	76	70	85	66	85	123	141	114	167	156
ENSMUSG00000042203	chr17	Tbc1d22b	29549788	29549994	4139	-0.29115	3.779804	0.067972	0.125341	0.026428	0	223	216	284	247	287	233	303	273	312	310
ENSMUSG00000025486	chr7	Sirt3	1.41E+08	1.41E+08	1570	-0.37909	4.317459	0.068051	0.125471	0.048859	0	316	443	404	408	264	393	395	372	484	355
ENSMUSG00000022860	chr16	Chodl	78930948	78931447	3820	-0.64589	4.534268	0.068078	0.125504	0.145754	0	564	262	717	290	546	237	497	833	396	144
ENSMUSG00000027968	chr3	Larp7	1.28E+08	1.28E+08	1880	0.391405	3.566118	0.068099	0.125526	0.050359	0	110	168	190	159	230	270	369	174	403	344
ENSMUSG00000052906	chr8	Ubxn8	33619586	33621700	2817	0.381989	2.498767	0.068252	0.125791	0.041405	0	72	72	90	69	100	112	126	131	199	171
ENSMUSG00000018040	chr15	Rrp7a	83113433	83116971	5411	0.289996	5.134667	0.068308	0.125876	0.028768	0	403	469	610	512	661	748	928	721	1132	985
ENSMUSG00000032719	chr1	Sbspon	15853862	15855862	2748	-0.66799	-0.07868	0.068353	0.125943	0.097904	0	23	6	22	19	19	9	11	17	23	19
ENSMUSG00000069372	chr18	Ctxn3	57468486	57468836	1472	0.999429	4.472096	0.068362	0.125943	0.34537	0	196	234	304	212	288	198	205	2460	239	298
ENSMUSG00000097769	chr18	Snhg4	35553371	35553469	4666	0.385875	2.483197	0.068423	0.126038	0.043158	0	77	66	98	69	87	130	121	149	165	156
ENSMUSG00000098974	chr19	Gm27505	5844638	5844747	110	0.496171	4.376944	0.068637	0.126415	0.085224	0	322	263	332	199	301	194	548	494	678	1000

ENSMUSG00000036026	chr17	Tmem63b	45660171	45660980	5098	-0.32197	6.183889	0.068676	0.126471	0.036689	0	1078	1301	1520	1480	1336	1110	1396	1953	1668	1419
ENSMUSG00000049680	chr11	Urgcp	5713417	5718263	5871	-0.30026	5.371224	0.068711	0.126518	0.031231	0	622	685	797	788	929	681	793	1088	979	778
ENSMUSG00000049872	chr10	Fam26e	34091352	34092515	1786	-0.59002	1.648907	0.068723	0.126524	0.105947	0	77	32	60	59	80	32	47	103	61	44
ENSMUSG00000024593	chr18	Megf10	57133090	57133730	7718	-0.51063	2.901635	0.068778	0.126608	0.085332	0	109	86	162	131	262	88	237	149	158	86
ENSMUSG00000083757	chr4	Rps15a-ps4	1.32E+08	1.32E+08	392	0.561951	0.686921	0.068822	0.126673	0.075949	0	23	16	25	12	25	32	55	44	35	41
ENSMUSG00000013921	chr7	Clip3	30291672	30291842	3991	0.400682	3.326374	0.06892	0.126836	0.052856	0	115	87	136	146	248	171	289	334	321	216
ENSMUSG00000026605	chr1	Cenpf	1.9E+08	1.9E+08	15433	0.515051	2.098591	0.068972	0.126916	0.082599	0	31	50	56	57	99	83	145	67	184	105
ENSMUSG00000022702	chr16	Hira	18877037	18877214	6132	-0.2818	4.55643	0.069034	0.127012	0.026472	0	317	411	484	439	508	385	507	487	632	475
ENSMUSG00000028771	chr5	Ptpn12	20986645	20987494	3509	0.315835	4.253771	0.06916	0.127227	0.033158	0	201	251	269	312	393	297	512	511	667	516
ENSMUSG00000026443	chr1	Lrrn2	1.33E+08	1.33E+08	3595	0.58708	1.530378	0.069243	0.127362	0.104738	0	34	18	36	36	65	54	124	57	111	48
ENSMUSG00000059355	chr8	Wdr83os	85080740	85081063	1031	0.316046	5.265271	0.069348	0.127538	0.034774	0	491	531	597	586	643	967	922	730	1219	1097
ENSMUSG00000056366	chr10	Fabp3-ps1	86731754	86732409	656	0.45852	5.336725	0.069458	0.127725	0.074449	0	426	629	590	785	347	867	848	1591	1316	823
ENSMUSG00000029192	chr5	Tbc1d14	36490604	36493114	9802	-0.28488	4.393127	0.069476	0.12774	0.026743	0	316	288	435	388	519	353	464	430	507	451
ENSMUSG00000026275	chr1	Ppp1r7	93342854	93343711	10495	-0.28276	4.559087	0.069511	0.127787	0.026681	0	374	376	459	452	494	440	497	444	575	509
ENSMUSG00000040957	chr18	Cables1	11839220	11840533	3397	0.526077	1.81534	0.069533	0.127811	0.082298	0	29	37	51	57	62	51	55	111	132	130
ENSMUSG00000003721	chr1	Insig2	1.21E+08	1.21E+08	3473	-0.27714	5.639339	0.069574	0.127849	0.026816	0	815	776	1023	861	1095	855	1069	1133	1161	1023
ENSMUSG00000032741	chr5	Tpcn1	1.21E+08	1.21E+08	4645	-0.30052	6.194284	0.069591	0.127849	0.032072	0	1112	1005	1340	1441	1940	1164	1490	1585	1954	1515
ENSMUSG00000034910	chr9	Pygo1	72925645	72925960	7916	-0.53235	3.967081	0.069575	0.127849	0.098669	0	301	229	319	351	336	172	198	642	227	239
ENSMUSG00000103392	chr3	RP23-436F15.5	10321712	10321720	536	-0.4936	2.013263	0.069583	0.127849	0.07441	0	62	67	104	67	90	49	108	39	107	88
ENSMUSG00000047370	chr7	Gm7367	60155538	60156170	633	-0.60576	0.178718	0.069648	0.127937	0.080023	0	19	19	23	29	15	16	13	21	21	26
ENSMUSG00000036270	chr8	Edc4	1.06E+08	1.06E+08	5497	-0.28377	4.697806	0.069657	0.127937	0.027224	0	412	370	488	514	605	407	527	596	705	511
ENSMUSG00000006462	chr2	A530013C23Rik	1.68E+08	1.68E+08	5964	0.666335	1.390793	0.069699	0.127964	0.139135	0	23	21	51	32	38	60	45	140	41	64
ENSMUSG00000027660	chr3	Skil	31095058	31095157	9694	-0.37564	3.838374	0.069695	0.127964	0.047314	0	186	215	254	331	374	221	408	245	375	208
ENSMUSG00000038126	chr5	Mphosph9	1.24E+08	1.24E+08	8544	-0.44335	2.070099	0.069693	0.127964	0.057536	0	54	62	108	80	99	64	110	75	72	84
ENSMUSG00000021265	chr12	Slc25a29	1.09E+08	1.09E+08	2606	-0.41085	2.825624	0.069724	0.127993	0.052905	0	98	134	139	159	136	150	109	149	140	141
ENSMUSG00000034681	chr17	Rnps1	24414675	24414734	1920	0.292615	5.346879	0.0698	0.128114	0.029855	0	518	489	689	631	742	815	953	1287	1154	1003
ENSMUSG00000036306	chr8	Lzts1	69132669	69136159	6993	0.491824	1.761978	0.069812	0.12812	0.070975	0	34	27	40	55	76	56	111	86	127	75
ENSMUSG00000034621	chr11	Gpatch8	1.02E+08	1.02E+08	8178	-0.36719	4.908181	0.070018	0.128482	0.047321	0	548	449	614	562	646	372	515	971	646	568
ENSMUSG00000040740	chr4	Slc25a34	1.42E+08	1.42E+08	2670	0.735735	3.573327	0.07012	0.128651	0.188031	0	140	157	168	168	87	99	202	877	372	204
ENSMUSG00000029247	chr5	Paics	76951307	76951835	3139	-0.31412	6.644279	0.07019	0.128761	0.035455	0	1429	1902	2364	1685	1863	1779	1901	2312	2318	2043
ENSMUSG00000018196	chr1	Glrx2	1.44E+08	1.44E+08	8772	-0.30154	4.941449	0.070282	0.12888	0.03142	0	529	538	670	523	546	567	627	640	670	675
ENSMUSG00000037190	chr9	Cyb561d2	1.08E+08	1.08E+08	1974	0.496062	1.697404	0.07028	0.12888	0.071747	0	22	42	65	33	59	68	94	61	109	98
ENSMUSG00000058927	chr19	Gm10053	24875686	24876634	949	-0.31022	4.407593	0.070282	0.12888	0.03258	0	326	402	465	373	377	402	461	367	545	423
ENSMUSG00000025885	chr18	Myo5b	74440936	74441052	9766	0.792757	0.054816	0.07032	0.128933	0.145365	0	15	7	14	13	6	8	25	19	58	33
ENSMUSG00000035441	chr11	Myo1d	80482126	80484382	6465	-0.44451	3.121215	0.070349	0.128968	0.066348	0	154	105	182	194	203	66	167	199	290	166
ENSMUSG00000038895	chr9	Zfp653	22055460	22055893	2132	0.455842	1.753169	0.070386	0.129019	0.056261	0	49	41	49	46	42	59	80	113	106	85
ENSMUSG00000021286	chr12	Zfyve21	1.12E+08	1.12E+08	1310	0.331018	3.505415	0.070427	0.129077	0.035039	0	162	128	168	157	221	204	285	371	328	281
ENSMUSG00000026858	chr2	Fam73b	30364233	30364305	6249	-0.35773	4.185896	0.070444	0.129092	0.043946	0	225	308	390	395	397	220	335	292	523	528
ENSMUSG00000034620	chr10	Tmem5	1.22E+08	1.22E+08	5614	-0.32464	4.506778	0.07047	0.129122	0.036109	0	362	406	506	404	418	368	463	622	472	411
ENSMUSG00000097413	chr18	A830052D11Rik	32359057	32359435	1130	-0.44516	1.773217	0.070554	0.129258	0.055234	0	43	65	77	71	66	56	53	70	73	77
ENSMUSG00000083692	chr16	Gm9575	50665008	50666346	1339	0.683143	-0.13103	0.070596	0.129318	0.088486	0	8	9	13	13	8	10	23	35	30	19
ENSMUSG00000031429	chrX	Psmd10	1.41E+08	1.41E+08	1469	0.348998	3.3561	0.070612	0.12933	0.038887	0	142	113	189	134	170	229	293	182	330	293
ENSMUSG00000020538	chr11	Srebf1	60199089	60200151	5634	0.485212	5.26153	0.070704	0.129482	0.084396	0	436	282	427	656	932	608	759	759	1479	1738
ENSMUSG00000043424	chr18	Eif3j2	43475418	43477796	2379	-0.55889	2.365632	0.070763	0.129573	0.102504	0	99	80	126	100	100	57	89	193	74	64
ENSMUSG00000066839	chr9	Ecsit	22072246	22072580	1684	-0.31338	6.241583	0.070781	0.129589	0.035259	0	1127	1419	1543	1506	1354	1479	1406	1537	1833	1554
ENSMUSG00000030431	chr7	Tmem238	4784595	4785279	1337	0.527142	0.971706	0.070878	0.129749	0.071086	0	13	29	25	27	33	53	45	46	57	51
ENSMUSG00000095098	chr19	Ccdc85b	5456789	5457397	609	0.34756	4.259161	0.070898	0.129769	0.041135	0	240	294	370	262	219	450	431	433	601	566
ENSMUSG00000029676	chr6	Pot1a	25743737	25744693	8669	-0.3275	3.465758	0.070991	0.129921	0.03459	0	183	180	232	202	222	158	221	296	274	194
ENSMUSG00000020826	chr11	Nos2	78920787	78920995	4192	-0.59508	2.168028	0.071002	0.129925	0.116574	0	44	89	89	148	73	56	79	39	144	105
ENSMUSG00000029599	chr5	Ddx54	1.21E+08	1.21E+08	3929	0.288715	5.10323	0.071031	0.129961	0.029096	0	386	400	568	565	695	670	793	877	1164	935
ENSMUSG00000042050	chr12	Wdr60	1.16E+08	1.16E+08	3725	-0.37408	3.228562	0.07108	0.130033	0.045349	0	150	144	218	179	189	122	167	275	187	196
ENSMUSG00000054199	chr3	Gon4l	88835231	88835296	7564	-0.297	3.97163	0.071113	0.130076	0.028984	0	252	230	343	262	363	213	345	383	363	343
ENSMUSG00000039887	chr3	Alg14	1.21E+08	1.21E+08	910	-0.35074	3.168269	0.071127	0.130084	0.038839	0	145	149	208	133	204	152	212	138	214	199
ENSMUSG00000004044	chr11	Ptrf	1.01E+08	1.01E+08	3587	0.29895	7.821323	0.071229	0.130231	0.03263	0	2692	2781	3748	3794	4040	4671	6198	4509	7378	6531
ENSMUSG00000025145	chr11	Lrrc45	1.21E+08	1.21E+08	3293	0.399269	2.647462	0.071229	0.130231	0.049193	0	83	77	101	64	121	114	152	136	205	219
ENSMUSG00000031605	chr8	Klhl2	64739863	64740974	3025	0.449572	2.919315	0.071235	0.130231	0.065739	0	85	98	99	110	135	108	163	146	292	323
ENSMUSG00000015053	chr6	Gata2	88193891	88194000	3351	0.460383	2.110451	0.071287	0.130308	0.06207	0	45	63	43	76	66	77	107	141	146	103
ENSMUSG00000039646	chr16	Vasn	4639941	4640148	3007	0.448811	3.742159	0.071425	0.130544	0.069846	0	182	108	163	149	359	229	487	248	517	345
ENSMUSG00000097994	chr6	Gm26982	1.14E+08	1.14E+08	1151	0.609263	0.479825	0.071548	0.130751	0.087768	0	17	16	18	16	17	17	29	55	34	47
ENSMUSG00000032624	chr17	Eml4	83350931	83351239	5445	0.417357	2.87577	0.071583	0.130797	0.056314	0	92	61	114	101	159	131	207	129	284	233
ENSMUSG00000044447	chr14	Dock5	67751928	67756522	10335	0.487178	1.48569	0.071652	0.130906	0.065365	0	34	28	41	36	49	43	86	49	99	96
ENSMUSG00000021591	chr13	Glrx	75839868	75840175	1345	-0.31365	4.378716	0.071771	0.131106	0.033816	0	330	416	426	387	334	356	443	442	520	397
ENSMUSG00000014245	chr11	Pigl	62458460	62458694	2268	0.449299	1.726274	0.07181	0.13116	0.058176	0	36	36	54	35	68	53	80	81	110	113
ENSMUSG00000042743	chr13	Sgtb	1.04E+08	1.04E+08	3072	-0.66838	-0.08017	0.071868	0.131249	0.101911	0	17	5	24	21	23	7	16	20	23	13
ENSMUSG00000001943	chr9	Vsig2	37539255	37539438	1170	0.766186	0.038582	0.071914	0.131315	0.140616	0	8	12	11	12	13	7	21	34	22	52
ENSMUSG00000030737	chr7	Slco2b1	99657804	99660176	5612	0.369098	4.18559	0.071955	0.131374	0.04715	0	258	169	293	299	307	286	392	692	501	526

ENSMUSG00000050890	chr4	Pdik1l	1.34E+08	1.34E+08	5810	-0.45403	1.74017	0.071969	0.131382	0.059204	0	44	72	60	58	81	42	77	63	90	54
ENSMUSG00000024286	chr18	Ccny	9314044	9316672	4017	-0.28905	6.287515	0.072036	0.131486	0.030193	0	1145	1251	1744	1497	1563	1326	1622	1837	1800	1595
ENSMUSG00000042165	chr3	Gm9774	92428032	92429423	1392	0.428271	2.476641	0.072387	0.132093	0.056579	0	65	75	90	79	78	120	133	210	149	113
ENSMUSG00000092345	chr4	Gm20503	59003210	59003557	1294	0.337173	3.327556	0.072382	0.132093	0.036613	0	109	119	158	144	214	183	279	204	336	308
ENSMUSG00000061533	chr12	Cep128	90998492	90999659	11591	0.607728	0.691731	0.072433	0.132159	0.097283	0	15	11	24	12	40	20	42	43	59	52
ENSMUSG00000021097	chr12	Clmn	1.05E+08	1.05E+08	11962	-0.49655	2.051596	0.072477	0.132223	0.078946	0	59	43	80	101	124	36	85	70	108	105
ENSMUSG00000041936	chr4	Agrn	1.56E+08	1.56E+08	9285	-0.31871	4.464983	0.072492	0.132231	0.035363	0	285	354	415	519	480	287	481	400	619	542
ENSMUSG00000020718	chr11	Polg2	1.07E+08	1.07E+08	4356	0.473845	1.903242	0.072505	0.132237	0.067036	0	39	54	71	36	54	71	86	134	95	105
ENSMUSG00000050014	chr15	Apol10b	77584158	77585811	1986	-0.58253	1.03103	0.072539	0.132282	0.096202	0	31	32	37	55	42	35	36	18	35	58
ENSMUSG00000037523	chr2	Mavs	1.31E+08	1.31E+08	3345	-0.31211	5.522222	0.072599	0.132375	0.035039	0	651	839	890	985	862	679	879	1204	1179	873
ENSMUSG00000034235	chr14	Usp54	20548912	20550460	8921	-0.47374	2.866515	0.072639	0.132412	0.075395	0	149	129	164	124	127	98	120	247	129	108
ENSMUSG00000041733	chr5	Coq5	1.15E+08	1.15E+08	2037	-0.3369	6.405509	0.07263	0.132412	0.041472	0	1215	1681	1803	1765	1354	1643	1609	1783	2162	1491
ENSMUSG00000027879	chr3	Sec22b	97901190	97901420	3709	0.312683	5.179022	0.072689	0.132486	0.034849	0	488	451	637	441	694	868	1086	714	1079	896
ENSMUSG00000036241	chr4	Ube2r2	41135743	41136246	4189	-0.30901	7.126503	0.072713	0.132512	0.035091	0	2253	2557	2997	2653	2332	2530	2762	3059	3174	2949
ENSMUSG00000030330	chr6	Ing4	1.25E+08	1.25E+08	6675	0.292955	4.990859	0.072736	0.132533	0.030067	0	448	426	573	428	498	629	804	723	934	996
ENSMUSG00000047539	chr1	Fbxo28	1.82E+08	1.82E+08	5318	-0.2939	4.566889	0.072744	0.132533	0.029748	0	365	347	525	414	544	364	446	611	551	511
ENSMUSG00000024604	chr18	Rbm22	60560736	60560879	5338	0.285711	4.329191	0.072758	0.132542	0.027541	0	267	265	321	311	340	429	541	553	601	436
ENSMUSG00000037706	chr7	Cd81	1.43E+08	1.43E+08	2270	0.326312	7.03391	0.072811	0.132621	0.039163	0	1639	1655	2234	1764	2494	2876	4562	2522	3946	3087
ENSMUSG00000040472	chr14	Rabggta	55715873	55716538	2630	0.290698	3.822075	0.072871	0.132713	0.027452	0	163	211	224	198	261	294	364	334	445	371
ENSMUSG00000021180	chr12	Rps6ka5	1.01E+08	1.01E+08	4406	-0.61524	2.321313	0.072971	0.132878	0.129004	0	91	86	91	121	106	35	85	193	102	47
ENSMUSG00000037890	chr5	Wdr19	65199696	65199760	4403	0.4883	1.486448	0.072991	0.132897	0.066159	0	44	25	32	33	53	51	87	72	102	59
ENSMUSG00000025403	chr10	Shmt2	1.28E+08	1.28E+08	2305	0.292691	5.200364	0.073088	0.133038	0.030438	0	410	487	609	604	661	795	812	846	1307	983
ENSMUSG00000046207	chr11	Pik3r6	68503019	68503247	3622	0.456882	1.721906	0.07308	0.133038	0.059269	0	32	38	50	57	48	53	103	66	126	91
ENSMUSG00000043279	chr5	Trim56	1.37E+08	1.37E+08	9281	-0.30503	3.982442	0.073116	0.133072	0.031041	0	235	200	339	345	350	256	294	338	372	385
ENSMUSG00000026674	chr1	Ddr2	1.7E+08	1.7E+08	9264	-0.40411	5.512304	0.073196	0.1332	0.059434	0	790	468	823	721	1674	726	1055	680	1138	1006
ENSMUSG00000040612	chr1	Ildr2	1.66E+08	1.66E+08	8251	-0.54754	1.376245	0.073305	0.133364	0.087387	0	43	27	48	60	76	39	53	32	85	34
ENSMUSG00000048832	chr19	Vps37c	10688815	10688979	2415	0.282717	5.12457	0.073302	0.133364	0.02832	0	397	447	563	593	640	783	878	796	1070	921
ENSMUSG00000030062	chr6	Rpn1	88084473	88084794	3642	0.336245	6.411818	0.073335	0.133401	0.041532	0	981	1066	1618	1037	1670	1758	2201	1480	3170	2610
ENSMUSG00000033323	chr18	Ctdp1	80407959	80408781	3910	0.43344	3.329149	0.073363	0.133434	0.064694	0	119	95	141	160	201	156	227	454	280	224
ENSMUSG00000009487	chr7	Otog	46240987	46241119	10043	0.672388	0.926176	0.073458	0.133589	0.127868	0	26	20	21	24	22	19	94	63	53	31
ENSMUSG00000031097	chr7	Tnni2	1.42E+08	1.42E+08	1497	-0.33956	13.07185	0.073491	0.133631	0.043035	0	135272	153982	189992	159163	162545	181634	144326	202639	161278	177243
ENSMUSG00000080836	chr5	Gm6444	1.23E+08	1.23E+08	458	-0.56924	0.842007	0.073573	0.133763	0.088314	0	32	43	24	42	26	30	37	25	40	29
ENSMUSG00000027933	chr3	Ints3	90391380	90391911	4460	-0.28325	4.734812	0.073619	0.13383	0.028091	0	408	404	569	487	583	385	631	495	795	537
ENSMUSG00000028456	chr4	Unc13b	43058953	43059285	13497	-0.44661	2.289189	0.073744	0.134039	0.064011	0	74	68	96	142	83	52	108	101	124	99
ENSMUSG00000047182	chr5	Irs3	1.38E+08	1.38E+08	2337	0.815182	0.758196	0.073821	0.13416	0.202796	0	13	16	11	12	45	18	30	25	69	99
ENSMUSG00000054893	chr7	Zfp667	6286579	6286654	4755	-0.36869	2.296117	0.073885	0.13426	0.039181	0	80	81	100	83	112	84	90	94	125	100
ENSMUSG00000029414	chr5	Kntc1	1.24E+08	1.24E+08	6961	0.600139	0.706514	0.073908	0.134283	0.0955	0	12	17	29	17	27	23	49	23	76	49
ENSMUSG00000036180	chr8	Gatad2a	69907069	69909974	5502	0.272783	5.029337	0.07392	0.134289	0.026276	0	395	402	559	502	629	655	833	884	1014	786
ENSMUSG00000029836	chr6	Cbx3	51470360	51470431	3229	-0.29228	4.188031	0.073958	0.134339	0.029318	0	300	315	341	328	379	240	400	442	470	376
ENSMUSG00000024135	chr17	Srbd1	85984665	85985483	3530	0.397653	2.212001	0.07408	0.13454	0.047246	0	50	45	81	68	87	80	140	134	141	110
ENSMUSG00000064317	chr10	Gm10146	78393309	78393756	448	0.497626	0.99031	0.074088	0.13454	0.06203	0	28	17	33	24	28	48	56	40	59	52
ENSMUSG00000021585	chr13	Cast	74694286	74694833	2894	-0.33519	6.059327	0.074125	0.134591	0.041337	0	1073	1088	1429	1266	1356	915	1224	2025	1566	1187
ENSMUSG00000038600	chr6	Atp6v0a4	38048483	38049083	4973	-0.82849	0.218013	0.074149	0.134616	0.201268	0	40	9	25	11	31	10	27	33	13	8
ENSMUSG00000044646	chr18	Zbtb7c	75820178	75820365	4729	0.607633	1.679437	0.074267	0.134813	0.119661	0	31	17	51	40	72	52	155	49	93	90
ENSMUSG00000002996	chr12	Hbp1	31926254	31927507	6167	-0.41152	6.480764	0.074289	0.134835	0.062839	0	1584	1533	2010	1607	1744	1055	1488	3163	1635	1614
ENSMUSG00000033706	chr6	Smyd5	85431989	85432100	3169	0.356282	3.36641	0.074327	0.134886	0.042069	0	104	138	170	154	188	221	267	174	402	290
ENSMUSG00000032077	chr9	Bud13	46283008	46283173	3980	0.345771	2.942937	0.07441	0.135019	0.037809	0	92	88	135	114	133	150	200	244	227	171
ENSMUSG00000022787	chr16	Wdr53	32247227	32247267	1523	0.390688	2.557963	0.074488	0.135143	0.047025	0	59	78	124	72	88	120	140	176	184	147
ENSMUSG00000029201	chr5	Ugdh	65413202	65414063	6799	0.376617	4.021906	0.074522	0.135186	0.050037	0	188	160	250	184	424	264	447	335	656	481
ENSMUSG00000040147	chrX	Maob	16709282	16710191	2789	-0.37959	3.796992	0.074621	0.135349	0.050418	0	226	244	291	320	211	209	214	231	340	419
ENSMUSG00000042607	chr6	Asb4	5383386	5383405	3932	-0.37248	3.34624	0.074773	0.135607	0.046637	0	126	221	257	166	179	161	185	245	235	201
ENSMUSG00000035104	chr6	Eva1a	82041043	82041267	2805	-0.66875	0.09657	0.074827	0.135671	0.114099	0	16	24	28	22	10	7	19	19	33	14
ENSMUSG00000035150	chrX	Eif2s3x	94188707	94190922	3812	-0.35975	5.429129	0.074828	0.135671	0.047507	0	682	686	986	792	912	485	758	1329	854	1005
ENSMUSG00000092417	chr17	Gpank1	35121455	35121550	1879	0.402693	3.100885	0.074861	0.135712	0.053436	0	129	112	133	119	108	156	187	321	219	241
ENSMUSG00000054675	chr5	Tmem119	1.14E+08	1.14E+08	2315	0.531213	3.722654	0.074903	0.13577	0.101693	0	186	89	188	129	326	287	625	176	430	295
ENSMUSG00000043602	chr11	Zfp3	70764209	70764549	2061	-0.34293	3.538003	0.074918	0.13578	0.039028	0	179	197	267	199	238	245	210	263	221	224
ENSMUSG00000029338	chr5	Antxr2	97882783	97886600	5427	-0.35424	4.957296	0.074931	0.135787	0.045481	0	535	348	620	527	940	474	777	574	900	492
ENSMUSG00000031851	chr8	Ntpcr	1.26E+08	1.26E+08	2673	0.295867	3.722683	0.074943	0.135791	0.0289	0	172	164	235	171	247	288	338	295	446	324
ENSMUSG00000020288	chr11	Ahsa2	23487882	23490570	4532	-0.31709	5.248433	0.074985	0.135846	0.036489	0	558	694	973	601	693	655	913	642	886	843
ENSMUSG00000097073	chr9	9430037G07Rik	88595325	88598247	3767	-0.72405	0.121209	0.074994	0.135846	0.139476	0	20	16	21	24	24	10	16	38	20	5
ENSMUSG00000020409	chr11	Slu7	43433744	43433819	4050	-0.33118	4.979617	0.075049	0.135921	0.039689	0	498	548	646	621	606	456	617	944	657	578
ENSMUSG00000074340	chr3	Ovgp1	1.06E+08	1.06E+08	3561	0.638549	0.938649	0.075055	0.135921	0.118372	0	27	23	31	17	18	32	49	91	34	48
ENSMUSG00000020904	chr11	Cfap52	67924806	67925233	2320	-0.71106	0.048379	0.075116	0.136014	0.127129	0	21	14	38	6	21	11	20	19	14	20
ENSMUSG00000038991	chr13	Txndc5	38500273	38501708	4298	0.382887	6.181147	0.075236	0.136215	0.054578	0	1014	685	1090	923	1630	1504	2364	1093	2701	2034
ENSMUSG00000020561	chr12	Twistnb	33429624	33429908	2324	-0.34729	3.318367	0.075298	0.13629	0.040205	0	146	187	221	160	213	156	216	261	225	158
ENSMUSG00000061731	chr15	Ext1	53064038	53068849	8077	-0.31105	4.309548	0.075298	0.13629	0.03386	0	309	283	401	364	490	311	518	308	570	376

ENSMUSG00000037185	chr15	Krt80	1.01E+08	1.01E+08	1774	0.509547	0.970107	0.075314	0.136302	0.067955	0	25	11	33	26	34	38	46	51	58	61
ENSMUSG00000045932	chr19	Ifit2	34550694	34551022	3927	0.666755	3.3152	0.075353	0.136355	0.16089	0	92	91	165	139	161	553	180	139	159	255
ENSMUSG00000006476	chr2	Nsmf	25054355	25054671	4896	0.317228	3.909962	0.075391	0.136405	0.034566	0	195	156	252	194	332	267	485	342	455	401
ENSMUSG00000006021	chr7	Kptn	16119895	16120181	3341	-0.35724	3.506368	0.075437	0.136471	0.043421	0	164	201	223	227	245	199	244	136	301	280
ENSMUSG00000030922	chr7	Lyrm1	1.2E+08	1.2E+08	1513	-0.43335	2.632958	0.075476	0.136523	0.060762	0	105	115	150	98	118	139	141	88	121	106
ENSMUSG00000007122	chr1	Casq1	1.72E+08	1.72E+08	1951	-0.32237	12.65388	0.075527	0.136597	0.039349	0	103848	93538	140645	107558	159893	141194	127428	104237	147478	137438
ENSMUSG00000071252	chr13	2210408I21Rik	77135540	77135630	4558	-0.55814	1.068476	0.075579	0.136675	0.090533	0	40	27	36	50	48	19	28	62	53	32
ENSMUSG00000023994	chr17	Nfya	48386885	48389342	7315	0.32693	3.538229	0.075593	0.136682	0.035508	0	153	125	187	177	218	187	328	237	416	357
ENSMUSG00000079283	chr1	2310009B15Rik	1.39E+08	1.39E+08	1750	0.380834	2.533822	0.07567	0.136803	0.044622	0	72	84	92	75	87	129	128	147	159	183
ENSMUSG00000002660	chr17	Clpp	56990264	56990513	1207	0.299065	4.667633	0.075916	0.137229	0.03169	0	310	373	410	414	378	533	566	762	717	671
ENSMUSG00000007950	chr8	Abhd8	71456700	71457377	1985	-0.31898	4.307264	0.075934	0.137244	0.035782	0	315	303	397	404	413	380	476	273	512	403
ENSMUSG00000052310	chr3	Slc39a1	90248172	90248259	2364	0.308393	6.147287	0.075956	0.137266	0.035358	0	900	887	1090	1010	1439	1474	2062	1306	2456	1920
ENSMUSG00000021905	chr14	Dph3	32080566	32081269	3555	-0.30547	5.555606	0.07597	0.137274	0.034248	0	757	865	1052	780	858	955	1000	870	1074	947
ENSMUSG00000027166	chr2	Dnajc24	1.06E+08	1.06E+08	1369	0.448222	1.707967	0.076064	0.137426	0.058959	0	31	46	47	33	68	60	94	76	122	79
ENSMUSG00000010047	chr9	Hyal2	1.08E+08	1.08E+08	3293	0.311548	3.838128	0.076183	0.137623	0.033163	0	149	180	252	238	249	311	381	271	496	387
ENSMUSG00000094114	chr13	Gm21967	1.2E+08	1.2E+08	1648	-0.54516	2.508702	0.076194	0.137625	0.102206	0	120	90	96	64	192	62	79	160	85	147
ENSMUSG00000032725	chr7	Folr2	1.02E+08	1.02E+08	1079	0.512692	4.16747	0.076242	0.137694	0.096606	0	239	103	292	188	450	397	400	245	693	745
ENSMUSG00000019907	chr10	Ppp1r12a	1.08E+08	1.08E+08	3403	-0.35194	3.780817	0.076304	0.137787	0.043033	0	214	167	302	265	355	168	324	377	289	253
ENSMUSG00000025873	chr13	Faf2	54621784	54621903	5084	0.303151	4.190463	0.076388	0.137921	0.032171	0	242	204	275	241	414	371	485	522	528	434
ENSMUSG00000039485	chr10	Tspyl4	34297442	34301320	3879	-0.44308	1.753717	0.076483	0.138075	0.05722	0	51	54	82	54	79	43	83	46	92	67
ENSMUSG00000057123	chr3	Gja5	97032416	97032485	3166	0.537562	2.48159	0.076585	0.138241	0.097825	0	63	80	67	95	61	97	269	79	162	156
ENSMUSG00000057137	chr6	Tmem140	34863146	34863340	5687	0.66409	4.905943	0.076692	0.138416	0.164152	0	359	334	482	407	336	404	476	2267	520	578
ENSMUSG00000079559	chr9	Gm684	51270258	51270925	1263	0.65089	0.027831	0.076741	0.138487	0.098809	0	14	8	14	6	17	19	30	15	47	21
ENSMUSG00000033773	chr5	Rpap2	1.08E+08	1.08E+08	3893	-0.38571	3.957883	0.076778	0.138535	0.053106	0	258	244	388	270	309	213	280	519	291	257
ENSMUSG00000024054	chr17	Smchd1	71344489	71345365	19319	-0.30564	4.170735	0.076835	0.138596	0.032754	0	272	224	418	339	431	233	419	342	513	401
ENSMUSG00000024747	chr19	Aldh1a7	20692953	20693535	2066	-0.78137	3.247462	0.076842	0.138596	0.223416	0	90	292	172	272	149	72	64	62	275	375
ENSMUSG00000026123	chr1	Plekhb2	34849976	34850063	7987	-0.33277	5.902262	0.076823	0.138596	0.041401	0	893	1104	1239	1292	988	1122	1192	883	1628	1354
ENSMUSG00000021418	chr13	Rpp40	35893472	35896925	6540	-0.34596	3.342401	0.076867	0.13862	0.039979	0	155	183	226	147	234	163	186	265	204	211
ENSMUSG00000022828	chr16	Gtf2e1	37509790	37511819	6285	-0.31666	3.60509	0.076875	0.13862	0.034045	0	199	232	226	225	227	190	263	302	284	219
ENSMUSG00000025915	chr1	Sgk3	9798107	9798246	14311	0.403597	2.759613	0.076898	0.138642	0.053132	0	79	94	97	103	104	102	173	132	263	238
ENSMUSG00000031935	chr9	Med17	15260352	15262438	3899	0.293668	3.634184	0.07699	0.13879	0.028236	0	181	160	207	161	214	227	327	336	387	317
ENSMUSG00000042814	chr2	Mcts2	1.53E+08	1.53E+08	917	0.376084	2.853923	0.077106	0.138982	0.045948	0	88	107	111	83	128	169	177	219	172	189
ENSMUSG00000018449	chr11	Rpain	70970213	70970587	2842	0.396657	2.81631	0.077284	0.139267	0.051375	0	99	99	104	83	111	132	194	255	185	152
ENSMUSG00000060244	chr1	Alyref2	1.72E+08	1.72E+08	1273	0.545077	0.975266	0.077275	0.139267	0.078259	0	23	24	22	20	37	43	72	30	61	51
ENSMUSG00000041096	chrX	Tspyl2	1.52E+08	1.52E+08	2820	0.361954	3.57546	0.077411	0.139476	0.04534	0	173	143	215	139	194	213	273	453	307	304
ENSMUSG00000020781	chr11	Tsen54	1.16E+08	1.16E+08	2458	0.337277	2.986701	0.077436	0.139503	0.036679	0	94	115	134	102	132	176	225	201	219	192
ENSMUSG00000070570	chr7	Slc17a7	45163921	45164144	2939	-0.71551	1.873402	0.077583	0.13975	0.175339	0	45	41	60	61	185	81	35	30	67	95
ENSMUSG00000029014	chr5	Dnajc2	21757267	21757409	5029	0.30687	4.393695	0.077643	0.13984	0.033409	0	247	307	386	332	283	418	499	645	607	531
ENSMUSG00000030804	chr7	Gm21974	1.28E+08	1.28E+08	2037	0.386276	4.169327	0.077722	0.139964	0.054277	0	235	184	273	228	395	404	614	247	618	494
ENSMUSG00000032301	chr9	Psma4	54950790	54950903	2370	0.319054	6.769118	0.077734	0.139968	0.038623	0	1311	1576	1885	1557	1767	2277	2481	3763	2765	2728
ENSMUSG00000036959	chrX	Bcorl1	48341358	48341483	8516	-0.30679	3.848063	0.07776	0.139996	0.032085	0	236	187	281	270	364	275	291	244	357	322
ENSMUSG00000039457	chr16	Ppl	5086291	5089828	6277	-0.65059	1.453776	0.077881	0.14019	0.138161	0	82	23	53	42	72	45	29	81	43	40
ENSMUSG00000040710	chr1	St8sia4	95587682	95591964	20091	-0.48723	2.859876	0.077888	0.14019	0.083963	0	121	117	192	173	93	55	113	164	218	174
ENSMUSG00000089989	chr7	Flt3l	45131188	45131431	3712	0.528273	1.712623	0.077983	0.140344	0.089614	0	55	21	63	26	53	55	86	81	98	120
ENSMUSG00000047976	chr6	Kcna1	1.27E+08	1.27E+08	8970	-0.45969	2.164384	0.078024	0.140399	0.067951	0	76	44	88	105	120	61	83	120	84	84
ENSMUSG00000034994	chr10	Eef2	81176631	81176729	3098	0.316744	10.11313	0.078079	0.140479	0.038616	0	11680	13822	17444	19555	20759	19455	26003	38065	32838	27968
ENSMUSG00000016024	chr2	Lbp	1.58E+08	1.58E+08	4831	0.330451	4.091727	0.078098	0.140496	0.039213	0	198	181	282	206	417	355	421	529	478	414
ENSMUSG00000026586	chr1	Prrx1	1.63E+08	1.63E+08	11066	-0.31975	5.906459	0.078236	0.140724	0.03856	0	1178	736	1012	1203	1442	880	1365	1360	1581	1096
ENSMUSG00000037058	chr18	Paip2	35598617	35598759	2789	-0.30646	6.905382	0.078272	0.140772	0.035798	0	1969	2227	2542	2043	2201	2060	2528	2972	2662	2219
ENSMUSG00000034807	chr8	Colgalt1	71611024	71611444	3179	0.288251	6.078579	0.078328	0.140853	0.031291	0	893	813	1062	898	1468	1292	1697	1616	2241	1897
ENSMUSG00000063087	chr18	Gm10125	5491503	5492097	7466	0.782536	-0.33595	0.078345	0.140867	0.159496	0	7	2	12	7	15	27	24	6	18	23
ENSMUSG00000022615	chr15	Tymp	89371931	89372465	2037	0.351065	3.191543	0.078384	0.140918	0.04149	0	94	126	170	144	130	223	207	238	311	199
ENSMUSG00000033845	chr1	Mrpl15	4773206	4774516	8487	0.317711	6.037406	0.078434	0.14099	0.038136	0	780	1003	1180	957	931	1719	1654	1538	1906	1563
ENSMUSG00000022948	chr16	Setd4	93583457	93583684	4702	0.606137	0.13584	0.0785	0.141089	0.072419	0	10	14	12	14	15	14	27	26	34	40
ENSMUSG00000020526	chr11	Znhit3	84910950	84911648	2136	-0.34368	3.046107	0.078581	0.141218	0.039251	0	149	155	176	126	151	133	172	178	180	177
ENSMUSG00000062866	chr10	Phactr2	13207717	13214273	11688	-0.27777	4.615773	0.07863	0.141288	0.027643	0	375	339	465	498	581	366	533	563	614	521
ENSMUSG00000049600	chr7	Zbtb45	13004936	13005328	2722	0.399937	2.499221	0.07874	0.141467	0.051615	0	64	70	65	102	98	121	165	111	206	139
ENSMUSG00000036323	chr5	Srp72	76974683	76974832	5717	-0.28026	5.720841	0.07876	0.141483	0.029442	0	872	819	1037	939	1170	772	1003	1309	1337	1176
ENSMUSG00000030254	chr6	Rad18	1.13E+08	1.13E+08	5796	0.525644	0.84701	0.078792	0.141524	0.06993	0	23	21	22	20	29	28	37	50	81	42
ENSMUSG00000042225	chrX	Ammecr1	1.43E+08	1.43E+08	5437	0.340253	3.174607	0.078837	0.141568	0.038318	0	101	105	145	128	188	152	287	199	311	233
ENSMUSG00000048174	chr1	Tmem81	1.33E+08	1.33E+08	2018	0.512539	0.993899	0.078832	0.141568	0.070125	0	23	27	27	21	31	55	47	46	44	61
ENSMUSG00000035559	chr8	Mpv17l2	70758649	70759024	955	0.33383	3.643365	0.078906	0.141673	0.038284	0	154	196	176	165	220	241	284	258	417	428
ENSMUSG00000020227	chr10	Irak3	1.2E+08	1.2E+08	3676	0.444464	2.28304	0.078922	0.141683	0.064835	0	46	55	78	64	99	58	112	167	177	142
ENSMUSG00000006673	chr9	Qrich1	1.09E+08	1.09E+08	7728	-0.29236	5.176176	0.079081	0.141937	0.031709	0	555	555	703	671	858	504	753	969	915	680
ENSMUSG00000015837	chr11	Sqstm1	50199366	50200947	3356	0.559995	8.821152	0.079104	0.141937	0.120554	0	4765	5270	7314	6749	6570	7828	7267	29320	8618	9134
ENSMUSG00000047126	chr11	Cltc	86694351	86695690	8499	-0.27822	7.443088	0.079087	0.141937	0.029755	0	2893	2447	3511	3181	4007	2575	3753	4021	4621	3567

ENSMUSG00000097565	chr13	Gm26965	67491152	67492150	1520	-0.50339	1.378687	0.079097	0.141937	0.076563	0	51	50	43	55	44	27	44	68	47	59
ENSMUSG00000019929	chr10	Dcn	97479500	97479789	2084	-0.48843	9.138524	0.079143	0.141988	0.091997	0	14243	5894	12291	7658	15228	6842	10980	19277	9736	7819
ENSMUSG00000072720	chr5	Myo18b	1.13E+08	1.13E+08	10698	-0.36279	8.862148	0.079389	0.142411	0.050979	0	6205	6362	9834	9655	12608	7011	7222	14425	10220	8597
ENSMUSG00000070047	chr8	Fat1	44935447	44935621	15586	-0.46989	4.528288	0.079623	0.142811	0.083082	0	469	167	460	379	828	317	623	322	615	408
ENSMUSG00000086938	chr19	4930481A15Rik	5406740	5407083	2240	0.717692	1.436915	0.079676	0.142888	0.173237	0	34	31	37	39	19	44	35	169	59	67
ENSMUSG00000032593	chr9	Amigo3	1.08E+08	1.08E+08	2543	-0.52147	1.625689	0.079729	0.142965	0.085479	0	44	51	68	60	76	50	82	23	79	56
ENSMUSG00000044018	chr4	Mrpl50	49512596	49514577	2114	-0.30289	5.711679	0.079835	0.143136	0.034764	0	879	999	1097	939	852	953	1124	1142	1212	1007
ENSMUSG00000024293	chr18	Esco1	10566602	10567646	4572	-0.28708	3.749756	0.079958	0.14333	0.028082	0	222	217	275	248	263	233	294	305	314	256
ENSMUSG00000068328	chr6	Aup1	83054653	83054832	1509	0.27121	5.69602	0.079964	0.14333	0.027624	0	699	696	878	776	864	1005	1199	1470	1520	1428
ENSMUSG00000000743	chr8	Chmp1a	1.23E+08	1.23E+08	3260	0.275276	5.955295	0.08008	0.14352	0.028686	0	792	903	1019	929	1026	1243	1518	1615	1843	1715
ENSMUSG00000020014	chr10	Cfap54	92775619	92776298	14460	-0.71819	-0.23036	0.08012	0.143554	0.130483	0	21	17	16	19	5	9	15	15	10	19
ENSMUSG00000099226	chrX	Mir7091	74274027	74274105	79	-0.51872	1.437138	0.08011	0.143554	0.080446	0	64	42	58	36	57	58	50	50	42	46
ENSMUSG00000010830	chr15	Kdelr3	79516408	79516640	1414	0.477543	4.066602	0.080141	0.143573	0.085437	0	243	142	239	145	419	376	607	209	646	447
ENSMUSG00000036989	chr7	Trim3	1.06E+08	1.06E+08	4569	0.292392	4.222877	0.080184	0.143633	0.030362	0	257	246	324	259	307	361	428	588	502	504
ENSMUSG00000018661	chr11	Cog1	1.14E+08	1.14E+08	4987	0.283476	4.228639	0.080259	0.143748	0.028613	0	233	219	335	274	359	360	438	579	556	463
ENSMUSG00000024036	chr17	Slc37a1	31295483	31295754	3626	0.542604	0.490082	0.080324	0.143846	0.06799	0	17	13	17	18	23	20	44	28	41	48
ENSMUSG00000027185	chr2	Nat10	1.04E+08	1.04E+08	7199	-0.27555	4.32968	0.080377	0.143921	0.02704	0	291	323	474	335	423	314	401	416	526	474
ENSMUSG00000074102	chr9	Rbm15b	1.07E+08	1.07E+08	6511	0.318922	3.618007	0.080393	0.143922	0.035311	0	155	132	168	185	277	209	365	296	409	320
ENSMUSG00000103125	chr18	RP23-407E2.6	36975941	36976278	429	-0.45698	1.935509	0.080398	0.143922	0.066033	0	62	44	80	59	126	48	88	79	76	79
ENSMUSG00000102836	chr18	RP23-407E2.5	36969916	36970137	313	-0.45698	1.935509	0.080409	0.143924	0.066039	0	62	44	80	59	126	48	88	79	76	79
ENSMUSG00000071661	chr19	Zbtb3	8802530	8802685	2037	-0.50628	0.657366	0.080424	0.143932	0.06629	0	26	32	25	26	37	18	37	21	38	32
ENSMUSG00000022676	chr16	Snai2	14705852	14706052	2031	0.444382	1.971393	0.080645	0.144308	0.063056	0	42	47	47	53	83	84	113	108	145	66
ENSMUSG00000063179	chr7	Pstk	1.31E+08	1.31E+08	2179	-0.28558	4.222049	0.080711	0.144408	0.029154	0	305	336	375	338	338	335	349	411	483	376
ENSMUSG00000020464	chr11	Pnpt1	29130744	29130918	3516	-0.30632	4.235866	0.080746	0.144452	0.03395	0	321	344	415	307	332	354	380	306	483	432
ENSMUSG00000035595	chr10	1600002K03Rik	80172944	80173174	678	0.434899	1.946598	0.080805	0.144521	0.058799	0	41	58	69	38	60	78	109	84	105	126
ENSMUSG00000044221	chr5	Grsf1	88659448	88660459	3036	-0.31413	6.850509	0.080806	0.144521	0.03826	0	1701	2141	2344	2360	2064	1931	2139	3043	2754	2118
ENSMUSG00000008604	chr3	Ubqln4	88553758	88553912	4147	-0.28256	6.396834	0.080828	0.144543	0.03069	0	1261	1419	1775	1619	1644	1579	1638	1784	1995	1819
ENSMUSG00000040875	chr9	Osbpl10	1.15E+08	1.15E+08	5139	-0.44579	1.799385	0.080869	0.144597	0.060936	0	46	50	96	62	79	51	79	75	87	46
ENSMUSG00000002279	chr17	Lmf1	25579174	25579379	13471	0.318401	3.511271	0.080926	0.144679	0.034627	0	139	155	177	175	194	225	299	209	404	343
ENSMUSG00000024926	chr19	Kat5	5603017	5603552	2008	0.286141	4.055374	0.081066	0.144912	0.028873	0	209	202	302	248	291	301	417	521	500	392
ENSMUSG00000026638	chr1	Irf6	1.93E+08	1.93E+08	7069	0.524881	0.374552	0.081076	0.144912	0.058818	0	13	14	19	20	15	24	39	31	39	31
ENSMUSG00000034192	chr6	Lsm3	91515928	91516078	1257	0.339097	3.964139	0.081089	0.144916	0.041468	0	196	228	292	220	199	401	442	288	458	411
ENSMUSG00000083012	chr5	Fam220a	1.44E+08	1.44E+08	2734	-0.31856	5.671328	0.081269	0.145218	0.038801	0	814	887	1135	985	870	1012	1005	1248	1051	887
ENSMUSG00000021916	chr14	Glt8d1	31001393	31001428	2521	0.328435	3.877828	0.081297	0.14522	0.038706	0	214	172	268	167	265	335	442	266	429	418
ENSMUSG00000028224	chr4	Nbn	15957925	15958110	2533	-0.28717	3.934569	0.081301	0.14522	0.028857	0	211	249	362	281	302	239	357	348	359	300
ENSMUSG00000049957	chr11	Ccdc137	1.2E+08	1.2E+08	3803	-0.33442	2.916312	0.081294	0.14522	0.036613	0	130	132	149	120	163	122	178	135	175	162
ENSMUSG00000037993	chr8	Dhx38	1.1E+08	1.1E+08	4197	0.287455	4.263959	0.08139	0.14536	0.02959	0	222	244	325	306	352	307	441	542	666	539
ENSMUSG00000019732	chr8	Calr3	72424176	72424755	1962	-0.48733	1.161001	0.081412	0.14538	0.070216	0	34	45	54	40	36	30	38	60	48	34
ENSMUSG00000039105	chr4	Atp6v1g1	63544772	63544999	1135	0.301665	7.300505	0.081443	0.145417	0.035528	0	2041	2082	2886	2249	2550	3624	3251	4565	4248	4427
ENSMUSG00000020185	chr10	E2f7	1.11E+08	1.11E+08	9009	0.634937	0.468284	0.081647	0.145762	0.112111	0	8	13	18	22	23	29	36	14	67	38
ENSMUSG00000041143	chr4	Tmco4	1.39E+08	1.39E+08	3596	0.344796	3.005929	0.081759	0.145943	0.040314	0	88	104	147	120	127	174	181	258	227	190
ENSMUSG00000003269	chr7	Cyth2	45806637	45807848	3515	0.306086	4.238453	0.081799	0.145977	0.033915	0	250	233	347	299	272	337	449	635	572	444
ENSMUSG00000046275	chr11	Tusc5	76679808	76680537	3302	1.188378	2.561032	0.081793	0.145977	0.517761	0	53	20	18	103	103	13	50	47	331	558
ENSMUSG00000061479	chr7	Snrpa	27187005	27187364	1754	0.312244	4.765111	0.081915	0.146166	0.036518	0	311	354	447	437	481	628	727	457	964	741
ENSMUSG00000045095	chr6	Magi1	93675455	93679002	7701	-0.39336	2.399367	0.081943	0.146196	0.05034	0	80	85	121	101	108	68	139	78	151	98
ENSMUSG00000042616	chr4	Oscp1	1.26E+08	1.26E+08	5254	0.57738	0.968288	0.081989	0.146259	0.097863	0	20	19	26	26	33	19	42	42	80	83
ENSMUSG00000003344	chr10	Btbd2	80642617	80643691	3586	-0.27606	4.725352	0.082073	0.146391	0.028169	0	453	391	517	517	533	421	531	651	658	533
ENSMUSG00000042379	chr13	Esm1	1.13E+08	1.13E+08	2097	0.717959	0.838245	0.082128	0.146471	0.164738	0	26	9	6	19	47	34	43	49	44	72
ENSMUSG00000020553	chr11	Pctp	89982665	89984756	2723	0.40274	2.456499	0.082141	0.146474	0.05304	0	57	88	76	69	96	131	127	111	168	175
ENSMUSG00000054206	chr10	Gzmm	79689020	79689465	1472	-0.59066	1.712434	0.082268	0.146681	0.119434	0	59	40	77	63	87	28	51	125	51	44
ENSMUSG00000002329	chr14	Mdp1	55657879	55659074	1733	0.331837	4.817144	0.082448	0.146946	0.041593	0	358	427	522	395	356	730	724	554	816	787
ENSMUSG00000005373	chr5	Mlxipl	1.35E+08	1.35E+08	5367	-0.37764	5.808178	0.082429	0.146946	0.055469	0	929	760	1240	1183	1210	1001	1065	570	1561	1521
ENSMUSG00000026663	chr1	Atf6	1.71E+08	1.71E+08	9231	-0.28612	5.468428	0.082448	0.146946	0.031277	0	732	675	878	869	903	691	1025	1122	1029	788
ENSMUSG00000027811	chr3	4930579G24Rik	79629079	79629356	1970	0.504734	1.281564	0.082553	0.147115	0.076301	0	21	33	42	26	39	46	68	37	106	67
ENSMUSG00000006931	chr11	Leprel4	1E+08	1E+08	2178	0.378949	3.407124	0.082746	0.147439	0.051986	0	164	91	189	100	231	205	338	255	340	257
ENSMUSG00000087236	chr1	Gm1305	1.8E+08	1.8E+08	3449	0.563415	0.896528	0.082812	0.147538	0.090712	0	23	24	26	11	34	35	46	73	50	39
ENSMUSG00000028028	chr3	Alpk1	1.28E+08	1.28E+08	6709	0.503289	0.805128	0.082827	0.147545	0.063548	0	19	15	25	24	31	24	52	39	61	52
ENSMUSG00000032553	chr9	Srprb	1.03E+08	1.03E+08	4287	-0.27229	5.23981	0.082971	0.14777	0.028116	0	621	550	773	614	919	589	806	725	1026	880
ENSMUSG00000047649	chr7	Cd3eap	19356849	19358016	1657	-0.34566	3.22186	0.082974	0.14777	0.041811	0	136	167	218	163	182	129	212	250	204	159
ENSMUSG00000045140	chr11	Pigw	84876315	84878512	2733	-0.37725	2.447007	0.083045	0.147876	0.046289	0	78	94	136	90	112	86	104	136	115	103
ENSMUSG00000034875	chr7	Nudt19	35547185	35548123	2680	-0.3011	5.250027	0.083078	0.147917	0.034664	0	666	692	776	664	665	764	692	782	892	801
ENSMUSG00000038406	chr7	Scaf1	45002948	45003371	8368	-0.29218	5.525756	0.083098	0.147933	0.032861	0	678	681	940	908	1062	652	906	1247	1217	855
ENSMUSG00000025154	chr19	Arhgap19	41766588	41770196	5140	0.296191	4.208668	0.083123	0.147952	0.031854	0	252	231	346	256	296	370	518	347	605	543
ENSMUSG00000047420	chr6	Fam180a	35312746	35313869	1528	-0.72082	0.767477	0.083141	0.147952	0.167191	0	39	23	32	27	49	15	34	63	16	14
ENSMUSG00000068580	chr2	Zfyve19	1.19E+08	1.19E+08	3255	0.351345	3.330503	0.083136	0.147952	0.043172	0	102	148	180	152	149	200	205	346	293	258
ENSMUSG00000014837	chr8	4931428F04Rik	1.05E+08	1.05E+08	3552	0.508309	1.314515	0.083252	0.148131	0.080072	0	32	22	31	24	57	56	73	40	95	64

ENSMUSG00000027422	chr2	Rrbp1	1.44E+08	1.44E+08	8786	0.450499	6.470415	0.083274	0.148151	0.080021	0	1066	720	1282	1078	2307	1639	2658	1133	3662	3137
ENSMUSG00000040502	chr10	March9	1.27E+08	1.27E+08	3037	0.489262	0.782928	0.083317	0.148209	0.062781	0	15	14	27	22	36	32	44	46	48	50
ENSMUSG00000024913	chr19	Lrp5	3584828	3585291	9738	-0.29667	5.05799	0.083344	0.148237	0.033533	0	442	481	625	727	827	462	686	754	981	659
ENSMUSG00000039853	chr4	Trim14	46493781	46495767	4338	0.630942	-0.04248	0.08339	0.148301	0.083895	0	9	10	12	16	9	27	18	17	29	30
ENSMUSG00000063870	chr6	Chd4	1.25E+08	1.25E+08	8019	0.28198	7.058984	0.083417	0.148329	0.031361	0	1601	1546	2332	2012	2702	2241	3484	3684	4409	3493
ENSMUSG00000013539	chr16	Tango2	18300825	18301552	7040	0.594805	5.028646	0.0835	0.148439	0.137932	0	439	438	431	467	343	531	501	2189	611	691
ENSMUSG00000020903	chr11	Stx8	67966193	67966517	7137	0.281831	4.198236	0.083499	0.148439	0.028512	0	254	256	320	273	264	394	440	438	565	501
ENSMUSG00000031754	chr8	Nudt21	94017770	94019704	2726	0.290009	3.513292	0.083548	0.148485	0.028642	0	147	151	176	162	217	226	259	313	360	301
ENSMUSG00000037032	chr7	Apbb1	1.06E+08	1.06E+08	4404	0.353634	3.671369	0.083545	0.148485	0.045172	0	166	155	215	208	180	226	495	241	415	297
ENSMUSG00000024667	chr19	Tmem216	10533865	10533955	1977	0.469778	1.251577	0.083576	0.148517	0.064867	0	22	23	45	26	46	55	52	51	72	77
ENSMUSG00000027378	chr2	Nphp1	1.28E+08	1.28E+08	2708	-0.31452	4.676887	0.083588	0.148519	0.037261	0	430	427	537	481	475	479	452	655	478	549
ENSMUSG00000025064	chr19	Col17a1	47646344	47647278	5765	0.600173	0.028081	0.08361	0.148538	0.08046	0	7	7	17	16	14	19	37	25	28	19
ENSMUSG00000080316	chr17	Spaca6	17830719	17830858	6897	0.605876	1.499569	0.083642	0.148576	0.12323	0	41	24	29	17	71	35	70	96	79	107
ENSMUSG00000074227	chr7	Spint2	29256331	29256837	1459	0.463698	1.672504	0.083664	0.148597	0.066681	0	28	38	53	53	45	68	67	59	111	114
ENSMUSG00000041696	chr9	Rasl12	65398488	65398667	3877	0.525854	2.819412	0.083717	0.148671	0.100148	0	73	73	99	126	106	80	142	118	332	327
ENSMUSG00000035842	chr17	Ddx11	66123520	66123692	4149	0.639647	0.753615	0.083815	0.148827	0.124003	0	10	19	18	14	44	25	47	25	65	66
ENSMUSG00000032892	chr11	Rangrf	68972484	68972741	1269	-0.33433	4.54324	0.083835	0.148842	0.042287	0	352	460	452	471	407	494	469	334	568	509
ENSMUSG00000030546	chr7	Plin1	79721164	79721759	1916	1.379254	4.18439	0.083886	0.148914	0.708648	0	180	33	29	239	380	32	130	60	1170	1894
ENSMUSG00000095990	chr17	Zfp97	17121415	17121537	2684	-0.65645	0.817271	0.08393	0.148973	0.141413	0	37	24	40	35	36	8	22	64	29	32
ENSMUSG00000052730	chr6	Gm5111	48589445	48589694	1140	0.461493	1.580394	0.083964	0.149014	0.065151	0	39	45	39	34	43	79	70	86	69	78
ENSMUSG00000019977	chr10	Hbs1l	21295979	21296176	4893	-0.27955	6.075809	0.084172	0.149365	0.03054	0	1011	1144	1415	1239	1368	1174	1396	1603	1484	1410
ENSMUSG00000020123	chr10	Avpr1a	1.22E+08	1.22E+08	2671	0.535823	1.111231	0.084187	0.149373	0.080588	0	28	25	31	22	33	23	47	73	88	60
ENSMUSG00000049878	chr4	Rlf	1.21E+08	1.21E+08	6990	-0.33465	4.102344	0.08421	0.149393	0.041612	0	291	251	356	315	388	252	372	515	335	285
ENSMUSG00000087177	chr10	E130307A14Rik	39621412	39622727	7141	-0.35959	2.665922	0.084279	0.149496	0.042055	0	98	100	129	120	144	121	101	143	142	128
ENSMUSG00000030403	chr7	Vasp	19256929	19257754	2438	0.36505	5.900862	0.084313	0.149535	0.052547	0	647	740	1096	783	1155	1387	1889	803	2003	1775
ENSMUSG00000030741	chr7	Spns1	1.26E+08	1.26E+08	3707	0.286581	4.906226	0.084322	0.149535	0.031104	0	444	357	512	403	538	563	686	925	858	811
ENSMUSG00000029344	chr5	Tpst2	1.12E+08	1.12E+08	2789	0.306623	4.005235	0.084464	0.149768	0.034065	0	217	214	275	250	229	350	382	302	565	473
ENSMUSG00000100370	chr7	Gm4790	39566946	39570556	3611	-0.36627	2.926383	0.084509	0.149828	0.04575	0	123	117	158	118	199	106	169	203	151	138
ENSMUSG00000027326	chr2	Casc5	1.19E+08	1.19E+08	8542	0.666127	0.286609	0.084611	0.14999	0.129045	0	9	4	13	14	34	21	20	34	44	41
ENSMUSG00000033952	chr1	Aspm	1.39E+08	1.39E+08	9866	0.605641	1.448651	0.084628	0.150001	0.124723	0	21	25	30	23	80	45	82	47	140	66
ENSMUSG00000040410	chr4	Fbxl4	22357543	22357681	3798	-0.43239	4.073804	0.084646	0.150014	0.0718	0	340	249	362	315	336	178	256	623	311	306
ENSMUSG00000069520	chr10	Tmem19	1.15E+08	1.15E+08	3010	0.287223	3.982221	0.08472	0.150125	0.029312	0	206	222	277	230	243	253	454	381	542	419
ENSMUSG00000046447	chr4	Camk2n1	1.38E+08	1.38E+08	4444	0.432119	3.166022	0.084749	0.150158	0.068006	0	132	80	118	143	159	150	189	395	227	228
ENSMUSG00000006850	chr18	Tmco6	36735068	36735256	1817	0.498619	2.685102	0.08489	0.150389	0.09004	0	83	78	110	77	88	115	127	331	141	143
ENSMUSG00000025470	chr7	Zfp511	1.4E+08	1.4E+08	1100	0.37808	2.328246	0.084949	0.150465	0.046334	0	71	50	98	60	80	102	140	114	174	123
ENSMUSG00000054611	chr19	Kdm2a	4314419	4319281	14294	-0.31271	5.7797	0.084955	0.150465	0.038442	0	893	817	1100	1024	1275	754	1077	1631	1292	994
ENSMUSG00000001768	chr2	Rin2	1.46E+08	1.46E+08	5399	0.35182	4.848846	0.084984	0.150498	0.047987	0	391	241	526	378	617	390	764	943	985	759
ENSMUSG00000093185	chr4	Gm25692	45396994	45397118	125	0.359561	2.381466	0.085096	0.150676	0.040134	0	69	61	76	82	85	99	118	137	169	151
ENSMUSG00000078866	chr2	Gm14420	1.77E+08	1.77E+08	2172	-0.47894	2.65483	0.085254	0.150936	0.08188	0	66	76	191	82	218	100	111	147	128	117
ENSMUSG00000090639	chr9	Gm20425	1.03E+08	1.03E+08	3028	0.462671	6.298209	0.085326	0.151044	0.08545	0	942	590	905	1127	2132	1353	2093	1248	2711	3423
ENSMUSG00000040213	chr3	Ccbl2	1.43E+08	1.43E+08	2619	0.42661	3.007411	0.085343	0.151055	0.065036	0	109	112	94	127	115	134	154	332	218	227
ENSMUSG00000043372	chr11	Hexim2	1.03E+08	1.03E+08	2373	0.442642	1.45342	0.085362	0.151069	0.058015	0	36	22	49	34	47	49	69	87	81	69
ENSMUSG00000074971	chr2	Fibin	1.1E+08	1.1E+08	2267	-0.5119	4.382905	0.085452	0.15121	0.102666	0	469	255	552	249	539	182	558	677	342	257
ENSMUSG00000010064	chr9	Slc38a3	1.08E+08	1.08E+08	5277	-0.3258	5.14207	0.085618	0.151485	0.041411	0	488	596	763	849	567	632	830	683	950	561
ENSMUSG00000056592	chr7	Zfp658	43562256	43562421	3495	0.527776	0.361142	0.085669	0.151556	0.069448	0	16	6	21	19	19	26	32	33	38	33
ENSMUSG00000030493	chr7	C230052I12Rik	35392275	35393091	1824	0.570153	0.785631	0.085721	0.151628	0.090893	0	17	25	20	23	22	26	51	23	70	60
ENSMUSG00000034259	chr15	Exosc4	76327397	76327663	1945	0.272474	4.301525	0.085792	0.151733	0.027244	0	247	281	368	276	312	422	488	471	608	517
ENSMUSG00000041346	chr11	Wrap53	69561758	69562019	2062	0.378103	2.545011	0.085907	0.151918	0.047607	0	65	73	101	103	73	138	146	128	176	164
ENSMUSG00000009640	chr4	Dmap1	1.18E+08	1.18E+08	2636	0.305753	3.875916	0.086042	0.152078	0.034228	0	164	207	253	216	253	354	348	276	475	423
ENSMUSG00000011305	chr17	Plin5	56111601	56112541	2087	0.679008	4.397173	0.08601	0.152078	0.181377	0	185	331	365	298	141	248	284	1500	551	453
ENSMUSG00000033446	chr14	Lpar6	73237895	73243294	5400	0.426872	2.642045	0.086023	0.152078	0.062886	0	71	87	102	100	73	93	147	128	232	240
ENSMUSG00000063882	chr4	Uqcrh	1.16E+08	1.16E+08	1237	0.352066	8.730846	0.08604	0.152078	0.050128	0	5272	7249	7415	5859	4833	11516	10528	10347	11205	10948
ENSMUSG00000020368	chr11	Canx	50293961	50296335	4693	0.280832	6.804182	0.08611	0.152179	0.031564	0	1351	1462	1814	1531	2358	2048	2932	2524	3801	3177
ENSMUSG00000078185	chr1	Chml	1.76E+08	1.76E+08	6117	-0.38347	1.91853	0.086122	0.152181	0.044906	0	57	59	79	78	78	52	84	68	100	75
ENSMUSG00000029772	chr6	Ahcyl2	29768011	29768317	11896	-0.30485	4.124038	0.08617	0.152228	0.034855	0	250	280	371	343	367	209	353	348	439	494
ENSMUSG00000046909	chr11	Tefm	80136678	80137279	1570	-0.29863	3.87568	0.086165	0.152228	0.032608	0	214	265	350	263	250	242	331	313	387	262
ENSMUSG00000031201	chrX	Brcc3	75416628	75416841	7887	-0.29653	4.038393	0.086196	0.152242	0.032359	0	274	299	359	263	301	299	334	390	363	314
ENSMUSG00000075053	chr13	Vdac3-ps1	18030324	18031629	1306	-0.31824	4.440312	0.0862	0.152242	0.038587	0	371	425	427	406	344	442	409	460	480	426
ENSMUSG00000024269	chr18	Tpgs2	25127223	25129903	6840	-0.41861	3.123354	0.086213	0.152245	0.06378	0	123	143	190	182	193	172	209	79	211	187
ENSMUSG00000044881	chr7	Coa4	1.01E+08	1.01E+08	1425	0.377601	2.240549	0.086288	0.152357	0.045673	0	56	52	95	69	65	102	132	115	139	120
ENSMUSG00000036412	chr18	Arsi	60911780	60912550	2975	0.578319	3.780306	0.086425	0.152579	0.131285	0	129	101	162	149	414	371	509	115	447	451
ENSMUSG00000018442	chr11	Derl2	71007164	71007347	8049	0.296488	4.119442	0.086499	0.152691	0.032506	0	236	237	310	204	311	351	422	367	540	553
ENSMUSG00000019997	chr10	Ctgf	24595442	24595788	2861	0.511684	5.180882	0.086812	0.153225	0.104586	0	475	351	572	462	656	708	1108	1896	797	394
ENSMUSG00000039236	chr7	Isg20	78913424	78913494	1826	0.651802	0.9334	0.086966	0.153476	0.140647	0	15	26	21	16	40	60	24	32	52	83
ENSMUSG00000022008	chr14	Gpalpp1	76086232	76090746	5448	-0.30687	3.918035	0.086982	0.153485	0.034951	0	251	230	321	272	319	202	308	436	354	280
ENSMUSG00000037465	chr15	Klf10	38294413	38296164	3045	0.365143	4.263117	0.087076	0.153631	0.051614	0	186	181	361	336	362	244	442	663	654	565

ENSMUSG00000050147	chr8	F2rl3	72761880	72762014	1751	-0.52423	1.328681	0.087254	0.153927	0.088992	0	33	44	55	48	62	45	56	18	70	45
ENSMUSG00000020894	chr11	Vamp2	69088490	69088627	3809	0.262621	5.548086	0.087439	0.154233	0.027135	0	635	542	793	737	861	1014	1208	1071	1435	1215
ENSMUSG00000015605	chr17	Srf	46546839	46549178	4093	-0.29982	6.439988	0.087565	0.154396	0.036177	0	1094	1496	1769	1754	1944	1737	1931	1468	2143	1732
ENSMUSG00000027984	chr3	Hadh	1.31E+08	1.31E+08	4977	0.347276	7.555044	0.087564	0.154396	0.049062	0	2079	3040	2778	3399	2329	3881	3553	5597	5900	5699
ENSMUSG00000047749	chr6	Zc3hav1l	38287396	38293137	6536	-0.52829	1.673743	0.087558	0.154396	0.094688	0	54	33	67	47	115	43	91	40	77	49
ENSMUSG00000003070	chr10	Efna2	80179482	80179890	2131	0.75575	0.14548	0.087602	0.154442	0.170818	0	13	1	17	12	20	24	44	10	39	29
ENSMUSG00000028405	chr4	Aco1	40143081	40143541	4496	0.370189	5.009471	0.08768	0.154559	0.054299	0	414	364	451	496	631	503	732	558	1175	1360
ENSMUSG00000096974	chr4	Gm26881	43046034	43046277	592	0.449999	1.405518	0.087836	0.154815	0.060048	0	27	29	44	34	47	62	48	60	87	85
ENSMUSG00000052926	chr8	Rnaseh2a	84956610	84957864	3509	0.286561	3.8137	0.087875	0.154863	0.029795	0	161	206	262	186	239	300	312	366	435	378
ENSMUSG00000007783	chr7	Cpt1c	44959373	44959675	2793	0.481955	1.507612	0.087905	0.154897	0.074258	0	42	22	40	25	64	55	75	65	85	93
ENSMUSG00000030527	chr7	Crtc3	80586627	80589951	9850	-0.31921	4.168682	0.088096	0.155214	0.038884	0	266	248	325	363	482	229	361	499	458	336
ENSMUSG00000023456	chr6	Tpi1	1.25E+08	1.25E+08	2209	-0.31025	11.42004	0.088128	0.155251	0.039579	0	40493	52344	62610	48378	48334	58303	52522	51745	62213	56489
ENSMUSG00000024941	chr19	Scyl1	5758427	5758696	2637	-0.28627	6.304546	0.088428	0.15576	0.033109	0	1219	1250	1599	1544	1654	1232	1476	2125	1883	1608
ENSMUSG00000020267	chr11	Hint1	54866383	54866600	872	0.30306	6.84924	0.088521	0.155903	0.0374	0	1537	1639	2201	1502	1709	2802	2657	3075	3004	3117
ENSMUSG00000044562	chr7	Rasip1	45627488	45627590	3202	0.349077	3.843215	0.088567	0.155951	0.045946	0	149	199	220	282	192	269	319	287	573	451
ENSMUSG00000057666	chr6	Gapdh	1.25E+08	1.25E+08	4133	-0.29972	12.72058	0.088571	0.155951	0.03706	0	94386	124188	143082	131322	128039	135041	117129	152120	155527	138390
ENSMUSG00000066677	chr1	Pydc3	1.74E+08	1.74E+08	5255	0.956472	0.564333	0.088591	0.155966	0.32138	0	12	7	17	13	32	80	9	15	22	69
ENSMUSG00000020642	chr12	Rnf144a	26306797	26310789	5163	-0.30663	3.766096	0.088659	0.156066	0.034551	0	173	178	278	325	314	213	277	307	331	289
ENSMUSG00000078713	chr4	Tomm5	45105208	45105644	868	0.343684	5.120004	0.088695	0.156111	0.046995	0	439	579	574	474	449	948	929	625	1052	914
ENSMUSG00000034126	chr12	Pomt2	87106866	87109293	5059	-0.35316	3.508783	0.088751	0.156188	0.046728	0	216	154	240	175	282	132	276	311	237	212
ENSMUSG00000038240	chr10	Pdss2	43221486	43222060	5963	-0.34652	4.478543	0.088878	0.156393	0.047071	0	357	435	450	440	370	477	471	287	593	438
ENSMUSG00000033453	chr9	Adamts15	30899155	30902789	5928	0.437324	2.989089	0.088908	0.156417	0.072181	0	67	75	95	118	219	131	274	191	211	251
ENSMUSG00000036916	chrX	Zfp280c	48541625	48543289	5236	-0.39918	2.048079	0.088915	0.156417	0.05286	0	75	62	84	72	93	52	95	84	74	104
ENSMUSG00000093904	chr8	Tomm20	1.27E+08	1.27E+08	4986	0.282747	5.630081	0.088935	0.156433	0.031892	0	636	717	851	741	765	961	1098	1571	1434	1276
ENSMUSG00000058835	chr2	Abi1	22940073	22942047	4032	0.277888	4.524902	0.088949	0.156438	0.029471	0	298	282	400	329	435	360	579	693	733	609
ENSMUSG00000075703	chr5	Ept1	30232581	30232815	10855	-0.26834	3.931357	0.089093	0.156671	0.026223	0	237	237	297	272	349	255	366	278	389	325
ENSMUSG00000071533	chr16	Pcnp	56007245	56007482	3115	-0.26036	4.902253	0.089327	0.157063	0.02631	0	483	496	629	490	618	513	660	631	742	624
ENSMUSG00000032867	chr5	Fbxw8	1.18E+08	1.18E+08	4978	0.275511	5.451042	0.089347	0.157077	0.030223	0	613	490	710	653	858	781	1045	1333	1357	1108
ENSMUSG00000023262	chr9	Acy1	1.06E+08	1.06E+08	2966	0.368861	2.695183	0.089369	0.157096	0.04816	0	91	64	97	100	114	137	142	195	156	201
ENSMUSG00000029993	chr6	Nfu1	87009236	87009389	2078	0.284775	5.297205	0.089401	0.157133	0.032228	0	539	542	733	532	599	914	983	1035	1017	1023
ENSMUSG00000071419	chr6	Rps15-ps2	58017506	58017943	438	0.280837	3.746428	0.089494	0.157276	0.028579	0	164	192	238	182	230	289	359	299	390	365
ENSMUSG00000000317	chr11	Bcl6b	70224128	70226143	3719	-0.49069	3.280962	0.089698	0.157615	0.094313	0	102	207	156	295	174	132	196	97	352	190
ENSMUSG00000021114	chr12	Atp6v1d	78842989	78843610	1403	0.292757	6.197566	0.089803	0.15778	0.034844	0	979	1086	1176	1133	1079	1664	1676	2114	2014	1875
ENSMUSG00000014226	chr1	Cacybp	1.6E+08	1.6E+08	2390	-0.28671	5.597913	0.089846	0.157835	0.033086	0	718	856	1196	765	912	787	1203	870	1183	1060
ENSMUSG00000009731	chrX	Kcnd1	7822289	7824963	5287	0.630146	0.277032	0.089894	0.157899	0.114436	0	11	7	18	8	30	20	23	23	44	48
ENSMUSG00000028409	chr4	Smu1	40736542	40737395	3119	0.265831	5.594279	0.089943	0.157965	0.02831	0	600	640	884	734	813	998	1218	1389	1291	1222
ENSMUSG00000024847	chr19	Aip	4114446	4114796	1937	-0.28092	5.829571	0.090216	0.158425	0.031911	0	877	948	1231	1015	1138	1107	1152	980	1386	1326
ENSMUSG00000051379	chr2	Flrt3	1.41E+08	1.41E+08	4865	-0.55504	0.243125	0.090313	0.158575	0.075064	0	25	11	23	23	28	19	14	23	28	20
ENSMUSG00000033356	chr15	Pus7l	94522688	94523651	3291	0.468461	1.316121	0.090377	0.158667	0.064002	0	27	33	35	28	44	49	69	40	91	77
ENSMUSG00000024142	chr17	Mlst8	24473550	24475951	3366	-0.27217	4.066499	0.090414	0.158713	0.027603	0	250	259	391	288	346	287	374	296	432	380
ENSMUSG00000056973	chr8	Ces1d	93166068	93166438	2369	0.993338	4.628977	0.090443	0.158743	0.394946	0	294	194	149	385	338	110	152	204	1167	2428
ENSMUSG00000026032	chr1	Ndufb3	58586384	58586670	763	0.337438	6.706263	0.090458	0.158749	0.046913	0	1355	1729	1779	1495	1205	2737	2525	2390	2887	2853
ENSMUSG00000069633	chr8	Pex11g	3457105	3459434	3397	0.389341	2.416177	0.090556	0.158901	0.051783	0	59	81	83	69	85	99	141	104	162	191
ENSMUSG00000036372	chr19	Tmem258	10204014	10204264	1611	0.320293	4.980078	0.090583	0.158927	0.041004	0	422	485	580	362	473	794	866	589	946	848
ENSMUSG00000027475	chr2	Kif3b	1.53E+08	1.53E+08	5635	0.32552	3.500891	0.090608	0.158952	0.039604	0	121	121	189	159	260	190	349	240	395	307
ENSMUSG00000031258	chrX	Xkrx	1.34E+08	1.34E+08	3024	0.667584	-0.15475	0.090664	0.159029	0.093727	0	14	8	12	9	7	21	20	12	30	30
ENSMUSG00000078427	chr10	Sarnp	1.29E+08	1.29E+08	1062	0.289118	4.732691	0.090819	0.159281	0.032871	0	349	373	513	358	394	623	753	570	752	677
ENSMUSG00000027447	chr2	Cst3	1.49E+08	1.49E+08	1266	0.298329	8.716404	0.090896	0.159376	0.037129	0	5921	5671	7501	5532	6819	9252	10064	13575	10633	10072
ENSMUSG00000062713	chr16	Sim2	94085260	94085990	3670	-0.82138	3.478042	0.09089	0.159376	0.269802	0	25	299	303	389	172	245	57	163	159	274
ENSMUSG00000030761	chr7	Myo7a	98051060	98051716	8524	0.426545	3.245599	0.09092	0.159398	0.069838	0	146	72	121	130	207	186	269	138	363	319
ENSMUSG00000020064	chr10	Herc4	63243797	63244163	4019	-0.28647	4.697724	0.090971	0.159449	0.032272	0	430	414	570	417	550	397	526	710	586	504
ENSMUSG00000091561	chr18	Gm6665	31819862	31819921	258	0.60463	0.084584	0.090972	0.159449	0.089857	0	11	9	8	18	17	30	22	29	21	29
ENSMUSG00000025260	chrX	Hsd17b10	1.52E+08	1.52E+08	1298	0.291303	5.637286	0.091038	0.159543	0.034415	0	604	722	847	773	776	994	1100	1577	1274	1408
ENSMUSG00000003948	chr11	Mmd	90187684	90188235	5386	0.497881	4.774802	0.091097	0.159627	0.101149	0	322	255	351	394	600	364	442	486	1013	1535
ENSMUSG00000044211	chr6	Gm7887	48524372	48525105	734	-0.57398	0.306617	0.091114	0.159636	0.090721	0	17	20	30	24	25	7	35	16	31	22
ENSMUSG00000051335	chr13	Gfod1	43195519	43201244	6654	-0.35883	2.787958	0.091259	0.159871	0.047391	0	104	113	117	156	151	73	149	144	191	157
ENSMUSG00000032123	chr9	Dpagt1	44326845	44327205	1905	0.286489	4.130463	0.091274	0.159877	0.031215	0	195	247	283	279	311	365	403	358	611	514
ENSMUSG00000022679	chr16	Mpv17l	13903161	13903280	3760	-0.50329	0.452884	0.091465	0.160191	0.064535	0	15	20	32	25	36	15	32	25	29	24
ENSMUSG00000089671	chr15	Gm16537	99715543	99715839	702	0.936485	0.417197	0.091531	0.160286	0.296492	0	4	20	9	25	9	15	22	12	115	36
ENSMUSG00000042121	chr5	Ssh1	1.14E+08	1.14E+08	8892	-0.30255	3.256089	0.091549	0.160298	0.033069	0	151	137	175	212	201	135	215	193	250	208
ENSMUSG00000058748	chr8	Zfp958	4625840	4625966	1401	-0.45686	1.808065	0.091655	0.160458	0.07009	0	61	54	89	64	63	49	55	105	76	52
ENSMUSG00000074576	chr2	Mocs3	1.68E+08	1.68E+08	1973	0.405481	1.722647	0.091664	0.160458	0.050498	0	39	44	54	42	50	53	97	88	118	75
ENSMUSG00000095588	chr4	Gm12350	34485832	34486293	462	0.373726	3.455276	0.091823	0.160716	0.053476	0	140	166	217	125	136	305	277	282	245	286
ENSMUSG00000020547	chr12	Bzw2	36091846	36092309	1860	-0.29175	6.829796	0.091844	0.160732	0.035338	0	1745	2049	2362	2061	2199	2362	2150	2249	2525	2477
ENSMUSG00000033720	chr6	Sfxn5	85213051	85215746	5743	0.46893	2.338866	0.0919	0.160807	0.080248	0	51	57	93	68	81	72	95	95	206	222
ENSMUSG00000045211	chr14	Nudt18	70577847	70578110	3716	0.337031	3.499032	0.09191	0.160807	0.042442	0	137	157	212	155	165	212	278	198	428	368

ENSMUSG00000029196	chr5	Tada2b	36473670	36476962	3791	-0.3469	4.143289	0.092007	0.160957	0.047623	0	299	279	331	338	400	230	338	576	395	278
ENSMUSG00000066613	chr5	Zfp932	1.1E+08	1.1E+08	3272	-0.42198	2.156933	0.092039	0.160993	0.063568	0	81	69	113	68	89	62	101	51	118	111
ENSMUSG00000038268	chr11	Ovca2	75175942	75178387	2670	0.315021	3.219721	0.092054	0.160999	0.035507	0	126	124	144	109	185	187	219	209	322	265
ENSMUSG00000086877	chrX	A230072C01Rik	20961684	20961712	1581	-0.49472	0.782838	0.092227	0.161281	0.069336	0	30	32	37	31	29	22	22	31	39	46
ENSMUSG00000024379	chr18	Tslp	32815383	32815403	1133	0.520265	0.538159	0.092357	0.161487	0.069355	0	20	12	22	18	20	30	25	42	39	48
ENSMUSG00000025934	chr1	Gsta3	21240589	21240659	4344	1.26201	0.269397	0.0924	0.161542	0.574522	0	4	3	4	15	29	1	6	28	39	109
ENSMUSG00000031351	chrX	Zfp185	72987339	72987519	3707	-0.69214	2.826966	0.092447	0.16159	0.191784	0	201	57	166	65	249	51	274	62	137	118
ENSMUSG00000063696	chr8	Gm8730	1.03E+08	1.03E+08	1075	0.339137	2.869349	0.092451	0.16159	0.040558	0	90	96	137	89	121	169	168	156	230	214
ENSMUSG00000030495	chr7	Slc7a10	35186385	35186650	2463	1.315779	1.641711	0.092499	0.161634	0.670216	0	28	4	1	28	88	8	45	32	140	296
ENSMUSG00000032399	chr9	Rpl4	64173387	64173433	1422	0.262621	9.093502	0.092496	0.161634	0.029087	0	6749	7229	9274	8004	10541	10982	13306	15502	15559	14168
ENSMUSG00000029063	chr4	Nadk	1.56E+08	1.56E+08	3747	0.354541	4.920561	0.09268	0.161881	0.051229	0	413	304	468	430	625	463	673	579	1138	1203
ENSMUSG00000030291	chr6	Med21	1.47E+08	1.47E+08	2102	-0.29591	4.320524	0.092673	0.161881	0.034291	0	327	358	464	343	327	354	453	452	424	387
ENSMUSG00000031730	chr8	Dhodh	1.1E+08	1.1E+08	6326	-0.3222	3.567443	0.092685	0.161881	0.039248	0	186	232	246	187	236	220	280	170	287	261
ENSMUSG00000101316	chr11	Gm12663	16635109	16636066	958	-0.51013	0.88999	0.092687	0.161881	0.07772	0	28	29	53	39	25	25	42	35	46	24
ENSMUSG00000041351	chr4	Rap1gap	1.38E+08	1.38E+08	6429	-0.4222	2.546348	0.092714	0.161907	0.065999	0	92	124	123	125	78	98	112	75	165	130
ENSMUSG00000038855	chr1	Itpkb	1.8E+08	1.8E+08	10463	-0.30753	5.168176	0.092725	0.161907	0.03858	0	461	535	671	912	760	519	737	632	1091	834
ENSMUSG00000018796	chr8	Acsl1	46471041	46471230	9449	-0.33787	7.957526	0.092936	0.162254	0.048154	0	3433	4558	4868	5529	4713	2818	3910	5701	7126	6707
ENSMUSG00000021975	chr14	Ints9	64950045	64950367	2677	0.271037	3.684844	0.092959	0.162274	0.026872	0	166	170	230	171	233	273	313	321	401	322
ENSMUSG00000029674	chr5	Limk1	1.35E+08	1.35E+08	7154	0.459575	2.391077	0.093002	0.162329	0.077945	0	57	45	78	59	132	86	177	84	209	154
ENSMUSG00000096401	chr8	Gm21811	20136502	20136663	930	-0.66159	0.281749	0.09305	0.162391	0.13567	0	39	12	35	13	16	18	16	22	19	27
ENSMUSG00000022231	chr15	Sema5a	32244813	32245299	10809	-0.3393	3.475109	0.093082	0.162406	0.043476	0	174	143	185	229	314	195	261	236	279	166
ENSMUSG00000048240	chr10	Gng7	80948624	80951746	3786	-0.48151	1.441756	0.093081	0.162406	0.075579	0	35	38	42	69	76	40	47	35	69	68
ENSMUSG00000024589	chr18	Nedd4l	64887756	64888095	8626	-0.32728	5.239113	0.093163	0.162515	0.043916	0	617	651	1088	483	675	697	822	769	873	717
ENSMUSG00000038910	chr17	Plcl2	50509547	50509937	4050	-0.31205	5.767471	0.093168	0.162515	0.040304	0	905	847	1063	1077	1141	842	983	1644	1116	1058
ENSMUSG00000026893	chr2	Gca	62664285	62664459	3409	-0.45391	1.295922	0.093341	0.162796	0.064153	0	33	56	43	50	45	44	43	46	57	43
ENSMUSG00000037933	chr13	Bicd2	49341549	49341641	6351	-0.29044	5.413518	0.093369	0.162825	0.03454	0	540	782	877	867	850	784	951	694	1058	973
ENSMUSG00000001763	chr6	Tspan33	29694222	29694544	5195	0.423966	1.562107	0.093405	0.162856	0.055253	0	34	31	46	43	50	58	98	75	95	56
ENSMUSG00000020778	chr11	Ten1	1.16E+08	1.16E+08	2728	0.323539	3.989036	0.09341	0.162856	0.040917	0	192	230	284	231	229	417	446	272	471	418
ENSMUSG00000040414	chr19	Slc25a28	43663822	43664643	1514	0.38287	4.252469	0.093485	0.162966	0.059143	0	217	257	341	296	261	341	332	830	482	514
ENSMUSG00000039901	chr19	9130011E15Rik	45818144	45818978	2896	-0.27861	3.854443	0.093551	0.16306	0.029144	0	245	221	316	225	315	242	297	350	329	296
ENSMUSG00000050382	chr7	Kif7	79698098	79698915	4581	0.579886	0.748662	0.093639	0.163193	0.104659	0	31	7	17	18	32	25	51	48	55	43
ENSMUSG00000046844	chr8	Vat1l	1.14E+08	1.14E+08	5462	0.751003	0.851101	0.093678	0.163225	0.194673	0	26	8	16	28	26	12	64	20	84	78
ENSMUSG00000096956	chr15	Snhg18	32240569	32241769	1482	0.350697	3.130874	0.09368	0.163225	0.046085	0	118	96	146	86	199	199	246	204	254	224
ENSMUSG00000030835	chr7	Nomo1	46033698	46033972	5936	-0.26745	6.142009	0.093697	0.163232	0.029687	0	1071	959	1477	1351	1657	1157	1368	1572	1812	1596
ENSMUSG00000026525	chr1	Opn3	1.76E+08	1.76E+08	1913	0.685066	0.584212	0.093746	0.163297	0.15468	0	20	5	16	22	26	15	38	20	73	61
ENSMUSG00000022792	chr16	Yars2	16302965	16303747	3149	-0.32278	3.782358	0.093891	0.163528	0.040409	0	204	291	283	261	213	267	288	249	323	281
ENSMUSG00000040249	chr10	Lrp1	1.28E+08	1.28E+08	17717	0.419155	7.486507	0.093902	0.163528	0.074365	0	2755	1109	2686	1969	4670	2837	5020	4078	7177	5471
ENSMUSG00000049891	chr8	Gm7984	75398511	75398738	534	-0.56844	0.464034	0.093992	0.163664	0.094512	0	17	35	34	26	16	23	28	19	23	28
ENSMUSG00000003308	chr9	Keap1	21229730	21230868	4664	-0.31357	6.416641	0.094167	0.163949	0.041291	0	1300	1398	1753	1542	1951	1479	1497	2442	1600	1760
ENSMUSG00000027227	chr2	Sord	1.22E+08	1.22E+08	2352	-0.28912	5.411019	0.094203	0.16399	0.03443	0	660	726	844	925	718	741	815	986	917	977
ENSMUSG00000044937	chr10	BC030307	86705811	86706017	4646	-0.48674	0.584816	0.094253	0.164058	0.062985	0	26	24	28	28	32	24	30	35	30	18
ENSMUSG00000064363	chrMT	mt-Nd4	10167	11544	1378	-0.3372	12.07986	0.094278	0.16408	0.048539	0	57091	75550	98903	109037	61000	78645	81023	79223	106245	100368
ENSMUSG00000026048	chr1	Ercc5	44147744	44149522	5864	-0.28807	3.984127	0.094297	0.164092	0.031981	0	249	300	318	257	314	280	333	387	354	291
ENSMUSG00000079317	chrX	Trappc2	1.66E+08	1.66E+08	3643	-0.31967	3.596997	0.094372	0.164202	0.038773	0	191	223	277	198	221	258	258	210	263	240
ENSMUSG00000028339	chr4	Col15a1	47208161	47208362	6349	-0.50215	7.368795	0.094416	0.164258	0.106813	0	2564	2087	3383	3407	5130	2641	4181	894	5404	3184
ENSMUSG00000018583	chr11	G3bp1	55469685	55469801	7064	-0.2755	7.15879	0.094535	0.164404	0.032104	0	2025	2247	3125	2421	3402	2616	3167	2477	3675	3145
ENSMUSG00000050555	chr9	Hyls1	35560820	35562104	5970	0.532852	0.446187	0.094526	0.164404	0.075394	0	13	11	23	20	19	21	35	22	52	46
ENSMUSG00000069114	chr3	Zbtb10	9250602	9252080	7414	-0.42002	2.628332	0.094519	0.164404	0.067693	0	97	120	99	116	150	58	136	181	151	95
ENSMUSG00000081049	chrX	Rps24-ps3	79195047	79195448	402	0.412037	2.035676	0.094549	0.164408	0.057882	0	38	68	69	51	59	94	92	99	117	127
ENSMUSG00000028901	chr4	Gmeb1	1.32E+08	1.32E+08	7857	-0.29346	3.440102	0.094693	0.164637	0.032138	0	173	159	193	211	261	140	249	243	286	228
ENSMUSG00000036944	chr15	Tmem71	66526212	66527934	2931	0.563175	0.903719	0.094729	0.164678	0.09865	0	14	25	24	25	31	32	36	87	45	44
ENSMUSG00000038530	chr1	Rgs4	1.7E+08	1.7E+08	3098	-0.31065	3.38705	0.094751	0.164696	0.036157	0	136	177	230	223	197	156	267	190	249	226
ENSMUSG00000057766	chr18	Ankrd29	12252362	12254701	3295	-0.63965	0.007553	0.094786	0.164736	0.10726	0	14	9	24	19	30	7	21	27	12	17
ENSMUSG00000043155	chr4	Hpdl	1.17E+08	1.17E+08	1804	0.45169	1.373715	0.094819	0.164772	0.062085	0	31	36	38	39	29	55	84	61	83	52
ENSMUSG00000066621	chr5	Tecpr1	1.44E+08	1.44E+08	9665	-0.2686	4.870016	0.094843	0.164793	0.029227	0	470	437	576	602	578	404	605	632	753	731
ENSMUSG00000015970	chr14	Chdh	30009023	30009233	6156	1.315536	0.820294	0.094877	0.164811	0.657739	0	17	7	1	30	21	3	10	12	110	155
ENSMUSG00000016477	chr13	E2f3	29906575	29910165	4794	-0.31915	4.24395	0.09487	0.164811	0.040636	0	234	264	433	361	497	264	358	536	493	328
ENSMUSG00000024312	chr17	Wdr46	33940660	33940806	2442	0.308354	3.354608	0.09491	0.164828	0.035837	0	103	130	165	138	233	210	245	269	344	247
ENSMUSG00000028945	chr5	Rheb	24802823	24803756	5540	-0.28494	5.751264	0.0949	0.164828	0.033823	0	830	931	1208	951	1008	890	1135	1411	1208	1000
ENSMUSG00000028407	chr4	Toporsos	40269569	40269719	1054	-0.30614	3.055673	0.094956	0.164868	0.033668	0	144	137	170	148	158	142	163	162	225	171
ENSMUSG00000052997	chr7	Uba2	34140689	34141466	4092	-0.25704	5.494221	0.094957	0.164868	0.027199	0	683	635	916	900	991	683	958	1000	1261	938
ENSMUSG00000034203	chr6	Chchd4	91464276	91465313	1245	0.300914	4.388715	0.095006	0.164932	0.036024	0	269	326	407	280	264	463	561	537	587	523
ENSMUSG00000006641	chr5	Slc5a6	31036036	31036953	3991	0.348137	2.724865	0.095026	0.164947	0.042457	0	80	95	102	90	110	126	150	138	239	208
ENSMUSG00000044167	chr3	Foxo1	52268336	52269422	8665	-0.28763	4.416853	0.095085	0.165027	0.032962	0	325	320	438	410	474	315	368	590	502	471
ENSMUSG00000103565	chr15	Sgsm3	81002628	81002664	2283	-0.29446	3.386721	0.095148	0.165117	0.032024	0	151	188	216	181	220	172	190	251	266	212
ENSMUSG00000027221	chr2	Chst1	92599707	92600148	2680	0.67228	2.030426	0.095262	0.165294	0.177057	0	39	35	37	73	73	37	54	82	160	257

ENSMUSG00000022774	chr16	Ncbp2	31948513	31948727	2305	0.274936	4.610373	0.095316	0.165366	0.030161	0	331	356	424	311	412	526	712	511	726	631
ENSMUSG00000079022	chr15	Col22a1	71795795	71799520	9203	-0.53734	6.232889	0.095353	0.16541	0.122442	0	1624	654	2025	746	2634	925	2121	1644	1925	650
ENSMUSG00000000392	chr2	Fap	62500943	62501288	5662	0.377437	4.616912	0.095435	0.165531	0.059148	0	306	226	404	297	587	537	988	416	683	589
ENSMUSG00000003131	chr9	Pafah1b2	45965311	45968966	4241	0.267458	4.979464	0.095466	0.165564	0.029098	0	378	394	517	440	688	545	861	815	1042	799
ENSMUSG00000040836	chr1	Gpr161	1.65E+08	1.65E+08	6962	-0.48747	1.327353	0.095499	0.165601	0.076654	0	45	27	36	55	77	40	55	47	58	36
ENSMUSG00000039741	chr11	Bahcc1	1.2E+08	1.2E+08	11118	-0.35807	3.004284	0.095595	0.165747	0.048564	0	112	124	144	162	212	102	120	181	205	216
ENSMUSG00000047757	chrX	Fancb	1.65E+08	1.65E+08	2983	-0.50164	0.310492	0.095677	0.165849	0.058899	0	21	19	21	27	25	17	19	24	27	25
ENSMUSG00000054455	chr2	Vapb	1.74E+08	1.74E+08	7131	-0.26349	7.348221	0.095678	0.165849	0.02961	0	2670	2584	3259	2874	3472	2945	3108	3587	4034	3567
ENSMUSG00000048330	chr7	Ric3	1.09E+08	1.09E+08	8561	-0.53847	0.552768	0.095698	0.165863	0.086727	0	20	39	26	26	24	16	20	35	39	24
ENSMUSG00000001802	chr7	Lrp3	35200027	35200415	4571	-0.32424	3.702037	0.095737	0.165909	0.040847	0	203	172	258	242	344	189	241	381	282	249
ENSMUSG00000050043	chr2	Tmx2	84671316	84672532	2330	-0.40544	5.640244	0.095763	0.165934	0.069546	0	778	965	1107	891	981	986	1203	394	1399	1023
ENSMUSG00000047260	chr11	Emc6	73175519	73176751	1415	0.292698	5.943588	0.095788	0.165956	0.036037	0	747	933	1112	920	877	1508	1405	1539	1730	1629
ENSMUSG00000022325	chr15	Pop1	34495304	34495415	3795	0.414547	2.117848	0.095881	0.166097	0.059685	0	46	66	75	46	70	92	119	76	171	113
ENSMUSG00000050666	chr14	Vstm4	32856756	32856966	2741	0.398813	3.020411	0.095911	0.166128	0.06276	0	85	72	128	105	204	174	295	151	217	222
ENSMUSG00000035770	chr8	Dync1li2	1.04E+08	1.04E+08	4633	-0.26293	6.475098	0.096039	0.166322	0.02925	0	1417	1302	1980	1482	1987	1489	1983	2000	2097	1860
ENSMUSG00000086784	chr7	Isoc2a	4877053	4877193	1088	0.304561	4.701209	0.096047	0.166322	0.03773	0	395	327	403	371	431	469	486	730	798	886
ENSMUSG00000028969	chr5	Cdk5	24418250	24419462	2050	0.300743	3.836425	0.096082	0.166362	0.034893	0	185	219	247	180	225	293	381	281	420	455
ENSMUSG00000047719	chr4	Ubiad1	1.48E+08	1.48E+08	2992	-0.2887	4.004123	0.096105	0.166382	0.032497	0	232	277	307	336	311	313	372	270	405	310
ENSMUSG00000080776	chr11	Gm12174	46727818	46728630	813	0.333143	2.824097	0.096119	0.166384	0.039633	0	94	81	115	113	113	162	154	155	247	192
ENSMUSG00000020691	chr11	Mettl2	1.05E+08	1.05E+08	3399	-0.34654	2.668855	0.096173	0.166457	0.042893	0	105	104	129	128	119	96	161	141	135	112
ENSMUSG00000017288	chr11	Vps53	76046226	76046582	5203	0.255108	4.593488	0.096187	0.16646	0.025989	0	290	312	417	355	474	503	572	617	706	654
ENSMUSG00000086474	chr11	9130204K15Rik	79781979	79782556	1462	0.795949	-0.44364	0.096219	0.166495	0.16044	0	12	10	5	5	5	23	10	24	10	23
ENSMUSG00000050891	chr15	Tatdn1	58890153	58890697	1366	-0.33908	3.73098	0.096233	0.166499	0.04556	0	223	275	308	212	195	248	241	312	314	236
ENSMUSG00000030042	chr6	Pole4	82618992	82619138	2509	-0.29247	4.452601	0.09627	0.166542	0.034503	0	321	365	521	348	465	373	515	319	620	481
ENSMUSG00000030108	chr6	Slc6a13	1.21E+08	1.21E+08	2904	0.587189	0.531923	0.0963	0.166558	0.111302	0	12	10	19	19	31	36	55	15	44	36
ENSMUSG00000043017	chr7	Ptgir	16906490	16906910	3334	0.415834	1.87298	0.096304	0.166558	0.058796	0	49	36	53	48	70	71	75	74	142	119
ENSMUSG00000028998	chr5	Tomm7	23838944	23839828	1125	0.321883	5.718462	0.09632	0.166565	0.043715	0	645	851	1005	680	686	1373	1350	1217	1332	1422
ENSMUSG00000097772	chr5	5430416N02Rik	1E+08	1E+08	3691	0.671226	-0.02817	0.096447	0.166765	0.125952	0	11	4	13	7	22	9	39	24	24	30
ENSMUSG00000038894	chr8	Irs2	10986980	10987014	4024	-0.66028	2.604833	0.09653	0.166887	0.176543	0	87	66	151	144	185	37	80	274	98	60
ENSMUSG00000056185	chr19	Snx32	5495278	5495648	1650	0.300146	3.073534	0.09661	0.167004	0.031825	0	112	105	149	121	136	174	217	210	249	221
ENSMUSG00000030222	chr6	Rerg	1.37E+08	1.37E+08	2563	-0.52723	0.725725	0.096683	0.16711	0.088992	0	23	27	36	41	28	16	33	43	44	17
ENSMUSG00000024481	chr18	4833403I15Rik	46850039	46850877	3219	-1.02532	1.221604	0.096713	0.167142	0.412603	0	68	35	61	58	27	8	10	123	25	10
ENSMUSG00000031633	chr8	Slc25a4	46206797	46207620	2353	-0.31276	11.85742	0.096753	0.167189	0.042409	0	56235	73404	80958	70443	58503	75155	72100	82302	85312	66620
ENSMUSG00000040731	chr5	Eif4h	1.35E+08	1.35E+08	2425	0.263339	7.126013	0.096802	0.167253	0.029726	0	1692	1808	2460	2048	2691	2607	3340	3364	4576	4069
ENSMUSG00000061126	chr17	Cyp4f39	32468462	32468683	1599	-0.50697	2.455166	0.096848	0.167312	0.101052	0	106	74	125	90	140	72	112	34	178	140
ENSMUSG00000040283	chr11	Btnl9	49165585	49169691	6054	0.570265	2.462098	0.09705	0.16764	0.128462	0	36	89	66	111	55	55	98	196	212	216
ENSMUSG00000028551	chr4	Cdkn2c	1.1E+08	1.1E+08	2686	0.448884	3.383599	0.09707	0.167653	0.081271	0	127	124	122	147	213	121	233	196	382	504
ENSMUSG00000073481	chr1	Marc2	1.85E+08	1.85E+08	6629	0.301713	5.801761	0.09709	0.167666	0.038561	0	573	903	1008	782	903	1229	1204	1304	1642	1781
ENSMUSG00000049657	chr4	Zbtb5	44991242	44995386	5606	-0.33243	2.947518	0.097122	0.167702	0.040962	0	133	89	176	134	189	112	141	162	211	172
ENSMUSG00000048280	chr13	Zfp738	67667437	67671611	5217	-0.45573	1.746481	0.097149	0.167727	0.074969	0	65	56	61	59	74	40	66	104	70	44
ENSMUSG00000103906	chr15	TIGD5	75909735	75914535	4801	0.468224	1.251241	0.097194	0.167783	0.067316	0	28	35	27	28	40	43	57	87	68	53
ENSMUSG00000028782	chr4	Bai2	1.3E+08	1.3E+08	6487	-0.68746	-0.08727	0.097276	0.167892	0.122506	0	8	9	23	23	28	11	29	11	12	13
ENSMUSG00000060657	chr16	Marf1	14109166	14111771	7765	-0.26859	4.957221	0.097281	0.167892	0.029739	0	524	478	641	575	607	444	695	787	718	654
ENSMUSG00000048661	chr10	Lemd3	1.21E+08	1.21E+08	4809	-0.31811	3.695823	0.097331	0.167957	0.039592	0	200	201	278	235	287	200	251	388	266	228
ENSMUSG00000000538	chr11	Tom1l2	60226714	60230241	8764	-0.28238	6.669422	0.0974	0.168055	0.0342	0	1549	1729	2246	1891	1900	1731	1880	2630	2414	2038
ENSMUSG00000100153	chr7	Gm5601	1.2E+08	1.2E+08	972	-0.37702	2.400338	0.097567	0.168322	0.051599	0	84	94	129	87	96	75	132	124	100	96
ENSMUSG00000059049	chr4	Frem1	82897920	82900598	13978	-0.54359	1.776571	0.097591	0.168343	0.110659	0	55	39	83	45	120	43	105	44	93	38
ENSMUSG00000031256	chrX	Cstf2	1.34E+08	1.34E+08	9180	-0.28373	3.569543	0.097672	0.168462	0.030723	0	182	179	260	205	264	176	268	203	361	254
ENSMUSG00000063410	chr14	Stk24	1.21E+08	1.21E+08	2676	-0.27145	4.50283	0.097741	0.168561	0.029822	0	378	307	423	454	513	324	461	565	564	495
ENSMUSG00000054708	chr10	Ankrd24	81628540	81628640	8142	-0.35452	2.484955	0.097776	0.1686	0.044438	0	86	82	144	105	103	105	108	100	136	114
ENSMUSG00000036545	chr11	Adamts2	50602084	50602299	9336	-0.34664	6.188965	0.097879	0.168756	0.051623	0	1295	750	1374	1205	2369	1092	1842	1236	1879	1513
ENSMUSG00000002365	chr17	Snx9	5841328	5841546	2411	-0.26412	4.715674	0.097941	0.168841	0.028526	0	467	377	487	453	611	374	623	570	661	577
ENSMUSG00000028175	chr3	Depdc1a	1.59E+08	1.59E+08	3323	0.673772	-0.0989	0.097973	0.168876	0.110503	0	6	18	8	7	13	13	23	16	42	27
ENSMUSG00000020444	chr11	Guk1	59183875	59184187	1835	0.278595	4.751479	0.098026	0.168946	0.031887	0	320	420	475	364	443	638	664	657	713	724
ENSMUSG00000051375	chr18	Pcdh1	38185914	38189942	8797	-0.35795	4.022155	0.098137	0.169116	0.052654	0	151	287	327	441	323	228	281	316	488	372
ENSMUSG00000031849	chr8	Comp	70373548	70373647	2425	-0.80182	5.150602	0.098326	0.169421	0.273603	0	950	190	785	247	1763	353	1277	566	713	150
ENSMUSG00000046062	chr1	Ppp1r15b	1.33E+08	1.33E+08	5594	0.283237	5.084777	0.098355	0.169449	0.033501	0	427	396	513	518	726	545	757	988	1144	973
ENSMUSG00000015790	chr2	Surf1	26913381	26913658	1753	0.294527	4.505888	0.098436	0.169534	0.035447	0	306	324	355	332	371	463	528	782	589	529
ENSMUSG00000031608	chr8	Galnt7	57523828	57526251	5253	-0.35062	2.729478	0.098441	0.169534	0.045793	0	103	95	146	107	171	78	120	148	203	139
ENSMUSG00000043943	chr9	Naalad2	18321951	18323623	4749	-0.33427	3.416979	0.098436	0.169534	0.043303	0	173	163	224	201	230	217	283	151	241	191
ENSMUSG00000013367	chr7	Iglon5	43472907	43474551	2619	0.747078	0.137342	0.098473	0.16956	0.178387	0	14	3	14	7	25	29	43	9	41	22
ENSMUSG00000022623	chr15	Shank3	89499623	89499919	8896	-0.32698	3.865787	0.09848	0.16956	0.043399	0	222	196	283	376	274	193	294	239	472	341
ENSMUSG00000005981	chr16	Trap1	4039971	4040224	2573	-0.27311	7.069	0.098653	0.169836	0.03233	0	2018	2296	2769	2588	2575	2437	2548	3166	3100	2854
ENSMUSG00000048376	chr13	F2r	95601804	95604937	3307	0.352879	3.608185	0.098672	0.169848	0.050063	0	153	114	202	202	227	212	486	300	369	229
ENSMUSG00000101335	chr9	Gm28229	88441500	88443652	2153	0.562479	0.562301	0.098746	0.169954	0.094985	0	12	25	21	10	24	40	38	27	34	48
ENSMUSG00000032109	chr9	Nlrx1	44252713	44253539	3980	-0.27544	4.425305	0.098761	0.169959	0.030752	0	332	274	411	441	524	325	401	457	568	531

ENSMUSG00000038457	chr8	Tmem255b	13435459	13435667	1224	-0.40882	1.86981	0.098805	0.170013	0.059508	0	69	70	72	64	61	45	71	57	101	91
ENSMUSG00000034429	chr15	Zfp707	75969123	75969404	3094	0.412819	1.676026	0.098837	0.170047	0.054161	0	41	43	50	39	47	55	70	94	124	75
ENSMUSG00000042429	chr1	Adora1	1.34E+08	1.34E+08	5785	1.085733	1.971305	0.098878	0.170096	0.477909	0	35	36	22	49	58	6	29	27	287	304
ENSMUSG00000062116	chr7	Zfp954	7114690	7116200	1999	0.354541	2.273364	0.099003	0.170291	0.042843	0	57	47	83	79	84	89	127	136	143	127
ENSMUSG00000016918	chr1	Sulf1	12692277	12692684	11294	-0.35025	4.501284	0.099068	0.170361	0.051534	0	473	232	400	382	653	265	584	470	564	472
ENSMUSG00000024972	chr19	Lgals12	7596660	7598171	2773	1.540355	1.83046	0.099068	0.170361	0.943714	0	15	5	5	42	87	3	43	2	195	386
ENSMUSG00000021481	chr13	Zfp346	55105311	55105518	4176	0.286199	4.288041	0.099223	0.170605	0.033046	0	269	256	303	302	329	340	471	661	520	506
ENSMUSG00000038486	chr3	Sv2a	96181151	96181303	4636	0.65614	-0.25922	0.09926	0.170647	0.093486	0	10	5	6	12	14	16	11	26	27	24
ENSMUSG00000020720	chr11	Psmd12	1.07E+08	1.07E+08	2649	0.341586	6.7993	0.099388	0.170847	0.050855	0	1320	1580	1862	1667	1761	2336	2342	4518	2660	2504
ENSMUSG00000041577	chr1	Prelp	1.34E+08	1.34E+08	3615	-0.36728	5.912351	0.099533	0.171075	0.058456	0	1072	672	1161	1123	1738	710	1185	1918	1325	1049
ENSMUSG00000022515	chr16	Anks3	4941415	4941797	2483	0.313269	3.681176	0.09956	0.171079	0.038891	0	181	155	242	150	224	232	320	437	319	335
ENSMUSG00000024993	chr19	Fam45a	60811585	60811673	6242	-0.33448	3.052075	0.099549	0.171079	0.043115	0	155	121	185	129	177	106	166	143	267	187
ENSMUSG00000002763	chr17	Pex6	46711463	46712384	3796	0.282367	4.689101	0.099811	0.17148	0.03282	0	369	339	433	414	368	459	550	644	870	811
ENSMUSG00000045275	chr16	Lca5l	96158407	96159867	6521	0.490864	0.794309	0.099818	0.17148	0.070676	0	25	18	21	15	34	43	39	48	45	44
ENSMUSG00000025227	chr19	Tmem180	46341121	46341170	2804	0.606362	0.863876	0.09991	0.171595	0.120283	0	20	27	17	21	26	23	39	25	86	76
ENSMUSG00000029145	chr5	Eif2b4	31187558	31187800	2594	0.315309	5.833085	0.099898	0.171595	0.042934	0	672	832	1012	837	877	1212	1242	2086	1498	1269
ENSMUSG00000020331	chr10	Hcn2	79716634	79717219	3195	0.51569	0.758333	0.100006	0.171738	0.080079	0	21	12	32	25	19	42	34	38	68	36
ENSMUSG00000034484	chr18	Snx2	53176365	53176487	2013	0.288897	5.213396	0.100029	0.171756	0.035411	0	492	474	627	456	757	663	744	1005	1192	1196
ENSMUSG00000024687	chr19	Osbp	11965844	11966296	4578	-0.28101	6.719839	0.10006	0.171788	0.034418	0	1630	1610	2082	2038	2341	1743	1970	2877	2492	2007
ENSMUSG00000038766	chr3	Gabpb2	95181766	95188975	15465	-0.29926	4.190458	0.100104	0.171843	0.036739	0	322	233	382	304	453	246	411	295	496	486
ENSMUSG00000024897	chr19	Apba1	23758876	23759091	6632	0.41547	2.033985	0.10034	0.172226	0.060706	0	60	29	57	69	72	69	122	108	122	115
ENSMUSG00000042305	chr1	Tmem183a	1.34E+08	1.34E+08	3564	0.265094	4.352695	0.100516	0.172506	0.028279	0	249	326	354	274	334	393	526	510	627	547
ENSMUSG00000004661	chr9	Arid3b	57790353	57790609	7976	-0.52988	1.647958	0.100657	0.172727	0.105018	0	73	32	56	59	83	28	59	102	55	50
ENSMUSG00000037339	chr5	Fam53a	33600351	33600880	9110	-0.26726	5.82463	0.100742	0.172852	0.03072	0	811	939	1199	1020	1222	1034	1151	1354	1255	1157
ENSMUSG00000027263	chr2	Tubgcp4	1.21E+08	1.21E+08	8395	-0.28523	3.772199	0.100793	0.172918	0.032263	0	201	217	298	239	300	207	321	208	380	331
ENSMUSG00000034457	chrX	Eda2r	97333840	97337450	5891	0.571481	4.063209	0.100853	0.172999	0.14018	0	200	185	245	203	289	191	413	1138	331	246
ENSMUSG00000041747	chr13	Utp15	98246845	98249376	4071	0.3209	2.914229	0.100875	0.173016	0.037857	0	106	92	109	102	144	134	165	209	252	214
ENSMUSG00000019710	chr3	Mrpl24	87919506	87919705	2255	0.264919	5.438077	0.100915	0.173039	0.029865	0	566	678	696	613	707	930	1032	1038	1268	1233
ENSMUSG00000024187	chr17	Itfg3	26211822	26213717	3981	0.261759	6.051425	0.100926	0.173039	0.029623	0	819	878	1088	1098	1163	1192	1534	1864	2209	1726
ENSMUSG00000041313	chr5	Slc7a1	1.48E+08	1.48E+08	7527	0.378506	3.125436	0.100911	0.173039	0.057798	0	125	62	128	112	213	167	256	210	316	202
ENSMUSG00000023885	chr17	Thbs2	14665500	14667520	5922	-0.51548	5.993622	0.101033	0.173201	0.116475	0	1627	427	1249	725	2396	678	1763	1368	1301	1081
ENSMUSG00000034902	chr10	Pip5k1c	81292963	81293152	5730	-0.26943	5.202305	0.101079	0.173259	0.030909	0	530	551	728	713	865	541	769	644	1095	906
ENSMUSG00000095334	chr7	Gm21984	1.27E+08	1.27E+08	822	0.63642	-0.02279	0.101289	0.173596	0.105	0	11	17	14	7	7	26	22	24	19	31
ENSMUSG00000085379	chr11	2310058D17Rik	58965748	58968579	3201	-0.60871	0.500939	0.101387	0.173743	0.120728	0	22	42	28	20	20	29	33	15	20	24
ENSMUSG00000017897	chr2	Eya2	1.66E+08	1.66E+08	2963	-0.54756	1.6078	0.101541	0.173964	0.112909	0	64	33	75	42	85	28	57	100	66	34
ENSMUSG00000021877	chr14	Arf4	26638074	26638486	2813	0.353066	5.99546	0.101534	0.173964	0.054739	0	848	611	1003	686	1646	1268	1887	1109	2331	1858
ENSMUSG00000021671	chr13	Poc5	96388294	96388531	3033	-0.34676	2.697731	0.101564	0.173982	0.045368	0	106	108	132	124	128	83	141	175	154	111
ENSMUSG00000035168	chr2	Tanc1	59612042	59612196	14570	-0.28989	3.771206	0.101674	0.174149	0.033738	0	183	201	274	300	301	164	307	308	359	312
ENSMUSG00000052921	chr11	Arhgef15	68943155	68944829	6483	-0.31587	4.015285	0.101731	0.174226	0.041349	0	212	273	308	422	270	252	293	302	475	373
ENSMUSG00000061650	chr11	Med9	59948206	59948478	1920	0.275142	4.292896	0.101745	0.174227	0.030852	0	290	259	371	265	281	412	511	533	550	478
ENSMUSG00000022999	chr15	Lmbr1l	98903921	98904508	4217	0.381584	2.626735	0.101829	0.174349	0.055077	0	83	83	82	84	106	92	145	214	156	199
ENSMUSG00000049300	chr3	Prmt6	1.1E+08	1.1E+08	4197	0.365213	2.310287	0.101846	0.174358	0.047892	0	49	71	74	63	100	89	157	111	162	125
ENSMUSG00000002319	chr14	Ipo4	55625400	55626041	5362	0.257275	5.830893	0.101877	0.17439	0.028703	0	672	709	941	866	1192	1099	1458	1479	1743	1479
ENSMUSG00000015126	chr17	Tsr3	25240170	25240364	1192	0.274368	4.079504	0.101928	0.174454	0.030346	0	232	237	293	221	285	371	391	495	458	417
ENSMUSG00000020312	chr10	Shc2	79617940	79620099	5537	0.476718	2.131334	0.102008	0.174571	0.089235	0	56	23	62	55	111	73	143	93	128	148
ENSMUSG00000000148	chr5	Brat1	1.41E+08	1.41E+08	6179	0.299041	3.251773	0.102038	0.174599	0.033668	0	107	147	155	129	168	170	242	275	295	240
ENSMUSG00000046020	chr2	Pofut1	1.53E+08	1.53E+08	9912	-0.28297	4.76769	0.102095	0.174675	0.033807	0	467	355	534	471	691	450	598	433	716	682
ENSMUSG00000099843	chr1	Gm7160	1.06E+08	1.06E+08	1417	0.741021	0.749638	0.102152	0.174752	0.205606	0	15	18	27	25	12	23	22	114	29	39
ENSMUSG00000025894	chr9	Aasdhppt	4294793	4296839	2870	-0.28631	4.188208	0.102195	0.174785	0.033587	0	279	304	399	294	397	316	350	491	429	316
ENSMUSG00000029029	chr4	Wrap73	1.54E+08	1.54E+08	4335	0.29217	3.482703	0.102197	0.174785	0.033172	0	132	163	219	137	183	226	311	252	327	309
ENSMUSG00000024413	chr18	Npc1	12189693	12191002	10725	0.628832	5.660518	0.102267	0.174884	0.173768	0	577	528	874	720	616	492	758	3870	1222	880
ENSMUSG00000032724	chr2	Abtb2	1.04E+08	1.04E+08	6032	-0.33063	3.636212	0.102314	0.174942	0.044399	0	163	229	182	286	289	216	287	284	290	196
ENSMUSG00000035666	chr2	Gtf3c4	28822299	28826797	7230	-0.36222	4.823081	0.102375	0.175026	0.056727	0	446	432	567	552	675	391	468	1001	575	445
ENSMUSG00000030879	chr7	Mrpl17	1.06E+08	1.06E+08	4153	0.262122	5.457625	0.102415	0.175072	0.02955	0	516	684	752	647	725	968	1086	1014	1326	1177
ENSMUSG00000042293	chr9	Gm5617	48495345	48495964	620	0.386234	1.897624	0.102438	0.17509	0.051759	0	44	45	62	49	63	84	82	117	117	77
ENSMUSG00000000282	chr11	Mnt	74830920	74831401	4627	0.331704	3.459975	0.102471	0.175121	0.043953	0	143	117	183	191	175	166	222	360	341	348
ENSMUSG00000031523	chr8	Dlc1	36567751	36570403	14694	-0.34293	4.856646	0.102482	0.175121	0.050927	0	458	368	506	609	799	342	514	464	863	870
ENSMUSG00000024970	chr19	AI846148	7356464	7358487	3183	0.318272	2.999868	0.102525	0.175171	0.038179	0	95	116	105	122	148	172	226	171	247	207
ENSMUSG00000029142	chr5	Mrpl33	31596935	31597021	7473	0.321324	6.04115	0.102537	0.175171	0.045414	0	883	1088	1200	782	865	1696	1687	1454	1746	1813
ENSMUSG00000024201	chr17	Kdm4b	56326062	56326229	4895	-0.31764	4.75229	0.10264	0.175327	0.043215	0	407	375	554	559	621	364	498	854	590	497
ENSMUSG00000022884	chr16	Eif4a2	23107444	23107820	5338	-0.33547	8.341362	0.102763	0.175514	0.050357	0	5022	5838	7690	5407	6254	5237	6164	10215	6041	5481
ENSMUSG00000025758	chr3	Plk4	40800019	40800283	5863	0.482242	1.337437	0.102789	0.175537	0.078711	0	39	25	37	24	43	33	72	51	112	71
ENSMUSG00000031357	chrX	Syap1	1.63E+08	1.63E+08	2351	-0.27821	4.990603	0.102844	0.17561	0.033243	0	542	490	677	611	574	426	627	845	807	678
ENSMUSG00000031385	chrX	Plxnb3	73757090	73757150	6493	-0.4867	0.909691	0.102903	0.17569	0.074827	0	35	24	30	46	40	21	46	30	53	28
ENSMUSG00000001657	chr15	Hoxc8	1.03E+08	1.03E+08	2832	0.682328	1.602774	0.102935	0.175723	0.184165	0	46	11	28	29	77	28	99	50	111	145
ENSMUSG00000037935	chr11	Smarce1	99209047	99210277	6650	0.253071	5.466792	0.102961	0.175745	0.027685	0	522	546	817	653	869	889	1152	1205	1317	1046

ENSMUSG00000027018	chr2	Hat1	71388958	71389304	2886	0.291375	4.023685	0.103001	0.175792	0.034435	0	233	251	281	195	242	367	408	361	568	378
ENSMUSG00000004814	chr5	Ccl24	1.36E+08	1.36E+08	1289	0.507968	1.371026	0.10302	0.175802	0.089986	0	43	20	33	25	50	45	58	46	98	98
ENSMUSG00000091754	chr14	Gm3636	6735685	6736817	1746	0.56721	0.814355	0.103174	0.176042	0.107522	0	17	31	26	11	25	57	41	31	59	38
ENSMUSG00000041658	chrX	Rragb	1.53E+08	1.53E+08	2258	-0.60666	0.347238	0.103227	0.176112	0.118569	0	19	28	13	38	20	13	22	35	24	17
ENSMUSG00000018800	chr11	Abca5	1.1E+08	1.1E+08	11437	-0.38738	3.527287	0.103278	0.176168	0.062788	0	223	154	243	213	254	132	223	397	248	167
ENSMUSG00000098715	chr6	Gm28053	48718607	48718701	350	-0.5611	0.052517	0.103286	0.176168	0.080627	0	9	21	18	27	20	12	18	15	27	19
ENSMUSG00000016510	chr5	Mtif3	1.47E+08	1.47E+08	5127	-0.28511	4.284613	0.103451	0.176425	0.033941	0	273	376	423	373	324	319	401	476	453	392
ENSMUSG00000073062	chrX	Zxdb	94724569	94730187	5619	-0.54243	0.081012	0.103461	0.176425	0.076242	0	25	14	19	16	22	12	24	22	22	13
ENSMUSG00000008855	chr11	Hdac5	1.02E+08	1.02E+08	8780	-0.34838	5.501351	0.103502	0.176473	0.053573	0	844	638	869	1013	845	522	815	1480	978	891
ENSMUSG00000020973	chr12	Dnaaf2	69189087	69190394	3390	0.426996	1.957722	0.103592	0.176604	0.067138	0	37	46	89	52	47	84	101	72	148	105
ENSMUSG00000000120	chr11	Ngfr	95568818	95571095	3446	0.728065	1.950517	0.103618	0.176626	0.221465	0	35	17	25	50	119	42	68	240	113	88
ENSMUSG00000035158	chr6	Mitf	97807058	97807287	6215	-0.31453	3.576895	0.103645	0.17665	0.04048	0	179	212	258	208	241	138	215	337	315	249
ENSMUSG00000019989	chr10	Enpp3	24773814	24774072	2815	-0.38711	2.340678	0.103668	0.176668	0.056031	0	71	65	95	116	132	58	115	117	142	82
ENSMUSG00000038622	chr15	Med30	52712445	52712686	871	0.355295	2.915544	0.103708	0.176692	0.048746	0	101	108	138	106	86	172	214	150	217	217
ENSMUSG00000044627	chr2	Swi5	32278816	32279131	5551	0.281783	6.194607	0.103695	0.176692	0.03513	0	990	1020	1368	963	1167	1694	1934	1525	2029	2120
ENSMUSG00000037049	chr7	Smpd1	1.06E+08	1.06E+08	2411	-0.25655	6.153143	0.103758	0.17672	0.029017	0	1122	1152	1434	1310	1447	1299	1468	1412	1964	1436
ENSMUSG00000039005	chr4	Tlr4	66827584	66827921	5556	0.42267	2.505023	0.103742	0.17672	0.069383	0	86	46	94	62	114	66	161	179	200	157
ENSMUSG00000058446	chr6	Znrf2	54816916	54817472	6176	-0.28964	4.92641	0.103762	0.17672	0.036293	0	454	624	583	565	527	435	586	742	718	725
ENSMUSG00000055745	chr15	Ldoc1l	84553398	84557823	4426	-0.33823	3.070803	0.103909	0.176948	0.044777	0	124	139	191	156	169	144	206	110	241	164
ENSMUSG00000079610	chr1	Ankrd39	36537507	36539534	4654	0.353214	2.725721	0.103971	0.177032	0.048685	0	77	72	133	82	120	157	154	206	166	158
ENSMUSG00000021277	chr12	Traf3	1.11E+08	1.11E+08	7350	-0.29478	4.756113	0.104011	0.177035	0.037154	0	357	343	614	470	762	421	697	505	724	503
ENSMUSG00000066036	chr4	Ubr4	1.39E+08	1.39E+08	17997	-0.37131	7.006214	0.104011	0.177035	0.061867	0	2237	1761	2803	2540	2842	1519	2149	4594	2720	2180
ENSMUSG00000074733	chr19	5830428H23Rik	61053840	61054421	6503	0.384866	2.320438	0.10401	0.177035	0.054936	0	67	66	75	61	84	99	158	81	152	159
ENSMUSG00000006998	chr16	Psmd2	20651652	20651851	4038	0.331501	7.970366	0.104228	0.177382	0.04955	0	3025	3171	4198	3823	4439	4524	5021	10358	6454	6209
ENSMUSG00000001786	chr10	Fbxo7	86021972	86022144	6180	0.327078	3.275312	0.104327	0.177528	0.041999	0	141	147	148	125	139	218	204	286	252	272
ENSMUSG00000054405	chr4	Dnajc8	1.33E+08	1.33E+08	2555	0.247803	5.360359	0.104374	0.177587	0.026584	0	533	530	729	625	726	906	1021	1038	1179	1026
ENSMUSG00000020459	chr11	Mtif2	29526408	29526487	3868	-0.29073	4.81193	0.104415	0.177634	0.036447	0	401	571	620	506	452	512	629	523	704	568
ENSMUSG00000007817	chr14	Zmiz1	25459185	25459556	12523	-0.34721	5.468815	0.104457	0.177685	0.053474	0	656	591	821	979	1147	427	889	1358	1105	858
ENSMUSG00000028932	chr5	Psmc2	21785283	21785517	5031	0.323575	6.911701	0.104488	0.177716	0.047035	0	1476	1727	2081	1673	1965	2549	2696	4640	2890	2663
ENSMUSG00000019917	chr10	Sept10	59164113	59164944	2539	-0.27163	3.334708	0.104514	0.177739	0.028324	0	154	159	203	188	213	155	230	207	255	218
ENSMUSG00000022808	chr16	Snx4	33251456	33251601	2442	0.256669	4.675776	0.104597	0.177857	0.027881	0	312	295	437	400	519	464	742	665	774	613
ENSMUSG00000052291	chr10	5330438D12Rik	1.17E+08	1.17E+08	2229	0.627845	-0.17805	0.104726	0.178055	0.093577	0	14	7	10	11	8	11	24	27	18	30
ENSMUSG00000102781	chr2	Pla2r1	60420013	60420302	4464	-0.44465	1.354234	0.104763	0.178096	0.069014	0	49	34	61	37	59	25	49	62	72	42
ENSMUSG00000029213	chr5	Commd8	72157000	72159893	3464	-0.26421	4.348064	0.104852	0.178224	0.029182	0	353	340	435	332	380	325	488	459	469	412
ENSMUSG00000030357	chr6	Fkbp4	1.28E+08	1.28E+08	2795	-0.27071	6.872322	0.105049	0.178537	0.032924	0	1775	1910	2439	2157	2442	2170	2576	1865	3091	2694
ENSMUSG00000019797	chr10	1700021F05Rik	43525121	43525408	1339	0.298043	5.562256	0.105133	0.178571	0.039256	0	543	707	823	778	665	1172	1096	893	1583	1307
ENSMUSG00000021461	chr13	Fancc	63304709	63305868	7884	0.367722	2.129244	0.105121	0.178571	0.048089	0	47	54	77	57	79	82	137	86	142	119
ENSMUSG00000071343	chr10	Gm10327	33808497	33809498	1002	-0.56696	0.174186	0.105083	0.178571	0.088973	0	19	22	19	27	16	23	12	23	22	17
ENSMUSG00000079355	chr9	Ackr4	1.04E+08	1.04E+08	5287	-0.87863	0.963424	0.10512	0.178571	0.307529	0	86	7	51	14	43	13	30	65	34	15
ENSMUSG00000082087	chr11	Gm12138	40672906	40673856	951	-0.47733	0.72147	0.105121	0.178571	0.065516	0	18	28	40	30	38	30	35	25	37	25
ENSMUSG00000068706	chr15	Gm10250	5120602	5121172	571	0.332795	4.813241	0.10517	0.178612	0.048233	0	341	490	458	429	313	732	658	755	812	637
ENSMUSG00000032125	chr9	Robo4	37401897	37402151	4107	-0.30633	4.123536	0.105192	0.178628	0.039714	0	218	286	380	431	289	258	354	326	452	439
ENSMUSG00000020949	chr12	Fkbp3	65062436	65062740	947	-0.30144	6.96479	0.105235	0.178678	0.040968	0	1878	2496	2702	2264	2053	2529	2567	2589	2622	2551
ENSMUSG00000003360	chr15	Ddx23	98645134	98646017	5452	-0.26414	5.920974	0.105294	0.178714	0.030909	0	817	923	1309	1124	1413	945	1237	1520	1483	1258
ENSMUSG00000024217	chr17	Snrpc	27839974	27840169	6217	0.264212	4.858899	0.105277	0.178714	0.029896	0	401	404	512	416	453	678	684	672	843	782
ENSMUSG00000066798	chr2	Zbtb6	37425500	37429923	5080	-0.36587	2.478619	0.105293	0.178714	0.051966	0	90	82	114	94	142	59	99	115	182	122
ENSMUSG00000019796	chr10	Lrp11	7589800	7590613	3418	0.41716	1.91292	0.105439	0.178938	0.06327	0	53	42	44	47	76	93	72	82	142	100
ENSMUSG00000064145	chr9	Arih2	1.09E+08	1.09E+08	7672	-0.3827	6.004519	0.105502	0.179022	0.065833	0	1110	1054	1409	1135	1357	873	1044	2361	1105	1075
ENSMUSG00000022136	chr14	Dnajc3	1.19E+08	1.19E+08	5190	-0.2692	5.72707	0.105591	0.179152	0.032061	0	856	733	1129	830	1347	824	1099	1323	1313	1065
ENSMUSG00000032503	chr9	Arpp21	1.12E+08	1.12E+08	17428	0.365011	4.526232	0.105641	0.179214	0.058376	0	253	263	287	380	516	446	912	385	841	472
ENSMUSG00000096780	chr17	Tmem181b-ps	6438524	6438843	4187	0.524594	1.686282	0.105731	0.179344	0.10669	0	51	28	37	28	70	72	62	53	100	141
ENSMUSG00000009549	chr2	Srp14	1.18E+08	1.18E+08	1195	0.288168	6.334702	0.105772	0.179364	0.037307	0	1009	1198	1539	1073	1233	2008	2010	2022	2043	2101
ENSMUSG00000029518	chr5	Rab35	1.16E+08	1.16E+08	2799	0.25607	4.992046	0.105771	0.179364	0.028211	0	390	422	542	521	548	577	707	915	1034	836
ENSMUSG00000048100	chr3	Taf13	1.09E+08	1.09E+08	3155	0.266213	4.451176	0.105781	0.179364	0.030034	0	261	301	409	301	389	488	531	559	550	621
ENSMUSG00000063568	chr6	Jazf1	52768797	52770380	2536	-0.49048	0.567079	0.105808	0.179388	0.068493	0	22	15	30	29	43	15	27	28	40	28
ENSMUSG00000024486	chr18	Hbegf	36504929	36506364	2373	-0.32775	4.626814	0.105871	0.179472	0.046699	0	315	355	612	448	607	463	627	320	726	426
ENSMUSG00000035184	chr14	Fam124a	62555737	62555914	4406	-0.48611	2.069214	0.105971	0.17962	0.094427	0	64	50	101	60	138	40	58	128	115	68
ENSMUSG00000031799	chr8	Tpm4	72134975	72135049	2203	0.352927	6.375054	0.105986	0.179623	0.056249	0	908	1117	1331	1257	1509	1608	2699	1061	3359	2353
ENSMUSG00000002147	chr10	Stat6	1.28E+08	1.28E+08	4402	0.278034	5.135916	0.106017	0.179654	0.033763	0	555	385	556	448	718	615	843	850	1246	1004
ENSMUSG00000010660	chr9	Plcd1	1.19E+08	1.19E+08	2651	0.275801	3.782457	0.106094	0.17968	0.03103	0	180	146	222	203	295	250	358	398	391	356
ENSMUSG00000022570	chr15	Tsta3	75924684	75924994	1311	-0.26365	4.299354	0.10607	0.17968	0.02913	0	297	351	417	340	378	324	394	492	480	392
ENSMUSG00000031284	chrX	Pak3	1.44E+08	1.44E+08	9552	-0.6015	0.093993	0.106097	0.17968	0.100532	0	9	18	17	21	36	13	27	11	26	15
ENSMUSG00000039648	chr2	Ccbl1	30185124	30185569	2923	-0.27949	3.972991	0.106082	0.17968	0.032153	0	213	251	313	358	298	297	284	316	403	343
ENSMUSG00000089911	chr3	Hiat1	1.17E+08	1.17E+08	4087	-0.24982	4.271196	0.106048	0.17968	0.025887	0	338	301	379	311	415	310	412	429	500	410
ENSMUSG00000074748	chr10	Atxn7l3b	1.13E+08	1.13E+08	3572	0.247894	5.132106	0.106227	0.179878	0.02662	0	455	433	546	543	715	639	929	876	1144	889
ENSMUSG00000007867	chr12	Ift43	86082561	86082640	775	0.367943	2.774726	0.106285	0.17991	0.053702	0	85	88	112	104	101	149	244	111	220	164

ENSMUSG00000018770	chr2	Atp5g3	73908447	73908707	2181	0.309565	9.541277	0.106276	0.17991	0.043861	0	8513	13008	11937	11756	9536	18707	17874	18298	22223	18188
ENSMUSG00000043131	chr6	Mob1a	83326016	83326267	4794	0.297794	5.244105	0.106279	0.17991	0.039154	0	536	441	539	493	851	644	1051	745	1375	1146
ENSMUSG00000025736	chr17	Jmjd8	25828867	25829163	2758	-0.34208	3.936667	0.106369	0.18003	0.049847	0	196	205	322	313	418	264	336	175	481	333
ENSMUSG00000032527	chr9	Pccb	1.01E+08	1.01E+08	2771	-0.27472	6.482129	0.106418	0.180091	0.034063	0	1328	1467	1631	1867	1878	1405	1567	2025	2158	2318
ENSMUSG00000060475	chr17	Wtap	12966796	12968051	5651	0.244942	4.597445	0.106437	0.1801	0.025244	0	341	308	425	344	429	493	599	614	756	599
ENSMUSG00000022858	chr16	Tra2b	22244549	22246866	5383	0.249618	5.008952	0.106539	0.180251	0.026855	0	447	426	569	426	589	604	835	733	1060	878
ENSMUSG00000096188	chr8	Cmtm4	1.04E+08	1.04E+08	7734	-0.31749	3.690326	0.10656	0.180265	0.042167	0	194	187	251	260	308	161	199	370	343	280
ENSMUSG00000024830	chr19	Rps6kb2	4156713	4157199	2445	0.271145	4.574836	0.106591	0.180296	0.031491	0	306	309	394	350	446	452	565	784	618	604
ENSMUSG00000020015	chr10	Cdk17	93160876	93161200	3643	0.320364	3.352181	0.106628	0.180336	0.041445	0	97	144	164	156	197	171	340	216	364	242
ENSMUSG00000022184	chr15	Fbxo4	3965445	3965792	2047	0.410653	2.197021	0.106662	0.180368	0.063009	0	45	62	58	66	92	63	109	167	144	122
ENSMUSG00000085829	chr14	Gm4285	75843379	75843982	902	0.516647	0.5384	0.106673	0.180368	0.074458	0	20	19	18	16	18	24	24	50	48	40
ENSMUSG00000032235	chr9	Ice2	69397906	69398053	7736	-0.35301	2.593278	0.106687	0.180369	0.048544	0	109	88	159	88	116	79	126	145	139	126
ENSMUSG00000027254	chr2	Map1a	1.21E+08	1.21E+08	12166	-0.38557	4.36855	0.106725	0.180413	0.06536	0	378	198	479	330	612	282	613	447	493	265
ENSMUSG00000015189	chr6	Casd1	4600840	4601301	4062	-0.25936	4.676463	0.106748	0.18043	0.028964	0	420	399	516	462	524	360	595	632	668	482
ENSMUSG00000035623	chr7	Rsf1	97579896	97580105	12635	-0.29803	4.13516	0.106833	0.180551	0.037752	0	267	253	323	347	437	230	376	506	405	328
ENSMUSG00000025939	chr1	Ube2w	16540790	16541789	4930	0.291567	3.454979	0.106939	0.180707	0.033703	0	161	144	178	129	204	191	333	287	322	272
ENSMUSG00000022346	chr15	Myc	61985341	61985951	2767	0.500318	3.151712	0.107083	0.180904	0.10846	0	95	61	88	85	307	175	215	185	379	269
ENSMUSG00000025465	chr7	Echs1	1.4E+08	1.4E+08	5274	0.341025	6.70713	0.107095	0.180904	0.05294	0	1319	1473	1524	1821	1485	1780	1929	4044	2825	3089
ENSMUSG00000093798	chr10	Gm8355	14745362	14746117	756	0.336858	3.757389	0.107076	0.180904	0.048354	0	136	200	234	176	252	367	395	223	359	375
ENSMUSG00000031534	chr8	Smim19	22462615	22463375	1458	0.285231	4.716645	0.107158	0.180989	0.035205	0	371	401	438	367	372	582	550	783	751	673
ENSMUSG00000032715	chr2	Trib3	1.52E+08	1.52E+08	2125	0.624518	0.561687	0.107199	0.181036	0.126682	0	14	21	28	17	8	17	24	55	53	48
ENSMUSG00000026791	chr2	Slc2a8	32972990	32973732	3209	0.321649	3.505896	0.107212	0.181037	0.042738	0	129	152	193	166	200	211	225	419	302	301
ENSMUSG00000032512	chr9	Wdr48	1.2E+08	1.2E+08	3821	-0.25677	4.046235	0.107226	0.181038	0.027234	0	246	235	361	308	359	231	402	340	455	345
ENSMUSG00000022536	chr16	Glyr1	5013906	5015602	3348	-0.2773	5.940911	0.107352	0.181228	0.034667	0	948	986	1290	1110	1301	794	1283	1690	1534	1251
ENSMUSG00000003527	chr16	Dgcr14	17900711	17902323	2819	0.299318	3.23241	0.107437	0.181351	0.034632	0	121	129	154	160	127	185	225	253	285	252
ENSMUSG00000035370	chr10	Adat3	80602880	80602949	4586	0.288705	4.75503	0.10757	0.181552	0.036548	0	342	318	443	376	569	602	679	463	952	777
ENSMUSG00000048218	chr15	Amigo2	97244074	97246597	2871	0.486128	1.628875	0.107727	0.181795	0.087731	0	30	28	43	66	41	63	85	43	117	103
ENSMUSG00000012609	chr12	Ttll5	85824659	85824731	15833	-0.35351	2.515996	0.107764	0.181836	0.048021	0	89	83	97	114	150	92	143	85	145	116
ENSMUSG00000029913	chr6	Prdm5	65778988	65779193	3711	0.399721	1.610305	0.108006	0.182222	0.055344	0	40	28	45	41	60	52	95	83	79	83
ENSMUSG00000028617	chr4	Lrrc42	1.07E+08	1.07E+08	2139	0.292695	3.331583	0.108022	0.182225	0.034192	0	139	99	165	165	186	199	274	213	332	272
ENSMUSG00000039515	chr2	Ppp2r4	30416039	30416332	5188	0.289804	6.473522	0.108055	0.182259	0.038296	0	1088	1165	1464	1269	1739	1859	2194	1536	3044	2858
ENSMUSG00000022272	chr15	Myo10	25622525	25623030	10122	-0.29342	6.181752	0.108167	0.182426	0.039106	0	856	1080	1668	1438	1759	1135	1806	1736	1701	1243
ENSMUSG00000020000	chr10	Moxd1	24223517	24223867	3198	-0.73086	0.056949	0.108254	0.18255	0.189356	0	13	14	11	22	42	8	29	6	35	9
ENSMUSG00000026509	chr1	Capn2	1.82E+08	1.82E+08	6345	0.267798	6.434606	0.108278	0.182553	0.032662	0	1089	1032	1515	1233	1764	1585	2400	1754	3011	2427
ENSMUSG00000034024	chr10	Cct2	1.17E+08	1.17E+08	1962	0.258323	6.978334	0.108282	0.182553	0.030565	0	1487	1621	2272	1875	2435	2386	3345	3648	3681	3012
ENSMUSG00000039253	chr11	Fn3krp	1.21E+08	1.21E+08	2520	0.326811	2.64685	0.1083	0.182562	0.04016	0	91	72	95	89	109	140	180	156	175	144
ENSMUSG00000021830	chr14	Txndc16	45134448	45135970	10360	-0.32932	4.219602	0.108389	0.18269	0.04733	0	385	244	405	297	395	270	398	559	397	295
ENSMUSG00000020741	chr11	Cluh	74649495	74649694	6502	-0.25423	7.331	0.10845	0.182751	0.029713	0	2259	2668	3301	3206	3226	2656	3244	3328	4403	3625
ENSMUSG00000083061	chr11	Gm12191	49678710	49679057	348	0.411665	1.486203	0.108452	0.182751	0.055091	0	43	28	46	38	37	63	77	66	79	72
ENSMUSG00000053835	chr17	H2-T24	36005695	36006789	2182	0.657738	1.680726	0.108496	0.182803	0.175379	0	24	42	34	63	35	62	79	25	96	183
ENSMUSG00000049119	chr4	Fam110b	5644090	5644410	8164	-0.3565	2.613213	0.108649	0.183039	0.049342	0	72	90	143	113	160	96	144	90	167	127
ENSMUSG00000079662	chr17	Ntn3	24203848	24206947	4894	-0.51287	0.610697	0.108755	0.183195	0.088398	0	29	15	37	22	41	15	38	18	44	27
ENSMUSG00000031673	chr8	Cdh11	1.03E+08	1.03E+08	4216	-0.55089	3.129307	0.109025	0.183627	0.133706	0	184	44	191	119	360	99	230	165	230	113
ENSMUSG00000044258	chr13	Ctla2a	60934155	60935028	1373	0.442894	3.351371	0.109076	0.18369	0.084518	0	108	199	174	150	62	199	262	262	328	316
ENSMUSG00000028465	chr4	Tln1	43531519	43532085	9801	0.288108	7.136715	0.109139	0.183775	0.038313	0	1702	1606	2182	2397	2812	2764	3527	2620	5378	4051
ENSMUSG00000031921	chr8	Terf2	1.07E+08	1.07E+08	4597	0.251897	3.926334	0.109232	0.183909	0.026091	0	195	170	266	237	296	293	388	383	499	368
ENSMUSG00000022973	chr16	Synj1	90936092	90939034	8085	0.287731	3.340776	0.109348	0.184082	0.033244	0	124	107	171	168	193	169	255	246	354	284
ENSMUSG00000051278	chr3	Zgrf1	1.28E+08	1.28E+08	7046	-0.54211	0.235214	0.109395	0.184139	0.078058	0	16	17	26	17	34	18	18	12	26	30
ENSMUSG00000043923	chr9	Ccdc84	44410160	44410364	1158	0.479919	1.180658	0.109488	0.184272	0.077877	0	32	16	47	28	28	33	62	49	84	71
ENSMUSG00000028032	chr3	Papss1	1.32E+08	1.32E+08	2599	0.328556	3.632561	0.109509	0.184285	0.045828	0	164	126	189	166	280	197	353	224	463	398
ENSMUSG00000078126	chr14	Rpl23a-ps3	34170655	34171168	514	0.480163	0.951823	0.109668	0.18453	0.071708	0	25	20	27	25	30	32	59	29	78	55
ENSMUSG00000030034	chr6	Ino80b	83121765	83122364	1503	0.300309	3.049955	0.109787	0.184709	0.034615	0	109	107	145	132	117	154	208	223	253	221
ENSMUSG00000024754	chr19	Tmem2	21778342	21778786	6667	-0.32761	4.437162	0.10993	0.184926	0.04751	0	303	344	537	369	477	393	566	243	539	494
ENSMUSG00000020453	chr11	Patz1	3288874	3289347	5904	0.312515	3.219484	0.109949	0.184937	0.039626	0	123	99	160	133	178	174	197	315	285	225
ENSMUSG00000055546	chr11	Timd4	46810800	46810869	2173	-0.75883	0.951666	0.110075	0.185126	0.232956	0	49	19	34	22	75	36	25	4	43	52
ENSMUSG00000023883	chr17	Phf10	14945009	14945184	4914	-0.25844	5.63898	0.11009	0.185129	0.030155	0	751	724	1080	932	1077	856	1059	1258	1079	1008
ENSMUSG00000037434	chr1	Slc30a1	1.92E+08	1.92E+08	5244	0.301987	3.694105	0.11023	0.185341	0.038098	0	143	179	247	218	173	222	299	300	439	419
ENSMUSG00000029135	chr5	Fosl2	32136472	32136805	5855	0.253651	4.522194	0.110269	0.185384	0.028022	0	256	275	423	361	454	487	525	591	718	587
ENSMUSG00000040621	chrX	Gemin8	1.66E+08	1.66E+08	2487	0.487499	0.478539	0.11035	0.185497	0.063385	0	19	15	18	15	22	33	36	24	47	35
ENSMUSG00000036885	chr3	Arhgef26	62338344	62340573	10116	-0.48614	1.003126	0.110372	0.185513	0.081276	0	25	27	59	41	38	18	54	39	47	32
ENSMUSG00000028165	chr3	Cisd2	1.35E+08	1.35E+08	4360	-0.2468	5.024777	0.110415	0.185563	0.026935	0	505	537	660	608	629	585	704	648	784	738
ENSMUSG00000039108	chr2	Lsm14b	1.8E+08	1.8E+08	2892	-0.25439	5.535825	0.110485	0.185658	0.029246	0	710	790	939	763	1016	761	997	1166	1131	881
ENSMUSG00000041471	chr14	Fam35a	34237041	34237586	3446	-0.40326	2.664199	0.110505	0.185669	0.067381	0	114	102	121	133	122	81	104	213	120	111
ENSMUSG00000011179	chr12	Odc1	17544873	17545168	2547	0.294201	6.657663	0.110565	0.185726	0.040094	0	1084	1775	1892	1268	1512	2140	2602	2733	3096	2399
ENSMUSG00000029563	chr6	Foxp2	14901349	14901761	13457	-0.52847	0.205694	0.110569	0.185726	0.084988	0	18	11	21	25	32	7	24	23	26	24
ENSMUSG00000031767	chr8	Nudt7	1.14E+08	1.14E+08	5618	0.340148	4.508667	0.110606	0.185726	0.051438	0	304	355	415	335	233	383	459	772	706	664

ENSMUSG00000050947	chr3	Amigo1	1.08E+08	1.08E+08	5540	-0.27473	5.800288	0.110596	0.185726	0.034398	0	843	847	1187	903	1368	1025	1181	1372	1119	1114
ENSMUSG00000061758	chr6	Akr1b10	34384218	34384407	3535	-0.3056	5.725018	0.110589	0.185726	0.042842	0	838	1038	1126	1024	781	1060	1233	922	1283	970
ENSMUSG00000023868	chr17	Pde10a	8525372	8525815	12598	-0.50181	2.131652	0.110716	0.185888	0.105662	0	87	26	138	83	97	45	86	115	97	78
ENSMUSG00000032846	chr13	Zswim6	1.08E+08	1.08E+08	5456	0.389124	1.74707	0.110764	0.185945	0.054418	0	34	38	47	54	64	55	103	70	120	89
ENSMUSG00000047205	chr11	Dusp18	3895240	3895517	4632	0.331416	3.327275	0.110825	0.186026	0.045983	0	101	132	146	202	154	159	237	330	327	256
ENSMUSG00000053475	chr2	Tnfaip6	52038009	52038269	1710	0.477856	1.704862	0.110852	0.186049	0.08963	0	42	27	43	26	87	66	111	64	114	76
ENSMUSG00000026248	chr1	Mrpl44	79776018	79776311	1644	0.263469	5.161406	0.11095	0.186189	0.031245	0	418	492	669	548	594	858	799	946	1000	895
ENSMUSG00000030983	chr7	Bccip	1.34E+08	1.34E+08	2038	-0.26012	5.510231	0.111008	0.186265	0.030633	0	689	753	955	884	856	893	981	861	1028	1025
ENSMUSG00000021540	chr13	Smad5	56703010	56703131	7420	-0.24567	5.402885	0.111068	0.186342	0.027177	0	642	643	826	720	1031	667	943	959	1117	856
ENSMUSG00000030545	chr7	Pex11a	79735957	79737910	2368	-0.31964	3.637868	0.111139	0.186439	0.044059	0	206	229	258	255	184	184	201	259	302	347
ENSMUSG00000028023	chr3	Pitx2	1.29E+08	1.29E+08	4726	0.487259	3.271861	0.111274	0.186642	0.104141	0	193	69	124	102	172	105	370	331	365	169
ENSMUSG00000038214	chr10	Bend3	43479140	43479372	6028	-0.3434	2.795399	0.111293	0.186653	0.047185	0	73	111	136	143	190	121	139	126	177	144
ENSMUSG00000038074	chr6	Fkbp14	54577604	54579686	4185	-0.46852	4.033527	0.111424	0.186849	0.099198	0	282	192	419	219	514	332	463	113	382	291
ENSMUSG00000021264	chr12	Yy1	1.09E+08	1.09E+08	2902	-0.28851	4.258638	0.111517	0.186983	0.036685	0	316	298	399	346	394	238	373	558	505	358
ENSMUSG00000035293	chr12	G2e3	51348061	51348444	7886	-0.37021	1.915338	0.111576	0.187059	0.050377	0	58	61	85	60	86	50	64	73	117	79
ENSMUSG00000027555	chr3	Car13	14641727	14641845	2299	0.676723	1.255233	0.111608	0.18709	0.184862	0	32	15	11	33	56	42	41	30	106	115
ENSMUSG00000029073	chr4	Cptp	1.56E+08	1.56E+08	2709	-0.27866	3.703575	0.111647	0.187133	0.032401	0	189	207	291	231	275	242	248	211	385	287
ENSMUSG00000002546	chr2	Golga2	32287384	32287470	5500	-0.26344	6.275708	0.111808	0.18738	0.032169	0	1193	1164	1493	1453	1799	1126	1558	2051	1886	1644
ENSMUSG00000007880	chr4	Arid1a	1.34E+08	1.34E+08	11476	-0.27377	5.331198	0.111908	0.187524	0.034176	0	677	522	689	781	1041	563	859	995	1072	808
ENSMUSG00000000416	chr6	Cttnbp2	18366478	18367616	8855	-0.66663	0.217252	0.111946	0.187565	0.153049	0	19	17	19	21	36	7	30	33	24	5
ENSMUSG00000034667	chr10	Xpot	1.22E+08	1.22E+08	5992	-0.24427	5.179109	0.112022	0.187671	0.026735	0	509	553	782	636	830	595	747	844	923	768
ENSMUSG00000062101	chr17	Zfp119b	55938381	55939993	2166	-0.4694	1.411363	0.112042	0.187681	0.082369	0	45	52	61	41	50	38	39	80	39	54
ENSMUSG00000042682	chr14	Selk	29968308	29968536	1240	0.251772	5.630039	0.112179	0.187883	0.028952	0	693	692	901	637	843	1093	1218	1203	1425	1306
ENSMUSG00000050229	chr1	Pigm	1.72E+08	1.72E+08	7554	0.295876	3.417471	0.112189	0.187883	0.036167	0	138	110	191	167	196	160	285	260	341	338
ENSMUSG00000020483	chr11	Dynll2	87979525	87981570	2736	-0.30003	8.053546	0.112247	0.187938	0.042477	0	3895	4312	5904	4811	5722	5431	5296	3488	6945	6494
ENSMUSG00000035342	chr19	Lzts2	45015176	45015323	2921	0.251492	4.608653	0.11225	0.187938	0.027776	0	302	287	429	412	438	429	582	704	727	663
ENSMUSG00000045107	chr14	Saysd1	20075646	20077644	2294	0.345444	2.830467	0.112307	0.188011	0.047832	0	90	112	111	90	108	161	210	148	172	215
ENSMUSG00000069008	chr3	Gm5537	58102609	58104269	1661	-0.65971	0.05189	0.11245	0.188227	0.145363	0	19	27	8	21	21	27	11	16	18	12
ENSMUSG00000073002	chr6	Vamp5	72368049	72369470	1648	0.301406	5.944128	0.112648	0.188537	0.042247	0	792	920	963	1041	831	1640	1614	1531	1541	1434
ENSMUSG00000038838	chr17	Vars2	35655634	35656652	5460	-0.26578	3.845269	0.112684	0.188574	0.030056	0	236	243	259	260	301	230	308	237	403	352
ENSMUSG00000036502	chrX	Tmem255a	38196573	38197298	4490	-0.54262	0.024688	0.112826	0.188788	0.07666	0	20	14	23	20	15	14	22	19	24	10
ENSMUSG00000029501	chr5	Ankle2	1.1E+08	1.1E+08	5259	-0.29434	4.88184	0.113011	0.189076	0.039396	0	491	452	659	525	583	447	538	897	659	542
ENSMUSG00000058975	chr7	Kcnc1	46396497	46398247	9128	-0.3193	6.35773	0.113031	0.189085	0.047851	0	1324	1167	1778	2088	1202	1571	1748	1768	2034	1336
ENSMUSG00000032113	chr9	Chek1	36708482	36710430	4635	0.648507	-0.08953	0.113172	0.1893	0.113638	0	20	5	13	5	10	14	24	20	34	28
ENSMUSG00000001999	chr2	Blvra	1.27E+08	1.27E+08	2446	0.311306	3.84184	0.113277	0.189451	0.042184	0	159	196	277	198	238	273	322	250	531	493
ENSMUSG00000050578	chr9	Mmp13	7272514	7272677	2675	1.083002	1.036936	0.113408	0.189649	0.514394	0	7	5	5	6	91	65	100	9	81	46
ENSMUSG00000051483	chr16	Cbr1	93607837	93608254	1237	0.26257	4.15705	0.113431	0.189663	0.029558	0	241	260	265	286	285	354	420	460	494	529
ENSMUSG00000078923	chr2	Ube2v1	1.68E+08	1.68E+08	2721	-0.24802	5.221245	0.113515	0.18978	0.027979	0	501	618	810	718	745	597	771	813	1037	789
ENSMUSG00000022557	chr15	Bop1	76452996	76453378	2476	0.252616	4.959574	0.113613	0.189883	0.028746	0	388	391	523	473	610	595	834	627	1071	855
ENSMUSG00000028232	chr4	Tmem68	3549041	3550579	3462	0.325954	2.525904	0.113591	0.189883	0.040912	0	77	73	88	68	115	104	156	133	193	156
ENSMUSG00000089798	chr5	1700028K03Rik	1.08E+08	1.08E+08	8149	-0.61976	0.909007	0.113617	0.189883	0.147188	0	29	21	48	33	55	19	54	10	64	24
ENSMUSG00000038141	chr17	Tmem181a	6270475	6270590	1869	0.39217	2.041052	0.113683	0.18997	0.058917	0	48	42	63	50	91	56	109	100	156	123
ENSMUSG00000038020	chr11	Rapgefl1	98836785	98837673	5677	0.518688	0.602398	0.113848	0.190224	0.080503	0	16	12	19	26	24	25	42	23	67	41
ENSMUSG00000031984	chr8	2810004N23Rik	1.25E+08	1.25E+08	1382	-0.2638	4.622662	0.113956	0.190381	0.03111	0	371	455	542	399	464	457	559	432	621	531
ENSMUSG00000042508	chr5	Dmtf1	9118801	9120138	11041	-0.28681	3.275431	0.114066	0.19054	0.033866	0	177	133	201	163	210	140	235	219	234	188
ENSMUSG00000032997	chr1	Chpf	75474569	75476226	3856	0.350399	4.406472	0.11444	0.191143	0.056444	0	299	161	333	259	539	381	733	412	698	571
ENSMUSG00000048546	chr15	Tob2	81848270	81851872	3994	-0.39814	5.827028	0.11457	0.191336	0.074834	0	685	884	1754	1191	943	931	887	1680	791	1317
ENSMUSG00000010048	chr9	Ifrd2	1.08E+08	1.08E+08	2637	-0.27494	5.064842	0.114656	0.191434	0.034629	0	499	644	688	568	638	699	632	647	791	717
ENSMUSG00000032563	chr9	Mrpl3	1.05E+08	1.05E+08	5961	-0.27923	5.564684	0.114652	0.191434	0.036371	0	759	886	928	943	755	863	1053	1065	1163	821
ENSMUSG00000053134	chr5	Supt7l	31514569	31515926	5347	-0.27027	3.615998	0.114848	0.191731	0.030974	0	191	215	239	231	231	180	293	289	304	231
ENSMUSG00000062949	chrX	Atp11c	60223290	60225793	7312	-0.42659	2.653819	0.114944	0.191868	0.079223	0	105	84	151	122	139	46	141	190	166	93
ENSMUSG00000029787	chr6	Avl9	56714927	56715214	7463	-0.35421	2.500676	0.115041	0.192008	0.050596	0	108	69	118	101	130	75	104	152	142	104
ENSMUSG00000047604	chr19	Frat2	41845978	41848132	2155	-0.37765	4.213786	0.115227	0.192294	0.06554	0	317	333	281	378	424	402	405	175	562	329
ENSMUSG00000046561	chr3	Arsj	1.26E+08	1.26E+08	3715	-0.51824	0.417073	0.115409	0.192576	0.080138	0	17	18	30	17	44	18	32	18	25	27
ENSMUSG00000028273	chr3	Pdlim5	1.42E+08	1.42E+08	6448	-0.3914	8.921292	0.115631	0.192923	0.073719	0	7873	9236	11267	9102	8083	6146	8123	18126	8990	7505
ENSMUSG00000037174	chr3	Elf2	51252720	51256985	9563	-0.25666	5.403023	0.115746	0.193082	0.030542	0	630	634	953	759	895	702	834	1111	1032	815
ENSMUSG00000038072	chr5	Galnt11	25222882	25223031	2993	-0.2804	3.713246	0.115755	0.193082	0.033867	0	202	164	302	273	265	195	327	228	356	284
ENSMUSG00000066152	chr4	Slc31a2	62262562	62262623	2033	-0.28244	3.404478	0.115878	0.193265	0.033959	0	192	177	215	168	206	137	242	243	267	231
ENSMUSG00000018417	chr1	Myo1b	51749765	51751296	10792	-0.25374	4.053059	0.11594	0.193345	0.028117	0	235	256	327	343	347	233	381	349	483	341
ENSMUSG00000040113	chr1	Mettl11b	1.64E+08	1.64E+08	1848	-0.46638	3.473692	0.116035	0.19348	0.099295	0	133	259	222	279	161	277	150	108	301	227
ENSMUSG00000042462	chr7	Dctpp1	1.27E+08	1.27E+08	676	0.285874	3.729059	0.116168	0.193678	0.035261	0	177	188	245	171	207	305	293	272	409	404
ENSMUSG00000015599	chr17	Ttbk1	46442448	46445557	6959	-0.93119	0.896089	0.116301	0.193878	0.369772	0	14	11	34	37	114	30	44	2	51	16
ENSMUSG00000028467	chr4	Gba2	43566928	43567467	4481	-0.2898	3.318119	0.116322	0.193888	0.035461	0	151	194	184	176	198	152	203	186	243	261
ENSMUSG00000029426	chr5	Scarb2	92443873	92444284	2110	-0.25146	6.353856	0.116446	0.194072	0.03004	0	1298	1218	1865	1320	1775	1401	1762	1860	2111	1592
ENSMUSG00000022122	chr14	Ednrb	1.04E+08	1.04E+08	4037	-0.37254	3.890864	0.116489	0.194097	0.06363	0	192	192	334	281	429	166	220	223	474	466
ENSMUSG00000025940	chr1	Tmem70	16665207	16665505	1820	-0.28663	6.026131	0.116477	0.194097	0.03904	0	963	1298	1437	1148	1074	1286	1484	1218	1511	1283

ENSMUSG00000025085	chr19	Ablim1	57032733	57037337	11949	-0.30967	5.441414	0.116568	0.194205	0.045415	0	649	652	913	991	813	451	954	1243	1036	916
ENSMUSG00000044533	chr17	Rps2	24718116	24718158	1830	0.259102	8.963606	0.116598	0.194232	0.03254	0	5783	7129	8821	7544	8862	11308	12368	10159	15776	13825
ENSMUSG00000028541	chr4	B4galt2	1.18E+08	1.18E+08	5031	0.377173	2.926861	0.116687	0.194357	0.061926	0	88	72	119	81	200	138	227	139	274	226
ENSMUSG00000082286	chr11	Pisd-ps1	3125904	3126058	1757	-0.39968	2.554839	0.116702	0.194357	0.068081	0	108	82	116	97	152	69	121	79	128	194
ENSMUSG00000053730	chr4	Tmem39b	1.3E+08	1.3E+08	2286	0.416998	1.526998	0.117021	0.194867	0.063556	0	26	35	39	38	63	53	64	60	98	99
ENSMUSG00000022425	chr15	Enpp2	54838898	54839536	3473	-0.39451	4.323381	0.117059	0.194905	0.072838	0	449	180	384	351	550	238	288	410	455	648
ENSMUSG00000040423	chr1	Rc3h1	1.61E+08	1.61E+08	11308	-0.34616	4.984588	0.117086	0.194927	0.056512	0	475	466	727	651	657	420	495	1118	670	550
ENSMUSG00000030733	chr7	Sh2b1	1.26E+08	1.26E+08	3422	-0.26744	6.370671	0.117157	0.195022	0.034157	0	1268	1146	1917	1247	2096	1435	1923	1827	1914	1634
ENSMUSG00000037788	chr6	Vopp1	57727807	57730230	9661	0.287446	3.202601	0.117181	0.195038	0.033938	0	118	119	132	151	165	181	237	189	325	248
ENSMUSG00000002504	chr17	Slc9a3r2	24639282	24640389	2257	-0.3026	5.035638	0.117203	0.195052	0.043076	0	516	524	648	826	475	484	767	759	852	588
ENSMUSG00000037669	chr12	1110057K04Rik	8208107	8208192	2748	0.293724	3.661689	0.117363	0.195272	0.037381	0	149	178	202	190	225	237	349	213	459	380
ENSMUSG00000038803	chr5	Ost4	30905885	30906766	1272	0.256243	5.538198	0.117351	0.195272	0.030859	0	644	620	857	634	777	1061	1219	933	1427	1237
ENSMUSG00000046417	chr11	Lrrc75a	62604884	62606246	2089	0.356405	2.546212	0.117542	0.195546	0.052568	0	70	68	95	71	121	135	190	103	188	135
ENSMUSG00000038236	chr6	Hoxa7	52214491	52216030	3761	0.285268	3.25941	0.117567	0.195563	0.03377	0	133	109	162	142	170	184	293	241	242	252
ENSMUSG00000031642	chr8	Sh3rf1	61224171	61224346	5181	0.394738	2.065357	0.117715	0.195786	0.06092	0	45	51	49	79	70	58	132	118	139	103
ENSMUSG00000022781	chr16	Pak2	32016290	32020266	6795	0.248766	5.290574	0.117796	0.195898	0.028737	0	517	556	605	572	731	648	1036	942	1360	1049
ENSMUSG00000024426	chr17	Atat1	35897595	35897915	4586	0.411777	1.935766	0.117881	0.196015	0.068124	0	47	47	53	43	78	78	123	55	129	114
ENSMUSG00000024165	chr17	Hn1l	24942156	24944678	2933	0.424349	3.367529	0.11802	0.196223	0.082508	0	111	108	159	130	236	170	294	114	489	347
ENSMUSG00000071757	chr15	Zhx2	57694665	57695004	4434	-0.27393	5.302552	0.118116	0.196359	0.035229	0	474	595	714	832	1047	729	878	808	952	778
ENSMUSG00000087598	chr7	Zfp111	24193947	24200042	10160	-0.39289	1.891523	0.118152	0.196396	0.059561	0	66	34	84	71	95	59	81	66	88	73
ENSMUSG00000027996	chr3	Sfrp2	83766321	83767043	2153	0.847502	3.830446	0.118188	0.196428	0.33922	0	93	49	57	88	633	205	256	164	910	699
ENSMUSG00000030083	chr6	Abtb1	88835915	88836452	1879	0.348417	4.688119	0.1182	0.196428	0.057222	0	299	318	443	433	400	457	510	1134	584	654
ENSMUSG00000022890	chr16	Atp5j	84827866	84827995	3130	-0.30746	8.444747	0.118382	0.196706	0.046207	0	5006	7494	7586	6517	5105	6927	7079	7473	7939	6512
ENSMUSG00000078652	chr11	Psme3	1.01E+08	1.01E+08	2949	0.24552	5.956634	0.118426	0.196756	0.028748	0	729	857	1126	874	1196	1249	1495	1600	1962	1579
ENSMUSG00000027438	chr2	Napb	1.49E+08	1.49E+08	7051	0.588484	3.12904	0.118593	0.196986	0.162031	0	123	84	151	98	120	122	180	596	113	184
ENSMUSG00000056228	chr8	Cars2	11514021	11514191	1846	-0.32141	3.991757	0.118584	0.196986	0.047113	0	219	321	330	299	291	317	347	195	382	391
ENSMUSG00000004791	chr12	Pgf	85166639	85167414	1582	-0.52004	0.879557	0.118693	0.197126	0.096138	0	47	22	33	31	39	34	41	16	41	36
ENSMUSG00000040688	chr17	Tbl3	24697949	24700785	5686	0.248286	4.374398	0.118706	0.197126	0.027675	0	240	284	330	313	422	413	501	467	699	557
ENSMUSG00000100347	chr1	Gm7895	94468715	94469887	1173	-0.44863	1.443433	0.118727	0.197138	0.077469	0	31	40	71	66	49	26	55	70	68	46
ENSMUSG00000026500	chr1	Cox20	1.78E+08	1.78E+08	883	0.352694	4.023554	0.118854	0.197325	0.057205	0	205	286	285	213	173	419	506	280	469	418
ENSMUSG00000037096	chr3	Gm9762	78966359	78966799	441	-0.42215	1.387399	0.119068	0.197656	0.061903	0	36	43	47	53	65	47	58	47	40	57
ENSMUSG00000073940	chr7	Hbb-bt	1.04E+08	1.04E+08	703	-0.47702	3.387612	0.119091	0.197671	0.106052	0	63	205	232	227	310	103	190	127	314	314
ENSMUSG00000015127	chr17	Unkl	25188397	25188492	5673	-0.47822	1.593753	0.119225	0.197845	0.093451	0	42	49	67	55	76	27	43	106	64	50
ENSMUSG00000071317	chr10	Bves	45335762	45335881	1607	-0.24809	5.704617	0.119213	0.197845	0.029226	0	807	782	1086	953	1120	1048	986	1117	1300	1063
ENSMUSG00000039795	chr3	Zfand1	10339953	10340905	6267	0.326119	2.846336	0.119284	0.19792	0.043343	0	100	97	142	92	91	140	207	176	203	195
ENSMUSG00000030671	chr7	Pde3b	1.14E+08	1.14E+08	6899	0.63019	2.934497	0.119401	0.19809	0.184048	0	111	52	67	100	168	60	124	120	353	465
ENSMUSG00000019850	chr10	Tnfaip3	19000910	19003015	7226	0.342699	3.106891	0.119623	0.198434	0.050376	0	125	94	146	142	117	125	209	185	334	287
ENSMUSG00000023912	chr17	Slc25a27	43641900	43643676	2687	-0.3805	2.356885	0.1199	0.198871	0.059441	0	79	76	141	94	89	83	107	127	80	108
ENSMUSG00000017837	chr11	Nkiras2	1.01E+08	1.01E+08	3578	0.244548	4.891587	0.119924	0.198886	0.027705	0	383	392	541	438	517	552	750	856	939	674
ENSMUSG00000035242	chr10	Oaz1	80826656	80826905	2558	0.258282	8.087853	0.119966	0.198933	0.032846	0	3435	3757	5063	3665	4876	6323	6250	6501	7458	7752
ENSMUSG00000054693	chr9	Adam10	70678997	70679259	4913	-0.25837	5.051333	0.120038	0.199029	0.031562	0	465	498	693	653	728	409	773	718	978	716
ENSMUSG00000069020	chr2	Urm1	29820075	29820206	4275	0.284736	4.472711	0.120138	0.19917	0.037453	0	266	367	424	313	278	503	583	528	659	548
ENSMUSG00000020359	chr11	Phykpl	51584757	51584879	9699	-0.2664	4.31393	0.120344	0.199487	0.032472	0	350	302	364	400	381	354	357	502	511	373
ENSMUSG00000078441	chr10	Scamp4	80602882	80602949	1863	0.276554	4.711843	0.120498	0.199671	0.035947	0	333	304	434	371	556	573	658	456	920	753
ENSMUSG00000098134	chr12	Rnf113a2	84417196	84418578	1383	0.421932	2.849098	0.120485	0.199671	0.079547	0	95	84	113	114	98	109	156	349	170	165
ENSMUSG00000104049	chr12	AC120402.1	84417194	84418310	1383	0.421932	2.849098	0.120478	0.199671	0.079544	0	95	84	113	114	98	109	156	349	170	165
ENSMUSG00000090381	chr14	Gm6158	24070074	24070637	564	0.584714	-0.13512	0.120519	0.199683	0.088828	0	7	8	6	12	21	11	25	23	31	24
ENSMUSG00000026698	chr1	Pigc	1.62E+08	1.62E+08	4250	0.286579	4.533786	0.120573	0.199748	0.038347	0	279	330	459	315	355	460	545	806	619	517
ENSMUSG00000078676	chr11	Casc3	98804905	98804986	4303	0.266276	4.926178	0.120616	0.199796	0.033292	0	402	411	489	453	545	493	747	1018	838	792
ENSMUSG00000000078	chr13	Klf6	5861489	5861842	4217	0.319597	5.279741	0.120677	0.199872	0.04918	0	509	380	624	801	572	571	858	1329	1202	1137
ENSMUSG00000038702	chr1	Dsel	1.12E+08	1.12E+08	5763	-0.37475	3.125112	0.120704	0.199893	0.063097	0	181	94	190	120	242	107	245	175	223	142
ENSMUSG00000027993	chr3	Trim2	84160439	84165249	18113	-0.34701	2.503663	0.120796	0.200022	0.049633	0	92	80	122	85	151	65	145	107	144	123
ENSMUSG00000034437	chr3	Gm9761	1.17E+08	1.17E+08	342	0.479062	0.65226	0.120814	0.200028	0.077894	0	17	9	34	17	27	32	46	32	55	35
ENSMUSG00000057969	chr9	Sema3b	1.08E+08	1.08E+08	4777	-0.43206	4.713885	0.121099	0.200475	0.090332	0	621	251	607	272	805	357	837	450	600	377
ENSMUSG00000006435	chr19	Neurl1a	47178820	47179551	4411	-0.27127	7.365772	0.12114	0.200519	0.0363	0	2349	2640	3722	3323	3073	3382	3619	3110	3563	3522
ENSMUSG00000005267	chr11	Zfp287	62700356	62700626	7632	-0.49354	0.841893	0.121201	0.200595	0.082473	0	39	21	33	35	39	41	27	23	38	34
ENSMUSG00000032911	chr9	Cspg4	56865104	56865277	8050	0.344655	4.399609	0.121215	0.200595	0.056359	0	256	198	292	391	430	309	688	343	833	651
ENSMUSG00000027465	chr2	Tbc1d20	1.52E+08	1.52E+08	4171	0.250465	5.781115	0.121324	0.200752	0.030265	0	660	754	903	860	1033	1009	1200	1341	1815	1674
ENSMUSG00000060152	chr5	Pop5	1.15E+08	1.15E+08	2296	-0.3043	4.243954	0.121358	0.200784	0.043186	0	302	367	433	321	301	394	387	272	486	418
ENSMUSG00000002578	chr10	Ikzf4	1.29E+08	1.29E+08	5995	-0.98303	0.98924	0.121389	0.200811	0.433201	0	16	58	11	10	125	31	48	10	55	7
ENSMUSG00000031342	chrX	Gpm6b	1.66E+08	1.66E+08	5600	-0.34813	3.01995	0.121411	0.200823	0.053265	0	146	110	152	112	242	130	218	157	191	130
ENSMUSG00000027854	chr3	Sike1	1.03E+08	1.03E+08	4627	-0.26111	4.609058	0.121455	0.200851	0.03173	0	369	389	534	418	516	431	650	394	630	483
ENSMUSG00000050490	chr10	Gm8394	85313488	85314439	952	0.537605	0.902124	0.121456	0.200851	0.110426	0	12	17	34	36	22	32	46	82	45	37
ENSMUSG00000036817	chr5	Sun1	1.39E+08	1.39E+08	7596	-0.27814	5.67215	0.12157	0.201015	0.037509	0	896	659	1079	885	1183	757	1195	1397	1044	972
ENSMUSG00000025512	chr7	Chid1	1.41E+08	1.41E+08	10799	0.330353	3.82238	0.121669	0.201155	0.050497	0	160	168	252	193	281	272	446	193	564	386
ENSMUSG00000006392	chr4	Med8	1.18E+08	1.18E+08	3001	0.249622	4.763104	0.121799	0.201298	0.029121	0	362	389	489	365	458	611	650	701	739	703

ENSMUSG00000025880	chr18	Smad7	75367529	75369568	4521	-0.36985	2.457515	0.121772	0.201298	0.057463	0	86	91	119	105	109	68	113	168	111	93
ENSMUSG00000096054	chr10	Syne1	5020203	5022247	11801	-0.28262	5.456941	0.121795	0.201298	0.038582	0	560	634	837	974	1072	672	900	1213	919	906
ENSMUSG00000104204	chr6	RP23-291E6.6	57684739	57687580	2842	-0.46271	1.142471	0.12201	0.201621	0.078632	0	23	43	48	46	47	31	64	28	44	42
ENSMUSG00000019338	chr3	Zfp687	95006590	95008213	5952	-0.26275	3.881792	0.122048	0.201646	0.03057	0	193	200	289	301	375	231	312	319	348	351
ENSMUSG00000052563	chr11	D930048N14Rik	51650954	51651213	3429	0.633113	-0.03201	0.122054	0.201646	0.116557	0	10	16	4	9	17	20	14	27	27	35
ENSMUSG00000041915	chr18	Ammecr1l	31759824	31760194	4769	-0.282	3.972571	0.122093	0.201686	0.036608	0	253	256	267	241	425	192	397	322	442	325
ENSMUSG00000066357	chr9	Wdr6	1.09E+08	1.09E+08	4163	0.332916	3.887808	0.122166	0.201784	0.05179	0	187	154	226	180	362	282	399	228	570	468
ENSMUSG00000039660	chr2	D2Wsu81e	30173453	30174185	3010	0.293618	3.074604	0.122258	0.20191	0.036687	0	98	104	143	113	174	156	212	188	255	266
ENSMUSG00000030284	chr6	Creld1	1.13E+08	1.13E+08	3816	0.252603	5.754401	0.122496	0.20228	0.031006	0	653	807	977	751	925	1157	1545	1186	1498	1429
ENSMUSG00000021622	chr13	Ckmt2	91853387	91853648	1486	-0.40415	10.48013	0.122574	0.202384	0.08165	0	20320	34972	28552	34263	13720	29743	26957	26144	34782	24152
ENSMUSG00000031753	chr8	Cog4	1.11E+08	1.11E+08	4053	-0.24954	6.129267	0.122617	0.202431	0.030512	0	1079	1173	1455	1328	1291	1215	1419	1651	1713	1452
ENSMUSG00000039065	chr15	Fam173b	31601852	31602149	5248	-0.28355	3.435788	0.122658	0.202476	0.034978	0	170	181	256	165	215	206	234	185	251	248
ENSMUSG00000025893	chr9	Kbtbd3	4309743	4309934	2310	-0.37435	2.808841	0.122831	0.202736	0.061599	0	102	144	166	125	111	151	161	95	149	137
ENSMUSG00000051403	chr7	Ppp1r37	19530967	19531426	2971	-0.23181	5.682716	0.122888	0.202806	0.026005	0	750	840	995	985	1065	840	1127	1119	1331	1116
ENSMUSG00000025499	chr7	Hras	1.41E+08	1.41E+08	3733	-0.29226	6.651253	0.122966	0.202911	0.04236	0	1475	1831	2126	1583	2250	2174	2198	1434	2461	2150
ENSMUSG00000039199	chr8	Zdhhc1	1.05E+08	1.05E+08	1737	0.267336	3.388893	0.123045	0.203017	0.030591	0	146	113	181	163	188	189	272	264	305	300
ENSMUSG00000037847	chr19	Nmrk1	18631950	18631999	3345	-0.37404	1.952159	0.123107	0.203095	0.057045	0	71	77	76	51	79	68	82	63	102	71
ENSMUSG00000027709	chr3	Mccc1	35959311	35960129	2977	-0.27012	5.326545	0.123276	0.20335	0.035472	0	576	700	761	774	848	604	714	742	1043	1178
ENSMUSG00000040506	chr2	Ambra1	91730134	91730379	6122	-0.25175	4.477793	0.12352	0.203728	0.02946	0	300	309	477	446	512	331	463	554	575	462
ENSMUSG00000039682	chr5	Lap3	45493374	45493561	3072	-0.24213	5.733493	0.123596	0.203828	0.028598	0	782	891	1164	988	983	888	1132	1211	1319	1142
ENSMUSG00000038822	chr10	Hace1	45577829	45578150	12851	-0.33198	2.20106	0.12362	0.203829	0.043917	0	70	75	91	70	118	62	97	94	119	100
ENSMUSG00000102752	chr1	Gm7694	1.7E+08	1.7E+08	3827	0.576455	-0.22434	0.123625	0.203829	0.086023	0	8	8	12	11	11	11	20	13	28	34
ENSMUSG00000027942	chr3	4933434E20Rik	90051636	90051693	6826	-0.26122	5.686144	0.123729	0.203975	0.033385	0	870	914	1122	829	912	1014	1043	1023	1165	1160
ENSMUSG00000027132	chr2	Katnbl1	1.12E+08	1.12E+08	4051	0.327279	2.375312	0.123775	0.204027	0.043209	0	58	66	103	62	91	114	134	134	151	125
ENSMUSG00000073542	chr18	Cep76	67617397	67619372	3979	-0.27022	3.281921	0.123815	0.204069	0.031367	0	155	150	203	180	194	152	228	209	267	173
ENSMUSG00000097316	chr1	Gm10516	1.92E+08	1.92E+08	2788	-0.41658	1.496475	0.123878	0.204148	0.068346	0	43	65	52	50	48	55	58	48	51	58
ENSMUSG00000021460	chr13	Auh	52835119	52835551	9580	-0.30662	5.288747	0.124016	0.204352	0.046122	0	617	700	848	764	647	617	685	1209	809	732
ENSMUSG00000032078	chr9	Zpr1	46273064	46273367	3583	0.262985	4.642071	0.124129	0.204513	0.03287	0	283	339	440	378	463	481	550	821	655	652
ENSMUSG00000029516	chr5	Cit	1.16E+08	1.16E+08	15387	0.446193	1.239405	0.124162	0.204542	0.075086	0	21	26	36	41	36	42	62	35	89	80
ENSMUSG00000068566	chr7	Myadm	3289038	3289325	3238	0.336492	6.733642	0.124378	0.204874	0.056767	0	1302	1167	1560	1768	2143	1954	3912	1495	4061	2704
ENSMUSG00000020019	chr10	Ntn4	93640681	93640775	3741	0.28187	3.868147	0.124446	0.204938	0.036545	0	189	169	191	239	314	298	426	407	438	289
ENSMUSG00000030077	chr6	Chl1	1.04E+08	1.04E+08	7751	0.662773	0.458081	0.124446	0.204938	0.167412	0	18	8	21	10	25	14	27	15	65	66
ENSMUSG00000001420	chr3	Tmem79	88328655	88329932	2912	0.59141	1.519448	0.124481	0.204971	0.153377	0	22	35	49	34	45	29	29	127	85	123
ENSMUSG00000024790	chr19	Sac3d1	6116004	6116587	1374	-0.30265	3.405128	0.124567	0.205087	0.040806	0	148	184	235	178	230	210	257	148	256	221
ENSMUSG00000067367	chr5	Lyar	38220470	38220635	2401	0.264294	3.84842	0.124585	0.205093	0.031303	0	200	197	274	192	220	291	349	297	477	420
ENSMUSG00000047221	chr5	Fam185a	21424958	21425576	3894	-0.28916	3.611367	0.124632	0.205147	0.037978	0	183	233	254	247	186	223	260	267	300	221
ENSMUSG00000029512	chr5	Ulk1	1.11E+08	1.11E+08	5213	-0.47585	6.053777	0.12467	0.205184	0.113338	0	1084	1103	1293	1473	1505	679	859	2996	1105	843
ENSMUSG00000040818	chr14	Dennd6a	26579578	26579862	5710	-0.27285	3.612727	0.124689	0.205191	0.033819	0	200	184	235	233	261	142	244	287	344	294
ENSMUSG00000083337	chr11	Gm11539	96248633	96249189	557	0.510355	0.126707	0.12476	0.205283	0.071904	0	17	10	11	15	14	25	21	27	38	24
ENSMUSG00000030556	chr7	Lrrc28	67513411	67515178	4834	-0.263	3.877497	0.124794	0.205315	0.031483	0	244	282	287	235	270	272	285	319	362	307
ENSMUSG00000044770	chr10	Scml4	42860370	42860853	7725	0.591717	1.580617	0.124854	0.20539	0.157022	0	26	25	39	25	84	88	118	26	101	66
ENSMUSG00000003190	chr7	Bcl2l12	44991222	44991454	1976	0.385506	2.694877	0.124901	0.205399	0.066105	0	93	77	108	63	122	151	200	89	210	192
ENSMUSG00000034064	chr16	Poglut1	38525137	38526781	4658	0.249793	3.77438	0.124904	0.205399	0.027522	0	198	165	236	190	251	254	392	319	422	347
ENSMUSG00000034684	chr9	Sema3f	1.08E+08	1.08E+08	5197	0.315472	3.084002	0.124879	0.205399	0.043788	0	84	108	120	157	159	171	216	167	316	227
ENSMUSG00000021024	chr12	Psma6	55384222	55384327	1234	0.288036	6.979545	0.12509	0.20568	0.041753	0	1581	1822	2292	1775	2006	2633	2725	4488	3219	2992
ENSMUSG00000032014	chr9	Oaf	43221278	43222839	2388	0.38195	4.417375	0.125261	0.205937	0.071676	0	260	200	328	253	543	477	824	275	712	531
ENSMUSG00000032187	chr9	Smarca4	21616169	21616400	6475	-0.26346	6.045354	0.125353	0.206063	0.034529	0	865	960	1350	1277	1659	1072	1401	1099	1987	1533
ENSMUSG00000036503	chr3	Rnf13	57736066	57736200	2676	-0.29603	5.091431	0.12541	0.206132	0.043147	0	608	551	683	550	735	400	712	1048	766	675
ENSMUSG00000022094	chr14	Slc39a14	70303469	70306812	10550	0.287486	4.045649	0.12553	0.206305	0.03859	0	231	207	298	198	307	262	363	583	509	412
ENSMUSG00000037907	chr11	Ankrd13b	77470485	77471823	3839	-0.28716	3.534636	0.125586	0.206374	0.037234	0	198	181	195	238	240	197	205	313	262	228
ENSMUSG00000021136	chr12	Smoc1	81026808	81027158	3496	0.98703	2.114752	0.125677	0.206498	0.464003	0	36	18	10	41	142	19	43	54	183	384
ENSMUSG00000024423	chr18	Impact	12972252	12972372	3432	0.397119	3.700452	0.125765	0.206619	0.075656	0	174	149	238	158	215	172	291	649	338	274
ENSMUSG00000024164	chr17	C3	57203970	57204154	5143	0.630211	6.465491	0.125801	0.206652	0.199359	0	969	464	911	965	2772	1185	1226	1103	3932	5582
ENSMUSG00000075266	chr10	Cenpw	30196011	30197226	1510	0.543852	0.255174	0.125892	0.206777	0.089802	0	16	9	16	19	13	14	21	32	51	36
ENSMUSG00000022607	chr15	Ptk2	73205105	73206260	4991	-0.24542	4.867443	0.126013	0.206933	0.028861	0	379	447	595	579	667	476	596	704	757	590
ENSMUSG00000051736	chr10	Fam229b	39118804	39119034	3331	0.436555	0.90329	0.126016	0.206933	0.060255	0	23	22	29	30	20	33	51	49	51	53
ENSMUSG00000085498	chr2	Gm14023	1.29E+08	1.29E+08	1781	-0.51233	-0.10031	0.12604	0.206948	0.08149	0	18	18	18	17	11	8	20	13	24	18
ENSMUSG00000057193	chr9	Slc44a2	21337828	21337962	3456	-0.24444	7.8823	0.126148	0.207085	0.030356	0	3988	3380	5090	3964	5052	4209	5492	4956	5837	4677
ENSMUSG00000079481	chrX	Nhsl2	1.02E+08	1.02E+08	16952	-0.35343	2.608412	0.126154	0.207085	0.053757	0	91	59	131	130	166	80	138	118	152	136
ENSMUSG00000059474	chr11	Mbtd1	93885852	93886062	13896	-0.34913	3.424991	0.126276	0.207261	0.057204	0	200	137	225	217	221	132	200	358	240	172
ENSMUSG00000022833	chr16	Ccdc14	34690616	34690831	4107	-0.39391	1.536464	0.1263	0.207276	0.059333	0	56	37	65	51	59	39	79	48	64	56
ENSMUSG00000028962	chr5	Slc4a2	24423837	24424151	6195	0.260107	4.449614	0.126331	0.207301	0.03211	0	297	239	390	293	457	353	631	489	745	598
ENSMUSG00000050640	chr5	Tmem150c	1E+08	1E+08	5555	-0.53055	0.337459	0.126419	0.207422	0.099218	0	29	17	19	21	30	9	37	23	30	16
ENSMUSG00000020869	chr11	Lrrc59	94629767	94630109	3073	0.259934	5.622241	0.126437	0.207427	0.033565	0	588	569	805	698	1149	881	1260	1066	1756	1392
ENSMUSG00000060227	chr2	Casc4	1.22E+08	1.22E+08	5858	-0.30405	3.590234	0.126616	0.207696	0.042888	0	206	146	264	208	295	152	277	317	334	190
ENSMUSG00000001062	chr8	Vps9d1	1.23E+08	1.23E+08	5153	-0.25314	4.182323	0.126675	0.207768	0.029929	0	275	273	413	365	318	302	384	328	493	431

ENSMUSG00000036242	chr14	3632451O06Rik	49681560	49682416	3663	0.408869	3.368578	0.127	0.208277	0.079725	0	168	76	147	96	261	167	382	315	305	204
ENSMUSG00000034403	chrX	Pja1	99465734	99468314	3324	0.278745	4.565959	0.127026	0.208283	0.037715	0	272	306	383	323	521	500	747	414	733	632
ENSMUSG00000051034	chr5	Zfp11	1.3E+08	1.3E+08	3929	-0.39184	1.305677	0.127034	0.208283	0.054573	0	31	38	51	49	60	39	53	37	67	47
ENSMUSG00000034931	chr11	Dhx8	1.02E+08	1.02E+08	5032	-0.25375	4.17275	0.127073	0.208322	0.030094	0	273	265	336	330	442	267	355	467	480	360
ENSMUSG00000024383	chr18	Map3k2	32163089	32163550	10791	-0.25967	3.459046	0.127156	0.208433	0.029665	0	186	150	223	179	264	176	237	225	302	229
ENSMUSG00000050373	chr2	Snx21	1.65E+08	1.65E+08	4760	0.243414	4.527856	0.127197	0.208475	0.028035	0	314	311	390	351	389	463	561	684	618	571
ENSMUSG00000029594	chr5	Rbm19	1.2E+08	1.2E+08	2963	-0.29573	3.137265	0.127282	0.208591	0.038843	0	121	126	173	169	225	118	179	205	264	164
ENSMUSG00000024817	chr19	Uhrf2	30030513	30030931	8590	0.264864	4.197544	0.127455	0.208849	0.03291	0	217	254	326	265	330	274	470	577	613	431
ENSMUSG00000026439	chr1	Rbbp5	1.32E+08	1.32E+08	3930	-0.25283	4.512353	0.127657	0.209129	0.030363	0	346	352	512	366	506	452	491	388	573	506
ENSMUSG00000030559	chr7	Rab38	88430273	88430603	1471	0.574645	0.098726	0.12766	0.209129	0.115056	0	12	6	13	6	29	22	34	19	39	21
ENSMUSG00000038628	chr2	Polr3k	1.82E+08	1.82E+08	3124	-0.31121	4.266531	0.127671	0.209129	0.046819	0	238	370	435	350	385	395	412	237	484	456
ENSMUSG00000051817	chr2	Sox12	1.52E+08	1.52E+08	4453	0.363884	1.966171	0.12786	0.209413	0.053876	0	38	37	67	67	73	75	82	105	138	104
ENSMUSG00000086329	chr2	Gm14233	1.31E+08	1.31E+08	439	0.427674	1.594644	0.127876	0.209415	0.073222	0	34	42	39	47	44	83	63	57	75	105
ENSMUSG00000059540	chr2	Tcea2	1.82E+08	1.82E+08	2704	0.445909	1.736991	0.127939	0.209494	0.081648	0	59	38	44	40	43	60	74	134	78	86
ENSMUSG00000025610	chr16	Map3k7cl	87553330	87553595	1652	-0.41279	4.29105	0.127974	0.209527	0.084508	0	351	211	568	260	517	372	561	233	563	228
ENSMUSG00000027803	chr3	Wwtr1	57455649	57459110	4779	-0.26692	5.430276	0.128037	0.209605	0.035525	0	569	651	819	883	1053	637	900	1176	1119	764
ENSMUSG00000043259	chr10	Fam13c	70440668	70440898	3520	-0.36715	3.069892	0.128067	0.209628	0.062289	0	115	150	189	185	142	107	154	271	157	159
ENSMUSG00000032120	chr9	C2cd2l	44309237	44311267	4334	-0.26414	3.999471	0.12814	0.209724	0.032975	0	211	288	341	278	339	223	351	297	531	325
ENSMUSG00000022964	chr16	Tmem50b	91574503	91576158	2446	-0.24054	4.478859	0.128196	0.209791	0.027419	0	284	372	441	419	511	363	519	473	562	470
ENSMUSG00000031478	chr8	Nek3	22128283	22128790	2153	-0.37173	1.83083	0.128307	0.209947	0.054521	0	58	70	73	58	66	64	76	78	76	57
ENSMUSG00000026568	chr1	Mpc2	1.65E+08	1.65E+08	7344	-0.31903	7.33885	0.128489	0.21022	0.052329	0	2621	3475	3267	3259	2030	3214	3027	3156	3797	3452
ENSMUSG00000000085	chr4	Scmh1	1.2E+08	1.2E+08	7731	-0.2495	4.827253	0.128522	0.21025	0.030295	0	435	435	527	556	624	468	557	750	679	565
ENSMUSG00000017778	chr13	Cox7c	86044816	86044908	1131	0.311849	7.915595	0.128615	0.210352	0.050117	0	2985	3891	4633	3494	2765	6221	6066	6771	5909	5627
ENSMUSG00000020250	chr10	Txnrd1	82859206	82859300	3417	-0.26594	6.098874	0.128613	0.210352	0.035899	0	1003	1220	1414	1281	1312	1030	1310	1904	1720	1334
ENSMUSG00000029534	chr6	St7	17692933	17693158	9109	-0.29527	3.076457	0.128646	0.210378	0.038442	0	118	150	169	150	184	137	212	161	233	139
ENSMUSG00000043445	chr17	Pgp	24470473	24471149	1027	-0.28326	5.014925	0.128717	0.210469	0.039897	0	475	650	725	583	492	630	585	714	816	631
ENSMUSG00000037720	chr5	Tmem33	67260565	67260806	7098	-0.2332	4.694256	0.12893	0.210792	0.026193	0	401	435	535	404	560	421	587	518	674	585
ENSMUSG00000061315	chr10	Naca	1.28E+08	1.28E+08	7034	0.293143	8.645053	0.129183	0.21118	0.04452	0	4646	4717	6414	6925	7672	7057	8986	15326	10993	9205
ENSMUSG00000072770	chr6	Acrbp	1.25E+08	1.25E+08	3277	0.509886	0.667908	0.12928	0.211314	0.094756	0	26	17	23	12	23	24	33	50	35	61
ENSMUSG00000085492	chr17	Trmt61b	71557027	71558343	2897	0.527267	0.669251	0.129306	0.211331	0.100853	0	16	17	31	13	25	25	37	21	62	63
ENSMUSG00000027006	chr2	Dnajc10	80315466	80315805	5004	-0.23283	5.247452	0.129341	0.211365	0.02683	0	616	604	766	607	838	631	841	780	1063	784
ENSMUSG00000067873	chrX	Htatsf1	57053583	57053765	4879	-0.2579	6.530815	0.129522	0.211636	0.034016	0	1429	1418	1973	1711	1908	1679	1747	2399	1961	1946
ENSMUSG00000022357	chr15	Klhl38	58314573	58315116	2212	1.116397	4.112712	0.129731	0.211926	0.613618	0	113	120	200	357	114	64	54	2277	151	183
ENSMUSG00000092192	chr9	Dyx1c1	72958785	72958997	1975	-0.56422	0.104226	0.129721	0.211926	0.10807	0	21	17	27	20	13	11	10	33	22	18
ENSMUSG00000026784	chr2	Pdss1	22895522	22895762	4248	-0.32307	3.290482	0.129783	0.211987	0.048427	0	116	198	221	211	150	164	229	165	270	185
ENSMUSG00000058254	chrX	Tspan7	10485158	10485238	7067	-0.23613	6.783243	0.129838	0.212051	0.028604	0	1675	1686	2149	2075	2405	1994	2202	2290	2993	2343
ENSMUSG00000020806	chr11	Rhbdf2	1.17E+08	1.17E+08	5293	0.392579	3.89403	0.129896	0.212121	0.076186	0	169	195	205	230	270	229	268	744	333	379
ENSMUSG00000059878	chr6	Zfp422	1.17E+08	1.17E+08	3625	0.245619	3.828975	0.130038	0.212328	0.027756	0	162	179	245	225	279	264	362	407	423	339
ENSMUSG00000026504	chr1	Sdccag8	1.77E+08	1.77E+08	4129	-0.30957	2.985245	0.130183	0.212523	0.043344	0	108	141	210	129	139	126	183	139	211	164
ENSMUSG00000026878	chr2	Rab14	35180205	35182447	5431	0.233975	6.501923	0.130188	0.212523	0.028006	0	1209	1208	1490	1368	1697	1681	2348	2466	2730	2263
ENSMUSG00000025374	chr10	Nabp2	1.28E+08	1.28E+08	2507	0.245748	5.120687	0.13025	0.212599	0.030008	0	434	490	566	525	643	787	744	787	1057	1006
ENSMUSG00000019194	chr7	Scn1b	31116524	31117136	1801	-0.27618	8.814418	0.130368	0.212766	0.039766	0	7143	7360	9464	8632	8511	10163	9320	7152	10619	9496
ENSMUSG00000062510	chr1	Nsl1	1.91E+08	1.91E+08	5303	0.564986	0.149188	0.13039	0.212771	0.105872	0	8	7	20	19	14	21	38	13	44	25
ENSMUSG00000081485	chr11	Gm12338	75599763	75599954	192	0.311678	5.872041	0.130402	0.212771	0.049781	0	747	944	1092	804	718	1557	1482	1650	1324	1364
ENSMUSG00000063320	chr10	1190007I07Rik	82619851	82620217	1197	-0.31929	3.405904	0.130559	0.213003	0.047848	0	175	217	211	195	161	230	216	188	222	217
ENSMUSG00000031486	chr8	Gpr124	27085583	27086211	5775	0.316092	3.925477	0.130694	0.213197	0.048945	0	157	148	248	215	389	253	478	285	573	407
ENSMUSG00000025373	chr10	Rnf41	1.28E+08	1.28E+08	4374	0.252471	3.997628	0.130749	0.213262	0.029926	0	182	233	279	222	301	318	467	320	495	424
ENSMUSG00000026158	chr1	Ogfrl1	23366424	23370448	8109	-0.31584	2.947877	0.130898	0.213458	0.045496	0	105	122	181	147	158	90	141	150	218	212
ENSMUSG00000098332	chr9	5031420N21Rik	73039718	73039865	2999	0.359985	2.278533	0.1309	0.213458	0.054945	0	66	67	85	58	69	119	129	87	135	147
ENSMUSG00000027412	chr2	Lpin3	1.61E+08	1.61E+08	3694	0.291042	3.008761	0.130959	0.213529	0.037483	0	101	88	153	105	158	140	233	187	272	202
ENSMUSG00000027593	chr2	Raly	1.55E+08	1.55E+08	3292	0.236891	6.084107	0.131099	0.213733	0.028649	0	813	977	1141	1043	1238	1338	1735	1588	2280	1685
ENSMUSG00000025810	chr8	Nrp1	1.28E+08	1.28E+08	5907	-0.2699	5.957465	0.131198	0.213819	0.0375	0	880	978	1227	1389	1203	800	1313	1152	2003	1473
ENSMUSG00000045790	chr5	Ccdc149	52374651	52376678	3317	-0.38669	1.529651	0.131198	0.213819	0.057566	0	47	54	48	47	69	35	64	67	57	62
ENSMUSG00000094724	chr17	Rnaset2b	6978860	6979098	2555	0.428799	1.697266	0.131173	0.213819	0.073496	0	45	44	43	53	34	81	85	57	126	72
ENSMUSG00000025722	chr7	Wdr73	80890723	80891909	3721	0.307755	2.792317	0.131223	0.213834	0.040515	0	77	111	109	94	117	124	178	159	220	208
ENSMUSG00000040174	chr2	Alkbh3	93980550	93980977	3159	0.253201	4.993325	0.131445	0.21417	0.031978	0	409	470	585	465	482	762	743	813	869	799
ENSMUSG00000083477	chr5	Gm5555	49552257	49553270	1014	0.558265	0.031112	0.131598	0.214395	0.093231	0	12	11	18	13	7	18	20	40	29	20
ENSMUSG00000021911	chr14	Parg	32201949	32202465	5778	-0.24313	4.544543	0.131619	0.214404	0.028735	0	322	402	515	378	501	383	526	557	569	455
ENSMUSG00000010453	chr1	Kansl3	36335730	36337651	6742	-0.26732	5.487407	0.13171	0.214527	0.036459	0	801	644	931	818	890	650	892	1309	1051	862
ENSMUSG00000028772	chr4	Zcchc17	1.3E+08	1.3E+08	4560	-0.25167	5.282043	0.131806	0.214634	0.031984	0	595	740	788	653	725	752	814	719	985	851
ENSMUSG00000031166	chrX	Wdr13	8123301	8125729	5277	-0.22783	4.57771	0.131807	0.214634	0.025142	0	361	387	473	430	497	379	546	537	602	507
ENSMUSG00000031712	chr8	Il15	82331637	82332024	1908	-0.42575	1.788004	0.131861	0.214696	0.079945	0	42	73	65	92	47	58	65	52	100	64
ENSMUSG00000038305	chr1	Spats2l	57774162	57774563	8041	0.449848	3.381868	0.132002	0.2149	0.10115	0	132	56	147	131	290	248	430	161	310	234
ENSMUSG00000019920	chr10	Lims1	58323466	58323687	4891	-0.27171	5.418417	0.132095	0.215002	0.037818	0	613	650	852	926	877	476	1000	1085	1191	863
ENSMUSG00000031145	chrX	Prickle3	7657260	7657500	4902	-0.31917	3.736671	0.132083	0.215002	0.049577	0	194	247	313	240	231	204	193	409	321	252
ENSMUSG00000012483	chr6	Rpa3	8255936	8256247	1136	0.359039	2.216231	0.132192	0.215114	0.053556	0	56	73	73	63	64	104	129	90	125	144

ENSMUSG00000036368	chr17	Rmdn2	79614900	79614987	1802	-0.3322	2.357211	0.132199	0.215114	0.047771	0	95	85	103	95	87	68	124	119	121	93
ENSMUSG00000047635	chr5	2810006K23Rik	1.24E+08	1.24E+08	2873	-0.29931	3.051777	0.132211	0.215114	0.040764	0	116	148	181	153	159	134	196	123	236	179
ENSMUSG00000016494	chr1	Cd34	1.95E+08	1.95E+08	7290	-0.26281	6.948787	0.132381	0.215366	0.03605	0	1755	1867	2414	2297	3048	2266	3030	1901	3325	2607
ENSMUSG00000002058	chr11	Unc119	78343482	78343786	2448	0.318771	3.308614	0.132401	0.215367	0.047979	0	99	125	189	147	178	215	239	155	346	324
ENSMUSG00000003154	chr6	Foxj2	1.23E+08	1.23E+08	5283	-0.29465	5.09512	0.132428	0.215367	0.044163	0	563	513	702	623	750	583	546	1074	746	602
ENSMUSG00000025731	chr17	0610011F06Rik	25875464	25875726	1109	-0.25138	4.663725	0.132413	0.215367	0.031102	0	387	432	561	442	468	500	509	571	557	525
ENSMUSG00000031380	chrX	Figf	1.64E+08	1.64E+08	2408	0.543945	2.282031	0.132547	0.215536	0.142963	0	36	68	71	75	74	69	62	261	89	174
ENSMUSG00000022035	chr14	Ccdc25	65837302	65837484	2227	-0.26567	5.130785	0.132582	0.215566	0.035658	0	498	620	785	562	735	704	840	547	836	749
ENSMUSG00000040479	chr2	Dgkz	91932824	91933525	6270	0.25453	5.751876	0.132655	0.21566	0.033273	0	664	669	944	774	1096	861	1218	1427	1687	1736
ENSMUSG00000020541	chr11	Tom1l1	90643465	90646309	7749	-0.3312	3.412152	0.132671	0.215661	0.052708	0	187	185	211	186	208	162	187	349	208	180
ENSMUSG00000027173	chr2	Depdc7	1.05E+08	1.05E+08	2096	0.443362	1.827148	0.132746	0.215757	0.086222	0	32	58	51	57	43	89	78	135	84	68
ENSMUSG00000052369	chr15	Tmem106c	97964229	97964503	1635	0.294655	2.99052	0.132998	0.216142	0.039026	0	110	84	129	104	168	151	222	167	257	220
ENSMUSG00000036856	chr4	Wnt4	1.37E+08	1.37E+08	4194	-0.32796	4.495751	0.13306	0.216217	0.054276	0	377	277	366	443	660	361	325	601	430	595
ENSMUSG00000034518	chr8	Hmgxb4	74993356	74993749	5227	-0.29024	2.970492	0.13312	0.216288	0.037805	0	118	111	168	155	166	112	201	138	215	159
ENSMUSG00000096944	chr4	Gm26722	1.29E+08	1.29E+08	1048	0.287611	3.863971	0.133191	0.216378	0.040241	0	160	211	305	189	228	335	417	414	349	315
ENSMUSG00000032060	chr9	Cryab	50752758	50753477	1185	0.258696	9.269157	0.133368	0.216641	0.03548	0	7375	7841	13411	9493	9126	12699	16878	13435	20919	15074
ENSMUSG00000036975	chr1	Tmem177	1.2E+08	1.2E+08	3341	-0.28486	3.803218	0.133394	0.216658	0.039262	0	223	235	295	315	191	248	301	275	346	289
ENSMUSG00000004633	chr6	Chn2	54039554	54040155	5745	0.412333	1.350196	0.133776	0.217252	0.061057	0	29	43	32	30	39	43	63	58	92	74
ENSMUSG00000031879	chr8	Fam96b	1.05E+08	1.05E+08	1075	0.29865	3.862083	0.133863	0.217343	0.043605	0	135	231	226	265	222	355	418	287	407	374
ENSMUSG00000037692	chr4	Ahdc1	1.33E+08	1.33E+08	8444	-0.25765	4.923167	0.133852	0.217343	0.033432	0	433	371	568	626	806	501	703	609	831	596
ENSMUSG00000020807	chr11	4933427D14Rik	72153929	72155438	5697	0.391052	1.532258	0.133997	0.21753	0.061603	0	37	26	57	30	54	51	68	91	82	78
ENSMUSG00000078572	chr11	1810043H04Rik	1.2E+08	1.2E+08	834	0.303866	3.744534	0.134009	0.21753	0.044649	0	161	234	234	180	172	346	348	277	391	333
ENSMUSG00000024457	chr17	Trim26	36837134	36837264	6868	-0.23927	4.348403	0.134166	0.217758	0.027772	0	323	277	408	390	450	353	388	401	526	510
ENSMUSG00000005204	chr11	Senp3	69673115	69673636	3632	0.227222	4.972584	0.134272	0.217904	0.025759	0	413	418	540	469	578	562	770	846	946	845
ENSMUSG00000001674	chr1	Ddx18	1.22E+08	1.22E+08	2483	0.236783	3.963817	0.134435	0.218118	0.026452	0	196	202	282	227	290	302	372	447	478	366
ENSMUSG00000100954	chr1	Gm10138	1.51E+08	1.51E+08	2843	0.568487	-0.0893	0.134429	0.218118	0.087821	0	8	14	5	17	11	17	23	27	26	23
ENSMUSG00000044952	chr7	Kctd21	97332327	97332371	2966	-0.32747	2.702002	0.134589	0.218343	0.048886	0	105	101	137	137	116	98	148	94	152	177
ENSMUSG00000022759	chr16	Lrrc74b	17544465	17545642	3941	-0.75331	-0.13115	0.134631	0.218359	0.239868	0	18	14	12	29	13	4	8	41	12	8
ENSMUSG00000028373	chr4	Astn2	65380803	65381689	4959	-0.49953	1.056145	0.134629	0.218359	0.102551	0	47	22	26	29	74	31	44	44	37	36
ENSMUSG00000007033	chr17	Hspa1l	34972703	34972862	2472	-0.26377	4.302194	0.134688	0.218404	0.034223	0	294	262	405	380	473	327	480	487	479	312
ENSMUSG00000041220	chr3	Elovl6	1.3E+08	1.3E+08	5951	0.916654	3.371945	0.13469	0.218404	0.428302	0	46	43	73	183	280	73	118	40	563	863
ENSMUSG00000035007	chr11	Rundc1	1.01E+08	1.01E+08	3223	0.247962	3.739053	0.134721	0.218429	0.028751	0	141	189	240	204	246	257	328	333	450	326
ENSMUSG00000024085	chr17	Man2a1	64600736	64601870	7223	0.33046	4.972524	0.134811	0.218498	0.056613	0	430	268	444	416	815	455	994	634	1222	881
ENSMUSG00000038520	chr7	Tbc1d17	44840901	44841420	3448	0.381005	5.201213	0.134795	0.218498	0.075758	0	490	497	596	539	520	555	707	1861	851	872
ENSMUSG00000064254	chr7	Ethe1	24587543	24587807	1484	0.272455	4.218417	0.134808	0.218498	0.036487	0	228	301	308	298	250	449	409	419	568	504
ENSMUSG00000026584	chr1	Scyl3	1.64E+08	1.64E+08	5802	-0.38304	2.692699	0.134988	0.218759	0.070092	0	125	91	148	98	144	60	115	208	145	129
ENSMUSG00000063445	chr16	Nmral1	4710059	4711603	3891	0.461509	1.832085	0.135049	0.218831	0.097445	0	36	39	63	36	73	103	84	39	126	111
ENSMUSG00000026179	chr1	Pnkd	74284930	74285137	7832	0.259103	5.213316	0.135179	0.219016	0.034387	0	453	538	607	663	536	768	1044	730	1197	989
ENSMUSG00000040652	chr9	Oaz2	65668001	65668177	2990	-0.2456	7.666468	0.135249	0.219105	0.032095	0	3109	3492	4263	3456	4077	3868	4048	4677	4556	4347
ENSMUSG00000032965	chr16	Ift57	49699233	49699549	2862	0.329888	2.383262	0.135339	0.219226	0.045898	0	61	76	83	83	73	82	137	154	170	130
ENSMUSG00000025270	chrX	Alas2	1.51E+08	1.51E+08	2403	-0.57538	1.674893	0.13541	0.219315	0.158183	0	19	48	40	83	133	23	58	51	87	82
ENSMUSG00000095930	chr13	Nim1k	1.2E+08	1.2E+08	8466	-0.4198	1.801526	0.135711	0.219776	0.07465	0	58	37	79	61	97	69	45	79	64	77
ENSMUSG00000034189	chr8	Hsdl1	1.2E+08	1.2E+08	3168	-0.23893	4.251737	0.135807	0.219906	0.02793	0	296	285	434	345	361	290	380	470	503	404
ENSMUSG00000045410	chr13	Akr1e1	4590757	4593298	3514	-0.24517	4.175421	0.135968	0.220141	0.029393	0	278	312	364	323	348	329	395	302	495	406
ENSMUSG00000020173	chr11	Cobl	12236608	12238059	8142	-0.23854	5.252623	0.136048	0.220194	0.029191	0	567	631	719	740	782	724	884	747	982	726
ENSMUSG00000024414	chr11	Mrpl27	94653767	94653841	985	0.250527	5.161312	0.136034	0.220194	0.03214	0	520	538	622	475	543	798	874	801	1027	1006
ENSMUSG00000052419	chr6	2610001J05Rik	13867735	13870740	3784	0.257307	4.832435	0.136042	0.220194	0.033588	0	364	457	491	383	452	632	727	573	844	824
ENSMUSG00000052974	chr7	Cyp2f2	27119909	27120015	2025	0.7166	0.902763	0.1361	0.220252	0.239887	0	18	11	15	14	57	32	15	49	44	114
ENSMUSG00000000194	chr2	Gpr107	31152316	31152481	12766	-0.22975	5.425107	0.13614	0.220291	0.027234	0	710	629	894	735	914	711	927	798	1227	988
ENSMUSG00000085667	chr4	Gm12992	1.32E+08	1.32E+08	5873	0.592108	0.026537	0.136248	0.220439	0.119338	0	6	11	21	9	14	19	17	16	56	23
ENSMUSG00000020134	chr11	Peli1	21091291	21091678	6553	-0.31486	3.558195	0.136291	0.220477	0.048857	0	153	222	258	241	207	156	208	363	274	224
ENSMUSG00000038578	chr4	Susd1	59314683	59315409	4766	0.527145	0.532557	0.136303	0.220477	0.107834	0	9	12	21	16	36	29	25	23	55	54
ENSMUSG00000019715	chr2	Gle1	29935426	29935598	6087	-0.23743	4.99086	0.136579	0.220897	0.028644	0	532	423	669	562	702	543	649	752	727	719
ENSMUSG00000068141	chr17	Gm10232	3044014	3044733	720	0.444743	1.025666	0.136661	0.221004	0.075742	0	16	35	25	25	35	55	49	44	65	44
ENSMUSG00000060301	chr10	2610008E11Rik	79064374	79068051	4229	-0.27483	3.972342	0.136773	0.22116	0.037035	0	253	282	301	256	331	301	304	415	300	304
ENSMUSG00000040093	chr2	Bmf	1.19E+08	1.19E+08	5253	0.389205	3.147244	0.136992	0.221488	0.074891	0	118	86	168	142	121	120	220	403	216	206
ENSMUSG00000003234	chr16	Abcf3	20548577	20548745	3557	0.259461	5.8819	0.137018	0.221505	0.035503	0	753	796	1061	895	979	1186	1338	1984	1596	1356
ENSMUSG00000033938	chr8	Ndufb7	83566671	83566930	4522	0.283007	7.39305	0.137131	0.22166	0.043024	0	1940	2765	2974	2594	2275	4409	3883	3726	4961	4269
ENSMUSG00000026618	chr1	Iars2	1.85E+08	1.85E+08	8885	-0.27892	6.314597	0.13718	0.221688	0.041469	0	1197	1379	1571	1534	1588	1126	1417	2433	1818	1627
ENSMUSG00000039842	chr8	Mcph1	18595131	18595635	7806	0.328082	2.360794	0.137169	0.221688	0.047173	0	61	62	85	80	86	89	102	168	156	143
ENSMUSG00000001240	chr11	Ramp2	1.01E+08	1.01E+08	3301	0.241588	6.051767	0.137238	0.221756	0.030759	0	869	923	1158	1095	1008	1366	1488	1590	2140	1830
ENSMUSG00000036764	chr10	Dnajc12	63382443	63382518	2740	-0.28001	3.231927	0.137314	0.221801	0.035699	0	152	139	221	168	175	181	190	207	204	190
ENSMUSG00000041168	chr17	Lonp1	56614301	56614563	2963	-0.24916	6.516057	0.137305	0.221801	0.033064	0	1244	1561	1761	1958	1769	1585	1762	2169	2223	2005
ENSMUSG00000067586	chr13	S1pr3	51408618	51408945	4484	-0.35913	3.777949	0.137289	0.221801	0.065717	0	164	223	291	332	280	225	275	128	451	342
ENSMUSG00000021686	chr13	Ap3b1	94358960	94359231	4020	0.238647	4.504055	0.137579	0.222203	0.02848	0	309	266	391	334	446	398	505	642	701	634
ENSMUSG00000014778	chr8	Fhod1	1.05E+08	1.05E+08	4666	-0.26769	5.568604	0.13762	0.222244	0.037638	0	593	773	1186	869	949	957	913	768	1278	1086

ENSMUSG00000023830	chr17	Igf2r	12682406	12684126	9438	-0.24055	7.065163	0.137667	0.222293	0.031041	0	2098	1805	2703	2384	3270	1971	3166	2965	3613	2770
ENSMUSG00000032198	chr9	Dock6	21800184	21800399	6556	-0.2868	4.109154	0.137683	0.222294	0.04164	0	220	265	327	436	335	206	367	433	423	403
ENSMUSG00000029722	chr5	Agfg2	1.38E+08	1.38E+08	3802	0.31592	2.792144	0.137705	0.222303	0.046642	0	86	61	107	114	148	118	180	174	201	217
ENSMUSG00000001305	chr1	Rrp15	1.87E+08	1.87E+08	3239	0.256922	3.368029	0.137787	0.222371	0.030482	0	112	141	165	170	195	199	265	276	319	246
ENSMUSG00000027562	chr3	Car2	14886273	14886371	2422	-0.39582	2.903066	0.137795	0.222371	0.076862	0	83	182	139	175	113	169	126	119	163	155
ENSMUSG00000091512	chr3	Lamtor3	1.38E+08	1.38E+08	1295	0.251909	5.137201	0.13778	0.222371	0.032812	0	498	516	593	486	566	727	800	1110	979	820
ENSMUSG00000084838	chr16	Gm10241	20176727	20177012	286	-0.50032	0.244594	0.137875	0.222473	0.075372	0	11	17	32	18	32	17	17	25	23	24
ENSMUSG00000059920	chr16	4930453N24Rik	64751751	64752176	5948	-0.25186	5.463748	0.137897	0.222483	0.033157	0	695	738	933	811	810	908	912	988	942	873
ENSMUSG00000050973	chr7	Gdpgp1	80232867	80233205	3132	-0.42253	0.895732	0.137916	0.222488	0.065904	0	26	28	29	42	46	26	29	30	57	38
ENSMUSG00000055302	chr5	Mrfap1	36794867	36795944	1648	0.255197	7.525786	0.137953	0.222522	0.035136	0	2346	2689	3555	2466	2978	4311	4914	3940	5070	4963
ENSMUSG00000047777	chr4	Phf13	1.52E+08	1.52E+08	3205	0.300378	2.941425	0.138054	0.222659	0.040779	0	102	103	102	106	155	141	160	226	257	201
ENSMUSG00000036305	chr15	Rpl39-ps	1.03E+08	1.03E+08	355	0.355711	2.184684	0.13816	0.222804	0.054708	0	53	70	88	44	70	84	140	109	139	113
ENSMUSG00000027777	chr3	Schip1	68064802	68065007	5102	-0.25608	6.485899	0.138429	0.223211	0.035163	0	1461	1601	1948	1561	1504	1642	1960	2023	2277	1603
ENSMUSG00000021280	chr12	Exoc3l4	1.11E+08	1.11E+08	2922	0.576393	3.954355	0.138524	0.223338	0.175944	0	84	194	284	115	401	588	577	111	429	366
ENSMUSG00000030214	chr6	Plbd1	1.37E+08	1.37E+08	2633	0.305277	4.507589	0.138545	0.223347	0.048121	0	189	383	366	441	304	449	561	500	809	635
ENSMUSG00000028461	chr4	Ccdc107	43492900	43493023	1547	0.254261	4.301034	0.138746	0.223645	0.03254	0	231	308	342	275	337	465	472	493	492	536
ENSMUSG00000028199	chr3	Cryz	1.55E+08	1.55E+08	6195	-0.28858	3.432126	0.139008	0.224041	0.040698	0	202	173	215	201	183	181	248	154	284	265
ENSMUSG00000091050	chr15	9330020H09Rik	98567324	98567525	2147	0.510911	0.061375	0.139037	0.224062	0.083395	0	7	10	19	15	14	24	20	37	26	20
ENSMUSG00000023266	chr17	Frs3	47689030	47689098	3128	-0.41742	1.775899	0.139088	0.224118	0.07704	0	69	53	71	56	69	47	71	107	56	51
ENSMUSG00000043122	chr12	A530016L24Rik	1.12E+08	1.12E+08	2636	1.118376	1.731328	0.139193	0.224262	0.628956	0	32	13	3	54	67	6	21	29	179	307
ENSMUSG00000024947	chr19	Men1	6334979	6335070	3458	0.258382	3.475837	0.139246	0.22432	0.031172	0	153	135	163	171	220	184	306	282	381	270
ENSMUSG00000018931	chr11	Natd1	60902246	60906121	4247	-0.23712	4.200213	0.139389	0.224524	0.027922	0	297	279	371	324	387	280	348	471	475	400
ENSMUSG00000021244	chr12	Ylpm1	84996321	84997356	9914	-0.23206	4.377613	0.139468	0.224625	0.026833	0	317	288	380	397	504	342	431	448	556	459
ENSMUSG00000024049	chr17	Myom1	71019521	71019651	5672	-0.30573	10.39098	0.139557	0.224742	0.051163	0	18149	21460	27085	28484	29777	22870	19862	42309	26866	26906
ENSMUSG00000024146	chr17	Cript	87025550	87025675	1712	-0.25474	4.99067	0.139773	0.225065	0.034047	0	559	590	690	487	521	512	693	731	805	648
ENSMUSG00000028487	chr4	Bnc2	84275095	84276447	8174	-0.50436	0.305169	0.139898	0.225186	0.089158	0	23	9	21	21	41	16	20	24	32	20
ENSMUSG00000086583	chr7	Gm15500	1.15E+08	1.15E+08	1019	0.230898	4.540836	0.139885	0.225186	0.026835	0	298	341	398	303	447	445	578	557	729	631
ENSMUSG00000097048	chr6	1600020E01Rik	86526271	86527974	2092	0.368579	1.596538	0.139897	0.225186	0.05706	0	38	40	50	32	53	69	72	90	71	77
ENSMUSG00000079144	chr1	A130010J15Rik	1.93E+08	1.93E+08	4403	-0.2987	2.634412	0.139965	0.225269	0.040729	0	99	94	135	109	130	96	118	109	200	129
ENSMUSG00000038172	chr4	Ttc39b	83220300	83227224	10199	0.315954	2.879054	0.139995	0.22529	0.046126	0	106	73	101	109	155	111	214	180	265	188
ENSMUSG00000030905	chr7	Crym	1.2E+08	1.2E+08	3391	-0.31817	2.715883	0.140018	0.225301	0.047841	0	103	136	111	127	116	92	150	148	139	147
ENSMUSG00000028247	chr4	Coq3	21879673	21879796	2997	-0.27674	5.039739	0.140058	0.22534	0.040424	0	481	680	750	559	498	640	695	631	829	651
ENSMUSG00000039530	chr8	Tusc3	39005867	39006200	1511	0.315664	3.155703	0.140079	0.225348	0.04868	0	139	83	161	92	189	171	248	193	315	226
ENSMUSG00000022505	chr16	Emp2	10281749	10284615	3440	0.282634	4.063059	0.140241	0.225581	0.04067	0	248	171	241	234	371	311	558	455	461	347
ENSMUSG00000045639	chr7	Zfp629	1.28E+08	1.28E+08	6723	0.246917	3.775942	0.140362	0.22575	0.029328	0	184	185	210	224	233	302	314	354	448	305
ENSMUSG00000021963	chr14	Sap18	57798180	57798354	3781	0.227379	5.357152	0.140438	0.22582	0.027101	0	554	575	714	629	667	857	1033	1006	1141	1097
ENSMUSG00000037204	chr15	Atg101	1.01E+08	1.01E+08	1230	0.279343	4.976839	0.14043	0.22582	0.041183	0	402	442	662	459	395	786	675	816	843	841
ENSMUSG00000021431	chr13	Snrnp48	38204939	38205128	1799	0.353758	2.953894	0.140638	0.226116	0.060472	0	102	107	134	99	116	128	181	322	181	187
ENSMUSG00000021120	chr12	Pigh	79080673	79082496	2349	0.370595	1.589932	0.140669	0.226139	0.055984	0	35	31	48	39	61	61	97	59	98	69
ENSMUSG00000027276	chr2	Jag1	1.37E+08	1.37E+08	5827	-0.27483	3.476584	0.14069	0.226146	0.037353	0	176	176	191	247	217	136	222	236	327	271
ENSMUSG00000063558	chr1	Aox1	58029931	58030058	8690	-0.30138	3.553358	0.140719	0.226167	0.045868	0	204	181	239	219	230	129	185	334	316	279
ENSMUSG00000027386	chr2	Fbln7	1.29E+08	1.29E+08	3228	0.370926	4.345622	0.140831	0.22632	0.07345	0	247	146	420	226	488	551	674	343	668	402
ENSMUSG00000026005	chr1	Rpe	66700831	66701028	3113	-0.3017	3.365069	0.140953	0.22649	0.045229	0	154	166	212	197	217	142	201	144	287	313
ENSMUSG00000043384	chrX	Gprasp1	1.36E+08	1.36E+08	8119	-0.24396	4.436183	0.141146	0.226774	0.030258	0	352	284	441	388	508	338	566	482	487	435
ENSMUSG00000006412	chr1	Pfdn2	1.71E+08	1.71E+08	1937	0.256324	5.638557	0.141323	0.227032	0.035247	0	618	743	875	762	774	1222	1042	1333	1294	1335
ENSMUSG00000024963	chr19	Dnajc4	6987911	6988108	1074	-0.2445	3.842042	0.141342	0.227036	0.02917	0	221	223	287	291	268	272	269	304	387	290
ENSMUSG00000011114	chr9	Tbrg1	37649182	37649503	3482	0.235451	5.187492	0.141404	0.227094	0.029156	0	513	486	611	472	717	704	951	1034	1072	837
ENSMUSG00000069678	chr6	Pcgf1	83077869	83078238	1471	0.326982	2.256698	0.141411	0.227094	0.046239	0	50	73	83	59	82	106	121	110	133	134
ENSMUSG00000020770	chr11	Unk	1.16E+08	1.16E+08	4438	0.316849	2.883259	0.141524	0.227246	0.047661	0	87	85	142	95	139	100	189	177	247	249
ENSMUSG00000027160	chr2	Ccdc34	1.1E+08	1.1E+08	6558	0.348225	2.120066	0.141555	0.227246	0.054902	0	47	49	72	65	82	108	110	78	160	99
ENSMUSG00000031065	chrX	Cdk16	20687954	20688361	4378	-0.23536	7.387677	0.141547	0.227246	0.030374	0	2407	2731	3363	3311	3331	2950	3278	3879	4301	3548
ENSMUSG00000043487	chr12	Acot6	84100654	84101428	3388	0.345557	2.112193	0.141668	0.227402	0.051662	0	40	52	72	82	66	81	109	111	155	101
ENSMUSG00000081087	chr2	Rps15a-ps7	1.52E+08	1.52E+08	392	0.331798	2.065129	0.141894	0.227738	0.047378	0	46	64	58	66	66	90	96	102	127	115
ENSMUSG00000021917	chr14	Spcs1	30999826	31000222	1546	0.262413	6.302035	0.141965	0.227799	0.037495	0	1092	1151	1526	999	1193	1677	2117	2317	1957	1878
ENSMUSG00000032184	chr9	Lysmd2	75625732	75626037	1200	0.35488	2.759354	0.141958	0.227799	0.061888	0	104	71	107	70	140	130	200	236	176	128
ENSMUSG00000061136	chr2	Prpf40a	53134704	53139270	10273	-0.29158	4.890172	0.142165	0.228093	0.045384	0	496	424	591	561	660	395	517	967	733	519
ENSMUSG00000031367	chrX	Ap1s2	1.64E+08	1.64E+08	4965	-0.22561	5.097684	0.142226	0.228165	0.026816	0	527	579	699	589	679	522	814	743	898	730
ENSMUSG00000026927	chr2	Sdccag3	26382802	26383694	3587	0.229528	4.553833	0.142312	0.228258	0.026763	0	319	327	396	336	421	425	646	507	760	640
ENSMUSG00000031652	chr8	N4bp1	86841139	86845041	6469	-0.23271	4.955839	0.142317	0.228258	0.028233	0	464	411	602	629	717	540	641	670	749	720
ENSMUSG00000045064	chr12	Zc2hc1c	85288591	85288785	4482	0.840346	0.928889	0.142529	0.228572	0.341405	0	16	23	20	17	31	23	17	177	27	20
ENSMUSG00000015981	chr7	Stk32c	1.39E+08	1.39E+08	2302	-0.53813	0.164336	0.142738	0.22888	0.107699	0	26	10	22	10	36	16	26	20	19	17
ENSMUSG00000075705	chr17	Msrb1	24736642	24736762	1258	0.281763	7.160127	0.142843	0.229022	0.043815	0	1691	2449	2493	2211	1787	3246	3076	4092	4151	3630
ENSMUSG00000029185	chr5	Fam114a1	64970071	64970144	2964	-0.35697	4.410765	0.142863	0.229027	0.068047	0	389	233	443	293	679	342	645	254	546	397
ENSMUSG00000035674	chr7	Ndufa3	3617373	3617407	858	0.282583	7.163183	0.142886	0.229038	0.044096	0	1789	2338	2289	2330	1903	3699	3077	3853	3843	3576
ENSMUSG00000034190	chr14	Chmp7	69716979	69718300	2706	-0.22745	5.570161	0.143281	0.229645	0.027823	0	715	823	972	846	907	772	1000	1137	1221	992
ENSMUSG00000050079	chr8	Rspry1	94601955	94602430	6425	-0.27054	3.493837	0.143321	0.229682	0.036125	0	157	176	231	194	275	143	243	302	299	213

ENSMUSG00000000934	chr15	Top1mt	75657035	75657214	1903	-0.26554	3.381989	0.143342	0.229689	0.033968	0	133	190	221	200	200	185	208	198	258	247
ENSMUSG00000001909	chr8	Trmt1	84686307	84686699	6306	0.332418	4.612181	0.143431	0.229804	0.059257	0	309	313	372	394	413	398	483	1123	610	556
ENSMUSG00000025409	chr10	Mbd6	1.27E+08	1.27E+08	4455	0.27044	4.029492	0.143534	0.229943	0.037087	0	228	206	252	240	305	214	388	480	511	519
ENSMUSG00000087589	chr1	D430040D24Rik	36557701	36559667	2830	0.520573	0.376222	0.143604	0.230028	0.095664	0	12	18	15	17	19	13	34	54	32	32
ENSMUSG00000003199	chr17	Mpnd	56005711	56005814	2305	-0.25311	5.530767	0.143697	0.23015	0.034685	0	676	811	1003	846	848	857	931	732	1214	1185
ENSMUSG00000038037	chr16	Socs1	10783808	10784921	1220	-0.6395	2.258573	0.143713	0.23015	0.212326	0	139	43	28	115	152	105	74	31	151	69
ENSMUSG00000058192	chr9	Zfp846	20581325	20581678	2861	-0.38459	1.394507	0.143754	0.230189	0.062109	0	52	48	48	42	48	37	51	39	64	69
ENSMUSG00000034881	chr10	Tbxa2r	81328732	81328917	1763	0.499345	0.30706	0.143958	0.23049	0.085731	0	11	12	17	14	25	26	44	16	42	27
ENSMUSG00000039382	chrX	Wdr45	7721973	7722230	2717	0.304125	4.438286	0.144085	0.230666	0.049099	0	315	264	348	332	349	378	464	894	512	526
ENSMUSG00000020705	chr11	Ddx42	1.06E+08	1.06E+08	4228	0.238316	5.225809	0.144148	0.230686	0.030318	0	517	502	608	517	725	634	882	1139	1143	962
ENSMUSG00000030870	chr7	Ubfd1	1.22E+08	1.22E+08	9629	0.308859	5.398833	0.144138	0.230686	0.052147	0	571	516	767	544	762	770	974	1783	1002	879
ENSMUSG00000040350	chr11	Trim7	48826140	48826279	7149	-0.34075	5.848915	0.144117	0.230686	0.063993	0	783	1024	1237	1024	1347	1124	1370	500	1629	1319
ENSMUSG00000024170	chr17	Telo2	25099570	25100120	8006	0.29306	3.164301	0.144235	0.2308	0.041213	0	142	117	133	120	148	171	223	177	353	234
ENSMUSG00000054408	chr8	Spcs3	54520433	54523395	3466	0.232524	5.426894	0.144276	0.230838	0.029018	0	620	556	814	553	764	777	1194	1013	1417	1073
ENSMUSG00000025226	chr19	Fbxl15	46328184	46328526	1348	0.387747	1.677848	0.144333	0.230876	0.06534	0	30	49	53	40	52	77	83	51	116	83
ENSMUSG00000062729	chr1	Ppox	1.71E+08	1.71E+08	4515	0.268748	3.483416	0.144333	0.230876	0.034939	0	159	160	186	144	187	187	259	275	338	369
ENSMUSG00000024436	chr17	Mrps18b	35910379	35910956	2089	0.240727	4.346419	0.144482	0.231087	0.029833	0	236	297	357	343	315	460	481	519	597	489
ENSMUSG00000027630	chr3	Tbl1xr1	22076652	22076954	8362	0.260648	5.132354	0.14456	0.231185	0.036592	0	498	467	593	395	720	640	870	1149	987	815
ENSMUSG00000037938	chr2	Chchd5	1.29E+08	1.29E+08	1727	0.291458	3.022317	0.144764	0.231486	0.040429	0	109	121	142	97	131	150	186	255	241	202
ENSMUSG00000022130	chr14	Tgds	1.18E+08	1.18E+08	2265	0.283939	2.776152	0.144997	0.231832	0.036479	0	92	97	117	88	113	128	169	164	226	185
ENSMUSG00000039033	chr2	Tasp1	1.4E+08	1.4E+08	3652	-0.30653	2.586357	0.1451	0.231943	0.043528	0	106	90	123	111	116	89	121	160	141	109
ENSMUSG00000041241	chr4	Mul1	1.38E+08	1.38E+08	4000	-0.23972	5.40627	0.145091	0.231943	0.031092	0	610	752	837	812	806	799	846	998	1069	800
ENSMUSG00000027716	chr3	Trpc3	36620482	36621397	5419	-0.36608	2.090439	0.145198	0.232071	0.062424	0	70	78	77	96	67	58	94	114	83	77
ENSMUSG00000070713	chr8	Gm10282	72304118	72305276	1159	0.373206	1.833388	0.145588	0.232668	0.063278	0	50	31	50	42	82	65	114	77	121	83
ENSMUSG00000034187	chr11	Nsf	1.04E+08	1.04E+08	8346	0.256974	4.366974	0.145637	0.23272	0.034535	0	247	257	338	332	403	367	480	396	802	619
ENSMUSG00000020156	chr10	Mum1	80226434	80226704	10361	0.245273	4.4116	0.145779	0.232921	0.031497	0	251	275	367	291	457	401	538	423	725	627
ENSMUSG00000015341	chr8	Golga7	23241353	23242631	2383	0.221139	5.208034	0.145915	0.233111	0.026201	0	482	500	678	546	647	736	975	915	1068	943
ENSMUSG00000003099	chr7	Ppp5c	17004640	17005171	3136	-0.23384	5.921044	0.145951	0.233141	0.030075	0	884	1016	1236	1189	1130	1063	1203	1399	1506	1317
ENSMUSG00000042354	chr14	Gnl3	31012434	31012634	1883	0.306805	4.809326	0.146024	0.23323	0.051338	0	333	365	513	353	545	532	641	1159	688	565
ENSMUSG00000051041	chr7	Olfml1	1.08E+08	1.08E+08	1685	-0.43313	2.476	0.146175	0.233445	0.095033	0	113	51	105	90	178	57	127	171	116	79
ENSMUSG00000057667	chr7	Bloc1s3	19505814	19507610	1824	0.299211	2.684955	0.146392	0.233765	0.040778	0	93	80	109	98	91	121	187	155	172	180
ENSMUSG00000042688	chr9	Mapk6	75369062	75369149	6675	-0.24481	5.427075	0.14643	0.233798	0.032776	0	547	628	954	847	972	603	1089	822	1271	886
ENSMUSG00000041921	chr2	Metap1d	71453276	71453398	4537	-0.26683	4.508335	0.146472	0.233839	0.03803	0	384	451	428	415	354	434	490	511	494	449
ENSMUSG00000047866	chr8	Lonp2	86624043	86624416	5346	-0.24246	5.894292	0.146638	0.234077	0.032507	0	936	921	1170	1188	1159	952	1080	1533	1438	1363
ENSMUSG00000035382	chr9	Pcsk7	45906569	45907039	3784	-0.23235	4.000752	0.146754	0.234208	0.027438	0	245	256	313	255	377	227	355	376	434	338
ENSMUSG00000036398	chr17	Ppp1r11	36948356	36949554	1975	0.242907	4.602745	0.146741	0.234208	0.031142	0	293	389	424	359	377	553	618	531	763	590
ENSMUSG00000052632	chr12	Asap2	21111748	21112169	5687	-0.29614	3.361772	0.146976	0.234534	0.044539	0	167	118	198	217	251	131	220	265	300	172
ENSMUSG00000040738	chr4	Ints8	11199158	11199451	7472	-0.24524	3.98692	0.147003	0.234551	0.030609	0	234	246	332	264	365	251	421	364	353	296
ENSMUSG00000001665	chr10	Gstt3	75774115	75775010	2627	0.316094	2.446933	0.147093	0.234667	0.047692	0	59	61	84	74	127	112	120	141	157	162
ENSMUSG00000043342	chr2	Hoxd9	74697727	74698833	2136	-0.51811	2.189288	0.14715	0.234731	0.136743	0	40	126	108	83	82	112	43	77	65	117
ENSMUSG00000058586	chr15	Serhl	83089506	83089765	7393	0.277843	4.516473	0.147275	0.234904	0.041118	0	299	414	347	337	288	510	502	617	725	556
ENSMUSG00000027890	chr3	Gstm4	1.08E+08	1.08E+08	1707	0.245966	3.814361	0.14737	0.235028	0.030477	0	185	207	238	188	248	312	313	338	385	410
ENSMUSG00000001865	chr3	Cpa3	20215620	20215992	1517	0.397107	2.100087	0.147505	0.235145	0.07691	0	53	45	50	45	114	104	99	106	98	139
ENSMUSG00000023206	chr2	Il15ra	11705290	11705578	4446	-0.27929	3.354331	0.147483	0.235145	0.039398	0	152	223	190	158	196	158	190	214	276	241
ENSMUSG00000026043	chr1	Col3a1	45311538	45311832	9816	-0.37886	11.43484	0.14753	0.235145	0.081598	0	36702	31732	54641	41635	108299	44341	78775	31278	77349	52421
ENSMUSG00000029265	chr5	Dr1	1.08E+08	1.08E+08	3478	-0.24759	4.369823	0.147504	0.235145	0.032571	0	331	316	406	390	427	263	487	538	561	383
ENSMUSG00000040323	chr1	Gm15429	1.62E+08	1.62E+08	798	0.436466	0.957576	0.147545	0.235145	0.076008	0	15	27	28	25	36	31	35	70	60	52
ENSMUSG00000096173	chr15	Gm3150	72913357	72913560	204	-0.43544	0.765388	0.147531	0.235145	0.078251	0	31	28	29	43	22	24	34	25	36	42
ENSMUSG00000092564	chr17	BC051226	33908182	33908586	979	0.456875	0.593592	0.14757	0.235157	0.069419	0	20	18	17	19	24	32	27	32	44	54
ENSMUSG00000058833	chr8	2810428I15Rik	70504292	70504509	1822	0.254854	5.388607	0.147829	0.235543	0.035866	0	505	591	786	628	680	1062	950	927	1067	1217
ENSMUSG00000060679	chr1	Mrps9	42851233	42851426	5524	0.259049	4.973598	0.147872	0.235585	0.036389	0	386	504	509	550	402	663	752	858	888	809
ENSMUSG00000034748	chr10	Sirt6	81621785	81622078	2785	0.335218	2.058764	0.148082	0.235892	0.049805	0	51	57	52	65	74	81	95	102	116	135
ENSMUSG00000005683	chr10	Cs	1.28E+08	1.28E+08	2828	-0.25096	9.789631	0.14817	0.236004	0.036005	0	12377	15658	16928	19316	15630	16103	16611	20709	23241	17621
ENSMUSG00000022864	chr16	D16Ertd472e	78544012	78545284	2453	-0.49481	0.624629	0.148196	0.236018	0.096505	0	14	16	35	48	32	16	34	32	37	24
ENSMUSG00000022556	chr15	Hsf1	76477445	76477717	2018	-0.22469	5.088646	0.148293	0.236146	0.027226	0	536	513	695	615	706	626	741	751	765	748
ENSMUSG00000020282	chr11	Rhbdf1	32209585	32210223	5433	0.259968	4.430319	0.14833	0.236165	0.03627	0	295	207	351	313	495	384	645	526	732	478
ENSMUSG00000071497	chr19	Nutf2-ps1	53588204	53589067	864	-0.38975	0.94609	0.148339	0.236165	0.054061	0	30	30	41	34	40	33	41	40	39	32
ENSMUSG00000026970	chr2	Rbms1	60750193	60752982	5473	0.255639	5.098857	0.148433	0.236288	0.035717	0	478	393	517	517	719	502	815	845	1278	1012
ENSMUSG00000055681	chr8	Cope	70302518	70302932	3353	0.230343	6.28044	0.148488	0.236347	0.029725	0	985	1164	1311	1087	1426	1676	1907	1955	2217	1994
ENSMUSG00000025410	chr10	Dctn2	1.27E+08	1.27E+08	1918	0.241805	6.851709	0.148586	0.236477	0.033067	0	1507	1611	1972	1720	2032	2258	2626	3673	3185	2837
ENSMUSG00000008200	chr2	Fnbp4	90745370	90745826	6583	0.251203	3.885907	0.148829	0.236836	0.032214	0	222	175	238	200	289	235	338	422	452	438
ENSMUSG00000006527	chr14	Sfmbt1	30714849	30714966	8629	-0.2477	3.559633	0.149027	0.237097	0.030437	0	176	163	240	201	296	176	235	278	293	276
ENSMUSG00000030553	chr7	Pgpep1l	68236608	68237122	955	0.363548	1.948078	0.149023	0.237097	0.059711	0	51	44	77	45	58	95	119	80	94	98
ENSMUSG00000022095	chr14	Fam160b2	70583296	70585183	4033	-0.2366	5.414819	0.149206	0.237299	0.030985	0	659	734	856	806	773	784	804	784	1213	996
ENSMUSG00000029642	chr5	Polr1d	1.47E+08	1.47E+08	1985	0.248861	6.029122	0.149185	0.237299	0.034794	0	797	1013	1167	942	1045	1572	1579	1670	1683	1650
ENSMUSG00000041671	chr6	Pyroxd1	1.42E+08	1.42E+08	4933	-0.2694	3.326633	0.149195	0.237299	0.036286	0	144	199	205	168	187	171	217	217	211	232

ENSMUSG00000026921	chr2	Egfl7	26580014	26580109	3581	0.273204	5.386379	0.149309	0.237436	0.041423	0	452	711	706	716	537	730	936	1080	1358	1291
ENSMUSG00000047371	chr7	Zfp768	1.27E+08	1.27E+08	2245	-0.23604	5.012715	0.149338	0.237456	0.03037	0	462	570	647	644	573	604	686	705	799	644
ENSMUSG00000027605	chr2	Acss2	1.56E+08	1.56E+08	10163	0.318051	5.295282	0.149652	0.237877	0.056729	0	403	454	540	824	717	573	754	911	1572	1416
ENSMUSG00000031883	chr8	Car7	1.05E+08	1.05E+08	2459	-0.51157	0.573129	0.149639	0.237877	0.111308	0	19	30	19	47	21	20	34	15	38	30
ENSMUSG00000097368	chr5	Gm10390	1.2E+08	1.2E+08	8066	-0.42973	1.009535	0.149655	0.237877	0.075969	0	26	36	38	46	39	29	46	21	45	52
ENSMUSG00000034863	chr8	Ano8	71476023	71476921	3753	-0.22767	4.220836	0.149721	0.237928	0.027179	0	295	289	384	367	334	295	426	363	524	408
ENSMUSG00000079083	chr9	Jrkl	13242790	13245741	2952	-0.34027	1.77538	0.149709	0.237928	0.051698	0	52	59	61	63	77	51	61	60	111	67
ENSMUSG00000067261	chr4	Foxd3	99656299	99658622	2324	-0.50936	0.039342	0.1498	0.238026	0.083163	0	12	18	20	20	23	17	24	22	10	16
ENSMUSG00000039671	chr2	Zmynd8	1.66E+08	1.66E+08	11031	0.265145	4.250022	0.149839	0.23806	0.037825	0	244	169	298	336	415	335	450	455	602	596
ENSMUSG00000025176	chr19	Hoga1	42045610	42046110	2259	0.624824	0.872007	0.149906	0.23814	0.180507	0	20	24	23	16	29	17	26	115	58	31
ENSMUSG00000028479	chr4	Gne	44034075	44037353	6358	-0.27855	3.252393	0.149975	0.238223	0.039222	0	172	122	163	171	243	161	188	163	248	241
ENSMUSG00000045319	chr2	Proser2	6097607	6101360	9563	0.459805	0.46753	0.150161	0.23849	0.078054	0	7	15	19	23	27	32	31	30	36	42
ENSMUSG00000023074	chrX	Mospd1	53344598	53344906	2085	-0.39432	5.754651	0.150246	0.238598	0.088557	0	1118	828	1055	1102	949	588	894	2198	980	793
ENSMUSG00000027957	chr3	Slc35a3	1.17E+08	1.17E+08	10173	-0.25201	3.21926	0.150435	0.238843	0.030921	0	135	136	198	175	201	136	190	196	269	206
ENSMUSG00000032897	chr4	Nfyc	1.21E+08	1.21E+08	2942	-0.22754	5.090621	0.150419	0.238843	0.028319	0	571	527	671	623	663	664	746	670	830	723
ENSMUSG00000066233	chr9	Tmem42	1.23E+08	1.23E+08	1044	-0.29488	2.978583	0.150598	0.239075	0.043252	0	135	144	169	118	147	146	144	194	182	146
ENSMUSG00000005936	chr17	Kctd20	28951950	28952023	4379	0.366172	5.944971	0.150623	0.23908	0.076505	0	767	746	1032	901	1067	909	1230	3150	1368	1427
ENSMUSG00000011158	chr12	Brf1	1.13E+08	1.13E+08	2755	0.234548	4.210921	0.150654	0.23908	0.029027	0	241	213	340	254	385	326	446	531	546	491
ENSMUSG00000053950	chr18	Adnp2	80126311	80130994	5012	0.288992	2.866997	0.150638	0.23908	0.040548	0	96	80	114	106	150	112	184	218	233	189
ENSMUSG00000059839	chr13	Zfp874b	67471514	67474951	3743	-0.39928	3.313777	0.150949	0.239521	0.086691	0	147	198	204	215	164	126	162	384	157	158
ENSMUSG00000001157	chr6	Gmcl1	86691768	86693051	3823	0.300893	2.56989	0.151167	0.239837	0.043729	0	78	73	103	68	118	118	147	123	184	183
ENSMUSG00000033697	chr15	Arhgap39	76723985	76725176	7367	0.330152	2.420763	0.151182	0.239837	0.051915	0	75	48	85	88	95	82	172	135	184	121
ENSMUSG00000021709	chr13	Erbb2ip	1.04E+08	1.04E+08	7939	-0.31561	5.556278	0.151378	0.240069	0.056679	0	693	731	940	909	1116	533	904	1679	1013	799
ENSMUSG00000032409	chr9	Atr	95857597	95857783	23492	-0.28469	3.033632	0.15138	0.240069	0.03998	0	137	109	185	133	187	126	143	152	225	216
ENSMUSG00000057497	chr6	Fam136a	86365683	86365819	1605	-0.24443	4.232512	0.15135	0.240069	0.031876	0	277	367	386	314	339	349	418	335	485	411
ENSMUSG00000019952	chr10	Poc1b	99107036	99107223	3748	0.318557	2.455759	0.151499	0.24023	0.047229	0	78	56	80	83	105	85	127	137	195	166
ENSMUSG00000056260	chr3	Lrif1	1.07E+08	1.07E+08	9192	-0.34385	2.764323	0.151548	0.24028	0.059876	0	125	124	147	100	126	97	135	208	127	121
ENSMUSG00000041079	chr16	Rwdd2b	87433407	87434626	2009	0.371816	1.985864	0.151595	0.240326	0.067128	0	41	37	78	55	75	87	128	60	131	103
ENSMUSG00000033985	chr4	Tesk2	1.17E+08	1.17E+08	4272	0.377892	1.323482	0.151677	0.240401	0.060954	0	27	22	48	39	40	42	78	72	67	58
ENSMUSG00000036537	chrX	Rnf113a1	37191245	37192467	1223	-0.43368	0.803501	0.151671	0.240401	0.071925	0	16	32	42	27	45	23	36	40	34	32
ENSMUSG00000097906	chr13	Gm9625	67810246	67811200	955	-0.32451	2.200241	0.151746	0.240483	0.048537	0	69	86	98	82	82	84	104	92	90	93
ENSMUSG00000056267	chr9	Cep70	99243367	99243490	4806	0.415233	1.282119	0.15179	0.240525	0.073977	0	24	36	46	28	32	39	79	46	65	83
ENSMUSG00000050910	chr11	Cdr2l	1.15E+08	1.15E+08	3700	0.432437	2.903068	0.151808	0.240527	0.101298	0	96	67	95	55	228	166	252	111	253	210
ENSMUSG00000029454	chr5	Mapkapk5	1.22E+08	1.22E+08	6209	-0.22996	5.447308	0.151951	0.240726	0.029623	0	721	707	940	793	745	757	908	979	1032	995
ENSMUSG00000078773	chr4	Rad54b	11558922	11559013	5782	-0.46228	0.95545	0.151978	0.240741	0.097506	0	44	28	52	21	34	26	46	24	61	29
ENSMUSG00000043300	chr3	B3galnt1	69574158	69575960	2028	0.365329	2.398948	0.152346	0.241296	0.066983	0	81	38	80	60	125	88	163	123	155	156
ENSMUSG00000029438	chr5	Bcl7a	1.23E+08	1.23E+08	8580	-0.29415	4.003569	0.152459	0.241447	0.046809	0	246	206	329	307	402	244	289	517	364	259
ENSMUSG00000059119	chr7	Nap1l4	1.44E+08	1.44E+08	2283	-0.23665	7.560821	0.152523	0.241521	0.03247	0	2924	3334	3910	3213	3614	3672	4213	3892	4370	3909
ENSMUSG00000044763	chr16	Trmt10c	56032609	56035291	3002	-0.25958	4.119473	0.152652	0.241698	0.036326	0	269	325	360	306	302	276	405	460	371	321
ENSMUSG00000033579	chr8	Fa2h	1.11E+08	1.11E+08	3008	0.470784	0.552927	0.152729	0.241772	0.08412	0	16	14	16	26	23	22	39	54	48	23
ENSMUSG00000062202	chr17	Btbd9	30215524	30220144	6857	-0.23768	3.620389	0.152734	0.241772	0.028908	0	190	190	252	225	250	184	262	223	358	300
ENSMUSG00000024134	chr17	Six2	85684277	85685513	2119	-0.49485	3.199964	0.152944	0.242076	0.13601	0	265	47	198	118	274	99	194	239	258	113
ENSMUSG00000005983	chr16	1700037C18Rik	3895179	3895414	3227	0.39976	1.101044	0.153116	0.242322	0.064225	0	30	30	34	25	26	44	49	42	65	71
ENSMUSG00000028080	chr3	Lrba	86224680	86224754	18270	-0.4061	4.996912	0.153189	0.242382	0.094553	0	528	499	606	708	694	318	472	1368	525	522
ENSMUSG00000040669	chr6	Phc1	1.22E+08	1.22E+08	5297	-0.26053	3.652353	0.153183	0.242382	0.035665	0	223	207	239	218	243	184	226	346	289	286
ENSMUSG00000040918	chr1	Slc19a2	1.64E+08	1.64E+08	3838	-0.41429	2.36804	0.153256	0.24246	0.089902	0	66	96	119	119	84	49	79	181	117	90
ENSMUSG00000021930	chr14	Spryd7	61531993	61535241	4002	-0.32718	5.363215	0.153394	0.242637	0.061343	0	588	748	948	775	757	603	682	1470	722	743
ENSMUSG00000066640	chr5	Fbxl18	1.43E+08	1.43E+08	12563	-0.22735	3.901993	0.153403	0.242637	0.02653	0	206	216	331	276	325	246	296	342	395	328
ENSMUSG00000025350	chr10	Rdh5	1.29E+08	1.29E+08	2809	0.24138	6.062182	0.153443	0.242672	0.033395	0	901	989	1200	945	1050	1562	1591	1724	1749	1716
ENSMUSG00000002688	chr12	Prkd1	50341231	50342220	3778	0.482647	1.692954	0.153466	0.242682	0.115095	0	44	44	27	47	52	29	72	111	85	136
ENSMUSG00000023032	chr15	Slc4a8	1.01E+08	1.01E+08	13021	-0.52284	1.330057	0.153597	0.24286	0.135492	0	62	31	71	46	27	31	31	85	51	36
ENSMUSG00000017737	chr2	Mmp9	1.65E+08	1.65E+08	3539	-0.79341	1.630712	0.153825	0.243194	0.336482	0	32	16	63	21	217	37	32	26	41	119
ENSMUSG00000033931	chr8	Rbm34	1.27E+08	1.27E+08	3429	0.317952	3.085267	0.153989	0.243425	0.052275	0	111	103	155	125	130	124	199	331	242	200
ENSMUSG00000027519	chr2	Rab22a	1.74E+08	1.74E+08	7206	-0.22752	5.928205	0.154015	0.243439	0.029634	0	979	986	1184	1139	1174	996	1311	1458	1405	1369
ENSMUSG00000044043	chr18	Pcdhb14	37447656	37456350	8695	-0.50079	0.560822	0.154416	0.244044	0.098911	0	27	12	37	22	41	24	41	20	32	17
ENSMUSG00000103922	chr1	RP23-34E15.4	4771131	4772199	1069	-0.48153	1.194512	0.154599	0.244306	0.109801	0	42	40	40	69	19	39	37	39	59	42
ENSMUSG00000029647	chr5	Pan3	1.47E+08	1.47E+08	7316	0.274175	3.523068	0.154693	0.244425	0.039279	0	169	128	170	166	233	173	280	363	314	339
ENSMUSG00000032434	chr9	Cmtm6	1.15E+08	1.15E+08	3352	0.273268	4.63341	0.154807	0.244578	0.041878	0	268	347	310	354	617	436	666	512	891	707
ENSMUSG00000028542	chr4	Slc6a9	1.18E+08	1.18E+08	5141	-0.29325	2.750035	0.154883	0.24467	0.042458	0	102	90	129	120	179	92	123	145	180	166
ENSMUSG00000022911	chr16	Arl13b	62793685	62795708	5087	-0.31575	2.218413	0.155007	0.244838	0.046936	0	83	58	95	79	112	68	95	112	121	83
ENSMUSG00000026887	chr2	Mrrf	36136389	36136699	2853	-0.25823	4.325127	0.155153	0.245021	0.036658	0	260	360	438	413	342	394	435	327	546	417
ENSMUSG00000028364	chr4	Tnc	63959785	63960543	7772	0.64349	6.106648	0.155176	0.245021	0.240442	0	867	303	1017	483	2051	857	4496	466	2661	1647
ENSMUSG00000030123	chr6	Plxnd1	1.16E+08	1.16E+08	7192	-0.28783	6.17231	0.155163	0.245021	0.048305	0	899	1138	1347	1756	1517	1108	1796	983	2317	1519
ENSMUSG00000034926	chr4	Dhcr24	1.07E+08	1.07E+08	4028	0.552925	3.356514	0.155236	0.245088	0.174553	0	72	53	93	131	383	196	333	108	406	389
ENSMUSG00000054648	chr8	Zfp869	69706332	69707694	1590	-0.40358	3.16645	0.155284	0.245137	0.08973	0	164	136	191	160	197	106	173	352	157	105
ENSMUSG00000071649	chr19	B3gat3	8920374	8920648	1601	0.241537	5.100002	0.155479	0.245415	0.033012	0	433	510	680	450	545	795	835	779	942	938

ENSMUSG00000034460	chr12	Six4	73099609	73104238	10855	-0.32196	4.052266	0.155638	0.245639	0.05808	0	264	270	310	361	322	219	335	583	311	262
ENSMUSG00000040006	chr10	Ginm1	7767947	7768585	2996	-0.25973	5.833043	0.155768	0.245816	0.039131	0	943	950	1171	993	1108	861	1010	1693	1264	1223
ENSMUSG00000020375	chr11	Rufy1	50389286	50389958	2764	-0.22293	4.583851	0.155901	0.245998	0.027336	0	347	426	457	444	470	404	483	519	601	573
ENSMUSG00000041757	chr1	Plekha6	1.33E+08	1.33E+08	10827	-0.31378	3.165143	0.156018	0.24611	0.052227	0	152	98	172	203	206	129	204	135	207	257
ENSMUSG00000068739	chr3	Sars	1.08E+08	1.08E+08	3653	0.230635	6.2602	0.156025	0.24611	0.030924	0	945	1109	1355	1194	1284	1612	1649	1953	2269	2159
ENSMUSG00000075040	chr2	Zfp408	91643669	91646473	4008	0.359648	2.183965	0.156009	0.24611	0.063914	0	48	39	93	69	82	59	131	109	142	152
ENSMUSG00000038046	chr11	Rnmtl1	76243715	76244086	1935	0.294052	3.699934	0.156082	0.246142	0.046607	0	147	225	232	196	155	319	295	304	454	282
ENSMUSG00000043099	chr11	Hic1	75164565	75167544	3750	-0.31734	3.705828	0.156078	0.246142	0.055437	0	222	155	233	285	318	207	411	170	338	232
ENSMUSG00000006369	chr15	Fbln1	85205949	85206212	4368	0.391123	4.247684	0.156212	0.24632	0.087919	0	331	106	211	223	525	407	657	415	593	433
ENSMUSG00000031111	chrX	Igsf1	49782536	49782952	5768	0.336427	2.453524	0.15628	0.246399	0.058474	0	49	49	102	78	131	121	153	113	173	140
ENSMUSG00000029376	chr5	Mthfd2l	90931196	90931433	2235	-0.3677	1.931358	0.156789	0.247174	0.067125	0	80	64	74	67	61	40	85	101	91	69
ENSMUSG00000025436	chr10	Xrcc6bp1	1.27E+08	1.27E+08	1362	0.416629	1.135455	0.156907	0.247331	0.075443	0	27	28	49	22	23	53	45	53	73	54
ENSMUSG00000032115	chr9	Hyou1	44379490	44379595	7230	0.282063	5.52368	0.157022	0.247484	0.046375	0	502	540	717	652	1128	829	1147	788	1705	1523
ENSMUSG00000040824	chr7	Snrpd2	19149722	19149894	613	0.233861	5.226477	0.157066	0.247498	0.031241	0	470	558	666	538	633	884	950	811	1033	990
ENSMUSG00000072214	chr16	Sept5	18621811	18622796	2127	0.363459	3.002014	0.157057	0.247498	0.071972	0	118	65	98	85	225	141	253	170	279	210
ENSMUSG00000022661	chr16	Cd200	45382135	45383457	3321	-0.25711	4.596556	0.157103	0.247528	0.03746	0	379	383	437	581	395	367	558	417	662	590
ENSMUSG00000020946	chr11	Gosr2	1.04E+08	1.04E+08	3266	-0.22158	6.242404	0.157179	0.247563	0.028671	0	1176	1126	1607	1376	1546	1212	1630	1806	1881	1653
ENSMUSG00000036461	chr14	Elf1	79481194	79481637	4314	0.264591	3.32915	0.157175	0.247563	0.036386	0	128	98	162	184	191	175	250	290	297	264
ENSMUSG00000040272	chr2	Accs	93833467	93835828	8364	0.383997	1.667845	0.157167	0.247563	0.067313	0	50	30	51	42	49	55	69	61	108	118
ENSMUSG00000020482	chr11	Ccdc117	5528887	5531533	3372	-0.29035	4.637482	0.157331	0.247775	0.048199	0	415	403	501	428	534	342	465	850	518	432
ENSMUSG00000027667	chr3	Zfp639	32510259	32510589	5475	-0.24084	4.481528	0.157696	0.248321	0.032262	0	350	384	419	398	457	394	464	599	498	412
ENSMUSG00000045160	chr6	Bola3	83349147	83349237	3211	-0.27588	6.23773	0.157811	0.248444	0.044887	0	1187	1455	1609	1456	1092	1639	1486	1450	1796	1476
ENSMUSG00000060181	chr10	Slc35e3	1.18E+08	1.18E+08	3482	0.331979	2.787611	0.157799	0.248444	0.058629	0	91	50	113	91	171	123	192	179	190	204
ENSMUSG00000055675	chr8	Kbtbd11	15011025	15011314	7137	0.428356	2.319419	0.1579	0.248556	0.099166	0	48	40	73	61	138	87	91	89	183	215
ENSMUSG00000054226	chr6	Tprkb	85915738	85915790	3491	-0.2457	4.537472	0.158011	0.248703	0.033769	0	365	435	500	326	464	444	509	500	502	492
ENSMUSG00000021496	chr13	Pcbd2	55727368	55727474	546	0.348804	2.357286	0.158081	0.248728	0.0594	0	64	88	72	68	71	130	123	91	176	134
ENSMUSG00000030583	chr7	Sipa1l3	29320372	29322287	16555	-0.30466	2.934973	0.15805	0.248728	0.048277	0	110	91	151	147	214	95	184	130	211	185
ENSMUSG00000030674	chr7	Qprt	1.27E+08	1.27E+08	2645	0.559141	0.76305	0.158069	0.248728	0.156128	0	25	10	16	8	51	42	55	31	38	51
ENSMUSG00000104372	chr11	AL663030.1	1.21E+08	1.21E+08	495	-0.40203	2.739053	0.158268	0.248994	0.087601	0	95	99	177	136	126	84	113	251	110	102
ENSMUSG00000057134	chr10	Ado	67544512	67548955	4444	-0.21536	5.216325	0.158483	0.249305	0.026483	0	538	613	752	682	750	640	763	769	1009	845
ENSMUSG00000047330	chr1	Kcne4	78816758	78816996	2657	-0.38754	1.36963	0.158535	0.249359	0.065998	0	36	31	49	45	81	41	39	51	74	50
ENSMUSG00000020520	chr11	Galnt10	57645442	57645717	5965	-0.28421	4.289579	0.158644	0.249501	0.045933	0	262	301	411	368	467	262	543	247	611	436
ENSMUSG00000038013	chr11	Wipf2	98863638	98863902	7819	-0.25362	3.489973	0.158912	0.249894	0.033508	0	171	158	232	212	248	202	204	210	265	304
ENSMUSG00000031788	chr8	Kifc3	95099832	95100452	3758	0.243443	3.796007	0.15904	0.250067	0.031577	0	178	170	222	211	283	225	425	302	475	348
ENSMUSG00000041935	chr15	AW549877	3982036	3986479	5083	-0.2674	4.342493	0.159076	0.250095	0.040551	0	311	316	379	389	456	250	384	633	484	412
ENSMUSG00000025008	chr19	Tctn3	40596446	40597542	3273	0.377339	1.802009	0.159129	0.25015	0.067881	0	39	60	42	38	65	78	104	61	112	91
ENSMUSG00000032449	chr9	Slc25a36	97074961	97079239	9594	-0.2364	4.895676	0.159596	0.250856	0.031724	0	382	474	591	537	732	567	618	697	656	614
ENSMUSG00000045427	chrX	Hnrnph2	1.35E+08	1.35E+08	4369	-0.2147	5.689067	0.159648	0.250909	0.026882	0	812	761	1097	853	1131	816	1248	1068	1406	1077
ENSMUSG00000026269	chr1	Rnpepl1	92910783	92911483	9467	-0.23113	5.953349	0.159718	0.250962	0.031471	0	890	911	1136	1312	1368	1030	1138	1437	1672	1406
ENSMUSG00000049038	chr10	Mterf2	85119435	85120814	1565	-0.3121	3.758109	0.159717	0.250962	0.054894	0	211	284	276	286	161	270	284	214	349	277
ENSMUSG00000018379	chr11	Srsf1	88047373	88048032	5710	0.242729	5.996888	0.159773	0.251019	0.034807	0	803	836	1176	855	1258	1133	1708	1223	2238	1898
ENSMUSG00000025140	chr11	Pycr1	1.21E+08	1.21E+08	3935	-0.40414	3.349182	0.15987	0.251144	0.09266	0	179	121	209	147	329	195	298	80	267	175
ENSMUSG00000022760	chr16	Thap7	17527982	17528740	1880	0.248092	3.267897	0.159954	0.25119	0.031248	0	134	125	168	148	151	189	237	258	260	262
ENSMUSG00000036553	chr5	Sh3tc1	35697180	35697568	5705	0.326512	2.783248	0.159929	0.25119	0.055264	0	64	103	110	128	96	100	164	168	250	218
ENSMUSG00000074207	chr3	Adh1	1.38E+08	1.38E+08	2233	0.485428	4.642112	0.159951	0.25119	0.138952	0	305	333	501	411	150	330	272	1119	768	953
ENSMUSG00000022914	chr16	Brwd1	95992092	95993977	20280	-0.24078	5.439762	0.160175	0.2515	0.033823	0	607	629	928	760	1053	702	991	1164	1014	764
ENSMUSG00000056014	chr5	A430033K04Rik	1.39E+08	1.39E+08	3900	-0.33763	1.646556	0.160187	0.2515	0.049187	0	47	44	59	64	72	56	51	64	79	64
ENSMUSG00000037752	chr4	Xkr8	1.33E+08	1.33E+08	4312	0.386242	1.811303	0.160266	0.251595	0.073611	0	31	35	54	50	82	59	107	56	123	112
ENSMUSG00000062929	chr12	Cfl2	54858817	54861237	2940	-0.24179	8.829115	0.160306	0.251629	0.035393	0	6614	7652	9808	7873	9347	7495	9556	12613	10552	8350
ENSMUSG00000027217	chr2	Tspan18	93201760	93204422	8175	-0.43137	3.135858	0.160404	0.251753	0.107101	0	84	117	165	275	210	87	121	115	318	262
ENSMUSG00000037315	chrX	Jade3	20425688	20425830	5084	0.477577	0.25628	0.160455	0.251806	0.074457	0	18	12	13	16	16	16	22	35	43	34
ENSMUSG00000050705	chr17	2310061I04Rik	35892677	35892966	2414	0.255055	5.848034	0.160494	0.251839	0.038483	0	685	922	922	1023	780	1274	1273	1602	1716	1411
ENSMUSG00000026864	chr2	Hspa5	34771970	34772146	4229	0.258187	8.246399	0.160566	0.251923	0.040362	0	3511	4132	5151	3779	6881	6990	7964	5623	9227	8684
ENSMUSG00000060288	chr4	Ppih	1.19E+08	1.19E+08	1894	0.336339	2.767881	0.160805	0.252269	0.060338	0	89	88	146	81	91	158	173	105	237	203
ENSMUSG00000035456	chr5	Prdm8	98180869	98181112	3119	-0.48746	0.001285	0.160851	0.252313	0.079391	0	16	8	21	25	20	12	18	13	27	20
ENSMUSG00000027834	chr3	Serpini1	75557547	75557642	7286	-0.4711	0.302552	0.160869	0.252313	0.080053	0	15	11	31	33	23	19	21	25	26	21
ENSMUSG00000049588	chr11	Ccdc69	55049731	55050558	1848	-0.35271	3.499935	0.16101	0.252505	0.069797	0	144	155	272	201	306	242	241	100	285	274
ENSMUSG00000045438	chr5	Cox19	1.39E+08	1.39E+08	3539	0.229498	5.050742	0.161227	0.252816	0.030455	0	440	476	575	476	572	782	838	683	984	851
ENSMUSG00000040990	chrX	Sh3kbp1	1.6E+08	1.6E+08	10100	-0.29542	5.491033	0.161323	0.252938	0.051997	0	707	852	1030	732	785	810	911	518	1237	1255
ENSMUSG00000054836	chr9	Elp6	1.1E+08	1.1E+08	2054	0.357451	2.135483	0.161373	0.252989	0.065988	0	43	52	89	60	74	118	107	70	125	135
ENSMUSG00000031672	chr8	Got2	95864134	95865251	2585	-0.27174	8.839294	0.161489	0.253142	0.044962	0	6159	8760	8372	10807	7287	7937	9210	11170	12333	7908
ENSMUSG00000098950	chr2	Gm28036	1.56E+08	1.56E+08	5823	-0.21778	5.522043	0.161614	0.253309	0.027853	0	732	708	877	789	1029	700	918	1146	1218	1010
ENSMUSG00000042303	chr15	Sgsm3	80977765	80977865	4358	-0.2369	3.558935	0.161709	0.253428	0.029606	0	171	207	239	204	236	207	222	275	306	245
ENSMUSG00000041895	chr11	Wipi1	1.1E+08	1.1E+08	4410	-0.24265	6.012214	0.161861	0.253638	0.035161	0	950	993	1376	1267	1272	1055	1217	1804	1584	1240
ENSMUSG00000075273	chr2	Ttc30b	75935849	75938585	2737	-0.3558	1.921152	0.161924	0.253709	0.063288	0	63	67	86	56	75	38	73	100	109	68
ENSMUSG00000021385	chr13	Ippk	49421311	49421466	2776	-0.25701	3.161695	0.162279	0.254235	0.034474	0	116	162	191	156	184	135	200	205	227	182

ENSMUSG00000032850	chr5	Rnft2	1.18E+08	1.18E+08	5593	-0.46139	0.847129	0.162314	0.254256	0.094123	0	27	27	42	27	45	30	36	12	44	47
ENSMUSG00000067825	chr6	Pex26	1.21E+08	1.21E+08	5667	-0.3116	2.504464	0.162329	0.254256	0.049384	0	87	95	98	82	160	100	97	106	158	124
ENSMUSG00000068697	chr14	Myoz1	20649102	20649609	1294	-0.27511	10.89366	0.162436	0.254395	0.046375	0	30992	31842	40075	35311	35080	37545	29549	53913	37222	39199
ENSMUSG00000025016	chr19	Tm9sf3	41210842	41215139	6144	-0.22131	6.976938	0.162551	0.254546	0.029656	0	1994	1868	2627	2056	2861	1898	2892	2922	3209	2754
ENSMUSG00000027893	chr3	Ahcyl1	1.08E+08	1.08E+08	6690	0.250348	5.520835	0.162684	0.254726	0.037212	0	616	543	794	650	929	657	988	1198	1607	1497
ENSMUSG00000040795	chr4	Iqcc	1.3E+08	1.3E+08	3188	0.266298	2.970361	0.162861	0.254975	0.035871	0	93	117	138	111	127	146	203	222	230	188
ENSMUSG00000036281	chr2	Snapc4	26362765	26363020	6622	0.330811	2.342754	0.162881	0.254977	0.055283	0	71	59	81	68	89	71	99	170	169	148
ENSMUSG00000015766	chr6	Eps8	1.37E+08	1.37E+08	5731	0.322696	3.475068	0.162929	0.254982	0.058809	0	155	81	191	169	238	147	232	312	436	344
ENSMUSG00000029790	chr6	Cep41	30653457	30655850	4979	0.461043	1.006122	0.162923	0.254982	0.093112	0	32	22	26	23	29	36	69	23	69	63
ENSMUSG00000079560	chr6	Hoxa3	52169062	52170742	6014	-0.36993	1.354906	0.16294	0.254982	0.063587	0	46	38	53	51	44	29	44	68	55	58
ENSMUSG00000048429	chr9	1810026J23Rik	21592722	21593070	3170	-0.23776	6.561863	0.163016	0.255074	0.034192	0	1419	1712	1879	1665	1822	1769	1864	2369	2227	1814
ENSMUSG00000005354	chr15	Txn2	77915047	77915857	4208	0.242572	7.895361	0.163058	0.255107	0.035974	0	2826	3787	4157	3783	3556	5693	5670	5606	6986	5915
ENSMUSG00000032376	chr9	Usp3	66514637	66518578	6848	0.327914	3.905011	0.163089	0.255107	0.062217	0	154	234	249	202	266	277	339	664	335	302
ENSMUSG00000052738	chr6	Suclg1	73248382	73248753	4617	-0.25757	8.259266	0.163093	0.255107	0.04064	0	4614	5983	6097	5830	5006	6146	5928	7240	7113	5777
ENSMUSG00000026620	chr1	Mark1	1.85E+08	1.85E+08	4356	-0.38058	1.907744	0.163187	0.255226	0.074309	0	46	54	55	101	94	42	64	91	109	74
ENSMUSG00000001774	chr9	Chordc1	18292267	18292460	2205	-0.24147	5.51038	0.163263	0.255315	0.034538	0	590	736	1130	738	975	921	1042	858	1064	935
ENSMUSG00000028878	chr4	Fam76a	1.33E+08	1.33E+08	3088	-0.25599	4.692771	0.163508	0.25567	0.038407	0	450	436	525	449	466	368	512	777	597	500
ENSMUSG00000061759	chr10	1700052N19Rik	4432467	4432711	8243	-0.24164	4.135945	0.16358	0.255753	0.032859	0	305	289	394	270	319	331	411	301	441	383
ENSMUSG00000021149	chr13	Gtpbp4	8972071	8973274	2977	0.248846	5.351154	0.163605	0.255763	0.036773	0	489	627	746	563	684	764	940	1389	1206	877
ENSMUSG00000026482	chr1	Rgl1	1.53E+08	1.53E+08	6907	0.32637	4.621305	0.163777	0.255975	0.063299	0	319	226	368	368	572	333	481	507	973	992
ENSMUSG00000042606	chr7	Hirip3	1.27E+08	1.27E+08	3023	0.284951	2.940358	0.163772	0.255975	0.043093	0	100	75	119	114	171	138	200	163	286	200
ENSMUSG00000076431	chr13	Sox4	28948919	28953713	4795	-0.3101	3.855938	0.163835	0.256036	0.05555	0	179	221	263	311	377	154	356	428	373	217
ENSMUSG00000079049	chr13	Serpinb1c	32881833	32882225	1353	-0.50949	0.378847	0.163979	0.256232	0.112022	0	20	23	43	12	22	17	27	11	37	27
ENSMUSG00000054808	chr7	Actn4	28893248	28894387	5026	0.260336	6.208151	0.164076	0.256354	0.041112	0	864	841	1133	1415	1417	1204	1968	1451	2828	2171
ENSMUSG00000056962	chr11	Jmjd6	1.17E+08	1.17E+08	4698	0.251796	4.810311	0.164164	0.256464	0.037255	0	317	459	506	398	446	710	728	675	726	651
ENSMUSG00000049969	chr4	Plekhf2	10988662	10991354	3039	0.228033	3.785104	0.164199	0.256489	0.028326	0	168	173	260	197	266	280	339	296	422	392
ENSMUSG00000032834	chr10	Pwp2	78170910	78172134	3871	0.23425	4.012937	0.164255	0.256547	0.030548	0	219	188	262	250	322	309	370	497	508	350
ENSMUSG00000021629	chr13	Slc30a5	1.01E+08	1.01E+08	3178	0.217849	4.287473	0.164364	0.256689	0.02654	0	260	245	320	283	405	345	528	517	593	475
ENSMUSG00000001741	chr7	Il16	83642848	83644076	7842	0.278297	2.82491	0.164451	0.256795	0.039968	0	94	69	110	128	130	131	178	166	235	192
ENSMUSG00000035517	chr4	Tdrd7	45965334	45965476	3958	0.245057	4.078432	0.164561	0.25691	0.033936	0	213	247	244	247	334	401	384	345	481	499
ENSMUSG00000097383	chr10	1500026H17Rik	89686371	89686519	3027	-0.54524	0.756817	0.164543	0.25691	0.142917	0	28	41	50	24	14	34	30	40	30	16
ENSMUSG00000021453	chr13	Gadd45g	51846678	51846832	1173	0.536067	5.265339	0.164741	0.257161	0.174784	0	447	214	778	894	300	846	572	2183	620	947
ENSMUSG00000005951	chr11	Shpk	73199460	73199680	2985	0.490686	0.830757	0.164768	0.257169	0.105488	0	19	21	15	32	28	21	33	49	51	77
ENSMUSG00000026014	chr1	Raph1	60482292	60490321	20498	-0.23979	4.720145	0.16482	0.257169	0.033689	0	391	413	444	580	548	386	540	706	678	525
ENSMUSG00000039634	chr4	Zfp189	49521176	49521251	3006	-0.33055	1.626619	0.164792	0.257169	0.050439	0	50	48	60	56	66	38	71	74	77	54
ENSMUSG00000059277	chr7	R74862	1.43E+08	1.43E+08	3889	0.493165	0.474306	0.16482	0.257169	0.098168	0	23	14	26	10	15	29	50	30	44	22
ENSMUSG00000029036	chr4	Atad3a	1.56E+08	1.56E+08	3765	0.244277	4.858934	0.16495	0.257254	0.034955	0	332	439	492	481	464	471	642	899	848	835
ENSMUSG00000038216	chr11	Pnmt	98386450	98386866	1154	0.740908	0.318261	0.164979	0.257254	0.263151	0	20	12	12	19	5	12	18	88	31	18
ENSMUSG00000039376	chr14	Synpo2l	20658946	20662465	4629	-0.27709	8.006346	0.164949	0.257254	0.047394	0	3592	3808	5180	5228	5976	5433	6713	3275	6309	5138
ENSMUSG00000057835	chr17	Zfp119a	55864892	55866650	2018	-0.41173	1.249303	0.164963	0.257254	0.079818	0	37	45	44	43	49	32	45	75	35	41
ENSMUSG00000067847	chr2	Romo1	1.56E+08	1.56E+08	747	0.248398	5.850477	0.164921	0.257254	0.037321	0	700	929	1024	842	878	1453	1309	1326	1598	1519
ENSMUSG00000087579	chr19	1500017E21Rik	36614052	36614481	3977	-0.37074	3.684009	0.164986	0.257254	0.080254	0	198	126	324	261	324	210	428	127	334	210
ENSMUSG00000006445	chr4	Epha2	1.41E+08	1.41E+08	4674	0.335524	2.20921	0.165006	0.257256	0.057509	0	55	46	93	70	73	80	112	90	201	120
ENSMUSG00000062590	chr1	Armc9	86154780	86154843	13006	0.361126	1.541	0.165068	0.257324	0.059038	0	33	36	49	37	51	39	100	71	86	77
ENSMUSG00000021379	chr13	Id4	48261427	48261938	1660	0.425766	0.508575	0.165088	0.257327	0.068334	0	14	14	19	25	22	32	37	27	54	27
ENSMUSG00000053119	chr6	Chmp3	71543797	71544033	3250	0.214884	5.868799	0.165132	0.257366	0.027732	0	747	816	1066	881	1012	1102	1462	1407	1758	1628
ENSMUSG00000046949	chr13	Nqo2	33964659	33964800	3974	-0.26841	4.860194	0.165392	0.257743	0.04289	0	431	558	616	536	479	601	608	412	829	611
ENSMUSG00000034220	chr1	Gpc1	92831645	92832097	5159	-0.21821	8.248875	0.165485	0.257828	0.029474	0	4444	4827	6146	5379	6684	5524	6356	6984	7975	5972
ENSMUSG00000055254	chr13	Ntrk2	58806596	58806852	13806	-0.38886	3.776168	0.165477	0.257828	0.08952	0	278	116	283	208	437	149	166	314	332	441
ENSMUSG00000034371	chr19	Dak	10592200	10592789	2253	0.334751	2.165541	0.165533	0.257875	0.0547	0	58	55	65	65	81	71	121	82	187	124
ENSMUSG00000030271	chr6	Ogg1	1.13E+08	1.13E+08	2034	0.345174	2.459487	0.165604	0.257955	0.064421	0	62	63	99	78	99	91	114	229	154	119
ENSMUSG00000000530	chr15	Acvrl1	1.01E+08	1.01E+08	4265	0.230723	4.109806	0.16572	0.258061	0.029671	0	254	220	263	270	310	336	476	342	580	449
ENSMUSG00000032118	chr9	Fez1	36821939	36822375	4029	0.291894	2.417096	0.165727	0.258061	0.041527	0	79	58	84	84	88	95	153	131	173	127
ENSMUSG00000094936	chr19	Rbm4	4784293	4785567	4940	0.237292	3.494076	0.165717	0.258061	0.029979	0	162	152	196	150	195	232	293	297	298	284
ENSMUSG00000043190	chr13	Rfesd	76001535	76003088	2906	-0.26099	3.411142	0.165877	0.258264	0.037074	0	180	175	237	188	175	197	201	235	225	253
ENSMUSG00000045576	chr3	St7l	1.05E+08	1.05E+08	7583	-0.29456	3.628047	0.165945	0.258341	0.049463	0	187	209	288	183	270	176	267	387	281	180
ENSMUSG00000036555	chr5	Iqce	1.41E+08	1.41E+08	12037	0.361564	2.195751	0.165995	0.258391	0.066253	0	70	41	65	62	91	72	130	77	178	144
ENSMUSG00000096433	chr17	Gm4944	22197265	22201809	4880	-0.33134	2.036681	0.166101	0.258526	0.053994	0	71	59	85	87	71	59	69	77	102	112
ENSMUSG00000052512	chr7	Nav2	48908716	48908745	32073	-0.26418	4.315094	0.166158	0.258568	0.040477	0	223	277	380	427	540	328	528	333	495	427
ENSMUSG00000084067	chr2	Gm14269	1.7E+08	1.7E+08	306	-0.48577	0.039149	0.166165	0.258568	0.083682	0	19	21	13	15	23	13	24	21	13	20
ENSMUSG00000034566	chr11	Atp5h	1.15E+08	1.15E+08	1465	0.267386	8.271379	0.166299	0.258747	0.044462	0	3487	5298	5202	5179	3958	7688	7335	7755	8761	7377
ENSMUSG00000031563	chr8	Wwc2	47826083	47828784	6546	-0.25849	4.075962	0.166362	0.258816	0.038585	0	280	206	306	348	401	219	374	454	465	299
ENSMUSG00000021514	chr13	Zfp369	65278814	65278987	5896	-0.37403	1.714805	0.166448	0.258892	0.069353	0	75	45	77	43	60	46	50	71	81	80
ENSMUSG00000053334	chr5	Ficd	1.14E+08	1.14E+08	3154	-0.25123	3.175003	0.166438	0.258892	0.033539	0	162	137	175	149	188	142	193	215	236	173
ENSMUSG00000004018	chr11	Fancl	26386135	26387310	3372	0.365808	1.861872	0.166666	0.259201	0.068451	0	36	33	70	51	73	67	94	58	130	121
ENSMUSG00000026113	chr1	Inpp4a	37299865	37300118	10387	-0.21832	4.375447	0.166748	0.259301	0.027231	0	339	310	368	390	452	336	444	504	502	449

ENSMUSG00000027944	chr3	Hax1	89995457	89995710	1117	0.225658	4.770365	0.166773	0.25931	0.029828	0	368	376	541	393	414	585	733	678	761	650
ENSMUSG00000070426	chr7	Rnf121	1.02E+08	1.02E+08	4427	-0.25057	4.819753	0.166821	0.259355	0.037262	0	446	478	652	450	528	564	672	423	689	635
ENSMUSG00000046836	chr1	Brox	1.83E+08	1.83E+08	5010	-0.22056	4.864002	0.166862	0.259362	0.028615	0	434	472	634	481	600	451	611	742	707	632
ENSMUSG00000066415	chr9	Msl2	1.01E+08	1.01E+08	5627	-0.21814	4.521576	0.166861	0.259362	0.027495	0	348	342	447	438	490	344	474	588	597	486
ENSMUSG00000029152	chr5	Ociad1	73292794	73292976	4132	0.234206	6.894507	0.16712	0.259733	0.033956	0	1634	1607	2162	1671	2065	2485	2969	3630	3001	2801
ENSMUSG00000042015	chr13	Wdr41	94976344	94976589	5029	-0.22172	4.717767	0.167333	0.260035	0.02868	0	421	399	540	481	520	513	538	482	650	630
ENSMUSG00000069763	chr11	Tmem100	90030348	90030743	1767	-0.38287	2.903346	0.167418	0.260138	0.084252	0	119	118	134	121	216	97	115	283	133	119
ENSMUSG00000001300	chr8	Efnb2	8617434	8620976	4324	-0.29203	3.425481	0.167463	0.260149	0.048509	0	140	148	208	280	211	134	195	294	288	225
ENSMUSG00000032727	chr13	Mier3	1.12E+08	1.12E+08	5846	-0.26969	2.895059	0.167461	0.260149	0.038404	0	123	101	135	135	183	95	165	164	198	168
ENSMUSG00000052676	chrX	Zmat1	1.35E+08	1.35E+08	5391	-0.41252	0.781873	0.167532	0.260228	0.072924	0	35	25	38	29	28	20	34	27	35	49
ENSMUSG00000036186	chr2	Fam69b	26628457	26628699	2476	0.378887	1.231865	0.167646	0.260375	0.062268	0	23	32	34	42	31	36	56	59	72	76
ENSMUSG00000032470	chr9	Mras	99385420	99388504	5134	-0.28767	3.49869	0.167673	0.260388	0.046657	0	131	209	228	183	292	220	264	162	327	209
ENSMUSG00000088559	chr1	Mir1981	1.85E+08	1.85E+08	82	0.565172	0.641151	0.167743	0.260467	0.146728	0	19	31	23	7	15	33	29	31	37	71
ENSMUSG00000004415	chr5	Col26a1	1.37E+08	1.37E+08	5844	0.393293	3.024053	0.167762	0.260468	0.090283	0	79	71	112	104	235	141	352	193	252	135
ENSMUSG00000022391	chr15	Rangap1	81704248	81705258	3211	0.243789	5.386048	0.167914	0.260674	0.036172	0	476	526	776	576	891	847	1071	744	1479	1196
ENSMUSG00000028369	chr4	Svep1	58042442	58043168	16117	-0.27765	5.175485	0.168084	0.260881	0.046805	0	598	339	890	545	1027	597	865	691	934	736
ENSMUSG00000034278	chr2	Dnajc17	1.19E+08	1.19E+08	1308	0.314748	2.383811	0.168085	0.260881	0.051996	0	66	56	90	95	74	131	132	123	125	140
ENSMUSG00000039191	chr5	Rbpj	53555779	53555903	5817	0.24907	5.129848	0.168123	0.260911	0.037606	0	454	356	582	465	870	583	866	858	1228	970
ENSMUSG00000021631	chr17	Mrps36-ps1	53866715	53867020	306	0.469373	1.024921	0.168202	0.261004	0.104989	0	29	36	22	25	19	63	60	38	50	44
ENSMUSG00000035266	chr5	Helq	1.01E+08	1.01E+08	5056	0.339267	1.787595	0.168507	0.261448	0.055529	0	46	38	64	49	50	62	76	74	109	119
ENSMUSG00000018541	chr11	Cwc25	97745481	97747469	5053	0.25411	3.177252	0.1686	0.261534	0.033856	0	136	103	156	127	161	158	222	252	267	244
ENSMUSG00000052305	chr7	Hbb-bs	1.04E+08	1.04E+08	863	-0.36916	6.372204	0.168588	0.261534	0.085074	0	547	1666	1599	1793	2360	1010	1416	1364	2290	2540
ENSMUSG00000033751	chr8	Gadd45gip1	84831522	84832640	2494	0.241937	5.194147	0.168627	0.261546	0.035356	0	456	552	634	626	505	859	879	765	1157	943
ENSMUSG00000032202	chr9	Rab27a	73044854	73045011	3879	0.391295	1.371197	0.168668	0.261582	0.070913	0	27	38	51	35	27	50	46	73	91	71
ENSMUSG00000039116	chr10	Gpr126	14402585	14405438	6505	-0.42682	1.110241	0.168744	0.26167	0.088308	0	34	20	38	44	67	27	37	27	67	53
ENSMUSG00000024007	chr17	Ppil1	29250803	29251725	2163	0.329667	3.629427	0.168789	0.26171	0.063782	0	149	175	228	149	210	287	337	137	456	389
ENSMUSG00000019831	chr10	Wasf1	40883475	40883609	2854	-0.5122	0.458953	0.168841	0.261761	0.123405	0	29	11	18	20	51	10	33	24	36	24
ENSMUSG00000002006	chrX	Pdzd4	73793359	73795920	3970	0.39722	1.363868	0.168921	0.261856	0.078314	0	33	14	44	40	50	60	71	46	85	65
ENSMUSG00000040697	chr4	Dnajc16	1.42E+08	1.42E+08	6510	-0.2233	4.51123	0.168999	0.261926	0.029028	0	305	334	508	429	492	365	462	584	577	469
ENSMUSG00000073643	chr1	Wdfy1	79702262	79705570	6488	-0.21794	4.689451	0.169004	0.261926	0.027884	0	377	353	510	518	574	403	524	633	647	583
ENSMUSG00000040365	chr11	Trim41	48806404	48807846	3511	0.226892	4.730773	0.169052	0.261971	0.030373	0	340	381	497	421	391	517	596	769	769	683
ENSMUSG00000073295	chrX	Nudt11	6047453	6048404	3036	-0.52394	0.472492	0.169139	0.262077	0.125324	0	18	27	21	35	27	14	20	47	14	29
ENSMUSG00000021715	chr13	Cwc27	1.05E+08	1.05E+08	2873	0.26415	3.483004	0.169456	0.262538	0.039105	0	138	168	190	163	179	256	211	333	291	305
ENSMUSG00000018427	chr11	Ypel2	86936425	86940688	4847	-0.31562	3.556965	0.169528	0.26257	0.058145	0	142	173	194	321	261	153	222	322	218	302
ENSMUSG00000028619	chr4	Tceanc2	1.07E+08	1.07E+08	7193	-0.25133	4.014765	0.169505	0.26257	0.036453	0	273	265	340	252	328	281	321	457	322	317
ENSMUSG00000037722	chr14	Gnpnat1	45376334	45378486	2629	-0.29445	2.743703	0.169552	0.26257	0.0473	0	97	116	135	89	178	90	172	134	160	144
ENSMUSG00000043639	chr19	Rbm20	53677306	53677592	6790	-0.33291	5.791549	0.169537	0.26257	0.069003	0	690	895	1229	1198	1192	914	914	2003	922	873
ENSMUSG00000022802	chr16	Lmln	33062521	33062734	6511	-0.34095	1.832586	0.169618	0.262642	0.05867	0	57	54	78	76	59	42	82	92	77	68
ENSMUSG00000042406	chr15	Atf4	80255184	80255685	1724	0.26439	7.303896	0.169738	0.262799	0.044014	0	2082	2338	2652	2200	2679	3362	3438	5618	3573	3867
ENSMUSG00000024787	chr19	Snx15	6119399	6119954	2184	0.239233	3.438989	0.169942	0.263085	0.03108	0	154	138	182	155	195	235	276	215	340	293
ENSMUSG00000001986	chrX	Gria3	41400854	41401257	9859	-0.37719	1.384353	0.169992	0.263134	0.06639	0	34	35	70	48	55	39	71	40	49	57
ENSMUSG00000035829	chr2	Ppp1r26	28446800	28446896	5619	-0.3927	1.348732	0.170165	0.263371	0.076243	0	55	36	53	35	54	29	57	72	51	41
ENSMUSG00000003153	chr6	Slc2a3	1.23E+08	1.23E+08	7245	0.514867	1.926624	0.170236	0.263451	0.150892	0	78	21	45	54	52	38	80	192	101	103
ENSMUSG00000029603	chr5	Dtx1	1.21E+08	1.21E+08	4663	-0.69166	0.195125	0.170325	0.26356	0.236361	0	3	10	28	30	44	13	8	34	30	10
ENSMUSG00000026873	chr2	Phf19	34893757	34896061	5036	0.374507	1.349658	0.170352	0.263569	0.065334	0	23	43	36	33	42	59	70	48	87	58
ENSMUSG00000035297	chr5	Cops4	1.01E+08	1.01E+08	5006	-0.2301	6.161848	0.170369	0.263569	0.03292	0	1043	1209	1380	1370	1445	1365	1457	1752	1621	1419
ENSMUSG00000030946	chr7	Lhpp	1.33E+08	1.33E+08	2085	-0.22532	4.205878	0.170573	0.263826	0.029134	0	290	254	368	343	411	362	356	335	485	434
ENSMUSG00000034252	chr9	Senp6	80066903	80067572	7016	-0.23218	5.262081	0.170572	0.263826	0.032943	0	611	614	769	689	771	602	873	1058	848	726
ENSMUSG00000020392	chr11	Cdkn2aipnl	51967661	51967957	1958	-0.28964	4.384789	0.170757	0.264077	0.050889	0	336	372	463	382	345	300	327	691	463	408
ENSMUSG00000032540	chr9	Abhd5	1.22E+08	1.22E+08	3618	-0.25828	5.040364	0.170773	0.264077	0.041124	0	508	570	596	618	687	419	568	593	1041	959
ENSMUSG00000026723	chr2	Trdmt1	13509014	13511690	3835	-0.32595	1.938425	0.171058	0.264488	0.052982	0	63	67	76	67	74	61	84	60	122	67
ENSMUSG00000029761	chr6	Cald1	34598500	34598665	7687	-0.24138	5.618966	0.171157	0.264582	0.036158	0	809	583	904	971	1230	681	1276	893	1386	1101
ENSMUSG00000053286	chr1	Trmt1l	1.51E+08	1.51E+08	8211	-0.22699	4.216755	0.171139	0.264582	0.029922	0	283	294	389	365	334	352	427	319	487	404
ENSMUSG00000014773	chr17	Dll1	15367354	15368035	4219	0.292389	2.88546	0.171346	0.264786	0.047243	0	84	83	87	135	164	125	193	183	242	205
ENSMUSG00000052296	chr7	Ppp6r1	4631501	4632244	3787	-0.21448	6.278185	0.171341	0.264786	0.02879	0	1215	1168	1549	1466	1573	1159	1729	1835	2115	1630
ENSMUSG00000054237	chr19	Fra10ac1	38188481	38188800	1402	0.2533	3.49141	0.171331	0.264786	0.036296	0	121	169	205	171	185	278	280	274	287	275
ENSMUSG00000024222	chr17	Fkbp5	28399095	28401151	6363	0.696653	5.400434	0.171425	0.264878	0.302432	0	515	607	848	360	305	365	464	3970	725	558
ENSMUSG00000056536	chr1	Pign	1.06E+08	1.06E+08	13595	-0.27554	2.969207	0.171484	0.264939	0.041565	0	139	97	178	122	180	103	157	175	204	190
ENSMUSG00000059939	chr4	9430015G10Rik	1.56E+08	1.56E+08	3695	0.409005	1.725954	0.171736	0.265299	0.089313	0	65	20	42	37	66	70	79	101	84	89
ENSMUSG00000084013	chr2	Gm14270	1.7E+08	1.7E+08	846	0.365239	1.423467	0.171835	0.265423	0.060598	0	35	41	37	41	31	55	75	52	89	69
ENSMUSG00000031641	chr8	Cbr4	61487734	61487990	3047	-0.27394	4.363232	0.171892	0.26548	0.045444	0	325	433	391	389	300	399	359	516	474	397
ENSMUSG00000029017	chr5	Pmpcb	21737141	21737276	5141	-0.2388	6.400864	0.171929	0.265508	0.035942	0	1190	1660	1665	1600	1448	1630	1773	1711	2115	1767
ENSMUSG00000028851	chr4	Nudc	1.34E+08	1.34E+08	1425	0.211323	5.492376	0.172007	0.265598	0.027406	0	568	624	729	737	828	891	1013	1052	1464	1244
ENSMUSG00000020530	chr11	Ggnbp2	84832361	84833213	4726	0.307599	5.48184	0.17217	0.265821	0.059291	0	639	622	756	574	721	708	992	2008	1105	952
ENSMUSG00000036103	chr18	Colec12	9707648	9707759	3322	-0.28468	4.65967	0.172221	0.265841	0.049646	0	480	252	520	367	741	372	662	573	594	464
ENSMUSG00000038417	chr10	Fig4	41188172	41188699	3263	-0.24572	3.433721	0.172222	0.265841	0.03399	0	191	143	221	177	246	143	251	247	308	215

ENSMUSG00000038563	chr7	Eftud1	82648614	82648649	4398	0.255004	3.307659	0.172303	0.265938	0.03523	0	128	157	150	143	163	176	226	291	330	234
ENSMUSG00000036636	chr17	Clcn7	25133391	25133614	5292	0.225717	4.74331	0.172523	0.266247	0.030409	0	380	381	448	376	464	449	585	649	966	771
ENSMUSG00000021974	chr14	Fgf9	58070547	58070647	4266	-0.54763	0.097094	0.172641	0.266399	0.124446	0	26	12	15	24	20	16	24	30	12	10
ENSMUSG00000027425	chr2	Csrp2bp	1.44E+08	1.44E+08	4699	-0.22488	4.429376	0.172939	0.266778	0.030185	0	357	342	355	446	420	357	450	523	559	429
ENSMUSG00000037266	chr4	Rsrp1	1.35E+08	1.35E+08	3349	0.287694	6.927621	0.172944	0.266778	0.052801	0	1957	1651	2233	1254	2007	2290	3178	2849	2678	4552
ENSMUSG00000047388	chr8	Atmin	1.17E+08	1.17E+08	4877	-0.23188	4.68162	0.172909	0.266778	0.032548	0	381	389	523	480	548	356	498	721	605	585
ENSMUSG00000033228	chr15	Scaf11	96411698	96414916	7724	-0.2844	5.45865	0.173002	0.266838	0.050831	0	657	602	876	913	1022	565	724	1497	1058	817
ENSMUSG00000047446	chr12	Arl4a	40005447	40005711	7701	0.287129	4.581042	0.173162	0.267054	0.050672	0	318	295	439	336	414	345	457	790	589	901
ENSMUSG00000020706	chr11	Ftsj3	1.06E+08	1.06E+08	4358	0.231248	5.193927	0.173188	0.267065	0.033104	0	429	501	689	477	743	743	817	1120	1042	872
ENSMUSG00000021597	chr13	Ankrd32	77043088	77044030	5881	-0.33778	2.716923	0.173324	0.267246	0.066141	0	100	131	122	137	108	70	169	176	172	95
ENSMUSG00000042380	chr4	Smim12	1.27E+08	1.27E+08	1022	0.233519	4.535034	0.173375	0.267294	0.032684	0	296	370	408	346	338	517	553	598	598	619
ENSMUSG00000051346	chr10	Spryd4	1.28E+08	1.28E+08	1570	-0.23454	5.212377	0.173532	0.267506	0.034064	0	525	682	741	687	692	737	817	661	1054	696
ENSMUSG00000026342	chr1	Slc35f5	1.26E+08	1.26E+08	2956	0.258516	4.62075	0.173751	0.267783	0.040839	0	339	329	430	333	435	411	702	882	629	497
ENSMUSG00000053168	chr15	9030619P08Rik	75427606	75428178	935	0.64136	0.308991	0.173737	0.267783	0.212071	0	6	11	21	17	20	23	12	15	29	81
ENSMUSG00000039801	chr15	2410089E03Rik	8169106	8169489	13017	-0.29924	2.648364	0.173823	0.267866	0.049379	0	96	82	116	118	166	69	159	140	168	124
ENSMUSG00000027822	chr3	Slc33a1	63933507	63933904	3548	-0.25014	3.46952	0.173892	0.267941	0.035746	0	184	188	227	164	234	170	280	178	285	269
ENSMUSG00000044424	chr19	Gm9493	23619742	23620320	579	0.398266	1.398852	0.173913	0.267944	0.078152	0	30	37	53	21	42	64	81	60	55	70
ENSMUSG00000026637	chr1	Traf5	1.92E+08	1.92E+08	4566	0.386	1.934579	0.173992	0.268037	0.079958	0	36	66	36	53	77	91	102	64	114	118
ENSMUSG00000052428	chr1	Tmco1	1.67E+08	1.67E+08	4764	-0.21777	5.136079	0.174135	0.268226	0.02932	0	613	560	749	550	669	564	825	652	993	791
ENSMUSG00000039529	chr18	Atp8b1	64528979	64531564	6440	0.308867	2.298014	0.174354	0.268534	0.047824	0	62	64	78	80	74	68	130	121	161	153
ENSMUSG00000020695	chr11	Mrc2	1.05E+08	1.05E+08	6674	0.368129	5.528022	0.174422	0.268609	0.086515	0	662	313	685	505	1307	858	1729	672	1634	1256
ENSMUSG00000029458	chr5	Brap	1.22E+08	1.22E+08	6284	-0.24452	5.147229	0.174813	0.269181	0.037359	0	551	552	731	644	734	486	691	1089	828	707
ENSMUSG00000024309	chr17	Pfdn6	33938821	33939111	1193	0.222836	4.660643	0.175044	0.26949	0.030099	0	314	391	424	372	437	592	603	545	753	656
ENSMUSG00000029484	chr5	Anxa3	96793385	96793563	1597	0.301735	4.216301	0.175053	0.26949	0.055994	0	234	215	244	314	387	358	498	241	761	575
ENSMUSG00000068523	chr3	Gng5	1.46E+08	1.47E+08	2738	-0.24028	6.606153	0.175091	0.269519	0.037041	0	1565	1781	2024	1839	1488	1864	2160	1953	2386	2000
ENSMUSG00000030145	chr6	Zfp248	1.18E+08	1.18E+08	5039	-0.37337	0.969749	0.17514	0.269564	0.05843	0	28	30	38	42	39	33	44	41	44	28
ENSMUSG00000015224	chr4	Cyp2j9	96568429	96568902	3337	0.513241	0.690658	0.175309	0.269795	0.123323	0	20	14	24	26	19	17	31	81	39	40
ENSMUSG00000067925	chrX	Cxx1a	53642488	53643682	1195	0.238117	4.188849	0.175368	0.269856	0.033716	0	247	268	259	306	299	448	442	380	569	437
ENSMUSG00000033411	chr2	Ctdspl2	1.22E+08	1.22E+08	9251	-0.33576	2.371202	0.175693	0.270325	0.061456	0	94	58	94	78	159	75	123	125	111	92
ENSMUSG00000058331	chr13	Zfp85	67747800	67749722	2312	-0.41497	0.872848	0.175804	0.270466	0.083169	0	26	32	56	28	25	23	37	47	35	33
ENSMUSG00000067924	chrX	Cxx1b	53669177	53670408	1232	0.240911	4.68051	0.175887	0.270564	0.035932	0	352	314	433	381	486	694	603	502	726	653
ENSMUSG00000070705	chr7	Eid2b	28277706	28280129	2424	-0.31873	2.219766	0.175912	0.270565	0.054161	0	81	80	103	75	83	55	90	127	121	89
ENSMUSG00000078853	chr11	Igtp	58199556	58199779	2022	0.410969	4.256843	0.175927	0.270565	0.106956	0	210	267	363	188	349	686	557	159	579	474
ENSMUSG00000035235	chr14	Trim13	61598226	61598346	1699	0.256374	3.126348	0.176055	0.270705	0.036947	0	95	112	184	130	142	166	252	205	258	220
ENSMUSG00000063694	chr6	Cycs	50562563	50565385	3404	-0.25897	8.248771	0.176076	0.270705	0.043672	0	4574	6106	7057	5194	4403	5995	6648	5817	7628	6036
ENSMUSG00000074652	chr2	Myh7b	1.56E+08	1.56E+08	6634	0.543585	1.111785	0.176067	0.270705	0.156469	0	42	14	36	30	14	27	74	75	87	28
ENSMUSG00000044573	chr12	Acp1	30893326	30895953	3221	0.219721	4.925267	0.17611	0.270727	0.029669	0	364	461	542	446	527	538	755	900	866	763
ENSMUSG00000049577	chr8	Zfpm1	1.22E+08	1.22E+08	3503	-0.31153	2.193155	0.176276	0.270951	0.052505	0	62	72	82	115	84	61	101	98	125	89
ENSMUSG00000085396	chrX	Firre	50555744	50555929	1439	-0.43372	0.775821	0.176307	0.270969	0.087173	0	42	27	30	25	30	22	33	39	24	43
ENSMUSG00000037997	chr6	Parp11	1.27E+08	1.27E+08	5720	0.376795	2.629404	0.176328	0.27097	0.082783	0	78	68	102	93	103	163	178	60	199	197
ENSMUSG00000014554	chr6	Dguok	83480217	83480436	2191	0.247084	3.647141	0.176352	0.270979	0.035181	0	154	193	231	194	171	274	311	264	358	362
ENSMUSG00000028101	chr3	Pias3	96696384	96696531	3918	0.262024	3.280322	0.176451	0.2711	0.039102	0	148	94	142	136	218	187	260	239	275	265
ENSMUSG00000000532	chr15	Acvr1b	1.01E+08	1.01E+08	4413	-0.37634	6.051236	0.176476	0.271108	0.091536	0	1376	729	1585	1153	1453	816	937	2687	1237	1047
ENSMUSG00000051255	chr19	Gm6563	23675844	23676712	869	0.309762	2.920797	0.176501	0.271117	0.054352	0	94	130	140	86	101	191	218	163	210	171
ENSMUSG00000026872	chr2	Zeb2	44983634	44989153	19658	-0.28449	4.615073	0.176737	0.271449	0.050871	0	403	254	458	499	670	246	512	574	652	649
ENSMUSG00000002812	chr11	Flii	60714123	60714447	5039	0.213965	6.363205	0.176786	0.271483	0.029394	0	950	1110	1448	1413	1481	1537	2110	2200	2440	2071
ENSMUSG00000022827	chr16	Rabl3	37539885	37539960	6369	0.269365	2.684795	0.176798	0.271483	0.038135	0	68	85	119	99	112	110	162	158	212	175
ENSMUSG00000017664	chr2	Slc35c2	1.65E+08	1.65E+08	3914	0.235183	4.482845	0.176844	0.271523	0.033774	0	306	295	404	303	406	484	535	397	727	676
ENSMUSG00000038007	chr4	Acer2	86874396	86874596	7159	0.456754	2.155464	0.176911	0.271596	0.12027	0	49	63	78	64	49	51	67	183	99	192
ENSMUSG00000034269	chr6	Setd5	1.13E+08	1.13E+08	12481	-0.25853	5.354152	0.177046	0.271773	0.042507	0	659	471	765	760	1129	516	923	1134	966	846
ENSMUSG00000057103	chr6	Cml1	85910154	85911020	1345	-0.41489	0.576207	0.177144	0.271894	0.07007	0	13	20	35	30	39	21	25	26	33	36
ENSMUSG00000006342	chr10	Susd2	75636619	75637370	3255	0.389481	2.18699	0.17721	0.271965	0.089693	0	37	34	96	72	93	91	153	62	172	118
ENSMUSG00000054021	chr13	Sirt5	43370710	43370868	1367	0.305825	3.114291	0.177234	0.271971	0.054396	0	106	124	139	166	96	209	210	160	283	239
ENSMUSG00000001767	chr2	Crnkl1	1.46E+08	1.46E+08	3844	0.236485	4.346223	0.177308	0.272055	0.034069	0	265	263	377	295	360	380	550	670	524	426
ENSMUSG00000019039	chr9	Dalrd3	1.09E+08	1.09E+08	2458	0.238402	3.317948	0.177573	0.272401	0.031417	0	134	133	164	160	164	203	254	214	284	292
ENSMUSG00000062110	chr5	Scfd2	74204816	74206395	8127	0.249691	3.420321	0.177562	0.272401	0.035031	0	150	147	165	169	174	165	306	318	324	247
ENSMUSG00000039781	chr11	Cep131	1.2E+08	1.2E+08	3833	0.36047	2.807556	0.177804	0.272724	0.077787	0	65	92	107	102	145	98	139	315	172	185
ENSMUSG00000024869	chr19	Nudt8	4000580	4000847	4298	0.259612	3.722494	0.177935	0.272895	0.039727	0	162	219	208	222	171	297	301	375	360	319
ENSMUSG00000014301	chr16	Pam16	4616464	4616633	857	0.259543	4.546194	0.178192	0.273219	0.04192	0	320	376	428	315	308	558	545	654	530	620
ENSMUSG00000014444	chr8	Piezo1	1.22E+08	1.22E+08	9933	0.234192	5.487803	0.178169	0.273219	0.035014	0	524	574	884	549	968	731	1198	1001	1578	1251
ENSMUSG00000033813	chr1	Tcea1	4857814	4857976	3017	-0.26334	4.557863	0.178205	0.273219	0.043475	0	363	372	503	374	543	293	441	760	542	476
ENSMUSG00000021012	chr12	Zc3h14	98746968	98747158	4184	-0.20886	5.514702	0.178349	0.27341	0.027643	0	680	726	970	822	899	779	969	1116	1174	913
ENSMUSG00000033933	chr6	Vhl	1.14E+08	1.14E+08	2997	0.240694	3.459974	0.178444	0.273525	0.033222	0	143	136	212	129	225	198	274	255	376	293
ENSMUSG00000037196	chr17	Pacrg	10403012	10403478	1572	0.513553	0.289759	0.178538	0.273638	0.114075	0	6	21	18	17	14	12	30	48	35	30
ENSMUSG00000026000	chr1	Lancl1	67000517	67003557	6863	-0.23123	5.193412	0.178637	0.27373	0.033783	0	564	619	783	656	661	738	689	885	851	714
ENSMUSG00000030225	chr6	Dera	1.38E+08	1.38E+08	1742	0.273079	3.151895	0.178621	0.27373	0.042387	0	92	145	158	120	150	190	192	202	256	280

ENSMUSG00000001138	chr1	Cnnm3	36511867	36513153	6420	0.287531	3.852138	0.178813	0.273968	0.050796	0	183	173	273	200	259	238	303	604	375	323
ENSMUSG00000018921	chr11	Pelp1	70392883	70393022	3561	0.221678	4.528186	0.178919	0.274101	0.030283	0	263	274	402	400	456	414	508	675	703	608
ENSMUSG00000015942	chr5	Gtf2ird2	1.34E+08	1.34E+08	5572	-0.31019	2.817801	0.178966	0.274142	0.055983	0	105	119	162	121	139	96	136	227	147	121
ENSMUSG00000029343	chr5	Crybb1	1.12E+08	1.12E+08	985	-0.41761	1.469081	0.179163	0.274384	0.094088	0	30	60	65	62	38	52	49	35	90	45
ENSMUSG00000062619	chr17	2310039H08Rik	46772635	46773407	773	0.265466	3.892017	0.179152	0.274384	0.042986	0	208	176	251	217	271	291	319	562	358	335
ENSMUSG00000050271	chr8	D8Ertd82e	36094828	36094988	9606	-0.31032	2.590005	0.179241	0.274473	0.05456	0	67	91	123	153	120	73	136	119	178	126
ENSMUSG00000056427	chr11	Slit3	35121224	35121711	6067	-0.35207	3.820701	0.179325	0.274541	0.077671	0	249	130	294	243	435	171	216	487	269	301
ENSMUSG00000092218	chr9	Gm20529	1.08E+08	1.08E+08	203	0.578853	0.306042	0.179314	0.274541	0.167876	0	13	13	18	8	24	24	47	5	44	39
ENSMUSG00000027677	chr3	Ttc14	33800195	33800436	11072	-0.24858	3.657451	0.179363	0.274568	0.036845	0	240	179	275	164	283	181	305	238	334	295
ENSMUSG00000031728	chr8	Zfp821	1.1E+08	1.1E+08	2127	0.276456	2.381981	0.179456	0.274681	0.039802	0	71	64	84	72	96	104	122	124	186	123
ENSMUSG00000023088	chr16	Abcc1	14361558	14361643	12366	-0.24205	5.074772	0.17961	0.274886	0.03736	0	558	463	626	570	857	448	619	949	900	728
ENSMUSG00000013523	chr2	Bcas1	1.7E+08	1.7E+08	3775	0.462928	0.465061	0.179648	0.274913	0.095704	0	25	9	21	13	21	20	52	34	43	25
ENSMUSG00000024998	chr19	Plce1	38481109	38481356	15998	-0.26426	3.560822	0.179956	0.275339	0.041341	0	165	162	266	209	283	192	361	199	275	218
ENSMUSG00000029823	chr6	Luc7l2	38551334	38551908	12084	-0.22042	6.509424	0.179966	0.275339	0.031754	0	1564	1334	1953	1379	1990	1484	1996	2166	2090	2079
ENSMUSG00000028833	chr4	Ncdn	1.27E+08	1.27E+08	3710	0.220705	4.185999	0.179986	0.27534	0.029245	0	261	226	257	272	387	338	477	412	601	469
ENSMUSG00000008398	chr10	Elk3	93247414	93250108	4550	0.24592	4.747815	0.180014	0.275352	0.038078	0	304	324	401	582	441	489	707	575	970	702
ENSMUSG00000022477	chr15	Aco2	81872309	81872548	3892	-0.25789	10.50353	0.180035	0.275353	0.044251	0	21228	26056	27201	32501	23804	24799	24994	40519	35674	28170
ENSMUSG00000041215	chr16	Yeats2	20141063	20141235	6116	-0.26628	3.089712	0.180058	0.275358	0.041078	0	145	100	162	152	220	113	206	175	240	174
ENSMUSG00000025854	chr5	Fam20c	1.39E+08	1.39E+08	4223	0.32539	4.740654	0.180127	0.275433	0.068469	0	254	247	419	403	724	429	652	428	1178	884
ENSMUSG00000036437	chr8	Npy1r	66697422	66697522	3007	-0.41657	1.108868	0.180551	0.276051	0.08568	0	40	24	37	55	42	40	26	55	51	34
ENSMUSG00000025425	chr18	St8sia5	77185853	77186225	2097	-0.29975	4.41	0.180607	0.276107	0.056999	0	311	329	393	488	434	515	384	258	654	386
ENSMUSG00000026019	chr1	Wdr12	60069785	60078241	11955	-0.20996	4.542678	0.180855	0.276424	0.02693	0	326	357	485	427	501	444	448	493	605	518
ENSMUSG00000029500	chr5	Pgam5	1.1E+08	1.1E+08	2373	0.226233	4.901361	0.180845	0.276424	0.032262	0	393	449	537	471	427	688	703	769	875	689
ENSMUSG00000037605	chr5	Lphn3	81020138	81021345	13291	-0.45609	0.134389	0.18088	0.276432	0.07921	0	19	15	21	10	34	15	18	19	26	22
ENSMUSG00000074846	chr2	Gm10774	1.27E+08	1.27E+08	204	0.418126	1.118234	0.181094	0.276729	0.089382	0	20	36	34	25	32	55	57	49	35	73
ENSMUSG00000027624	chr2	Epb4.1l1	1.56E+08	1.56E+08	11528	0.322691	4.02869	0.181204	0.276866	0.06618	0	208	126	214	270	416	228	354	351	641	593
ENSMUSG00000102422	chr3	SCHIP1	67892232	67892321	2369	-0.23165	6.436411	0.181323	0.277018	0.035342	0	1396	1543	1868	1496	1438	1613	1910	1958	2224	1561
ENSMUSG00000044338	chr2	Aplnr	85136225	85139923	3699	-0.35968	5.398115	0.181445	0.277173	0.08519	0	452	915	843	1101	596	659	971	413	1456	909
ENSMUSG00000071632	chr16	2510002D24Rik	18836578	18836619	1486	-0.26253	3.683406	0.181503	0.277231	0.041739	0	200	241	292	211	210	235	236	350	282	240
ENSMUSG00000013150	chr8	Gfod2	1.06E+08	1.06E+08	4608	-0.26559	3.079163	0.18155	0.277242	0.040117	0	118	138	168	138	208	178	158	149	221	175
ENSMUSG00000052105	chr17	Mtcl1	66336982	66338154	9268	0.338582	2.723178	0.181543	0.277242	0.067848	0	74	74	104	84	152	106	272	166	195	116
ENSMUSG00000020454	chr11	Eif4enif1	3202392	3202556	6370	-0.2257	4.995505	0.181725	0.277465	0.032409	0	465	461	650	635	674	500	677	890	733	626
ENSMUSG00000022507	chr16	1810013L24Rik	8830100	8830685	4066	-0.28048	5.507821	0.181736	0.277465	0.051591	0	767	838	903	815	792	654	823	1543	971	796
ENSMUSG00000028703	chr4	Lrrc41	1.16E+08	1.16E+08	3713	0.24667	4.521446	0.181954	0.277766	0.038382	0	301	304	377	293	487	367	543	809	678	526
ENSMUSG00000028114	chr3	Mettl14	1.23E+08	1.23E+08	5119	-0.21805	3.9709	0.182305	0.278272	0.028481	0	247	261	340	261	289	274	377	349	381	300
ENSMUSG00000048007	chrX	Timm8a1	1.35E+08	1.35E+08	1421	0.344545	2.146948	0.182372	0.278344	0.064718	0	39	78	72	66	61	103	132	80	138	110
ENSMUSG00000050953	chr10	Gja1	56377300	56377518	3105	-0.25875	4.727078	0.182402	0.278359	0.042892	0	483	279	572	435	672	377	474	584	650	747
ENSMUSG00000029191	chr5	Rfc1	65261852	65263146	6000	-0.20994	4.514303	0.182605	0.278638	0.027397	0	345	351	431	428	492	369	484	417	636	582
ENSMUSG00000029863	chr6	Casp2	42264985	42265197	6986	0.260337	2.987583	0.182635	0.278652	0.038241	0	125	89	142	113	125	141	194	228	232	206
ENSMUSG00000029089	chr5	Pacrgl	48372392	48372495	1464	0.423094	1.379903	0.182717	0.278717	0.095409	0	40	18	41	41	38	32	69	106	79	52
ENSMUSG00000031503	chr8	Col4a2	11312805	11313114	6619	-0.24255	8.52032	0.18271	0.278717	0.039524	0	4430	5201	7690	8232	8181	5673	8262	6325	12090	7694
ENSMUSG00000036687	chr5	Tmem184a	1.4E+08	1.4E+08	5277	-0.51948	-0.18932	0.182759	0.27872	0.109031	0	18	18	9	10	22	6	16	17	27	12
ENSMUSG00000037664	chr7	Cdkn1c	1.43E+08	1.43E+08	1931	0.353756	6.605022	0.182759	0.27872	0.083651	0	547	1055	1664	1585	2599	2029	3668	1786	3184	2138
ENSMUSG00000014859	chr8	E2f4	1.05E+08	1.05E+08	1992	0.205583	4.730478	0.182973	0.279009	0.026448	0	315	379	437	438	490	537	706	638	807	626
ENSMUSG00000034612	chr10	Chst11	82985498	82985982	5527	0.425205	2.379485	0.183002	0.279009	0.108124	0	66	46	88	67	101	51	108	84	241	229
ENSMUSG00000043929	chrX	Klhl15	94234599	94234653	9741	0.352848	1.438523	0.18301	0.279009	0.060722	0	39	37	37	29	48	40	71	86	79	68
ENSMUSG00000028861	chr4	Mrps15	1.26E+08	1.26E+08	1693	0.227161	5.393343	0.183139	0.279176	0.033502	0	517	626	679	731	659	978	1026	852	1232	1161
ENSMUSG00000101795	chr1	Gm5835	1.43E+08	1.43E+08	1270	-0.33627	1.967292	0.183193	0.279227	0.064387	0	91	60	63	72	64	47	79	85	102	88
ENSMUSG00000059842	chr2	Zfp341	1.55E+08	1.55E+08	3299	-0.36402	1.589468	0.183386	0.279491	0.069805	0	26	52	71	50	82	41	67	69	61	61
ENSMUSG00000025702	chr6	March8	1.16E+08	1.16E+08	6536	-0.22944	5.41294	0.183453	0.279561	0.034402	0	646	667	938	758	837	574	905	1215	1082	842
ENSMUSG00000007030	chr17	Vwa7	35016579	35016767	4313	-0.29356	3.810079	0.183611	0.279741	0.053788	0	183	228	315	275	292	235	227	460	240	281
ENSMUSG00000046727	chr18	Cystm1	36345619	36345840	2840	-0.24553	7.01304	0.183596	0.279741	0.040344	0	1966	2342	2770	2244	2315	2776	2380	3045	2771	2566
ENSMUSG00000032105	chr9	Pdzd3	44247312	44248016	2181	0.529638	-0.01341	0.183739	0.279906	0.123052	0	10	9	10	19	12	29	20	16	45	12
ENSMUSG00000022885	chr16	St6gal1	23224740	23225229	4916	0.274196	3.452695	0.184069	0.280378	0.045974	0	112	112	206	182	226	158	271	233	391	366
ENSMUSG00000061665	chr17	Cd2ap	42792951	42796369	5399	-0.23325	4.309959	0.184115	0.280416	0.034208	0	291	290	355	392	469	265	395	559	501	422
ENSMUSG00000091509	chr14	Gm17066	1.05E+08	1.05E+08	1113	0.33078	1.982243	0.184202	0.280518	0.057108	0	48	60	62	44	70	70	87	84	127	137
ENSMUSG00000038717	chr9	Atp5l	44913250	44913466	511	0.268314	8.195526	0.184417	0.280784	0.048683	0	3843	5001	4884	4522	3560	7151	6754	8836	7245	6767
ENSMUSG00000047547	chr13	Cltb	54592401	54594042	4868	0.268641	6.365687	0.184399	0.280784	0.048328	0	929	1234	1546	1258	1278	1711	1602	3033	1949	2103
ENSMUSG00000010663	chr19	Fads1	10182888	10183264	3456	0.410494	4.454296	0.184523	0.280914	0.11183	0	218	123	228	287	799	455	634	387	855	615
ENSMUSG00000032103	chr9	Pus3	35558595	35558733	2972	-0.2838	3.480729	0.184608	0.281012	0.049422	0	149	210	256	201	199	189	240	329	227	172
ENSMUSG00000041809	chr1	Efhc1	20951626	20951796	2208	0.541956	-0.12128	0.18472	0.281152	0.140614	0	10	1	18	7	21	17	29	25	17	23
ENSMUSG00000021615	chr13	Xrcc4	89774027	89776408	4213	-0.28532	2.551346	0.184987	0.281527	0.044912	0	85	104	148	82	113	94	123	131	140	121
ENSMUSG00000029641	chr5	Rasl11a	1.47E+08	1.47E+08	1126	0.441285	0.456761	0.185081	0.281639	0.086851	0	5	16	24	23	23	30	31	37	45	27
ENSMUSG00000100017	chr14	2410022M11Rik	56811953	56815597	3645	0.505946	0.728334	0.18515	0.281713	0.128202	0	26	15	28	23	13	27	16	48	67	58
ENSMUSG00000024875	chr19	Yif1a	5088538	5088748	1493	0.205477	5.102848	0.185401	0.282064	0.027101	0	477	488	537	543	605	702	861	758	1083	896
ENSMUSG00000026779	chr2	Mastl	23115606	23118592	5777	0.451995	0.017478	0.185518	0.282211	0.086779	0	10	5	18	12	20	19	28	14	34	28

ENSMUSG00000031314	chrX	Taf1	1.02E+08	1.02E+08	8428	-0.21709	4.011938	0.185634	0.282357	0.028914	0	273	205	314	294	366	224	355	371	422	381
ENSMUSG00000001018	chr3	Snapin	90488026	90489593	2290	-0.23464	6.118705	0.185668	0.282378	0.036805	0	1104	1096	1619	1202	1248	1250	1386	1867	1609	1289
ENSMUSG00000041506	chr9	Rrp9	1.06E+08	1.06E+08	2788	0.210433	3.950627	0.185772	0.282505	0.02647	0	227	212	272	217	258	319	368	392	458	386
ENSMUSG00000028675	chr4	Pnrc2	1.36E+08	1.36E+08	2213	-0.20421	5.3051	0.186082	0.28293	0.027136	0	582	600	756	706	910	660	815	952	984	877
ENSMUSG00000038526	chr3	Car14	95897768	95898212	2543	-0.26355	5.170589	0.186092	0.28293	0.045967	0	726	505	641	683	692	639	525	986	772	861
ENSMUSG00000037410	chr9	Tbc1d2b	90202027	90205222	8799	0.245846	4.233616	0.186118	0.282938	0.038542	0	269	167	308	276	437	303	555	450	599	497
ENSMUSG00000070953	chr2	Rabepk	34777556	34779529	3814	0.27659	2.897567	0.1863	0.283184	0.043198	0	99	109	137	106	100	161	158	159	251	214
ENSMUSG00000060098	chr8	Prmt7	1.06E+08	1.06E+08	6125	-0.20779	5.180016	0.186377	0.283269	0.028042	0	486	609	758	633	771	632	706	819	906	857
ENSMUSG00000025466	chr7	Fuom	1.4E+08	1.4E+08	3272	0.262007	3.935358	0.186489	0.283395	0.042948	0	191	258	247	247	194	375	366	285	476	421
ENSMUSG00000091994	chr10	E130317F20Rik	79851381	79854511	3265	-0.44854	1.021344	0.186501	0.283395	0.111104	0	48	26	53	25	35	34	16	48	55	40
ENSMUSG00000026603	chr1	Smyd2	1.9E+08	1.9E+08	2717	0.347932	7.236087	0.186576	0.283479	0.082425	0	1306	2643	2401	2708	1912	4089	2404	5622	3268	3762
ENSMUSG00000034255	chr11	Arhgap27	1.03E+08	1.03E+08	6415	0.334416	2.84135	0.186702	0.283638	0.067409	0	69	103	126	151	68	126	198	149	246	213
ENSMUSG00000027405	chr2	Nop56	1.3E+08	1.3E+08	4099	0.207568	4.838812	0.18696	0.283997	0.027581	0	365	415	521	401	515	545	732	632	978	719
ENSMUSG00000038253	chr6	Hoxa5	52201754	52202831	1877	0.383545	1.016684	0.186979	0.283997	0.066813	0	26	30	28	21	33	39	57	58	41	56
ENSMUSG00000083899	chr11	Gm12346	77293444	77294873	2255	0.362125	1.568525	0.187156	0.284234	0.071904	0	28	36	52	36	60	57	96	42	94	89
ENSMUSG00000021186	chr12	Fbln5	1.02E+08	1.02E+08	5829	-0.2161	4.673258	0.187182	0.284242	0.029842	0	421	359	513	430	574	454	490	660	614	520
ENSMUSG00000049191	chrX	Rgag4	1.02E+08	1.02E+08	4761	0.431897	1.10079	0.187235	0.284292	0.105474	0	30	8	34	22	55	47	58	46	63	58
ENSMUSG00000033460	chrX	Armcx1	1.35E+08	1.35E+08	3227	0.328236	2.462137	0.187341	0.284423	0.06298	0	74	69	73	63	124	101	211	107	161	126
ENSMUSG00000030605	chr7	Mfge8	79133769	79134546	2125	0.253297	6.108658	0.187588	0.284766	0.043447	0	977	600	983	1160	1628	1199	1672	1730	2368	1910
ENSMUSG00000038022	chr6	Fam188b	55203383	55203569	4270	0.329801	1.627157	0.187729	0.284948	0.05398	0	46	36	48	48	41	51	71	88	109	74
ENSMUSG00000046862	chr4	Pramef8	1.43E+08	1.43E+08	4176	-0.2473	3.255016	0.187751	0.284951	0.036392	0	115	173	204	163	209	139	205	216	219	236
ENSMUSG00000029587	chr5	Zfp12	1.43E+08	1.43E+08	5821	-0.2958	3.421754	0.18787	0.285101	0.054853	0	175	161	229	178	242	152	191	371	221	178
ENSMUSG00000004952	chr5	Rasa4	1.36E+08	1.36E+08	6191	0.21567	4.827055	0.187969	0.285219	0.030172	0	362	377	491	480	480	570	656	698	735	878
ENSMUSG00000067430	chr17	Zfp763	33016863	33019969	3557	-0.37858	1.3305	0.188104	0.285393	0.074772	0	32	29	71	48	54	28	58	66	57	40
ENSMUSG00000074415	chr9	2610203C20Rik	41376397	41376676	12655	0.30278	2.642488	0.188136	0.28541	0.052955	0	85	63	120	76	121	79	181	171	196	180
ENSMUSG00000037965	chr16	Zc3h7a	11136592	11137485	9160	0.243131	4.24161	0.188646	0.286153	0.037596	0	292	248	328	224	347	294	513	380	616	620
ENSMUSG00000040723	chr1	Rcsd1	1.66E+08	1.66E+08	10131	-0.23255	6.884052	0.188711	0.286189	0.036985	0	1749	1638	2580	2346	2430	2082	2029	3212	3014	2321
ENSMUSG00000063765	chr15	Chadl	81678296	81678756	4965	-0.41992	0.403435	0.188698	0.286189	0.074037	0	16	20	30	19	35	24	30	14	30	25
ENSMUSG00000083097	chr2	Gm14494	1.54E+08	1.54E+08	435	0.386539	0.935444	0.188996	0.286588	0.073208	0	20	22	41	19	30	50	40	54	48	43
ENSMUSG00000027472	chr2	Pdrg1	1.53E+08	1.53E+08	2443	-0.22457	6.503317	0.189037	0.286619	0.034373	0	1425	1634	1902	1469	1686	1854	1949	1825	2089	1931
ENSMUSG00000031015	chr7	Swap70	1.1E+08	1.1E+08	4032	0.242854	3.750169	0.189152	0.286763	0.036798	0	162	150	217	206	304	214	338	280	477	415
ENSMUSG00000020814	chr11	Mxra7	1.17E+08	1.17E+08	2391	0.264016	4.195941	0.189322	0.28699	0.045433	0	272	188	315	248	375	387	650	308	568	414
ENSMUSG00000038552	chr5	Fndc4	31292255	31293486	2261	0.440414	1.874984	0.189356	0.28701	0.117607	0	59	18	48	37	96	72	134	58	131	88
ENSMUSG00000006678	chrX	Pola1	93304767	93305816	8813	0.373556	1.611037	0.189404	0.28705	0.075575	0	33	29	40	45	71	47	84	50	125	92
ENSMUSG00000063808	chr7	Gpatch1	35276536	35276811	3295	0.377725	3.083596	0.189684	0.287444	0.091835	0	98	103	136	135	138	123	149	448	212	175
ENSMUSG00000026991	chr2	Pkp4	59160850	59161128	5707	-0.28601	4.15825	0.189793	0.287576	0.053876	0	205	311	417	405	298	233	267	527	478	390
ENSMUSG00000048720	chr19	Tbc1d12	38836579	38837446	4209	-0.34862	2.052669	0.189831	0.287603	0.070514	0	67	55	91	64	109	47	110	115	90	59
ENSMUSG00000027634	chr2	Ndrg3	1.57E+08	1.57E+08	8388	-0.21029	5.191244	0.189923	0.287711	0.029365	0	630	556	647	595	842	571	788	831	871	899
ENSMUSG00000027329	chr2	Spef1	1.31E+08	1.31E+08	2747	0.346952	2.172218	0.189977	0.287753	0.069591	0	41	76	71	61	74	92	133	64	169	124
ENSMUSG00000033029	chr15	1700088E04Rik	79129349	79130537	5292	-0.47213	0.082356	0.189992	0.287753	0.10296	0	14	20	32	18	10	12	17	21	33	14
ENSMUSG00000040188	chr9	Scamp2	57560944	57561110	2341	0.223155	5.963868	0.190057	0.287789	0.033902	0	764	810	1107	861	1324	1357	1585	1190	1981	1737
ENSMUSG00000041130	chr17	Zfp598	24669752	24669973	3286	-0.22747	4.379546	0.190052	0.287789	0.033375	0	305	331	373	369	502	310	408	585	473	459
ENSMUSG00000017300	chr2	Tnnc2	1.65E+08	1.65E+08	800	-0.25085	13.35413	0.190332	0.288142	0.043912	0	154931	181695	228388	181176	204651	246590	189237	183224	219889	251241
ENSMUSG00000067931	chr17	Zfp948	21567046	21567245	2612	-0.32817	1.595946	0.190319	0.288142	0.054986	0	39	58	59	43	76	46	68	52	76	64
ENSMUSG00000039735	chr3	Fnbp1l	1.23E+08	1.23E+08	5408	-0.2834	3.218202	0.190821	0.28885	0.051154	0	123	130	200	229	169	94	205	199	276	224
ENSMUSG00000017167	chr11	Cntnap1	1.01E+08	1.01E+08	5875	-0.41604	1.532061	0.190992	0.289078	0.099467	0	52	47	59	35	77	38	54	28	66	98
ENSMUSG00000022706	chr16	Mrpl40	18872018	18872662	1214	0.225486	4.31303	0.191173	0.28932	0.032842	0	244	287	406	288	299	471	463	429	607	505
ENSMUSG00000036863	chr3	Syde2	1.46E+08	1.46E+08	5495	-0.47113	0.821774	0.191205	0.289336	0.116461	0	35	18	30	33	49	13	31	61	37	25
ENSMUSG00000026843	chr2	Fubp3	31572651	31572953	5914	0.253522	3.612952	0.19131	0.289372	0.040546	0	154	140	222	160	263	190	380	375	363	249
ENSMUSG00000036721	chr13	Zscan12	21362827	21362872	2228	-0.35372	2.523847	0.191255	0.289372	0.077543	0	77	94	125	128	109	69	94	207	110	102
ENSMUSG00000051427	chr11	Ccdc157	4141123	4143935	5589	-0.34867	2.532927	0.191312	0.289372	0.074158	0	103	73	130	68	170	65	152	138	99	134
ENSMUSG00000059981	chr7	Taok2	1.27E+08	1.27E+08	9247	-0.20375	5.106168	0.191287	0.289372	0.027578	0	562	457	712	613	752	528	730	711	994	813
ENSMUSG00000085945	chr7	2310014F06Rik	1.13E+08	1.13E+08	659	-0.49685	0.123025	0.191502	0.289627	0.11586	0	11	29	18	21	18	16	24	12	36	11
ENSMUSG00000023944	chr17	Hsp90ab1	45567775	45568124	2999	0.217268	10.13103	0.191706	0.289904	0.033132	0	13009	14886	21466	17228	20966	20947	26752	34982	31116	27107
ENSMUSG00000022323	chr15	Hrsp12	34484021	34484535	3192	-0.32102	2.760769	0.191886	0.290114	0.062964	0	111	109	159	106	138	144	136	74	160	174
ENSMUSG00000028567	chr4	Txndc12	1.09E+08	1.09E+08	2253	0.23666	3.601783	0.19188	0.290114	0.034923	0	150	135	192	207	250	251	311	223	410	336
ENSMUSG00000025701	chr6	Alox5	1.16E+08	1.16E+08	4106	0.423666	1.30419	0.191939	0.290155	0.10233	0	25	16	37	28	68	45	64	37	91	83
ENSMUSG00000028140	chr3	Mrpl9	94443336	94443494	1601	0.257255	6.134749	0.191955	0.290155	0.045622	0	895	1151	1183	1145	890	1458	1545	2369	1893	1604
ENSMUSG00000029439	chr5	Sfswap	1.3E+08	1.3E+08	3302	0.222263	3.983603	0.192091	0.290328	0.03112	0	202	207	247	247	316	257	399	501	439	393
ENSMUSG00000059195	chr4	Gm12715	1.04E+08	1.04E+08	1128	0.342894	2.41597	0.192178	0.290428	0.072237	0	55	59	75	73	131	91	171	77	213	146
ENSMUSG00000056917	chr19	Sipa1	5651185	5651562	3868	0.243909	4.066502	0.192227	0.290471	0.038578	0	175	209	292	280	336	299	480	283	596	485
ENSMUSG00000066554	chr5	Gm10167	1.48E+08	1.48E+08	1479	0.421066	0.214	0.192409	0.290714	0.068405	0	11	8	21	18	18	23	27	23	43	26
ENSMUSG00000010021	chr11	Kif19a	1.15E+08	1.15E+08	4068	0.449426	0.432028	0.192473	0.290779	0.088484	0	25	12	13	11	26	19	38	29	47	37
ENSMUSG00000021938	chr14	Pspc1	56722441	56723280	4003	0.256388	3.142666	0.192546	0.290857	0.039938	0	90	119	175	134	153	182	241	165	287	240
ENSMUSG00000032580	chr9	Rbm5	1.08E+08	1.08E+08	15434	0.221427	5.373173	0.192606	0.290916	0.03317	0	600	587	586	581	830	789	1014	1272	1100	1014
ENSMUSG00000032306	chr9	Mpi	57544256	57544938	3142	-0.2393	6.014563	0.192709	0.29104	0.03951	0	934	1150	1206	1375	1133	1394	1310	1130	1720	1301

ENSMUSG00000006307	chr7	Kmt2b	30568858	30569436	9596	-0.24274	4.634624	0.192829	0.291189	0.039432	0	413	325	472	450	603	302	492	735	609	543
ENSMUSG00000059751	chr13	Rps3a3	1.09E+08	1.09E+08	795	0.524166	-0.25401	0.192917	0.291258	0.113207	0	6	7	14	5	19	9	27	13	24	29
ENSMUSG00000089889	chr5	0610040B10Rik	1.43E+08	1.43E+08	683	0.398341	0.798372	0.192917	0.291258	0.070094	0	20	27	28	24	17	33	34	53	52	45
ENSMUSG00000031736	chr8	Crnde	92326038	92326266	2012	0.452435	0.207025	0.192955	0.291284	0.085495	0	14	17	20	10	12	16	42	24	28	32
ENSMUSG00000021595	chr13	Nsun2	69533746	69533910	5737	0.202587	5.723031	0.193005	0.291328	0.027972	0	685	739	976	713	1006	1063	1223	1326	1629	1365
ENSMUSG00000024078	chr17	Ttc27	74717750	74718011	2820	-0.23461	3.260251	0.193139	0.291499	0.032956	0	127	158	224	166	188	148	224	182	252	221
ENSMUSG00000029397	chr5	Rchy1	91948904	91949864	2894	-0.21061	5.334641	0.193197	0.291554	0.029854	0	627	605	889	663	846	811	914	810	917	861
ENSMUSG00000027881	chr3	Prpf38b	1.09E+08	1.09E+08	4750	0.224027	4.761698	0.193274	0.29159	0.033647	0	296	330	432	435	628	528	684	566	832	809
ENSMUSG00000032294	chr9	Pkm	59656368	59656649	2599	-0.22674	11.71713	0.19327	0.29159	0.036364	0	47132	59361	70199	61710	64753	70607	58310	67684	84026	78025
ENSMUSG00000035949	chr2	Fbxw2	34804514	34805999	6661	-0.24374	5.52913	0.193284	0.29159	0.040859	0	710	758	963	896	837	656	860	1441	1026	958
ENSMUSG00000021319	chr13	Sfrp4	19623175	19623877	1756	0.550306	3.428177	0.193414	0.291742	0.206593	0	92	65	80	124	404	191	472	78	472	304
ENSMUSG00000035936	chr13	Aldh5a1	24907579	24911766	5647	-0.24487	3.443294	0.193427	0.291742	0.037384	0	151	177	218	242	188	195	189	205	317	254
ENSMUSG00000058440	chr6	Nrf1	30047988	30048113	10282	0.24573	3.544919	0.193517	0.291847	0.037756	0	175	130	163	179	241	211	258	377	354	273
ENSMUSG00000047767	chr7	Atg16l2	1.01E+08	1.01E+08	3881	0.352152	1.965571	0.193626	0.291979	0.068939	0	65	51	55	46	58	55	107	138	96	104
ENSMUSG00000025785	chr9	Exosc7	1.23E+08	1.23E+08	1843	0.22728	3.709478	0.193671	0.291982	0.031954	0	190	199	216	179	206	299	310	293	381	342
ENSMUSG00000039623	chr5	Ap5z1	1.42E+08	1.42E+08	3817	0.303248	2.473724	0.193669	0.291982	0.054474	0	80	63	76	77	113	84	117	132	186	196
ENSMUSG00000038371	chr7	Sbf2	1.1E+08	1.1E+08	12127	-0.23764	4.069113	0.19372	0.292024	0.036665	0	266	203	333	331	395	225	337	476	406	361
ENSMUSG00000025340	chr5	Rabgef1	1.3E+08	1.3E+08	4168	-0.25469	6.212738	0.194049	0.292489	0.045251	0	1062	1337	1562	1244	1536	1171	1440	2353	1511	1371
ENSMUSG00000022023	chr14	Wbp4	79459937	79462129	3452	-0.20777	4.849328	0.194253	0.292765	0.02877	0	407	476	617	555	518	490	692	623	704	607
ENSMUSG00000040363	chrX	Bcor	12036740	12037917	7190	-0.2797	4.386774	0.194831	0.293603	0.052803	0	292	288	347	405	612	307	427	652	520	302
ENSMUSG00000036022	chrX	Fam122b	53243415	53246290	4409	0.37496	1.264462	0.195216	0.294152	0.069945	0	33	31	30	38	33	39	72	38	82	76
ENSMUSG00000020099	chr10	Unc5b	60762610	60765373	5852	-0.27326	3.494381	0.195483	0.294523	0.048429	0	147	154	185	293	252	169	288	191	352	203
ENSMUSG00000031328	chrX	Flna	74223461	74223977	9400	0.294053	7.087076	0.195637	0.294716	0.061293	0	1696	1388	1995	2371	2899	2399	3272	1923	6155	4274
ENSMUSG00000032578	chr9	Cish	1.07E+08	1.07E+08	6419	-0.85058	5.431048	0.195654	0.294716	0.49769	0	608	1056	56	950	2005	759	985	121	1727	105
ENSMUSG00000017119	chr11	Nbr1	1.02E+08	1.02E+08	6871	-0.26647	6.635413	0.195715	0.294775	0.050168	0	1508	1504	2093	1874	2139	1436	1796	3417	2168	1714
ENSMUSG00000047766	chr9	Lrrc49	60568859	60570598	6310	0.307095	2.20704	0.195871	0.294979	0.054698	0	46	65	71	56	103	77	123	143	146	99
ENSMUSG00000031399	chrX	Fam3a	74384719	74385435	2485	0.261217	4.166868	0.195968	0.29506	0.045646	0	245	215	291	273	340	314	391	716	472	380
ENSMUSG00000036873	chr3	2410004B18Rik	1.46E+08	1.46E+08	2029	-0.24482	3.798533	0.195956	0.29506	0.038547	0	193	271	288	226	271	300	323	237	333	267
ENSMUSG00000023452	chr5	Pisd	32736301	32737454	3814	0.210259	4.672245	0.196126	0.295266	0.029284	0	311	370	443	393	455	432	632	544	910	720
ENSMUSG00000031666	chr8	Rbl2	91070057	91070406	6963	-0.41936	5.638715	0.196162	0.295288	0.124029	0	967	695	1048	969	1080	501	664	2388	753	652
ENSMUSG00000032011	chr9	Thy1	44043384	44043476	1735	0.422002	5.045252	0.196341	0.295526	0.125344	0	360	274	587	329	896	768	1286	238	1250	896
ENSMUSG00000022526	chr15	Zfp251	76852148	76854614	3497	-0.24843	3.410887	0.196413	0.295602	0.038954	0	156	150	223	179	262	138	235	301	260	203
ENSMUSG00000052423	chr1	B4galt3	1.71E+08	1.71E+08	5467	0.242822	3.246066	0.196505	0.295708	0.035896	0	153	114	177	135	135	169	251	231	300	247
ENSMUSG00000047712	chr10	Ust	8204753	8207670	4284	-0.40866	2.028068	0.196596	0.295812	0.104138	0	77	38	99	47	130	33	80	116	97	83
ENSMUSG00000024683	chr19	Mrpl16	11770415	11770524	1122	-0.24445	5.285661	0.196622	0.29582	0.041379	0	486	751	871	791	609	801	755	822	921	815
ENSMUSG00000021943	chr14	Gdf10	33923587	33924202	2507	-0.24629	3.857151	0.196663	0.295834	0.039589	0	255	177	325	286	267	278	232	262	442	332
ENSMUSG00000039852	chr4	Rere	1.5E+08	1.5E+08	8525	-0.28989	6.51005	0.196674	0.295834	0.05966	0	1416	1472	1735	1759	2004	1165	1415	3328	1901	1788
ENSMUSG00000038965	chr16	Ube2l3	17152013	17154282	5599	-0.20296	7.121103	0.196705	0.295848	0.029213	0	2127	2226	2741	2505	2852	2567	2728	2954	3675	3175
ENSMUSG00000024583	chr18	Txnl1	63662801	63664332	2558	0.24449	5.879751	0.196804	0.295936	0.041943	0	814	834	1091	840	898	1118	1348	2122	1459	1360
ENSMUSG00000031770	chr8	Herpud1	94386438	94386738	2333	-0.23586	6.5268	0.196806	0.295936	0.03936	0	1537	1585	1936	1561	1648	1681	1769	2557	1909	1856
ENSMUSG00000035601	chr4	Trmt10b	45297127	45297195	2641	-0.29308	2.024605	0.19689	0.29603	0.047188	0	74	64	73	76	77	74	81	70	105	88
ENSMUSG00000021806	chr14	Nid2	19751257	19751565	4884	-0.25676	5.303431	0.196912	0.296031	0.045836	0	602	419	733	719	1207	625	1047	718	1117	730
ENSMUSG00000004056	chr7	Akt2	27591552	27591879	7131	-0.20507	7.80662	0.196996	0.296076	0.03001	0	3215	3248	4767	3879	5152	3761	4924	5213	5202	5153
ENSMUSG00000032264	chr9	Zw10	49055581	49055787	2895	-0.21338	3.574852	0.197004	0.296076	0.02788	0	175	185	265	198	244	216	263	235	311	255
ENSMUSG00000055799	chr6	Tcf7l1	72626378	72627793	3924	0.274892	3.060886	0.197006	0.296076	0.046864	0	127	90	102	141	163	122	212	247	261	227
ENSMUSG00000015804	chr5	Med28	45520221	45520484	5010	0.224894	4.951634	0.197107	0.296195	0.034558	0	456	427	558	412	516	733	836	579	881	822
ENSMUSG00000020473	chr11	Aebp1	5861947	5862398	4058	0.282266	5.767873	0.197139	0.296211	0.056424	0	692	454	881	656	1564	1047	1748	1410	1576	1205
ENSMUSG00000029851	chr6	Fam115c	42623019	42624615	4775	0.309999	2.084266	0.197376	0.296535	0.053749	0	63	51	65	54	75	80	118	73	159	112
ENSMUSG00000002900	chr12	Lamb1	31265234	31265344	9917	0.247425	6.660336	0.197441	0.2966	0.043608	0	1322	935	1567	1584	2492	1824	3173	2207	3320	2432
ENSMUSG00000051978	chr8	Erich1	14027565	14028153	1579	-0.35672	0.728758	0.197517	0.296683	0.059883	0	24	30	35	29	29	20	42	32	37	31
ENSMUSG00000064210	chr15	Ano6	95790843	95791056	5640	-0.20512	6.184648	0.197778	0.297042	0.029595	0	996	1040	1437	1366	1748	1189	1567	1662	1937	1571
ENSMUSG00000035967	chrX	Ddx26b	56454857	56455316	7173	-0.24867	3.266359	0.197876	0.297157	0.03882	0	146	145	227	153	201	120	237	185	232	257
ENSMUSG00000075268	chr19	Gm10819	16267061	16267621	561	-0.34406	1.248139	0.198052	0.297389	0.062339	0	28	43	53	51	39	34	43	54	66	41
ENSMUSG00000052488	chr8	Cherp	72460489	72461355	3794	0.202043	4.57155	0.198334	0.297781	0.027209	0	292	300	408	376	483	399	567	639	748	639
ENSMUSG00000000031	chr7	H19	1.43E+08	1.43E+08	2372	0.261379	12.05251	0.198425	0.297853	0.049413	0	30909	59467	90618	78034	69208	82103	118283	105914	126417	110099
ENSMUSG00000028648	chr4	Ndufs5	1.24E+08	1.24E+08	860	0.248507	6.52303	0.198409	0.297853	0.044059	0	1210	1437	1784	1339	1177	2398	2240	2257	2303	2220
ENSMUSG00000021906	chr14	Oxnad1	32085374	32085566	5769	-0.25904	4.828083	0.198743	0.298297	0.046671	0	440	541	605	550	407	583	665	413	781	558
ENSMUSG00000030751	chr7	Psma1	1.14E+08	1.14E+08	2103	0.249967	6.407728	0.198804	0.298324	0.044591	0	1134	1233	1565	1231	1281	1606	1848	3151	2110	1991
ENSMUSG00000059518	chr5	Znhit1	1.37E+08	1.37E+08	1860	0.223395	4.683464	0.198799	0.298324	0.033905	0	356	387	424	395	394	622	639	519	696	707
ENSMUSG00000021555	chr13	Naa35	59585259	59585292	5780	0.204477	4.334676	0.199	0.298587	0.02743	0	244	302	357	313	343	382	529	436	611	566
ENSMUSG00000029576	chr5	Radil	1.42E+08	1.42E+08	4803	-0.3734	1.280865	0.199159	0.298792	0.076074	0	43	19	55	40	69	29	48	50	65	50
ENSMUSG00000023007	chr15	Prpf40b	99295087	99295273	4952	-0.20587	3.935253	0.199331	0.298986	0.027187	0	229	249	294	282	307	249	337	348	340	374
ENSMUSG00000097412	chr10	1810014B01Rik	86685601	86685737	1661	-0.29679	2.79223	0.199318	0.298986	0.056767	0	111	124	110	150	129	101	120	123	262	131
ENSMUSG00000021794	chr14	Glud1	34310727	34311342	4089	-0.21749	7.029423	0.199521	0.299239	0.034028	0	2060	2089	2457	2596	2483	1961	2554	3487	3265	2915
ENSMUSG00000037017	chr5	Zscan21	1.38E+08	1.38E+08	3198	0.316331	4.249541	0.199552	0.299252	0.069334	0	267	274	294	249	314	310	363	916	448	407
ENSMUSG00000073374	chr17	C030034I22Rik	69417402	69421632	4231	0.413545	0.319641	0.199574	0.299252	0.072045	0	15	13	20	13	21	16	43	32	29	33

ENSMUSG00000022338	chr15	Eny2	44428111	44428242	2429	0.226586	4.717131	0.199752	0.299488	0.035084	0	347	422	482	370	379	532	729	749	651	616
ENSMUSG00000032714	chr10	Syde1	78584503	78585911	3288	0.272253	3.335326	0.199838	0.299584	0.048552	0	134	92	166	150	228	153	259	196	384	316
ENSMUSG00000085479	chr11	9430073C21Rik	67195680	67197472	2173	0.763078	1.860184	0.199917	0.29967	0.391395	0	29	27	34	103	19	36	47	52	406	33
ENSMUSG00000069939	chr11	Gm12070	26786633	26787634	1002	-0.39575	1.509928	0.199977	0.299727	0.091578	0	40	69	49	35	68	58	32	63	74	50
ENSMUSG00000016487	chr6	Ppfibp1	1.47E+08	1.47E+08	9790	0.250422	5.130827	0.200039	0.299766	0.044054	0	499	379	668	492	654	509	972	1251	1052	706
ENSMUSG00000021417	chr13	Eci2	34977748	34978066	2615	0.3295	6.091211	0.200046	0.299766	0.078028	0	808	964	1113	1149	982	1069	1241	3409	1632	1498
ENSMUSG00000060427	chr8	Zfp868	69610857	69612455	2893	-0.3356	2.387302	0.200184	0.29994	0.069279	0	73	96	122	80	111	85	105	166	96	74
ENSMUSG00000028452	chr4	Vcp	42979963	42980634	4851	0.215329	8.976594	0.200436	0.300285	0.033782	0	5895	6953	8902	7843	9671	10490	11136	15403	13025	12702
ENSMUSG00000020308	chr10	Tpgs1	79669410	79669783	1101	0.21876	3.837581	0.200469	0.300302	0.031124	0	181	212	249	213	239	346	344	338	371	360
ENSMUSG00000074364	chr7	Ehd2	15946977	15950792	5100	-0.25662	6.818077	0.200556	0.300401	0.047642	0	1452	1697	1948	2827	2386	1574	2244	1813	3508	3123
ENSMUSG00000061518	chr1	Cox5b	36691484	36691689	1552	0.242773	8.472924	0.201096	0.301176	0.042999	0	4085	5759	5676	6710	4636	8547	8185	8542	10775	8573
ENSMUSG00000022665	chr16	Ccdc80	45093402	45093597	4140	0.295007	6.084253	0.201185	0.30123	0.062954	0	868	554	1193	845	1793	1351	2365	1120	2303	1660
ENSMUSG00000026806	chr2	Ddx31	28840406	28840860	3534	0.254488	2.723303	0.201197	0.30123	0.038409	0	95	84	115	83	119	133	159	154	231	155
ENSMUSG00000033068	chr2	Entpd6	1.51E+08	1.51E+08	4775	-0.26647	3.43184	0.201192	0.30123	0.046642	0	157	148	206	216	261	171	208	150	283	333
ENSMUSG00000035762	chr13	Tmem161b	84222314	84222434	2572	-0.25134	3.134498	0.201265	0.301299	0.040229	0	151	168	181	134	146	132	190	205	217	188
ENSMUSG00000019080	chr15	Mfsd3	76701542	76702350	2169	-0.22686	3.26727	0.20159	0.301753	0.031957	0	164	132	221	158	188	166	204	191	254	215
ENSMUSG00000030717	chr7	Nupr1	1.27E+08	1.27E+08	2514	0.297307	3.958318	0.201718	0.301912	0.060904	0	316	107	251	192	293	250	403	402	468	488
ENSMUSG00000035845	chr15	Alg12	88805244	88806054	2356	-0.26476	2.382887	0.201938	0.302209	0.040377	0	88	82	109	82	107	85	104	95	136	127
ENSMUSG00000058809	chr11	Gm12141	41498737	41500458	1722	-0.31159	2.258338	0.202041	0.302329	0.05856	0	86	81	105	95	62	91	109	91	101	93
ENSMUSG00000045795	chr7	Whamm	81571292	81571909	3069	0.386038	3.341378	0.202188	0.302518	0.103196	0	129	120	173	132	176	142	168	577	227	212
ENSMUSG00000023079	chr5	Gtf2ird1	1.34E+08	1.34E+08	4834	0.241492	3.067258	0.202272	0.30261	0.036296	0	103	101	128	119	191	157	215	224	258	199
ENSMUSG00000048970	chrX	C1galt1c1	38630785	38632123	1449	-0.21752	3.628898	0.202494	0.302909	0.030393	0	206	201	241	196	258	223	309	221	319	255
ENSMUSG00000009894	chr11	Snap47	59407134	59407810	2651	-0.22917	4.722772	0.202563	0.30298	0.036513	0	347	499	542	464	519	532	647	427	695	516
ENSMUSG00000004768	chr1	Rab23	33719887	33720173	8285	-0.28489	2.880056	0.202754	0.303167	0.051491	0	140	75	138	124	200	132	171	137	195	132
ENSMUSG00000022758	chr16	P2rx6	17561885	17562183	3995	-0.26932	3.955272	0.202752	0.303167	0.049749	0	250	291	306	295	249	272	267	472	277	323
ENSMUSG00000069835	chr11	Sat2	69622024	69622332	1424	0.312388	2.035955	0.202736	0.303167	0.057961	0	45	48	83	61	63	77	89	144	118	89
ENSMUSG00000004789	chr12	Dlst	85110833	85110959	2767	-0.23364	8.496316	0.202866	0.303302	0.040156	0	4730	6870	6962	7679	6117	6992	7038	6391	10310	8059
ENSMUSG00000030613	chr7	Ccdc90b	92561149	92561635	1801	-0.20611	3.998357	0.20292	0.30335	0.027904	0	235	272	351	267	297	274	387	346	387	329
ENSMUSG00000007564	chr17	Ppp2r1a	20945311	20945583	3375	0.202199	6.968653	0.203094	0.303577	0.0298	0	1620	1604	2137	2037	2389	2588	2859	2803	4166	3305
ENSMUSG00000021273	chr14	Fdft1	63145153	63146968	2860	0.489265	5.681797	0.203172	0.303629	0.17391	0	680	629	618	866	728	716	619	3745	872	970
ENSMUSG00000023249	chr9	Parp3	1.06E+08	1.06E+08	3699	-0.20161	6.452314	0.203156	0.303629	0.029476	0	1398	1437	1771	1512	1679	1400	1994	2107	2240	1805
ENSMUSG00000066042	chr4	Med18	1.32E+08	1.32E+08	1998	0.39126	0.876174	0.203261	0.303714	0.073771	0	35	20	20	20	28	30	48	52	51	49
ENSMUSG00000084145	chr11	Gm12263	59474284	59475765	1482	-0.5036	-0.00185	0.203273	0.303714	0.118339	0	14	19	15	22	19	10	17	36	15	10
ENSMUSG00000025157	chr19	Zdhhc16	41933472	41933665	1830	-0.20238	4.324861	0.203416	0.303895	0.027381	0	277	319	408	335	460	352	459	380	485	490
ENSMUSG00000023723	chr11	Mrps23	88204388	88204485	1560	0.225816	6.318913	0.203453	0.303918	0.037035	0	1005	1276	1392	1222	1201	1958	1855	2062	2136	1885
ENSMUSG00000030595	chr7	Nfkbib	28758251	28759008	2169	0.228902	4.495691	0.203516	0.303979	0.036373	0	328	252	394	331	435	411	513	768	561	570
ENSMUSG00000041794	chr9	Myrip	1.2E+08	1.2E+08	5440	-0.42094	0.336269	0.203621	0.304103	0.084247	0	18	20	19	33	22	16	19	36	29	18
ENSMUSG00000023000	chr15	Dhh	98893031	98894560	2363	-0.42789	0.378765	0.20372	0.304217	0.09419	0	17	20	15	38	26	12	25	24	41	22
ENSMUSG00000039678	chr2	Tbc1d13	30133746	30133912	4719	0.223589	4.722854	0.203811	0.304321	0.034884	0	358	340	453	360	531	503	653	464	907	822
ENSMUSG00000013936	chr5	Myl2	1.22E+08	1.22E+08	1950	1.052523	5.096962	0.203957	0.304506	0.774447	0	9	564	12	915	305	890	123	2309	1547	510
ENSMUSG00000074771	chr2	Ankef1	1.37E+08	1.37E+08	7185	1.064551	0.633662	0.204044	0.304603	0.737906	0	19	2	3	21	32	2	13	3	86	135
ENSMUSG00000039458	chr15	Mtmr12	12205028	12205279	4785	-0.26118	2.732793	0.204296	0.304945	0.042711	0	91	112	114	124	160	89	152	131	208	131
ENSMUSG00000024370	chr18	Cdc23	34630951	34631301	9500	-0.20345	4.527115	0.20439	0.305053	0.028387	0	385	322	500	368	491	377	589	462	618	463
ENSMUSG00000020475	chr11	Pgam2	5801640	5801839	840	-0.2797	11.37535	0.204423	0.30507	0.058062	0	37739	47971	59919	48196	49350	67940	50515	32940	63307	58649
ENSMUSG00000034800	chr2	Zfp661	1.28E+08	1.28E+08	5165	-0.32206	1.85618	0.204533	0.305201	0.062213	0	72	61	55	73	62	63	63	92	80	67
ENSMUSG00000026036	chr1	Nif3l1	58445151	58445634	7763	-0.23126	3.853627	0.20474	0.305476	0.035684	0	225	234	337	237	264	293	347	228	356	309
ENSMUSG00000009406	chrX	Elk1	20933395	20935548	5381	-0.20517	3.863345	0.205065	0.305929	0.027462	0	220	229	291	225	338	240	325	347	358	302
ENSMUSG00000047443	chr1	Fam132b	91366430	91366648	2815	-0.42132	1.213812	0.205124	0.305951	0.102892	0	43	21	57	35	62	34	78	37	41	32
ENSMUSG00000097617	chr9	Gm10687	44123768	44125293	1651	0.443364	0.966279	0.205112	0.305951	0.106324	0	26	25	22	27	29	30	38	25	77	84
ENSMUSG00000032374	chr9	Plod2	92542223	92542568	5392	0.37703	3.511148	0.205156	0.305965	0.100936	0	137	102	133	110	369	209	460	161	375	302
ENSMUSG00000045625	chr16	Pigz	31933851	31934043	2541	0.494099	0.1568	0.205282	0.306121	0.126378	0	8	8	19	7	30	19	40	15	41	24
ENSMUSG00000020775	chr11	Mrpl38	1.16E+08	1.16E+08	2550	0.218016	5.61032	0.205333	0.306164	0.034317	0	570	740	834	878	727	1159	1142	1089	1478	1214
ENSMUSG00000028854	chr4	Slc9a1	1.33E+08	1.33E+08	5324	0.211307	4.125283	0.205495	0.306373	0.030182	0	218	191	294	307	350	289	416	468	574	457
ENSMUSG00000038239	chr7	Hrc	45335290	45337374	2410	-0.20981	10.06998	0.205575	0.306458	0.032855	0	15606	16197	21274	20710	23103	22389	20135	23736	26050	22774
ENSMUSG00000068040	chr2	Tm9sf4	1.53E+08	1.53E+08	7281	-0.20344	5.281438	0.205873	0.306869	0.029543	0	577	529	780	686	944	620	881	706	1121	933
ENSMUSG00000079297	chrX	Gm2223	33505661	33507010	1350	-0.37151	1.766361	0.205945	0.306944	0.084075	0	71	49	69	56	66	38	50	111	62	78
ENSMUSG00000032531	chr9	Amotl2	1.03E+08	1.03E+08	6289	-0.22158	4.330715	0.205984	0.306969	0.034001	0	277	268	421	424	433	290	409	377	535	576
ENSMUSG00000019872	chr10	Smpdl3a	57794335	57794409	2065	-0.26583	5.8869	0.206107	0.307086	0.051965	0	994	954	1237	1122	1055	810	976	2019	1260	1212
ENSMUSG00000042523	chr12	Dnal1	84114366	84114399	6938	-0.2713	2.899651	0.206093	0.307086	0.047544	0	142	82	157	150	145	105	200	151	169	160
ENSMUSG00000037577	chr17	Ephx3	32183770	32185121	2502	-0.47045	-0.09233	0.206132	0.307091	0.105837	0	11	15	16	20	21	12	22	4	22	24
ENSMUSG00000020589	chr12	Fam49a	12262139	12262238	4846	0.23944	3.66206	0.206234	0.307183	0.038765	0	194	120	217	177	265	244	376	357	332	275
ENSMUSG00000028664	chr4	Ephb2	1.37E+08	1.37E+08	12608	0.476262	2.173463	0.206238	0.307183	0.154658	0	56	19	61	51	133	77	218	58	137	113
ENSMUSG00000091475	chr17	2810468N07Rik	25570811	25571101	1349	0.416756	0.46951	0.20636	0.30733	0.081436	0	16	16	17	13	30	23	44	46	31	26
ENSMUSG00000036086	chr1	Zranb3	1.28E+08	1.28E+08	9079	-0.30615	2.84741	0.206458	0.307444	0.06435	0	144	126	131	115	132	87	116	116	276	175
ENSMUSG00000020836	chr11	Coro6	77462411	77462754	3011	-0.27991	6.899806	0.206531	0.307519	0.05826	0	1906	2014	2251	2773	1865	1789	2190	3987	2677	1937
ENSMUSG00000103970	chr9	RP23-250G8.14	1.09E+08	1.09E+08	1146	-0.31366	1.458961	0.206624	0.307624	0.053362	0	43	47	45	45	67	40	51	67	70	51

ENSMUSG00000023186	chr9	Vwa5a	38718268	38718387	4899	-0.2113	5.323997	0.206724	0.307741	0.032234	0	684	543	881	603	903	561	817	984	1152	878
ENSMUSG00000038623	chr7	Tm6sf1	81859001	81859540	5921	0.242806	5.064101	0.206922	0.308003	0.042426	0	399	462	540	595	557	530	1183	739	1200	655
ENSMUSG00000041798	chr11	Gck	5900820	5901087	3033	0.501255	1.707608	0.207023	0.308119	0.170757	0	14	63	65	48	27	119	42	67	108	84
ENSMUSG00000042348	chr13	Arl15	1.14E+08	1.14E+08	3364	-0.25726	2.994749	0.207125	0.308238	0.042161	0	137	105	128	150	202	119	200	138	210	180
ENSMUSG00000061894	chr4	Zscan20	1.29E+08	1.29E+08	8375	-0.3163	1.649587	0.207155	0.308249	0.055169	0	59	42	76	49	57	57	64	67	66	61
ENSMUSG00000030471	chr7	Zdhhc13	48789003	48789137	2410	0.323728	2.492963	0.207218	0.308311	0.065282	0	79	92	97	55	82	89	186	101	210	146
ENSMUSG00000024130	chr17	Abca3	24351950	24352251	8797	-0.21452	4.121672	0.207316	0.30839	0.031505	0	273	212	338	329	423	242	385	355	475	442
ENSMUSG00000039697	chr10	Ncoa7	30645584	30647651	5336	-0.27759	2.565348	0.207309	0.30839	0.048433	0	74	78	123	119	150	68	140	129	152	137
ENSMUSG00000029672	chr6	Fam3c	22306520	22308538	3713	0.232559	3.832245	0.207548	0.308702	0.036977	0	196	146	246	202	313	267	426	260	473	377
ENSMUSG00000019487	chr17	Trip10	57249451	57249571	2290	-0.24872	6.598162	0.207676	0.308841	0.046025	0	1545	1639	2081	1811	1655	1797	1856	2897	1956	1685
ENSMUSG00000040123	chr14	Zmym5	56790585	56794500	5541	-0.26441	4.347037	0.207686	0.308841	0.049895	0	351	315	423	332	428	276	386	695	377	411
ENSMUSG00000022469	chr15	Rapgef3	97744770	97745666	6336	-0.24252	3.224735	0.20783	0.309022	0.039195	0	147	168	167	196	151	126	210	210	260	199
ENSMUSG00000058914	chr15	C1qtnf3	10952332	10952537	2557	0.478355	4.701646	0.208004	0.309247	0.168926	0	362	218	439	216	620	431	1677	212	707	530
ENSMUSG00000022400	chr15	Rbx1	81466316	81466450	1655	0.208849	6.12877	0.208096	0.309349	0.032169	0	924	1048	1266	998	1168	1620	1708	1583	1941	1822
ENSMUSG00000030170	chr6	Wnt5b	1.19E+08	1.19E+08	2654	0.513823	0.557625	0.208117	0.309349	0.153316	0	17	8	8	23	39	16	48	36	68	25
ENSMUSG00000005674	chr1	Tomm40l	1.71E+08	1.71E+08	5135	-0.25034	5.636903	0.208143	0.309354	0.046194	0	740	935	1118	882	799	1029	1172	656	1317	1097
ENSMUSG00000025034	chr19	Trim8	46501648	46503013	3230	0.2001	4.938007	0.208297	0.30955	0.028325	0	384	485	494	466	539	605	818	669	941	797
ENSMUSG00000003477	chr6	Inmt	55170626	55171277	1600	1.006813	3.005596	0.208322	0.309553	0.716214	0	133	50	113	89	41	20	29	1070	43	61
ENSMUSG00000015776	chr2	Med22	26905262	26908301	3614	0.197352	4.507103	0.20863	0.309978	0.026952	0	318	306	400	306	439	421	513	561	719	632
ENSMUSG00000086429	chr6	Gt(ROSA)26Sor	1.13E+08	1.13E+08	1695	-0.31525	2.094613	0.208676	0.310014	0.063993	0	63	93	80	61	88	49	70	109	121	95
ENSMUSG00000020677	chr11	Ddx52	83942062	83942264	3332	0.217183	4.174171	0.208838	0.310193	0.032428	0	263	238	330	257	297	318	444	583	502	413
ENSMUSG00000022635	chr15	Zcrb1	93386097	93386283	3074	-0.22893	5.951262	0.208842	0.310193	0.038785	0	1026	1085	1299	1105	998	1301	1406	1171	1329	1334
ENSMUSG00000049091	chr7	Sephs2	1.27E+08	1.27E+08	1359	-0.20591	4.409179	0.208875	0.310209	0.029683	0	298	358	433	384	424	311	410	552	550	491
ENSMUSG00000003617	chr3	Cp	19957054	19957429	9566	-0.27982	4.236005	0.208952	0.310291	0.056433	0	335	205	381	330	495	194	302	494	476	553
ENSMUSG00000029093	chr5	Sorcs2	36017180	36019392	8803	0.289605	3.368489	0.209029	0.310371	0.057905	0	149	90	151	145	247	148	366	215	379	237
ENSMUSG00000074221	chr7	Zfp568	29983955	29984228	7183	-0.24427	5.105361	0.209087	0.310423	0.043476	0	436	499	712	575	958	547	1037	694	853	555
ENSMUSG00000066149	chr4	Cdc26	62383654	62384538	7180	0.204837	4.341335	0.209189	0.310541	0.029086	0	262	292	392	296	323	423	489	558	538	500
ENSMUSG00000026424	chr1	Gpr37l1	1.35E+08	1.35E+08	2269	-0.44796	0.253335	0.209319	0.310635	0.102257	0	19	20	9	29	29	12	19	19	38	24
ENSMUSG00000038077	chr6	Kcna6	1.27E+08	1.27E+08	5945	-0.48762	0.20408	0.209287	0.310635	0.123477	0	14	15	11	16	51	19	21	16	25	22
ENSMUSG00000038489	chr7	Polr2l	1.41E+08	1.41E+08	1650	0.221422	5.094676	0.209314	0.310635	0.035621	0	427	516	616	530	530	867	776	711	947	924
ENSMUSG00000023913	chr17	Pla2g7	43568098	43568170	2905	0.226146	5.078211	0.20938	0.310692	0.036924	0	557	490	554	457	499	655	968	685	932	1006
ENSMUSG00000042492	chr7	Tbc1d10b	1.27E+08	1.27E+08	4690	0.201516	5.600657	0.209435	0.310741	0.029878	0	551	609	845	734	1090	1026	1230	1134	1513	1152
ENSMUSG00000071655	chr19	Ubxn1	8871559	8871585	1068	0.233484	7.381161	0.209614	0.310972	0.04116	0	1670	2471	3535	2517	2711	4052	3546	4207	4632	4341
ENSMUSG00000028145	chr3	Them4	94310132	94310288	1730	-0.25571	3.326211	0.209712	0.311084	0.044239	0	161	193	209	168	163	194	228	145	259	230
ENSMUSG00000018566	chr11	Slc2a4	69942539	69943572	3478	-0.24541	8.543141	0.209751	0.311109	0.045672	0	6220	6436	7953	7077	5743	6748	6226	10696	8230	7609
ENSMUSG00000035778	chr2	Ggta1	35400179	35402802	4709	0.214178	4.144758	0.209935	0.311349	0.031612	0	238	204	340	326	254	320	466	456	541	438
ENSMUSG00000030652	chr7	Coq7	1.19E+08	1.19E+08	4003	0.2404	5.708768	0.209994	0.311403	0.042878	0	585	905	859	889	715	1330	1278	1082	1530	1305
ENSMUSG00000010554	chr11	Mettl16	74770830	74770984	13817	-0.23711	4.006816	0.210541	0.31218	0.039549	0	228	283	301	281	355	279	348	209	484	412
ENSMUSG00000028744	chr4	Pqlc2	1.39E+08	1.39E+08	3516	0.228721	3.226664	0.210615	0.312257	0.034531	0	127	104	171	125	194	166	219	269	287	234
ENSMUSG00000023991	chr17	Foxp4	47867133	47868803	4926	0.235858	3.527878	0.210686	0.312328	0.037828	0	145	121	193	158	278	180	316	308	383	280
ENSMUSG00000034951	chr7	Cog7	1.22E+08	1.22E+08	3328	0.191175	4.203326	0.210879	0.312488	0.024904	0	250	235	305	295	350	352	443	456	540	497
ENSMUSG00000036073	chr4	Galt	41755228	41755652	2471	0.220729	4.59906	0.210836	0.312488	0.034768	0	315	357	371	433	372	493	542	763	653	568
ENSMUSG00000038456	chr6	Dennd2a	39462378	39463451	5429	0.277962	3.426246	0.210884	0.312488	0.054436	0	117	96	160	156	301	191	331	218	362	278
ENSMUSG00000048481	chr7	Mypop	18991245	18991354	2175	-0.30673	2.435707	0.21085	0.312488	0.05992	0	114	81	106	95	90	107	131	77	113	122
ENSMUSG00000021427	chr13	Ssr1	37971401	37979806	9306	0.236776	6.157379	0.211231	0.312969	0.042188	0	943	851	1188	906	1667	1450	1910	1209	2526	2004
ENSMUSG00000025083	chr19	Afap1l2	56912361	56913408	5591	-0.31317	2.426748	0.21129	0.313023	0.063948	0	62	64	107	113	157	80	118	73	149	138
ENSMUSG00000034949	chr10	Zfr2	81233155	81233242	7483	0.359959	1.079636	0.211572	0.313407	0.070337	0	31	19	28	23	47	29	57	58	74	50
ENSMUSG00000034157	chr12	Cipc	86947043	86947250	4863	-0.23423	5.431814	0.211743	0.313593	0.040839	0	680	750	875	786	776	690	806	1339	939	833
ENSMUSG00000038463	chr1	Olfml2b	1.71E+08	1.71E+08	3095	0.366305	5.520043	0.211733	0.313593	0.101456	0	627	310	638	497	1400	998	1765	590	1659	1060
ENSMUSG00000067274	chr5	Rplp0	1.16E+08	1.16E+08	1659	0.194661	9.542357	0.211795	0.313637	0.029055	0	9465	10496	13469	10778	14216	15195	18267	19703	20463	19033
ENSMUSG00000091811	chr7	Inafm1	16272014	16273692	1679	0.209097	3.692346	0.212065	0.314003	0.02965	0	154	159	233	203	256	258	294	354	340	355
ENSMUSG00000032579	chr9	Hemk1	1.07E+08	1.07E+08	3646	-0.24053	3.642421	0.212223	0.314204	0.040086	0	162	255	258	205	238	230	263	190	354	296
ENSMUSG00000050914	chr8	Ankrd37	45996902	45997125	1403	-0.39462	1.226882	0.212258	0.314222	0.092192	0	21	57	59	30	48	39	53	49	38	46
ENSMUSG00000020160	chr11	Meis1	18879817	18885651	10532	-0.34992	2.303294	0.212522	0.314546	0.081791	0	47	109	117	86	97	106	66	89	97	131
ENSMUSG00000037369	chrX	Kdm6a	18162575	18163172	8158	-0.38854	3.677992	0.21251	0.314546	0.111183	0	231	190	267	216	307	102	170	536	179	305
ENSMUSG00000031979	chr8	Cog2	1.25E+08	1.25E+08	4778	-0.20341	4.175768	0.21275	0.314849	0.02916	0	247	315	345	332	371	247	442	382	493	416
ENSMUSG00000021139	chr12	Gm20498	81358860	81359344	3241	-0.21491	5.460023	0.212817	0.314902	0.0343	0	700	766	1013	667	783	869	920	964	964	977
ENSMUSG00000027371	chr2	Fahd2a	1.27E+08	1.27E+08	1463	-0.24477	3.996309	0.212831	0.314902	0.042665	0	251	293	324	321	230	296	290	426	339	328
ENSMUSG00000018707	chr12	Dync1h1	1.11E+08	1.11E+08	15658	-0.22523	7.463332	0.213277	0.315528	0.038895	0	2728	2359	3633	3367	3955	2569	3550	5297	4237	3429
ENSMUSG00000022387	chr15	Brd1	88687300	88688480	8138	-0.23199	4.864469	0.213315	0.31555	0.039658	0	436	445	554	581	613	452	556	909	696	510
ENSMUSG00000064080	chr6	Fbln2	91212455	91212900	5876	0.213	6.425033	0.213424	0.315677	0.034466	0	1064	957	1344	1488	1890	1407	2204	2085	2862	2375
ENSMUSG00000064371	chrMT	mt-Tt	15289	15355	67	0.431191	0.798615	0.213522	0.315789	0.10859	0	8	22	38	31	18	30	37	63	49	40
ENSMUSG00000005069	chr6	Pex5	1.24E+08	1.24E+08	3943	0.196197	5.175399	0.213654	0.315951	0.028193	0	533	448	585	565	680	625	912	1003	1002	974
ENSMUSG00000005501	chr1	Usp40	87945119	87948596	11871	-0.20118	4.060234	0.213904	0.316256	0.028225	0	222	261	323	332	354	235	371	396	460	364
ENSMUSG00000020832	chr11	Eral1	78073376	78074174	2268	-0.20417	4.522925	0.213951	0.316256	0.029936	0	348	395	489	422	383	427	468	517	593	475
ENSMUSG00000038388	chr6	Mpp6	50110241	50110464	2843	-0.22083	6.079776	0.213913	0.316256	0.036944	0	1099	1096	1366	1140	1367	1199	1295	1921	1428	1379

ENSMUSG00000067995	chr14	Gtf2f2	75896937	75897653	1467	0.218561	3.387675	0.213952	0.316256	0.031675	0	125	155	176	159	186	226	264	242	273	288
ENSMUSG00000027394	chr2	Ttl	1.29E+08	1.29E+08	5945	-0.22156	3.943442	0.214114	0.316423	0.034528	0	215	251	308	310	293	269	405	248	451	289
ENSMUSG00000031925	chr9	Maml2	13619990	13621675	6138	-0.29851	2.555535	0.214156	0.316423	0.060052	0	90	73	125	114	139	58	125	175	150	110
ENSMUSG00000040594	chr11	Ranbp17	33211795	33213498	8833	0.460683	-0.29458	0.214119	0.316423	0.074701	0	7	8	10	11	14	11	23	23	27	13
ENSMUSG00000072825	chr12	Cep170b	1.13E+08	1.13E+08	6642	-0.31274	4.035245	0.214141	0.316423	0.071813	0	264	202	296	258	525	230	302	593	307	259
ENSMUSG00000045237	chrX	1110012L19Rik	70385877	70386151	1094	-0.2403	3.884323	0.214289	0.316586	0.041038	0	246	285	323	224	234	260	299	380	294	324
ENSMUSG00000033735	chr6	Spr	85133678	85134288	1230	-0.22616	4.917512	0.214582	0.316984	0.037941	0	457	535	652	527	531	583	587	454	865	762
ENSMUSG00000090086	chr5	AI480526	1.23E+08	1.23E+08	4725	0.349823	2.57645	0.214611	0.316993	0.083669	0	108	59	88	75	97	73	130	209	135	226
ENSMUSG00000020484	chr11	Xbp1	5520659	5521200	3248	0.202208	6.13991	0.214786	0.317217	0.031097	0	921	885	1291	916	1534	1375	1703	1808	2080	1854
ENSMUSG00000035198	chr11	Tubg1	1.01E+08	1.01E+08	2266	-0.2082	4.801122	0.214858	0.31729	0.031664	0	385	446	594	521	554	547	540	475	809	645
ENSMUSG00000034110	chr5	Kctd7	1.3E+08	1.3E+08	4368	-0.27848	2.541733	0.214978	0.317433	0.052151	0	114	106	92	92	114	71	132	144	138	127
ENSMUSG00000038150	chr11	Ormdl3	98581256	98582847	2184	0.224088	5.51375	0.21531	0.317891	0.037771	0	656	606	813	685	746	724	961	1044	1465	1635
ENSMUSG00000000938	chr6	Hoxa10	52231197	52232780	3270	-0.22206	4.125696	0.215345	0.317907	0.034909	0	296	258	372	251	394	353	441	324	411	326
ENSMUSG00000092868	chr15	Mir5113	80940039	80940120	82	0.322169	1.490088	0.215694	0.318389	0.056212	0	42	37	45	35	40	68	62	74	77	66
ENSMUSG00000020363	chr11	Gfpt2	49794178	49794243	5591	-0.31328	3.655689	0.215858	0.318563	0.071405	0	202	109	216	226	445	204	349	173	321	264
ENSMUSG00000050106	chr11	Tmc8	1.18E+08	1.18E+08	3056	0.504817	0.157537	0.215844	0.318563	0.131504	0	10	12	4	24	19	18	30	15	40	37
ENSMUSG00000040441	chr10	Slc26a10	1.27E+08	1.27E+08	2215	0.380692	1.677569	0.215959	0.31866	0.094785	0	22	41	50	69	43	52	77	52	111	123
ENSMUSG00000073555	chr18	Gm4951	60212080	60212169	2645	0.568446	0.120522	0.21597	0.31866	0.187285	0	7	7	13	18	23	50	15	11	28	26
ENSMUSG00000040620	chr11	Dhx33	70984091	70987427	10031	-0.21086	3.641209	0.216018	0.318697	0.03025	0	164	202	258	218	278	187	296	309	310	247
ENSMUSG00000030616	chr7	Sytl2	90348699	90348892	6888	0.270496	3.897559	0.216144	0.318849	0.054143	0	165	156	228	181	426	322	494	322	360	375
ENSMUSG00000054204	chr12	Fam150b	30884322	30885039	1509	-0.57159	-0.16108	0.216196	0.318892	0.184204	0	24	13	18	16	8	4	9	28	11	25
ENSMUSG00000070803	chr4	Cited4	1.21E+08	1.21E+08	1249	-0.41281	5.122829	0.216571	0.319411	0.130724	0	337	595	817	588	1081	841	881	168	894	639
ENSMUSG00000009035	chr15	Tmem184b	79360684	79362885	3434	-0.24121	5.327475	0.2167	0.31955	0.04417	0	619	527	714	768	1047	688	991	514	1086	1038
ENSMUSG00000024491	chr18	Rbm27	42275353	42275592	6431	-0.22201	3.996728	0.216711	0.31955	0.035328	0	266	222	307	286	354	215	308	471	410	325
ENSMUSG00000034401	chr4	Spata6	1.12E+08	1.12E+08	5616	0.263005	2.617588	0.216775	0.319575	0.044072	0	59	82	114	91	118	99	140	155	213	174
ENSMUSG00000036634	chr7	Mag	30899176	30899698	4072	0.391611	0.754439	0.216773	0.319575	0.076507	0	26	16	18	30	23	39	42	29	61	39
ENSMUSG00000054426	chr3	A930005H10Rik	1.16E+08	1.16E+08	2385	0.298225	2.417621	0.217329	0.320358	0.05868	0	66	87	83	84	67	127	120	168	142	109
ENSMUSG00000100309	chr1	Gm6644	55444074	55445024	951	-0.28065	2.437197	0.217471	0.320533	0.049412	0	71	73	121	97	135	110	126	96	134	92
ENSMUSG00000067377	chrX	Tspan6	1.34E+08	1.34E+08	2060	0.271146	3.025644	0.217556	0.320624	0.049972	0	111	105	134	116	143	160	285	136	285	171
ENSMUSG00000027082	chr2	Tfpi	84432855	84433184	5463	0.307594	2.512035	0.217724	0.320839	0.064354	0	71	58	109	51	139	98	148	123	227	142
ENSMUSG00000045005	chr1	Fzd5	64730558	64736853	6915	0.343902	1.913431	0.217821	0.320946	0.076613	0	35	34	62	72	71	48	131	104	130	75
ENSMUSG00000024990	chr19	Rbp4	38116620	38116909	1297	0.77238	2.067949	0.218026	0.321215	0.443087	0	30	20	13	62	138	22	49	33	162	360
ENSMUSG00000023243	chr14	Kcnk5	20140058	20142457	3364	-0.42216	0.77871	0.218167	0.321388	0.100968	0	29	15	26	42	46	23	36	50	31	22
ENSMUSG00000028106	chr3	Rprd2	95759873	95766420	8419	-0.23685	4.457645	0.218198	0.321399	0.041774	0	416	309	413	347	494	332	413	681	532	395
ENSMUSG00000028884	chr4	Rpa2	1.33E+08	1.33E+08	2993	0.218853	4.229375	0.218251	0.321444	0.03479	0	271	282	341	219	322	435	416	484	479	501
ENSMUSG00000042670	chr2	Immp1l	1.06E+08	1.06E+08	955	-0.25007	5.121904	0.218431	0.321675	0.047665	0	643	640	798	478	552	782	669	710	712	752
ENSMUSG00000059058	chr1	Tma7-ps	1.72E+08	1.72E+08	195	-0.38883	0.979378	0.218565	0.321804	0.089107	0	28	47	46	32	23	34	28	47	43	38
ENSMUSG00000094685	chr7	Gm5900	1.05E+08	1.05E+08	1266	-0.46832	0.109558	0.218561	0.321804	0.114747	0	14	28	14	28	10	17	21	22	20	17
ENSMUSG00000002870	chr6	Mcm2	88883475	88884110	3370	0.317492	3.629183	0.218627	0.32186	0.074907	0	150	142	218	142	277	250	333	128	541	373
ENSMUSG00000079362	chr5	Gbp6	1.05E+08	1.05E+08	7842	-0.40007	1.84236	0.21876	0.322022	0.106611	0	30	60	63	115	67	73	50	67	64	92
ENSMUSG00000027823	chr3	Gmps	63976106	63976310	8105	0.199304	5.22742	0.219057	0.322425	0.029945	0	445	572	604	606	680	725	807	1041	1122	982
ENSMUSG00000002748	chr5	Baz1b	1.35E+08	1.35E+08	10794	-0.18837	5.803969	0.219087	0.322435	0.027162	0	893	780	1108	991	1222	950	1228	1165	1571	1215
ENSMUSG00000031644	chr8	Nek1	60993195	60993763	7886	-0.24254	2.89047	0.219128	0.32246	0.039982	0	137	101	150	136	138	102	188	165	184	152
ENSMUSG00000033166	chr14	Dis3	99076634	99077465	3722	-0.21354	3.583285	0.219289	0.322664	0.03162	0	185	164	254	217	256	169	255	318	318	240
ENSMUSG00000021236	chr12	Entpd5	84373857	84377380	6039	-0.21167	4.213145	0.219434	0.322842	0.032737	0	303	245	397	348	371	290	411	296	571	461
ENSMUSG00000035305	chr4	Ror1	1E+08	1E+08	5762	-0.3462	1.860866	0.21949	0.322891	0.078129	0	64	40	74	66	92	41	90	109	75	52
ENSMUSG00000003032	chr4	Klf4	55527143	55528300	3049	-0.27764	4.007647	0.219718	0.323135	0.05719	0	257	130	307	307	510	237	366	407	391	297
ENSMUSG00000024325	chr17	Ring1	34020792	34021483	3243	0.203023	4.014517	0.219694	0.323135	0.029133	0	225	211	288	250	274	285	382	490	426	427
ENSMUSG00000041779	chr1	Tram2	20996299	21001635	6661	0.271925	3.750943	0.219726	0.323135	0.054965	0	171	111	189	182	390	214	359	372	430	355
ENSMUSG00000019814	chr10	Ltv1	13178640	13178996	1766	-0.20583	4.648442	0.219851	0.323209	0.031587	0	384	436	509	425	475	445	617	398	697	567
ENSMUSG00000027364	chr2	Usp50	1.27E+08	1.27E+08	3093	0.360537	1.279653	0.219881	0.323209	0.078083	0	22	42	38	31	36	60	61	52	48	78
ENSMUSG00000041375	chr7	Ccdc9	16274042	16274416	5507	0.207361	4.393682	0.219893	0.323209	0.031556	0	293	232	404	289	425	335	493	552	655	618
ENSMUSG00000090247	chr10	Bloc1s1	1.29E+08	1.29E+08	1288	0.209047	6.075428	0.21983	0.323209	0.033923	0	918	1021	1207	973	1072	1580	1534	1750	1773	1693
ENSMUSG00000098176	chr15	Ccdc166	75979872	75982455	2584	0.465583	0.059385	0.219888	0.323209	0.111189	0	7	12	16	24	6	20	32	17	31	27
ENSMUSG00000030105	chr6	Arl8b	1.09E+08	1.09E+08	2928	-0.20673	6.671854	0.219922	0.323217	0.03347	0	1588	1633	2103	1838	1949	1777	1988	2751	2470	2031
ENSMUSG00000072623	chr6	Zfp9	1.18E+08	1.18E+08	3968	-0.25467	3.266659	0.220063	0.323391	0.045127	0	174	114	183	161	244	154	221	261	222	157
ENSMUSG00000028717	chr4	Tal1	1.15E+08	1.15E+08	4379	-0.36777	1.073249	0.220285	0.323676	0.081552	0	28	35	46	53	27	29	32	33	61	54
ENSMUSG00000082456	chr11	Gm11598	1E+08	1E+08	357	0.432382	0.134923	0.220304	0.323676	0.086275	0	12	11	23	9	16	28	21	17	32	34
ENSMUSG00000083179	chr4	Gm12693	94935621	94936103	483	-0.3404	1.411083	0.22034	0.323693	0.068166	0	36	45	64	48	48	56	59	36	50	60
ENSMUSG00000019808	chr10	Adat2	13552894	13553361	1466	-0.32069	1.370437	0.220396	0.323707	0.057611	0	47	40	45	39	61	43	57	37	62	61
ENSMUSG00000031517	chr8	Gpm6a	54954728	54955315	3336	-0.51224	-0.18932	0.220382	0.323707	0.123456	0	9	17	23	14	15	13	6	27	21	9
ENSMUSG00000052364	chrX	B630019K06Rik	8892382	8894964	2583	0.455992	-0.19125	0.22045	0.323752	0.102501	0	11	4	11	9	20	22	20	13	33	16
ENSMUSG00000057421	chrX	Las1l	95935335	95935649	8143	-0.20121	5.2078	0.220562	0.323882	0.030795	0	562	631	786	595	718	630	781	945	836	800
ENSMUSG00000020876	chr11	Snx11	96767555	96769322	4232	0.210653	3.659836	0.220674	0.324013	0.03064	0	185	177	207	186	211	264	311	265	353	374
ENSMUSG00000018677	chr11	Slc25a39	1.02E+08	1.02E+08	2756	0.23075	6.004582	0.220898	0.324307	0.041605	0	786	906	1086	1076	1075	1298	1601	1016	2202	2044
ENSMUSG00000055839	chr17	Tceb2	23824740	23824979	508	0.221855	6.785945	0.221057	0.324506	0.038865	0	1405	1699	2220	1389	1789	2765	2562	2520	3023	2800

ENSMUSG00000018425	chr11	Dhx40	86768846	86770261	4233	-0.24003	4.293283	0.221229	0.324724	0.043224	0	265	314	431	394	369	270	392	629	447	361
ENSMUSG00000031862	chr8	Atp13a1	69791163	69791641	3915	0.197309	4.433969	0.221277	0.32476	0.028519	0	301	265	346	313	464	376	517	506	695	621
ENSMUSG00000054814	chr5	Usp46	73998463	74002137	5533	-0.23085	3.808005	0.221334	0.324767	0.038474	0	204	188	214	268	401	218	257	305	374	354
ENSMUSG00000079555	chr5	Haus3	34153921	34154106	1950	0.26024	2.393283	0.221352	0.324767	0.041887	0	75	66	76	78	96	95	155	127	138	141
ENSMUSG00000099210	chr7	Mir7051	43457497	43457569	73	0.370406	1.803707	0.221349	0.324767	0.089065	0	51	47	44	66	33	72	54	111	96	111
ENSMUSG00000035919	chr9	Bbs9	22475715	22476055	6243	-0.26195	2.580752	0.221381	0.324776	0.04545	0	101	105	120	102	105	93	142	144	153	97
ENSMUSG00000017639	chr11	Rab11fip4	79591212	79591434	7451	0.486497	0.26986	0.2215	0.324909	0.129965	0	17	8	18	11	23	24	23	12	36	55
ENSMUSG00000022803	chr16	Popdc2	38362209	38363147	2360	-0.24039	6.250616	0.221541	0.324909	0.045507	0	1088	1292	1630	1380	1504	1510	2051	965	1921	1659
ENSMUSG00000030534	chr7	Vps33b	80269649	80270079	3343	-0.27277	2.277889	0.221566	0.324909	0.047431	0	91	69	101	65	111	73	116	88	127	104
ENSMUSG00000037949	chr9	Ano10	1.22E+08	1.22E+08	2599	-0.19555	5.361676	0.221547	0.324909	0.029312	0	564	698	784	758	864	667	809	976	991	1033
ENSMUSG00000038780	chr5	Smurf1	1.45E+08	1.45E+08	6336	-0.19505	4.464646	0.22176	0.325159	0.028104	0	340	304	398	396	543	324	501	468	641	495
ENSMUSG00000027559	chr3	Car3	14863512	14863605	2865	-0.52155	10.06642	0.221795	0.325176	0.215315	0	5287	26695	19290	32369	22122	19260	7396	9581	21024	44738
ENSMUSG00000015176	chr19	Nolc1	46075863	46076149	3634	0.193981	4.986413	0.221842	0.32521	0.028457	0	378	447	520	478	660	634	731	714	1087	804
ENSMUSG00000074064	chr8	Mlycd	1.19E+08	1.19E+08	2968	0.343605	5.930552	0.22189	0.325247	0.093321	0	734	966	1136	883	713	1035	1025	3179	1421	1254
ENSMUSG00000034173	chr5	Zbed5	1.3E+08	1.3E+08	2583	0.421039	-0.05579	0.222139	0.325551	0.076418	0	10	8	14	8	22	19	28	18	23	26
ENSMUSG00000036686	chr8	Cc2d1a	84132828	84133257	3710	-0.19184	3.979586	0.222145	0.325551	0.026298	0	238	255	312	258	339	238	318	347	446	381
ENSMUSG00000085783	chr16	Gm9816	62717037	62718450	1414	-0.28508	1.938267	0.222338	0.325765	0.049284	0	58	52	69	79	88	76	77	76	88	74
ENSMUSG00000091905	chr12	Gm6395	64786192	64786439	1491	0.461935	0.070369	0.222329	0.325765	0.109934	0	9	13	8	19	17	17	24	45	23	18
ENSMUSG00000029781	chr6	Fkbp9	56832059	56832427	3314	-0.23699	6.921582	0.2224	0.325821	0.044663	0	2168	1404	2343	1795	3433	2044	3127	2007	3271	2617
ENSMUSG00000049760	chr17	2410015M20Rik	56607452	56607841	755	0.213756	5.60199	0.222551	0.326007	0.035589	0	600	772	927	745	682	1164	1173	1103	1344	1229
ENSMUSG00000035203	chr7	Epn1	5080235	5080477	2807	-0.19981	7.059633	0.222942	0.326546	0.031781	0	1804	2165	2586	2757	2618	2457	2754	2582	3633	3087
ENSMUSG00000022324	chr15	Matn2	34306680	34306908	3583	-0.31229	4.376872	0.22311	0.326757	0.07548	0	445	169	458	254	634	316	614	354	516	370
ENSMUSG00000029669	chr6	Tspan12	21771395	21772936	2626	-0.24004	3.772768	0.223235	0.326873	0.043161	0	201	232	278	305	203	171	305	254	450	313
ENSMUSG00000030351	chr6	Tspan11	1.28E+08	1.28E+08	4380	0.334095	2.65846	0.223236	0.326873	0.082311	0	62	49	87	99	178	137	226	117	202	127
ENSMUSG00000030727	chr7	Rabep2	1.26E+08	1.26E+08	5322	0.954428	4.85598	0.223278	0.326899	0.697528	0	65	275	93	908	292	78	132	133	4019	808
ENSMUSG00000016349	chr2	Eef1a2	1.81E+08	1.81E+08	2084	-0.21204	10.4016	0.223444	0.327108	0.036291	0	17914	21117	24726	27286	31273	28797	24314	28606	34349	28744
ENSMUSG00000089838	chr1	Gm2962	1.71E+08	1.71E+08	336	0.341439	2.990017	0.223473	0.327116	0.086686	0	77	145	185	82	85	228	209	199	167	190
ENSMUSG00000042895	chr15	Abra	41865293	41866352	1762	-0.29012	7.060096	0.223774	0.327523	0.067548	0	1639	3361	1966	2988	1989	2679	2940	2858	3251	2147
ENSMUSG00000021990	chr14	Spata13	60634001	60634183	9102	-0.3006	2.761777	0.223875	0.327601	0.065021	0	71	101	127	200	122	84	157	144	180	147
ENSMUSG00000022685	chr16	Parn	13537964	13538902	2902	0.226769	3.470546	0.223872	0.327601	0.036105	0	149	138	192	164	207	164	252	360	351	276
ENSMUSG00000008140	chr7	Emc10	44489937	44490970	2917	0.199494	5.928676	0.223937	0.327657	0.03134	0	820	769	1095	908	1172	1287	1475	1188	1970	1699
ENSMUSG00000056050	chr1	Mia3	1.83E+08	1.83E+08	4431	-0.23972	6.290158	0.224202	0.328009	0.045838	0	1286	1122	1680	1399	1615	1110	1548	2589	1709	1427
ENSMUSG00000002968	chr7	Med25	44879391	44879514	2297	-0.21201	5.574007	0.224317	0.328112	0.035252	0	652	726	950	991	967	759	862	1365	1123	1039
ENSMUSG00000038611	chr7	Phrf1	1.41E+08	1.41E+08	6765	0.203	4.309438	0.224319	0.328112	0.030431	0	279	243	286	329	401	327	488	582	587	503
ENSMUSG00000034432	chr1	Cops8	90602981	90603627	4448	-0.20084	6.305098	0.224378	0.328163	0.032001	0	1263	1319	1686	1293	1476	1568	1677	1732	1891	1640
ENSMUSG00000029027	chr4	Dffb	1.54E+08	1.54E+08	2351	0.386547	0.660157	0.224558	0.328373	0.076089	0	19	17	21	21	29	23	38	41	32	61
ENSMUSG00000039834	chr2	Zfp335	1.65E+08	1.65E+08	4743	-0.20161	3.775089	0.224569	0.328373	0.029002	0	232	191	245	235	318	228	313	295	393	260
ENSMUSG00000097785	chr19	B230217O12Rik	57323385	57324062	1642	-0.45775	0.053952	0.224734	0.328579	0.099022	0	27	14	12	16	22	21	14	21	16	20
ENSMUSG00000025964	chr1	Adam23	63445891	63446412	17907	-0.38963	1.927692	0.224759	0.328582	0.104865	0	55	27	102	45	140	58	78	63	104	76
ENSMUSG00000042289	chr7	Hsd3b7	1.28E+08	1.28E+08	6154	0.220795	4.91216	0.224901	0.32873	0.037665	0	415	345	494	440	648	415	669	877	987	901
ENSMUSG00000044702	chr7	Palb2	1.22E+08	1.22E+08	5424	0.493043	-0.27221	0.224908	0.32873	0.10821	0	16	9	6	6	12	15	14	14	34	23
ENSMUSG00000032459	chr9	Mrps22	98588730	98588926	3991	-0.21211	4.279212	0.22505	0.328903	0.033659	0	275	340	441	335	340	386	430	332	549	393
ENSMUSG00000019528	chr3	Gyg	20122084	20122864	2344	-0.22692	8.145304	0.225106	0.32895	0.041693	0	4668	4497	5640	5288	5310	5150	5326	8434	5972	5247
ENSMUSG00000019303	chr11	Psmc3ip	1.01E+08	1.01E+08	1818	0.396999	0.735984	0.225286	0.329178	0.084431	0	27	13	24	22	26	29	38	29	79	37
ENSMUSG00000028394	chr4	Pole3	62522649	62524110	2040	0.185013	4.500411	0.225731	0.329793	0.02545	0	318	303	396	333	415	473	536	548	681	561
ENSMUSG00000003378	chr7	Grik5	25009853	25010794	3836	0.304589	2.143422	0.225976	0.330047	0.063786	0	59	39	55	63	112	88	119	131	121	96
ENSMUSG00000028698	chr4	Pik3r3	1.16E+08	1.16E+08	5300	-0.22248	3.468655	0.225947	0.330047	0.03495	0	141	167	230	231	227	198	292	208	275	210
ENSMUSG00000032883	chr1	Acsl3	78657825	78658103	4357	-0.24016	4.842269	0.22596	0.330047	0.045059	0	417	572	500	410	685	516	758	676	669	427
ENSMUSG00000045827	chr13	Serpinb9	33003250	33003344	3494	-0.27394	2.849189	0.226382	0.330604	0.052921	0	98	128	151	138	136	132	161	86	201	176
ENSMUSG00000000253	chr13	Gmpr	45507444	45507743	1871	-0.2209	7.094498	0.22718	0.331735	0.039621	0	2104	2368	2704	2578	2453	2985	2331	3132	3112	2922
ENSMUSG00000021241	chr12	Isca2	84773270	84773371	868	0.217007	4.698994	0.227328	0.331883	0.036218	0	357	434	467	378	334	573	633	588	752	688
ENSMUSG00000099681	chr11	1700052K11Rik	1.05E+08	1.05E+08	3708	-0.27971	2.088015	0.227329	0.331883	0.050371	0	64	60	99	78	83	77	97	62	104	99
ENSMUSG00000019467	chr10	Arhgef25	1.27E+08	1.27E+08	2387	0.242372	3.940626	0.227406	0.331961	0.044699	0	248	146	267	188	332	318	479	270	482	388
ENSMUSG00000042918	chr7	Mamstr	45639977	45640030	4877	0.257981	5.960655	0.227454	0.331996	0.053929	0	613	679	1412	737	1451	1349	1736	1058	1879	1888
ENSMUSG00000031659	chr8	Adcy7	88272403	88272613	6330	0.345867	4.54947	0.227589	0.332157	0.095638	0	363	149	360	296	591	419	858	260	844	721
ENSMUSG00000035868	chr17	3110052M02Rik	21657582	21657611	1383	-0.43938	0.037355	0.227664	0.332232	0.106628	0	22	17	18	17	15	7	34	16	24	14
ENSMUSG00000036438	chr17	Calm2	87433412	87434055	1467	-0.23507	7.74429	0.227851	0.332415	0.045226	0	3578	3500	4141	3654	4445	4038	4831	2629	6022	5553
ENSMUSG00000037773	chr2	Pced1a	1.3E+08	1.3E+08	5072	-0.2448	2.627298	0.227862	0.332415	0.039832	0	108	90	142	99	113	104	131	131	167	121
ENSMUSG00000094910	chr12	D430019H16Rik	1.05E+08	1.05E+08	5786	0.528356	0.488852	0.227823	0.332415	0.180504	0	11	6	11	24	39	17	65	26	54	20
ENSMUSG00000045948	chr7	Mrps12	28739641	28739979	1040	0.205365	4.948508	0.227919	0.332464	0.032898	0	371	490	604	455	461	701	758	751	858	751
ENSMUSG00000042105	chr7	Inpp5f	1.29E+08	1.29E+08	8323	0.307673	2.224788	0.227956	0.332484	0.061324	0	65	62	59	72	81	52	122	128	153	149
ENSMUSG00000035351	chr10	Nup37	88146992	88147072	1362	0.262822	2.31094	0.228143	0.33272	0.042849	0	70	76	77	69	73	98	117	118	150	137
ENSMUSG00000029097	chr5	Trmt44	35557206	35558055	4151	-0.34374	0.977684	0.228333	0.332927	0.067058	0	30	29	41	26	52	22	34	40	46	54
ENSMUSG00000031255	chrX	Sytl4	1.34E+08	1.34E+08	5125	0.375225	0.378552	0.22833	0.332927	0.069936	0	9	14	23	18	24	25	35	21	39	38
ENSMUSG00000025025	chr19	Mxi1	53310506	53310973	5619	-0.26861	5.103816	0.228423	0.333024	0.057828	0	596	490	637	711	693	479	570	1254	718	611
ENSMUSG00000042106	chr9	Fam212a	1.08E+08	1.08E+08	1156	0.343225	1.643847	0.228838	0.333593	0.074098	0	38	44	35	49	55	64	56	54	114	110

ENSMUSG00000084786	chr9	Ubl5	20642878	20644893	3468	0.215355	5.945309	0.229032	0.333842	0.037453	0	840	946	1149	873	916	1530	1516	1332	1628	1602
ENSMUSG00000019853	chr10	Hebp2	18540123	18541332	1910	0.402456	0.707438	0.229086	0.33386	0.096078	0	23	16	21	19	31	30	55	19	41	58
ENSMUSG00000028639	chr4	Ybx1	1.19E+08	1.19E+08	2531	-0.18882	8.504779	0.229093	0.33386	0.029389	0	5232	5936	7221	7048	6863	6448	7425	7844	9681	8317
ENSMUSG00000032913	chr3	Lrig2	1.04E+08	1.04E+08	7111	-0.22145	3.305015	0.230004	0.335151	0.034837	0	150	124	181	187	251	151	201	198	263	253
ENSMUSG00000029076	chr4	Sdf4	1.56E+08	1.56E+08	6115	0.19496	6.631684	0.230055	0.335191	0.031017	0	1525	1265	1724	1394	1811	1826	2308	2801	2869	2591
ENSMUSG00000030780	chr7	BC017158	1.28E+08	1.28E+08	5526	0.301915	2.435353	0.23043	0.335701	0.065612	0	66	44	89	73	135	77	138	114	199	172
ENSMUSG00000073888	chr4	Ccl27a	41769467	41769654	2377	0.286429	2.342952	0.230483	0.335745	0.055478	0	59	89	87	72	62	121	109	129	153	121
ENSMUSG00000021144	chr12	Mta1	1.13E+08	1.13E+08	3104	0.195245	4.771614	0.230682	0.335963	0.029815	0	346	324	456	436	585	466	657	799	797	698
ENSMUSG00000077450	chr17	Rab11b	33742484	33747813	6109	0.215983	6.351282	0.230659	0.335963	0.038178	0	1014	1155	1385	1293	1472	1519	1793	2850	2281	1794
ENSMUSG00000034724	chr5	Cnot6l	96070333	96077392	10313	-0.20199	4.759816	0.230967	0.336344	0.032108	0	363	384	559	553	580	358	655	650	781	540
ENSMUSG00000026648	chr2	Dclre1c	3424131	3424326	9316	0.334521	1.582331	0.231218	0.336674	0.074496	0	40	24	43	46	63	45	82	54	90	110
ENSMUSG00000071001	chr4	Hrct1	43727188	43728639	1452	0.455544	1.003017	0.231252	0.336687	0.130929	0	30	26	20	35	19	28	28	87	48	66
ENSMUSG00000060639	chr13	Hist1h4i	22040636	22041362	727	-0.25636	5.239942	0.231623	0.337192	0.05305	0	530	633	965	533	802	964	752	675	694	793
ENSMUSG00000031539	chr8	Ap3m2	22787354	22789453	3467	0.254569	3.224325	0.231788	0.337396	0.048162	0	117	119	179	116	180	205	224	152	270	321
ENSMUSG00000024902	chr19	Mrpl11	4962306	4962515	2882	0.219601	5.423752	0.231943	0.337586	0.039015	0	527	740	775	640	587	1023	1023	1064	1098	1099
ENSMUSG00000031072	chr7	Oraov1	1.45E+08	1.45E+08	4400	-0.20586	3.681522	0.232079	0.337749	0.030911	0	186	206	283	196	277	230	323	228	315	285
ENSMUSG00000068250	chr6	Amn1	1.49E+08	1.49E+08	4300	0.319804	1.794329	0.232135	0.337796	0.065577	0	58	42	64	42	41	68	108	89	79	89
ENSMUSG00000097885	chr3	5031434O11Rik	51560035	51560208	3731	0.563568	0.553264	0.232222	0.337886	0.197946	0	27	20	17	13	11	14	24	87	28	37
ENSMUSG00000020630	chr12	Rnaseh1	28649602	28649816	1457	0.231297	2.723147	0.232462	0.338199	0.036016	0	81	98	104	99	117	136	168	156	199	161
ENSMUSG00000022807	chr16	Osbpl11	33185071	33186000	4520	-0.20945	4.319166	0.232502	0.3382	0.034431	0	301	296	396	389	405	236	380	504	588	492
ENSMUSG00000032375	chr9	Aph1b	66775202	66779380	5163	-0.27769	2.35137	0.232511	0.3382	0.054053	0	82	64	107	76	138	61	102	137	125	111
ENSMUSG00000021493	chr13	Pdlim7	55495795	55496020	4849	-0.20828	8.653874	0.232568	0.338247	0.036304	0	5792	6619	8135	6628	9120	8940	7856	7658	9185	9270
ENSMUSG00000031196	chrX	F8	75172715	75173010	9905	-0.42686	0.186533	0.232966	0.33879	0.082599	0	12	19	35	14	22	20	22	15	23	24
ENSMUSG00000082274	chr2	Gm14026	1.29E+08	1.29E+08	1789	-0.47538	-0.2177	0.233082	0.338923	0.111888	0	18	7	17	19	14	9	22	20	19	6
ENSMUSG00000028419	chr4	Chmp5	40948407	40948676	1519	0.1951	4.976835	0.233185	0.339038	0.030141	0	416	471	623	448	481	608	837	677	990	825
ENSMUSG00000029061	chr4	Mmp23	1.56E+08	1.56E+08	2340	0.397721	2.926292	0.233216	0.339047	0.12511	0	109	56	114	63	215	190	274	73	260	196
ENSMUSG00000033983	chr11	Coil	88970252	88970272	3520	-0.25994	2.179433	0.233316	0.339156	0.045029	0	68	75	75	77	111	78	88	82	121	105
ENSMUSG00000028677	chr4	Rnf220	1.17E+08	1.17E+08	7229	0.18506	5.616594	0.233505	0.339396	0.027752	0	678	676	841	726	914	947	1154	1412	1346	1220
ENSMUSG00000037957	chr12	Wdr20	1.11E+08	1.11E+08	5593	-0.21667	3.373639	0.233605	0.339505	0.034238	0	153	157	200	196	221	153	211	290	256	206
ENSMUSG00000038332	chr10	Sesn1	41810574	41811300	3327	0.40084	5.314745	0.233635	0.339513	0.133233	0	480	430	542	598	846	520	705	2579	717	728
ENSMUSG00000031951	chr8	Tmem231	1.12E+08	1.12E+08	2887	-0.36717	1.002525	0.233734	0.339587	0.08484	0	33	22	43	34	51	16	61	41	46	35
ENSMUSG00000035725	chrX	Prkx	77761411	77763891	5807	0.216557	3.371772	0.233734	0.339587	0.033642	0	127	151	164	154	198	188	274	199	363	280
ENSMUSG00000040720	chr4	1110037F02Rik	11485958	11486105	7138	-0.18808	4.332889	0.233778	0.339614	0.027252	0	323	277	401	360	435	287	449	490	527	460
ENSMUSG00000019933	chr10	2310015B20Rik	70204664	70204759	1180	-0.25665	5.178631	0.2339	0.339756	0.053795	0	635	645	761	588	623	842	843	759	528	743
ENSMUSG00000027864	chr3	Ptgfrn	1.01E+08	1.01E+08	5902	-0.30022	5.85828	0.233978	0.339833	0.074926	0	1109	521	1116	889	1842	911	1868	784	1463	1079
ENSMUSG00000020534	chr11	Shmt1	60788104	60789316	3883	-0.2282	3.674455	0.234053	0.339872	0.038943	0	169	213	259	201	313	281	209	247	351	265
ENSMUSG00000058351	chr14	Smim4	31088869	31089026	592	0.312669	2.931087	0.234046	0.339872	0.073955	0	91	135	124	134	63	192	159	214	206	188
ENSMUSG00000089764	chr17	Gm16580	26269336	26270379	1044	0.38139	0.247163	0.23414	0.339963	0.058457	0	12	16	17	18	15	24	26	28	37	28
ENSMUSG00000022313	chr15	Utp23	51877429	51877710	2992	0.268439	2.435572	0.234389	0.340288	0.047912	0	81	85	90	70	70	112	135	121	176	135
ENSMUSG00000034930	chr6	Rtkn	83135463	83135585	3943	-0.20297	4.176218	0.234457	0.340351	0.031444	0	254	260	405	272	443	326	433	322	452	420
ENSMUSG00000036197	chr15	Gxylt1	93239742	93245129	6704	0.211858	3.407389	0.234557	0.34046	0.032778	0	123	129	172	173	227	183	291	228	343	288
ENSMUSG00000100599	chr15	1700120C14Rik	99251788	99252001	1731	0.248129	4.412581	0.234621	0.340518	0.049495	0	314	303	396	303	287	633	457	449	502	567
ENSMUSG00000041429	chr17	Nthl1	24632682	24632854	1080	0.321778	1.231077	0.234706	0.340606	0.06133	0	28	22	49	33	36	50	57	61	53	67
ENSMUSG00000020190	chr10	Mknk2	80665332	80667332	3065	0.301681	8.071215	0.234907	0.340862	0.076827	0	3124	3383	4108	4867	4730	4402	4828	13132	5760	6364
ENSMUSG00000029389	chr5	Ddx55	1.25E+08	1.25E+08	5121	0.269792	2.26813	0.234993	0.340951	0.050542	0	45	65	98	69	84	89	132	95	143	146
ENSMUSG00000029911	chr6	Ssbp1	40471352	40471459	3319	0.206849	4.789603	0.235133	0.341117	0.034189	0	368	417	513	440	383	598	620	791	739	674
ENSMUSG00000102644	chr5	THAP6	91962389	91962978	4119	-0.28446	2.179732	0.235324	0.341359	0.056076	0	77	78	86	93	69	80	116	77	120	76
ENSMUSG00000086965	chr16	Gm16314	18498901	18498951	865	-0.43231	-0.13937	0.235412	0.341451	0.099299	0	20	10	19	8	22	7	23	16	24	13
ENSMUSG00000020893	chr11	Per1	69095217	69095303	5631	0.27375	4.883099	0.235532	0.341554	0.06167	0	495	306	597	404	417	567	554	1174	654	774
ENSMUSG00000025050	chr19	Pcgf6	47033619	47034685	2098	-0.27297	2.183855	0.235526	0.341554	0.051049	0	72	86	98	62	88	74	114	78	120	88
ENSMUSG00000024571	chr18	Gm16286	80206765	80206901	3075	0.196244	5.973508	0.235758	0.341846	0.031964	0	772	905	1105	914	1217	1312	1339	1801	1722	1613
ENSMUSG00000029559	chr5	2210016L21Rik	1.15E+08	1.15E+08	3303	0.198705	4.168511	0.236	0.34216	0.030524	0	198	294	313	273	313	390	460	415	516	442
ENSMUSG00000021464	chr13	Ror2	53109312	53111668	4242	0.426656	1.464732	0.236311	0.34254	0.130575	0	41	9	59	27	58	38	99	65	101	59
ENSMUSG00000096549	chr17	Prickle4	47688517	47688839	1962	-0.3662	0.025675	0.236304	0.34254	0.059081	0	16	18	19	17	17	14	20	18	22	21
ENSMUSG00000035086	chr11	Becn1	1.01E+08	1.01E+08	7065	-0.18223	5.76212	0.236396	0.342627	0.027321	0	827	844	1072	958	1122	1011	1211	1080	1353	1257
ENSMUSG00000069208	chr13	Zfp825	74480517	74481150	822	-0.29744	2.091365	0.236421	0.342627	0.060983	0	72	77	83	70	80	66	90	126	89	65
ENSMUSG00000033849	chr1	B3galt2	1.44E+08	1.44E+08	9288	0.404119	2.895842	0.236541	0.342766	0.13047	0	78	52	55	148	209	84	190	140	292	303
ENSMUSG00000022750	chr16	Klhl22	17759618	17759694	5745	0.214902	4.884562	0.236641	0.342874	0.037537	0	416	359	503	454	555	487	694	1044	745	730
ENSMUSG00000034216	chr2	Vps18	1.19E+08	1.19E+08	4786	0.213499	4.0896	0.236735	0.342975	0.035469	0	202	213	311	279	317	255	349	418	602	544
ENSMUSG00000049086	chr2	Bmyc	25706739	25707721	983	0.253991	2.384623	0.237088	0.34345	0.04495	0	57	61	95	74	109	88	163	126	152	126
ENSMUSG00000025141	chr11	Myadml2	1.21E+08	1.21E+08	992	-0.20428	6.341471	0.237319	0.343749	0.035001	0	1256	1164	1870	1341	1671	1712	1712	1826	1911	1513
ENSMUSG00000036611	chr9	Eepd1	25481547	25481896	2935	-0.30915	5.805177	0.237362	0.343775	0.080656	0	1032	810	865	1197	1237	854	792	2200	985	929
ENSMUSG00000024871	chr19	Doc2g	4003321	4003401	3027	0.510759	-0.16022	0.237636	0.344111	0.137836	0	9	12	16	15	1	12	19	25	24	29
ENSMUSG00000067818	chr2	Myl9	1.57E+08	1.57E+08	1162	0.313672	6.243009	0.237644	0.344111	0.08357	0	634	882	1293	1208	1781	1935	2013	759	2804	2292
ENSMUSG00000008373	chr7	Prpf31	3629985	3630056	5439	0.208605	4.563031	0.237778	0.34427	0.034946	0	270	347	429	346	444	466	519	439	833	723
ENSMUSG00000020994	chr12	Pnn	59066919	59067115	3469	0.205927	4.711975	0.237825	0.344302	0.034302	0	344	318	479	373	535	408	598	861	760	671

ENSMUSG00000000876	chr2	Pxmp4	1.55E+08	1.55E+08	3114	-0.1962	4.167448	0.237994	0.34451	0.030127	0	265	292	352	308	383	276	314	428	477	467
ENSMUSG00000008892	chr8	Vdac3	22577075	22577602	1423	-0.21552	8.231727	0.238081	0.344558	0.039765	0	4813	5355	6307	5332	4912	6346	5912	7083	6613	5996
ENSMUSG00000024038	chr17	Ndufv3	31520115	31520261	2490	0.221239	6.690809	0.238068	0.344558	0.04154	0	1149	1608	1645	1925	1600	2506	2208	2094	3271	2826
ENSMUSG00000031616	chr8	Ednra	77663031	77665116	5476	0.26551	2.689526	0.238126	0.344558	0.051135	0	86	66	107	103	124	87	224	152	198	162
ENSMUSG00000038225	chr8	Primpol	46575579	46576721	6309	0.304308	1.643739	0.23812	0.344558	0.061782	0	39	33	55	48	52	75	70	50	96	97
ENSMUSG00000101841	chr11	Gm11993	9149778	9150597	820	-0.45513	-0.19242	0.238191	0.344615	0.111921	0	17	8	12	21	18	9	18	19	27	6
ENSMUSG00000073838	chr7	Tufm	1.26E+08	1.26E+08	1776	0.222046	6.9102	0.238303	0.344742	0.041957	0	1285	2012	1912	2188	1807	2868	2845	2516	3835	2982
ENSMUSG00000035279	chr7	Ssc5d	4925844	4925979	4284	-0.36711	6.0429	0.238366	0.344796	0.114467	0	1356	445	1265	763	2614	1046	2036	1004	1708	966
ENSMUSG00000000567	chr11	Sox9	1.13E+08	1.13E+08	4135	0.322294	2.007007	0.238509	0.344962	0.075275	0	51	43	56	40	106	78	114	78	164	82
ENSMUSG00000001946	chr9	Esam	37528078	37528290	2867	0.2356	5.00065	0.238531	0.344962	0.04579	0	331	494	535	651	423	553	689	702	1161	998
ENSMUSG00000023353	chr5	Agap3	24452177	24452534	3207	0.195526	5.015934	0.238562	0.344972	0.031093	0	426	444	546	514	587	512	765	1019	937	826
ENSMUSG00000046442	chr11	Ppm1e	87226906	87231928	6702	-0.3891	0.447566	0.238702	0.345109	0.079004	0	19	17	34	27	25	21	33	18	20	36
ENSMUSG00000080896	chrX	Gm14567	38969817	38969990	174	-0.43429	0.023669	0.238707	0.345109	0.091042	0	18	22	16	16	16	18	27	14	13	19
ENSMUSG00000040715	chr4	Rsc1a1	1.42E+08	1.42E+08	1749	-0.38129	4.422573	0.238839	0.345263	0.121919	0	376	237	430	441	567	190	268	1003	379	340
ENSMUSG00000044477	chr17	Zfand3	30005087	30005308	2616	-0.21282	6.399548	0.238888	0.345263	0.038451	0	1340	1371	1659	1602	1561	1350	1624	2515	1913	1707
ENSMUSG00000083364	chrX	Llph-ps2	13218210	13218602	393	0.401726	0.067788	0.238869	0.345263	0.076676	0	14	8	21	12	13	21	23	32	21	27
ENSMUSG00000029471	chr5	Camkk2	1.23E+08	1.23E+08	4843	0.222345	3.805906	0.239372	0.345926	0.038653	0	200	157	221	173	335	224	412	298	467	374
ENSMUSG00000042211	chr18	Fbxo38	62504069	62504880	4388	-0.20956	4.748375	0.239406	0.345939	0.035983	0	409	407	533	488	574	357	593	810	625	537
ENSMUSG00000016262	chr1	Sertad4	1.93E+08	1.93E+08	3850	0.327421	3.308789	0.239604	0.34619	0.086942	0	144	63	144	130	266	190	403	172	322	197
ENSMUSG00000005687	chr3	Bcas2	1.03E+08	1.03E+08	4390	0.190894	5.004176	0.239798	0.346433	0.029721	0	472	472	527	477	530	725	797	681	935	824
ENSMUSG00000032215	chr9	Rsl24d1	73113426	73113480	1716	0.195251	4.998589	0.239998	0.34665	0.031191	0	399	535	559	470	502	693	829	766	917	751
ENSMUSG00000055652	chr7	Klhl25	75848338	75848484	3385	-0.26705	2.540214	0.239981	0.34665	0.050905	0	78	78	140	93	144	93	115	87	166	153
ENSMUSG00000021266	chr12	Wars	1.09E+08	1.09E+08	3447	-0.18874	5.153676	0.240365	0.347144	0.029336	0	507	512	730	717	713	657	767	629	1004	832
ENSMUSG00000022701	chr16	2610015P09Rik	43889800	43890038	4230	0.344373	1.208016	0.240642	0.347507	0.069668	0	36	34	29	25	36	34	60	73	57	65
ENSMUSG00000061882	chr5	Ccdc62	1.24E+08	1.24E+08	4306	0.269771	2.06916	0.240891	0.347831	0.049076	0	59	58	71	51	70	101	97	89	120	111
ENSMUSG00000014606	chr11	Slc25a11	70644196	70644921	2120	-0.21841	8.163453	0.241142	0.348157	0.041379	0	3897	5569	5511	5967	4522	5831	5882	6103	7402	5496
ENSMUSG00000026639	chr1	Lamb3	1.93E+08	1.93E+08	6612	-0.37243	1.067347	0.241421	0.34852	0.091652	0	50	33	23	39	41	32	51	25	58	41
ENSMUSG00000037461	chr1	Ints7	1.92E+08	1.92E+08	7319	0.253783	3.514482	0.241444	0.34852	0.051204	0	132	134	212	167	231	210	305	157	407	382
ENSMUSG00000066270	chr9	Gm10157	1.19E+08	1.19E+08	343	0.335456	1.421837	0.24163	0.348752	0.075866	0	35	32	52	35	36	72	57	86	56	56
ENSMUSG00000002847	chr16	Pla1a	38396119	38396535	1972	-0.27432	2.357606	0.241926	0.349144	0.054651	0	90	56	123	94	102	71	117	87	120	142
ENSMUSG00000020423	chr1	Btg2	1.34E+08	1.34E+08	2743	0.284634	5.089635	0.242189	0.349486	0.069392	0	304	312	405	692	928	702	989	994	1066	607
ENSMUSG00000021578	chr13	Ccdc127	74350309	74350408	9559	-0.1858	5.27592	0.242307	0.349621	0.028781	0	615	594	797	653	784	683	815	989	957	772
ENSMUSG00000042116	chr4	Vwa1	1.56E+08	1.56E+08	3623	-0.19368	4.291557	0.242375	0.349682	0.030045	0	317	273	366	396	387	328	432	497	514	359
ENSMUSG00000004096	chr9	Cwc15	14500617	14500781	1111	0.197864	5.97142	0.242627	0.349943	0.033484	0	825	896	1069	1007	1072	1447	1519	1673	1489	1572
ENSMUSG00000029307	chr5	Dmp1	1.04E+08	1.04E+08	2760	-0.48406	0.251562	0.242604	0.349943	0.14974	0	25	9	18	12	46	12	35	11	29	22
ENSMUSG00000029415	chr5	Sdad1	92284010	92286870	5020	-0.22132	4.232905	0.242632	0.349943	0.039987	0	275	314	365	331	402	265	344	599	414	401
ENSMUSG00000017969	chr2	Ptgis	1.67E+08	1.67E+08	2567	-0.40411	3.473006	0.24288	0.350228	0.136886	0	285	86	222	90	388	124	349	257	258	135
ENSMUSG00000031174	chrX	Rpgr	10073621	10073828	7247	-0.32846	1.382637	0.242863	0.350228	0.071423	0	44	29	63	32	71	32	54	65	67	46
ENSMUSG00000007476	chr2	Lrrc8a	30237715	30237805	4308	-0.19481	4.13605	0.242953	0.350297	0.03041	0	284	265	289	365	352	268	372	441	463	375
ENSMUSG00000006215	chr4	Zbtb17	1.41E+08	1.41E+08	3877	-0.20512	4.482862	0.243012	0.350345	0.034196	0	276	349	418	486	478	408	412	564	514	504
ENSMUSG00000018160	chr11	Med1	98152154	98152963	8753	-0.1833	4.604235	0.243079	0.350405	0.02723	0	345	340	526	480	478	377	558	577	624	531
ENSMUSG00000056666	chr6	Retsat	72598475	72598796	3537	0.220457	5.05176	0.243186	0.350524	0.040894	0	416	448	590	542	562	545	567	1088	1032	969
ENSMUSG00000021750	chr14	Fam107a	8296274	8298797	3870	-0.46474	0.892264	0.243381	0.350768	0.155342	0	26	37	58	36	13	21	20	61	45	29
ENSMUSG00000038119	chr9	Cdon	35421128	35421183	7715	-0.30371	5.159551	0.243421	0.350789	0.079079	0	560	300	652	534	1388	531	1067	720	813	609
ENSMUSG00000026930	chr2	Gpsm1	26315515	26315720	5383	0.275078	2.664593	0.243462	0.350812	0.057819	0	95	60	104	75	144	115	191	198	167	126
ENSMUSG00000041623	chr11	D11Wsu47e	1.14E+08	1.14E+08	2382	0.283113	2.162238	0.243737	0.351171	0.058807	0	48	60	84	54	87	116	118	76	142	104
ENSMUSG00000031949	chr8	Adat1	1.12E+08	1.12E+08	4399	-0.29817	1.471287	0.243804	0.351231	0.055803	0	35	47	50	59	57	48	59	63	68	43
ENSMUSG00000029033	chr4	Acap3	1.56E+08	1.56E+08	5367	0.195335	3.761686	0.243974	0.35144	0.029409	0	202	144	233	226	249	256	319	341	447	329
ENSMUSG00000032643	chr4	Fhl3	1.25E+08	1.25E+08	1683	0.331759	6.6719	0.244026	0.351478	0.096067	0	983	1801	1977	1865	774	1752	1985	4348	2801	2400
ENSMUSG00000018559	chr11	Ctdnep1	69981156	69981585	2182	0.188292	7.075024	0.244147	0.351615	0.030905	0	1771	1859	2268	2232	2404	3033	3058	2987	4136	3496
ENSMUSG00000096210	chr15	H1f0	79028212	79030498	2287	0.193122	7.138948	0.244399	0.351942	0.032576	0	1774	1887	2742	2244	2387	2557	3250	4269	4030	3502
ENSMUSG00000040415	chr10	Dtx3	1.27E+08	1.27E+08	2572	0.189147	4.738408	0.244476	0.352016	0.029352	0	405	330	482	388	474	445	748	595	783	770
ENSMUSG00000025193	chr19	Cutc	43752996	43753220	1422	-0.20517	3.893213	0.244647	0.352152	0.0333	0	245	239	282	236	319	266	276	410	340	301
ENSMUSG00000025371	chr11	Chmp6	1.2E+08	1.2E+08	2432	0.187918	4.784617	0.244635	0.352152	0.029051	0	374	423	506	392	440	551	621	729	791	722
ENSMUSG00000045973	chr4	Slc25a51	45395923	45400179	5510	-0.18348	6.250535	0.244634	0.352152	0.029086	0	1173	1190	1495	1392	1508	1271	1522	1758	1907	1878
ENSMUSG00000071359	chr10	Tbpl1	22703879	22705895	3271	0.18715	3.970504	0.244685	0.352171	0.027382	0	181	219	303	228	297	277	417	347	506	411
ENSMUSG00000092260	chr8	Zfp963	69741639	69743610	2299	0.287658	2.226761	0.244723	0.352189	0.059762	0	66	57	69	62	91	86	100	174	109	115
ENSMUSG00000032946	chr19	Rasgrp2	6399340	6399517	12384	-0.2697	3.038103	0.244847	0.35233	0.058245	0	156	146	164	154	108	111	157	207	165	223
ENSMUSG00000057967	chr11	Fgf18	33117430	33118031	1187	-0.47022	0.986567	0.244949	0.35244	0.161616	0	35	11	38	35	71	18	71	40	37	21
ENSMUSG00000041353	chrX	Tmem29	1.5E+08	1.5E+08	7621	0.312104	1.567543	0.245304	0.352914	0.063948	0	41	37	46	29	61	54	66	57	96	100
ENSMUSG00000069844	chr11	Sco1	67052670	67052916	3925	-0.21033	3.276442	0.245334	0.352921	0.033285	0	168	153	199	162	174	186	212	195	255	189
ENSMUSG00000002833	chr17	Hdgfrp2	56079657	56079826	2251	0.181198	4.868882	0.2455	0.353086	0.027261	0	366	394	557	425	557	515	720	813	857	731
ENSMUSG00000031557	chr8	Plekha2	25039144	25043038	5397	0.226861	4.622729	0.245497	0.353086	0.043507	0	338	246	520	344	471	494	675	385	857	711
ENSMUSG00000041035	chr19	Dpcd	45560615	45560707	1995	0.21346	3.404039	0.245811	0.353497	0.035128	0	139	139	195	172	166	248	226	219	321	294
ENSMUSG00000002602	chr7	Axl	25757273	25759013	5033	0.24887	6.317089	0.246226	0.35391	0.054485	0	1185	624	1224	1032	2186	1491	2350	1894	2510	1930
ENSMUSG00000020265	chr10	Sumo3	77606097	77606341	3826	0.180188	5.97998	0.246217	0.35391	0.028024	0	809	918	1148	953	1117	1249	1499	1550	1886	1652

ENSMUSG00000034042	chr4	Gpbp1l1	1.17E+08	1.17E+08	4158	-0.18365	4.437081	0.246221	0.35391	0.027601	0	327	322	413	390	475	313	435	518	568	549
ENSMUSG00000044330	chr3	Gm9790	85915783	85916070	288	0.284059	3.056451	0.246178	0.35391	0.064075	0	96	161	136	110	105	240	192	181	211	204
ENSMUSG00000097320	chr7	C630016N16Rik	30729579	30729854	1416	0.320295	1.15514	0.246208	0.35391	0.066622	0	26	25	28	31	49	46	42	69	54	62
ENSMUSG00000020963	chr12	Tshr	91400994	91401254	4873	0.719235	0.830512	0.246336	0.354027	0.411543	0	15	6	11	28	48	7	35	10	53	144
ENSMUSG00000049184	chr8	Purg	33386325	33387531	2119	-0.27418	1.748158	0.246358	0.354027	0.049656	0	48	54	70	55	74	51	85	61	70	79
ENSMUSG00000040250	chr6	Asun	1.47E+08	1.47E+08	3968	-0.19511	3.843885	0.246477	0.35416	0.029743	0	172	236	281	246	354	242	328	291	366	332
ENSMUSG00000021079	chr12	Timm9	71123173	71123686	1018	0.224649	4.076078	0.246562	0.35421	0.041656	0	194	289	315	229	258	440	429	351	428	423
ENSMUSG00000092176	chr17	Gm20460	34614484	34614778	1572	-0.17671	4.57009	0.246561	0.35421	0.025565	0	378	339	473	395	526	382	495	538	662	539
ENSMUSG00000098462	chr19	Gm27694	5799000	5799085	86	-0.38608	2.64623	0.246642	0.354288	0.124935	0	191	75	112	66	130	52	102	129	138	219
ENSMUSG00000016940	chr11	Kctd2	1.15E+08	1.15E+08	3009	0.193638	4.118009	0.24673	0.354377	0.030216	0	230	240	274	254	353	349	379	390	497	537
ENSMUSG00000031391	chrX	L1cam	73853778	73855266	7347	0.404651	1.093666	0.246994	0.354719	0.113133	0	23	29	27	31	35	38	59	17	86	75
ENSMUSG00000051238	chr9	Swsap1	21955753	21956004	1846	0.27898	1.900952	0.247036	0.354743	0.053918	0	40	57	72	49	56	71	117	79	109	90
ENSMUSG00000066637	chr12	Ttc32	9029997	9030196	1000	-0.25792	2.995808	0.247079	0.354768	0.051133	0	106	145	169	139	160	183	166	133	150	188
ENSMUSG00000017344	chr11	Vtn	78499091	78499622	2030	0.208265	4.68746	0.247203	0.354861	0.036909	0	305	289	459	457	507	632	662	459	777	659
ENSMUSG00000040767	chr11	Snrnp25	32205415	32205663	1041	0.261146	2.70571	0.247221	0.354861	0.052009	0	72	116	121	78	98	158	152	142	188	170
ENSMUSG00000061360	chr15	Phf5a	81865319	81865892	937	0.203119	5.161354	0.247178	0.354861	0.035325	0	477	558	648	462	620	884	928	713	1026	861
ENSMUSG00000051864	chr15	Tbc1d22a	86214459	86214636	3229	0.178848	4.545351	0.24744	0.355139	0.026111	0	276	342	411	380	419	413	581	579	734	603
ENSMUSG00000018340	chr11	Anxa6	54979108	54979521	2930	0.185073	8.234823	0.247711	0.355455	0.030537	0	3686	4302	5272	4706	5704	6301	7963	6209	9465	7573
ENSMUSG00000053626	chr8	Tll1	64014770	64016180	4928	-0.3579	1.065757	0.247712	0.355455	0.082232	0	20	36	40	26	71	30	44	35	54	44
ENSMUSG00000028334	chr4	Nans	46489248	46489490	4581	0.234569	4.439384	0.247778	0.355513	0.046658	0	283	285	377	271	458	441	505	317	761	731
ENSMUSG00000024006	chr17	Stk38	28970885	28972676	8489	0.188421	5.319635	0.248321	0.356232	0.030454	0	510	566	718	613	712	781	1005	763	1244	1192
ENSMUSG00000033737	chrX	Fndc3c1	1.06E+08	1.06E+08	6315	0.297468	1.622734	0.248331	0.356232	0.06241	0	29	29	46	56	67	55	98	75	85	71
ENSMUSG00000011658	chr7	Fuz	44896079	44896362	5003	-0.19684	4.20322	0.248464	0.356386	0.031512	0	294	300	379	308	351	397	371	348	436	418
ENSMUSG00000036585	chr18	Fgf1	38838673	38842121	4648	-0.24267	4.363264	0.248728	0.356729	0.050635	0	401	307	355	454	308	276	477	577	568	324
ENSMUSG00000070699	chr7	Sars2	28741968	28742282	1910	-0.20651	3.96018	0.248786	0.356775	0.034914	0	205	292	281	296	307	283	348	243	454	360
ENSMUSG00000053754	chr14	Chd8	52198151	52199152	12599	-0.18578	5.128517	0.248976	0.356984	0.029477	0	548	457	678	610	846	524	782	878	878	776
ENSMUSG00000061461	chr5	Smim20	53267106	53267358	6494	-0.23271	5.885473	0.248984	0.356984	0.047726	0	942	1107	1175	1031	1016	1419	1342	877	1410	1166
ENSMUSG00000021548	chr13	Ccnh	85189408	85189652	3105	-0.20085	4.172425	0.249111	0.35713	0.033209	0	297	290	395	300	315	355	415	295	467	411
ENSMUSG00000030664	chr7	Sox6os	1.16E+08	1.16E+08	420	-0.33551	1.268492	0.249584	0.357771	0.072546	0	32	46	40	41	58	45	36	59	39	57
ENSMUSG00000024997	chr19	Prdx3	60864051	60864719	1478	-0.2039	7.468306	0.249873	0.358148	0.0373	0	2539	3447	3589	3158	2940	3359	3402	4187	4323	3828
ENSMUSG00000052821	chrX	Cysltr1	1.07E+08	1.07E+08	5142	0.34146	1.110036	0.250054	0.358371	0.078581	0	19	19	30	31	56	39	59	37	69	66
ENSMUSG00000036534	chr8	Slc38a7	95835920	95837671	4144	0.225091	3.137455	0.250114	0.358419	0.038648	0	121	113	157	142	136	140	203	194	305	272
ENSMUSG00000090626	chr9	Tex9	72450394	72451875	8798	-0.32662	1.060988	0.250751	0.359294	0.070537	0	39	25	38	34	51	28	50	25	57	50
ENSMUSG00000050989	chr4	Sepn1	1.35E+08	1.35E+08	3619	0.238748	4.509535	0.25093	0.359514	0.049423	0	308	232	359	326	545	482	668	328	812	602
ENSMUSG00000021835	chr14	Bmp4	46383520	46384712	2224	-0.25958	2.692833	0.251356	0.360086	0.051802	0	125	92	117	108	137	101	116	193	150	118
ENSMUSG00000091537	chr9	Tma7	1.09E+08	1.09E+08	1359	-0.19514	5.705891	0.251396	0.360107	0.033597	0	849	930	1114	799	922	1053	1092	982	1350	1165
ENSMUSG00000031105	chrX	Slc25a14	48623413	48623508	2364	0.345703	0.860341	0.251549	0.360289	0.07284	0	17	31	29	22	26	27	54	33	55	57
ENSMUSG00000073375	chr17	Lrrc30	67630965	67632723	1759	-0.48622	6.493571	0.251675	0.360431	0.212096	0	1419	1569	2461	2089	1187	976	1049	4876	683	993
ENSMUSG00000040302	chr5	Rbm48	3583978	3584807	3071	-0.28686	2.171219	0.251815	0.360596	0.063467	0	80	85	75	80	80	66	90	135	106	69
ENSMUSG00000043496	chr6	Tril	53815466	53820830	5365	0.243206	3.745413	0.252176	0.361075	0.05048	0	173	107	242	176	352	259	408	332	412	281
ENSMUSG00000031824	chr8	6430548M08Rik	1.2E+08	1.2E+08	6626	-0.23836	5.02243	0.252204	0.361078	0.049934	0	325	610	833	489	719	519	588	938	750	676
ENSMUSG00000039069	chr2	Mtg2	1.8E+08	1.8E+08	5949	-0.1827	3.841525	0.252509	0.361476	0.026717	0	217	250	271	231	294	252	321	312	371	304
ENSMUSG00000025439	chr7	Clns1a	97696634	97696869	1515	0.184028	5.090118	0.252659	0.361636	0.029315	0	445	514	618	485	593	751	832	713	1059	859
ENSMUSG00000036822	chr4	Topors	40259601	40263081	3856	-0.24306	3.487894	0.252673	0.361636	0.048777	0	162	129	238	199	303	136	221	337	301	214
ENSMUSG00000064339	chrMT	mt-Rnr2	1094	2675	1582	-0.33129	9.137652	0.252726	0.361675	0.099951	0	7291	12314	11398	13784	6598	7465	7036	20661	10444	12506
ENSMUSG00000032599	chr9	Ip6k2	1.09E+08	1.09E+08	4067	0.197055	3.506133	0.252906	0.361896	0.030603	0	157	145	221	142	218	208	285	302	328	287
ENSMUSG00000096606	chr7	Gm4980	99624082	99627103	3022	0.232497	6.224414	0.252938	0.361905	0.048749	0	779	1293	1244	1157	1245	2015	1442	1515	2150	2149
ENSMUSG00000050192	chr3	Eif5a2	28781276	28781413	5027	-0.32947	0.994095	0.253106	0.362106	0.070376	0	36	35	38	30	37	19	50	46	54	32
ENSMUSG00000032526	chr9	Deb1	1.22E+08	1.22E+08	517	-0.22635	5.268826	0.253298	0.362343	0.04549	0	617	792	802	624	571	859	809	696	896	814
ENSMUSG00000022814	chr16	Umps	33954782	33956935	3484	0.254778	3.198298	0.253448	0.362521	0.053135	0	134	97	170	118	179	170	225	137	332	307
ENSMUSG00000020387	chr11	Jade2	51813455	51817657	10760	-0.26322	2.484419	0.253521	0.362588	0.053838	0	93	94	117	106	88	89	98	163	127	107
ENSMUSG00000021807	chr14	2700060E02Rik	19811402	19812237	1510	0.19943	6.607129	0.253641	0.362666	0.035997	0	1248	1492	1875	1373	1575	2339	2361	2494	2471	2311
ENSMUSG00000031787	chr8	Katnb1	95081201	95081304	3425	-0.21259	3.125795	0.253654	0.362666	0.035194	0	120	138	193	157	171	135	213	163	214	215
ENSMUSG00000033540	chr5	Idua	1.09E+08	1.09E+08	4204	0.195137	3.477655	0.253651	0.362666	0.029966	0	140	138	198	183	207	208	255	323	338	258
ENSMUSG00000016356	chr2	Col20a1	1.81E+08	1.81E+08	4193	-0.26841	2.58199	0.25389	0.362891	0.057009	0	124	67	104	105	140	82	136	159	154	100
ENSMUSG00000028618	chr4	Tmem59	1.07E+08	1.07E+08	2056	0.192778	6.658428	0.253881	0.362891	0.033621	0	1510	1362	1811	1300	1896	1856	2458	3051	2743	2474
ENSMUSG00000036840	chr8	Siah1a	86723940	86725856	2107	0.241513	3.244894	0.253855	0.362891	0.046856	0	137	129	159	128	163	166	241	347	223	205
ENSMUSG00000014905	chr12	Dnajb9	44205897	44207405	1865	-0.3162	4.729004	0.254004	0.362978	0.089531	0	481	422	532	480	523	304	428	1156	460	399
ENSMUSG00000048911	chr2	Rnf24	1.31E+08	1.31E+08	6801	-0.33125	2.181798	0.253992	0.362978	0.085938	0	65	52	93	64	153	58	87	55	147	125
ENSMUSG00000004945	chr17	Tmem242	5410870	5411467	1837	-0.21912	5.905323	0.254087	0.36306	0.043236	0	966	1190	1285	932	929	1282	1329	1107	1410	1246
ENSMUSG00000032126	chr9	Hmbs	44336350	44336845	1755	0.196256	4.300679	0.254137	0.363094	0.03233	0	282	284	322	309	320	435	451	369	652	543
ENSMUSG00000002846	chr16	Timmdc1	38498347	38499083	1784	-0.20215	4.990778	0.254274	0.363252	0.035906	0	450	602	674	580	504	635	696	586	857	658
ENSMUSG00000028047	chr3	Thbs3	89215180	89215324	4823	0.331475	4.760705	0.254435	0.363407	0.099023	0	408	152	465	234	822	433	999	565	927	653
ENSMUSG00000092327	chr5	Gm20488	1.49E+08	1.49E+08	2996	-0.27828	3.638999	0.25442	0.363407	0.066124	0	212	130	255	192	371	180	423	259	263	183
ENSMUSG00000101104	chr1	Gm29247	44091463	44091591	676	0.291854	2.023793	0.254486	0.363443	0.062655	0	49	64	64	40	81	79	136	78	109	107
ENSMUSG00000020121	chr10	Srgap1	1.22E+08	1.22E+08	9132	0.355261	1.854703	0.254561	0.363513	0.09775	0	36	39	36	68	81	47	137	56	128	103

ENSMUSG00000021792	chr14	Fam213a	40993740	40994637	2948	0.331532	4.039824	0.254637	0.363583	0.09697	0	205	167	216	347	277	178	244	361	626	795
ENSMUSG00000014602	chr1	Kif1a	93015464	93018499	9330	-0.38961	0.799868	0.254694	0.363627	0.10512	0	45	20	21	31	38	15	41	43	46	26
ENSMUSG00000086915	chr10	Gm16365	39558496	39558712	1408	-0.41904	0.797941	0.254744	0.363662	0.116489	0	19	32	43	35	30	48	23	16	40	34
ENSMUSG00000064128	chr14	Cenpj	56526761	56527111	4363	-0.26929	1.917648	0.254858	0.363787	0.052296	0	60	59	77	75	65	59	99	59	94	82
ENSMUSG00000004032	chr3	Gstm5	1.08E+08	1.08E+08	1278	-0.21538	5.684949	0.254988	0.363787	0.041612	0	764	857	1156	886	948	1067	934	1412	999	1028
ENSMUSG00000030231	chr6	Plekha5	1.4E+08	1.4E+08	5133	-0.30068	2.818882	0.254939	0.363787	0.076038	0	130	81	147	112	181	63	172	220	181	109
ENSMUSG00000037643	chr3	Prkci	30995747	30996085	5551	0.239879	3.03058	0.25499	0.363787	0.046509	0	107	81	126	121	194	117	200	208	286	231
ENSMUSG00000078919	chr2	Dpm1	1.68E+08	1.68E+08	7489	0.249575	5.487732	0.254917	0.363787	0.056197	0	624	618	869	617	681	926	921	1821	926	996
ENSMUSG00000097868	chr2	A330069E16Rik	91237146	91237401	887	-0.35236	0.704429	0.25492	0.363787	0.076037	0	24	31	37	25	27	36	37	25	35	23
ENSMUSG00000025408	chr10	Ddit3	1.27E+08	1.27E+08	1713	0.227759	3.132927	0.255266	0.364143	0.041231	0	125	116	147	152	122	189	231	167	250	252
ENSMUSG00000030956	chr7	Fam53b	1.33E+08	1.33E+08	6911	-0.21513	4.823497	0.255368	0.364252	0.040684	0	313	375	522	693	676	439	543	650	755	689
ENSMUSG00000030409	chr7	Dmpk	19083849	19084154	4330	-0.20993	8.410188	0.255654	0.364621	0.040666	0	4083	5461	6433	6988	7833	6603	6964	5267	8958	8976
ENSMUSG00000052371	chr2	Hoxd3os1	74703248	74703622	2872	-0.44998	0.687206	0.255765	0.364743	0.141253	0	7	44	39	33	24	28	23	29	28	41
ENSMUSG00000098708	chr7	Gm27252	63896533	63896559	717	-0.51452	0.143101	0.255798	0.364752	0.183633	0	20	25	22	22	9	14	14	45	12	12
ENSMUSG00000059554	chr10	Ccdc28a	18213676	18214178	2964	-0.2856	2.622345	0.25596	0.364945	0.066104	0	110	127	119	114	74	116	128	144	113	129
ENSMUSG00000038079	chr1	Tmem237	59100590	59101198	2389	0.276461	1.689952	0.256092	0.365089	0.053153	0	43	33	52	45	65	57	79	62	116	91
ENSMUSG00000081228	chr5	Gm16089	1.38E+08	1.38E+08	336	-0.32049	1.356918	0.256114	0.365089	0.07174	0	37	52	49	44	46	59	45	53	60	36
ENSMUSG00000015932	chr2	Dstn	1.44E+08	1.44E+08	1911	0.184926	5.36024	0.256493	0.365592	0.030366	0	550	506	671	650	856	647	1038	929	1431	1147
ENSMUSG00000033006	chr15	Sox10	79154913	79156641	2713	0.36901	1.481871	0.256565	0.365658	0.10306	0	40	19	28	40	72	51	62	95	103	46
ENSMUSG00000015289	chrX	Lage3	74351276	74353002	2021	0.198792	4.236864	0.256845	0.365981	0.033674	0	275	279	328	270	296	437	429	410	480	558
ENSMUSG00000020109	chr10	Dnajb12	59879556	59879810	3369	-0.22811	5.650396	0.256832	0.365981	0.04726	0	785	788	1012	911	1030	794	927	1718	1024	898
ENSMUSG00000074649	chr2	BC029722	1.56E+08	1.56E+08	1615	0.188109	5.021287	0.25701	0.366179	0.031161	0	425	506	594	505	482	725	800	736	909	831
ENSMUSG00000040105	chr19	Ppapdc2	28963953	28966811	2859	0.361162	2.119463	0.257156	0.366348	0.105483	0	47	41	73	85	66	45	89	80	156	204
ENSMUSG00000061458	chr12	Nol10	17348458	17348619	3020	0.206272	3.568555	0.257374	0.366622	0.035468	0	125	166	242	145	249	252	283	267	356	313
ENSMUSG00000002014	chrX	Ssr4	73787028	73787306	3096	0.181443	5.550557	0.257517	0.366788	0.029586	0	675	635	889	587	891	966	1159	1090	1308	1269
ENSMUSG00000035944	chr15	Ttc38	85832306	85832419	3842	0.243039	2.785669	0.257753	0.367086	0.045552	0	89	100	102	113	113	112	135	211	211	199
ENSMUSG00000070044	chr8	Fam149a	45336717	45339372	5954	0.295404	1.943977	0.257796	0.367109	0.066023	0	42	37	70	56	81	62	115	61	142	111
ENSMUSG00000041632	chr13	Mrps27	99344786	99344875	1848	-0.19988	5.173711	0.257908	0.367231	0.035759	0	494	626	778	697	613	759	730	674	1036	700
ENSMUSG00000001444	chr11	Tbx21	97098071	97099378	2488	0.369075	0.42625	0.258247	0.367676	0.078236	0	22	11	24	15	18	22	44	26	31	40
ENSMUSG00000025133	chr7	Ints4	97480956	97481150	3243	-0.17438	4.689527	0.258427	0.367895	0.026265	0	372	406	549	439	522	461	532	615	652	559
ENSMUSG00000092650	chr13	Gm25241	81065477	81065560	84	0.476269	0.044917	0.258524	0.367995	0.117747	0	10	22	13	7	11	19	20	15	45	29
ENSMUSG00000052298	chr11	Cdc42se2	54717456	54719724	3661	0.180076	5.37356	0.258735	0.368257	0.029075	0	534	591	799	570	762	727	1054	1185	1172	1017
ENSMUSG00000000579	chr17	Dynlt1c	6601671	6601836	3777	0.317876	0.87545	0.25894	0.368511	0.058204	0	27	22	24	24	31	42	43	37	53	48
ENSMUSG00000051177	chr2	Plcb1	1.35E+08	1.35E+08	8685	-0.3309	1.970605	0.258991	0.368546	0.087599	0	58	48	103	71	82	37	66	57	114	134
ENSMUSG00000021846	chr14	Peli2	48120869	48121233	5849	-0.26486	3.36244	0.259087	0.368611	0.060326	0	168	144	195	224	199	132	183	368	216	186
ENSMUSG00000026200	chr1	Glb1l	75198236	75198354	5905	0.314064	1.333835	0.25909	0.368611	0.06989	0	31	23	36	31	62	49	60	44	92	71
ENSMUSG00000024812	chr19	Tjp2	24094523	24095590	4591	0.278743	3.144168	0.259347	0.368938	0.066112	0	81	96	153	195	142	130	228	153	357	283
ENSMUSG00000029681	chr5	Bcl7b	1.35E+08	1.35E+08	2404	0.175504	4.499226	0.259479	0.369089	0.026616	0	285	303	398	363	428	449	503	623	647	566
ENSMUSG00000019818	chr10	Cd164	41519414	41519700	4449	-0.18108	7.276787	0.259507	0.36909	0.030544	0	2278	2360	3106	2491	3655	2375	3637	3769	3938	3353
ENSMUSG00000024493	chr18	Lars	42202350	42202718	3856	-0.17455	5.586916	0.259553	0.369118	0.027454	0	627	687	1025	880	1091	817	1080	1104	1237	1039
ENSMUSG00000036339	chr14	Tmem260	48446128	48446335	8165	-0.24379	2.797513	0.259831	0.369399	0.047965	0	132	86	121	128	156	111	181	106	193	150
ENSMUSG00000060671	chr3	Atp8b2	89939481	89941431	8561	-0.24081	4.458616	0.259786	0.369399	0.051926	0	350	218	385	387	696	285	610	447	616	428
ENSMUSG00000061535	chr5	C1qtnf7	43515569	43515986	4136	0.40469	0.91277	0.259825	0.369399	0.115158	0	29	12	23	22	43	24	55	76	52	31
ENSMUSG00000038188	chr11	Scarf1	75513540	75513690	2887	0.249327	3.103282	0.259866	0.369411	0.050333	0	119	129	98	153	141	161	202	164	275	284
ENSMUSG00000037536	chr14	Fbxo34	47472561	47472717	3726	-0.19064	3.562129	0.259978	0.369533	0.029555	0	158	200	251	202	237	187	267	287	298	245
ENSMUSG00000030612	chr7	Mrpl46	78775236	78775725	1392	-0.19717	4.61527	0.260038	0.369579	0.034451	0	348	454	533	450	377	473	522	476	649	531
ENSMUSG00000040667	chr11	Nup88	70943058	70943322	8144	0.194533	5.305829	0.260346	0.36998	0.034456	0	456	536	762	614	736	763	936	1286	1017	896
ENSMUSG00000074671	chr2	Tspyl3	1.53E+08	1.53E+08	3072	0.342983	1.1759	0.26049	0.370145	0.082909	0	33	20	41	30	35	43	65	27	85	65
ENSMUSG00000104348	chr1	RP23-59N15.4	1.93E+08	1.93E+08	2573	-0.44896	1.385265	0.260789	0.370533	0.170868	0	66	28	46	48	54	38	65	9	93	52
ENSMUSG00000044475	chr10	Ascc1	60002805	60002907	1578	0.192629	4.026967	0.26084	0.370568	0.031828	0	207	221	330	242	268	337	356	478	408	424
ENSMUSG00000085741	chr2	5430405H02Rik	1.57E+08	1.57E+08	3851	0.35201	0.532373	0.260872	0.370575	0.071307	0	23	13	28	17	17	29	28	30	45	44
ENSMUSG00000024287	chr18	Thoc1	9958180	9958246	3855	0.201256	3.470207	0.261021	0.370749	0.032628	0	153	170	205	142	180	201	273	252	331	323
ENSMUSG00000029195	chr5	Klb	65348386	65349236	3464	0.918398	0.355833	0.261056	0.37076	0.712516	0	4	2	2	22	40	1	8	11	66	100
ENSMUSG00000010608	chr12	Rbm25	83631236	83631356	17376	-0.21823	5.759074	0.261108	0.370796	0.044132	0	823	812	1219	861	1186	676	1100	1752	1279	1086
ENSMUSG00000052137	chr4	Rbm12b2	12089439	12089727	3468	0.278327	1.901252	0.261207	0.370898	0.055802	0	58	51	54	46	63	70	91	111	85	105
ENSMUSG00000021972	chr14	Hmbox1	64811600	64813419	9681	-0.17967	3.985076	0.261274	0.370956	0.027166	0	237	245	302	269	351	250	320	336	405	424
ENSMUSG00000062038	chr5	Gm10108	13121449	13121766	318	-0.35518	1.461245	0.261399	0.371095	0.098928	0	46	60	58	58	22	50	47	48	65	63
ENSMUSG00000034463	chr14	Scara3	65919395	65921188	3405	-0.26896	4.234468	0.261532	0.371246	0.065082	0	318	161	309	295	687	290	383	470	465	385
ENSMUSG00000055531	chr10	Cpsf6	1.17E+08	1.17E+08	10510	0.194946	4.730239	0.261647	0.37137	0.033924	0	371	351	400	379	570	457	576	854	770	658
ENSMUSG00000023008	chr15	Fmnl3	99317225	99318372	5021	0.199957	3.972183	0.261767	0.371503	0.034057	0	200	204	250	294	265	275	497	336	529	335
ENSMUSG00000031303	chrX	Map3k15	1.6E+08	1.6E+08	4348	0.69295	1.158241	0.261806	0.37152	0.40444	0	14	25	10	60	22	10	20	21	190	93
ENSMUSG00000062352	chr12	Itgb1bp1	21240825	21241109	3321	0.187876	4.351868	0.261893	0.371606	0.030465	0	298	293	348	307	332	393	405	488	657	601
ENSMUSG00000002396	chr8	Ocel1	71371298	71371985	7133	0.271646	2.124135	0.261996	0.371676	0.055514	0	53	51	77	74	68	71	112	76	168	128
ENSMUSG00000047044	chr19	D030056L22Rik	18713193	18713659	1677	0.255893	2.431019	0.261975	0.371676	0.048623	0	95	73	83	73	72	109	130	133	165	136
ENSMUSG00000045672	chr4	Col27a1	63214004	63214404	13022	0.395626	2.749604	0.262283	0.372045	0.14099	0	101	31	75	72	216	96	244	101	227	228
ENSMUSG00000075593	chr5	Gal3st4	1.38E+08	1.38E+08	3252	-0.46723	-0.03755	0.262533	0.372361	0.142507	0	13	9	27	11	28	6	26	11	36	11

ENSMUSG00000027848	chr3	Olfml3	1.04E+08	1.04E+08	4014	0.287349	5.316052	0.262623	0.372451	0.077243	0	692	292	650	395	1026	781	1476	701	1272	906
ENSMUSG00000034543	chr11	Morc2a	3649494	3650146	6013	-0.2215	4.6021	0.262694	0.372513	0.044494	0	383	351	503	432	520	315	471	816	524	495
ENSMUSG00000040374	chr3	Pex2	5560188	5561764	2270	-0.17712	4.677473	0.262941	0.372825	0.02787	0	379	417	521	441	505	398	608	643	615	540
ENSMUSG00000002012	chrX	Pnck	73655994	73656386	1971	-0.19859	3.401425	0.262983	0.372847	0.031966	0	156	175	208	182	215	217	200	213	278	225
ENSMUSG00000046671	chr4	Mtfr1l	1.35E+08	1.35E+08	5370	-0.18716	6.761095	0.263257	0.373197	0.032973	0	1622	1708	2345	1984	1986	2276	2269	2143	2706	2327
ENSMUSG00000021179	chr12	Nrde2	1E+08	1E+08	3723	0.192305	3.379409	0.263335	0.373269	0.029774	0	135	134	192	170	175	191	240	270	298	289
ENSMUSG00000030842	chr7	Lamtor1	1.02E+08	1.02E+08	1366	0.186061	6.732991	0.263368	0.373277	0.032617	0	1364	1655	1894	1595	1774	2430	2584	2300	3059	2752
ENSMUSG00000051306	chr5	Usp42	1.44E+08	1.44E+08	6238	-0.2575	2.785727	0.263647	0.373635	0.053936	0	83	104	136	138	167	101	124	214	160	127
ENSMUSG00000046562	chr5	Unc119b	1.15E+08	1.15E+08	4603	-0.18564	4.441659	0.264035	0.374147	0.030452	0	337	303	437	320	553	330	541	489	580	446
ENSMUSG00000003039	chr8	Fam32a	72219730	72219860	1910	0.189359	4.381091	0.264191	0.374329	0.031472	0	281	247	325	372	403	306	541	509	692	582
ENSMUSG00000024841	chr19	Eif1ad	5366813	5367210	2469	0.176819	4.577971	0.264252	0.374378	0.027543	0	329	340	433	368	391	487	523	628	753	563
ENSMUSG00000002308	chr17	Cd320	33843091	33843291	2592	0.185053	3.693098	0.264484	0.374667	0.028706	0	158	184	230	199	236	263	309	335	328	351
ENSMUSG00000098792	chr11	Gm27401	1.17E+08	1.17E+08	173	0.422601	-0.11657	0.264511	0.374667	0.088045	0	8	13	15	12	10	16	29	26	13	24
ENSMUSG00000019923	chr10	Zwint	72654845	72654977	4434	0.351086	5.43536	0.264589	0.374702	0.116541	0	561	542	743	593	741	571	686	2662	919	810
ENSMUSG00000028642	chr4	4930538K18Rik	1.19E+08	1.19E+08	1452	-0.44413	0.455335	0.264587	0.374702	0.142064	0	38	13	36	16	20	17	24	44	16	25
ENSMUSG00000028798	chr4	Eif3i	1.3E+08	1.3E+08	3702	0.179325	6.584924	0.264719	0.374847	0.030391	0	1286	1381	1796	1392	1666	1978	2229	2622	2626	2392
ENSMUSG00000003423	chr7	Pih1d1	45154303	45154420	2024	0.202941	4.807647	0.264977	0.375125	0.037698	0	342	418	497	422	491	678	659	474	859	797
ENSMUSG00000035202	chr9	Lars2	1.23E+08	1.23E+08	3881	-0.30231	9.132637	0.264944	0.375125	0.087673	0	8359	12568	10932	6019	13737	10830	7201	11627	8855	19002
ENSMUSG00000055407	chr7	Map6	99267447	99269313	6958	0.252597	2.366184	0.264996	0.375125	0.049047	0	62	60	67	85	115	80	123	125	182	143
ENSMUSG00000039531	chr10	Zufsp	33926936	33927621	2364	0.251403	2.252362	0.2651	0.375233	0.046013	0	61	64	84	79	66	95	129	93	157	121
ENSMUSG00000024678	chr19	Ms4a4d	11536801	11537160	1513	0.249985	3.387991	0.265196	0.37533	0.054716	0	183	107	169	137	195	228	222	377	251	220
ENSMUSG00000097204	chr3	Gm17690	96167464	96169652	3467	0.386919	1.026238	0.265397	0.375577	0.107916	0	27	29	30	18	35	28	49	94	50	35
ENSMUSG00000092356	chr2	Gm20532	26586639	26586681	780	0.207472	3.92299	0.265593	0.375815	0.037181	0	182	236	284	267	190	260	335	389	501	424
ENSMUSG00000031812	chr8	Map1lc3b	1.22E+08	1.22E+08	7517	0.272926	7.53196	0.265646	0.375852	0.071519	0	2492	2434	3209	2735	3136	3132	3538	8881	4008	3926
ENSMUSG00000027774	chr3	Gfm1	67430096	67430322	4419	-0.20701	6.968378	0.265711	0.375905	0.040961	0	1629	2438	2590	2448	2009	2499	2496	2921	2984	2535
ENSMUSG00000038497	chr8	Tmco3	13288013	13288387	4533	-0.19196	3.919918	0.265939	0.376189	0.0318	0	222	214	328	281	305	271	389	238	420	330
ENSMUSG00000059511	chr13	Gm20563	62006666	62006941	276	0.331549	0.580909	0.26603	0.376281	0.067063	0	20	18	20	16	29	37	36	26	38	42
ENSMUSG00000074405	chr7	Zfp865	5020376	5020655	3873	0.244295	3.653848	0.266249	0.376551	0.053088	0	180	149	197	169	267	200	267	514	338	268
ENSMUSG00000001520	chr6	Nrip2	1.28E+08	1.28E+08	3602	0.323777	1.590437	0.266371	0.376685	0.081442	0	31	32	38	60	56	56	72	42	107	105
ENSMUSG00000007415	chr5	Gatad1	3632932	3634030	4125	-0.18294	5.73289	0.266759	0.377195	0.031481	0	844	919	1051	970	890	1026	1170	1083	1326	1174
ENSMUSG00000028995	chr5	Fam126a	23915276	23915537	7107	-0.20503	3.674519	0.266936	0.377407	0.036294	0	170	173	226	225	363	188	284	239	383	304
ENSMUSG00000030098	chr6	Grip2	91761509	91763606	5849	-0.2648	3.124678	0.267057	0.377502	0.061162	0	100	194	154	137	202	121	259	128	240	182
ENSMUSG00000056919	chr9	Cep162	87189577	87192922	11607	-0.24237	2.031596	0.267046	0.377502	0.043074	0	61	64	90	64	85	72	85	87	103	81
ENSMUSG00000074738	chr4	B930041F14Rik	1.56E+08	1.56E+08	2140	0.301026	1.530626	0.267376	0.377914	0.066987	0	51	24	37	36	61	60	65	73	82	78
ENSMUSG00000022749	chr16	Tbc1d23	57168866	57170440	3648	-0.19804	4.007398	0.267638	0.378245	0.034966	0	290	245	335	246	307	227	336	453	371	361
ENSMUSG00000071847	chr18	Apcdd1	62922327	62922721	2799	-0.37916	2.58025	0.267665	0.378245	0.130432	0	134	50	98	103	179	44	77	106	170	223
ENSMUSG00000020349	chr11	Ppp2ca	52098681	52099150	7490	0.182386	7.18904	0.267801	0.37836	0.032065	0	1912	2113	2641	2242	2507	2884	3642	4269	4059	3218
ENSMUSG00000039007	chr15	Cpq	33083129	33083322	1923	-0.20065	4.697633	0.267776	0.37836	0.036891	0	460	341	530	374	626	496	587	411	659	651
ENSMUSG00000038522	chr10	AI317395	40001575	40003589	2729	-0.36078	1.599232	0.267895	0.378455	0.105778	0	31	75	64	56	48	38	43	95	88	42
ENSMUSG00000028578	chr4	Caap1	94500081	94501416	3591	0.305005	0.997809	0.268008	0.378575	0.058614	0	18	24	37	27	37	33	47	42	66	59
ENSMUSG00000067928	chr17	Zfp760	21707741	21707893	4209	-0.29757	1.405709	0.268153	0.378741	0.064318	0	59	31	49	37	60	36	60	55	60	59
ENSMUSG00000037089	chr17	Slc35b2	45563964	45564773	2326	0.172004	4.839764	0.268274	0.378847	0.026825	0	386	420	481	402	557	517	740	740	880	679
ENSMUSG00000083854	chr7	Dnajc19-ps	1.04E+08	1.04E+08	351	-0.38806	0.518589	0.268282	0.378847	0.096742	0	24	30	25	31	15	30	33	18	32	22
ENSMUSG00000005672	chr5	Kit	75574916	75575118	5831	-0.34218	1.687502	0.268322	0.378864	0.095723	0	45	69	50	62	64	42	46	38	96	108
ENSMUSG00000026455	chr1	Klhl12	1.34E+08	1.34E+08	11395	-0.19122	4.68425	0.268395	0.378928	0.03333	0	366	426	561	449	483	507	528	665	569	492
ENSMUSG00000032504	chr9	Pdcd6ip	1.14E+08	1.14E+08	6903	0.173161	5.969246	0.268808	0.379434	0.028501	0	847	751	1125	985	1253	1107	1522	1641	1924	1614
ENSMUSG00000078670	chr7	Fam174b	73740307	73740828	2678	-0.3359	1.046861	0.268802	0.379434	0.074753	0	26	25	49	37	51	42	40	23	50	48
ENSMUSG00000027377	chr2	Mall	1.28E+08	1.28E+08	2006	-0.29748	2.400197	0.26889	0.379472	0.075472	0	53	89	115	132	92	103	106	62	163	113
ENSMUSG00000030352	chr6	Tspan9	1.28E+08	1.28E+08	4732	-0.26503	5.758633	0.268888	0.379472	0.06752	0	618	739	1064	1257	1349	988	1502	527	1607	1155
ENSMUSG00000019471	chr9	Cdc37	21138541	21139963	2456	0.175309	6.75839	0.269042	0.379648	0.029632	0	1363	1517	1842	1858	1924	2326	2545	2491	3299	2724
ENSMUSG00000047193	chr9	Dync2h1	6928503	6929623	16161	-0.29368	2.148498	0.269126	0.379701	0.071581	0	95	52	77	74	102	61	85	140	96	75
ENSMUSG00000081824	chr16	BC002163	42955631	42955949	319	0.242971	3.218344	0.269134	0.379701	0.051502	0	109	168	146	140	132	254	211	221	229	224
ENSMUSG00000001127	chrX	Araf	20797814	20797881	6541	-0.18178	6.121656	0.269228	0.379795	0.031625	0	1110	1077	1379	1182	1434	1158	1441	1871	1638	1494
ENSMUSG00000022215	chr14	Fitm1	55575617	55575947	969	-0.19134	7.650278	0.269323	0.379871	0.035629	0	2857	3129	3990	3916	4055	4495	4178	3812	5171	3965
ENSMUSG00000029207	chr5	Apbb2	66298861	66302709	10551	-0.22495	5.146628	0.269337	0.379871	0.047997	0	568	483	757	776	596	556	621	1153	781	685
ENSMUSG00000050931	chr3	Sgms2	1.31E+08	1.31E+08	5873	-0.35283	2.549318	0.269371	0.37988	0.110237	0	96	66	96	54	249	66	131	95	153	158
ENSMUSG00000041881	chr17	Ndufa7	33824591	33824680	1701	0.186167	6.741917	0.269407	0.379892	0.033508	0	1404	1612	1811	1759	1732	2460	2405	2800	2838	2644
ENSMUSG00000013822	chr9	Elof1	22112989	22113679	1092	0.179886	4.741478	0.269729	0.380308	0.029563	0	374	406	489	374	435	548	609	627	744	771
ENSMUSG00000032316	chr9	Clk3	57750711	57751121	2494	0.185029	5.037859	0.269898	0.380507	0.031806	0	464	505	547	472	557	620	741	982	859	860
ENSMUSG00000024799	chr19	Tm7sf2	6062821	6063073	3484	0.222818	3.04554	0.269958	0.380553	0.042221	0	89	109	124	138	175	184	175	206	209	242
ENSMUSG00000045201	chr14	Lrrc3b	15357519	15358761	1835	-0.43707	0.449014	0.270004	0.380579	0.137774	0	10	31	29	39	13	27	16	28	24	30
ENSMUSG00000024206	chr17	Rfx2	56775897	56777074	3353	0.335185	1.926659	0.270041	0.380593	0.097247	0	37	37	41	44	123	51	105	90	137	109
ENSMUSG00000071226	chr6	Cecr2	1.21E+08	1.21E+08	13306	-0.24151	3.575607	0.270092	0.380626	0.052024	0	182	170	236	191	306	181	215	399	219	244
ENSMUSG00000062270	chr9	Morf4l1	90091665	90092402	9754	0.212804	7.146902	0.270142	0.380657	0.04418	0	2009	1908	2697	1852	2523	2496	3357	5180	3377	3291
ENSMUSG00000024535	chr18	Snx24	53245662	53245852	1880	-0.187	3.852594	0.270479	0.381094	0.030104	0	220	209	285	252	319	291	338	252	343	332
ENSMUSG00000029640	chr5	Usp12	1.47E+08	1.47E+08	4639	-0.17554	4.48324	0.270595	0.381219	0.027987	0	317	348	490	374	458	359	564	421	649	477

ENSMUSG00000038777	chr3	Sema6c	95160457	95160702	5935	-0.21403	6.908006	0.270665	0.381278	0.044681	0	1854	1616	2270	2373	2748	2510	2816	1560	3331	2713
ENSMUSG00000044938	chr9	Klhl31	77636500	77636787	6494	-0.19953	8.671629	0.270886	0.38155	0.039173	0	5699	6780	8956	6474	8746	8925	8677	7506	8371	9999
ENSMUSG00000025357	chr10	Dgka	1.29E+08	1.29E+08	2808	-0.20399	3.569638	0.271173	0.381916	0.036543	0	185	185	220	216	249	170	215	346	279	275
ENSMUSG00000058558	chr5	Rpl5	1.08E+08	1.08E+08	3920	0.172291	7.856943	0.271204	0.381921	0.029143	0	3172	3211	4026	3340	4530	4369	6080	6175	6461	5630
ENSMUSG00000017670	chr2	Elmo2	1.65E+08	1.65E+08	6652	-0.18228	4.621508	0.271411	0.382135	0.030645	0	394	323	456	411	620	394	516	466	757	588
ENSMUSG00000026077	chr1	Npas2	39193731	39194009	4791	0.444253	1.550466	0.271388	0.382135	0.179647	0	17	11	27	49	108	59	98	79	74	66
ENSMUSG00000015134	chr7	Aldh1a3	66390892	66392761	4615	0.395588	1.899714	0.271701	0.382504	0.141482	0	28	20	32	61	134	66	97	104	130	88
ENSMUSG00000029505	chr5	Ep400	1.11E+08	1.11E+08	13971	-0.18483	4.779466	0.271895	0.382738	0.031819	0	477	329	513	469	670	424	589	678	723	600
ENSMUSG00000032968	chr1	Inha	75507077	75507518	1475	-0.23622	3.272239	0.272023	0.382879	0.048177	0	129	185	224	129	201	222	199	181	224	183
ENSMUSG00000033364	chr1	Usp37	74435511	74439478	11081	-0.19544	3.364829	0.272093	0.382939	0.032357	0	155	137	201	185	243	166	258	195	302	203
ENSMUSG00000001707	chr13	Eef1e1	38645698	38646310	1032	-0.21217	3.510706	0.27215	0.382941	0.039582	0	182	188	241	170	234	228	267	167	339	225
ENSMUSG00000022853	chr16	Ehhadh	21761287	21763336	3018	-0.27526	2.845315	0.272124	0.382941	0.067329	0	78	135	117	159	163	83	106	197	183	193
ENSMUSG00000044149	chrX	Nkrf	36887540	36890512	3268	0.29638	1.562436	0.272208	0.382983	0.065413	0	45	41	39	27	61	49	74	78	107	64
ENSMUSG00000030494	chr7	Rhpn2	35334170	35334411	6304	0.490834	1.158179	0.272252	0.383006	0.204712	0	21	23	26	46	31	20	43	148	49	31
ENSMUSG00000038733	chr1	Wdr26	1.81E+08	1.81E+08	7848	-0.209	7.351993	0.27242	0.383204	0.043078	0	2410	2563	3518	2952	3236	2367	3430	5234	3664	3026
ENSMUSG00000034932	chr10	Mrpl54	81264713	81264997	825	0.193195	5.499315	0.272736	0.383609	0.035904	0	551	729	876	675	672	1086	1054	1001	1229	1188
ENSMUSG00000039810	chr10	Zc3h10	1.29E+08	1.29E+08	4384	0.211355	2.892133	0.272766	0.383613	0.036494	0	99	111	120	100	136	147	170	204	233	166
ENSMUSG00000031214	chrX	Ophn1	98554277	98558405	13100	0.218677	3.010826	0.272874	0.383725	0.039435	0	119	93	124	115	167	132	210	168	271	234
ENSMUSG00000017307	chr2	Acot8	1.65E+08	1.65E+08	1994	0.246806	2.680214	0.273007	0.383873	0.050597	0	88	88	104	83	119	128	168	101	198	208
ENSMUSG00000073627	chr1	C130036L24Rik	86359574	86360007	6437	0.387071	0.682267	0.273069	0.383922	0.104384	0	14	22	30	19	24	35	21	67	40	33
ENSMUSG00000019505	chr11	Ubb	62551171	62551595	1675	0.261597	8.729309	0.273134	0.383974	0.067986	0	5298	5771	7270	5887	8237	7946	8197	19594	9168	8541
ENSMUSG00000040964	chr4	Arhgef10l	1.41E+08	1.41E+08	5693	-0.19545	6.064426	0.27329	0.384143	0.037132	0	776	947	1450	1351	1545	1341	1556	1179	1764	1406
ENSMUSG00000072494	chr14	Ppp1r3e	54872669	54873312	2508	-0.27922	1.326449	0.273309	0.384143	0.05405	0	47	36	49	34	56	38	49	53	58	58
ENSMUSG00000041846	chr12	Smek1	1.01E+08	1.01E+08	4594	-0.16905	4.43112	0.273562	0.384459	0.026028	0	333	320	437	378	438	344	467	539	567	458
ENSMUSG00000061887	chr4	Ssbp3	1.07E+08	1.07E+08	6582	0.170227	4.365639	0.273898	0.384892	0.026385	0	249	271	360	318	433	370	548	522	607	505
ENSMUSG00000020952	chr12	Scfd1	51377580	51377636	2091	-0.17897	4.166236	0.274188	0.385261	0.028991	0	289	292	373	251	383	303	427	358	452	422
ENSMUSG00000001383	chr18	Zmat2	36793923	36793959	2257	0.197149	6.190005	0.274422	0.38555	0.038256	0	925	1036	1479	967	1302	1755	1751	1423	1964	2100
ENSMUSG00000024253	chr17	Dync2li1	84626496	84626576	1324	0.265565	2.110976	0.274566	0.385713	0.056689	0	67	48	79	61	64	79	141	118	99	98
ENSMUSG00000026766	chr2	Mmadhc	50279881	50280402	2012	-0.19648	6.853081	0.274656	0.385761	0.038244	0	1651	2130	2468	2028	1970	2212	2401	2979	2622	2237
ENSMUSG00000037772	chr7	Mrpl23	1.43E+08	1.43E+08	1777	0.191753	5.037308	0.274638	0.385761	0.035313	0	439	476	618	448	575	822	814	774	768	819
ENSMUSG00000027722	chr3	Spata5	37419896	37420500	3788	0.214595	3.028253	0.274917	0.386088	0.039581	0	80	127	139	118	164	177	190	203	250	189
ENSMUSG00000032119	chr9	Hinfp	44295673	44296580	2100	-0.34386	1.355529	0.275119	0.386333	0.092263	0	49	21	56	34	76	26	45	50	72	67
ENSMUSG00000018433	chr11	Nol11	1.07E+08	1.07E+08	5357	0.173443	3.969554	0.275418	0.38662	0.02663	0	195	226	241	247	318	304	422	367	470	370
ENSMUSG00000022034	chr14	Esco2	65819038	65820098	4010	0.43337	-0.09202	0.27542	0.38662	0.091937	0	14	8	13	8	16	15	20	12	41	26
ENSMUSG00000022951	chr16	Rcan1	92391953	92393628	2506	-0.31715	6.842222	0.275435	0.38662	0.100335	0	1116	2519	2835	1576	2702	1997	3547	1128	3942	1516
ENSMUSG00000029131	chr5	Dnajb6	29735688	29736116	5721	0.211185	5.771858	0.275424	0.38662	0.043847	0	632	796	985	849	981	968	1254	2063	1383	1154
ENSMUSG00000032481	chr9	Smarcc1	1.1E+08	1.1E+08	5672	0.169344	5.046998	0.275478	0.386642	0.027185	0	444	431	546	515	673	621	912	716	998	851
ENSMUSG00000040606	chr4	Kazn	1.42E+08	1.42E+08	10721	-0.30834	1.65902	0.27555	0.386702	0.075574	0	63	22	77	56	70	46	66	66	82	63
ENSMUSG00000096403	chr6	Gm9825	7981829	7983430	1602	0.317564	1.041293	0.275711	0.386889	0.065755	0	30	23	22	29	41	27	55	56	67	52
ENSMUSG00000025815	chr2	Dhtkd1	5896115	5898812	6333	0.476137	0.737982	0.275787	0.386957	0.173602	0	29	17	12	23	26	22	24	94	30	41
ENSMUSG00000051154	chr2	Commd3	18672384	18672407	2330	-0.18542	5.990336	0.275835	0.386985	0.033785	0	946	1179	1243	1091	1142	1274	1432	1267	1520	1385
ENSMUSG00000039738	chr16	Slx4	3979105	3980172	7657	-0.22637	2.682235	0.276116	0.38734	0.043395	0	106	89	102	108	170	92	130	144	181	143
ENSMUSG00000031841	chr8	Cdh13	1.18E+08	1.18E+08	11144	-0.17469	7.02953	0.276459	0.387782	0.030442	0	1986	1900	2580	2517	2620	2353	2935	3010	3567	2483
ENSMUSG00000026064	chr1	Ptp4a1	30940302	30943323	5763	0.234362	4.437449	0.276562	0.387887	0.052538	0	277	311	437	302	328	288	433	843	594	597
ENSMUSG00000026826	chr2	Nr4a2	57106830	57108412	4059	-0.40002	0.513119	0.276609	0.387914	0.122606	0	32	10	17	22	48	12	34	27	40	25
ENSMUSG00000027695	chr3	Pld1	27938695	27938750	12961	-0.2309	2.718988	0.276641	0.38792	0.045278	0	102	109	109	106	162	90	162	169	151	130
ENSMUSG00000096232	chr16	0610012G03Rik	31948024	31948353	417	0.203977	4.942936	0.276743	0.388023	0.04028	0	396	450	619	499	404	797	680	725	841	727
ENSMUSG00000069874	chr11	Irgm2	58199618	58199779	3621	-0.27669	4.987492	0.276943	0.388265	0.075242	0	486	578	482	452	916	844	593	365	928	550
ENSMUSG00000069920	chr8	B3gnt9	1.05E+08	1.05E+08	2516	-0.30897	2.667027	0.276983	0.388281	0.086613	0	120	61	147	83	181	90	218	89	153	109
ENSMUSG00000015748	chr3	Prpf3	95830124	95830965	5661	0.186303	3.846663	0.277168	0.388462	0.031586	0	189	191	290	191	263	336	357	296	406	367
ENSMUSG00000068015	chr14	Lrch1	74754674	74757143	4706	0.243223	2.612342	0.277153	0.388462	0.049864	0	59	82	117	103	103	85	192	156	181	158
ENSMUSG00000084168	chr11	Atp5l2-ps	97768060	97768371	312	-0.41041	1.130209	0.277434	0.388796	0.146719	0	47	54	19	50	22	37	26	48	67	36
ENSMUSG00000022151	chr15	Ttc33	5185525	5185572	2163	-0.21546	4.659757	0.277485	0.388805	0.044927	0	405	402	563	439	448	361	507	838	557	463
ENSMUSG00000048874	chr1	Phf3	30802339	30805942	14190	-0.22301	4.937975	0.277497	0.388805	0.048667	0	484	461	575	527	720	378	627	1057	699	559
ENSMUSG00000042202	chr4	Slc35e2	1.56E+08	1.56E+08	6574	0.238349	2.615015	0.277544	0.388831	0.049776	0	83	63	107	71	146	120	183	133	173	153
ENSMUSG00000038286	chr13	Bphl	34037641	34037769	1209	-0.17962	4.0223	0.277889	0.389275	0.02924	0	246	259	366	268	296	313	362	294	430	368
ENSMUSG00000025733	chr17	Rhot2	25838457	25839494	4442	-0.20808	6.541179	0.278041	0.389449	0.043477	0	1295	1842	1932	1796	1363	1867	1831	1663	2658	2054
ENSMUSG00000035615	chr4	Frmpd1	45184875	45184957	5324	0.484852	1.115237	0.278117	0.389476	0.203643	0	10	31	52	20	33	45	121	19	58	36
ENSMUSG00000052798	chr10	Nup107	1.18E+08	1.18E+08	3111	0.208638	3.205296	0.278099	0.389476	0.037851	0	130	103	141	137	203	157	271	188	296	244
ENSMUSG00000028944	chr5	Prkag2	24862744	24863887	6480	-0.2295	4.40548	0.278211	0.389568	0.050635	0	264	422	496	335	385	454	442	288	497	562
ENSMUSG00000019779	chr10	Frk	34483400	34484369	4799	-0.30215	0.899247	0.27843	0.389835	0.062858	0	26	21	36	31	53	27	38	32	54	37
ENSMUSG00000034334	chr13	Fam151b	92449622	92450252	1381	0.344003	0.911987	0.278462	0.389841	0.083269	0	30	15	33	16	38	39	48	60	46	37
ENSMUSG00000028607	chr4	Cpt2	1.08E+08	1.08E+08	2391	0.22009	6.189852	0.278592	0.389984	0.048469	0	841	1207	1121	1398	992	1272	1339	2211	2292	2134
ENSMUSG00000035637	chr4	Grhpr	44981395	44981534	1603	0.177789	4.957873	0.278623	0.389988	0.030507	0	385	476	535	453	584	730	687	746	929	721
ENSMUSG00000038517	chr11	Tbkbp1	97136171	97137675	3975	0.204878	3.236516	0.278725	0.390091	0.036204	0	118	126	134	174	172	160	203	243	316	259
ENSMUSG00000022602	chr15	Arc	74669083	74669993	3057	-0.40542	0.138939	0.278844	0.39014	0.108219	0	11	23	29	21	12	12	26	11	33	22

ENSMUSG00000032418	chr9	Me1	86581371	86582907	3848	-0.30357	7.508311	0.27882	0.39014	0.093471	0	2817	2717	3845	3723	3771	2123	1980	2611	5018	7768
ENSMUSG00000034449	chr11	Dhrs11	84820856	84821301	1603	0.234463	4.672497	0.278827	0.39014	0.053425	0	320	439	428	458	266	543	475	793	736	646
ENSMUSG00000027679	chr3	Dnajc19	34057758	34058114	1015	-0.20924	5.057692	0.278943	0.390167	0.042865	0	525	615	744	537	527	764	631	616	763	759
ENSMUSG00000028999	chr5	Rint1	23787711	23787882	6972	-0.2035	3.315017	0.278948	0.390167	0.036329	0	180	147	185	139	233	174	192	187	282	242
ENSMUSG00000043889	chr13	Gm8399	81064684	81064992	1119	0.365218	0.727996	0.278934	0.390167	0.08615	0	21	31	25	15	19	34	36	28	64	44
ENSMUSG00000022529	chr16	Zfp263	3744093	3744767	4521	0.216818	3.288732	0.279037	0.390251	0.041753	0	150	122	161	123	193	151	250	318	245	255
ENSMUSG00000019326	chr11	Aoc3	1.01E+08	1.01E+08	4621	0.396206	4.701064	0.279349	0.39057	0.157066	0	277	186	294	468	706	261	482	307	1099	1447
ENSMUSG00000025510	chr7	Cd151	1.41E+08	1.41E+08	2010	0.178903	6.617287	0.279293	0.39057	0.032152	0	1208	1368	1788	1703	1635	1698	2140	2735	3000	2699
ENSMUSG00000055538	chr14	Zcchc24	25711642	25715402	4557	0.285998	6.806131	0.279344	0.39057	0.082944	0	1563	1295	1697	1635	2290	1770	2157	5714	2364	2268
ENSMUSG00000030056	chr6	Isy1	87818447	87819203	1620	0.178109	4.138005	0.279669	0.390938	0.029522	0	193	247	313	292	339	367	430	371	505	495
ENSMUSG00000030966	chr7	Trim21	1.03E+08	1.03E+08	2775	0.302877	1.975282	0.279654	0.390938	0.081195	0	41	48	59	64	77	109	77	53	116	132
ENSMUSG00000025488	chr7	Cox8b	1.41E+08	1.41E+08	362	-0.21467	8.24586	0.279759	0.391024	0.04704	0	4837	6213	5808	5574	4237	6476	6149	6496	6905	6286
ENSMUSG00000052631	chr6	Sh2d6	72513644	72513854	1737	-0.44422	0.503272	0.280199	0.391599	0.143694	0	19	14	32	16	52	32	16	23	16	40
ENSMUSG00000037300	chr8	Ttc13	1.25E+08	1.25E+08	10190	0.172381	4.567719	0.280392	0.391829	0.028416	0	320	276	429	359	493	461	628	580	602	643
ENSMUSG00000026975	chr2	Dph7	24962400	24962625	2365	0.252808	2.123597	0.280504	0.391946	0.049996	0	67	53	73	61	69	66	119	110	115	134
ENSMUSG00000057788	chr8	Ddx49	70292866	70293687	2928	0.177774	4.248444	0.280566	0.391994	0.029388	0	223	284	332	301	347	348	379	513	610	513
ENSMUSG00000037363	chr8	Letm2	25578492	25578804	2098	-0.25424	1.980099	0.280891	0.39235	0.050375	0	66	52	80	66	89	57	85	103	82	84
ENSMUSG00000040236	chr8	Trappc5	3676299	3676603	2546	-0.18216	4.989245	0.280888	0.39235	0.032365	0	444	600	655	514	588	625	728	674	800	618
ENSMUSG00000055923	chr5	Aasdh	76873659	76874313	6287	-0.22659	2.358847	0.280906	0.39235	0.043405	0	89	81	102	87	93	76	107	100	125	138
ENSMUSG00000025591	chr8	Tma16	66474330	66476909	4752	-0.24999	2.712595	0.280953	0.392376	0.055522	0	102	124	153	98	106	121	105	177	163	121
ENSMUSG00000022024	chr14	Sugt1	79587691	79587866	1951	-0.20586	5.709383	0.281271	0.392743	0.042645	0	884	848	1092	910	911	822	1066	1653	1089	1012
ENSMUSG00000022897	chr16	Dyrk1a	94570010	94570534	8251	-0.22529	6.152119	0.281273	0.392743	0.051454	0	1169	1058	1412	1214	1568	1206	1379	2416	1457	1119
ENSMUSG00000043858	chr7	Nup62	44816088	44816483	2851	0.171875	4.837492	0.281406	0.39289	0.028765	0	329	374	479	470	615	609	714	666	839	690
ENSMUSG00000020451	chr11	Limk2	3344256	3345884	6099	0.172987	3.934456	0.281732	0.393306	0.027334	0	201	205	286	219	289	287	432	394	397	368
ENSMUSG00000024759	chr19	Atl3	7494040	7494361	6698	-0.22701	4.56365	0.281813	0.393378	0.051027	0	407	258	475	383	639	241	455	542	726	647
ENSMUSG00000031840	chr8	Rab3a	70754679	70754868	2226	-0.20399	4.987624	0.282067	0.393693	0.040985	0	429	491	658	600	673	735	625	457	873	708
ENSMUSG00000038695	chr7	Josd2	44467980	44468190	2466	0.174306	5.233645	0.282127	0.393738	0.029965	0	474	566	736	542	631	762	991	991	1002	882
ENSMUSG00000019302	chr11	Atp6v0a1	1.01E+08	1.01E+08	6556	-0.17775	6.536285	0.282399	0.394078	0.032134	0	1394	1272	1914	1695	2024	1673	1642	1891	2709	2305
ENSMUSG00000024782	chr19	Ak3	29020833	29022946	3120	-0.17896	6.532452	0.282532	0.394224	0.032655	0	1312	1535	1685	1790	1882	1617	1986	1601	2789	2233
ENSMUSG00000048731	chr17	Ggnbp1	26973217	26973314	6943	-0.19793	4.011011	0.282588	0.394225	0.037102	0	291	288	324	249	259	332	335	319	361	376
ENSMUSG00000072381	chr3	Gm10355	1.01E+08	1.01E+08	519	-0.34208	0.077336	0.28259	0.394225	0.064509	0	18	16	22	16	18	20	17	15	24	23
ENSMUSG00000026657	chr2	Frmd4a	4017717	4018019	23350	0.215092	3.528306	0.28272	0.394367	0.043375	0	145	109	183	205	258	222	318	200	399	312
ENSMUSG00000020873	chr11	Slc35b1	95384692	95385113	2223	0.17326	5.233597	0.282783	0.394415	0.029658	0	535	524	631	539	721	821	903	760	1143	1012
ENSMUSG00000031848	chr8	Lsm4	70673248	70673457	1038	0.178421	5.142494	0.282968	0.394555	0.031495	0	404	539	689	544	593	762	780	758	1099	969
ENSMUSG00000057329	chr1	Bcl2	1.07E+08	1.07E+08	9157	-0.26394	2.357392	0.282967	0.394555	0.062031	0	75	69	108	73	143	55	120	146	123	98
ENSMUSG00000070284	chr9	Gmppb	1.08E+08	1.08E+08	2785	0.313712	3.210211	0.282969	0.394555	0.095834	0	122	91	165	101	217	182	309	81	383	253
ENSMUSG00000101609	chr7	Kcnq1ot1	1.43E+08	1.43E+08	84395	0.430601	1.158658	0.283013	0.394576	0.157495	0	42	16	26	19	48	16	52	60	58	105
ENSMUSG00000049532	chr14	Sall2	52311172	52315663	5433	0.291111	1.853982	0.283085	0.394637	0.07281	0	34	38	44	62	91	65	118	69	123	81
ENSMUSG00000033196	chr11	Myh2	67171027	67171088	7137	0.478714	9.584113	0.283206	0.394766	0.235058	0	7173	7648	2116	27526	8091	9371	17703	26892	38164	16843
ENSMUSG00000063760	chr10	Rnf217	31493193	31502731	11013	-0.16994	4.483289	0.283261	0.394803	0.027479	0	351	321	390	406	512	385	498	542	583	445
ENSMUSG00000029440	chr5	Psmd9	1.23E+08	1.23E+08	4562	0.169636	4.63016	0.283415	0.394978	0.027839	0	299	355	453	391	450	558	563	601	697	609
ENSMUSG00000001507	chr11	Itga3	95044474	95045763	5710	0.22847	2.752462	0.283603	0.395201	0.044527	0	86	85	94	117	130	109	136	175	244	187
ENSMUSG00000069049	chrY	Eif2s3y	1010543	1010685	4161	-1.00276	5.071836	0.283645	0.395219	0.979336	0	638	738	840	768	735	691	890	1	1022	3
ENSMUSG00000002820	chr9	Atg4d	21265299	21265717	2541	-0.18842	5.393488	0.283864	0.395485	0.035587	0	657	700	881	733	746	917	831	723	1050	1007
ENSMUSG00000019087	chrX	Atp6ap1	74297097	74297321	3026	0.176866	7.457797	0.283968	0.39559	0.032344	0	2479	2365	3245	2393	3362	3952	4174	3651	5215	4695
ENSMUSG00000097125	chr17	Gm26885	29461896	29462147	1688	-0.37689	0.2368	0.28419	0.395859	0.094357	0	9	12	33	29	22	13	27	24	22	25
ENSMUSG00000019539	chr7	Rcn3	45082913	45083363	1604	0.338441	5.703835	0.284345	0.396034	0.118072	0	729	350	847	509	1557	1157	1842	495	2079	1299
ENSMUSG00000063458	chr14	1700112E06Rik	22019712	22019908	2714	0.293664	1.535149	0.284619	0.396376	0.069208	0	26	46	39	38	62	74	62	57	80	82
ENSMUSG00000101628	chr1	Gm28177	52077261	52077300	3532	0.280217	4.079773	0.285087	0.396988	0.078942	0	206	201	292	282	296	536	409	167	476	510
ENSMUSG00000039209	chr16	Rpl39l	10170226	10170324	831	0.517344	-0.01554	0.285205	0.397073	0.211452	0	9	3	8	7	36	12	23	12	35	41
ENSMUSG00000040331	chr7	Nsmce4a	1.31E+08	1.31E+08	2597	0.200681	4.878862	0.285178	0.397073	0.040075	0	484	404	519	403	447	575	673	988	730	673
ENSMUSG00000039456	chr16	Morc3	93832121	93832348	4178	0.180591	4.156998	0.28554	0.397499	0.0313	0	258	186	339	248	378	320	501	448	512	431
ENSMUSG00000031577	chr8	Tti2	31150316	31151499	5039	0.215777	3.189981	0.285678	0.397651	0.042318	0	109	134	170	131	155	160	188	313	253	221
ENSMUSG00000009376	chr6	Met	17463800	17464248	7679	-0.2067	4.457351	0.285759	0.397723	0.042359	0	378	289	344	372	594	304	413	641	589	452
ENSMUSG00000011837	chr8	Snapc2	4253102	4253304	1513	0.183002	3.72035	0.285791	0.397729	0.030455	0	162	222	208	185	243	259	329	305	413	325
ENSMUSG00000031820	chr8	Babam1	71396855	71397020	1592	-0.16646	5.911545	0.285869	0.397797	0.028256	0	869	1009	1145	1066	1222	1068	1271	1252	1709	1347
ENSMUSG00000033885	chr14	Pxk	8098213	8098416	2840	-0.16947	3.89514	0.28614	0.398055	0.026522	0	221	222	265	253	357	237	323	329	422	330
ENSMUSG00000041879	chr1	Ipo9	1.35E+08	1.35E+08	8233	-0.16827	5.282481	0.28611	0.398055	0.028324	0	543	519	823	697	902	619	817	820	1119	942
ENSMUSG00000059895	chr15	Ptp4a3	73723145	73723515	4619	0.367903	8.580829	0.286116	0.398055	0.141324	0	5401	5011	5720	6558	4860	5935	5198	24557	6705	7412
ENSMUSG00000020027	chr10	Socs2	95385362	95388395	9531	-0.38453	3.658962	0.286406	0.398384	0.149584	0	118	386	104	141	435	237	328	250	310	139
ENSMUSG00000003033	chr8	Ap1m1	72240018	72240243	3150	0.163024	4.75219	0.286737	0.398737	0.025793	0	355	368	499	427	474	452	667	680	855	698
ENSMUSG00000015478	chr17	Rnf5	34601091	34601666	1483	0.207743	4.338334	0.286775	0.398737	0.042534	0	260	291	355	327	324	456	527	288	685	571
ENSMUSG00000029624	chr5	Ptcd1	1.45E+08	1.45E+08	3271	-0.24195	3.905223	0.286769	0.398737	0.058007	0	271	207	299	298	268	191	284	544	315	265
ENSMUSG00000068134	chr2	Zfp120	1.5E+08	1.5E+08	4376	-0.25399	3.425159	0.286754	0.398737	0.062702	0	174	163	235	200	196	136	180	399	235	190
ENSMUSG00000095567	chr4	Noc2l	1.56E+08	1.56E+08	2867	0.166811	5.26487	0.286911	0.398887	0.027977	0	489	499	724	572	766	729	883	846	1238	1080
ENSMUSG00000055116	chr7	Arntl	1.13E+08	1.13E+08	2904	-0.27097	3.686447	0.287198	0.399245	0.071748	0	117	174	293	237	389	218	300	397	231	190

ENSMUSG00000030067	chr6	Foxp1	98925338	98930234	14266	0.182147	3.764778	0.287349	0.399415	0.030873	0	182	149	241	235	259	219	316	362	407	389
ENSMUSG00000093133	chr11	Gm25994	1.07E+08	1.07E+08	101	-0.2463	3.28371	0.287487	0.399567	0.059346	0	193	167	173	127	207	96	219	274	211	246
ENSMUSG00000031684	chr8	Slc10a7	78509335	78509674	3630	-0.22727	2.617639	0.287549	0.399612	0.045949	0	97	88	118	110	135	75	121	114	190	166
ENSMUSG00000097062	chr11	Gm17586	1.21E+08	1.21E+08	908	0.253955	2.246142	0.287698	0.39978	0.055441	0	58	62	76	64	96	108	100	155	132	89
ENSMUSG00000022637	chr16	Cblb	52031549	52031685	6323	0.235783	4.017861	0.287988	0.400107	0.055244	0	238	182	299	219	306	250	321	685	443	345
ENSMUSG00000028522	chr4	Mier1	1.03E+08	1.03E+08	12513	-0.21396	4.239069	0.287992	0.400107	0.045622	0	286	278	385	352	394	238	363	645	456	349
ENSMUSG00000085289	chr18	Gm15337	39367038	39370316	3888	-0.36521	0.665504	0.288047	0.400145	0.091626	0	25	27	32	18	40	37	28	17	30	38
ENSMUSG00000032788	chr10	Pdxk	78436744	78440913	5124	0.240087	4.174681	0.288501	0.400694	0.057347	0	309	211	261	265	321	294	372	282	736	650
ENSMUSG00000068114	chr15	Ccdc134	82127922	82128049	2043	0.231081	4.156863	0.288475	0.400694	0.053969	0	185	226	375	212	397	375	642	286	468	457
ENSMUSG00000026688	chr1	Mgst3	1.67E+08	1.67E+08	1097	0.247681	6.581265	0.288554	0.400727	0.064433	0	1228	1583	1596	1728	1033	1956	2015	3690	2292	2048
ENSMUSG00000022142	chr15	Nup155	8109313	8109602	6402	-0.1789	3.724064	0.288648	0.400819	0.030299	0	228	193	250	211	284	193	315	274	410	270
ENSMUSG00000033308	chr3	Dpyd	1.19E+08	1.19E+08	8040	0.421729	1.29286	0.288728	0.400849	0.157307	0	31	26	16	41	53	24	30	104	74	87
ENSMUSG00000082284	chrX	H3f3a-ps1	1.02E+08	1.02E+08	410	0.357598	0.534309	0.288725	0.400849	0.084694	0	15	21	25	9	29	27	31	48	33	36
ENSMUSG00000030917	chr7	Tmem159	1.2E+08	1.2E+08	1926	0.201476	3.235591	0.288801	0.400909	0.036011	0	126	142	158	151	142	156	226	281	268	240
ENSMUSG00000037999	chr5	Arap2	62602445	62604656	8716	-0.33611	1.442274	0.288835	0.400917	0.101311	0	42	38	53	57	56	22	37	40	99	85
ENSMUSG00000085133	chr14	B930095G15Rik	1.21E+08	1.21E+08	2792	0.46266	0.348604	0.289008	0.401117	0.165984	0	13	8	20	20	22	12	30	70	18	27
ENSMUSG00000025982	chr1	Sf3b1	54985169	54987492	11370	0.182055	6.765153	0.289158	0.401284	0.034805	0	1473	1533	1966	1432	2147	1831	2603	3439	3007	2680
ENSMUSG00000031627	chr8	Irf2	46739745	46739936	2484	0.178692	4.111705	0.289523	0.401751	0.030677	0	234	229	307	285	293	352	326	469	563	429
ENSMUSG00000074781	chr10	Ube2n	95515162	95515237	3851	-0.19808	5.818422	0.289837	0.402146	0.040882	0	915	956	1198	842	1108	1175	1283	809	1436	1383
ENSMUSG00000042082	chr13	Arsb	93771679	93772092	3989	-0.22645	3.828211	0.289969	0.402289	0.050247	0	213	142	286	240	427	227	380	211	396	321
ENSMUSG00000000149	chr5	Gna12	1.41E+08	1.41E+08	3416	0.179968	5.489924	0.290007	0.402302	0.033409	0	501	592	795	841	812	863	1181	848	1473	1248
ENSMUSG00000022159	chr14	Rab2b	52261759	52263817	4163	0.259642	2.151969	0.290057	0.402331	0.057514	0	63	35	79	73	84	67	104	117	134	137
ENSMUSG00000000693	chr6	Loxl3	83034173	83034289	4196	0.318073	3.802564	0.29023	0.402531	0.104113	0	197	79	238	147	410	245	398	177	593	429
ENSMUSG00000024949	chr19	Sf1	6363690	6364118	6211	0.167131	6.131432	0.290846	0.403343	0.029259	0	863	923	1235	1108	1439	1399	1626	1880	2054	1693
ENSMUSG00000031107	chrX	Rbmx2	48695004	48695120	1872	0.286503	1.281919	0.290903	0.403343	0.061254	0	27	30	37	37	45	51	46	44	89	71
ENSMUSG00000041153	chr4	Osgin2	15997121	15999000	5571	0.216994	2.678132	0.29089	0.403343	0.040371	0	84	95	115	90	101	115	190	135	201	156
ENSMUSG00000038806	chr1	Sde2	1.81E+08	1.81E+08	3471	0.205413	3.501912	0.290983	0.403412	0.040564	0	118	145	179	181	263	196	243	362	355	260
ENSMUSG00000034430	chr6	Zxdc	90369492	90370568	8564	0.28552	4.318173	0.291348	0.403878	0.084237	0	251	288	334	273	348	273	379	1044	484	375
ENSMUSG00000066551	chr5	Hmgb1	1.49E+08	1.49E+08	4944	0.178223	6.780616	0.291504	0.404014	0.033652	0	1645	1572	1991	1551	1810	2186	2435	3267	3024	2673
ENSMUSG00000070407	chr11	Hs3st3b1	63885792	63889745	4911	-0.35916	0.282771	0.291497	0.404014	0.089985	0	17	17	26	18	29	16	25	29	38	9
ENSMUSG00000057738	chr2	Sptan1	29965560	29965785	11428	-0.17967	6.451602	0.291583	0.404083	0.034174	0	1239	1198	1680	1804	1909	1191	2269	1722	2567	2005
ENSMUSG00000048450	chr5	Msx1	37820485	37821700	3097	-0.28394	1.784163	0.291768	0.404298	0.067313	0	58	38	66	62	88	73	79	61	91	47
ENSMUSG00000039047	chr3	Pigk	1.53E+08	1.53E+08	9367	-0.16934	5.178925	0.292094	0.404711	0.029273	0	537	490	766	619	822	662	869	637	1001	816
ENSMUSG00000104279	chr1	RP24-252K15.4	1.78E+08	1.78E+08	1870	0.30475	0.886995	0.29214	0.404733	0.070152	0	19	24	25	27	36	35	40	66	46	37
ENSMUSG00000038671	chr2	Arfrp1	1.81E+08	1.81E+08	4320	0.18134	4.755731	0.29217	0.404734	0.03338	0	338	448	506	367	440	616	664	650	685	687
ENSMUSG00000094446	chr13	Gm6344	55085777	55086259	483	0.274697	2.210985	0.292511	0.405166	0.069359	0	53	59	39	91	101	100	111	109	156	104
ENSMUSG00000014294	chr18	Ndufa2	36742332	36742658	572	0.201952	7.21927	0.292561	0.405195	0.043681	0	1986	2534	2698	2141	2068	3788	3258	3592	3815	3821
ENSMUSG00000022428	chr15	Cby1	79659227	79659293	1119	-0.19149	3.385011	0.292627	0.405246	0.034037	0	143	157	223	206	198	196	232	181	312	214
ENSMUSG00000023020	chr15	Cox14	99725618	99725848	723	0.205094	6.526654	0.292785	0.405411	0.044886	0	1124	1552	1756	1341	1322	2501	2205	2044	2517	2026
ENSMUSG00000029345	chr5	Tfip11	1.12E+08	1.12E+08	4086	-0.16751	4.215363	0.292834	0.405411	0.027406	0	289	248	401	346	359	290	394	456	506	404
ENSMUSG00000040260	chr17	Daam2	49456022	49458747	6045	-0.24776	3.917833	0.292829	0.405411	0.062036	0	235	174	321	241	423	248	531	209	370	252
ENSMUSG00000029504	chr5	Ddx51	1.11E+08	1.11E+08	5248	0.192691	3.453225	0.292867	0.405415	0.034266	0	161	151	194	141	199	167	324	294	323	259
ENSMUSG00000031701	chr8	Dnaja2	85537640	85539407	2839	-0.21181	7.611477	0.292931	0.405464	0.048245	0	2904	3324	4030	3407	3856	3442	3758	6392	3975	3355
ENSMUSG00000068206	chr15	Pick1	79229173	79229420	7770	-0.18378	5.04913	0.293308	0.405945	0.034787	0	493	561	646	610	613	657	619	848	700	738
ENSMUSG00000049097	chr3	Ankrd34a	96596636	96596808	2583	-0.32266	1.056562	0.293729	0.406486	0.079131	0	33	26	46	27	56	45	30	29	60	42
ENSMUSG00000029427	chr5	Zcchc8	1.24E+08	1.24E+08	4286	0.173455	3.695372	0.293968	0.406777	0.027894	0	193	169	215	201	230	226	326	358	377	313
ENSMUSG00000031803	chr8	B3gnt3	71691719	71693155	2103	0.280623	2.372545	0.294145	0.406981	0.070771	0	69	85	69	96	55	87	119	111	227	123
ENSMUSG00000039347	chr6	Atp6v0e2	48537569	48537854	1832	-0.1709	5.536446	0.294262	0.407103	0.030544	0	753	778	896	770	880	929	971	1066	1055	1013
ENSMUSG00000008206	chr8	Cers4	4493026	4493068	12268	0.238783	2.166145	0.294394	0.407244	0.048522	0	53	49	71	87	78	72	110	117	130	130
ENSMUSG00000024713	chr19	Pcsk5	17432832	17433775	9346	-0.32861	3.591786	0.294657	0.407568	0.112014	0	268	69	209	152	451	136	334	212	320	263
ENSMUSG00000042719	chr5	Naa25	1.21E+08	1.21E+08	8298	-0.28211	5.34862	0.294776	0.407691	0.085079	0	647	614	877	768	836	523	662	1764	749	573
ENSMUSG00000037072	chr3	Sep15	1.45E+08	1.45E+08	2104	-0.1743	6.672965	0.294963	0.40791	0.032665	0	1700	1664	2169	1527	1946	1815	2444	1863	2842	2274
ENSMUSG00000045104	chr19	Gm5514	21938079	21938384	306	0.509109	-0.33698	0.295052	0.407991	0.168359	0	9	6	5	22	4	13	20	9	34	20
ENSMUSG00000028309	chr4	Rnf20	49632006	49632033	7288	-0.16624	5.032963	0.295193	0.408146	0.028336	0	474	463	728	515	741	556	801	734	795	709
ENSMUSG00000052713	chr18	Zfp608	54888045	54889081	6112	-0.22999	2.611063	0.295269	0.408211	0.048065	0	86	75	112	150	124	88	127	150	153	134
ENSMUSG00000025190	chr19	Got1	43499752	43500557	2539	-0.2165	8.275686	0.295319	0.408238	0.051043	0	4241	5957	5744	7308	4119	6407	6334	5856	8369	6311
ENSMUSG00000045176	chr11	2310047M10Rik	69059717	69061578	1862	0.170922	4.282984	0.295515	0.408469	0.02924	0	250	275	381	290	330	437	447	502	509	477
ENSMUSG00000025413	chr4	Ttc4	1.07E+08	1.07E+08	3568	-0.17527	5.34083	0.295564	0.408496	0.032061	0	569	671	870	667	820	861	934	751	969	870
ENSMUSG00000029047	chr4	Pex10	1.55E+08	1.55E+08	3298	-0.21598	3.120297	0.295662	0.408591	0.044116	0	138	153	213	134	130	159	162	191	224	193
ENSMUSG00000092085	chr1	Gm17224	1.72E+08	1.72E+08	500	0.98256	2.13025	0.295705	0.408609	0.974314	0	11	45	6	136	33	10	7	7	627	113
ENSMUSG00000032688	chr18	Malt1	65430963	65431398	5073	0.277077	2.25717	0.295786	0.40868	0.069586	0	54	60	82	70	90	45	108	135	171	158
ENSMUSG00000040040	chr14	Ift88	57424062	57424187	4628	-0.26643	2.24285	0.295846	0.408722	0.06485	0	91	63	92	90	86	63	89	147	87	106
ENSMUSG00000042436	chr11	Mfap4	61485431	61485485	1922	0.334984	6.356383	0.296189	0.409155	0.121853	0	1292	475	1166	921	2398	1815	3530	973	2686	1689
ENSMUSG00000078349	chr4	AW011738	1.56E+08	1.56E+08	1848	-0.37514	0.732684	0.296436	0.409456	0.113005	0	22	36	21	38	30	33	17	45	25	37
ENSMUSG00000030257	chr6	Srgap3	1.13E+08	1.13E+08	9852	0.325705	2.469191	0.296469	0.40946	0.105417	0	85	26	93	58	154	87	184	133	200	114
ENSMUSG00000014668	chr5	Chfr	1.1E+08	1.1E+08	3169	-0.16905	4.367564	0.296791	0.409863	0.028662	0	330	310	460	346	372	361	495	477	485	436

ENSMUSG00000026869	chr2	Psmd5	34852088	34852833	3750	0.165304	4.39036	0.296831	0.409878	0.027449	0	266	301	404	311	367	450	481	531	622	486
ENSMUSG00000036712	chr8	Cyld	88697028	88697099	8035	-0.17521	4.89435	0.296967	0.410025	0.031866	0	487	411	563	529	649	469	681	820	673	609
ENSMUSG00000026127	chr1	Imp4	34439851	34439927	8553	0.197412	4.091059	0.297047	0.410095	0.039119	0	237	255	279	212	336	310	425	285	624	505
ENSMUSG00000085315	chr2	A430018G15Rik	52425012	52425155	1713	0.364285	0.045314	0.297083	0.410103	0.080686	0	8	13	16	13	18	10	20	33	34	27
ENSMUSG00000044017	chr5	Gpr133	1.29E+08	1.29E+08	8321	-0.23432	3.807407	0.297139	0.41014	0.056214	0	229	146	244	221	449	175	365	228	398	358
ENSMUSG00000005609	chr7	Ctr9	1.11E+08	1.11E+08	6544	-0.16701	4.769626	0.297294	0.410155	0.028699	0	366	397	583	473	614	432	608	510	821	661
ENSMUSG00000014601	chr3	Strip1	1.08E+08	1.08E+08	3231	-0.1621	4.871686	0.297372	0.410155	0.027065	0	451	421	608	504	605	503	642	555	794	740
ENSMUSG00000024095	chr17	Hnrnpll	80029487	80030540	11677	-0.16883	4.071079	0.297387	0.410155	0.028442	0	273	233	310	306	362	252	339	356	534	389
ENSMUSG00000024219	chr17	Anks1	27909340	27909646	7143	-0.20648	4.330991	0.297302	0.410155	0.043991	0	284	283	288	368	600	346	469	313	598	468
ENSMUSG00000028954	chr5	Nub1	24685815	24686022	3455	0.230184	5.304879	0.297335	0.410155	0.056831	0	548	489	722	626	652	625	737	1703	976	936
ENSMUSG00000031734	chr8	Irx3	91798525	91798976	2611	0.397828	0.669879	0.297202	0.410155	0.130009	0	13	20	34	32	7	31	49	27	58	34
ENSMUSG00000035390	chr7	Brsk1	4690604	4690720	3594	0.330781	0.782267	0.297336	0.410155	0.088561	0	16	12	30	20	45	28	60	36	48	39
ENSMUSG00000047417	chr10	Rexo1	80540922	80542824	7155	-0.17553	3.895702	0.297244	0.410155	0.030144	0	200	199	295	296	338	210	309	358	399	366
ENSMUSG00000028649	chr4	Macf1	1.23E+08	1.23E+08	26689	-0.18746	6.474846	0.297634	0.410435	0.038195	0	1352	1116	1772	1718	2044	1196	2597	1700	2511	1868
ENSMUSG00000042308	chr7	Setd1a	1.28E+08	1.28E+08	6795	-0.1915	4.410296	0.297649	0.410435	0.037863	0	297	295	377	417	523	277	407	620	562	473
ENSMUSG00000025369	chr10	Smarcc2	1.28E+08	1.28E+08	5027	-0.16913	5.635681	0.297687	0.410446	0.030539	0	801	679	928	906	1099	693	1060	1299	1290	1173
ENSMUSG00000013465	chr2	Nelfb	25199712	25200466	3432	0.162732	4.869383	0.297738	0.410476	0.027106	0	396	421	532	464	479	524	726	662	908	805
ENSMUSG00000047084	chr7	Ngrn	80261215	80261423	1714	0.185171	4.430741	0.297797	0.410516	0.035117	0	294	340	385	330	314	504	589	526	540	472
ENSMUSG00000008429	chr9	Herpud2	25108130	25109005	2744	-0.24458	5.329245	0.297841	0.410536	0.06449	0	625	585	833	696	928	519	710	1575	770	711
ENSMUSG00000021678	chr13	F2rl1	95511732	95514281	2754	0.377089	0.408238	0.298058	0.410794	0.10167	0	17	17	18	18	18	26	53	13	34	35
ENSMUSG00000015023	chr8	Ddx19a	1.11E+08	1.11E+08	2957	-0.1722	4.243179	0.298146	0.410875	0.029802	0	287	262	386	330	418	281	395	526	477	404
ENSMUSG00000047423	chr19	AI837181	5425157	5425308	1529	0.172363	5.327228	0.298246	0.410972	0.03165	0	457	538	756	614	823	812	937	1187	1147	863
ENSMUSG00000072955	chrX	Tmsb15l	1.37E+08	1.37E+08	816	-0.3638	0.341178	0.298492	0.41127	0.090737	0	21	30	19	19	20	30	20	22	23	23
ENSMUSG00000026427	chr1	Eif2d	1.31E+08	1.31E+08	7374	-0.16284	4.813158	0.298566	0.411292	0.027543	0	452	438	538	505	533	474	538	655	775	663
ENSMUSG00000038212	chr13	Hiatl1	65064663	65066861	3925	-0.1742	3.876424	0.298593	0.411292	0.030329	0	227	213	286	252	323	189	311	330	466	342
ENSMUSG00000090077	chr2	Lime1	1.81E+08	1.81E+08	2304	0.183659	3.288157	0.298598	0.411292	0.031697	0	129	134	185	124	189	176	251	246	267	264
ENSMUSG00000099411	chr16	2310015D24Rik	13514131	13516487	3035	-0.32173	4.054775	0.298653	0.411327	0.109757	0	292	219	394	290	352	483	381	99	370	322
ENSMUSG00000021884	chr14	Hacl1	31552905	31552990	5123	-0.2006	2.858805	0.298973	0.411727	0.037015	0	115	122	133	125	143	107	136	170	202	172
ENSMUSG00000026697	chr1	Myoc	1.63E+08	1.63E+08	2074	-0.38633	5.200478	0.299063	0.41181	0.16252	0	1037	294	669	507	968	561	565	1599	367	526
ENSMUSG00000029821	chr6	Dfna5	50189369	50190982	7375	0.369375	0.142628	0.299412	0.41225	0.089445	0	8	17	9	14	25	18	31	18	38	28
ENSMUSG00000032497	chr9	Lrrfip2	1.11E+08	1.11E+08	3260	0.172175	5.973601	0.299458	0.412272	0.03207	0	855	906	1090	984	1086	1280	1421	1872	1654	1494
ENSMUSG00000099471	chr1	Gm8451	1.27E+08	1.27E+08	447	0.380604	0.306929	0.299599	0.412425	0.092481	0	16	15	10	22	18	21	24	22	58	28
ENSMUSG00000080824	chr6	Gm9001	75782358	75782756	399	-0.43824	-0.09763	0.299728	0.412523	0.14652	0	26	16	18	7	13	21	16	23	13	9
ENSMUSG00000100826	chr7	D7Ertd715e	59307924	59309726	26093	-0.29185	0.578297	0.299729	0.412523	0.060061	0	27	25	27	25	24	18	33	26	37	35
ENSMUSG00000026743	chr2	Mllt10	18055237	18055371	5907	-0.25519	3.879978	0.300055	0.412883	0.068449	0	255	203	299	260	319	191	220	582	303	264
ENSMUSG00000029205	chr5	Chrna9	65934921	65935034	3018	-0.52718	1.131312	0.300081	0.412883	0.27512	0	10	49	54	38	62	29	16	24	20	110
ENSMUSG00000039361	chr7	Picalm	90130232	90130702	4174	-0.16617	6.793658	0.300081	0.412883	0.030328	0	1577	1803	2029	1972	2449	1742	2666	2698	2915	2259
ENSMUSG00000026456	chr1	Cyb5r1	1.34E+08	1.34E+08	4437	0.167106	6.701884	0.300318	0.413127	0.030676	0	1427	1418	1936	1579	1846	2383	2586	2426	2942	2410
ENSMUSG00000027244	chr2	Atg13	91674618	91676463	4368	-0.21163	5.068353	0.300306	0.413127	0.048331	0	570	486	622	619	704	449	577	1158	764	692
ENSMUSG00000001134	chrX	Uxt	20941722	20941797	1639	0.18944	4.017395	0.300649	0.413542	0.036742	0	196	262	321	201	277	368	380	434	379	413
ENSMUSG00000016308	chrX	Ube2a	36874358	36874529	1662	0.169007	4.940345	0.300824	0.413742	0.030104	0	438	454	564	427	516	694	770	726	808	748
ENSMUSG00000036371	chr6	Serbp1	67266979	67267409	6685	-0.16199	8.027876	0.300865	0.413757	0.029164	0	3844	4031	5345	4604	5277	4660	5457	6429	6460	5696
ENSMUSG00000022517	chr16	Mgrn1	4886100	4886473	3293	-0.16956	5.830866	0.300975	0.413811	0.031325	0	803	899	1028	1192	1103	882	1266	1197	1781	1219
ENSMUSG00000027510	chr2	Rbm38	1.73E+08	1.73E+08	2869	-0.18949	6.92748	0.300955	0.413811	0.039672	0	1674	1906	2487	2672	2081	2624	2832	2426	2814	2384
ENSMUSG00000054381	chr7	Zfp747	1.27E+08	1.27E+08	2657	-0.26435	1.331836	0.301012	0.413811	0.05205	0	32	36	47	47	62	43	52	55	64	44
ENSMUSG00000097333	chr13	Zfp87	67515781	67518112	2865	0.260855	2.048564	0.301054	0.413811	0.060598	0	63	35	73	55	84	63	93	132	134	98
ENSMUSG00000103988	chr3	Dnajc19	34077454	34077524	333	-0.20263	5.042161	0.301031	0.413811	0.044058	0	517	611	742	523	517	764	627	612	741	755
ENSMUSG00000004865	chr17	Srpk1	28587648	28590241	9647	-0.15851	4.430232	0.301268	0.414064	0.025577	0	335	326	411	358	469	385	485	427	619	466
ENSMUSG00000026209	chr1	Dnpep	75307896	75308709	4289	0.17019	5.482012	0.301598	0.414477	0.031112	0	580	669	722	771	750	797	969	1321	1309	1147
ENSMUSG00000025505	chr7	Tmem80	1.41E+08	1.41E+08	3178	-0.18089	3.584646	0.301764	0.414631	0.031775	0	185	189	258	197	229	231	255	211	299	303
ENSMUSG00000030766	chr7	Arhgap17	1.23E+08	1.23E+08	3583	0.169767	4.44741	0.30183	0.414631	0.029738	0	255	297	376	392	397	372	493	601	611	624
ENSMUSG00000038776	chr1	Ephx1	1.81E+08	1.81E+08	1950	0.179052	4.010631	0.301813	0.414631	0.032139	0	255	175	271	286	267	289	365	449	527	375
ENSMUSG00000041000	chr4	Trim62	1.29E+08	1.29E+08	5015	0.301804	0.859134	0.301776	0.414631	0.066772	0	15	20	38	23	34	33	34	51	53	50
ENSMUSG00000044098	chr3	Rsbn1	1.04E+08	1.04E+08	6861	-0.2739	2.929059	0.302091	0.414948	0.076309	0	122	90	129	160	196	85	127	278	181	134
ENSMUSG00000020325	chr10	Fstl3	79777272	79777397	2445	0.32911	1.163902	0.302304	0.415199	0.093923	0	42	17	43	29	26	44	83	42	58	50
ENSMUSG00000030347	chr6	D6Wsu163e	1.27E+08	1.27E+08	2238	0.207356	2.876032	0.302386	0.415271	0.040404	0	84	117	137	92	133	117	188	180	228	204
ENSMUSG00000025200	chr19	Cwf19l1	44108644	44110660	3574	0.243722	2.108146	0.303053	0.416146	0.051658	0	51	54	73	72	73	94	79	91	157	115
ENSMUSG00000017734	chr2	Dbndd2	1.64E+08	1.64E+08	4389	0.178617	4.31866	0.303131	0.416212	0.032999	0	300	295	371	281	296	469	492	425	563	491
ENSMUSG00000025020	chr19	Slit1	41600257	41601700	5921	0.274194	1.230513	0.303345	0.416464	0.059246	0	29	26	42	37	36	45	77	53	68	44
ENSMUSG00000021257	chr12	Angel1	86700502	86702441	4463	-0.18761	3.273352	0.303482	0.416611	0.033808	0	171	127	203	181	169	161	208	220	267	196
ENSMUSG00000032649	chr1	Colgalt2	1.52E+08	1.52E+08	4245	-0.24554	2.659371	0.303646	0.416753	0.057573	0	111	74	112	145	123	117	177	105	162	104
ENSMUSG00000056851	chr15	Pcbp2	1.02E+08	1.02E+08	2868	0.167326	7.360306	0.30362	0.416753	0.031372	0	2160	2021	2915	2851	3070	3012	3735	4736	4610	4247
ENSMUSG00000054676	chr7	1600014C10Rik	38183217	38183521	3931	-0.19984	5.237869	0.303713	0.416803	0.043675	0	561	616	707	721	755	725	747	493	1050	1086
ENSMUSG00000070283	chr9	Ndufaf3	1.09E+08	1.09E+08	1815	0.179447	3.98451	0.303823	0.416914	0.032284	0	225	261	268	232	231	340	365	342	496	408
ENSMUSG00000030509	chr7	Asb7	66644565	66647925	6226	-0.18539	3.289276	0.303902	0.41698	0.033035	0	143	124	212	190	201	143	245	216	265	201
ENSMUSG00000063480	chr15	Nhp2l1	82041319	82042368	2130	0.159205	5.535804	0.304117	0.417234	0.027497	0	628	694	828	686	813	969	1171	1010	1348	1199

ENSMUSG00000041126	chr11	H2afv	6427229	6428432	1633	-0.16419	5.143789	0.304367	0.417536	0.02897	0	561	581	700	589	672	675	808	828	825	719
ENSMUSG00000013846	chr15	St3gal1	67102875	67106830	4985	0.185753	4.812049	0.304504	0.417682	0.037173	0	368	296	462	467	631	437	833	571	978	731
ENSMUSG00000016833	chr5	Mrps18c	1.01E+08	1.01E+08	1076	0.181588	4.596454	0.304577	0.417705	0.034843	0	358	390	424	351	337	557	596	556	641	609
ENSMUSG00000024891	chr19	Slc29a2	5024006	5024277	2472	0.219534	2.835875	0.304581	0.417705	0.044382	0	116	109	98	105	106	152	188	179	207	155
ENSMUSG00000040843	chr1	Tiprl	1.65E+08	1.65E+08	5473	0.179616	4.606604	0.30474	0.417849	0.034399	0	324	371	485	291	433	532	707	539	629	578
ENSMUSG00000042613	chr3	Pbxip1	89436706	89436780	4674	-0.17691	8.712431	0.304765	0.417849	0.035464	0	6233	6195	9259	7394	8316	7047	8323	12065	9670	8743
ENSMUSG00000063849	chr9	Ppcdc	57412668	57414726	2747	0.209513	2.714628	0.304776	0.417849	0.040881	0	105	79	119	86	111	136	149	142	206	178
ENSMUSG00000021866	chr14	Anxa11	25842156	25842295	4135	-0.20468	5.857555	0.304857	0.417918	0.046711	0	925	863	1130	1089	1179	730	1211	1954	1350	1089
ENSMUSG00000014609	chr11	Chrne	70614883	70615128	1690	0.189846	4.001651	0.304985	0.417969	0.037227	0	258	219	239	228	290	331	357	515	382	376
ENSMUSG00000027111	chr2	Itga6	71745616	71745650	9025	-0.19707	5.02598	0.30496	0.417969	0.042662	0	446	477	663	757	561	485	676	530	1169	767
ENSMUSG00000032047	chr9	Acat1	53580522	53582665	3758	-0.19295	7.420749	0.304931	0.417969	0.042055	0	2386	3215	3250	3665	2556	2891	3317	4445	4190	3819
ENSMUSG00000043801	chr17	Oaz1-ps	17345456	17345935	681	0.1666	5.555319	0.305041	0.418004	0.030442	0	596	704	870	695	835	1037	1059	1047	1275	1339
ENSMUSG00000024353	chr18	Mzb1	35647266	35647726	905	0.398	-0.30768	0.305196	0.418093	0.087601	0	7	8	11	11	14	15	20	24	10	23
ENSMUSG00000027286	chr2	Lrrc57	1.21E+08	1.21E+08	2227	-0.18022	3.921399	0.305168	0.418093	0.033492	0	279	250	306	240	246	283	370	303	391	299
ENSMUSG00000033883	chr3	D3Ertd254e	36159522	36159648	6503	-0.24318	1.994386	0.30519	0.418093	0.051595	0	61	47	71	80	98	60	75	78	103	104
ENSMUSG00000021327	chr13	Zkscan3	21387013	21388706	7817	-0.19388	4.123354	0.305366	0.418284	0.039734	0	314	243	323	277	392	234	489	461	402	316
ENSMUSG00000087331	chr15	1810021B22Rik	89071196	89071336	896	0.292467	1.069352	0.305686	0.418682	0.063678	0	31	31	25	35	25	38	56	55	61	47
ENSMUSG00000080002	chr5	Gm5566	1.5E+08	1.5E+08	459	0.381831	0.007062	0.305899	0.418931	0.090911	0	5	19	9	14	18	18	21	28	28	24
ENSMUSG00000003031	chr6	Cdkn1b	1.35E+08	1.35E+08	4552	-0.22574	5.128018	0.30606	0.419111	0.056621	0	552	524	708	659	705	406	719	1290	747	620
ENSMUSG00000026429	chr1	Ube2t	1.35E+08	1.35E+08	4832	-0.28964	2.071497	0.306283	0.419375	0.081089	0	65	76	116	73	45	89	85	63	111	82
ENSMUSG00000023110	chr14	Prmt5	54507187	54507947	3958	-0.15884	5.397538	0.306514	0.419567	0.027541	0	632	657	919	676	837	787	908	899	1181	874
ENSMUSG00000024750	chr19	Zfand5	21272278	21272742	6193	-0.29713	7.633266	0.306503	0.419567	0.100412	0	3382	3036	4061	3732	4068	2540	2958	9081	3328	2751
ENSMUSG00000038175	chr13	Mylip	45389742	45390043	3062	0.282348	3.871722	0.306455	0.419567	0.086911	0	192	129	306	260	221	177	279	704	346	371
ENSMUSG00000068686	chr2	Cd59b	1.04E+08	1.04E+08	1300	-0.35107	1.10901	0.306591	0.419629	0.108528	0	31	39	53	35	36	58	35	19	60	37
ENSMUSG00000014504	chr18	Srp19	34330847	34331111	3630	0.175438	5.009775	0.306702	0.419723	0.033461	0	433	495	620	454	509	675	798	943	851	684
ENSMUSG00000029699	chr5	Ssc4d	1.36E+08	1.36E+08	2976	0.343487	0.293253	0.306719	0.419723	0.078171	0	12	15	20	13	23	12	31	37	31	37
ENSMUSG00000027611	chr2	Procr	1.56E+08	1.56E+08	2031	-0.21419	3.169074	0.306824	0.419741	0.046437	0	145	136	207	149	163	137	147	269	206	205
ENSMUSG00000032633	chr11	Flcn	59791408	59792811	4322	-0.18533	5.506157	0.306796	0.419741	0.038217	0	719	697	912	858	839	631	954	1403	1041	952
ENSMUSG00000073147	chr5	5031425E22Rik	23382308	23382529	5142	0.28159	3.386007	0.306811	0.419741	0.084693	0	126	122	183	197	154	142	200	506	216	262
ENSMUSG00000051256	chr6	Jagn1	1.13E+08	1.13E+08	1201	0.157522	4.679531	0.306862	0.419752	0.026355	0	352	346	467	378	481	559	611	600	756	607
ENSMUSG00000042178	chr7	Armc5	1.28E+08	1.28E+08	3834	0.172975	3.91459	0.307144	0.420097	0.030788	0	197	184	296	197	319	272	382	316	457	442
ENSMUSG00000061559	chr9	Wdr61	54714735	54717125	4669	0.170412	4.087355	0.307266	0.420222	0.029774	0	236	260	305	215	311	310	428	479	467	409
ENSMUSG00000021275	chr12	Tecpr2	1.11E+08	1.11E+08	7830	-0.22986	2.479971	0.307305	0.420233	0.051901	0	93	72	96	114	122	59	136	134	144	128
ENSMUSG00000038936	chr1	Sccpdh	1.8E+08	1.8E+08	7562	0.174815	5.865256	0.307348	0.420251	0.034185	0	791	793	1151	834	1015	1144	1667	1659	1444	1253
ENSMUSG00000029174	chr5	Tbc1d1	64159451	64160505	7140	0.198518	5.206825	0.307584	0.42049	0.043692	0	587	467	520	515	778	685	846	1299	1039	729
ENSMUSG00000087165	chr11	2010001A14Rik	57795499	57795794	714	0.346421	0.249691	0.307561	0.42049	0.084381	0	18	11	17	21	12	31	23	30	24	31
ENSMUSG00000032745	chr13	Gpbp1	1.11E+08	1.11E+08	3905	-0.17285	5.783658	0.307678	0.420577	0.033305	0	834	871	1149	924	1102	984	1325	1445	1222	1022
ENSMUSG00000027479	chr2	Mapre1	1.54E+08	1.54E+08	7811	0.169507	6.117556	0.307751	0.420586	0.032298	0	858	957	1297	1050	1334	1431	1772	1305	2278	1833
ENSMUSG00000028437	chr4	Ubap1	41348996	41349231	3583	-0.18155	5.690236	0.307741	0.420586	0.036737	0	728	795	1061	953	1065	911	985	1531	1080	1085
ENSMUSG00000048495	chr1	Tyw5	57388237	57388752	2672	0.295357	1.440246	0.307775	0.420586	0.071846	0	35	49	34	45	28	54	74	57	79	72
ENSMUSG00000028212	chr4	Ccne2	11191351	11191544	3495	-0.27531	1.643484	0.308494	0.421526	0.071427	0	55	49	71	54	47	33	65	76	106	50
ENSMUSG00000003352	chr15	Cacnb3	98632220	98632520	3120	0.225326	2.460832	0.308694	0.421717	0.048221	0	66	55	100	87	115	95	175	116	174	127
ENSMUSG00000022283	chr15	Pabpc1	36595661	36596099	5768	0.174777	6.952516	0.308682	0.421717	0.034872	0	1332	1602	2175	2082	2685	1953	2962	3206	4167	3309
ENSMUSG00000042229	chr1	Rabif	1.34E+08	1.34E+08	2861	-0.1699	3.783157	0.308738	0.421735	0.029444	0	217	205	274	235	282	235	334	234	413	302
ENSMUSG00000060981	chr13	Hist1h4h	23531050	23531522	473	-0.21665	3.081126	0.308792	0.421767	0.047026	0	112	164	185	160	125	161	166	204	204	164
ENSMUSG00000030888	chr7	Rrp8	1.06E+08	1.06E+08	3072	0.165157	4.06834	0.309018	0.422034	0.028057	0	234	231	329	221	303	298	432	455	473	409
ENSMUSG00000041084	chr3	Ostc	1.31E+08	1.31E+08	1058	0.216317	5.067893	0.309112	0.422109	0.052504	0	448	404	620	425	724	754	970	429	1200	870
ENSMUSG00000082319	chrX	Gm8822	81820384	81822730	2347	0.382877	-0.08006	0.309134	0.422109	0.081458	0	10	7	10	19	15	12	26	17	33	25
ENSMUSG00000082516	chr2	Gm13342	22410525	22410731	207	-0.43318	0.177159	0.309221	0.422186	0.15489	0	19	23	22	29	5	28	15	15	24	20
ENSMUSG00000020032	chr10	Nuak1	84370905	84375387	5625	-0.1998	4.433187	0.309271	0.422213	0.043684	0	287	328	406	481	427	283	578	616	523	360
ENSMUSG00000048126	chr1	Col6a3	90765923	90765933	11963	-0.30512	8.515437	0.30938	0.422321	0.107252	0	6022	3136	8027	4843	13163	6023	12126	3367	10379	6744
ENSMUSG00000103171	chr3	DNAJC19	34078662	34078845	393	-0.20038	5.014797	0.30957	0.422537	0.044606	0	511	600	734	501	507	759	617	602	727	728
ENSMUSG00000070576	chr5	Mn1	1.11E+08	1.11E+08	6940	-0.21179	5.384067	0.309636	0.422586	0.050606	0	910	439	757	862	740	766	1030	1011	994	684
ENSMUSG00000056770	chr12	Setd3	1.08E+08	1.08E+08	6035	-0.17275	6.80435	0.309872	0.422866	0.03416	0	1726	1814	2264	1947	2119	1932	2214	3060	2517	2483
ENSMUSG00000097177	chr9	9330159M07Rik	88840236	88840726	6831	-0.336	2.174219	0.310275	0.423375	0.116582	0	90	82	73	86	74	57	65	189	87	59
ENSMUSG00000029144	chr5	Gtf3c2	31156005	31157767	6359	-0.16153	4.971234	0.310474	0.423597	0.028663	0	486	455	672	478	691	460	665	763	857	742
ENSMUSG00000042472	chr12	Zfp410	84316859	84317174	2697	-0.1607	4.066861	0.310499	0.423597	0.026473	0	244	246	354	298	336	300	392	391	413	339
ENSMUSG00000028295	chr4	Smim8	34768664	34769147	1510	0.208307	3.833366	0.310735	0.423877	0.046378	0	203	212	285	216	169	375	332	349	340	337
ENSMUSG00000078772	chr4	Gm12353	19605451	19605536	554	-0.25409	2.529346	0.310783	0.423901	0.064336	0	98	107	111	120	71	129	108	117	138	105
ENSMUSG00000004127	chr3	Trmt10a	1.38E+08	1.38E+08	7976	0.288584	1.37298	0.311227	0.424255	0.069973	0	29	43	37	32	45	49	81	38	87	67
ENSMUSG00000021552	chr13	Gkap1	58233351	58233658	1518	-0.20101	3.711942	0.311217	0.424255	0.042668	0	200	222	293	199	249	204	303	396	264	241
ENSMUSG00000022064	chr14	Pibf1	99099433	99100129	3271	-0.25402	2.843977	0.311184	0.424255	0.067615	0	140	83	142	149	129	107	161	227	164	97
ENSMUSG00000027404	chr2	Snrpb	1.3E+08	1.3E+08	1976	0.164445	6.757768	0.311141	0.424255	0.031078	0	1368	1588	1893	1734	1948	2431	2467	2346	3226	2820
ENSMUSG00000070493	chr5	Chchd2	1.3E+08	1.3E+08	2269	0.198295	8.131839	0.311092	0.424255	0.045668	0	3689	4909	5290	3941	3693	6796	6088	7561	7004	6971
ENSMUSG00000078249	chr11	Hmga1-rs1	1.21E+08	1.21E+08	1626	0.331778	0.824004	0.311108	0.424255	0.094899	0	16	22	17	29	40	26	27	56	71	41
ENSMUSG00000033191	chr4	Tie1	1.18E+08	1.18E+08	4917	-0.22414	5.354562	0.311374	0.424415	0.05735	0	441	704	927	1054	541	632	739	799	1342	969

ENSMUSG00000031434	chrX	Morc4	1.4E+08	1.4E+08	6051	0.213337	3.659615	0.311554	0.424618	0.049341	0	147	149	190	173	332	276	374	211	332	370
ENSMUSG00000028455	chr4	Stoml2	43027690	43028293	3022	0.168461	5.727234	0.311808	0.42488	0.032125	0	680	835	962	822	842	1167	1132	1380	1506	1311
ENSMUSG00000073755	chr4	5730409E04Rik	1.27E+08	1.27E+08	2891	-0.1649	4.473583	0.311803	0.42488	0.029072	0	321	347	445	392	456	423	408	505	527	559
ENSMUSG00000024070	chr17	Prkd3	78949405	78952030	11017	-0.19188	4.164595	0.311986	0.425039	0.039938	0	272	215	334	292	510	221	389	451	500	420
ENSMUSG00000031901	chr8	Dus2	1.06E+08	1.06E+08	3367	0.221533	3.24525	0.311986	0.425039	0.051026	0	122	128	147	144	185	192	295	126	320	256
ENSMUSG00000021519	chr13	Mterf3	66906968	66907183	4652	-0.19656	3.957309	0.312214	0.425308	0.041807	0	237	265	359	246	268	215	346	478	353	296
ENSMUSG00000021607	chr13	Mrpl36	73331009	73331091	899	-0.18694	4.940712	0.31231	0.425396	0.03911	0	484	574	675	488	473	641	721	560	731	656
ENSMUSG00000020514	chr11	Mrpl22	58171661	58171713	981	0.172821	4.440293	0.312417	0.425438	0.032406	0	272	347	421	317	334	484	577	507	555	525
ENSMUSG00000020844	chr11	Nxn	76257198	76258747	3239	0.168952	5.530649	0.312378	0.425438	0.032249	0	502	733	815	814	764	915	1024	1227	1324	1212
ENSMUSG00000021376	chr13	Tpmt	47025170	47025477	1914	-0.27783	1.41359	0.312432	0.425438	0.06152	0	40	36	38	52	72	51	57	53	53	55
ENSMUSG00000022639	chr16	5330426P16Rik	50719294	50720546	4679	0.243754	2.490906	0.312633	0.42567	0.058509	0	92	50	104	75	104	110	169	95	199	133
ENSMUSG00000022528	chr16	Hes1	30064384	30064536	2037	0.238624	3.038505	0.312684	0.425697	0.059063	0	84	117	142	175	101	154	251	140	260	229
ENSMUSG00000031077	chr7	Fadd	1.45E+08	1.45E+08	3903	0.232877	2.870898	0.312732	0.42572	0.055432	0	88	95	147	102	126	116	193	111	275	236
ENSMUSG00000061371	chr10	Zfp873	82058417	82058496	1893	-0.35885	0.0531	0.312834	0.425818	0.084784	0	19	9	28	13	21	9	22	23	22	22
ENSMUSG00000058587	chr9	Tmod3	75497796	75500150	3578	-0.16835	4.539849	0.313193	0.426263	0.031361	0	353	352	414	490	435	329	559	467	732	511
ENSMUSG00000032501	chr15	Trib1	59648350	59649522	5699	0.199793	4.803744	0.313296	0.42632	0.04498	0	327	381	359	470	648	617	747	501	1059	580
ENSMUSG00000037827	chr6	Gm5884	1.29E+08	1.29E+08	2259	0.246854	2.27085	0.313295	0.42632	0.060506	0	50	63	92	75	84	96	107	177	113	100
ENSMUSG00000026889	chr2	Rbm18	36116079	36117974	5740	-0.1612	5.376058	0.313347	0.426347	0.029197	0	611	681	846	695	826	755	900	1040	941	905
ENSMUSG00000024906	chr19	Mus81	5482345	5483029	3567	-0.18912	4.478173	0.313412	0.426395	0.03921	0	330	331	494	351	488	482	508	309	595	512
ENSMUSG00000030272	chr6	Camk1	1.13E+08	1.13E+08	6067	0.165111	5.11561	0.313454	0.426409	0.030506	0	482	463	663	512	611	730	878	653	1047	963
ENSMUSG00000020849	chr11	Ywhae	75732869	75733091	2568	-0.16178	8.662629	0.313701	0.426703	0.030761	0	5768	6974	8219	6992	7753	7900	8344	8658	10247	9289
ENSMUSG00000017314	chr11	Mpp2	1.02E+08	1.02E+08	4807	-0.2782	1.63996	0.313892	0.426921	0.071071	0	46	36	53	73	72	39	69	42	91	85
ENSMUSG00000038705	chr2	Gmeb2	1.81E+08	1.81E+08	4988	-0.17892	3.230054	0.313983	0.427003	0.031046	0	147	152	179	148	199	175	194	197	252	200
ENSMUSG00000059323	chr15	Tonsl	76622088	76622350	5815	0.155956	5.608817	0.314169	0.427214	0.027518	0	668	755	822	755	829	1011	1181	1131	1422	1243
ENSMUSG00000027596	chr2	a	1.55E+08	1.55E+08	1169	-0.25777	1.615111	0.314335	0.427398	0.061434	0	36	48	64	68	56	36	84	64	79	58
ENSMUSG00000035399	chr2	Oser1	1.63E+08	1.63E+08	2600	0.297249	3.591254	0.314493	0.427572	0.099258	0	126	171	206	195	201	206	236	647	211	217
ENSMUSG00000043067	chr9	Dpy19l1	24411776	24414423	6350	0.19913	3.895025	0.314704	0.427816	0.0431	0	225	142	241	211	348	245	445	274	513	400
ENSMUSG00000036615	chr3	Rfxap	54803115	54804575	2242	-0.17138	3.966652	0.315059	0.428256	0.030886	0	248	222	326	308	270	310	345	347	349	339
ENSMUSG00000057963	chr12	Itpk1	1.03E+08	1.03E+08	3320	0.223835	3.484161	0.315222	0.428435	0.054407	0	94	154	185	184	254	168	215	275	354	406
ENSMUSG00000022394	chr15	L3mbtl2	81663889	81664024	5945	-0.17445	3.522281	0.315391	0.428624	0.031545	0	161	182	237	176	263	157	285	241	330	258
ENSMUSG00000018882	chr11	Mrpl45	97315716	97315939	2596	-0.20111	5.97371	0.315875	0.429238	0.047235	0	857	1245	1401	1145	899	1301	1380	997	1757	1361
ENSMUSG00000001569	chr5	Nom1	29434664	29435643	4895	0.190385	4.088171	0.315918	0.429256	0.039696	0	240	217	304	239	326	293	403	609	477	329
ENSMUSG00000026035	chr1	Ppil3	58430994	58431330	4291	0.174723	3.390294	0.316025	0.429358	0.03076	0	153	130	178	166	189	219	277	213	319	259
ENSMUSG00000089715	chr15	Cbx6	79823896	79828978	6290	0.182089	5.405293	0.316139	0.429471	0.038208	0	637	430	679	579	1041	683	1162	1013	1391	1082
ENSMUSG00000039145	chr2	Camk1d	5293457	5299101	7427	0.279902	2.670248	0.316341	0.429704	0.083683	0	112	41	81	76	171	104	207	154	188	156
ENSMUSG00000061589	chr10	Dot1l	80755206	80755524	8705	-0.17334	5.25139	0.316476	0.429803	0.034573	0	615	517	640	751	856	528	869	694	1185	983
ENSMUSG00000100807	chr9	Gm29521	1.02E+08	1.02E+08	3749	-0.3776	0.792207	0.316469	0.429803	0.135668	0	42	39	24	30	14	22	21	44	53	31
ENSMUSG00000040648	chr1	Ppip5k2	97706048	97707830	14381	0.237111	2.156035	0.316667	0.429978	0.053398	0	51	45	84	65	95	62	114	103	151	131
ENSMUSG00000043284	chr11	Tmem11	60864452	60865348	1745	0.183767	5.280268	0.316656	0.429978	0.038882	0	429	650	765	595	586	891	850	1086	1022	910
ENSMUSG00000029729	chr5	Zkscan1	1.38E+08	1.38E+08	8541	0.204377	3.953758	0.316852	0.430145	0.04635	0	199	177	304	227	304	244	384	594	393	315
ENSMUSG00000055491	chr19	Pprc1	46044886	46045062	7516	0.185628	4.188734	0.316841	0.430145	0.037917	0	258	239	242	239	453	337	424	431	665	429
ENSMUSG00000019802	chr10	Sec63	42761496	42761888	8787	0.153083	5.557674	0.316917	0.43019	0.026801	0	644	618	790	762	922	826	1138	1297	1377	1178
ENSMUSG00000025393	chr10	Atp5b	1.28E+08	1.28E+08	4237	-0.17892	11.6006	0.316961	0.430207	0.038279	0	43544	58333	57909	62355	50365	57342	61097	77579	80730	62705
ENSMUSG00000029016	chr4	Clcn6	1.48E+08	1.48E+08	5933	0.194075	2.999618	0.317	0.430218	0.037545	0	110	87	128	137	158	144	183	174	266	228
ENSMUSG00000029249	chr5	Rest	77265491	77265788	7222	-0.16153	3.970639	0.317048	0.430242	0.027267	0	233	215	300	295	342	288	326	385	399	317
ENSMUSG00000066880	chr8	Zfp617	71908635	71908738	3024	-0.27102	3.80722	0.31728	0.430514	0.083362	0	197	235	325	232	290	164	268	587	259	195
ENSMUSG00000020163	chr10	Uqcr11	80402997	80403155	641	0.186054	7.874401	0.317433	0.430624	0.041217	0	3058	3981	4208	3732	3113	5633	5289	5692	6503	5702
ENSMUSG00000066057	chr17	Gm1976	94759944	94761577	1912	-0.28312	0.812423	0.317454	0.430624	0.059804	0	26	25	31	38	33	20	43	33	45	37
ENSMUSG00000099519	chr1	Gm29253	75171731	75171988	5231	-0.17285	7.031363	0.317435	0.430624	0.035339	0	2026	2002	2538	2342	2685	2510	2548	3543	2878	2717
ENSMUSG00000025066	chr19	Sfr1	47731756	47731821	1583	0.162338	6.36718	0.317539	0.430697	0.030928	0	1139	1220	1450	1216	1466	1829	2128	1996	2154	1969
ENSMUSG00000031568	chr8	Rwdd4a	47533664	47533943	3352	-0.15631	4.395683	0.317746	0.430936	0.026686	0	313	321	469	363	384	360	448	486	579	453
ENSMUSG00000024072	chr17	Yipf4	74489493	74489794	2133	0.166513	4.297722	0.318084	0.43131	0.029926	0	259	331	320	292	326	345	494	540	566	484
ENSMUSG00000024955	chr19	Esrra	6910977	6912010	2539	-0.18383	6.374819	0.318082	0.43131	0.039941	0	1209	1608	1576	1562	1315	1708	1714	1482	2214	1899
ENSMUSG00000022210	chr14	Dhrs4	55478758	55479033	1390	0.187058	4.780664	0.31834	0.431614	0.039799	0	330	420	432	537	405	555	512	738	779	817
ENSMUSG00000014867	chr2	Surf4	26920040	26922171	3281	0.162886	7.35937	0.318438	0.431662	0.031623	0	2087	2048	2759	2517	3712	2940	3893	4480	4918	4148
ENSMUSG00000024778	chr19	Fas	34290659	34290744	1801	0.214148	2.466881	0.318437	0.431662	0.043038	0	73	79	94	86	86	100	108	143	178	157
ENSMUSG00000028173	chr3	Wls	1.6E+08	1.6E+08	3304	0.180979	4.932962	0.31863	0.43188	0.037611	0	388	381	511	439	700	512	1035	674	972	633
ENSMUSG00000028521	chr4	Slc35d1	1.03E+08	1.03E+08	8528	-0.19544	2.981566	0.318919	0.432167	0.038042	0	135	107	171	121	166	154	184	145	200	164
ENSMUSG00000029141	chr5	Slc4a1ap	31526995	31527684	4759	0.166151	4.053372	0.318926	0.432167	0.030122	0	215	223	348	224	299	347	397	455	452	377
ENSMUSG00000041594	chr14	Tmtc4	1.23E+08	1.23E+08	7367	-0.29384	1.282795	0.318935	0.432167	0.084183	0	44	30	54	37	52	22	53	37	95	49
ENSMUSG00000021360	chr13	Gcnt2	40859768	40861273	7038	0.235067	2.772579	0.319215	0.432504	0.056017	0	92	106	124	113	74	103	146	185	242	190
ENSMUSG00000055013	chr1	Agap1	89454806	89455592	17469	-0.16571	4.66476	0.319339	0.43263	0.030994	0	385	320	510	501	537	380	687	489	719	543
ENSMUSG00000020956	chr12	Dtd2	51988312	51988855	3108	0.224053	2.532971	0.319547	0.432869	0.050874	0	52	97	93	93	104	114	142	159	139	157
ENSMUSG00000074282	chr7	Zfp94	24301704	24303873	3510	-0.26834	0.997926	0.319695	0.433027	0.057099	0	28	34	41	28	44	27	41	50	45	40
ENSMUSG00000037791	chr11	Phf12	77982754	77983377	4909	-0.18844	4.056232	0.319729	0.433031	0.039528	0	262	184	312	314	425	212	347	453	471	354
ENSMUSG00000103109	chr11	RP23-263M10.12	73080683	73083604	2922	-0.34626	0.024835	0.320081	0.433466	0.079718	0	20	13	12	14	28	12	23	22	23	16

ENSMUSG00000020076	chr10	Ddx50	62616023	62616516	2527	-0.15836	5.316502	0.320284	0.433697	0.028909	0	601	596	778	645	909	685	864	1028	943	860
ENSMUSG00000039354	chr1	Smarcal1	72583251	72583438	5728	-0.16463	4.385955	0.320366	0.433766	0.030069	0	257	318	418	417	446	324	480	537	532	432
ENSMUSG00000031231	chrX	Cox7b	1.06E+08	1.06E+08	1214	-0.19855	8.450024	0.320645	0.434101	0.047693	0	5113	7125	7470	6196	4813	6938	7240	8801	7792	6784
ENSMUSG00000035504	chr10	Reep6	80329953	80330345	2506	0.421809	1.563385	0.320724	0.434166	0.1927	0	30	17	29	51	82	26	41	52	121	155
ENSMUSG00000098650	chr11	Gm28048	22834744	22837195	2746	0.166324	5.538559	0.320854	0.434299	0.032412	0	633	699	908	649	755	1066	1167	975	1258	1211
ENSMUSG00000066838	chr7	Zfp772	7202122	7204359	2772	-0.27409	1.27466	0.320887	0.434302	0.063836	0	35	48	45	31	54	39	44	41	57	66
ENSMUSG00000052962	chr6	Mrpl35	71813003	71816287	3715	-0.1701	5.082129	0.320959	0.434357	0.033533	0	467	633	685	623	558	662	746	654	876	761
ENSMUSG00000092607	chr3	Scnm1	95129536	95129883	1885	0.167609	4.268609	0.321141	0.43456	0.031187	0	260	295	355	280	313	459	435	417	561	477
ENSMUSG00000069135	chr17	Fgfr1op	8165501	8165698	4008	-0.16286	4.020801	0.321176	0.434566	0.028658	0	242	255	373	276	279	304	355	358	412	345
ENSMUSG00000037071	chr19	Scd1	44394451	44398118	4836	0.706174	8.06101	0.321666	0.435187	0.58627	0	2144	1085	810	5586	8155	918	2204	677	15761	22287
ENSMUSG00000010751	chr7	Tnfrsf22	1.44E+08	1.44E+08	4289	0.261641	1.938596	0.321788	0.435309	0.066658	0	43	45	61	75	60	73	123	57	113	111
ENSMUSG00000078202	chr2	Nrarp	25180758	25183339	2582	-0.28964	2.773037	0.321861	0.435365	0.093577	0	77	112	138	175	120	115	178	53	216	158
ENSMUSG00000032413	chr9	Rasa2	96539300	96542475	15856	0.279575	2.105301	0.321906	0.435384	0.081966	0	60	30	66	53	116	54	105	111	150	130
ENSMUSG00000087178	chr7	A230056P14Rik	55962531	55962672	2354	-0.44824	-0.0221	0.322122	0.435632	0.163586	0	9	18	29	20	11	25	21	4	23	14
ENSMUSG00000037148	chr8	Arhgap10	77250366	77251007	3038	-0.1557	5.533968	0.322371	0.435845	0.028303	0	596	674	982	872	995	829	1042	1100	1170	963
ENSMUSG00000038122	chr10	Tbc1d32	56014298	56017704	7235	-0.25223	1.539143	0.32237	0.435845	0.055909	0	49	38	57	51	62	52	67	44	62	74
ENSMUSG00000091580	chr16	Gm6467	21896506	21896931	609	0.338603	1.186107	0.322374	0.435845	0.105607	0	32	39	29	32	24	31	41	98	61	54
ENSMUSG00000044244	chr9	Il20rb	1E+08	1E+08	4206	0.320066	1.205158	0.322515	0.435951	0.093175	0	32	22	44	30	36	25	39	88	84	56
ENSMUSG00000062931	chr10	Zfp938	82224850	82226593	2128	-0.21356	2.792788	0.322504	0.435951	0.046954	0	110	121	171	94	116	129	156	147	156	147
ENSMUSG00000020715	chr11	Ern1	1.06E+08	1.06E+08	8173	-0.20339	3.585487	0.322787	0.436276	0.045938	0	184	160	238	214	281	146	244	391	301	227
ENSMUSG00000033420	chr6	Antxr1	87133854	87137355	5263	-0.27787	5.700313	0.322873	0.43635	0.093048	0	1021	382	987	692	1829	688	1770	956	1231	892
ENSMUSG00000022415	chr15	Syngr1	80091334	80091492	4808	-0.17612	4.495362	0.32292	0.436371	0.035543	0	335	406	493	362	385	423	373	491	602	573
ENSMUSG00000020346	chr11	Mgat1	49244191	49244339	4733	0.151772	5.455228	0.323321	0.43687	0.02703	0	557	583	785	696	873	842	1031	948	1416	1185
ENSMUSG00000099041	chr2	Gm28035	30240567	30240677	4238	-0.21675	4.582692	0.323762	0.437424	0.0554	0	328	461	405	525	400	381	374	792	527	497
ENSMUSG00000065954	chr8	Tacc1	25154552	25159820	7695	0.182544	4.809079	0.323918	0.437591	0.038831	0	367	294	451	525	576	390	662	689	1026	792
ENSMUSG00000024376	chr18	Epb4.1l4a	33796327	33797470	3853	-0.25385	1.700723	0.32424	0.437984	0.061702	0	53	46	60	74	53	57	89	51	73	66
ENSMUSG00000041115	chrX	Iqsec2	1.52E+08	1.52E+08	6980	-0.1667	4.390675	0.324627	0.438464	0.031796	0	303	366	338	429	397	389	431	430	626	433
ENSMUSG00000026211	chr1	Obsl1	75479310	75479371	8467	-0.18745	6.851138	0.32472	0.438546	0.042838	0	1597	1790	2545	1848	2596	2253	3238	1630	2993	2451
ENSMUSG00000091896	chr18	Ube2d2a	35771559	35772012	2483	0.155442	5.217012	0.324917	0.43877	0.028333	0	472	566	669	557	671	788	948	799	1117	910
ENSMUSG00000035227	chr7	Spcs2	99837569	99839883	2815	0.162319	6.006858	0.324955	0.438777	0.031669	0	946	878	1123	953	1159	1312	1290	1659	1838	1810
ENSMUSG00000027429	chr2	Sec23b	1.45E+08	1.45E+08	6302	0.181083	4.193893	0.325245	0.439084	0.037522	0	219	255	293	256	419	377	463	311	663	468
ENSMUSG00000053898	chr7	Ech1	28825217	28825412	2284	0.202992	7.301598	0.325241	0.439084	0.050534	0	2027	2509	2613	2874	2066	2602	2972	5526	4505	4234
ENSMUSG00000000916	chr5	Nsun5	1.35E+08	1.35E+08	3142	0.206725	2.597276	0.325493	0.439376	0.042339	0	66	102	109	82	102	107	155	145	193	151
ENSMUSG00000047793	chr1	Sned1	93235841	93236201	9491	-0.21989	3.827106	0.325663	0.439537	0.055685	0	282	132	291	191	395	196	268	285	399	398
ENSMUSG00000062012	chr17	Zfp13	23575845	23577111	2439	0.282871	1.1416	0.325676	0.439537	0.068476	0	26	21	31	36	46	29	54	44	85	64
ENSMUSG00000033585	chr7	Ndn	62348277	62349928	1652	0.217825	4.515526	0.325882	0.439772	0.056599	0	301	248	368	261	625	500	625	334	805	614
ENSMUSG00000027007	chr2	Ssfa2	79635352	79635744	5599	-0.17812	4.062686	0.326381	0.440286	0.036581	0	294	236	288	332	317	220	305	439	464	421
ENSMUSG00000028015	chr3	Ctso	81932601	81932775	5123	-0.17583	3.51767	0.326422	0.440286	0.033771	0	204	143	215	196	254	173	253	210	332	295
ENSMUSG00000035310	chr5	Lin54	1E+08	1E+08	5820	-0.29646	2.562529	0.326401	0.440286	0.098174	0	111	74	130	108	114	64	105	242	123	80
ENSMUSG00000045252	chr7	Zfp574	25077205	25077386	4236	0.209552	3.17609	0.326418	0.440286	0.04782	0	111	108	145	152	183	134	198	325	279	197
ENSMUSG00000049396	chr11	Gemin4	76210571	76213923	3734	0.200216	2.773121	0.326376	0.440286	0.040482	0	89	87	101	111	138	140	155	136	237	179
ENSMUSG00000052331	chr1	Ankrd44	54645340	54648335	14175	-0.18815	3.122713	0.326564	0.440435	0.037205	0	135	121	170	139	210	114	215	190	222	212
ENSMUSG00000063229	chr7	Ldha	46841475	46841652	2982	-0.19647	11.65784	0.326727	0.440612	0.04803	0	45458	57371	70804	53611	60971	74699	61759	45610	81657	83028
ENSMUSG00000099034	chr15	2810039B14Rik	75642129	75642511	6418	-0.32947	0.123707	0.326784	0.440646	0.081064	0	12	17	17	19	29	19	21	10	31	23
ENSMUSG00000034858	chr9	Fam214a	74953053	74953278	4521	-0.25404	4.47954	0.326961	0.440842	0.077551	0	398	259	470	416	494	254	342	908	440	433
ENSMUSG00000021732	chr13	Fgf10	1.19E+08	1.19E+08	4601	0.67111	-0.22583	0.327049	0.440917	0.451178	0	5	4	4	12	24	4	2	10	32	62
ENSMUSG00000031161	chrX	Hdac6	7930120	7930537	5817	0.197628	3.062551	0.327399	0.441346	0.041837	0	102	99	157	140	150	116	196	258	253	222
ENSMUSG00000022367	chr15	Has2	56665627	56668588	4237	0.302354	1.128962	0.327757	0.441743	0.080912	0	28	17	36	31	46	41	63	31	89	49
ENSMUSG00000098972	chr2	Mir8093	32687630	32687766	137	-0.35941	0.034763	0.32774	0.441743	0.08403	0	13	15	19	13	29	16	28	11	26	15
ENSMUSG00000021116	chr12	Eif2s1	78861819	78862180	3405	-0.15744	5.456923	0.327867	0.441805	0.02981	0	731	749	903	643	813	801	982	906	1159	994
ENSMUSG00000022353	chr15	Mtss1	58941244	58944130	4965	0.176686	4.467922	0.327842	0.441805	0.036214	0	243	321	327	395	453	337	543	475	750	679
ENSMUSG00000026279	chr1	Thap4	93701935	93705655	6519	-0.17494	4.653922	0.328032	0.441985	0.036065	0	370	475	519	449	385	512	499	570	640	510
ENSMUSG00000028879	chr4	Stx12	1.33E+08	1.33E+08	3188	0.149444	5.360299	0.328075	0.441992	0.02656	0	546	587	752	622	747	764	1001	1121	1179	982
ENSMUSG00000031667	chr8	Aktip	91112041	91112611	2992	-0.15716	5.289965	0.328102	0.441992	0.029515	0	589	691	778	659	701	732	880	858	943	877
ENSMUSG00000059834	chr3	Sclt1	41626720	41627234	7569	-0.23427	2.027246	0.328176	0.442006	0.055089	0	67	54	82	73	86	45	100	108	94	86
ENSMUSG00000103651	chr19	RP24-245M20.4	4762103	4765171	3069	-0.40959	-0.07438	0.328157	0.442006	0.136444	0	17	4	14	18	31	16	10	27	16	16
ENSMUSG00000070304	chr9	Scn2b	45117876	45118093	4562	-0.33894	0.091042	0.328302	0.442133	0.075184	0	17	10	22	19	24	12	16	27	31	16
ENSMUSG00000075010	chr19	AW112010	11047617	11048093	770	0.228981	2.991311	0.328688	0.44261	0.056906	0	106	111	136	145	100	189	169	147	203	270
ENSMUSG00000038058	chr6	Nod1	54923942	54925009	4415	-0.16539	3.896763	0.328961	0.442898	0.030728	0	187	276	282	251	314	252	325	277	433	357
ENSMUSG00000041491	chr19	Cep78	15955774	15956403	2548	0.236264	1.839527	0.328966	0.442898	0.050946	0	50	51	47	47	71	64	95	73	109	101
ENSMUSG00000042210	chr9	Abhd14a	1.06E+08	1.06E+08	2087	-0.17033	3.452457	0.329065	0.442988	0.031338	0	186	177	220	169	204	204	261	224	282	220
ENSMUSG00000003662	chr2	Ciao1	1.27E+08	1.27E+08	3197	0.158197	5.303831	0.329125	0.443026	0.030025	0	524	585	752	607	638	811	974	1077	1022	940
ENSMUSG00000002105	chr2	Slc39a13	91061791	91062978	4869	-0.16776	4.92394	0.329212	0.4431	0.03352	0	526	422	640	440	661	532	799	518	823	672
ENSMUSG00000024271	chr18	Elp2	24603961	24604132	2789	0.154583	4.892847	0.32937	0.443227	0.027999	0	440	388	476	502	531	564	780	621	915	785
ENSMUSG00000025878	chr13	Uimc1	55027880	55028718	5085	0.152312	3.995694	0.329369	0.443227	0.025757	0	218	219	289	225	309	322	410	384	434	394
ENSMUSG00000022437	chr15	Samm50	84192233	84192384	1673	0.170823	7.34854	0.329421	0.443251	0.036412	0	1823	2538	3016	2768	2668	3726	3629	3415	4943	4349

ENSMUSG00000051116	chr5	Gm8121	57608567	57609067	501	-0.28746	1.127713	0.329463	0.443265	0.074406	0	35	48	42	30	35	46	39	46	41	45
ENSMUSG00000032182	chr9	Yipf2	21588709	21589558	2150	0.221293	2.41874	0.329763	0.443626	0.049123	0	72	80	80	75	96	91	114	105	198	163
ENSMUSG00000026374	chr1	Tsn	1.18E+08	1.18E+08	9046	0.151478	5.575613	0.329905	0.443773	0.027808	0	650	657	941	630	914	934	1250	1096	1381	1198
ENSMUSG00000060601	chr7	Nr1h2	44549616	44550131	3366	-0.16387	4.71074	0.329985	0.443838	0.031864	0	436	388	489	464	524	386	582	741	617	560
ENSMUSG00000034480	chrX	Diap2	1.3E+08	1.3E+08	11553	-0.20837	2.802172	0.330221	0.444112	0.047043	0	99	85	138	155	146	85	143	151	195	186
ENSMUSG00000030823	chr7	9130019O22Rik	1.27E+08	1.27E+08	3878	-0.26798	1.251461	0.330941	0.445038	0.066273	0	27	42	42	34	67	30	43	48	70	56
ENSMUSG00000078762	chr7	Haus5	30653711	30654055	3455	0.273074	1.832857	0.331212	0.445359	0.073563	0	48	47	74	43	49	52	88	57	145	112
ENSMUSG00000022562	chr15	Oplah	76296597	76296781	5596	-0.18186	5.132227	0.331402	0.445547	0.040537	0	479	646	538	737	684	542	573	859	971	920
ENSMUSG00000022687	chr16	Boc	44485045	44485799	4456	-0.28422	3.803586	0.331416	0.445547	0.097514	0	286	114	324	205	369	179	300	517	310	161
ENSMUSG00000032612	chr9	Usp4	1.08E+08	1.08E+08	8628	-0.15384	6.505542	0.331466	0.445571	0.029419	0	1190	1398	1966	1686	1807	1617	1931	2000	2418	2088
ENSMUSG00000020056	chr10	Ccdc53	88201093	88201292	4536	0.166567	4.429495	0.331647	0.44577	0.032392	0	328	328	394	283	342	475	554	457	583	562
ENSMUSG00000020362	chr11	Cnot6	49671503	49675405	6610	-0.15354	4.439486	0.331717	0.445821	0.027593	0	328	306	422	377	483	318	528	434	673	478
ENSMUSG00000002608	chr7	Ccdc97	25711106	25713113	3939	0.154091	5.418589	0.332163	0.446377	0.029021	0	519	571	789	658	876	800	1031	1230	1247	956
ENSMUSG00000050846	chr15	Zfp623	75940952	75941159	2463	-0.20001	2.472765	0.332337	0.446567	0.041457	0	88	92	95	94	118	87	123	134	153	101
ENSMUSG00000037415	chr8	Ranbp10	1.06E+08	1.06E+08	5308	-0.20795	5.195318	0.332566	0.446832	0.053323	0	562	490	745	667	845	595	745	1286	688	608
ENSMUSG00000036114	chr4	Rpp25l	41712033	41712814	856	0.178845	4.649721	0.332955	0.447312	0.038379	0	354	412	488	339	345	576	531	685	679	597
ENSMUSG00000015377	chr15	Dennd6b	89182217	89185109	4607	0.192717	3.241947	0.333394	0.447814	0.041592	0	133	116	192	144	146	167	219	316	242	221
ENSMUSG00000028603	chr4	Scp2	1.08E+08	1.08E+08	3478	-0.16154	6.915194	0.33338	0.447814	0.032964	0	1755	2037	2360	2160	2307	2087	2159	2844	3140	3095
ENSMUSG00000021765	chr13	Fst	1.14E+08	1.14E+08	2337	-0.30704	3.294688	0.333781	0.448167	0.113516	0	206	83	179	125	327	109	160	382	225	149
ENSMUSG00000026819	chr2	Slc25a25	32414487	32416322	7862	-0.32574	4.929219	0.333819	0.448167	0.132762	0	474	362	993	663	353	784	564	271	427	978
ENSMUSG00000037104	chr17	Socs5	87107679	87108047	4392	-0.16146	3.930674	0.3337	0.448167	0.029633	0	234	208	271	305	325	269	339	267	417	387
ENSMUSG00000048120	chr19	Entpd1	40612366	40612523	5580	0.165981	4.238166	0.333801	0.448167	0.032179	0	229	233	377	344	305	321	529	380	599	518
ENSMUSG00000092544	chr8	Gm20422	69742862	69743269	1358	-0.25975	1.676948	0.333727	0.448167	0.067706	0	55	42	68	49	71	45	54	102	78	53
ENSMUSG00000018809	chr11	Smyd4	75348433	75348751	4329	0.245192	2.32022	0.333944	0.448213	0.063812	0	89	62	98	55	66	81	130	163	128	119
ENSMUSG00000020180	chr10	Snrpd3	75517551	75518125	3434	0.16256	6.02494	0.33395	0.448213	0.033056	0	879	950	1257	969	1066	1484	1370	1596	1786	1713
ENSMUSG00000024137	chr17	E4f1	24443792	24444337	2561	0.191851	3.244978	0.333949	0.448213	0.040789	0	122	116	171	162	164	149	203	312	249	261
ENSMUSG00000019158	chr7	Tmem160	16452779	16453170	814	0.164346	4.321165	0.334017	0.448259	0.031911	0	243	308	379	299	339	450	440	449	520	573
ENSMUSG00000021367	chr13	Edn1	42301270	42301958	2344	-0.34251	1.115417	0.334172	0.448423	0.117719	0	32	34	41	55	31	25	25	76	35	53
ENSMUSG00000049489	chr11	Fam58b	78750506	78751729	1224	0.177824	3.272216	0.334527	0.448857	0.034935	0	106	138	203	144	164	207	251	214	286	225
ENSMUSG00000078908	chr8	Mon1b	1.14E+08	1.14E+08	5156	-0.20517	2.806222	0.334563	0.448861	0.046518	0	104	88	120	141	172	83	154	145	210	174
ENSMUSG00000090996	chr2	Gm20458	1.64E+08	1.64E+08	1369	0.168568	4.607261	0.334645	0.448929	0.033986	0	383	358	443	351	354	566	596	501	695	619
ENSMUSG00000045282	chr7	Tmem86b	4628042	4628753	1220	0.34196	0.118527	0.335036	0.449409	0.087957	0	16	11	14	13	18	19	26	12	33	39
ENSMUSG00000032348	chr9	Gsta4	78191966	78192064	957	-0.24489	3.020989	0.335257	0.449619	0.070154	0	102	166	129	180	143	184	148	98	239	185
ENSMUSG00000033819	chr15	Ppp1r16a	76671615	76671762	4119	-0.15022	4.347246	0.335241	0.449619	0.026393	0	322	302	376	351	434	342	395	492	545	479
ENSMUSG00000038365	chr8	Fbxo25	13907806	13907863	2008	-0.17345	3.391473	0.335467	0.449845	0.033092	0	156	176	221	179	187	202	246	235	247	204
ENSMUSG00000049516	chr7	Spty2d1	46990396	46993386	5223	-0.18599	3.32277	0.335491	0.449845	0.038403	0	144	119	191	170	276	148	248	196	260	242
ENSMUSG00000039640	chr11	Mrpl12	1.2E+08	1.2E+08	1532	0.191461	7.186724	0.335665	0.450035	0.046922	0	1741	2537	2598	2427	1915	3642	3407	2752	4484	3688
ENSMUSG00000063145	chr2	Bbs5	69647171	69647342	2445	0.246716	1.755523	0.33576	0.450119	0.060551	0	42	52	70	40	45	59	92	98	81	84
ENSMUSG00000051391	chr5	Ywhag	1.36E+08	1.36E+08	5500	-0.15176	8.217499	0.335928	0.450301	0.029616	0	4340	4315	5985	5230	6510	5527	5902	6113	8140	7283
ENSMUSG00000000776	chr14	Polr3d	70438748	70439578	2156	-0.15268	4.039484	0.336047	0.450414	0.026736	0	248	245	337	304	306	296	404	326	452	336
ENSMUSG00000020402	chr11	Vdac1	52360860	52361152	2620	-0.17701	9.959117	0.336078	0.450414	0.040502	0	14757	16264	19236	19417	18302	19096	18697	29036	22333	18748
ENSMUSG00000015937	chr13	H2afy	56073619	56074392	6809	0.160392	5.945362	0.3375	0.452276	0.032559	0	833	890	1099	954	1076	1330	1475	1174	1838	1758
ENSMUSG00000026965	chr2	Anapc2	25272478	25272677	3445	0.144593	5.448695	0.338506	0.45358	0.026018	0	586	628	719	671	863	846	1022	1072	1298	1121
ENSMUSG00000033439	chr3	Trmt13	1.17E+08	1.17E+08	5035	0.28504	1.190819	0.338599	0.453661	0.076814	0	37	32	31	19	44	37	78	46	62	58
ENSMUSG00000005124	chr15	Wisp1	66891320	66891634	5518	-0.36528	3.416138	0.338721	0.453781	0.166957	0	217	67	242	96	416	135	376	97	343	159
ENSMUSG00000018858	chr11	Ict1	1.15E+08	1.15E+08	3332	0.162049	4.795013	0.339084	0.454223	0.032439	0	316	435	518	440	476	649	655	581	846	662
ENSMUSG00000066258	chr7	Trim12a	1.04E+08	1.04E+08	5781	0.266132	2.468284	0.33917	0.454294	0.081222	0	58	76	99	94	86	118	124	70	150	229
ENSMUSG00000020536	chr11	Llgl1	60699723	60699941	4862	0.157612	4.379767	0.339404	0.454564	0.030142	0	251	234	359	354	467	366	487	558	646	517
ENSMUSG00000026707	chr2	Nsun6	14995131	14996546	5006	-0.26352	1.026058	0.339458	0.454593	0.061004	0	28	26	45	40	40	28	37	56	51	36
ENSMUSG00000030779	chr7	Rbbp6	1.23E+08	1.23E+08	8752	-0.17554	5.106957	0.339643	0.454796	0.038788	0	562	466	593	658	781	533	679	1067	819	678
ENSMUSG00000032869	chr2	Psmf1	1.52E+08	1.52E+08	6441	0.165315	4.179884	0.339853	0.45501	0.032454	0	252	262	298	283	321	317	381	582	503	449
ENSMUSG00000039914	chr10	Coq10a	1.28E+08	1.28E+08	2502	-0.19134	8.106642	0.339869	0.45501	0.0479	0	4212	5283	5539	5266	3848	6292	5813	5861	6148	5333
ENSMUSG00000025037	chrX	Maoa	16619698	16619913	4167	-0.16546	3.517707	0.340159	0.455354	0.030867	0	160	201	229	167	250	198	265	260	276	251
ENSMUSG00000021950	chr14	Anxa8	34085981	34086076	1880	0.495014	1.366189	0.340212	0.455382	0.291871	0	55	8	16	14	80	15	48	76	121	93
ENSMUSG00000022621	chr15	Rabl2	89582533	89583430	2960	0.245304	1.451266	0.340268	0.455412	0.053209	0	39	29	47	45	41	45	82	67	76	65
ENSMUSG00000006800	chr2	Sulf2	1.66E+08	1.66E+08	5818	0.282616	4.919436	0.3403	0.455412	0.102983	0	442	195	379	399	938	476	1144	404	1132	805
ENSMUSG00000063931	chr7	Pepd	34912379	34912454	3079	0.165298	5.154915	0.340434	0.455547	0.034377	0	521	448	640	520	682	707	920	605	1109	1070
ENSMUSG00000034998	chr17	Foxn2	88440711	88440884	7357	-0.20237	3.578211	0.340469	0.45555	0.049234	0	189	151	220	235	274	146	229	396	309	224
ENSMUSG00000022579	chr15	Gpihbp1	75596628	75596730	2554	0.192922	4.839686	0.341392	0.45674	0.04693	0	341	437	536	556	334	549	543	876	867	730
ENSMUSG00000024045	chr17	Akap8	32303676	32305706	3695	0.146433	4.849702	0.341545	0.45689	0.026546	0	401	351	531	440	576	546	710	750	804	720
ENSMUSG00000084319	chr6	Tpt1-ps3	99877816	99878334	519	-0.15881	7.203592	0.34157	0.45689	0.033017	0	2140	2574	2907	2581	2732	2829	3189	3539	3405	3160
ENSMUSG00000038845	chr11	Phb	95666957	95667042	2805	-0.16565	7.075709	0.341657	0.456938	0.035945	0	1961	2408	2883	2409	2163	2677	2853	2596	3656	3017
ENSMUSG00000071659	chr19	Hnrnpul2	8819401	8820813	5726	0.151466	6.732406	0.341674	0.456938	0.029874	0	1491	1328	1952	1639	2059	1857	2519	3013	3103	2647
ENSMUSG00000094518	chr13	Gm6421	1.17E+08	1.17E+08	411	-0.34981	0.468398	0.341705	0.456938	0.102818	0	28	19	22	31	20	34	20	33	27	16
ENSMUSG00000044600	chr8	Smim7	72565188	72567808	3266	0.17059	6.378659	0.341786	0.457002	0.037869	0	1151	1257	1637	1068	1414	1657	2128	2552	2154	1733
ENSMUSG00000034853	chr4	Acot11	1.07E+08	1.07E+08	6056	-0.23724	3.476235	0.342038	0.457295	0.070193	0	121	208	203	277	185	137	197	165	424	304

ENSMUSG00000049950	chr2	Rpp38	3328949	3329873	1042	0.228322	2.125382	0.342123	0.457365	0.054716	0	69	63	72	57	63	97	85	126	116	108
ENSMUSG00000014402	chr7	Tsg101	46888949	46889704	2730	0.146487	5.370889	0.342207	0.457433	0.027091	0	554	606	715	668	727	819	1034	1060	1093	1044
ENSMUSG00000048175	chr15	Asb8	98134637	98136438	2410	0.165852	6.852931	0.342514	0.457799	0.036049	0	1675	1673	2028	1790	1880	2367	2425	3604	3248	2565
ENSMUSG00000042035	chr3	Igsf3	1.01E+08	1.01E+08	7389	0.220405	3.507235	0.342708	0.458014	0.059847	0	164	100	174	142	311	200	391	242	377	223
ENSMUSG00000050565	chr1	Tor1aip2	1.56E+08	1.56E+08	9218	-0.15188	6.377336	0.342889	0.458211	0.029983	0	1207	1269	1642	1459	1763	1572	1771	2037	1985	1765
ENSMUSG00000085779	chr10	Atcayos	81194609	81194722	4375	-0.28696	7.083799	0.343028	0.458352	0.108762	0	2377	2320	2804	2258	2614	1902	1710	6262	1948	2239
ENSMUSG00000014177	chr11	Tvp23b	62879455	62879595	2235	0.179163	3.082095	0.343264	0.458592	0.035149	0	116	124	136	115	165	144	222	182	260	240
ENSMUSG00000021707	chr13	Dhfr	92354783	92355344	5290	0.214754	2.37237	0.343273	0.458592	0.049535	0	66	72	94	79	81	113	144	86	176	120
ENSMUSG00000027963	chr3	Extl2	1.16E+08	1.16E+08	3446	-0.16215	3.655208	0.343319	0.458609	0.030566	0	197	201	249	185	275	227	291	219	361	288
ENSMUSG00000052533	chr2	Nup188	30286397	30286470	6241	0.181646	3.684786	0.343734	0.459079	0.039261	0	194	128	193	212	282	186	328	357	440	304
ENSMUSG00000061981	chr11	Flot2	78037931	78038112	2740	0.154271	6.457754	0.343737	0.459079	0.031158	0	1132	1188	1464	1566	1614	1709	1800	2378	2665	2283
ENSMUSG00000027108	chr2	Ola1	73092801	73093724	3561	-0.15669	6.063956	0.343929	0.459291	0.031931	0	894	1163	1386	1087	1374	1282	1651	1338	1644	1428
ENSMUSG00000020263	chr10	Appl2	83600033	83601041	5949	0.207034	4.077937	0.344136	0.459523	0.053484	0	288	199	276	240	293	262	417	673	387	361
ENSMUSG00000027804	chr3	Ppid	79591342	79591557	4638	-0.20062	5.562615	0.344313	0.459671	0.052538	0	759	799	1103	692	853	1031	1273	571	1200	1002
ENSMUSG00000030335	chr6	Mrpl51	1.25E+08	1.25E+08	3357	0.176568	6.975988	0.344309	0.459671	0.04128	0	1540	2120	2428	1977	1717	3024	2884	2957	3353	3168
ENSMUSG00000078994	chr13	Zfp429	67389309	67391064	2134	0.296923	0.592965	0.344365	0.459695	0.070759	0	16	17	19	31	22	23	38	30	41	50
ENSMUSG00000087095	chr19	Emx2os	59425104	59429261	5023	0.324162	-0.10566	0.344475	0.459798	0.061442	0	14	9	13	11	14	14	21	21	28	24
ENSMUSG00000034757	chr11	Tmub2	1.02E+08	1.02E+08	2544	0.144475	4.425192	0.344521	0.459816	0.025112	0	298	314	381	318	385	396	540	535	633	530
ENSMUSG00000032594	chr9	Ip6k1	1.08E+08	1.08E+08	6487	0.174631	5.341978	0.344683	0.459988	0.039483	0	569	492	730	589	825	638	875	1444	1090	993
ENSMUSG00000020257	chr9	Wdr82	1.06E+08	1.06E+08	6338	-0.14924	5.280647	0.344815	0.46005	0.028466	0	636	625	705	631	801	716	945	851	998	778
ENSMUSG00000046186	chr9	Cd109	78615546	78615952	6900	0.270604	3.538241	0.344794	0.46005	0.092822	0	184	76	219	116	302	146	372	194	506	309
ENSMUSG00000078566	chr7	Bnip3	1.39E+08	1.39E+08	2265	0.379461	7.360077	0.34483	0.46005	0.191001	0	2087	2349	2717	2426	2242	2041	2149	12276	2462	2548
ENSMUSG00000049281	chr9	Scn3b	40269216	40270047	5546	0.278629	2.375905	0.345014	0.460251	0.091162	0	91	60	76	42	116	117	148	175	126	76
ENSMUSG00000028958	chr5	Tmub1	24445458	24446273	1879	-0.16925	3.632185	0.345148	0.460386	0.03389	0	222	209	219	198	229	251	247	285	306	253
ENSMUSG00000021497	chr13	Txndc15	55714650	55714844	1521	-0.14608	5.040887	0.345221	0.460439	0.026906	0	498	519	675	518	680	605	719	705	825	779
ENSMUSG00000042333	chr4	Tnfrsf14	1.55E+08	1.55E+08	1158	-0.42589	-0.24065	0.345279	0.460472	0.183185	0	26	10	8	8	19	3	20	9	29	18
ENSMUSG00000001403	chr2	Ube2c	1.65E+08	1.65E+08	2600	0.656017	5.845654	0.345407	0.460598	0.558504	0	210	820	244	1785	607	310	317	225	6734	1805
ENSMUSG00000043909	chr2	Trp53bp1	1.21E+08	1.21E+08	14164	0.175324	4.196521	0.345608	0.460777	0.03797	0	264	231	365	267	308	310	640	352	565	417
ENSMUSG00000060038	chr8	Dhps	85071757	85072053	2324	0.166652	3.763553	0.345604	0.460777	0.032274	0	189	224	218	217	200	264	296	347	427	338
ENSMUSG00000068290	chr2	Ddrgk1	1.31E+08	1.31E+08	2084	0.162533	5.967832	0.345679	0.460828	0.034683	0	873	874	1222	896	1067	1239	1354	1859	1532	1675
ENSMUSG00000000959	chr14	Oxa1l	54360841	54360917	2534	0.166872	5.855035	0.345754	0.460839	0.036447	0	736	874	995	1060	854	1156	1248	1736	1654	1333
ENSMUSG00000042524	chr15	Sun2	79724070	79725560	4969	-0.17232	7.205338	0.345728	0.460839	0.039628	0	2236	2321	2780	2858	2842	2398	2538	4384	3468	3400
ENSMUSG00000097530	chr7	Kansl2-ps	72672818	72674278	1461	-0.23566	2.265168	0.345798	0.460853	0.062981	0	66	88	92	89	90	68	115	148	86	87
ENSMUSG00000024805	chr19	Pcgf5	36379067	36379159	1659	0.188194	3.580569	0.345874	0.46091	0.042888	0	178	162	204	177	202	265	269	402	268	248
ENSMUSG00000019055	chr4	Plod1	1.48E+08	1.48E+08	6765	0.148906	6.156513	0.345925	0.460933	0.029138	0	933	879	1302	1185	1400	1330	1818	1535	2250	1886
ENSMUSG00000016756	chr13	Cmah	24327420	24327488	9972	-0.43118	1.78808	0.345964	0.460941	0.229186	0	48	31	62	43	155	57	82	9	86	102
ENSMUSG00000061474	chr13	Mrps36	1.01E+08	1.01E+08	1274	-0.18164	5.073322	0.346128	0.461116	0.042664	0	490	632	659	643	523	777	773	631	774	652
ENSMUSG00000041777	chr2	Cir1	73283105	73285035	3159	0.3047	3.58993	0.346285	0.461281	0.11941	0	134	165	228	171	199	136	243	714	232	217
ENSMUSG00000026820	chr2	Ptges2	32395896	32396550	5058	0.16991	5.349625	0.34649	0.461509	0.037391	0	474	697	696	737	561	833	884	966	1339	1031
ENSMUSG00000034793	chr11	G6pc3	1.02E+08	1.02E+08	2226	-0.15301	5.156761	0.346872	0.461973	0.029998	0	521	568	693	616	740	662	662	921	851	818
ENSMUSG00000046997	chr9	Spsb4	96943482	96944704	4484	0.304891	1.21151	0.347039	0.462151	0.098472	0	28	24	26	27	63	44	79	30	80	55
ENSMUSG00000037254	chr2	Itih2	10094593	10094901	3315	0.315135	1.204916	0.347102	0.462191	0.111803	0	28	16	51	16	58	36	58	81	66	45
ENSMUSG00000021127	chr12	Zfp36l1	80107760	80110548	2984	0.184472	5.198126	0.347697	0.462939	0.044552	0	510	369	554	741	712	524	991	1177	1102	820
ENSMUSG00000029550	chr5	Sppl3	1.15E+08	1.15E+08	4240	0.14989	4.931242	0.347801	0.463017	0.028639	0	464	394	487	440	631	588	716	835	873	727
ENSMUSG00000096537	chr13	1190003K10Rik	64481246	64481857	1097	0.684262	-0.58881	0.347823	0.463017	0.475997	0	11	0	16	5	3	0	25	26	27	5
ENSMUSG00000026174	chr1	Rqcd1	74506058	74506461	3826	0.146728	4.550379	0.348109	0.463353	0.026568	0	348	326	440	347	384	440	555	559	749	581
ENSMUSG00000044465	chr7	Fam160a2	1.05E+08	1.05E+08	11569	-0.14959	3.948386	0.348211	0.463444	0.026677	0	229	225	314	268	320	257	302	385	393	367
ENSMUSG00000025956	chr1	Mettl21a	64606473	64608137	3005	0.16561	3.668018	0.348475	0.463752	0.032824	0	174	186	219	184	229	263	312	380	316	273
ENSMUSG00000032127	chr9	Vps11	44348106	44348584	3179	0.185387	4.779103	0.348593	0.463863	0.044419	0	382	379	440	484	443	426	526	1013	773	688
ENSMUSG00000058793	chr2	Cds2	1.32E+08	1.32E+08	9125	0.155925	5.73989	0.348687	0.463923	0.031985	0	647	764	878	1006	923	877	1207	1423	1661	1477
ENSMUSG00000068742	chr2	Cry2	92403646	92405820	6320	0.325662	4.993721	0.348705	0.463923	0.141648	0	507	356	502	418	570	383	440	2063	622	614
ENSMUSG00000022899	chr16	Slc15a2	36750178	36751954	7360	-0.84167	-0.05875	0.348822	0.464034	0.842859	0	35	18	34	0	4	0	36	1	11	29
ENSMUSG00000039086	chr2	Ss18l1	1.8E+08	1.8E+08	4343	-0.22873	1.97092	0.349053	0.464298	0.05468	0	43	62	73	68	105	68	81	94	99	70
ENSMUSG00000040447	chr11	Spns2	72451638	72453115	4083	0.368955	4.911519	0.349146	0.464376	0.18207	0	263	506	510	521	370	389	347	2112	601	485
ENSMUSG00000002732	chr2	Fkbp7	76663044	76663352	1485	0.22142	3.789619	0.349262	0.464441	0.062821	0	249	117	241	144	322	269	455	231	416	363
ENSMUSG00000015697	chr3	Setdb1	95323525	95324190	6853	0.147864	4.418986	0.349238	0.464441	0.027094	0	287	285	377	360	383	373	521	614	612	507
ENSMUSG00000054150	chr12	Syne3	1.05E+08	1.05E+08	5532	-0.28969	2.223786	0.349497	0.464709	0.103794	0	75	54	73	76	152	32	73	112	169	117
ENSMUSG00000027091	chr2	Zc3h15	83644435	83644727	2789	0.15257	5.7565	0.349675	0.464808	0.030807	0	680	860	980	769	982	1052	1359	1511	1470	1231
ENSMUSG00000029462	chr5	Vps29	1.22E+08	1.22E+08	3089	0.155326	4.57503	0.349706	0.464808	0.030227	0	321	393	429	346	373	444	619	505	737	636
ENSMUSG00000032179	chr9	Bmp5	75775364	75776582	4025	-0.23673	3.862668	0.349677	0.464808	0.072173	0	285	126	351	188	385	187	425	392	331	227
ENSMUSG00000038967	chr11	Pdk2	95026258	95027322	3163	-0.17841	8.440823	0.349656	0.464808	0.043415	0	4924	5680	5818	7793	6458	6527	5802	9790	8337	7344
ENSMUSG00000020744	chr11	Slc25a19	1.16E+08	1.16E+08	4026	-0.22692	5.359423	0.349859	0.464967	0.069044	0	545	728	858	793	766	739	792	377	1254	1295
ENSMUSG00000016257	chr2	Slmo2	1.74E+08	1.74E+08	1860	0.1627	5.907545	0.349941	0.465032	0.035296	0	731	932	1110	983	959	1304	1534	1111	1938	1519
ENSMUSG00000039536	chr2	Stau1	1.67E+08	1.67E+08	6065	0.162126	5.457376	0.350056	0.46514	0.03487	0	557	515	761	742	928	784	1032	1432	1215	955
ENSMUSG00000042660	chr18	Wdr55	36760239	36760480	1498	0.157263	3.718567	0.350355	0.465493	0.029379	0	185	193	237	186	229	272	289	300	375	370
ENSMUSG00000027560	chr2	Dok5	1.71E+08	1.71E+08	1768	0.279603	2.534125	0.350405	0.465514	0.096398	0	55	64	119	106	91	125	214	58	215	123

ENSMUSG00000009995	chrX	Taz	74281912	74282040	5364	-0.15592	5.256712	0.350639	0.46574	0.031955	0	618	623	847	610	645	680	877	916	869	852
ENSMUSG00000033295	chr4	Ptprf	1.18E+08	1.18E+08	9130	-0.23922	3.089236	0.350642	0.46574	0.071801	0	112	90	138	147	301	110	238	139	262	173
ENSMUSG00000002768	chr17	Mea1	46681137	46681205	840	0.160148	4.598868	0.350926	0.466072	0.032802	0	336	338	412	408	405	536	588	425	786	643
ENSMUSG00000037016	chr3	Frem2	53513939	53517041	12347	-0.3085	2.112816	0.351274	0.466489	0.114316	0	65	40	60	74	166	60	135	90	112	49
ENSMUSG00000011306	chr8	Sugp1	70042813	70043080	2287	0.163244	4.217767	0.351691	0.466998	0.033562	0	235	263	358	306	298	330	402	603	512	441
ENSMUSG00000029287	chr5	Tgfbr3	1.07E+08	1.07E+08	6545	-0.21597	5.368383	0.351988	0.467348	0.063026	0	781	524	793	678	939	503	715	1561	941	768
ENSMUSG00000022022	chr14	Mtrf1	79397772	79398036	1862	-0.17842	3.248786	0.352044	0.467378	0.038472	0	160	153	197	164	155	169	178	242	212	225
ENSMUSG00000051906	chr8	Cd209f	4102787	4103249	1528	-0.45602	1.711528	0.352214	0.467558	0.25787	0	46	23	82	30	145	40	33	30	46	164
ENSMUSG00000037408	chr1	Cnnm4	36471620	36473085	4829	-0.20736	3.902421	0.352322	0.467657	0.055707	0	212	198	270	402	248	240	449	213	432	296
ENSMUSG00000020738	chr11	Sumo2	1.16E+08	1.16E+08	1736	-0.14866	4.484882	0.352556	0.467832	0.027889	0	306	356	483	369	457	407	567	450	545	496
ENSMUSG00000041975	chr2	Mettl8	70964561	70965679	5594	-0.19634	2.803645	0.352499	0.467832	0.046079	0	118	113	141	107	134	121	173	102	175	181
ENSMUSG00000049307	chr9	Fut4	14748459	14752122	3664	0.297735	0.786244	0.352525	0.467832	0.086279	0	21	16	25	21	40	22	54	26	53	57
ENSMUSG00000000339	chr3	Rtca	1.16E+08	1.16E+08	1880	-0.16019	4.668268	0.352702	0.467937	0.033301	0	350	461	531	424	462	460	488	681	612	542
ENSMUSG00000047434	chr16	Xxylt1	30955627	30957734	3412	-0.21888	2.933343	0.352685	0.467937	0.05709	0	78	99	160	162	196	122	195	106	224	178
ENSMUSG00000042156	chr14	Dzip1	1.19E+08	1.19E+08	4744	0.306211	1.781734	0.352821	0.46805	0.114297	0	41	22	54	33	109	54	128	73	81	95
ENSMUSG00000039936	chr4	Pik3cd	1.5E+08	1.5E+08	6259	0.193166	4.15631	0.353015	0.468263	0.047788	0	301	212	244	307	307	294	478	281	622	576
ENSMUSG00000024870	chr19	Rab1b	5099207	5100572	1835	0.148088	6.983593	0.353509	0.468873	0.030062	0	1652	1871	2175	2088	2229	2558	2727	3107	3866	3298
ENSMUSG00000005846	chr16	Rsl1d1	11192970	11193737	2258	0.169676	5.972323	0.353599	0.468931	0.039178	0	831	917	1197	854	1145	1231	1493	2104	1558	1313
ENSMUSG00000027374	chr2	Mrps5	1.28E+08	1.28E+08	6578	-0.15177	5.13257	0.353621	0.468931	0.030497	0	516	613	673	666	584	677	760	738	901	781
ENSMUSG00000020658	chr12	Efr3b	3962554	3966547	6547	-0.23402	3.311393	0.353815	0.469144	0.071597	0	119	176	154	268	165	160	239	113	323	240
ENSMUSG00000039929	chr16	Urb1	90751527	90752178	8190	0.201163	2.595746	0.354292	0.469731	0.046182	0	84	69	85	85	144	107	129	154	186	172
ENSMUSG00000026811	chr2	St6galnac6	32599709	32599836	4815	-0.15052	5.769367	0.354515	0.469982	0.030476	0	792	860	1139	848	1177	1094	1163	1225	1253	1231
ENSMUSG00000032551	chr9	1110059G10Rik	1.23E+08	1.23E+08	3361	0.240371	2.873988	0.354924	0.470479	0.070793	0	109	120	109	103	103	108	193	298	174	143
ENSMUSG00000042055	chr7	Wdr11	1.3E+08	1.3E+08	10372	-0.14528	4.702454	0.35505	0.470567	0.027601	0	402	391	482	464	542	376	557	625	690	660
ENSMUSG00000097167	chr3	Gm16740	95217457	95218058	956	0.358693	0.175669	0.355058	0.470567	0.119658	0	12	5	26	18	15	13	19	44	35	25
ENSMUSG00000060935	chr10	Tmem263	85102627	85102997	3778	0.182844	4.05751	0.355316	0.470863	0.043811	0	240	180	280	200	419	355	507	308	510	376
ENSMUSG00000024513	chr18	Mbd2	70568189	70568967	3214	-0.14251	5.054181	0.355369	0.470889	0.02703	0	521	520	602	593	664	503	749	764	967	742
ENSMUSG00000042507	chr12	Elmsan1	84149176	84152561	7611	-0.16768	4.027349	0.355441	0.470939	0.036251	0	232	233	311	288	385	192	387	444	478	320
ENSMUSG00000046861	chr4	Hectd3	1.17E+08	1.17E+08	4901	-0.1497	4.943067	0.356201	0.471901	0.029824	0	435	510	629	524	601	457	674	827	802	663
ENSMUSG00000026047	chr1	Kdelc1	44106546	44107104	3199	0.182354	3.138687	0.356651	0.472452	0.040221	0	95	128	172	118	176	156	268	177	275	215
ENSMUSG00000002617	chr17	Zfp40	23173869	23177364	4482	-0.26355	1.046992	0.356834	0.472646	0.07088	0	32	29	45	27	49	26	54	27	64	43
ENSMUSG00000057411	chr17	Fam173a	25790508	25790778	800	0.164365	4.582072	0.356866	0.472646	0.035613	0	335	371	394	362	405	589	530	442	719	639
ENSMUSG00000031432	chrX	Prps1	1.4E+08	1.4E+08	1993	-0.16693	5.050334	0.357063	0.472862	0.03752	0	524	574	654	475	688	623	619	940	752	670
ENSMUSG00000028582	chr4	Cc2d1b	1.09E+08	1.09E+08	4771	-0.1535	4.718556	0.357139	0.472917	0.03117	0	452	361	515	409	582	420	487	687	708	618
ENSMUSG00000039202	chr7	Abhd2	79273201	79273339	10571	0.217996	3.593359	0.357346	0.473146	0.062058	0	172	105	204	199	259	182	415	171	450	323
ENSMUSG00000032558	chr9	Nphp3	1.04E+08	1.04E+08	6639	-0.30589	1.01714	0.357483	0.473282	0.100369	0	31	13	46	33	61	19	36	45	62	45
ENSMUSG00000026404	chr1	Ddx59	1.36E+08	1.36E+08	2953	-0.19024	2.964594	0.357626	0.473426	0.044868	0	132	116	154	146	136	121	142	231	185	164
ENSMUSG00000004937	chr10	Sgta	81044075	81045003	1969	0.148052	6.532292	0.358046	0.473892	0.030472	0	1179	1361	1699	1541	1547	1941	2014	2263	2718	2397
ENSMUSG00000030264	chr6	Thumpd3	1.13E+08	1.13E+08	3888	-0.14909	4.075388	0.35803	0.473892	0.027835	0	228	256	384	265	355	297	409	367	439	348
ENSMUSG00000066361	chr12	Serpina3c	1.04E+08	1.04E+08	2213	0.480618	1.741661	0.358115	0.473937	0.299968	0	40	19	20	53	99	25	37	35	138	224
ENSMUSG00000041112	chr13	Elmo1	20090596	20090771	10113	0.192488	3.417221	0.358241	0.474058	0.046708	0	139	108	225	170	195	158	267	205	449	280
ENSMUSG00000022040	chr14	Ephx2	66084377	66084760	2035	0.255536	4.904327	0.358702	0.474507	0.090024	0	374	461	389	609	405	385	425	634	1063	1397
ENSMUSG00000028416	chr4	Bag1	40936398	40936676	1349	0.153546	6.959715	0.358707	0.474507	0.033066	0	1561	1912	2268	2049	2027	2698	2739	2771	3637	3406
ENSMUSG00000038697	chr8	Taf5l	1.24E+08	1.24E+08	3033	-0.16411	3.809707	0.358631	0.474507	0.033298	0	181	194	282	276	312	270	316	354	304	275
ENSMUSG00000042608	chr4	Stk40	1.26E+08	1.26E+08	4117	-0.14868	6.04675	0.358717	0.474507	0.030471	0	906	1028	1379	1183	1336	1339	1474	1348	1607	1484
ENSMUSG00000033543	chr9	Gtf2a2	70012550	70012661	4047	0.168849	4.660464	0.358771	0.474533	0.038103	0	378	413	463	318	388	582	615	689	619	564
ENSMUSG00000007877	chr11	Tcap	98383811	98383956	948	0.275542	10.389	0.358854	0.474562	0.107517	0	25764	18315	20903	24084	8410	24851	23092	54318	34215	34437
ENSMUSG00000016427	chrX	Ndufa1	37187588	37187741	419	0.175314	6.690534	0.358861	0.474562	0.043164	0	1387	1612	2156	1506	1381	2523	2394	2592	2474	2568
ENSMUSG00000058240	chr16	Cryzl1	91689322	91689915	4353	-0.15764	3.613629	0.358941	0.474623	0.030873	0	179	221	237	203	225	223	281	227	318	293
ENSMUSG00000034639	chr6	Setmar	1.08E+08	1.08E+08	1765	-0.25844	2.195738	0.359155	0.47486	0.078864	0	87	78	85	88	64	108	113	57	92	98
ENSMUSG00000040852	chr17	Plekhh2	84511895	84511964	6886	0.318725	2.130738	0.359349	0.475071	0.131706	0	51	30	57	70	119	53	195	144	104	62
ENSMUSG00000024507	chr18	Hsd17b4	50128201	50128409	3404	-0.14814	5.771762	0.360371	0.476376	0.030493	0	777	884	1105	1022	1000	844	1065	1281	1504	1408
ENSMUSG00000037236	chr18	Matr3	35562146	35562259	9869	-0.18349	6.109164	0.360504	0.476507	0.047402	0	1094	1013	1362	1127	1569	898	1537	2310	1660	1197
ENSMUSG00000028845	chr4	Tekt2	1.26E+08	1.26E+08	1900	0.34259	-0.26234	0.360546	0.476517	0.100866	0	7	3	18	10	17	9	21	23	21	22
ENSMUSG00000059820	chr9	AU019823	50605240	50607936	5321	0.168581	3.417089	0.360664	0.476627	0.034881	0	144	156	166	150	218	185	272	322	314	222
ENSMUSG00000090394	chr1	4930523C07Rik	1.6E+08	1.6E+08	10195	-0.18448	2.825608	0.360837	0.476811	0.040722	0	105	84	146	155	137	106	155	161	202	150
ENSMUSG00000006732	chr10	Mettl1	1.27E+08	1.27E+08	2907	-0.16987	4.161557	0.360998	0.476921	0.037794	0	281	300	403	219	377	362	415	406	412	341
ENSMUSG00000021013	chr12	Ttc8	98920574	98920783	2749	-0.19518	2.211196	0.361008	0.476921	0.043105	0	80	60	89	82	95	73	105	87	116	116
ENSMUSG00000031021	chr7	Tmem9b	1.1E+08	1.1E+08	2002	0.151237	5.327957	0.361024	0.476921	0.031336	0	543	636	752	610	610	894	962	924	1127	985
ENSMUSG00000028776	chr4	Tinagl1	1.3E+08	1.3E+08	4358	-0.16586	5.040545	0.361237	0.477156	0.03803	0	422	555	615	765	528	464	748	767	913	770
ENSMUSG00000039656	chr17	Rxrb	34031812	34032223	3698	-0.17585	5.328598	0.361473	0.477423	0.042985	0	614	649	806	697	786	637	835	1324	808	768
ENSMUSG00000024829	chr19	Mrpl21	3282901	3283171	2011	0.160118	5.037299	0.361759	0.477755	0.035143	0	387	551	617	509	508	742	883	716	865	791
ENSMUSG00000060708	chr5	Bloc1s4	36747374	36748679	1306	0.193363	2.604854	0.361849	0.477828	0.044469	0	70	92	127	84	94	135	148	145	159	152
ENSMUSG00000028218	chr4	Fam92a	12153409	12153978	4683	0.175718	2.97023	0.361932	0.477893	0.03653	0	108	96	163	112	131	152	218	186	222	181
ENSMUSG00000027642	chr2	Rpn2	1.57E+08	1.57E+08	4430	0.179038	6.707422	0.362004	0.477905	0.045685	0	1354	1249	1879	1440	2402	2113	2678	1565	3545	3166
ENSMUSG00000037990	chr10	Sh3rf3	58813359	58814126	7242	-0.33748	0.404698	0.36201	0.477905	0.120793	0	30	11	27	8	41	18	31	23	31	25

ENSMUSG00000032640	chr7	Chsy1	66109515	66110227	4167	0.227398	3.028495	0.362088	0.477961	0.06769	0	117	76	135	99	206	146	280	119	280	204
ENSMUSG00000024082	chr17	Ndufaf7	78937135	78937201	2303	-0.1544	4.346582	0.362417	0.47835	0.031739	0	282	390	392	348	357	392	439	391	560	456
ENSMUSG00000042548	chr2	Asxl1	1.53E+08	1.53E+08	7428	0.202444	4.172172	0.363658	0.479943	0.056108	0	237	193	278	304	400	237	371	725	529	410
ENSMUSG00000062937	chr4	Mtap	89137122	89137524	3226	-0.16237	4.251266	0.363827	0.48012	0.035474	0	304	320	355	277	416	345	379	300	608	479
ENSMUSG00000043903	chr8	Gm22	1.22E+08	1.22E+08	3082	0.326869	1.856384	0.364023	0.480332	0.137305	0	50	30	42	38	107	75	148	35	120	81
ENSMUSG00000027375	chr2	Mal	1.28E+08	1.28E+08	2778	-0.22355	2.315196	0.364227	0.480556	0.061858	0	90	57	114	100	79	62	117	129	146	82
ENSMUSG00000022365	chr15	Derl1	57869502	57871906	3145	0.148289	6.594984	0.364399	0.480737	0.031493	0	1276	1247	1857	1348	2018	1864	2312	2182	2677	2835
ENSMUSG00000104394	chr1	RP23-306B14.3	1.87E+08	1.87E+08	2262	-0.30839	0.143924	0.364605	0.480964	0.072547	0	18	22	16	16	21	22	23	21	24	15
ENSMUSG00000034118	chr5	Tpst1	1.3E+08	1.3E+08	2789	0.19774	4.194888	0.364728	0.48108	0.054353	0	280	135	342	214	488	346	507	410	557	465
ENSMUSG00000029176	chr5	Anapc4	52834015	52834392	5902	0.141956	5.416906	0.364831	0.481169	0.028054	0	573	635	780	622	779	849	1012	1171	1178	1001
ENSMUSG00000011958	chr9	Bnip2	69989466	69989689	3455	-0.14395	6.336298	0.364878	0.481186	0.029539	0	1213	1319	1635	1369	1535	1514	1848	1601	2072	1905
ENSMUSG00000020105	chr10	Lrig3	1.26E+08	1.26E+08	4050	0.2263	2.214225	0.365045	0.481269	0.061982	0	62	43	72	83	93	64	122	159	122	109
ENSMUSG00000024019	chr17	Cmtr1	29660595	29660771	7890	-0.16623	5.545006	0.365041	0.481269	0.039101	0	676	718	915	875	946	715	875	1502	1105	940
ENSMUSG00000029392	chr5	Rilpl1	1.24E+08	1.24E+08	2247	-0.23067	6.618367	0.364985	0.481269	0.076906	0	1595	1824	2213	1774	1320	1533	1600	3763	1996	1586
ENSMUSG00000025144	chr11	Stra13	1.21E+08	1.21E+08	1077	-0.15238	3.940081	0.365082	0.481271	0.030412	0	275	238	302	246	271	291	292	318	434	355
ENSMUSG00000034424	chr8	Gcsh	1.17E+08	1.17E+08	1579	-0.14738	4.90657	0.365162	0.48133	0.029682	0	385	510	628	529	582	572	678	597	737	716
ENSMUSG00000039617	chr3	Gm7488	21049565	21050248	684	0.292888	0.374866	0.365274	0.481433	0.064301	0	12	20	20	21	16	26	31	26	43	28
ENSMUSG00000040102	chr6	Klhl42	1.47E+08	1.47E+08	6267	-0.2062	2.493282	0.365624	0.481848	0.05368	0	116	69	98	79	135	78	115	111	174	134
ENSMUSG00000032349	chr9	Elovl5	77917364	77917526	3522	0.167892	4.518194	0.365858	0.482111	0.038765	0	233	305	372	407	506	368	535	457	815	702
ENSMUSG00000081249	chr11	Gm11517	96795439	96795825	387	0.333857	0.494784	0.36593	0.482159	0.115637	0	20	14	16	18	29	39	26	48	17	34
ENSMUSG00000026727	chr2	Rsu1	13076821	13077607	9299	0.149872	4.909039	0.366118	0.482285	0.030811	0	390	432	516	481	558	521	835	567	1028	784
ENSMUSG00000053647	chr5	Gper1	1.39E+08	1.39E+08	2537	0.278142	1.091205	0.36613	0.482285	0.074539	0	29	26	32	43	21	44	62	41	68	45
ENSMUSG00000069833	chr19	Ahnak	8989284	8989429	18543	0.152701	7.997665	0.366062	0.482285	0.033963	0	4107	2916	4612	3708	4971	4139	5815	6868	7900	7088
ENSMUSG00000102070	chr1	Gm28661	24614885	24615565	681	-0.21564	3.451786	0.3662	0.482332	0.062894	0	134	221	235	244	127	221	196	181	324	252
ENSMUSG00000020189	chr10	Osbpl8	1.11E+08	1.11E+08	7152	0.191658	4.389457	0.366878	0.483171	0.050776	0	281	237	359	344	423	245	405	498	855	692
ENSMUSG00000046808	chr5	Atp10d	72203329	72203563	7848	-0.23331	1.33499	0.366907	0.483171	0.056949	0	44	33	41	54	47	32	55	54	63	60
ENSMUSG00000034509	chr17	Mad2l1bp	46147390	46148284	1269	0.174738	4.101268	0.36702	0.483274	0.041074	0	205	321	299	255	242	385	421	430	530	339
ENSMUSG00000028807	chr4	Zbtb8a	1.29E+08	1.29E+08	2321	0.241045	1.256087	0.367059	0.48328	0.056699	0	36	25	36	36	42	37	64	46	78	68
ENSMUSG00000006906	chr6	Stambp	83543206	83544036	2157	0.158179	3.340719	0.367205	0.483425	0.03049	0	135	143	181	149	186	162	279	258	307	243
ENSMUSG00000001508	chr11	Sgca	94962791	94963080	1735	-0.16556	7.492637	0.36728	0.483478	0.040039	0	2704	2829	3440	3223	3732	3547	3317	5269	3876	3536
ENSMUSG00000038954	chr17	Supt3	44777152	44777428	4121	0.186702	2.535388	0.36743	0.483538	0.042008	0	71	68	114	81	117	102	157	119	169	166
ENSMUSG00000044345	chr19	Marveld1	42147400	42149559	4304	0.165318	4.44126	0.367376	0.483538	0.037554	0	335	231	352	293	515	345	594	453	734	592
ENSMUSG00000074884	chr2	Serf2	1.21E+08	1.21E+08	5455	0.156315	7.995553	0.367425	0.483538	0.035816	0	3238	4075	5044	3842	3884	5862	6592	5683	6995	5985
ENSMUSG00000020591	chr12	Ntsr2	16653470	16654123	1547	0.344632	0.108696	0.36822	0.484473	0.095526	0	7	22	14	13	15	26	18	26	37	20
ENSMUSG00000032059	chr9	Alg9	50775019	50775518	3889	0.183923	3.520109	0.368214	0.484473	0.044859	0	150	129	190	183	249	201	319	172	403	341
ENSMUSG00000059586	chr15	Nsmce2	59374198	59374355	3281	0.156282	3.555746	0.368245	0.484473	0.030614	0	187	159	205	184	179	243	287	277	342	284
ENSMUSG00000051557	chr4	Pusl1	1.56E+08	1.56E+08	2329	0.198593	2.547696	0.368602	0.484896	0.048752	0	76	80	106	64	125	111	156	106	184	165
ENSMUSG00000075224	chr2	Lrrc55	85162334	85163513	4080	-0.41012	0.305745	0.368689	0.484964	0.178744	0	12	11	25	26	39	25	35	7	39	9
ENSMUSG00000034880	chr8	Mrpl34	71464926	71465067	645	0.185717	4.599418	0.368975	0.485294	0.048517	0	310	408	420	424	297	631	595	423	699	612
ENSMUSG00000024317	chr18	Rnf138	21001341	21001540	3110	-0.20418	2.590053	0.369023	0.485311	0.051388	0	84	88	140	73	155	85	139	151	138	134
ENSMUSG00000001156	chr6	Mxd1	86647044	86651079	4662	0.20604	2.950978	0.369065	0.48532	0.055274	0	98	92	137	129	140	129	168	278	155	219
ENSMUSG00000032652	chr6	Crebl2	1.35E+08	1.35E+08	3923	-0.23072	3.291421	0.3692	0.485452	0.072536	0	186	134	182	177	193	131	159	379	177	193
ENSMUSG00000054793	chr7	Cadm4	24482023	24482162	2161	0.19089	2.259358	0.369343	0.485593	0.040144	0	62	68	82	74	79	92	115	122	152	105
ENSMUSG00000003166	chr16	Dgcr2	17839482	17842777	6638	-0.1443	5.523065	0.369709	0.486028	0.029755	0	721	626	828	804	1079	743	968	1209	1242	960
ENSMUSG00000030279	chr6	C2cd5	1.43E+08	1.43E+08	4468	0.143746	3.854126	0.369996	0.486359	0.02665	0	198	204	252	206	284	270	376	307	432	385
ENSMUSG00000043987	chr9	Cep164	45766946	45768363	5980	0.229892	2.370314	0.370255	0.486654	0.06464	0	78	48	78	68	123	66	136	107	190	157
ENSMUSG00000090625	chr2	Gm20721	1.74E+08	1.74E+08	1484	0.760634	2.36048	0.370467	0.486887	0.802537	0	16	59	27	151	52	9	11	14	714	110
ENSMUSG00000030521	chr7	Mphosph10	64376576	64376804	3651	0.155045	4.02157	0.370776	0.4872	0.032587	0	201	218	315	244	309	296	388	523	430	348
ENSMUSG00000074406	chr7	Zfp628	4915217	4915405	3524	-0.17261	3.081398	0.370751	0.4872	0.037355	0	105	118	153	168	208	143	186	176	253	170
ENSMUSG00000099233	chr16	Gm27883	19883799	19883900	102	-0.27869	3.206224	0.370936	0.487364	0.106358	0	127	96	212	135	298	222	289	85	212	137
ENSMUSG00000054715	chr7	Zscan22	12897815	12897943	3501	-0.21385	1.875006	0.371113	0.487551	0.054486	0	62	57	66	64	71	50	91	57	119	78
ENSMUSG00000000295	chr10	Hddc2	31313382	31313483	3509	0.192722	3.345689	0.37132	0.487612	0.04936	0	137	176	187	141	133	260	236	203	255	278
ENSMUSG00000029179	chr5	Zcchc4	52775409	52775594	10890	0.190643	2.830742	0.371281	0.487612	0.044903	0	124	86	123	106	103	134	161	201	230	152
ENSMUSG00000034135	chr9	Sik3	46012820	46013130	7102	-0.16735	5.319469	0.371372	0.487612	0.040511	0	595	602	712	748	878	641	657	1264	1011	820
ENSMUSG00000042797	chr7	Aqp11	97726379	97726704	1322	0.267375	0.469143	0.371353	0.487612	0.064485	0	14	21	21	18	23	32	26	25	43	37
ENSMUSG00000058325	chr7	Dock1	1.35E+08	1.35E+08	6807	-0.16963	3.868942	0.371345	0.487612	0.039215	0	214	171	317	248	359	199	303	259	471	401
ENSMUSG00000097787	chr19	2700046G09Rik	32389216	32389376	1641	0.244388	0.913788	0.371296	0.487612	0.057266	0	17	26	33	28	33	37	49	36	56	48
ENSMUSG00000036941	chr18	Elac1	73735038	73739300	4971	-0.1597	3.537703	0.371411	0.487618	0.033432	0	182	191	233	190	217	189	230	326	281	246
ENSMUSG00000053600	chr17	Zfp472	32965814	32965929	2376	0.267891	0.951027	0.371642	0.487862	0.071616	0	33	22	32	19	32	33	43	50	75	36
ENSMUSG00000099364	chr1	5730419F03Rik	78595031	78596859	2092	0.332946	0.713433	0.371667	0.487862	0.118099	0	11	18	39	24	23	18	72	33	49	31
ENSMUSG00000039307	chr11	Hexdc	1.21E+08	1.21E+08	4723	-0.17816	2.946313	0.371894	0.488113	0.040787	0	99	129	194	117	141	127	182	155	196	178
ENSMUSG00000028868	chr4	Wasf2	1.33E+08	1.33E+08	6258	0.156121	5.504295	0.37205	0.488272	0.035316	0	613	493	715	835	965	656	1145	1155	1502	1229
ENSMUSG00000020212	chr10	Mdm1	1.18E+08	1.18E+08	3149	0.259537	1.01296	0.372609	0.488951	0.058859	0	21	32	30	30	32	30	57	44	67	49
ENSMUSG00000048332	chr3	Lhfp	53041528	53041774	2108	-0.17497	4.7106	0.372639	0.488951	0.043532	0	411	273	558	427	696	415	699	677	621	455
ENSMUSG00000009210	chr11	2310007L24Rik	1.06E+08	1.06E+08	1724	-0.19742	2.30297	0.372748	0.489049	0.046463	0	89	81	101	73	85	97	96	104	121	106
ENSMUSG00000102918	chr18	PCDHGB6	37806364	37809743	5499	0.183191	6.179797	0.373047	0.489395	0.049952	0	1076	598	1198	995	1951	1290	2070	1742	2276	1697

ENSMUSG00000020079	chr10	Supv3l1	62429209	62429834	2969	-0.14825	4.037746	0.373162	0.489499	0.029735	0	237	281	329	309	270	315	355	365	422	346
ENSMUSG00000054072	chr18	Iigp1	60376029	60376130	3121	0.279945	3.470493	0.373364	0.489717	0.112989	0	112	196	185	153	180	464	200	135	258	270
ENSMUSG00000023806	chr17	Rsph3b	6904716	6905120	1614	0.180387	3.114421	0.373792	0.490232	0.04144	0	128	123	167	136	110	181	187	219	242	229
ENSMUSG00000048997	chr3	Atxn7l2	1.08E+08	1.08E+08	4817	0.189768	2.912927	0.373962	0.490362	0.046687	0	85	116	126	128	124	154	179	225	157	198
ENSMUSG00000074217	chr8	2210011C24Rik	84010222	84010492	1413	-0.23526	2.025659	0.373952	0.490362	0.06649	0	74	67	86	49	83	90	95	76	71	86
ENSMUSG00000000325	chr16	Arvcf	18348182	18348456	6425	-0.15009	4.078331	0.374003	0.49037	0.030195	0	259	219	341	285	389	324	331	427	429	341
ENSMUSG00000030138	chr6	Bms1	1.18E+08	1.18E+08	4286	-0.14225	5.271547	0.374404	0.490803	0.029197	0	482	620	756	691	860	636	809	975	1038	843
ENSMUSG00000037235	chr5	Mxd4	34173887	34177149	3882	-0.14351	5.938771	0.374381	0.490803	0.030405	0	928	819	1154	1116	1406	883	1434	1418	1799	1368
ENSMUSG00000026203	chr1	Dnajb2	75236406	75236589	4249	-0.18239	5.88449	0.374475	0.490808	0.049454	0	967	958	1421	879	1001	1005	1229	1873	1133	1147
ENSMUSG00000046441	chr8	Cmtr2	1.1E+08	1.1E+08	4115	-0.20076	2.283351	0.374479	0.490808	0.048446	0	64	65	85	88	132	82	98	113	142	88
ENSMUSG00000006676	chr9	Usp19	1.08E+08	1.08E+08	7048	-0.14334	7.291439	0.374578	0.490843	0.030845	0	2211	2348	3215	2747	3308	2770	3292	4090	3999	3214
ENSMUSG00000079111	chr5	Kdelr2	1.43E+08	1.43E+08	1846	0.17938	5.219533	0.374612	0.490843	0.04748	0	503	404	692	452	927	724	1145	618	1305	871
ENSMUSG00000086370	chrX	Ftx	1.04E+08	1.04E+08	7598	0.293776	0.597452	0.374593	0.490843	0.085044	0	26	8	26	22	24	18	43	35	46	42
ENSMUSG00000021044	chr12	Adck1	88360554	88360595	2330	-0.16046	4.437364	0.374672	0.490875	0.036686	0	323	434	423	367	327	419	422	476	569	486
ENSMUSG00000044847	chr11	Lsm11	45928269	45934023	6453	-0.19366	2.476512	0.374713	0.490882	0.046124	0	79	81	107	94	132	93	125	85	180	122
ENSMUSG00000020153	chr10	Ndufs7	80249121	80249204	1718	0.168333	7.735021	0.3749	0.49108	0.042815	0	2664	3720	3577	3595	2977	5298	4665	5023	5844	5114
ENSMUSG00000034839	chr9	Larp6	60712989	60713405	2440	0.315557	1.073296	0.374971	0.491127	0.120827	0	30	11	33	27	51	27	42	91	53	47
ENSMUSG00000025137	chr11	Pcyt2	1.21E+08	1.21E+08	4346	0.14509	4.993591	0.375092	0.491239	0.030215	0	400	450	595	532	550	610	666	727	933	973
ENSMUSG00000038344	chrX	Txlng	1.63E+08	1.63E+08	7541	-0.25403	2.852888	0.375172	0.491297	0.089191	0	120	111	161	113	145	76	130	299	145	115
ENSMUSG00000045503	chr2	Sys1	1.64E+08	1.64E+08	4958	0.158726	4.263527	0.37522	0.491313	0.035123	0	286	283	336	306	283	446	479	359	524	525
ENSMUSG00000034820	chr19	Cpsf7	10525244	10525327	3604	0.146861	4.62793	0.375292	0.491361	0.030433	0	360	338	413	360	485	428	610	759	641	588
ENSMUSG00000030774	chr7	Pak1	97842935	97843141	3065	-0.15354	5.787105	0.375588	0.491627	0.034915	0	690	981	1074	1074	1028	1072	1151	988	1524	1360
ENSMUSG00000047879	chr18	Usp14	9995432	9996248	5974	0.172754	5.405987	0.375589	0.491627	0.044074	0	518	659	813	600	738	697	974	1578	1102	896
ENSMUSG00000079614	chr18	Seh1l	67774876	67775120	3516	0.141655	4.834985	0.375602	0.491627	0.028741	0	360	408	577	378	556	556	722	730	804	673
ENSMUSG00000052040	chr7	Klf13	63886347	63891797	7535	-0.13722	5.439592	0.375788	0.491825	0.027427	0	590	626	819	820	971	721	879	971	1239	1047
ENSMUSG00000031570	chr8	Ppapdc1b	25720061	25720151	2546	0.215467	3.083017	0.376129	0.492225	0.064255	0	129	87	145	89	208	176	254	122	283	222
ENSMUSG00000054099	chr5	Slc25a40	8422850	8423039	2777	-0.209	2.092867	0.376396	0.492528	0.053931	0	80	66	93	66	66	57	101	95	100	103
ENSMUSG00000021290	chr12	2010107E04Rik	1.12E+08	1.12E+08	365	0.177257	7.583125	0.376573	0.492712	0.047786	0	2531	3537	3494	2719	2497	4895	4559	4296	5165	4453
ENSMUSG00000015522	chr3	Arnt	95434388	95434561	8007	-0.17099	5.613921	0.376773	0.492752	0.043592	0	797	651	955	833	1126	733	908	1638	1173	933
ENSMUSG00000021217	chr7	Tshz3	36698118	36698289	5456	0.252772	2.065879	0.376746	0.492752	0.085175	0	73	28	63	50	102	78	135	105	131	72
ENSMUSG00000021508	chr13	Cxcl14	56288647	56289807	1823	0.186032	5.982541	0.376781	0.492752	0.052154	0	1152	611	1118	897	1163	1626	1377	1087	1833	1828
ENSMUSG00000033207	chr19	Mamdc2	23302609	23303686	3338	0.299824	2.204511	0.37669	0.492752	0.124697	0	75	35	64	33	139	75	193	86	139	93
ENSMUSG00000042699	chr1	Dhx9	1.53E+08	1.53E+08	9603	0.142968	5.814765	0.37677	0.492752	0.030297	0	792	688	995	878	1147	985	1401	1162	1915	1525
ENSMUSG00000025781	chr2	Atp5c1	10056016	10056161	1908	-0.16598	9.340701	0.377076	0.493092	0.042209	0	9760	12222	12957	11901	9644	13617	13859	15398	14448	12965
ENSMUSG00000056486	chr2	Chn1	73610660	73613196	5146	0.229818	2.014186	0.37723	0.493246	0.064279	0	53	47	73	75	54	69	144	76	126	86
ENSMUSG00000015467	chr17	Egfl8	34613349	34613581	1761	0.266612	1.203456	0.377293	0.493272	0.082178	0	21	20	34	29	68	42	46	56	80	59
ENSMUSG00000030286	chr6	Emc3	1.14E+08	1.14E+08	2422	0.147702	6.279165	0.377321	0.493272	0.032839	0	1051	1054	1493	1176	1401	1570	1747	2333	2003	1811
ENSMUSG00000071654	chr19	Uqcc3	8880016	8880616	829	0.160116	5.209022	0.377841	0.493905	0.037997	0	414	605	742	565	585	911	837	776	1078	897
ENSMUSG00000040310	chr2	Alx4	93642384	93643088	7060	-0.3951	1.414119	0.377933	0.493932	0.214665	0	68	13	63	22	84	21	93	56	73	24
ENSMUSG00000097908	chr5	4933404O12Rik	1.37E+08	1.37E+08	4101	-0.28597	0.708828	0.377922	0.493932	0.076739	0	33	14	32	34	29	28	31	27	34	42
ENSMUSG00000037149	chr12	Ddx1	13219308	13219628	2507	-0.14113	6.856413	0.378069	0.494063	0.030191	0	1769	1740	2214	2015	2440	2200	2464	2826	2747	2538
ENSMUSG00000024160	chr17	Spsb3	24886643	24886760	2719	-0.14561	5.194045	0.378241	0.494242	0.031086	0	519	633	739	603	708	736	818	658	964	857
ENSMUSG00000026273	chr1	Mterf4	93299211	93301584	5271	0.162481	3.365302	0.378325	0.494304	0.034632	0	138	157	198	152	156	202	252	295	277	229
ENSMUSG00000057229	chr7	Atp5sl	25619414	25619460	2916	-0.17531	4.625416	0.378516	0.494507	0.045246	0	321	480	502	532	314	461	500	570	655	508
ENSMUSG00000101166	chr7	Gm28496	44246726	44246808	2991	0.262162	0.877959	0.378731	0.494741	0.064412	0	24	22	25	25	36	29	62	38	57	37
ENSMUSG00000026914	chr2	Psmd14	61711694	61711873	2820	0.15564	5.92525	0.379411	0.495536	0.036579	0	743	947	1148	905	1058	1094	1374	1984	1602	1412
ENSMUSG00000057530	chr4	Ece1	1.38E+08	1.38E+08	5300	-0.18201	5.717961	0.37939	0.495536	0.050293	0	701	862	1073	1133	890	690	985	1781	1233	1102
ENSMUSG00000015133	chr7	Lrrk1	66226912	66226941	9487	0.165049	3.732595	0.379951	0.496194	0.037941	0	202	131	243	214	259	229	433	283	405	294
ENSMUSG00000035834	chr13	Polr3g	81673843	81676122	3936	0.22919	1.497532	0.380048	0.496275	0.061233	0	23	37	58	44	50	58	75	54	76	79
ENSMUSG00000028899	chr4	Taf12	1.32E+08	1.32E+08	4038	-0.14681	4.771725	0.381435	0.498039	0.031476	0	418	445	536	492	489	566	632	501	652	638
ENSMUSG00000022312	chr15	Eif3h	51786558	51786825	1253	0.145578	6.747882	0.381532	0.498118	0.032639	0	1422	1585	1925	1696	1889	2228	2447	3121	2739	2537
ENSMUSG00000098917	chr8	Mir7654	8690093	8690162	70	-0.28826	0.462253	0.381588	0.498145	0.079465	0	15	14	37	31	23	24	27	19	39	27
ENSMUSG00000071037	chr17	Camkmt	85090726	85090863	972	0.38774	-0.50323	0.381633	0.498156	0.126026	0	5	13	10	6	9	9	20	5	24	23
ENSMUSG00000032555	chr9	Topbp1	1.03E+08	1.03E+08	11122	-0.15148	3.88167	0.381797	0.498323	0.03233	0	218	205	291	239	350	212	334	262	485	363
ENSMUSG00000101225	chr7	1700008J07Rik	1.28E+08	1.28E+08	2432	-0.22572	1.597413	0.381919	0.498436	0.055487	0	44	36	63	54	71	51	51	78	66	69
ENSMUSG00000079484	chr2	Phyhd1	30266203	30266625	2657	0.244972	3.91982	0.38197	0.498455	0.089106	0	144	304	231	286	160	301	227	601	355	402
ENSMUSG00000028454	chr4	Pigo	43017635	43018038	4283	-0.17803	3.268699	0.382346	0.498899	0.043984	0	116	159	188	166	227	153	237	135	290	246
ENSMUSG00000054604	chr16	Cggbp1	64851996	64852236	4522	0.138203	4.841166	0.382396	0.498917	0.028091	0	377	383	484	408	645	542	678	659	874	762
ENSMUSG00000039384	chr1	Dusp10	1.84E+08	1.84E+08	3042	-0.20283	5.58738	0.38259	0.499076	0.063069	0	456	861	641	909	1509	955	1225	1044	1146	793
ENSMUSG00000055200	chr7	Sertad3	27473768	27473871	1324	0.194555	2.941488	0.382582	0.499076	0.052408	0	69	124	135	108	161	181	201	134	245	181
ENSMUSG00000021782	chr14	Dlg5	24133953	24135673	8491	-0.20737	2.96062	0.382962	0.499515	0.059299	0	115	73	147	152	219	93	191	207	205	151
ENSMUSG00000040389	chr3	Wdr47	1.09E+08	1.09E+08	4394	-0.19177	2.579384	0.383057	0.499591	0.049627	0	98	94	115	115	99	91	169	112	177	101
ENSMUSG00000026748	chr2	Plxdc2	16356304	16357237	6947	-0.18211	5.122395	0.38342	0.500018	0.050328	0	626	333	641	581	963	574	995	818	819	595
ENSMUSG00000024205	chr11	Rpl36-ps2	76601319	76601629	311	0.359263	0.32014	0.384318	0.501142	0.129008	0	21	25	11	17	6	29	30	28	39	24
ENSMUSG00000009733	chr15	Tfcp2	1.01E+08	1.01E+08	3250	-0.15667	3.231727	0.384451	0.501268	0.033368	0	166	124	187	153	191	147	203	234	242	207
ENSMUSG00000024182	chr17	Axin1	26138688	26139041	3828	0.142053	4.351481	0.384595	0.501408	0.029159	0	283	269	338	289	448	357	469	588	599	491

ENSMUSG00000046573	chr13	Lyrm4	35978797	35979907	1515	0.20288	2.311984	0.385003	0.501893	0.050759	0	56	77	83	93	66	92	119	142	130	124
ENSMUSG00000042272	chr2	Sestd1	77180340	77187260	9857	0.164075	3.966213	0.385269	0.502191	0.039086	0	225	178	276	247	307	253	350	549	383	384
ENSMUSG00000027282	chr2	Mtch2	90847155	90847385	8490	0.146319	7.101715	0.385475	0.502414	0.033635	0	1805	2142	2486	2151	2261	2919	2934	3689	3606	3571
ENSMUSG00000017466	chr11	Timp2	1.18E+08	1.18E+08	3896	0.187516	7.903688	0.38573	0.502699	0.055727	0	3802	1954	4221	3131	6029	4316	7731	6285	6851	4713
ENSMUSG00000024966	chr19	Stip1	7020696	7021171	2173	-0.15929	6.851843	0.385869	0.502784	0.03988	0	1669	1792	2751	1859	2156	2366	2819	1754	3184	2576
ENSMUSG00000098816	chr7	Gm27786	1.43E+08	1.43E+08	70	0.756751	0.640512	0.385837	0.502784	0.79954	0	4	19	9	39	15	1	3	8	198	31
ENSMUSG00000032350	chr9	Gclc	77754535	77754959	3423	-0.17895	3.159044	0.38601	0.50292	0.04388	0	121	118	198	171	186	114	194	264	216	190
ENSMUSG00000008305	chr4	Tle1	72117142	72118391	8711	-0.18326	4.067008	0.386107	0.503	0.050272	0	236	317	296	315	305	243	289	576	390	330
ENSMUSG00000028964	chr4	Park7	1.51E+08	1.51E+08	2479	-0.17607	9.080627	0.386527	0.5035	0.049366	0	7501	8918	12467	9175	10088	13451	9744	11852	9861	12557
ENSMUSG00000026083	chr1	Eif5b	37998010	37998324	9753	0.14585	6.93567	0.386646	0.50356	0.033547	0	1470	1753	2336	1992	2208	2221	2518	3460	3408	3443
ENSMUSG00000085408	chr4	C530005A16Rik	1.17E+08	1.17E+08	2436	-0.27105	0.876388	0.386624	0.50356	0.086841	0	35	27	25	30	42	26	31	61	33	33
ENSMUSG00000097392	chr5	D930016D06Rik	1.05E+08	1.05E+08	4509	0.233329	2.674932	0.3867	0.503583	0.077712	0	89	87	90	92	124	91	162	280	141	119
ENSMUSG00000019718	chr12	L3hypdh	72073428	72074036	2679	0.28967	1.509545	0.387062	0.504007	0.106545	0	41	30	34	32	71	31	75	44	99	113
ENSMUSG00000046806	chr6	3110062M04Rik	34871771	34874695	4269	-0.19797	2.344949	0.3872	0.504139	0.05053	0	66	86	108	82	106	95	97	76	138	138
ENSMUSG00000037206	chr9	Islr	58156265	58158230	2354	0.198097	6.162777	0.387277	0.504192	0.062103	0	1002	656	1005	1084	1957	1451	2524	1170	2191	1624
ENSMUSG00000030397	chr7	Mark4	19426075	19426411	2259	-0.16385	3.463406	0.387549	0.504373	0.038178	0	164	139	200	224	248	138	241	296	320	232
ENSMUSG00000041199	chr17	Rpusd1	25727751	25727847	1703	0.188482	2.272828	0.387536	0.504373	0.043121	0	64	71	85	72	76	104	103	105	155	122
ENSMUSG00000056763	chr1	Cspp1	10037987	10039342	17553	0.216758	1.925449	0.387533	0.504373	0.057549	0	56	43	59	58	70	54	123	108	96	86
ENSMUSG00000093290	chr7	Mir3572	3655962	3656047	86	0.289569	0.443885	0.387562	0.504373	0.076317	0	26	11	18	15	24	18	36	37	39	33
ENSMUSG00000034893	chr14	Cog3	75702351	75704060	4222	-0.1367	3.968006	0.387701	0.504507	0.026162	0	212	246	318	247	350	258	356	364	398	361
ENSMUSG00000078941	chr13	Ak6	1.01E+08	1.01E+08	2769	-0.14149	5.583594	0.387776	0.504558	0.030943	0	672	853	1027	780	851	915	1062	1121	1214	981
ENSMUSG00000083443	chr6	Gm15519	1.13E+08	1.13E+08	1566	-0.29608	0.431639	0.387878	0.504642	0.095801	0	17	34	26	21	16	18	22	34	24	34
ENSMUSG00000036091	chr9	Hyal3	1.08E+08	1.08E+08	1948	0.237943	1.710359	0.387947	0.504685	0.070287	0	47	35	57	53	51	54	54	121	92	81
ENSMUSG00000042185	chr9	Nfrkb	31386192	31386270	9953	-0.167	3.478461	0.388011	0.504721	0.039125	0	162	157	218	162	293	172	224	321	282	223
ENSMUSG00000024665	chr19	Fads2	10064164	10064314	1508	-0.2784	2.496019	0.38811	0.504803	0.111389	0	64	45	84	91	252	79	150	106	143	113
ENSMUSG00000039737	chr5	Prkrip1	1.36E+08	1.36E+08	3967	0.155448	3.734534	0.388997	0.505908	0.034602	0	172	203	283	184	201	289	357	312	360	297
ENSMUSG00000103983	chr1	RP23-395H6.2	1.71E+08	1.71E+08	5577	0.370376	-0.21533	0.389151	0.506061	0.110075	0	13	6	11	10	15	7	25	11	29	30
ENSMUSG00000022656	chr16	Pvrl3	46387706	46395272	12747	0.207186	2.903667	0.389562	0.506547	0.059981	0	106	76	119	116	162	97	289	171	217	165
ENSMUSG00000030323	chr6	Ift122	1.16E+08	1.16E+08	7953	-0.14896	4.600312	0.39004	0.507121	0.033373	0	316	350	517	431	536	458	586	379	737	533
ENSMUSG00000029227	chr5	Fip1l1	74535449	74535761	10442	0.157337	4.701034	0.390168	0.50724	0.038187	0	290	322	505	399	570	415	601	873	688	630
ENSMUSG00000025035	chr19	Arl3	46531109	46531386	822	-0.14514	5.455456	0.390318	0.507388	0.03272	0	701	653	978	714	799	958	941	913	1097	890
ENSMUSG00000042589	chr5	Cux2	1.22E+08	1.22E+08	8015	-0.40243	0.02481	0.390521	0.507604	0.182636	0	24	10	24	12	18	8	40	12	30	6
ENSMUSG00000031533	chr8	Mrps31	22411340	22411584	1536	-0.15445	4.78625	0.39069	0.507776	0.03655	0	368	486	587	526	443	571	536	662	706	539
ENSMUSG00000055897	chr2	Ppp4r1l-ps	1.74E+08	1.74E+08	12025	0.174015	3.00735	0.390789	0.507858	0.041819	0	120	92	146	103	168	126	214	194	211	245
ENSMUSG00000013089	chr16	Etv5	22381309	22383691	4103	-0.15711	4.462389	0.39093	0.507944	0.037456	0	380	282	450	340	497	332	508	653	526	413
ENSMUSG00000025995	chr1	Wdr75	45795166	45795604	4900	0.134243	4.022272	0.390904	0.507944	0.02608	0	202	218	308	250	320	312	389	437	446	389
ENSMUSG00000018893	chr15	Mb	77015489	77016072	1252	-0.32471	10.02456	0.391043	0.508044	0.170265	0	11752	26148	16114	34108	4693	16256	23168	27873	26663	14471
ENSMUSG00000039637	chr16	Coro7	4626133	4627499	7420	0.1589	3.974329	0.391191	0.508165	0.037338	0	199	212	254	244	334	295	400	249	518	483
ENSMUSG00000090946	chr12	Ccdc71l	32378704	32382943	4240	0.178176	3.04043	0.39121	0.508165	0.043949	0	136	88	165	120	128	160	190	161	263	240
ENSMUSG00000050945	chr18	Zfp438	5210031	5211198	3209	-0.2092	1.881927	0.391351	0.508301	0.056804	0	74	47	75	58	67	63	86	58	110	76
ENSMUSG00000010057	chr9	Nprl2	1.08E+08	1.08E+08	2013	0.179551	3.148854	0.391527	0.508482	0.045715	0	124	130	153	142	133	211	217	143	264	246
ENSMUSG00000031634	chr8	Ufsp2	45975528	45975588	2566	-0.14049	5.240905	0.391671	0.508621	0.030585	0	572	624	771	604	731	742	794	866	840	907
ENSMUSG00000072582	chr11	Ptrh2	86683985	86684123	3132	0.141124	3.945922	0.391749	0.508674	0.028794	0	221	221	301	209	264	328	389	360	403	383
ENSMUSG00000032320	chr9	Rcn2	56041845	56042204	4745	0.130387	5.173085	0.391861	0.508773	0.026153	0	523	492	657	514	693	681	951	865	1052	857
ENSMUSG00000038535	chr9	Zfp280d	72274860	72275029	19017	-0.21481	3.480939	0.391921	0.508803	0.069866	0	216	130	226	192	233	142	217	426	237	179
ENSMUSG00000018820	chr19	Zfyve27	42163951	42164050	8623	0.179907	3.918455	0.392028	0.508846	0.048353	0	227	200	258	232	256	202	303	560	382	433
ENSMUSG00000028669	chr4	Pithd1	1.36E+08	1.36E+08	2477	0.137811	4.723562	0.392026	0.508846	0.028845	0	353	393	525	372	453	515	662	715	713	609
ENSMUSG00000039873	chr2	Neurl2	1.65E+08	1.65E+08	1014	0.150499	4.379	0.392346	0.509212	0.034628	0	267	289	344	331	417	516	417	429	572	578
ENSMUSG00000042428	chr15	Mgat3	80173721	80173838	4665	-0.26665	1.280888	0.392391	0.509222	0.087586	0	49	18	40	46	63	40	55	56	65	33
ENSMUSG00000032381	chr9	Fam96a	66126611	66126970	1240	0.138478	5.132025	0.392438	0.509236	0.029717	0	417	540	701	530	602	663	913	727	1057	943
ENSMUSG00000029386	chr5	Tctn2	1.25E+08	1.25E+08	8318	0.245237	1.174378	0.392803	0.50966	0.075443	0	24	18	40	30	57	57	49	44	65	55
ENSMUSG00000028348	chr4	Murc	48663514	48664029	2054	-0.14144	7.561406	0.393137	0.510046	0.032522	0	2683	2698	4008	3401	3894	3812	4674	4013	4391	3865
ENSMUSG00000052957	chr13	Gas1	60174405	60177365	2961	0.175789	5.469167	0.393195	0.510073	0.049635	0	668	360	792	661	1065	789	1357	1272	1201	868
ENSMUSG00000001366	chr9	Fbxo9	78081499	78082088	3103	-0.17604	5.779117	0.393277	0.510132	0.049734	0	876	806	1178	913	1104	962	1009	1891	1165	929
ENSMUSG00000010755	chr7	Cars	1.44E+08	1.44E+08	4639	-0.1391	5.281634	0.393532	0.510368	0.030279	0	536	673	707	618	875	720	797	945	947	887
ENSMUSG00000085881	chr13	Gm15912	74008152	74008464	578	0.288965	0.625372	0.393524	0.510368	0.088784	0	17	27	22	20	21	30	24	57	33	39
ENSMUSG00000050394	chrX	Armcx6	1.35E+08	1.35E+08	2486	0.256305	1.62157	0.393675	0.510505	0.087572	0	29	38	47	46	70	68	110	37	97	66
ENSMUSG00000022711	chr16	Pmm2	8637674	8637828	4519	0.141215	4.323313	0.39376	0.510567	0.029557	0	242	322	331	345	337	378	478	422	654	529
ENSMUSG00000034341	chr11	Wbp2	1.16E+08	1.16E+08	3177	0.138258	6.1476	0.393862	0.510652	0.030722	0	921	952	1249	1193	1347	1373	1452	1907	2015	1923
ENSMUSG00000097571	chrX	Jpx	1.03E+08	1.03E+08	4785	-0.32483	0.270184	0.394054	0.510853	0.119395	0	31	13	22	21	15	8	20	36	27	27
ENSMUSG00000021253	chr12	Tgfb3	86056744	86057938	3384	0.178811	5.379481	0.394287	0.511107	0.051484	0	564	434	702	658	953	758	1661	840	1072	824
ENSMUSG00000046010	chr11	Zfp830	82764345	82765935	1591	-0.17457	3.427646	0.394386	0.511188	0.044178	0	154	170	255	167	204	194	214	326	234	193
ENSMUSG00000052031	chr17	Tagap1	6954965	6957024	2358	-0.15006	3.658014	0.394598	0.511415	0.032069	0	174	198	250	242	239	264	294	227	312	279
ENSMUSG00000057054	chr11	Inca1	70688361	70688749	1377	0.253928	1.487653	0.394706	0.511507	0.080538	0	24	52	46	38	45	40	51	90	77	88
ENSMUSG00000053297	chr6	AI854703	48626764	48627113	4156	-0.27755	0.4497	0.39479	0.511568	0.076754	0	24	16	31	23	23	17	17	39	36	27
ENSMUSG00000021506	chr13	Pitx1	55825051	55826611	2656	-0.38607	-0.1334	0.395002	0.51179	0.150725	0	17	6	11	10	36	20	21	10	13	17

ENSMUSG00000025169	chr11	Ogfod3	1.21E+08	1.21E+08	1308	0.148003	3.506531	0.395036	0.51179	0.030942	0	169	153	204	172	193	243	240	258	329	309
ENSMUSG00000019984	chr10	Med23	24869986	24870146	6692	-0.15352	3.210176	0.395117	0.511847	0.032179	0	122	134	182	168	209	149	219	175	275	207
ENSMUSG00000009575	chr15	Cbx5	1.03E+08	1.03E+08	9006	-0.14306	5.889766	0.395885	0.512795	0.032986	0	891	757	1241	983	1394	987	1615	1123	1630	1263
ENSMUSG00000022463	chr15	Srebf2	82147266	82147490	4989	0.229699	5.023173	0.396088	0.512985	0.086068	0	323	308	408	479	1081	639	1033	425	1087	943
ENSMUSG00000028483	chr4	Snapc3	83417724	83418054	6760	0.162726	2.843024	0.396217	0.512985	0.035418	0	94	93	135	112	126	138	204	156	210	167
ENSMUSG00000029510	chr5	Gpc2	1.38E+08	1.38E+08	8309	0.298937	0.867848	0.396143	0.512985	0.112987	0	21	15	39	20	36	18	67	28	76	40
ENSMUSG00000035640	chr10	Dos	80130451	80132251	4996	-0.2719	0.361741	0.396118	0.512985	0.080743	0	16	20	18	22	34	15	34	19	42	19
ENSMUSG00000039568	chr16	Ubald1	4874778	4875869	5538	0.155563	5.24181	0.396207	0.512985	0.038745	0	509	543	607	598	729	725	775	1283	876	950
ENSMUSG00000022098	chr14	Bmp1	70474557	70475249	3757	0.19178	5.611	0.396376	0.513143	0.060195	0	691	415	805	612	1401	947	1539	812	1577	1249
ENSMUSG00000037640	chr7	Zfp60	27731389	27731470	8390	0.20451	3.183476	0.396713	0.513492	0.062991	0	118	114	182	130	158	138	215	376	189	202
ENSMUSG00000039357	chr14	Fut11	20694968	20695698	3344	-0.1867	3.026336	0.39672	0.513492	0.050523	0	143	81	175	119	212	114	217	169	219	172
ENSMUSG00000097287	chr5	D130017N08Rik	1.44E+08	1.44E+08	4122	-0.21933	1.537708	0.396771	0.51351	0.062691	0	53	37	52	58	52	39	58	45	94	74
ENSMUSG00000031913	chr8	Vps4a	1.07E+08	1.07E+08	2522	-0.13982	6.141085	0.396819	0.513524	0.031748	0	1037	1139	1457	1188	1357	1394	1424	1737	1713	1502
ENSMUSG00000026073	chr1	Il1r2	40074079	40074248	1908	0.317042	0.215389	0.397015	0.513633	0.108901	0	10	11	27	11	21	22	13	21	41	41
ENSMUSG00000028676	chr4	Srsf10	1.36E+08	1.36E+08	7003	0.136497	4.602705	0.396995	0.513633	0.028806	0	338	309	464	333	501	436	650	508	702	682
ENSMUSG00000044674	chr5	Fzd1	4753873	4758035	4163	0.208149	3.161495	0.396951	0.513633	0.065357	0	143	85	141	101	227	112	271	257	310	184
ENSMUSG00000020728	chr11	Cep112	1.08E+08	1.08E+08	6175	0.301413	0.616198	0.39706	0.513644	0.093757	0	21	20	17	22	26	17	62	38	45	25
ENSMUSG00000053390	chr17	Zfp952	32993129	32993258	4368	-0.17826	2.557716	0.397169	0.513737	0.044044	0	90	88	126	104	107	70	126	142	167	142
ENSMUSG00000020928	chr11	Higd1b	1.03E+08	1.03E+08	847	-0.25935	1.612998	0.397214	0.513747	0.093696	0	43	47	84	67	28	50	66	42	88	73
ENSMUSG00000038319	chr5	Kcnh2	24319589	24320149	4845	0.242547	2.924475	0.397631	0.514238	0.090926	0	73	93	128	104	189	167	197	70	310	217
ENSMUSG00000020228	chr10	Helb	1.2E+08	1.2E+08	5011	-0.14437	3.402037	0.397731	0.514319	0.02948	0	142	162	223	176	224	171	251	218	312	223
ENSMUSG00000055003	chr6	Lrtm2	1.19E+08	1.19E+08	4102	-0.40264	1.571941	0.397818	0.514384	0.246175	0	99	12	78	36	47	25	115	29	96	37
ENSMUSG00000037287	chr9	Tbcel	42412316	42416149	5556	-0.16921	4.787869	0.398007	0.51458	0.045767	0	416	388	551	505	592	406	562	957	607	495
ENSMUSG00000050148	chrX	Ubqln2	1.53E+08	1.54E+08	3344	-0.16569	3.947335	0.398624	0.51533	0.042369	0	242	230	301	261	325	236	270	512	400	278
ENSMUSG00000020130	chr10	Tbc1d15	1.15E+08	1.15E+08	3773	-0.26654	4.771419	0.39872	0.515357	0.116742	0	480	420	579	441	564	258	414	1351	512	368
ENSMUSG00000024501	chr18	Dpysl3	43320979	43324420	6265	0.231593	5.217013	0.398705	0.515357	0.08847	0	595	294	594	440	998	726	1483	471	1273	777
ENSMUSG00000020601	chr12	Trib2	15791727	15794076	4290	-0.16364	4.724331	0.399266	0.516016	0.04281	0	364	447	384	440	707	475	729	558	721	425
ENSMUSG00000031586	chr8	Rbpms	33782643	33784186	4022	-0.19843	3.422825	0.399332	0.516048	0.061332	0	125	243	164	235	166	175	180	226	266	314
ENSMUSG00000044986	chr15	Tst	78399556	78400030	1096	-0.16268	4.458014	0.399366	0.516048	0.04225	0	303	343	366	436	492	315	398	376	674	696
ENSMUSG00000005148	chr14	Klf5	99298691	99299222	1721	-0.26197	1.53253	0.399439	0.516095	0.093456	0	55	40	56	46	58	39	95	64	76	27
ENSMUSG00000029591	chr5	Ung	1.14E+08	1.14E+08	2566	0.174126	3.103849	0.399836	0.516514	0.044622	0	109	127	158	139	132	214	183	167	294	190
ENSMUSG00000032121	chr9	Tmem218	37208333	37208405	1019	0.22461	2.041195	0.399838	0.516514	0.066323	0	52	58	85	54	60	74	117	61	165	98
ENSMUSG00000028688	chr4	Toe1	1.17E+08	1.17E+08	2979	0.161799	3.063571	0.400088	0.516788	0.037244	0	94	121	138	139	163	159	175	242	248	197
ENSMUSG00000018574	chr11	Acadvl	70010183	70010436	2686	0.191038	8.487151	0.400126	0.516789	0.061477	0	4357	6402	5434	7116	4095	6405	6281	12071	10900	9278
ENSMUSG00000021130	chr12	Galnt16	80518990	80519345	3920	-0.17834	3.568461	0.40024	0.516888	0.048251	0	173	112	233	215	340	175	306	204	349	276
ENSMUSG00000034292	chr1	Traf3ip1	91494647	91494888	3712	-0.1793	2.352725	0.400364	0.517	0.04228	0	74	75	91	98	109	75	109	136	129	104
ENSMUSG00000045248	chr8	Med26	72494558	72497106	3040	-0.17586	3.39499	0.400432	0.517039	0.045058	0	149	129	205	208	246	239	243	173	215	252
ENSMUSG00000032026	chr9	Rexo2	48468514	48468946	1075	0.135373	5.551272	0.400511	0.517044	0.029881	0	589	738	908	654	844	994	1090	1147	1267	1191
ENSMUSG00000053774	chr16	Ubxn7	32332252	32332360	10318	0.163713	4.312358	0.400504	0.517044	0.042506	0	246	259	347	294	431	291	465	729	511	459
ENSMUSG00000021476	chr13	Habp4	64161866	64162334	2566	-0.12783	5.074976	0.400656	0.517184	0.025969	0	495	529	627	572	718	616	785	738	873	738
ENSMUSG00000049115	chr13	Agtr1a	30336441	30336589	2467	-0.20752	2.425588	0.401148	0.51777	0.062532	0	105	70	84	75	141	74	95	154	126	127
ENSMUSG00000047963	chr5	Stbd1	92603051	92603337	1985	0.194058	7.214893	0.401352	0.517986	0.063653	0	1305	2322	3199	1884	3079	3931	3895	2138	4233	4039
ENSMUSG00000020102	chr10	Slc16a7	1.25E+08	1.25E+08	3890	0.385595	0.470038	0.401555	0.518199	0.193884	0	22	4	24	21	22	11	39	12	54	59
ENSMUSG00000074698	chr2	Csnk2a1	1.52E+08	1.52E+08	7089	-0.1373	6.768446	0.401661	0.518288	0.031566	0	1693	1757	2217	1778	2073	2145	2352	2621	2608	2290
ENSMUSG00000042857	chr13	Gm9776	94355839	94358818	2980	0.282371	0.074362	0.401714	0.518307	0.064903	0	9	14	21	11	17	19	29	22	30	22
ENSMUSG00000036099	chr10	Vezt	93939165	93939300	20631	-0.15916	4.581233	0.401841	0.518423	0.040743	0	412	319	505	399	473	352	443	767	551	525
ENSMUSG00000023068	chr10	Nus1	52417547	52418168	4876	0.134036	5.24329	0.401948	0.518465	0.029011	0	479	556	677	550	767	656	878	839	1298	1015
ENSMUSG00000063873	chr2	Slc24a3	1.45E+08	1.45E+08	4564	0.316868	2.231798	0.401924	0.518465	0.153856	0	66	44	56	81	96	52	75	53	173	262
ENSMUSG00000038836	chr6	Agbl3	34780432	34781059	11075	-0.28028	0.514486	0.402153	0.518681	0.101005	0	33	21	21	20	26	14	32	47	26	23
ENSMUSG00000025723	chr7	Nmb	80902227	80902503	793	0.34855	0.846426	0.40219	0.518681	0.163877	0	27	25	37	15	19	30	26	97	33	33
ENSMUSG00000065887	chr4	n-R5s185	53860652	53860770	119	-0.23676	1.365009	0.402276	0.518743	0.070456	0	31	46	58	46	44	38	68	68	44	47
ENSMUSG00000036352	chr2	Ubac1	25998543	25999067	2632	-0.14591	7.754236	0.402611	0.519127	0.036111	0	2979	3659	4439	3735	4142	4856	4703	4139	5170	4698
ENSMUSG00000045999	chr17	AY036118	39847526	39848829	1304	0.886826	2.673789	0.402653	0.519133	1.235647	0	6	121	11	147	69	3	2	7	715	352
ENSMUSG00000022434	chr15	Fam118a	85037062	85037244	2543	0.196171	2.427656	0.402816	0.519245	0.055405	0	51	81	88	89	105	124	129	87	176	142
ENSMUSG00000054942	chr3	Fam73a	1.52E+08	1.52E+08	5355	-0.16628	3.06572	0.402785	0.519245	0.040555	0	127	143	172	131	157	150	193	223	188	152
ENSMUSG00000027646	chr2	Src	1.57E+08	1.57E+08	4371	0.184331	2.877489	0.403215	0.519712	0.050179	0	105	77	124	81	191	131	195	180	232	170
ENSMUSG00000076258	chr16	Gm23935	11144125	11144181	57	0.247845	7.81594	0.403291	0.519761	0.104657	0	2559	4724	4890	2254	2468	6015	3304	5403	4540	8522
ENSMUSG00000028886	chr4	Eya3	1.33E+08	1.33E+08	5647	0.126425	4.751534	0.403524	0.520013	0.025311	0	364	346	495	417	540	475	633	672	831	689
ENSMUSG00000015943	chr3	Bola1	96196588	96197279	1082	0.177697	3.524546	0.403664	0.520097	0.049128	0	139	200	226	163	159	307	248	269	268	289
ENSMUSG00000023852	chr17	Chd1	15704967	15705312	8721	-0.15662	4.193417	0.403632	0.520097	0.039108	0	307	269	299	312	418	262	368	574	447	371
ENSMUSG00000020941	chr11	Map3k14	1.03E+08	1.03E+08	6550	0.163831	3.197583	0.403723	0.520124	0.040435	0	109	119	152	145	198	159	231	298	235	197
ENSMUSG00000010205	chr9	Raver1	21074168	21075496	3440	0.136746	4.995326	0.404003	0.52039	0.030443	0	382	410	534	564	669	570	699	908	1004	740
ENSMUSG00000057541	chr5	Pus7	23740648	23741976	5171	-0.15344	3.763551	0.404004	0.52039	0.03579	0	209	174	279	231	307	218	284	404	327	260
ENSMUSG00000024560	chr18	Cxxc1	74216131	74216482	2618	-0.12736	4.247898	0.404251	0.52061	0.024857	0	285	258	367	350	400	317	455	413	503	433
ENSMUSG00000047867	chr6	Gimap6	48701582	48702823	3496	-0.15742	4.115884	0.404241	0.52061	0.039761	0	250	288	351	368	250	280	346	317	494	487
ENSMUSG00000073535	chr1	Gm5532	1.56E+08	1.56E+08	2206	0.437783	0.01854	0.404334	0.520669	0.246405	0	8	15	7	31	1	20	23	30	36	14

ENSMUSG00000044086	chr6	Lmod3	97238528	97238871	2242	0.161284	7.456129	0.404395	0.5207	0.044473	0	2306	2500	3107	3163	2720	4212	5017	2837	5654	3836
ENSMUSG00000019494	chr5	Cops6	1.38E+08	1.38E+08	2525	0.132783	6.361297	0.404682	0.520942	0.029715	0	1108	1203	1485	1371	1363	1727	1985	1999	2288	1991
ENSMUSG00000058620	chr2	Adra2b	1.27E+08	1.27E+08	4014	-0.25668	0.841163	0.404696	0.520942	0.078503	0	28	26	33	40	27	31	35	53	31	29
ENSMUSG00000072258	chr1	Taf1a	1.83E+08	1.83E+08	2409	-0.18482	2.366702	0.404664	0.520942	0.047745	0	87	84	105	75	98	80	106	145	117	106
ENSMUSG00000040280	chr10	Ndufa4l2	1.28E+08	1.28E+08	960	-0.17867	3.548348	0.404855	0.521098	0.049065	0	206	135	222	179	301	246	305	162	297	253
ENSMUSG00000052446	chr8	Zfp961	71951038	71951103	3950	0.226871	1.702382	0.404912	0.521123	0.063377	0	53	49	53	40	44	57	78	58	105	103
ENSMUSG00000085227	chr5	6330418K02Rik	1.38E+08	1.38E+08	1339	0.293927	0.478189	0.405068	0.521275	0.100154	0	15	15	20	17	31	38	31	13	41	41
ENSMUSG00000031775	chr8	Pllp	94674895	94676279	1889	0.285669	1.012835	0.405842	0.522222	0.098616	0	24	27	14	40	38	26	45	71	56	50
ENSMUSG00000028139	chr3	Riiad1	94464983	94465095	813	0.278846	1.416283	0.406213	0.522651	0.110934	0	33	43	46	40	29	52	43	112	45	71
ENSMUSG00000007850	chr11	Hnrnph1	50376990	50377147	5842	-0.1559	6.333106	0.406259	0.522662	0.041515	0	1282	1185	1860	1182	1623	1345	2111	1156	2414	1979
ENSMUSG00000024594	chr18	Prrc1	57354733	57354891	4801	-0.14768	5.465267	0.406454	0.522865	0.036621	0	626	759	752	675	1078	677	1036	1248	1107	840
ENSMUSG00000103766	chr3	RHBG	88243380	88243448	1524	0.276005	0.668384	0.406584	0.522983	0.098253	0	31	13	26	16	26	38	30	49	28	41
ENSMUSG00000053333	chr1	Dis3l2	86703808	86703871	8901	0.14806	3.866557	0.406633	0.522998	0.033641	0	206	215	228	258	232	278	313	441	379	362
ENSMUSG00000036285	chr5	Noa1	77294182	77294556	4029	-0.13579	4.198204	0.406883	0.523223	0.028816	0	242	295	384	357	321	345	399	394	468	422
ENSMUSG00000099481	chr7	Xndc1	1.02E+08	1.02E+08	5278	0.20273	2.172689	0.406884	0.523223	0.05832	0	72	51	90	47	84	94	112	82	128	134
ENSMUSG00000027488	chr2	Snta1	1.54E+08	1.54E+08	3094	0.151875	7.655097	0.407022	0.523351	0.039902	0	2657	2984	3659	3304	3307	4128	3739	6507	5353	4888
ENSMUSG00000020289	chr11	Nprl3	32225628	32226835	7572	-0.1297	3.979748	0.407086	0.523385	0.025557	0	251	216	331	266	311	281	345	359	423	345
ENSMUSG00000032637	chr7	Atxn2l	1.26E+08	1.26E+08	4782	0.141333	5.33537	0.407488	0.523853	0.033272	0	596	485	714	608	821	560	962	1053	1297	1161
ENSMUSG00000021635	chr13	Rad17	1.01E+08	1.01E+08	2846	-0.14675	3.972241	0.407667	0.523996	0.033743	0	199	258	347	302	266	268	356	416	362	323
ENSMUSG00000035545	chr7	Leng8	4137039	4137122	6391	0.163468	5.371688	0.407674	0.523996	0.045072	0	690	480	776	532	788	547	947	1192	1111	1372
ENSMUSG00000024120	chr17	Lrpprc	84705247	84705472	8504	-0.14009	6.670193	0.407781	0.524084	0.033746	0	1455	1691	1890	2070	1758	2050	2220	2165	2709	2108
ENSMUSG00000073415	chr17	Gm10501	34976899	34978751	2200	-0.25064	1.028144	0.407841	0.524112	0.069842	0	33	22	42	35	47	37	37	58	42	32
ENSMUSG00000025077	chr19	Dclre1a	56529167	56529662	6384	0.191241	2.104188	0.407897	0.52413	0.04822	0	52	58	60	76	82	81	106	84	128	126
ENSMUSG00000069631	chr11	Strada	1.06E+08	1.06E+08	5569	-0.13603	5.036447	0.40793	0.52413	0.030619	0	496	499	657	560	658	537	695	927	812	676
ENSMUSG00000057176	chr7	Gm166	1.28E+08	1.28E+08	2535	0.270981	0.851388	0.408153	0.524368	0.080105	0	22	30	26	25	24	26	43	28	77	49
ENSMUSG00000055760	chr17	Gemin6	80224441	80224670	1428	0.185872	2.537917	0.40835	0.524572	0.048076	0	93	84	109	71	85	105	130	166	152	156
ENSMUSG00000048402	chr1	Gli2	1.19E+08	1.19E+08	6869	-0.25254	1.616361	0.408481	0.524692	0.086425	0	44	27	61	53	93	46	93	69	66	43
ENSMUSG00000019782	chr10	Rwdd1	33996555	33996848	1136	-0.14757	5.807756	0.408541	0.52472	0.037163	0	799	1064	1150	966	882	1102	1189	1251	1272	1324
ENSMUSG00000047648	chr10	Fbxo30	11281330	11281500	5197	-0.23485	4.001133	0.408692	0.524816	0.092662	0	223	259	319	294	352	169	271	727	327	225
ENSMUSG00000078651	chr11	Aoc2	1.01E+08	1.01E+08	2543	0.314883	-0.17238	0.408682	0.524816	0.094581	0	6	11	19	7	16	8	24	19	25	27
ENSMUSG00000030871	chr7	Ears2	1.22E+08	1.22E+08	5152	-0.15287	3.16	0.40873	0.524817	0.033558	0	127	144	175	146	189	181	191	174	240	189
ENSMUSG00000024761	chr19	Gm16437	7668287	7668793	507	-0.30514	0.336921	0.408996	0.52511	0.114755	0	23	25	23	23	12	12	19	43	27	23
ENSMUSG00000029802	chr6	Abcg2	58584523	58584535	4987	-0.15236	4.776269	0.409047	0.525126	0.038244	0	376	420	690	398	543	585	688	503	694	523
ENSMUSG00000000094	chr11	Tbx4	85886422	85886562	3401	0.242543	2.265558	0.409459	0.525558	0.088675	0	68	52	44	65	136	84	138	125	183	75
ENSMUSG00000074166	chr7	AW146154	41478880	41481499	3405	-0.23979	1.81969	0.40943	0.525558	0.082361	0	58	66	77	61	45	45	59	116	74	76
ENSMUSG00000038187	chr7	Btbd10	1.13E+08	1.13E+08	5801	-0.15984	3.254109	0.409663	0.525771	0.038149	0	151	116	187	169	219	180	240	151	253	219
ENSMUSG00000002379	chr17	Ndufa11	56717762	56717942	2661	0.15843	7.173549	0.409955	0.526097	0.043856	0	1838	2439	2486	2479	2014	3723	3099	3172	4098	3413
ENSMUSG00000037152	chr3	Ndufc1	51404677	51405619	1495	-0.17506	7.185825	0.410472	0.526666	0.053716	0	2206	3034	3061	2252	2123	3548	3119	2720	3246	2954
ENSMUSG00000040488	chr7	Ltbp4	27305136	27305550	6463	-0.14579	7.232198	0.410474	0.526666	0.037184	0	2217	1755	2625	3159	3614	2562	3784	3157	4382	2909
ENSMUSG00000031583	chr8	Wrn	33234384	33236459	6372	-0.20392	2.135271	0.410663	0.526859	0.060276	0	86	49	66	73	113	64	88	88	111	120
ENSMUSG00000039063	chr2	Echdc3	6188465	6189651	2685	-0.1889	3.145759	0.410812	0.527011	0.056744	0	115	167	162	175	156	176	117	179	221	258
ENSMUSG00000035247	chr12	Hectd1	51743722	51744658	9048	-0.26858	7.530926	0.410895	0.527059	0.126792	0	3025	2641	3805	3557	3923	1933	2800	9479	3001	2336
ENSMUSG00000005078	chr12	Jkamp	72085589	72085673	2692	-0.14427	3.803072	0.410957	0.52709	0.032544	0	223	187	288	223	305	247	347	223	388	342
ENSMUSG00000022479	chr15	Vdr	97854425	97857631	5650	0.42866	-0.49878	0.411223	0.527382	0.198754	0	5	5	7	3	24	3	24	12	27	17
ENSMUSG00000030979	chr7	Uros	1.34E+08	1.34E+08	3576	-0.15952	4.330514	0.411502	0.527691	0.042085	0	309	350	403	331	363	438	480	273	505	493
ENSMUSG00000028910	chr4	Mecr	1.32E+08	1.32E+08	3041	0.150733	4.297085	0.411623	0.527796	0.037118	0	233	314	367	332	297	392	409	394	586	629
ENSMUSG00000036966	chr15	Spryd3	1.02E+08	1.02E+08	2927	0.161623	3.929045	0.41179	0.527962	0.042706	0	200	183	252	197	383	273	404	251	553	417
ENSMUSG00000004098	chr9	Col5a3	20770050	20770978	6809	0.21153	7.414673	0.411904	0.528059	0.079107	0	2611	1482	2690	2219	4515	3169	5001	1965	5853	5702
ENSMUSG00000028556	chr4	Dock7	98936665	98937300	8115	0.171015	4.132496	0.411992	0.528124	0.048949	0	258	150	302	240	454	246	477	510	511	444
ENSMUSG00000067370	chr17	B3galt4	33949909	33951477	1569	0.229045	1.163065	0.412042	0.528138	0.057073	0	28	37	41	27	30	41	54	53	65	57
ENSMUSG00000022370	chr15	Mrpl13	55534094	55534337	7936	0.163173	5.460617	0.412141	0.528217	0.045924	0	619	795	802	603	586	1144	1043	896	1206	1043
ENSMUSG00000024542	chr18	Cep192	67800107	67800186	8091	0.192687	2.343433	0.412713	0.528901	0.055797	0	76	47	81	72	117	89	132	98	196	116
ENSMUSG00000027810	chr3	Eif2a	58525821	58526086	6118	-0.15071	5.408341	0.412764	0.528917	0.039232	0	654	688	906	688	785	643	880	1347	974	852
ENSMUSG00000001576	chr17	Ergic1	26561489	26561632	6456	-0.16364	5.849999	0.412926	0.529027	0.046663	0	756	764	1160	978	1536	1084	1365	747	1729	1461
ENSMUSG00000028463	chr4	Car9	43506966	43507395	2304	0.307344	0.669948	0.412925	0.529027	0.121939	0	13	26	30	20	22	39	25	17	47	63
ENSMUSG00000022450	chr15	Ndufa6	82350139	82350371	560	-0.16221	7.405392	0.413043	0.529128	0.046673	0	2496	3247	3589	3102	2298	3657	3372	3977	3887	3495
ENSMUSG00000043542	chr3	Zc2hc1a	7503483	7503527	3508	-0.17466	2.751007	0.413182	0.529253	0.045799	0	105	101	131	119	133	99	160	192	171	111
ENSMUSG00000055943	chr2	Emc7	1.12E+08	1.12E+08	5826	0.132914	5.701625	0.413217	0.529253	0.030485	0	767	732	984	737	918	1021	1184	1511	1368	1238
ENSMUSG00000029545	chr5	Acads	1.15E+08	1.15E+08	2269	0.15727	6.683844	0.41351	0.529579	0.043669	0	1094	1788	1909	1864	1399	2042	2069	2719	3109	2736
ENSMUSG00000070822	chr7	Zscan18	12768092	12769745	3626	0.238045	1.102002	0.413857	0.529947	0.070323	0	31	26	36	31	32	37	79	37	64	43
ENSMUSG00000097820	chr9	E530011L22Rik	1.22E+08	1.22E+08	3304	0.261532	0.655484	0.413874	0.529947	0.076681	0	26	13	21	30	21	28	40	46	47	27
ENSMUSG00000050088	chr17	1600012H06Rik	14943184	14943319	3294	-0.13326	3.989348	0.414231	0.530355	0.028458	0	266	226	308	235	351	253	390	308	433	390
ENSMUSG00000055917	chr12	Zfp277	40315046	40315903	2454	0.14481	3.266513	0.414458	0.530473	0.030942	0	125	126	170	161	177	179	229	265	292	208
ENSMUSG00000063235	chr2	Ptpmt1	90908716	90911319	3684	-0.13647	4.976111	0.414396	0.530473	0.031688	0	478	541	662	512	538	617	670	590	827	778
ENSMUSG00000074479	chr3	Gm10704	88576410	88577139	730	0.194908	1.687928	0.414476	0.530473	0.047575	0	45	44	52	42	60	64	87	77	80	79
ENSMUSG00000091989	chr7	Gm17257	80507787	80508254	468	-0.25635	0.54135	0.414421	0.530473	0.07312	0	27	23	26	24	23	26	20	35	44	21

ENSMUSG00000004748	chr11	Mtfp1	4091480	4092299	1738	-0.19562	5.821929	0.41472	0.530736	0.067704	0	774	1147	1153	1159	720	1399	1126	739	1615	1188
ENSMUSG00000030990	chr7	Pgap2	1.02E+08	1.02E+08	4531	-0.12404	4.617888	0.414769	0.530749	0.025467	0	375	371	508	421	458	426	557	514	663	585
ENSMUSG00000028989	chr4	Angptl7	1.48E+08	1.48E+08	2157	-0.72614	5.775323	0.414931	0.530907	0.900329	0	2833	277	1579	285	441	84	310	4143	200	50
ENSMUSG00000020225	chr10	Tmbim4	1.2E+08	1.2E+08	2581	0.138291	5.290603	0.41502	0.530972	0.033114	0	505	559	822	561	673	877	1059	769	1110	935
ENSMUSG00000057363	chr1	Uxs1	43746966	43750362	5097	-0.14205	4.115201	0.415195	0.531147	0.032754	0	245	249	381	289	361	325	428	270	479	417
ENSMUSG00000019986	chr10	Ahi1	20952547	20952752	5093	0.273554	1.427936	0.415331	0.531272	0.116098	0	39	15	46	28	73	33	100	48	87	69
ENSMUSG00000004567	chr8	Mcoln1	3500457	3500627	3260	-0.12898	4.416833	0.415376	0.531273	0.027485	0	336	328	409	374	406	361	414	532	553	519
ENSMUSG00000042842	chr13	Serpinb6b	32965209	32965543	2200	-0.24189	1.236255	0.415447	0.531273	0.082049	0	38	32	56	37	43	32	78	29	66	41
ENSMUSG00000053192	chr3	Mllt11	95219135	95220463	1923	0.218481	6.111312	0.415441	0.531273	0.085137	0	861	1026	1394	1029	1013	1387	1308	3281	1219	1299
ENSMUSG00000057286	chr11	St6galnac2	1.17E+08	1.17E+08	7090	-0.22719	1.850894	0.415524	0.531323	0.074393	0	48	52	69	95	52	51	67	75	77	110
ENSMUSG00000089682	chr14	Bcl2l2	54883377	54883506	4462	-0.12641	5.151677	0.415618	0.531345	0.027402	0	531	580	679	636	656	586	802	880	890	811
ENSMUSG00000097656	chr6	Gm26712	57689433	57689649	217	-0.17107	4.530282	0.415617	0.531345	0.050064	0	340	456	424	413	376	580	509	344	572	473
ENSMUSG00000024538	chr18	Ppic	53406341	53407065	1286	0.155214	5.827321	0.415713	0.531367	0.042595	0	926	581	1005	741	1284	1032	1800	1427	1584	1153
ENSMUSG00000028937	chr4	Acot7	1.52E+08	1.52E+08	2124	0.137386	4.491361	0.41568	0.531367	0.031526	0	247	336	399	412	394	457	571	446	727	552
ENSMUSG00000020676	chr11	Ccl11	82057823	82058042	1082	-0.14844	3.92104	0.416079	0.531787	0.036167	0	304	181	300	236	300	242	324	401	371	334
ENSMUSG00000003438	chr7	Timm50	28305516	28306030	2684	0.13563	5.320089	0.416208	0.531902	0.03189	0	475	643	706	640	708	886	863	840	1215	1056
ENSMUSG00000028560	chr4	Usp1	98923810	98924243	3733	0.132212	3.955016	0.416399	0.532098	0.027895	0	203	214	260	228	333	278	333	416	499	373
ENSMUSG00000054435	chr6	Gimap4	48684549	48684623	1837	-0.19555	3.198421	0.416523	0.532206	0.063859	0	109	188	169	208	126	148	238	125	276	216
ENSMUSG00000037062	chr3	Sh3glb1	1.45E+08	1.45E+08	3949	-0.14078	7.671765	0.416614	0.532274	0.03573	0	2755	3410	3835	4276	3509	3303	4581	5389	5304	4161
ENSMUSG00000000355	chrX	Mcts1	38600578	38600778	1571	0.15817	4.85696	0.416718	0.532357	0.043323	0	411	500	553	368	422	735	689	664	687	710
ENSMUSG00000028540	chr4	Dph2	1.18E+08	1.18E+08	3030	-0.19184	1.984949	0.416861	0.532491	0.05015	0	47	62	85	70	84	72	82	74	124	73
ENSMUSG00000028078	chr3	Dclk2	86786151	86792111	10553	-0.28583	0.079604	0.416943	0.53252	0.084531	0	22	12	20	10	25	12	24	27	21	18
ENSMUSG00000047694	chrX	Yipf6	98936316	98936345	7149	-0.12831	4.10608	0.416961	0.53252	0.026634	0	243	277	360	271	350	282	408	365	446	420
ENSMUSG00000022754	chr16	Tmem45a	56805161	56806776	3056	-0.26864	2.534869	0.417004	0.532526	0.116946	0	101	49	120	61	209	98	191	64	132	119
ENSMUSG00000092367	chr7	Gm20479	27352649	27352756	556	0.30292	0.226014	0.417505	0.533117	0.104229	0	11	15	11	27	15	24	30	13	37	34
ENSMUSG00000026834	chr2	Acvr1c	58267453	58275043	9292	0.686888	1.246418	0.417661	0.533227	0.791236	0	18	2	5	33	95	1	11	28	127	178
ENSMUSG00000063802	chr7	Hspbp1	4660521	4660845	1488	0.148509	4.493998	0.417668	0.533227	0.03739	0	278	356	441	358	339	477	507	397	733	651
ENSMUSG00000056698	chr6	Elmod3	72565922	72566863	3560	0.172228	3.155907	0.417872	0.533438	0.047087	0	112	125	155	153	147	157	177	319	247	192
ENSMUSG00000024999	chr19	Noc3l	38788128	38789697	3977	-0.14969	3.258877	0.418005	0.533559	0.033501	0	133	151	209	144	202	188	216	214	238	188
ENSMUSG00000004105	chr2	Angptl2	33216069	33216453	6286	-0.18799	7.305833	0.418525	0.534124	0.06418	0	2746	1462	3020	2394	4828	2626	4721	2358	4714	3047
ENSMUSG00000022160	chr14	Mettl3	52294668	52295093	3987	0.135471	3.54299	0.418505	0.534124	0.028847	0	157	162	195	179	230	256	273	256	324	296
ENSMUSG00000032567	chr9	Aste1	1.05E+08	1.05E+08	6367	0.197504	1.458016	0.418779	0.534349	0.050006	0	35	31	46	37	59	53	60	61	82	75
ENSMUSG00000039109	chr13	F13a1	36867178	36868918	3927	0.218696	5.780385	0.418761	0.534349	0.086426	0	832	358	967	644	1588	817	1291	942	1962	2052
ENSMUSG00000072915	chr11	Gm12258	58847158	58847259	4429	0.246661	0.651581	0.418943	0.534509	0.062792	0	25	19	25	14	29	25	36	41	44	41
ENSMUSG00000021484	chr13	Lman2	55343833	55347037	4315	-0.14612	6.684325	0.419301	0.534917	0.038611	0	1379	1448	2106	1796	2422	1815	2434	1522	3037	2685
ENSMUSG00000026896	chr2	Ifih1	62595798	62598088	8165	0.211598	2.746868	0.419389	0.53498	0.072511	0	90	75	88	134	126	178	152	93	175	217
ENSMUSG00000015083	chr2	C8g	25498651	25498823	1493	-0.26412	0.513978	0.420467	0.536306	0.080398	0	21	18	24	34	25	30	15	28	36	32
ENSMUSG00000016128	chr5	Stard13	1.51E+08	1.51E+08	8044	-0.14898	3.493009	0.42062	0.536363	0.035251	0	165	125	214	220	273	171	286	255	282	251
ENSMUSG00000024425	chr18	Ndfip1	38418975	38419176	930	-0.1406	5.523919	0.420606	0.536363	0.035173	0	712	627	1028	701	997	736	1058	1321	1152	848
ENSMUSG00000032537	chr9	Ephb1	1.02E+08	1.02E+08	6487	0.285018	1.371536	0.420628	0.536363	0.128916	0	21	25	60	43	42	67	92	25	90	43
ENSMUSG00000087687	chr8	Pet100	3621551	3621611	1189	0.159182	3.951913	0.420903	0.536664	0.043164	0	208	245	311	220	222	405	377	310	359	402
ENSMUSG00000087366	chr4	Junos	95051534	95051765	4117	0.245264	0.608043	0.421051	0.536803	0.060094	0	16	22	24	27	19	25	33	38	44	41
ENSMUSG00000048310	chr8	Pskh1	1.06E+08	1.06E+08	3255	-0.13624	4.300284	0.42121	0.536956	0.031719	0	294	326	346	376	365	309	401	553	499	429
ENSMUSG00000005102	chr2	Eif2ak4	1.18E+08	1.18E+08	7457	-0.1734	2.488312	0.421406	0.537152	0.04475	0	86	76	105	103	122	66	133	138	144	134
ENSMUSG00000098973	chr9	Mir6236	1.1E+08	1.1E+08	123	-0.23068	6.095036	0.421441	0.537152	0.097289	0	1055	1593	1348	715	1365	1540	882	1366	1012	2317
ENSMUSG00000022965	chr16	Ifngr2	91547072	91547232	3313	-0.14857	6.325386	0.42188	0.537661	0.040167	0	1203	1327	1546	1376	1573	1850	1857	1236	2002	1802
ENSMUSG00000027236	chr2	Eif3j1	1.22E+08	1.22E+08	5830	-0.18419	6.583123	0.422096	0.537888	0.062328	0	1560	1550	2141	1489	1757	1517	1798	3592	1742	1719
ENSMUSG00000024096	chr17	Ralbp1	65848433	65850195	4335	0.143915	5.049377	0.422201	0.537972	0.036832	0	403	388	603	590	673	520	724	1088	969	786
ENSMUSG00000040794	chr2	C1qtnf4	90885860	90886003	1290	0.268441	2.075141	0.422324	0.53806	0.121158	0	63	49	78	46	77	86	64	209	70	84
ENSMUSG00000042997	chr3	Nhlrc3	53448588	53452649	5601	0.165795	3.129448	0.422347	0.53806	0.043669	0	128	93	170	134	162	111	237	213	292	240
ENSMUSG00000049287	chr11	Iba57	59155369	59158659	4885	0.141017	4.162018	0.422583	0.538311	0.033849	0	197	279	324	300	319	353	402	543	494	383
ENSMUSG00000029106	chr5	Add1	34573664	34573913	6066	-0.12673	6.280506	0.422671	0.538373	0.029253	0	1179	1050	1472	1483	1627	1188	1837	1787	2236	1726
ENSMUSG00000026917	chr2	Wdr5	27515157	27515280	3596	0.14934	5.045689	0.423298	0.539122	0.039963	0	383	479	535	517	720	586	713	1144	923	687
ENSMUSG00000022848	chr16	Dirc2	35694062	35698020	5395	-0.15716	5.946583	0.423503	0.539283	0.045232	0	1021	1005	1273	1091	987	1102	1123	1940	1366	1216
ENSMUSG00000043366	chr7	Olfr78	1.03E+08	1.03E+08	3496	-0.33262	0.144013	0.423482	0.539283	0.15585	0	28	20	17	12	15	11	15	9	32	41
ENSMUSG00000030232	chr6	Aebp2	1.41E+08	1.41E+08	8111	-0.14165	4.998522	0.423564	0.539312	0.035598	0	469	445	646	619	629	530	715	955	757	578
ENSMUSG00000022707	chr16	Gbe1	70313949	70314295	5352	-0.16158	5.88661	0.423778	0.539485	0.04803	0	796	1087	1084	1310	872	882	997	1662	1640	1399
ENSMUSG00000030826	chr7	Bcat2	45570153	45570399	3899	0.161771	6.032057	0.42376	0.539485	0.047927	0	1016	864	1030	1025	1202	972	1217	1765	1718	2467
ENSMUSG00000026155	chr1	Smap1	23844846	23845357	3575	0.123607	4.48046	0.424057	0.539741	0.025994	0	293	300	414	352	430	378	554	606	653	536
ENSMUSG00000027363	chr2	Usp8	1.27E+08	1.27E+08	4193	-0.12452	4.786104	0.424025	0.539741	0.027216	0	415	416	500	493	578	404	648	681	757	617
ENSMUSG00000036528	chr7	Ppfibp2	1.08E+08	1.08E+08	4729	0.175409	3.254804	0.42413	0.539784	0.050664	0	136	120	140	155	192	134	246	349	263	189
ENSMUSG00000001870	chr17	Ltbp1	75005568	75006361	10480	0.163705	4.945184	0.424226	0.539807	0.048625	0	446	255	561	426	798	489	918	831	921	673
ENSMUSG00000063727	chr15	Tnfrsf11b	54250619	54252382	2818	-0.39651	0.813806	0.424209	0.539807	0.243749	0	28	8	14	20	97	25	39	15	52	39
ENSMUSG00000050103	chr12	Agmo	37241641	37242167	6285	0.225213	1.878894	0.42479	0.540475	0.075112	0	63	33	54	60	65	47	71	128	113	98
ENSMUSG00000010538	chr3	Tsacc	88282757	88282984	1112	0.261024	1.09381	0.42493	0.540564	0.09505	0	36	27	38	16	37	54	47	64	37	50
ENSMUSG00000027309	chr2	4930402H24Rik	1.31E+08	1.31E+08	10659	-0.17535	3.63253	0.424938	0.540564	0.053918	0	186	172	232	256	249	133	256	200	386	416

ENSMUSG00000020361	chr11	Hspa4	53259814	53261815	5528	0.126077	7.046134	0.425005	0.5406	0.029546	0	1599	1762	2509	2157	2644	2645	3333	3002	4047	3114
ENSMUSG00000078317	chrX	F8a	73228291	73230795	2505	0.149133	3.099643	0.425122	0.540699	0.033982	0	111	129	138	138	154	161	243	193	232	212
ENSMUSG00000004609	chr7	Cd33	43527456	43529008	2571	0.266815	1.225075	0.425183	0.540726	0.108602	0	35	21	27	30	58	20	69	84	64	53
ENSMUSG00000030816	chr7	Rnf40	1.28E+08	1.28E+08	4154	0.124714	5.377595	0.425229	0.540735	0.027864	0	554	583	789	686	708	749	1008	1152	1144	1012
ENSMUSG00000024537	chr18	Psmg2	67641599	67641735	1059	0.159136	4.473205	0.425578	0.541129	0.045062	0	325	361	454	252	341	566	582	427	589	517
ENSMUSG00000019809	chr10	Pex3	13523842	13523943	4740	0.148684	3.494002	0.425812	0.541328	0.034864	0	180	173	191	156	175	179	255	293	371	293
ENSMUSG00000020525	chr11	Ppm1d	85311244	85311923	3173	0.201502	2.863082	0.425799	0.541328	0.067635	0	85	108	121	109	136	88	154	300	208	159
ENSMUSG00000001518	chr6	Itfg2	1.28E+08	1.28E+08	5069	-0.14562	3.557737	0.425899	0.541388	0.035204	0	195	194	209	189	233	198	268	330	263	232
ENSMUSG00000024392	chr17	Bag6	35135178	35135471	6215	-0.12708	7.023821	0.426035	0.541512	0.030096	0	1970	1828	2422	2400	2782	2277	2636	3255	3526	2864
ENSMUSG00000005823	chr17	Gpr108	57234914	57235366	2095	0.122439	4.984838	0.426981	0.542633	0.026636	0	450	429	538	499	616	635	694	734	921	861
ENSMUSG00000058655	chr15	Eif4b	1.02E+08	1.02E+08	3853	0.180687	7.645813	0.426996	0.542633	0.061605	0	2574	2752	3593	3186	3635	3047	3725	8780	4776	4543
ENSMUSG00000031948	chr8	Kars	1.12E+08	1.12E+08	2249	0.124685	6.516859	0.427125	0.542748	0.028932	0	1280	1221	1619	1501	1714	1847	2035	2433	2610	2203
ENSMUSG00000039244	chr5	E130309D02Rik	1.43E+08	1.43E+08	4639	-0.1472	3.46534	0.427175	0.542761	0.035738	0	140	203	207	176	238	209	236	189	318	266
ENSMUSG00000039349	chr1	C130074G19Rik	1.85E+08	1.85E+08	3035	0.211903	4.909013	0.427257	0.542816	0.082669	0	302	478	483	607	437	345	454	775	967	1314
ENSMUSG00000041609	chr5	Ccdc64	1.16E+08	1.16E+08	5932	0.250165	1.532769	0.427546	0.543133	0.093869	0	39	47	53	29	43	32	78	108	94	49
ENSMUSG00000102824	chr1	RP23-411B11.2	1.89E+08	1.89E+08	381	-0.16519	2.903168	0.427884	0.543513	0.043876	0	133	112	119	157	124	141	143	172	183	171
ENSMUSG00000025375	chr11	Aatk	1.2E+08	1.2E+08	7159	0.200871	3.209436	0.428008	0.54357	0.068996	0	154	88	127	145	201	96	231	211	292	344
ENSMUSG00000057265	chr12	Ccdc176	84409071	84409255	2234	-0.26471	0.324513	0.428002	0.54357	0.090936	0	26	22	11	22	23	16	19	31	36	23
ENSMUSG00000090088	chr10	Gm15934	45287311	45287633	525	0.305101	0.169096	0.428328	0.543927	0.122366	0	11	18	23	13	11	29	18	35	14	32
ENSMUSG00000034083	chr6	Ccdc174	91878053	91878186	9188	0.157391	3.274036	0.42846	0.543971	0.040678	0	137	136	149	151	182	161	212	325	237	244
ENSMUSG00000038828	chr5	Tmem214	30869579	30869818	6024	-0.12701	5.084673	0.428481	0.543971	0.029238	0	552	471	609	531	810	527	813	745	1009	733
ENSMUSG00000052763	chr6	Zfp212	47920476	47920749	3002	0.175981	3.333663	0.428452	0.543971	0.053138	0	104	147	202	162	174	151	227	379	236	246
ENSMUSG00000028331	chr4	5830415F09Rik	46376505	46377248	2271	0.195199	1.533139	0.429165	0.54479	0.050508	0	32	44	46	41	55	48	79	75	75	72
ENSMUSG00000029034	chr4	Cpsf3l	1.56E+08	1.56E+08	3067	0.121933	4.285743	0.429605	0.545299	0.025319	0	291	264	361	295	341	370	457	460	593	493
ENSMUSG00000027074	chr2	Slc43a3	84936579	84936644	4464	-0.1677	4.672312	0.429717	0.54539	0.052012	0	475	348	482	492	431	316	429	851	620	609
ENSMUSG00000075284	chr2	Wipf1	73429610	73432465	5896	0.172364	4.49189	0.429833	0.545488	0.054452	0	362	186	328	341	575	347	687	418	738	633
ENSMUSG00000064138	chr13	Fam172a	77708690	77708853	4019	-0.13759	3.422478	0.43052	0.546309	0.031404	0	178	152	224	159	221	162	223	261	297	251
ENSMUSG00000040705	chr7	A930016O22Rik	19418812	19419553	1214	0.69449	4.673488	0.43064	0.546411	0.880554	0	62	495	62	718	228	57	41	58	3503	645
ENSMUSG00000038583	chr10	Pln	53337686	53337795	2480	0.253961	0.719748	0.430753	0.546455	0.075882	0	20	24	24	31	17	29	43	30	63	34
ENSMUSG00000059772	chr7	Slx1b	1.27E+08	1.27E+08	3521	0.169681	2.445555	0.430716	0.546455	0.042933	0	83	67	88	78	105	100	124	109	177	157
ENSMUSG00000021704	chr13	Mtx3	92844787	92844867	6275	-0.18109	2.931674	0.430811	0.546478	0.054095	0	118	99	150	146	161	108	223	127	147	222
ENSMUSG00000068079	chr2	Tcf15	1.52E+08	1.52E+08	980	-0.21792	2.646106	0.431114	0.546813	0.082559	0	74	102	111	176	88	118	182	78	148	138
ENSMUSG00000028577	chr4	Plaa	94567514	94569909	6441	0.170978	5.829912	0.43124	0.546923	0.055402	0	726	817	1037	914	974	951	1218	2381	1338	1115
ENSMUSG00000022332	chr15	Khdrbs3	68928420	68928833	1887	-0.23246	2.979255	0.431282	0.546926	0.095806	0	123	120	139	191	125	130	185	58	297	189
ENSMUSG00000022664	chr16	Slc35a5	45139573	45142212	8105	-0.17094	2.605538	0.431549	0.547163	0.047093	0	97	77	122	87	155	79	155	143	151	138
ENSMUSG00000027011	chr2	Ube2e3	78868124	78868597	4390	0.126311	4.440011	0.431547	0.547163	0.027696	0	305	330	398	324	363	385	516	468	724	573
ENSMUSG00000048096	chr1	Lmod1	1.35E+08	1.35E+08	3948	0.245693	2.231256	0.431799	0.54743	0.104294	0	71	20	62	88	118	66	112	111	179	128
ENSMUSG00000024097	chr17	Srsf7	80200089	80201602	2279	0.152719	4.675062	0.432048	0.547695	0.04277	0	392	336	474	338	477	512	713	363	837	728
ENSMUSG00000000399	chr6	Ndufa9	1.27E+08	1.27E+08	1322	0.146055	8.00571	0.432377	0.548013	0.041221	0	2946	4435	4520	4605	3698	5905	5495	6619	7004	6176
ENSMUSG00000001632	chr6	Brpf1	1.13E+08	1.13E+08	6714	0.141241	3.863609	0.432361	0.548013	0.034656	0	200	172	236	227	327	225	300	431	444	393
ENSMUSG00000027845	chr3	Dclre1b	1.04E+08	1.04E+08	8152	0.176868	1.941921	0.432646	0.548285	0.047365	0	40	47	75	62	73	65	89	103	115	95
ENSMUSG00000057337	chr10	Chst3	60181532	60186883	6497	-0.26911	0.848618	0.432671	0.548285	0.101542	0	22	17	33	28	61	20	59	31	42	31
ENSMUSG00000002625	chr17	Akap8l	32321425	32321785	2075	0.19166	4.526838	0.433034	0.548544	0.068976	0	290	276	411	377	456	341	495	1054	439	515
ENSMUSG00000059734	chr19	Ndufs8	3908870	3909074	963	-0.14134	7.048897	0.432998	0.548544	0.038515	0	1932	2466	2494	2524	2028	2717	2834	2786	3505	2765
ENSMUSG00000078515	chr4	Ddi2	1.42E+08	1.42E+08	9553	-0.22834	6.263433	0.433021	0.548544	0.100406	0	1387	858	1487	1427	1828	874	1184	3519	1345	1327
ENSMUSG00000087574	chr11	C030037D09Rik	88718645	88719017	4199	-0.19479	1.967604	0.432989	0.548544	0.05602	0	52	73	80	70	64	70	102	62	96	86
ENSMUSG00000023330	chr2	Dtwd1	1.26E+08	1.26E+08	1350	0.209123	1.991037	0.433358	0.548885	0.065591	0	70	64	64	38	59	87	87	101	103	103
ENSMUSG00000024566	chr18	Atp9b	80734143	80736149	5397	0.127029	4.285261	0.433382	0.548885	0.028291	0	287	243	309	318	399	329	443	471	580	564
ENSMUSG00000037624	chr1	Kcnk2	1.89E+08	1.89E+08	4943	0.275546	1.582788	0.433425	0.548889	0.124883	0	49	19	53	27	75	29	111	93	82	61
ENSMUSG00000049354	chr11	Dcaf7	1.06E+08	1.06E+08	6133	-0.12332	5.971245	0.433471	0.548896	0.028761	0	869	905	1153	1181	1394	1086	1532	1319	1759	1347
ENSMUSG00000022751	chr16	Nit2	57156671	57157166	1280	-0.13098	4.541032	0.433576	0.548929	0.031019	0	351	406	477	378	401	446	473	578	570	503
ENSMUSG00000039501	chr2	Znfx1	1.67E+08	1.67E+08	8189	-0.14719	4.756607	0.43355	0.548929	0.039525	0	354	366	533	530	614	603	483	485	641	733
ENSMUSG00000005299	chr5	Letm1	33739673	33742612	9650	-0.13172	6.268896	0.434024	0.549447	0.03326	0	1030	1273	1414	1594	1403	1410	1565	1517	2265	1874
ENSMUSG00000040713	chr1	Creg1	1.66E+08	1.66E+08	2362	-0.12963	5.814984	0.434155	0.549562	0.031901	0	946	758	1198	930	1088	919	1182	1516	1419	1250
ENSMUSG00000022724	chr16	Mina	59471775	59471945	5290	-0.14383	4.340859	0.434241	0.54962	0.037453	0	283	327	403	305	465	393	482	287	610	477
ENSMUSG00000020307	chr10	Cdc34	79682195	79682590	1262	-0.14091	7.81105	0.434355	0.549715	0.038632	0	3061	3867	4931	3915	3869	5010	4484	4835	5133	5055
ENSMUSG00000101102	chr1	Gm28609	1.33E+08	1.33E+08	463	-0.26146	0.255427	0.434397	0.549718	0.080121	0	15	26	18	25	15	19	23	29	26	20
ENSMUSG00000030602	chr7	Pak4	28399549	28401617	7845	0.142201	4.528235	0.434444	0.549727	0.037103	0	333	254	335	353	577	371	640	553	773	524
ENSMUSG00000022610	chr15	Mapk12	89130585	89131218	1889	-0.1362	7.094316	0.434762	0.550078	0.035967	0	2194	2023	2835	2397	2484	2703	2817	3591	2916	2970
ENSMUSG00000044791	chr9	Setd2	1.11E+08	1.11E+08	8350	-0.14489	5.202904	0.434851	0.550141	0.039634	0	569	487	683	669	844	521	747	1174	918	744
ENSMUSG00000037003	chr15	Tenc1	1.02E+08	1.02E+08	4728	-0.14373	5.33553	0.43496	0.550229	0.039316	0	712	542	691	791	785	584	737	1215	1062	912
ENSMUSG00000041720	chr16	Pi4ka	17280351	17280620	11257	-0.12899	4.538401	0.435158	0.550428	0.030598	0	333	368	435	410	479	347	469	448	721	642
ENSMUSG00000026098	chr1	Pms1	53189187	53189498	7542	-0.20909	1.118188	0.435328	0.550594	0.058409	0	29	44	34	37	41	36	46	44	48	51
ENSMUSG00000068267	chr2	Cenpb	1.31E+08	1.31E+08	4886	-0.1258	7.421897	0.435597	0.550883	0.030884	0	2442	2498	3471	3240	3363	2759	3296	4053	4836	4373
ENSMUSG00000050549	chr3	5730508B09Rik	1.28E+08	1.28E+08	1603	0.233554	2.008698	0.435704	0.550969	0.086538	0	58	65	78	53	42	62	75	72	143	153
ENSMUSG00000040025	chr4	Ythdf2	1.32E+08	1.32E+08	4572	0.136058	4.293869	0.435801	0.551041	0.033381	0	260	258	336	327	381	321	423	643	582	437

ENSMUSG00000023328	chr5	Ache	1.37E+08	1.37E+08	4623	-0.12707	5.874183	0.436231	0.551535	0.030961	0	939	816	1214	960	1204	1018	1493	1177	1771	1137
ENSMUSG00000099876	chrY	Gm29650	1048393	1049134	742	0.575558	-0.36797	0.436415	0.551716	0.510727	0	7	6	16	5	12	31	29	0	31	0
ENSMUSG00000022967	chr16	Ifnar1	91485238	91485416	5879	0.134028	4.427371	0.43649	0.551761	0.03258	0	288	255	366	356	461	305	525	499	742	606
ENSMUSG00000059201	chr6	Lep	29060220	29060248	3354	0.679046	1.653359	0.436853	0.552169	0.835919	0	57	11	5	54	65	5	17	3	123	312
ENSMUSG00000045008	chr10	9030612E09Rik	43174704	43176562	1859	-0.20084	1.117322	0.437021	0.552331	0.05369	0	34	29	50	38	35	35	47	40	57	48
ENSMUSG00000038335	chr11	Tsr1	74898071	74898215	3837	-0.15444	5.01306	0.437339	0.552682	0.045271	0	432	491	700	485	766	510	695	1068	717	561
ENSMUSG00000022678	chr16	Nde1	14163275	14163368	3205	-0.11908	5.014488	0.437555	0.552767	0.026367	0	506	494	630	509	670	614	691	687	893	725
ENSMUSG00000027531	chr3	Impa1	10311956	10315301	5437	0.147933	4.298688	0.437485	0.552767	0.040356	0	258	274	382	301	342	394	517	286	618	603
ENSMUSG00000028211	chr4	Trp53inp1	11156431	11156547	6475	-0.22551	4.032098	0.437597	0.552767	0.096832	0	209	213	394	307	371	147	247	731	339	308
ENSMUSG00000028869	chr4	Gnl2	1.25E+08	1.25E+08	3683	0.14391	5.021764	0.437668	0.552767	0.039454	0	443	422	614	496	612	590	710	1160	796	699
ENSMUSG00000032309	chr9	Fbxo22	55208925	55209188	2394	-0.11865	4.602366	0.437528	0.552767	0.025614	0	374	384	477	376	496	440	532	556	652	533
ENSMUSG00000034758	chr10	Tle6	81590904	81591139	3088	-0.20154	1.323383	0.437647	0.552767	0.054746	0	30	43	50	46	47	47	46	44	66	59
ENSMUSG00000087269	chr2	D330023K18Rik	31146457	31146785	1249	0.221491	1.682856	0.437685	0.552767	0.077587	0	41	52	67	38	40	73	56	104	74	78
ENSMUSG00000030738	chr7	Eif3c	1.27E+08	1.27E+08	3383	0.130409	7.150055	0.438181	0.553155	0.03351	0	1810	1952	2477	2327	2836	2530	3102	4401	3968	3374
ENSMUSG00000031537	chr8	Ikbkb	22659212	22660459	19078	0.122349	4.402698	0.438164	0.553155	0.027029	0	296	277	345	351	422	396	528	445	609	595
ENSMUSG00000046380	chr15	Jrk	74702301	74707864	5853	-0.19894	1.534567	0.438192	0.553155	0.057031	0	49	32	54	50	68	34	65	61	85	66
ENSMUSG00000061104	chr8	Gm10094	95825354	95826133	780	0.170318	2.346887	0.438153	0.553155	0.046022	0	73	70	80	70	99	101	103	156	135	119
ENSMUSG00000090258	chr12	Churc1	76765538	76765638	5693	0.144148	5.159881	0.438158	0.553155	0.039864	0	472	570	749	488	541	903	847	841	872	823
ENSMUSG00000026836	chr2	Acvr1	58388644	58389178	4829	-0.13376	3.923589	0.438274	0.553207	0.032174	0	199	245	247	305	326	231	398	332	446	294
ENSMUSG00000015149	chr7	Sirt2	28766735	28766867	3568	-0.12758	6.382996	0.438441	0.553367	0.031776	0	1218	1253	1697	1535	1586	1468	1651	2244	2100	1834
ENSMUSG00000027956	chr3	Tmem144	79812564	79814146	3487	0.250679	0.689794	0.438636	0.553513	0.07502	0	20	23	18	30	23	34	43	24	43	47
ENSMUSG00000047583	chr3	Tyw3	1.55E+08	1.55E+08	4499	-0.19878	1.498903	0.438626	0.553513	0.056211	0	38	47	70	42	48	49	52	53	79	66
ENSMUSG00000023964	chr6	Calcr	3685677	3687643	3913	-0.28553	-0.08811	0.438829	0.553655	0.075763	0	12	17	24	11	14	14	20	22	17	16
ENSMUSG00000025857	chr5	Heatr2	1.39E+08	1.39E+08	3514	-0.14808	3.712512	0.438819	0.553655	0.039049	0	169	203	253	267	256	220	224	392	323	283
ENSMUSG00000028179	chr3	Cth	1.58E+08	1.58E+08	2263	0.342546	0.579938	0.439049	0.553883	0.179391	0	17	17	17	25	26	10	14	64	33	63
ENSMUSG00000033350	chr9	Chst2	95399292	95406473	7328	0.233711	1.784928	0.439386	0.554258	0.089366	0	44	49	43	41	81	71	113	38	111	91
ENSMUSG00000075028	chr2	Prdm11	92965151	92975861	17044	-0.23642	0.597402	0.439548	0.554411	0.069322	0	19	15	27	28	42	17	34	27	43	34
ENSMUSG00000026885	chr2	Ttll11	35751241	35752492	4024	0.206168	1.779076	0.439933	0.554796	0.06731	0	50	42	59	44	64	70	80	118	64	78
ENSMUSG00000036639	chr5	Nudt1	1.4E+08	1.4E+08	1390	0.219578	2.57467	0.439899	0.554796	0.084737	0	78	94	112	67	100	164	140	64	171	186
ENSMUSG00000024855	chr19	Pacs1	5133688	5135025	4339	0.153053	3.695231	0.440234	0.555074	0.041709	0	171	151	207	277	212	189	267	353	450	354
ENSMUSG00000026764	chr2	Kif5c	49619298	49619787	7142	0.228119	0.600155	0.440234	0.555074	0.069637	0	17	14	26	23	30	27	41	21	44	46
ENSMUSG00000038848	chr2	Ythdf1	1.81E+08	1.81E+08	3316	-0.13635	5.374312	0.440309	0.555118	0.035849	0	596	610	811	760	864	747	767	1251	996	822
ENSMUSG00000001065	chr8	Zfp276	1.23E+08	1.23E+08	5530	-0.1576	3.097748	0.440399	0.555181	0.045355	0	166	136	120	156	157	124	191	169	271	197
ENSMUSG00000010476	chr7	Ebf3	1.37E+08	1.37E+08	5021	-0.15286	3.371406	0.440677	0.55543	0.04052	0	110	152	212	206	237	169	184	241	261	284
ENSMUSG00000036106	chr15	Prr5	84669620	84669705	1917	0.196772	2.641181	0.440651	0.55543	0.069474	0	84	55	115	76	160	131	193	91	193	159
ENSMUSG00000028397	chr4	Kdm4c	74242497	74242640	5823	-0.14935	3.350815	0.440752	0.555474	0.03893	0	165	128	210	172	221	151	222	303	250	199
ENSMUSG00000021703	chr13	Serinc5	92611138	92611287	5316	-0.17364	3.973456	0.441258	0.55603	0.056432	0	217	153	279	288	489	216	478	356	416	269
ENSMUSG00000030759	chr7	Far1	1.14E+08	1.14E+08	8055	-0.1372	3.983431	0.441273	0.55603	0.034549	0	274	203	301	231	379	235	411	282	468	380
ENSMUSG00000024580	chr18	Grpel2	61712440	61716127	4030	-0.12618	4.441455	0.441553	0.556331	0.029483	0	319	368	443	374	374	411	493	519	512	466
ENSMUSG00000038544	chr4	Inip	59769637	59772459	5995	0.166882	2.477645	0.442209	0.557108	0.045264	0	72	79	99	89	91	105	143	95	179	159
ENSMUSG00000021832	chr14	Psmc6	45329824	45329932	1564	-0.16843	6.808625	0.442273	0.557138	0.056944	0	1690	1910	2500	1708	2088	1873	2145	4018	2165	1990
ENSMUSG00000002345	chr8	2310045N01Rik	70139499	70139772	2743	0.139592	3.235503	0.442411	0.557166	0.031904	0	152	123	153	136	175	174	219	226	293	236
ENSMUSG00000023175	chr10	Bsg	79704491	79704584	1814	0.131502	9.05892	0.442416	0.557166	0.035022	0	8555	6707	9181	7863	10251	11046	10910	15558	14003	13169
ENSMUSG00000032718	chr6	Mansc1	1.35E+08	1.35E+08	2373	-0.2136	0.895015	0.442352	0.557166	0.059445	0	30	21	35	40	33	29	34	38	54	38
ENSMUSG00000036957	chr7	Lrfn3	30355514	30356103	2861	-0.19013	1.968542	0.442511	0.557235	0.053181	0	53	49	87	64	93	83	78	75	107	72
ENSMUSG00000074754	chr2	Gm561	1.45E+08	1.45E+08	471	-0.18358	4.101203	0.442875	0.557642	0.064726	0	315	333	391	247	197	416	361	321	342	379
ENSMUSG00000100863	chr4	Gm12669	91805547	91806555	1009	0.157469	2.888707	0.442976	0.557719	0.043185	0	88	112	143	110	125	162	154	170	181	224
ENSMUSG00000018143	chr5	Mafk	1.4E+08	1.4E+08	3901	0.221791	4.267458	0.443033	0.55774	0.096626	0	219	238	315	388	325	308	335	1018	411	321
ENSMUSG00000021713	chr13	Ppwd1	1.04E+08	1.04E+08	2367	-0.16417	2.324833	0.443168	0.557859	0.042838	0	81	67	93	90	105	70	105	128	145	101
ENSMUSG00000015363	chr15	Trabd	89075124	89075214	5591	0.128023	5.193236	0.443329	0.558011	0.031709	0	479	560	646	566	661	678	708	1059	1052	965
ENSMUSG00000025264	chrX	Tsr2	1.51E+08	1.51E+08	3805	0.146683	3.325059	0.443408	0.55806	0.037445	0	147	126	217	139	160	160	240	278	268	279
ENSMUSG00000042787	chr9	Exog	1.19E+08	1.19E+08	3887	-0.18851	2.005765	0.443681	0.558352	0.05595	0	60	65	85	61	79	70	104	58	91	105
ENSMUSG00000022475	chr15	Hdac7	97792664	97793742	5530	0.127984	4.461313	0.443884	0.558557	0.030771	0	307	250	363	397	449	350	547	625	643	536
ENSMUSG00000010051	chr9	Hyal1	1.08E+08	1.08E+08	3777	-0.17048	2.889709	0.443967	0.558611	0.049986	0	122	78	153	118	188	96	140	177	204	200
ENSMUSG00000021192	chr12	Golga5	1.02E+08	1.02E+08	2897	-0.14182	4.774387	0.444111	0.558696	0.038969	0	402	439	536	476	539	428	586	880	606	524
ENSMUSG00000038909	chr11	Kat7	95274259	95275887	5536	0.126792	4.888103	0.444116	0.558696	0.030792	0	387	421	500	469	591	480	728	903	848	667
ENSMUSG00000028427	chr4	Aqp7	41033074	41034459	2828	0.202015	3.822425	0.444235	0.558795	0.077964	0	173	184	254	303	171	168	257	299	460	618
ENSMUSG00000097006	chr17	9530082P21Rik	23743234	23743421	4842	0.255621	2.138398	0.444318	0.55885	0.11951	0	48	36	95	73	83	68	75	219	79	100
ENSMUSG00000032333	chr9	Stoml1	58253164	58253399	1987	0.135759	3.423807	0.4448	0.559405	0.031783	0	156	147	213	149	182	189	232	283	311	292
ENSMUSG00000038462	chr13	Uqcrfs1	30540308	30541341	1363	-0.1537	8.838258	0.444976	0.559575	0.048376	0	6453	9160	9136	8937	5853	9183	9268	11102	11435	9201
ENSMUSG00000074182	chr3	Znhit6	1.46E+08	1.46E+08	2813	0.132325	3.334695	0.445543	0.560238	0.030459	0	125	125	188	182	182	195	230	253	298	247
ENSMUSG00000027615	chr3	Hps3	19995945	19997029	9103	0.152714	2.936527	0.445808	0.560519	0.039538	0	94	119	129	103	155	118	197	200	205	216
ENSMUSG00000038194	chr7	Lhb	45418353	45418525	2501	-0.29013	0.454871	0.446028	0.560746	0.103442	0	25	20	34	15	24	39	22	21	30	19
ENSMUSG00000041939	chr5	Mvk	1.14E+08	1.14E+08	2674	0.162446	3.36671	0.446157	0.560857	0.049314	0	108	129	160	164	261	205	243	165	346	312
ENSMUSG00000047485	chrX	Klhl34	1.58E+08	1.58E+08	1935	0.367533	2.062059	0.446568	0.561323	0.250469	0	42	56	21	148	19	74	93	167	152	56
ENSMUSG00000004221	chrX	Ikbkg	74393290	74393405	8110	-0.13312	4.579023	0.446749	0.561499	0.034352	0	375	377	511	355	465	369	504	706	617	470

ENSMUSG00000034321	chr19	Exosc1	41922980	41924088	1622	-0.13457	3.224438	0.446896	0.561632	0.031415	0	143	153	166	150	197	143	199	222	259	217
ENSMUSG00000064368	chrMT	mt-Nd6	13552	14070	519	-0.32948	6.660669	0.447345	0.562146	0.222343	0	1284	1297	1157	4174	1399	865	952	902	5443	3126
ENSMUSG00000040078	chr6	Gm9769	85843980	85844459	480	-0.18247	2.679623	0.447453	0.562231	0.05867	0	106	71	123	114	154	86	134	207	137	129
ENSMUSG00000034729	chr17	Mrps10	47368887	47368954	8079	0.122936	4.792868	0.447539	0.562236	0.029199	0	378	439	497	408	479	592	606	662	760	725
ENSMUSG00000044150	chrX	A830080D01Rik	1.6E+08	1.6E+08	4869	-0.23684	0.737761	0.447507	0.562236	0.08152	0	28	26	31	18	40	14	40	33	55	32
ENSMUSG00000019826	chr10	Zbtb24	41450396	41450530	2828	0.186629	2.077725	0.447686	0.562327	0.056646	0	47	54	92	61	71	62	87	135	127	107
ENSMUSG00000026788	chr2	Zbtb43	33450287	33455123	5225	-0.1644	3.975188	0.447692	0.562327	0.052313	0	250	238	222	280	395	214	347	535	324	304
ENSMUSG00000029136	chr5	Rbks	31624439	31624656	1489	0.248419	0.778053	0.447785	0.562392	0.076787	0	18	24	30	25	26	20	32	47	47	61
ENSMUSG00000021420	chr13	Fars2	36117411	36118005	2125	-0.13183	4.291288	0.448073	0.562703	0.033126	0	260	326	356	425	327	389	422	412	515	425
ENSMUSG00000003444	chr7	Med29	28386146	28387024	1281	-0.13832	3.787154	0.448317	0.562907	0.035286	0	206	229	309	207	249	291	325	259	386	257
ENSMUSG00000024077	chr17	Strn	78649913	78655659	8858	-0.15041	3.653654	0.44828	0.562907	0.042807	0	177	153	221	256	307	145	251	291	383	347
ENSMUSG00000058492	chr9	Scp2-ps2	1.23E+08	1.23E+08	432	0.181953	2.133293	0.448553	0.563152	0.0546	0	50	56	95	67	70	70	85	122	124	135
ENSMUSG00000028256	chr3	Odf2l	1.45E+08	1.45E+08	2584	-0.17352	2.377796	0.44864	0.563211	0.050349	0	92	83	109	66	101	100	134	92	126	106
ENSMUSG00000019969	chr12	Psen1	83688203	83688293	3114	0.118099	5.015659	0.448944	0.563541	0.027261	0	500	422	518	487	662	619	745	790	977	805
ENSMUSG00000051341	chr17	Zfp52	21555046	21555075	2175	-0.20611	1.69619	0.449308	0.563947	0.071981	0	47	64	64	61	42	52	62	95	79	54
ENSMUSG00000055319	chr7	Sec23ip	1.29E+08	1.29E+08	4578	0.137633	4.989621	0.450004	0.564769	0.037936	0	448	389	561	471	676	512	735	1096	875	679
ENSMUSG00000029101	chr5	Rgs12	34949445	34949524	7910	0.167121	2.72249	0.450099	0.564838	0.049482	0	65	81	109	132	131	101	149	180	235	153
ENSMUSG00000022544	chr16	Fam86	5244152	5245385	2649	-0.13726	3.569567	0.450271	0.564991	0.034403	0	142	220	244	206	219	233	246	234	327	269
ENSMUSG00000102717	chr1	RP23-211F21.1	1.36E+08	1.36E+08	3246	0.92372	-0.03231	0.450303	0.564991	1.498594	0	0	18	1	22	4	0	1	0	138	12
ENSMUSG00000066191	chr4	Anks6	47015669	47016816	5237	-0.18559	1.367352	0.450469	0.565148	0.05029	0	43	37	51	36	55	41	60	47	71	55
ENSMUSG00000024735	chr19	Prpf19	10895231	10895468	7278	-0.13799	7.785801	0.451401	0.566266	0.039933	0	3103	3291	4412	4042	4582	3819	4560	6875	4823	4292
ENSMUSG00000044751	chr11	Gm12231	55118101	55118795	695	0.142284	3.984377	0.45149	0.566327	0.039245	0	191	248	314	268	223	387	389	379	367	369
ENSMUSG00000055334	chr9	Snupn	56950878	56950953	1391	-0.14895	3.225275	0.452146	0.567098	0.038786	0	133	135	215	163	172	206	215	166	228	199
ENSMUSG00000014303	chr16	Glis2	4594713	4594935	4373	0.170583	3.721659	0.452563	0.567569	0.057698	0	221	110	190	158	372	250	382	287	392	315
ENSMUSG00000001995	chr8	Sipa1l2	1.25E+08	1.25E+08	6365	0.139293	3.770216	0.452703	0.567694	0.036355	0	177	175	200	228	307	202	349	350	502	293
ENSMUSG00000028088	chr3	Fmo5	97628804	97628901	5675	-0.15974	2.755649	0.452748	0.567698	0.044568	0	118	102	143	110	111	111	132	180	154	157
ENSMUSG00000005374	chr5	Tbl2	1.35E+08	1.35E+08	5968	-0.13375	3.935956	0.452974	0.56793	0.033515	0	208	203	295	231	420	263	381	289	399	369
ENSMUSG00000001467	chr5	Cyp51	4081145	4083303	4286	0.279268	3.65225	0.45312	0.56801	0.160723	0	108	95	144	197	446	237	291	93	456	546
ENSMUSG00000053289	chr9	Ddx10	53098454	53099262	3368	0.138415	3.622582	0.45309	0.56801	0.035243	0	183	163	210	200	214	191	279	399	334	302
ENSMUSG00000026646	chr2	Suv39h2	3455815	3458729	4410	-0.22032	1.075634	0.453183	0.568038	0.069909	0	29	26	42	42	44	49	36	29	59	43
ENSMUSG00000078789	chr11	Dph1	75177643	75178387	2690	0.153315	3.042945	0.453243	0.568062	0.040455	0	115	134	133	101	159	128	190	225	245	224
ENSMUSG00000062014	chr14	Gmfb	46808149	46811823	4446	0.116566	5.108683	0.453356	0.568153	0.027187	0	498	427	624	544	684	565	924	834	1025	876
ENSMUSG00000051234	chr9	Rnf7	96470937	96471852	1328	0.131991	6.483027	0.453462	0.568233	0.03649	0	1215	1429	1747	1271	1430	2096	2303	1858	2353	2174
ENSMUSG00000059142	chr17	Zfp945	22846697	22852766	10173	-0.17718	2.754902	0.453843	0.56866	0.057293	0	110	113	144	107	113	106	131	221	140	129
ENSMUSG00000029838	chr6	Ptn	36715663	36715762	2021	-0.32331	2.910854	0.453885	0.56866	0.210124	0	134	55	150	53	333	111	288	74	244	69
ENSMUSG00000039067	chr8	Psmd7	1.08E+08	1.08E+08	1599	0.139111	7.162401	0.454335	0.569173	0.041041	0	1763	2201	2863	2069	2526	3080	3230	4534	3327	3115
ENSMUSG00000093752	chr2	Gm20716	1.68E+08	1.68E+08	5288	0.134132	6.346332	0.454404	0.569207	0.037847	0	1090	1104	1532	1227	1562	1569	1788	2718	2010	1786
ENSMUSG00000032621	chr13	Srek1	1.04E+08	1.04E+08	3985	-0.12606	4.213132	0.454469	0.569238	0.030746	0	276	262	384	281	423	272	425	474	430	470
ENSMUSG00000036327	chr2	Qsox2	26208637	26211459	4644	0.149233	2.934026	0.454656	0.569369	0.039027	0	93	109	135	103	163	111	206	196	228	198
ENSMUSG00000056313	chr8	1810011O10Rik	24437180	24438984	1805	0.171016	4.054803	0.454634	0.569369	0.057748	0	228	244	251	383	167	263	414	358	519	519
ENSMUSG00000008318	chr7	Relt	1.01E+08	1.01E+08	3279	-0.18062	4.13754	0.454944	0.569678	0.065573	0	170	259	412	325	426	364	484	183	487	395
ENSMUSG00000021694	chr13	Ercc8	1.08E+08	1.08E+08	7657	-0.1627	2.261739	0.455186	0.56993	0.043749	0	58	82	103	82	92	77	107	100	116	120
ENSMUSG00000020537	chr11	Drg2	60454591	60454743	2716	0.116034	4.656632	0.455526	0.570304	0.026777	0	327	355	460	381	505	495	543	680	740	597
ENSMUSG00000033545	chr8	Znrf1	1.12E+08	1.12E+08	7018	-0.12225	5.96804	0.455623	0.570371	0.031261	0	908	1006	1200	1192	1121	1214	1420	1167	1740	1450
ENSMUSG00000056412	chr4	Gm12396	40775259	40775564	306	0.207964	1.746089	0.455662	0.570371	0.073064	0	44	61	66	36	42	76	87	91	74	73
ENSMUSG00000040339	chr3	Fam102b	1.09E+08	1.09E+08	5702	-0.15479	4.384617	0.456134	0.570869	0.04863	0	374	235	466	278	504	271	526	611	452	452
ENSMUSG00000070867	chr4	Trabd2b	1.14E+08	1.14E+08	6617	-0.24693	2.586666	0.456143	0.570869	0.119775	0	95	46	112	128	169	76	98	60	179	234
ENSMUSG00000022476	chr15	Polr3h	81915030	81916665	2514	0.136787	3.16821	0.456281	0.570991	0.033942	0	126	122	176	122	164	187	210	185	278	229
ENSMUSG00000002944	chr5	Cd36	17781690	17783349	3927	0.208902	8.281954	0.456353	0.57103	0.093693	0	3811	4927	5357	6089	3601	3446	3975	11875	11025	9806
ENSMUSG00000028622	chr4	Mrpl37	1.07E+08	1.07E+08	4460	-0.1282	6.478295	0.45674	0.571461	0.034892	0	1309	1611	1656	1573	1555	1900	1917	1774	2292	1967
ENSMUSG00000023828	chr17	Slc22a3	12419972	12421497	3501	0.345681	0.788174	0.456799	0.571483	0.203072	0	16	18	21	35	29	10	24	21	77	90
ENSMUSG00000024403	chr17	Atp6v1g2	35233660	35233890	2510	-0.21807	1.401949	0.456957	0.571629	0.078082	0	54	40	68	32	33	47	59	48	61	60
ENSMUSG00000027242	chr2	Wdr76	1.22E+08	1.22E+08	6305	-0.20294	1.391303	0.457232	0.571851	0.069793	0	49	29	50	39	61	38	54	36	77	74
ENSMUSG00000029480	chr5	Dhx37	1.25E+08	1.25E+08	4139	0.155199	2.820055	0.457229	0.571851	0.044303	0	72	78	130	129	152	132	154	172	246	162
ENSMUSG00000030400	chr7	Ercc2	19382010	19382059	4170	-0.11616	4.00775	0.457258	0.571851	0.025782	0	226	260	318	247	346	258	376	356	443	374
ENSMUSG00000027699	chr3	Ect2	27097222	27098488	5202	0.303322	1.110485	0.457461	0.572002	0.166376	0	20	22	30	24	61	16	64	32	129	40
ENSMUSG00000075289	chr19	Carns1	4164324	4166564	3968	-0.12908	4.842994	0.45745	0.572002	0.034091	0	456	493	526	464	541	551	549	626	642	798
ENSMUSG00000003865	chr7	Gys1	45434844	45435170	4789	-0.12758	8.65113	0.457743	0.572199	0.03522	0	5259	6517	7704	8461	7082	8311	8335	8960	10555	8386
ENSMUSG00000049999	chr2	Ppp1r3d	1.78E+08	1.78E+08	3267	0.195925	1.723617	0.45771	0.572199	0.068956	0	42	28	54	52	78	62	53	88	96	101
ENSMUSG00000056216	chr7	Cebpg	35046422	35050932	4935	-0.11849	5.412283	0.45774	0.572199	0.029054	0	538	683	859	771	868	739	879	1034	1054	1053
ENSMUSG00000024892	chr19	Pcx	4510472	4510581	4272	0.267045	6.445189	0.457802	0.572222	0.153106	0	869	1176	1277	1734	1585	763	979	1325	3595	4991
ENSMUSG00000005312	chr13	Ubqln1	58176156	58178028	3686	0.129498	6.077397	0.457855	0.572224	0.035586	0	806	988	1166	1135	1316	1170	1392	2141	1855	1698
ENSMUSG00000034168	chr12	Irf2bpl	86880703	86884814	4112	-0.13183	5.213733	0.457887	0.572224	0.036152	0	493	458	655	849	817	595	879	685	1086	930
ENSMUSG00000063253	chr8	Scoc	83434493	83436040	2062	-0.13751	4.695555	0.458137	0.572485	0.038532	0	364	453	595	354	499	560	619	440	628	593
ENSMUSG00000075279	chr2	Mrpl23-ps1	74591330	74591909	580	0.154366	2.934904	0.45821	0.572525	0.043481	0	99	114	123	120	140	199	156	167	217	176
ENSMUSG00000026308	chr1	Klhl30	91351016	91351135	3089	-0.14841	7.072008	0.458282	0.572563	0.047392	0	1661	1861	2866	2420	3226	2929	3788	2023	3577	2455

ENSMUSG00000078680	chr4	Mup10	60578260	60578512	1391	-0.92833	0.544675	0.458634	0.572951	1.635561	0	49	13	15	68	0	0	106	8	0	0
ENSMUSG00000036570	chr7	Fxyd1	31051681	31051815	709	0.125318	8.112639	0.45874	0.573032	0.034102	0	3725	3937	4740	4594	5148	6617	6257	7082	6957	6267
ENSMUSG00000078484	chr4	Klhl17	1.56E+08	1.56E+08	3014	-0.14654	3.188344	0.458833	0.573097	0.040286	0	129	140	178	141	211	148	233	136	267	228
ENSMUSG00000050628	chr11	Ubald2	1.16E+08	1.16E+08	1532	0.136277	4.120743	0.459253	0.573466	0.037205	0	216	242	342	306	273	327	339	554	446	443
ENSMUSG00000059409	chr17	Ppp2r5d	46682991	46684126	2926	-0.12147	5.113478	0.459213	0.573466	0.030574	0	491	455	632	684	774	539	763	903	988	708
ENSMUSG00000087381	chr4	Gm16008	1.56E+08	1.56E+08	1324	0.24705	0.719327	0.459172	0.573466	0.091692	0	25	11	34	21	28	18	46	53	37	43
ENSMUSG00000100774	chr1	Gm7329	65095227	65095436	210	-0.33326	0.187819	0.459362	0.57355	0.160818	0	15	15	18	27	23	12	8	13	26	51
ENSMUSG00000049800	chr11	Sertad2	20543253	20543760	6352	-0.16119	3.970302	0.459464	0.573626	0.053338	0	231	259	286	304	289	208	283	574	386	280
ENSMUSG00000059273	chr7	Zc3h4	16401196	16401306	6049	-0.12889	4.86983	0.459591	0.573733	0.034603	0	472	415	538	530	591	417	606	876	795	592
ENSMUSG00000021639	chr13	Gtf2h2	1E+08	1E+08	4372	-0.13544	3.64261	0.459877	0.574038	0.03567	0	188	222	288	184	196	235	290	250	332	272
ENSMUSG00000039234	chr3	Sec24d	1.23E+08	1.23E+08	3856	-0.18591	4.394276	0.460071	0.574228	0.072665	0	399	190	382	286	648	316	635	295	696	394
ENSMUSG00000020692	chr11	Nle1	82900768	82901050	3233	0.145069	2.894482	0.460521	0.574687	0.03754	0	104	113	122	107	134	147	179	161	192	218
ENSMUSG00000028601	chr4	Echdc2	1.08E+08	1.08E+08	2287	-0.16301	3.020658	0.460506	0.574687	0.052137	0	147	147	167	118	118	136	150	181	182	234
ENSMUSG00000020069	chr10	Hnrnph3	63014664	63015714	3151	0.121544	3.985889	0.460805	0.574937	0.028245	0	211	242	264	264	275	288	402	318	480	442
ENSMUSG00000022185	chr14	Acin1	54642161	54643048	8649	0.12065	5.845644	0.460795	0.574937	0.030986	0	902	708	924	891	1186	984	1391	1553	1638	1463
ENSMUSG00000037216	chr1	Lipt1	37871738	37872031	2051	0.165761	2.324932	0.460865	0.57496	0.047158	0	61	72	106	80	67	100	111	131	139	124
ENSMUSG00000019578	chr17	Ubxn6	56067045	56068683	5685	0.130458	5.49802	0.461122	0.575209	0.036183	0	654	646	798	699	792	849	935	1491	1094	1106
ENSMUSG00000058979	chr6	Cecr5	1.21E+08	1.21E+08	3355	-0.13809	4.417337	0.461148	0.575209	0.039415	0	322	405	459	358	293	439	463	444	554	450
ENSMUSG00000047264	chr8	Zfp358	3493138	3493309	1999	0.138607	4.664044	0.461379	0.575445	0.039977	0	332	375	413	455	426	504	455	837	644	631
ENSMUSG00000058900	chr13	Rsl1	67173207	67173253	1648	-0.22409	0.498702	0.461651	0.575733	0.071239	0	23	19	33	22	22	18	40	33	31	21
ENSMUSG00000066892	chr9	Fbxl12	20618118	20618410	5090	0.165911	2.360747	0.461763	0.575821	0.046823	0	86	78	75	77	74	90	129	134	145	126
ENSMUSG00000038876	chr10	Rnf146	29344178	29347883	4454	-0.13983	5.284739	0.46218	0.576289	0.041781	0	591	647	760	643	759	650	765	1282	891	718
ENSMUSG00000035354	chr7	Uvrag	98886743	98888592	3438	0.141219	3.755729	0.462381	0.576487	0.039622	0	200	166	222	216	265	224	299	476	354	293
ENSMUSG00000036403	chr5	Cep135	76588698	76588924	7188	0.247056	0.937685	0.462428	0.576494	0.086797	0	25	28	21	31	32	24	57	27	75	53
ENSMUSG00000030216	chr6	Wbp11	1.37E+08	1.37E+08	5029	0.11714	5.268114	0.462598	0.576652	0.028918	0	499	518	670	691	716	688	844	1096	1141	928
ENSMUSG00000044894	chr11	Uqcrq	53427922	53429150	1831	0.145879	8.208386	0.462638	0.576652	0.047013	0	3848	5306	5477	4913	3511	6873	6530	7517	8264	6730
ENSMUSG00000029499	chr5	Pxmp2	1.1E+08	1.1E+08	1200	0.139142	4.712735	0.462882	0.576852	0.040651	0	355	437	454	418	391	605	516	775	621	629
ENSMUSG00000097353	chr10	A430046D13Rik	1.28E+08	1.28E+08	1997	-0.14868	4.299981	0.462878	0.576852	0.045741	0	291	362	391	319	347	406	366	596	392	372
ENSMUSG00000035696	chr4	Rnf38	44126210	44129656	8336	0.130077	3.740989	0.463217	0.577217	0.032532	0	187	172	247	214	243	186	333	390	412	325
ENSMUSG00000026617	chr1	Bpnt1	1.85E+08	1.85E+08	2263	-0.12639	4.195091	0.463355	0.577338	0.032234	0	249	292	358	314	384	342	446	285	507	461
ENSMUSG00000053329	chr10	D10Jhu81e	78162067	78162718	1363	-0.13357	7.391865	0.463861	0.577916	0.03947	0	2544	2749	3313	3228	2734	3407	3089	4428	3814	3727
ENSMUSG00000039706	chr5	Ldb2	44472133	44473512	2485	0.160761	2.584149	0.463931	0.577951	0.046484	0	77	73	93	93	134	106	128	185	189	124
ENSMUSG00000002981	chr7	Clptm1	19631581	19633962	4130	0.116444	6.085276	0.464047	0.578044	0.029421	0	920	905	1244	1086	1314	1187	1440	1815	2116	1756
ENSMUSG00000035790	chr16	Cep19	32099800	32100111	1751	0.144862	3.587903	0.464313	0.578324	0.041696	0	163	186	197	203	190	259	270	388	294	234
ENSMUSG00000017978	chr6	Cadps2	23262773	23263716	9572	-0.30729	-0.1628	0.464483	0.578431	0.108223	0	11	8	16	11	30	14	24	8	24	14
ENSMUSG00000035107	chr16	Dcbld2	58408443	58408951	8401	0.162138	3.532924	0.464482	0.578431	0.054085	0	174	93	185	174	299	183	378	235	341	295
ENSMUSG00000026087	chr1	Mrpl30	37890477	37890584	3226	-0.13321	6.267513	0.464578	0.578497	0.038953	0	1171	1400	1559	1309	1213	1712	1551	1644	1908	1641
ENSMUSG00000024319	chr17	Vps52	33955812	33956182	3876	-0.10967	5.352065	0.464752	0.578662	0.02547	0	580	599	806	703	871	739	938	857	1115	941
ENSMUSG00000020740	chr11	Gga3	1.16E+08	1.16E+08	6245	0.120165	4.013378	0.465238	0.579214	0.029054	0	199	216	290	269	322	317	418	306	460	455
ENSMUSG00000035367	chr13	Rmi1	58402597	58402789	3522	0.162204	2.465684	0.465515	0.579507	0.04807	0	85	80	90	74	96	135	117	118	144	146
ENSMUSG00000033272	chr18	Slc35a4	36679215	36679623	3275	-0.11427	6.186377	0.465662	0.579638	0.028583	0	999	1160	1455	1262	1465	1344	1629	1611	2032	1558
ENSMUSG00000053963	chr1	6330403A02Rik	1.8E+08	1.8E+08	6552	-0.32455	-0.21184	0.466013	0.580023	0.120944	0	13	4	11	20	25	12	17	8	26	18
ENSMUSG00000040848	chr1	Sft2d2	1.65E+08	1.65E+08	5702	-0.11328	5.249267	0.466238	0.580252	0.027491	0	575	545	672	655	868	635	889	754	1105	914
ENSMUSG00000070643	chr1	Sox13	1.33E+08	1.33E+08	4312	-0.14697	2.901526	0.466408	0.58041	0.042215	0	118	112	123	155	137	101	145	181	231	175
ENSMUSG00000002831	chr17	Plin4	56100591	56102330	5777	-0.21539	7.641539	0.466554	0.580527	0.104178	0	3169	3150	4607	3464	3512	1956	2376	9069	4084	4290
ENSMUSG00000027551	chr2	Zfp64	1.69E+08	1.69E+08	5918	0.18729	2.791843	0.466586	0.580527	0.068328	0	99	92	111	102	129	92	136	291	191	147
ENSMUSG00000042557	chr9	Sin3a	57072040	57072063	5385	-0.13386	4.433936	0.466863	0.58082	0.037797	0	299	307	392	402	500	304	449	678	567	421
ENSMUSG00000011171	chr12	Vipr2	1.16E+08	1.16E+08	4463	-0.26742	1.493474	0.466911	0.580828	0.132921	0	63	27	51	34	76	36	54	107	64	29
ENSMUSG00000052593	chr12	Adam17	21323509	21325626	7154	0.130583	5.239067	0.467024	0.580916	0.036926	0	513	482	663	592	781	623	1074	626	1308	1054
ENSMUSG00000035772	chr2	Mrps2	28468066	28468142	2919	0.120976	4.733362	0.467084	0.580938	0.031072	0	296	388	528	475	445	566	613	578	828	641
ENSMUSG00000019179	chr5	Mdh2	1.36E+08	1.36E+08	2089	-0.1313	9.829571	0.467414	0.581297	0.039055	0	11494	16713	17473	18579	14641	18711	18668	20420	23496	19365
ENSMUSG00000039031	chr10	Arhgap18	26753421	26753502	3884	0.148796	3.931074	0.467816	0.581745	0.046413	0	132	216	255	321	290	269	359	279	507	472
ENSMUSG00000039703	chr11	Nploc4	1.2E+08	1.2E+08	4776	0.201885	6.673104	0.468104	0.58205	0.091859	0	1234	1395	1859	1688	1784	1440	1747	5372	2248	1924
ENSMUSG00000101249	chr1	Gm29216	24615706	24616197	492	-0.16777	3.650497	0.468219	0.58214	0.059158	0	166	229	264	288	140	260	202	288	324	287
ENSMUSG00000036693	chr5	Nop14	34638532	34638651	2734	0.134594	4.274248	0.468286	0.582172	0.038096	0	220	295	351	312	363	325	396	666	545	432
ENSMUSG00000073802	chr4	Cdkn2b	89306289	89307314	1393	-0.25605	-0.0677	0.468644	0.582565	0.091914	0	12	17	20	16	13	8	25	10	29	22
ENSMUSG00000089872	chr1	Rps6kc1	1.91E+08	1.91E+08	9741	-0.12007	4.435954	0.468783	0.582685	0.030251	0	385	282	401	330	485	358	462	461	568	576
ENSMUSG00000044285	chr14	Gm1821	46084126	46084815	690	0.222459	2.798696	0.468838	0.582701	0.101594	0	79	113	124	95	117	107	100	280	112	256
ENSMUSG00000042854	chr2	Trp53rk	1.67E+08	1.67E+08	5755	0.178795	1.628704	0.468899	0.582724	0.05457	0	32	43	62	46	53	67	85	56	90	72
ENSMUSG00000033416	chr10	Gucd1	75351111	75352902	8206	0.280112	6.111326	0.469117	0.582944	0.17688	0	1067	929	1199	1082	860	780	916	4801	1110	1193
ENSMUSG00000034158	chr16	Lrrc58	37868389	37868980	8604	-0.18858	5.319772	0.469203	0.582998	0.079588	0	572	564	813	726	911	428	653	1729	853	723
ENSMUSG00000096687	chr10	AA474331	39890018	39892929	3833	0.22477	1.996165	0.469319	0.58309	0.097003	0	59	40	107	41	55	52	101	154	103	83
ENSMUSG00000054051	chr14	Ercc6	32513521	32513599	8422	-0.14948	2.849814	0.469929	0.583795	0.043661	0	119	99	165	103	143	105	139	143	239	178
ENSMUSG00000029162	chr5	Khk	30921556	30922007	1670	0.135899	3.854589	0.469983	0.58381	0.038029	0	202	212	254	233	238	287	269	475	370	345
ENSMUSG00000081272	chr2	Gm13509	49308155	49309462	1308	0.132816	3.095076	0.470406	0.584283	0.03213	0	114	121	134	133	173	151	206	213	260	209
ENSMUSG00000002635	chr7	Pdcd2l	34184499	34184811	1315	-0.11879	3.700724	0.470818	0.584689	0.028467	0	206	223	226	209	252	228	311	276	345	289

ENSMUSG00000030711	chr7	Sult1a1	1.27E+08	1.27E+08	1507	0.185243	4.288719	0.470784	0.584689	0.075078	0	281	258	410	323	239	252	283	625	517	773
ENSMUSG00000087635	chr2	Gm13414	34649514	34650240	727	-0.30851	0.120979	0.471126	0.58502	0.129345	0	16	16	17	16	28	17	15	43	12	15
ENSMUSG00000006418	chr2	Rnf114	1.67E+08	1.67E+08	3356	0.136792	5.19837	0.471361	0.585259	0.041462	0	473	612	702	574	530	739	768	1162	858	909
ENSMUSG00000028277	chr4	Ube2j1	33031416	33031616	3530	0.114957	5.245765	0.471431	0.585294	0.02879	0	521	577	707	547	683	639	926	1055	1104	906
ENSMUSG00000005804	chr2	Bloc1s6	1.23E+08	1.23E+08	3899	0.110947	4.630429	0.471484	0.585307	0.026009	0	342	365	450	386	437	514	609	545	721	599
ENSMUSG00000026553	chr1	Copa	1.72E+08	1.72E+08	9427	-0.1167	7.154462	0.471529	0.58531	0.031077	0	2327	1832	2743	2284	3306	2374	3419	2953	4024	3313
ENSMUSG00000070738	chr1	Dgkd	87853287	87853456	6850	0.11709	5.690512	0.471871	0.585682	0.030459	0	738	658	891	868	994	774	1168	1428	1590	1398
ENSMUSG00000016619	chr15	Nup50	84923428	84923650	4741	0.114051	4.618596	0.472489	0.586396	0.027576	0	323	391	420	368	459	486	537	559	784	619
ENSMUSG00000004054	chr19	Map3k11	5689131	5689266	3801	0.129535	4.459203	0.472541	0.586409	0.035761	0	257	314	350	451	376	362	481	492	815	577
ENSMUSG00000028826	chr4	Tmem57	1.35E+08	1.35E+08	6744	-0.15722	4.521618	0.472892	0.586791	0.054825	0	371	334	441	356	525	299	406	861	530	445
ENSMUSG00000025280	chr14	Polr3a	24448694	24449222	4683	-0.14009	3.118497	0.473026	0.586904	0.038853	0	152	107	151	146	201	133	178	225	245	183
ENSMUSG00000064208	chr10	Gm10145	27936364	27936828	465	-0.21699	0.475365	0.473458	0.587389	0.057596	0	24	17	29	20	27	24	24	29	32	31
ENSMUSG00000049422	chr10	Chchd10	75935573	75936004	939	0.134995	8.428066	0.473672	0.587601	0.042341	0	4281	5844	5681	6386	4909	8441	7626	7379	10238	7990
ENSMUSG00000041396	chr1	Mettl18	1.64E+08	1.64E+08	1513	-0.17668	1.681405	0.474256	0.588254	0.054946	0	58	50	59	52	55	59	86	63	73	59
ENSMUSG00000073792	chr4	Alg6	99715664	99715706	8544	-0.17422	2.202472	0.474283	0.588254	0.058506	0	99	74	87	61	72	75	111	84	128	101
ENSMUSG00000000378	chr11	Ccm2	6546887	6547029	3666	0.129556	3.636651	0.47451	0.588483	0.033547	0	169	176	180	213	247	203	305	246	437	342
ENSMUSG00000032577	chr9	Mapkapk3	1.07E+08	1.07E+08	5542	-0.1227	5.208901	0.474641	0.588593	0.03357	0	534	608	729	569	783	667	810	1045	862	719
ENSMUSG00000043488	chr19	Frmd8os	5845623	5845750	612	0.33637	0.478662	0.474742	0.588664	0.19904	0	16	17	15	21	26	14	13	86	27	28
ENSMUSG00000062169	chr1	Cnih4	1.81E+08	1.81E+08	3783	-0.11641	5.063124	0.474912	0.588823	0.030034	0	514	525	685	558	611	661	821	618	926	706
ENSMUSG00000078247	chr17	Airn	12741311	12741424	3583	-0.19605	2.405839	0.474997	0.588876	0.076642	0	109	57	119	90	89	96	105	169	89	99
ENSMUSG00000075389	chr11	2810410L24Rik	1.2E+08	1.2E+08	3028	0.226613	1.172386	0.475064	0.588906	0.08829	0	31	26	48	22	40	50	43	82	45	46
ENSMUSG00000053414	chr16	Hunk	90386397	90386716	5009	-0.19372	1.561209	0.475193	0.589013	0.062812	0	39	33	61	58	68	49	86	51	78	49
ENSMUSG00000048078	chr7	Tenm4	96171244	96171493	21030	0.290739	2.580819	0.475353	0.589159	0.186685	0	64	52	59	75	209	77	104	57	215	324
ENSMUSG00000027787	chr3	Nmd3	69721985	69722122	10155	0.157664	4.405374	0.475757	0.589606	0.055563	0	254	323	425	329	336	358	451	868	476	432
ENSMUSG00000036955	chr10	2510003E04Rik	62538626	62540056	6547	-0.12462	4.755208	0.476191	0.590092	0.034602	0	400	448	545	458	488	437	580	806	683	508
ENSMUSG00000034473	chr16	Sec22a	35311131	35314287	5221	0.133736	3.217611	0.4763	0.590174	0.033999	0	144	142	159	131	151	172	220	225	308	209
ENSMUSG00000036833	chr2	Pnpla7	24976033	24976313	7496	0.225905	5.255082	0.476391	0.590234	0.118262	0	536	484	664	644	599	534	601	2251	690	686
ENSMUSG00000047363	chr2	Cstad	30595040	30595074	1229	-0.25198	0.414275	0.476524	0.590345	0.090365	0	16	27	30	15	25	33	27	26	22	21
ENSMUSG00000071256	chr17	Zfp213	23556769	23558312	2672	0.183593	2.14714	0.477011	0.590896	0.061971	0	69	76	68	48	73	94	115	73	136	120
ENSMUSG00000024422	chr17	Dhx16	35879819	35880118	4094	0.117126	4.155269	0.477061	0.590905	0.02923	0	213	241	306	321	350	323	465	356	528	496
ENSMUSG00000020255	chr10	D10Wsu102e	83360221	83360373	3509	0.13288	3.198329	0.477152	0.590965	0.034193	0	130	126	146	141	182	141	225	199	304	259
ENSMUSG00000032733	chr9	Snx33	56917200	56918704	4564	-0.16729	3.115658	0.477566	0.591371	0.058469	0	165	84	146	128	247	116	171	218	232	219
ENSMUSG00000043311	chr17	D17H6S53E	35126373	35126450	2280	0.125762	3.613615	0.477549	0.591371	0.03225	0	159	180	237	211	180	253	295	279	390	266
ENSMUSG00000035329	chr12	Fbxo33	59200655	59202679	4466	0.181397	1.90431	0.478031	0.591894	0.057945	0	49	51	54	61	70	53	68	97	139	105
ENSMUSG00000001552	chr11	Jup	1E+08	1E+08	6436	0.158893	6.43647	0.478277	0.592096	0.059458	0	924	1003	1412	1829	1766	1386	1749	3447	2326	1794
ENSMUSG00000021910	chr14	Nisch	31170930	31172178	13198	0.120602	6.61366	0.478279	0.592096	0.034109	0	1305	1101	1716	1588	2256	1609	2711	2124	3062	2556
ENSMUSG00000002767	chr17	Mrpl2	46646229	46646398	1170	0.129977	5.921226	0.478538	0.592311	0.03924	0	758	1006	1022	1112	881	1367	1205	1540	1690	1521
ENSMUSG00000039849	chr2	Pcif1	1.65E+08	1.65E+08	6544	0.128225	4.513838	0.478496	0.592311	0.036551	0	297	289	374	405	465	374	469	762	690	504
ENSMUSG00000046387	chr18	Pcdhb17	37484795	37489454	4660	-0.19796	1.601549	0.478841	0.592633	0.073883	0	46	26	56	53	88	37	81	67	83	57
ENSMUSG00000029134	chr5	Plb1	32232708	32232791	8859	-0.22132	1.332022	0.47955	0.593457	0.08691	0	26	36	41	59	59	52	33	67	46	59
ENSMUSG00000030094	chr6	Xpc	91489305	91490266	5490	0.153229	3.554193	0.479755	0.593658	0.050276	0	169	171	188	178	212	171	264	459	295	250
ENSMUSG00000036904	chr18	Fzd8	9212856	9216201	3346	-0.15454	2.332197	0.48019	0.594068	0.045089	0	81	61	88	102	105	90	98	128	128	102
ENSMUSG00000040746	chr11	Rnf167	70647235	70647313	3539	0.120614	5.006544	0.480215	0.594068	0.03325	0	450	421	570	544	587	644	653	975	770	825
ENSMUSG00000098702	chr18	1500015A07Rik	61726390	61728254	2296	0.214454	1.255021	0.480135	0.594068	0.072789	0	31	44	31	32	36	44	49	80	56	56
ENSMUSG00000017781	chr11	Pitpna	75588097	75588352	4129	-0.14818	7.384651	0.480467	0.594076	0.052406	0	1818	3269	3595	3038	2944	3751	3015	2728	4265	4532
ENSMUSG00000036199	chr8	Ndufa13	69894188	69894410	1243	0.134336	8.285478	0.480479	0.594076	0.043232	0	4292	5359	5963	4632	4294	7643	6957	7704	7812	7349
ENSMUSG00000058318	chr2	Phf21a	92093117	92093153	8561	-0.11902	4.060579	0.480416	0.594076	0.030246	0	262	206	301	281	411	267	364	394	416	425
ENSMUSG00000060579	chr14	Fhit	9550092	9550398	1491	0.236411	0.925684	0.480382	0.594076	0.097696	0	16	36	34	26	25	46	27	62	50	39
ENSMUSG00000073563	chr18	Csnk1g3	53862113	53862600	4394	0.116817	3.815308	0.480354	0.594076	0.028868	0	169	193	257	216	298	241	386	372	390	318
ENSMUSG00000078974	chr11	Sec61g	16500530	16501807	2464	0.128168	5.207811	0.480321	0.594076	0.037749	0	511	638	724	489	553	851	907	778	1054	871
ENSMUSG00000024359	chr18	Hspa9	34937414	34938393	3932	-0.12127	8.943037	0.480596	0.594167	0.035317	0	6759	8928	9391	9510	7856	9369	10193	11280	13115	10998
ENSMUSG00000086725	chr11	A630052C17Rik	29170909	29172951	2203	-0.23274	0.316313	0.481049	0.594675	0.082314	0	18	28	20	15	22	16	29	34	24	21
ENSMUSG00000043153	chr12	Ispd	36381519	36382024	2690	-0.18674	1.740973	0.481314	0.594896	0.063689	0	47	33	69	62	84	53	83	64	107	53
ENSMUSG00000063888	chr17	Rpl7l1	46773907	46775736	2606	0.112266	5.577571	0.481284	0.594896	0.029189	0	587	740	891	705	921	917	1223	950	1517	1216
ENSMUSG00000011960	chr15	Ccnt1	98538689	98544608	9157	-0.12902	4.307626	0.481586	0.595178	0.036942	0	280	260	376	335	496	302	398	606	509	396
ENSMUSG00000027999	chr3	Pla2g12a	1.3E+08	1.3E+08	1654	0.179955	4.905414	0.481708	0.595276	0.075787	0	353	502	446	673	321	616	453	1086	803	723
ENSMUSG00000008976	chr16	Gabpa	84834925	84835023	5687	-0.14619	4.464845	0.481953	0.595307	0.04998	0	409	406	348	354	375	259	493	683	619	429
ENSMUSG00000022205	chr15	Sub1	11981339	11984297	3930	0.109685	5.676841	0.481991	0.595307	0.028044	0	685	749	935	815	924	1015	1210	1384	1315	1236
ENSMUSG00000022337	chr15	Emc2	43477229	43477325	1245	-0.1251	6.216651	0.481841	0.595307	0.037059	0	1075	1326	1566	1247	1217	1584	1724	1599	1746	1539
ENSMUSG00000022863	chr16	Btg3	78359860	78360538	1439	0.173908	1.515167	0.481922	0.595307	0.05217	0	30	34	47	48	60	56	63	76	87	60
ENSMUSG00000022992	chr15	Kansl2	98518821	98519547	2417	-0.13018	5.532218	0.481787	0.595307	0.039656	0	659	769	951	808	840	823	969	1438	979	896
ENSMUSG00000061411	chr2	Nol4l	1.53E+08	1.53E+08	9083	-0.20403	1.564019	0.481952	0.595307	0.080036	0	33	43	38	62	84	30	81	62	78	66
ENSMUSG00000041712	chr12	Ubr7	1.03E+08	1.03E+08	3247	-0.12224	4.446577	0.482053	0.595331	0.033628	0	314	346	428	380	425	346	477	645	583	390
ENSMUSG00000024576	chr18	Csnk1a1	61555274	61555873	10502	-0.11829	7.658091	0.482106	0.595342	0.033645	0	3026	3197	4050	3380	3910	3528	4797	5515	4769	3929
ENSMUSG00000038065	chr6	Mturn	54681624	54681931	5695	-0.17753	3.571072	0.482688	0.596009	0.071355	0	207	143	219	219	264	130	223	471	246	232
ENSMUSG00000026626	chr1	Ppp2r5a	1.91E+08	1.91E+08	9607	-0.13786	6.757602	0.483022	0.596367	0.045744	0	1639	1546	2017	2105	2181	1708	2032	1753	2942	3718

ENSMUSG00000063810	chr6	Alms1	85587531	85588026	9986	-0.25451	0.714489	0.483105	0.596417	0.105833	0	21	16	23	26	59	28	34	45	37	20
ENSMUSG00000047613	chr4	A430005L14Rik	1.54E+08	1.54E+08	1552	0.111297	3.964231	0.483293	0.596596	0.026325	0	198	233	288	260	267	309	354	381	440	396
ENSMUSG00000051232	chr11	Tmem199	78507055	78507805	1902	0.117949	3.716751	0.483344	0.596605	0.028995	0	167	200	264	189	228	229	307	316	391	355
ENSMUSG00000040860	chr4	Crocc	1.41E+08	1.41E+08	8266	-0.19675	1.674739	0.483482	0.596723	0.071805	0	36	39	74	55	79	39	71	45	105	86
ENSMUSG00000022718	chr16	Dgcr8	18253948	18255605	7286	-0.11356	3.922056	0.48362	0.59684	0.027746	0	230	221	276	235	356	230	359	327	404	386
ENSMUSG00000019837	chr10	Gtf3c6	40249203	40249831	1020	-0.13621	4.009404	0.483742	0.596937	0.041219	0	232	247	367	276	282	335	373	219	431	417
ENSMUSG00000059278	chr11	Naa38	69395487	69395681	890	-0.12713	4.5295	0.483872	0.597045	0.036779	0	330	429	457	379	396	510	526	398	582	524
ENSMUSG00000006526	chr14	Tmem110	30825590	30825890	4058	-0.13792	3.539608	0.483965	0.597106	0.041151	0	188	137	217	177	307	157	239	327	307	268
ENSMUSG00000031839	chr8	Hsbp1	1.19E+08	1.19E+08	1163	0.117224	6.463582	0.484038	0.597143	0.032966	0	1175	1366	1631	1430	1438	2013	2079	1963	2340	2209
ENSMUSG00000001642	chr6	Akr1b3	34303934	34304339	3933	-0.12268	7.36513	0.48448	0.597581	0.036482	0	2145	2767	3242	2870	3382	3663	3659	2926	4166	3796
ENSMUSG00000043065	chr16	Spice1	44347121	44347506	5416	-0.19215	1.900088	0.484462	0.597581	0.074472	0	63	44	80	68	71	35	80	121	94	74
ENSMUSG00000061904	chr10	Slc25a3	91116574	91117124	5550	0.131961	9.613761	0.484535	0.597596	0.042611	0	9710	13883	13127	14355	10467	17752	16830	18506	22944	19048
ENSMUSG00000023170	chr11	Gps2	69913888	69914074	1604	0.122264	4.246132	0.484699	0.597664	0.033327	0	246	281	332	327	322	339	397	608	494	459
ENSMUSG00000025432	chr10	Avil	1.27E+08	1.27E+08	3398	-0.25538	1.281032	0.48474	0.597664	0.132006	0	56	34	43	29	49	34	27	77	32	77
ENSMUSG00000041781	chr12	Cpsf2	1.02E+08	1.02E+08	5315	-0.11005	4.937082	0.48477	0.597664	0.027739	0	441	459	633	504	627	533	692	787	822	605
ENSMUSG00000049134	chr19	Nrap	56320035	56320302	5507	-0.16067	9.72492	0.484806	0.597664	0.063223	0	12088	10603	14731	20077	17669	14314	14615	30846	19015	13952
ENSMUSG00000052751	chr6	Repin1	48593883	48594052	3975	0.164893	4.621091	0.48477	0.597664	0.063813	0	346	363	381	407	422	391	481	1091	629	437
ENSMUSG00000020921	chr11	Tmem101	1.02E+08	1.02E+08	2021	0.112743	3.920549	0.484849	0.597664	0.027721	0	182	214	299	231	292	316	389	323	451	346
ENSMUSG00000038151	chr10	Prdm1	44437177	44440242	5492	-0.23523	1.005705	0.485203	0.598046	0.112534	0	26	35	41	49	20	20	50	24	65	53
ENSMUSG00000047881	chr5	Rell1	63908896	63911151	3863	0.11941	3.706894	0.485346	0.598118	0.03053	0	175	152	216	238	266	239	331	300	440	283
ENSMUSG00000078490	chr4	C030017K20Rik	1.55E+08	1.55E+08	9951	-0.2398	0.575615	0.485375	0.598118	0.10785	0	29	25	36	9	27	17	41	23	45	27
ENSMUSG00000098178	chr17	Yam1	39846958	39848788	1831	-0.23825	12.17414	0.48539	0.598118	0.138939	0	52403	75188	88793	60808	153073	69097	50441	81587	61899	228176
ENSMUSG00000020231	chr10	Dip2a	76259429	76259722	8215	-0.13241	3.431364	0.485618	0.598346	0.03732	0	160	118	221	182	272	154	265	218	318	256
ENSMUSG00000052675	chr7	Zfp112	24112314	24112436	4095	-0.24749	2.342893	0.486451	0.599319	0.137367	0	95	75	108	82	90	66	78	243	62	76
ENSMUSG00000100691	chr8	2010320M18Rik	70776815	70777823	1009	0.142156	3.16465	0.486579	0.599423	0.044495	0	107	126	189	131	156	217	183	239	202	225
ENSMUSG00000000794	chr3	Kcnn3	89520164	89521404	7391	0.259922	2.024342	0.486687	0.599502	0.144839	0	52	45	46	72	88	43	190	132	108	39
ENSMUSG00000051989	chr16	Smim11	92301286	92301343	972	0.140227	4.858892	0.486796	0.599583	0.046626	0	356	477	530	503	415	759	734	477	785	728
ENSMUSG00000040037	chr3	Negr1	1.57E+08	1.57E+08	6725	-0.35525	0.026945	0.486863	0.599613	0.254536	0	16	4	8	22	39	3	19	10	34	33
ENSMUSG00000019794	chr10	Katna1	7726000	7726123	2195	0.119653	4.076782	0.486966	0.599626	0.031862	0	226	247	320	248	305	327	414	315	466	521
ENSMUSG00000044199	chr10	S1pr4	81497745	81500132	2388	0.247162	0.466069	0.487004	0.599626	0.093039	0	13	12	24	31	18	14	27	34	50	41
ENSMUSG00000054855	chr15	Rnd1	98663421	98663890	2967	-0.19639	0.826207	0.486971	0.599626	0.053379	0	27	22	34	30	38	30	33	36	42	42
ENSMUSG00000024210	chr17	Ip6k3	27143969	27145322	2307	0.122417	6.456969	0.487089	0.599678	0.036587	0	1166	1187	1697	1445	1556	2132	1922	2157	2709	1669
ENSMUSG00000005950	chr11	P2rx5	73160421	73160733	2395	0.148189	4.062398	0.487147	0.599687	0.05012	0	174	307	305	282	238	321	431	255	571	484
ENSMUSG00000070476	chr2	Fam217b	1.78E+08	1.78E+08	4559	0.1743	2.0538	0.487184	0.599687	0.059876	0	61	44	65	52	100	75	96	73	151	114
ENSMUSG00000017144	chr2	Rnd3	51130438	51132545	4432	0.135238	3.66177	0.487231	0.599692	0.040251	0	173	196	171	177	284	259	365	235	417	267
ENSMUSG00000020070	chr10	Rufy2	62980223	62980332	8108	-0.15945	2.291831	0.487342	0.599775	0.050068	0	76	56	103	90	103	79	96	134	140	85
ENSMUSG00000031891	chr8	Hsd11b2	1.06E+08	1.06E+08	1845	0.33966	0.959123	0.487686	0.600146	0.254476	0	8	19	26	15	76	59	67	11	57	40
ENSMUSG00000019863	chr10	Qrsl1	43874188	43874706	3442	-0.13682	4.260418	0.487932	0.600395	0.043323	0	259	352	396	359	289	432	418	299	526	429
ENSMUSG00000000489	chr15	Pdgfb	79995900	79997257	2918	0.130745	5.033808	0.488187	0.600652	0.041248	0	394	306	588	607	775	660	790	614	1049	896
ENSMUSG00000025474	chr7	Tubgcp2	1.4E+08	1.4E+08	3085	-0.13611	4.169826	0.488271	0.600652	0.042922	0	327	202	315	349	378	273	317	548	475	393
ENSMUSG00000027498	chr2	Cstf1	1.72E+08	1.72E+08	3504	0.110888	4.458307	0.488258	0.600652	0.027858	0	283	323	380	378	395	403	518	626	605	505
ENSMUSG00000036218	chr15	Pdzrn4	92396915	92397505	4179	0.244008	-0.1069	0.488375	0.600727	0.072115	0	11	10	13	16	13	12	21	27	31	15
ENSMUSG00000004558	chr14	Ndrg2	51905271	51906306	2157	0.136582	10.61758	0.488767	0.601155	0.04659	0	21451	22898	27363	27529	25254	32035	29777	55550	36316	36250
ENSMUSG00000049504	chr3	Proser1	53463666	53464319	5084	-0.1533	3.213175	0.488865	0.601222	0.052392	0	136	103	146	179	259	112	184	243	247	246
ENSMUSG00000010045	chr9	Tmem115	1.08E+08	1.08E+08	2194	0.113153	4.399246	0.488959	0.601285	0.029141	0	304	300	387	296	402	393	506	612	590	450
ENSMUSG00000002957	chr7	Ap2a2	1.42E+08	1.42E+08	4639	0.110542	6.153802	0.489302	0.601548	0.029822	0	961	954	1223	1130	1488	1335	1587	1572	2161	2019
ENSMUSG00000003135	chr1	Cnot11	39534992	39535047	3508	-0.11795	4.811057	0.489322	0.601548	0.032804	0	400	457	609	480	485	469	633	780	690	563
ENSMUSG00000019883	chr10	Echdc1	29313166	29313297	3317	-0.17466	4.315219	0.48935	0.601548	0.073537	0	270	334	357	360	441	293	352	197	676	712
ENSMUSG00000026798	chr2	Coq4	29787493	29788357	3399	0.142894	2.953476	0.489293	0.601548	0.042696	0	75	135	135	130	132	151	192	170	240	188
ENSMUSG00000035505	chr5	Cox18	90214724	90215175	2009	0.154426	2.484283	0.489422	0.601548	0.048964	0	62	88	84	106	93	122	108	131	180	135
ENSMUSG00000050379	chrX	Sept6	36911326	36913254	9882	0.169097	2.919668	0.489434	0.601548	0.065179	0	113	64	135	87	203	134	242	142	246	169
ENSMUSG00000057880	chr16	Abat	8513429	8513574	7748	-0.191	2.466301	0.489587	0.601682	0.075831	0	54	62	95	116	173	98	122	156	112	99
ENSMUSG00000027257	chr2	Pacsin3	91255954	91256190	4327	0.121587	7.822584	0.489669	0.60173	0.036864	0	2945	3548	4270	3775	3485	5097	4941	6069	5602	5472
ENSMUSG00000033249	chr8	Hsf4	1.05E+08	1.05E+08	1753	0.184555	2.305614	0.49008	0.602182	0.072888	0	71	68	94	65	80	90	82	192	103	129
ENSMUSG00000037370	chr10	Enpp1	24637914	24641976	10257	0.187119	3.209107	0.490167	0.602235	0.081948	0	154	60	126	128	264	149	317	185	308	196
ENSMUSG00000035469	chr14	Rcbtb1	59201209	59201304	6010	-0.12353	4.119041	0.490359	0.602417	0.035086	0	258	233	321	321	385	243	343	521	455	389
ENSMUSG00000009907	chr1	Vps4b	1.07E+08	1.07E+08	8905	0.106216	4.724887	0.490832	0.602762	0.026025	0	373	363	496	392	505	449	626	660	850	643
ENSMUSG00000020790	chr11	Ankfy1	72690006	72690034	11332	0.125358	4.731139	0.490809	0.602762	0.037659	0	377	284	472	399	618	507	652	461	844	787
ENSMUSG00000021340	chr13	Gpld1	24943152	24943249	3584	0.232933	0.249433	0.490739	0.602762	0.071624	0	15	11	16	17	25	15	32	20	36	36
ENSMUSG00000027739	chr3	Rab33b	51483920	51484112	3538	0.156851	3.302082	0.490685	0.602762	0.054873	0	136	145	169	138	183	138	210	392	253	217
ENSMUSG00000071604	chr19	Fam189a2	23972751	23973631	2547	-0.11195	4.967461	0.490857	0.602762	0.029619	0	480	483	582	554	604	611	611	787	741	724
ENSMUSG00000007589	chr14	Tinf2	55679083	55679409	1736	-0.11958	3.488703	0.491112	0.602839	0.031024	0	191	175	204	177	217	212	213	260	301	259
ENSMUSG00000024831	chr19	Ighmbp2	3260924	3261635	4101	-0.15791	2.277585	0.491137	0.602839	0.049787	0	72	71	96	89	92	73	79	139	137	102
ENSMUSG00000032816	chr9	Igdcc4	65101486	65101598	6366	-0.11276	5.784352	0.491032	0.602839	0.031025	0	820	711	1149	949	1202	910	1470	1156	1617	1082
ENSMUSG00000044080	chr3	S100a1	90511034	90511364	694	0.144487	6.204537	0.491133	0.602839	0.051713	0	950	1318	1263	1372	827	1583	1425	1661	2221	2130
ENSMUSG00000080850	chr4	Gm12439	48675156	48675520	365	0.125808	4.508818	0.491048	0.602839	0.038014	0	307	260	472	361	433	548	603	410	559	602

ENSMUSG00000059316	chr2	Slc27a4	29802634	29802960	4412	0.115941	4.342762	0.491475	0.603199	0.031014	0	247	297	369	299	421	375	512	375	704	519
ENSMUSG00000003345	chr10	Csnk1g2	80622780	80622950	2511	-0.10785	6.388326	0.491561	0.603204	0.028695	0	1180	1206	1689	1546	1674	1614	1845	1823	2190	1909
ENSMUSG00000074506	chr3	Gm10705	87207545	87208005	461	-0.22103	0.29287	0.491566	0.603204	0.078629	0	25	11	17	22	27	20	29	21	35	18
ENSMUSG00000056328	chr11	Myh1	67200052	67200124	6353	0.175599	12.65987	0.491734	0.603357	0.077982	0	74496	100089	96505	162990	64744	104650	171856	192959	239386	108711
ENSMUSG00000020898	chr11	Ctc1	69015911	69016165	6797	0.117411	3.785434	0.492185	0.603857	0.030336	0	201	170	242	225	264	245	321	270	442	404
ENSMUSG00000052609	chr12	Plekhg3	76533560	76533818	4955	0.137301	3.397926	0.492256	0.603891	0.042321	0	126	122	159	176	263	162	257	219	334	326
ENSMUSG00000033805	chr5	Ephx4	1.07E+08	1.07E+08	1646	-0.25234	0.028129	0.492369	0.603976	0.071413	0	18	10	21	13	23	17	22	23	17	19
ENSMUSG00000069919	chr11	Hba-a1	32283511	32283801	812	0.216092	5.243816	0.492653	0.604271	0.116797	0	175	559	514	742	1022	580	722	582	1516	1486
ENSMUSG00000027776	chr3	Il12a	68690644	68690741	1701	-0.18564	1.02499	0.492746	0.604331	0.05795	0	34	33	41	29	35	38	33	44	52	45
ENSMUSG00000036913	chr8	Trim67	1.25E+08	1.25E+08	8817	-0.38519	-0.11714	0.492962	0.604542	0.292993	0	2	22	22	25	7	6	5	14	26	36
ENSMUSG00000101878	chr6	Gm8203	1.16E+08	1.16E+08	387	0.172826	1.559331	0.493191	0.60477	0.051802	0	35	42	52	43	52	61	62	55	92	83
ENSMUSG00000029166	chr5	Mapre3	30814641	30814898	3407	0.154519	6.0614	0.493404	0.604923	0.060111	0	796	956	1236	1077	1241	1382	1214	2701	1344	1419
ENSMUSG00000041645	chr12	Ddx24	1.03E+08	1.03E+08	3157	-0.1115	5.786973	0.493372	0.604923	0.030677	0	796	841	1065	985	1110	948	1130	1526	1435	1158
ENSMUSG00000024968	chr19	Rcor2	7267325	7267424	3135	0.282651	1.265174	0.493529	0.605023	0.181581	0	30	13	40	25	72	56	86	14	72	65
ENSMUSG00000046546	chr16	Fam43a	30599723	30602797	3075	-0.12376	3.990663	0.493754	0.605246	0.036443	0	200	283	298	289	307	203	342	324	547	399
ENSMUSG00000023967	chr17	Mrps18a	46110986	46111129	3690	0.13006	5.580216	0.493859	0.605321	0.042008	0	553	819	911	848	647	1156	1004	1093	1297	1202
ENSMUSG00000022052	chr14	Ppp2r2a	67014057	67016653	4036	-0.1101	5.933005	0.493919	0.605341	0.029992	0	836	1019	1115	1016	1321	1217	1341	1309	1595	1359
ENSMUSG00000014633	chr8	Cmc2	1.17E+08	1.17E+08	2043	0.134387	4.25085	0.494342	0.605805	0.042985	0	253	324	357	289	270	483	471	329	521	478
ENSMUSG00000020319	chr11	Wdpcp	21572235	21572370	5934	-0.18968	1.335364	0.494526	0.605977	0.06365	0	30	35	50	41	64	43	61	64	61	36
ENSMUSG00000097445	chr9	Gm26631	57531287	57533585	2505	0.778773	0.537949	0.494642	0.60606	1.370884	0	2	12	2	54	8	0	0	2	195	29
ENSMUSG00000103104	chr17	Riok2	17374332	17374670	3196	0.14135	4.103182	0.494681	0.60606	0.047609	0	235	248	335	260	278	307	340	658	416	363
ENSMUSG00000036613	chr12	Tssc1	28751828	28752004	1692	-0.16805	2.881479	0.494736	0.606073	0.063511	0	109	132	130	115	156	136	164	78	215	213
ENSMUSG00000019961	chr10	Tmpo	91147571	91149758	6478	-0.1076	5.353786	0.494882	0.606141	0.028485	0	628	641	824	615	835	639	902	1056	1133	897
ENSMUSG00000036860	chr11	Mrpl55	59202486	59202659	1027	0.125117	4.783638	0.494883	0.606141	0.0378	0	371	452	441	503	399	649	668	586	840	579
ENSMUSG00000081967	chr2	Gm14017	1.21E+08	1.21E+08	386	-0.2767	0.109395	0.494922	0.606141	0.112785	0	16	17	24	19	14	22	17	21	38	7
ENSMUSG00000037894	chr3	H2afz	1.38E+08	1.38E+08	1776	0.12076	5.765339	0.495087	0.606289	0.036403	0	732	837	1049	722	1015	1149	1337	926	1794	1430
ENSMUSG00000040690	chr4	Col16a1	1.3E+08	1.3E+08	6750	-0.23241	6.010876	0.495151	0.606313	0.137134	0	1280	394	1207	604	2583	911	2294	906	1720	1180
ENSMUSG00000052658	chr9	5830454E08Rik	1.21E+08	1.21E+08	727	-0.26242	0.140028	0.495244	0.606374	0.10751	0	10	20	23	24	15	12	22	37	16	20
ENSMUSG00000005907	chr5	Pex1	3596066	3596517	7740	-0.13933	2.741982	0.495605	0.606762	0.041587	0	93	103	145	103	138	90	171	127	189	168
ENSMUSG00000032998	chr4	Foxj3	1.2E+08	1.2E+08	10973	-0.11699	5.026277	0.495792	0.606937	0.033392	0	511	449	607	613	651	583	663	948	768	662
ENSMUSG00000066043	chr4	Phactr4	1.32E+08	1.32E+08	4960	-0.1057	4.011832	0.496156	0.60733	0.025566	0	231	245	320	289	307	261	334	376	464	386
ENSMUSG00000036353	chr3	P2ry12	59216271	59218256	2379	0.228162	0.849922	0.496264	0.607377	0.101296	0	28	14	31	16	44	39	55	44	52	23
ENSMUSG00000054312	chr3	Mrps21	95862634	95862932	1282	0.125751	5.883092	0.496282	0.607377	0.039906	0	816	958	1094	897	905	1480	1413	1127	1554	1495
ENSMUSG00000038930	chr7	Rccd1	80316596	80317050	3630	-0.19778	2.270684	0.496775	0.607926	0.085459	0	69	70	115	60	115	75	149	45	133	119
ENSMUSG00000037085	chr15	Trmt12	58872649	58876781	4133	0.151414	2.701277	0.496836	0.607946	0.049798	0	87	97	121	99	101	138	159	99	219	176
ENSMUSG00000026879	chr2	Gsn	35279663	35279718	2977	-0.16232	10.12469	0.497548	0.608764	0.068447	0	25021	11067	20534	15335	26942	17295	18292	33836	22925	30359
ENSMUSG00000074466	chr3	Gm15417	89391850	89392506	1669	-0.13478	4.229419	0.497621	0.6088	0.043527	0	280	344	388	283	326	418	362	443	343	464
ENSMUSG00000103400	chr1	RP24-229G16.1	1.66E+08	1.66E+08	2041	0.252851	-0.03501	0.498028	0.609243	0.087135	0	9	11	10	15	22	9	27	27	32	18
ENSMUSG00000023147	chr16	Wrb	96145407	96145578	4261	-0.15071	3.092303	0.498318	0.609545	0.05263	0	124	142	172	131	174	166	206	100	253	213
ENSMUSG00000098022	chr7	Zfp82	30054489	30057764	6041	0.181936	1.017786	0.498387	0.609575	0.054191	0	22	23	39	31	37	34	52	49	50	54
ENSMUSG00000036256	chr5	Igfbp7	77349240	77349499	1213	0.127695	7.014588	0.498436	0.609582	0.042134	0	1700	1766	2394	2123	2383	2515	3619	1936	4729	3184
ENSMUSG00000028443	chr4	Nudt2	41465151	41465180	845	-0.12291	3.501935	0.498669	0.609813	0.034027	0	168	194	206	205	199	243	247	225	295	236
ENSMUSG00000055239	chr6	Kcmf1	72841114	72843130	3251	-0.15837	7.232579	0.498726	0.609828	0.06515	0	2332	2378	3033	2863	2579	2404	2487	5832	2858	2856
ENSMUSG00000038990	chr2	Cables2	1.8E+08	1.8E+08	4597	-0.11526	3.8378	0.49984	0.611136	0.031107	0	227	217	282	270	231	261	339	261	379	355
ENSMUSG00000032498	chr9	Mlh1	1.11E+08	1.11E+08	4818	-0.13997	2.904628	0.500201	0.611524	0.042739	0	129	98	144	114	166	155	162	138	166	192
ENSMUSG00000037260	chr8	Hgsnat	25944459	25945315	2679	-0.10935	4.643077	0.500577	0.611929	0.029163	0	387	330	515	416	528	375	607	647	595	586
ENSMUSG00000015202	chr10	Cnksr3	7119063	7120586	3837	0.152704	2.248205	0.501203	0.61264	0.050061	0	45	67	87	80	93	85	122	111	168	93
ENSMUSG00000017715	chr11	Pgs1	1.18E+08	1.18E+08	5333	0.108717	4.871377	0.501312	0.61272	0.029158	0	396	463	541	395	551	577	649	647	890	784
ENSMUSG00000022512	chr16	Cldn1	26356642	26359200	3247	-0.2175	2.255312	0.50158	0.612993	0.113304	0	77	88	73	93	84	48	105	176	145	44
ENSMUSG00000026576	chr1	Atp1b1	1.64E+08	1.64E+08	3081	0.165737	6.714744	0.50178	0.613184	0.072045	0	1368	1767	1737	2343	839	2071	2726	2639	3479	2126
ENSMUSG00000070371	chr7	Prss36	1.28E+08	1.28E+08	3221	-0.14829	2.218337	0.501979	0.613372	0.044954	0	62	68	108	70	97	77	96	86	135	116
ENSMUSG00000016344	chr2	Ppdpf	1.81E+08	1.81E+08	1336	0.118653	4.828581	0.502254	0.613635	0.035344	0	371	435	576	441	441	652	673	520	860	723
ENSMUSG00000030269	chr6	Mtmr14	1.13E+08	1.13E+08	2874	0.198436	4.339347	0.502283	0.613635	0.100874	0	306	273	346	336	292	296	316	1095	436	363
ENSMUSG00000022545	chr16	Ercc4	13109684	13110141	6730	0.139949	2.887867	0.502339	0.61365	0.044415	0	66	115	132	116	159	120	174	189	221	199
ENSMUSG00000027905	chr3	Ddx20	1.06E+08	1.06E+08	4142	0.130557	3.381593	0.502415	0.613688	0.038856	0	161	152	181	145	180	197	220	335	285	221
ENSMUSG00000025494	chr7	Sigirr	1.41E+08	1.41E+08	1990	0.203458	1.324958	0.502778	0.614078	0.074669	0	35	40	46	35	28	33	58	58	68	87
ENSMUSG00000029346	chr5	Srrd	1.12E+08	1.12E+08	1638	0.183509	1.941724	0.503291	0.614649	0.066242	0	40	74	55	63	57	72	84	70	129	114
ENSMUSG00000022881	chr16	Rfc4	23113943	23114107	1534	-0.15244	2.573601	0.503385	0.61471	0.051908	0	90	114	122	80	106	112	108	102	180	150
ENSMUSG00000028484	chr4	Psip1	83455680	83457079	5082	-0.11467	4.513818	0.503583	0.614897	0.032753	0	359	332	477	318	505	345	574	577	664	422
ENSMUSG00000009281	chr6	Rarres2	48569698	48569805	708	0.140886	4.555442	0.503971	0.615198	0.050922	0	365	274	336	298	612	468	405	651	584	744
ENSMUSG00000030401	chr7	Rtn2	19282662	19282865	2034	-0.12304	9.644996	0.503927	0.615198	0.040522	0	12212	12185	15282	13624	16582	18186	15209	21226	16588	16282
ENSMUSG00000032440	chr9	Tgfbr2	1.16E+08	1.16E+08	4785	-0.1155	6.02403	0.504007	0.615198	0.034841	0	949	861	1081	1127	1709	1032	1690	1512	1802	1312
ENSMUSG00000054499	chr7	Dedd2	25202840	25203931	1828	0.199246	2.808265	0.504004	0.615198	0.095595	0	99	95	97	137	103	75	142	329	175	151
ENSMUSG00000005043	chr11	Sgsh	1.19E+08	1.19E+08	4414	0.151804	2.924579	0.504189	0.615325	0.054609	0	103	65	162	118	157	128	191	131	248	236
ENSMUSG00000022962	chr16	Gart	91621186	91621748	3992	-0.10924	5.581568	0.504226	0.615325	0.030764	0	694	741	934	795	996	878	886	1308	1287	1009
ENSMUSG00000057409	chr17	Zfp53	21491256	21491316	2058	-0.19074	1.277927	0.504285	0.615325	0.074557	0	43	26	62	37	41	25	48	64	65	57

ENSMUSG00000060739	chr13	Nsa2	97129427	97131228	2686	0.10493	5.479037	0.504288	0.615325	0.028179	0	599	639	840	738	770	800	1067	1253	1275	1012
ENSMUSG00000026773	chr2	Pfkfb3	11471433	11474543	7561	-0.21925	6.969736	0.504377	0.615379	0.128038	0	985	2354	2171	2863	3035	1352	1370	3829	1998	5029
ENSMUSG00000029326	chr5	Enoph1	1E+08	1E+08	1826	0.141625	2.860578	0.504535	0.615518	0.04527	0	89	119	128	104	128	171	170	127	227	179
ENSMUSG00000015971	chr14	Actr8	29978337	29978588	2121	0.132707	4.682284	0.504698	0.615622	0.044867	0	368	382	433	386	463	450	543	968	588	559
ENSMUSG00000054728	chr13	Phactr1	42680623	42680926	9611	-0.16485	1.567163	0.504709	0.615622	0.05472	0	39	39	50	60	68	37	60	68	90	67
ENSMUSG00000078768	chr7	Zfp566	30077337	30078618	1728	-0.20625	0.769501	0.504767	0.615638	0.067426	0	19	23	38	32	34	24	42	46	36	27
ENSMUSG00000041057	chr17	Wdr43	71616215	71616485	3450	0.133678	4.801063	0.504918	0.615676	0.046003	0	368	373	493	420	578	444	596	1077	685	596
ENSMUSG00000048763	chr11	Hoxb3	96323326	96323445	4251	-0.26746	-0.04536	0.5049	0.615676	0.137644	0	20	7	20	17	16	6	18	34	27	10
ENSMUSG00000070605	chr4	Gm13251	1.46E+08	1.46E+08	4550	0.260736	0.095602	0.504977	0.615676	0.105043	0	10	18	7	17	21	23	24	15	24	36
ENSMUSG00000078517	chr4	Emc1	1.39E+08	1.39E+08	6683	0.10521	5.496205	0.504947	0.615676	0.028561	0	658	619	884	688	779	905	1124	1167	1150	1076
ENSMUSG00000021693	chr13	Kif2a	1.07E+08	1.07E+08	7046	-0.11566	3.759432	0.505114	0.61579	0.031645	0	207	163	247	244	322	201	303	342	394	287
ENSMUSG00000032044	chr9	Rpusd4	35267865	35268078	2647	0.123089	3.42619	0.505703	0.61641	0.034937	0	132	179	220	149	170	204	261	271	283	276
ENSMUSG00000037326	chr17	Capn15	25959556	25959733	3520	-0.1563	2.186329	0.505712	0.61641	0.050879	0	70	45	90	79	116	72	94	99	121	110
ENSMUSG00000029718	chr5	Pcolce	1.38E+08	1.38E+08	3823	0.20008	7.269619	0.505942	0.616637	0.107692	0	2378	1226	2574	1445	4797	3820	5092	1651	4751	3821
ENSMUSG00000036452	chr18	Arhgap26	38601534	38601697	17331	0.175706	2.585137	0.506176	0.616856	0.071537	0	69	81	104	98	114	75	115	247	149	151
ENSMUSG00000069089	chr13	Cdk7	1.01E+08	1.01E+08	7595	-0.11094	4.222623	0.506212	0.616856	0.029812	0	290	251	371	305	407	328	458	488	453	355
ENSMUSG00000074811	chr19	Hps6	46003478	46006173	2696	0.147468	2.222042	0.506331	0.616948	0.045879	0	61	66	78	60	99	91	116	90	159	109
ENSMUSG00000021819	chr14	Zswim8	20707552	20708056	6072	-0.11811	5.176274	0.506593	0.617212	0.036273	0	547	459	676	627	867	487	777	1067	987	775
ENSMUSG00000080772	chr4	Gm12543	59833677	59834219	543	0.219249	0.729206	0.506661	0.617241	0.075085	0	26	16	24	24	30	18	36	35	58	53
ENSMUSG00000002679	chr12	Med6	81573557	81573960	1447	0.130275	3.024313	0.507045	0.617492	0.038269	0	117	116	156	127	122	169	206	200	193	204
ENSMUSG00000020397	chr11	Med7	46436925	46437009	2871	0.119758	3.550546	0.507025	0.617492	0.034156	0	152	182	236	170	189	268	277	283	296	272
ENSMUSG00000030869	chr7	Ndufab1	1.22E+08	1.22E+08	6883	0.137867	7.683844	0.507031	0.617492	0.0514	0	2417	3692	4084	3442	2523	5255	5013	4155	5530	4783
ENSMUSG00000053004	chr6	Hrh1	1.14E+08	1.14E+08	4450	-0.23694	-0.05994	0.506917	0.617492	0.096192	0	16	10	8	16	29	12	22	13	26	21
ENSMUSG00000020899	chr11	Pfas	68985697	68988273	7933	-0.1256	3.446108	0.507171	0.617536	0.038132	0	209	134	183	185	230	174	199	236	337	277
ENSMUSG00000037134	chr8	Prmt10	77549397	77549736	5679	0.115469	3.34761	0.507149	0.617536	0.030027	0	126	156	166	169	192	197	229	247	307	248
ENSMUSG00000028412	chr4	Slc44a1	53440413	53440716	6945	-0.10942	5.16751	0.507473	0.61785	0.030944	0	609	421	694	602	811	596	885	850	991	731
ENSMUSG00000003134	chr1	Tbc1d8	39371492	39372786	5239	0.116368	3.618263	0.508041	0.618348	0.032042	0	157	180	195	203	244	223	372	301	312	271
ENSMUSG00000022351	chr15	Sqle	59315077	59316129	5546	0.319745	2.831249	0.507958	0.618348	0.267832	0	42	33	70	76	346	150	158	52	236	317
ENSMUSG00000029209	chr5	Gnpda2	69573108	69573156	6858	-0.14229	2.278595	0.508061	0.618348	0.04222	0	75	75	85	78	105	67	110	118	121	117
ENSMUSG00000086922	chr6	Gm13835	31141979	31142663	685	-0.11709	4.132274	0.508002	0.618348	0.03367	0	253	303	300	314	339	369	382	432	384	359
ENSMUSG00000039461	chr9	Tcta	1.08E+08	1.08E+08	1838	0.180095	5.050687	0.508221	0.618488	0.086415	0	462	486	671	497	457	488	610	1654	722	617
ENSMUSG00000027133	chr2	Nop10	1.12E+08	1.12E+08	1109	0.127072	5.233241	0.50863	0.618932	0.04263	0	563	622	731	480	570	906	846	1020	872	842
ENSMUSG00000036752	chr2	Tubb4b	25222160	25223368	2088	-0.11536	7.776547	0.508794	0.619076	0.036198	0	2545	3494	5114	3296	4900	4341	5028	4562	5550	4959
ENSMUSG00000031595	chr8	Pdgfrl	40926212	40926425	3126	0.194114	4.008992	0.50884	0.619078	0.099485	0	313	108	249	139	466	286	618	315	471	317
ENSMUSG00000097487	chr11	Ptges3l	1.01E+08	1.01E+08	2108	-0.16562	6.524915	0.50898	0.619195	0.074346	0	1195	1718	2179	1269	1793	2489	2284	995	2110	1965
ENSMUSG00000002949	chr8	Timm44	4259731	4260255	3664	-0.12066	6.334641	0.50948	0.619678	0.039389	0	1154	1515	1629	1458	1172	1645	1635	1755	2168	1773
ENSMUSG00000031683	chr8	Lsm6	78804865	78808245	4076	-0.11603	5.580633	0.50944	0.619678	0.035577	0	747	744	1077	686	904	1021	1166	1066	1031	985
ENSMUSG00000087138	chr7	Gm15545	44986900	44987370	1976	0.217542	0.670741	0.509512	0.619678	0.084342	0	22	18	26	23	26	20	30	64	39	35
ENSMUSG00000034007	chr9	Scaper	55549883	55550871	5158	-0.13405	2.891637	0.509671	0.619817	0.041381	0	106	108	119	148	162	112	157	208	184	159
ENSMUSG00000002205	chr7	Vrk3	44748413	44748651	3098	0.111069	4.449786	0.509812	0.619879	0.031014	0	316	330	442	319	332	429	472	577	594	561
ENSMUSG00000070436	chr7	Serpinh1	99345375	99346422	2435	0.20823	8.171664	0.509775	0.619879	0.118853	0	3490	2857	5112	3626	8010	6313	10278	1868	10205	7732
ENSMUSG00000022013	chr14	Dnajc15	77826217	77826470	648	-0.1234	5.403063	0.510122	0.620147	0.040636	0	587	812	850	763	621	904	848	817	1064	1042
ENSMUSG00000045996	chr15	Polr2k	36174010	36174081	624	-0.13216	3.673564	0.510086	0.620147	0.043523	0	203	248	262	185	193	255	253	333	282	272
ENSMUSG00000002416	chr6	Ndufb2	39592574	39592712	5628	-0.13614	7.147206	0.510487	0.620373	0.05081	0	2056	2911	3011	2276	1932	3263	2916	3080	3364	2862
ENSMUSG00000020843	chr11	Timm22	76406952	76407143	3183	-0.12287	5.208728	0.510469	0.620373	0.039998	0	534	658	769	545	700	816	919	582	1020	758
ENSMUSG00000027170	chr2	Eif3m	1.05E+08	1.05E+08	2590	-0.11105	6.324213	0.51043	0.620373	0.033371	0	1150	1368	1699	1236	1484	1457	1750	2106	2013	1638
ENSMUSG00000056679	chrX	Gpr173	1.52E+08	1.52E+08	5109	0.220973	0.144022	0.510462	0.620373	0.065601	0	14	9	17	16	22	14	29	27	28	29
ENSMUSG00000037703	chr2	Lzts3	1.31E+08	1.31E+08	4252	0.16116	2.06285	0.510765	0.620657	0.054195	0	57	45	55	69	99	62	108	109	127	103
ENSMUSG00000024104	chr6	Fam21	1.16E+08	1.16E+08	4294	0.132622	5.146789	0.511155	0.621076	0.046897	0	458	523	650	536	657	491	774	1360	890	832
ENSMUSG00000063200	chr13	Nol7	43398376	43398658	1811	-0.10922	5.530882	0.511397	0.621315	0.031801	0	681	790	954	764	792	947	1013	1085	1127	964
ENSMUSG00000005465	chr8	Il27ra	84030287	84031192	2657	0.279204	0.053439	0.511825	0.621781	0.122346	0	10	13	23	16	8	10	29	12	39	33
ENSMUSG00000039684	chr10	Gm5422	31248140	31251045	2906	0.187929	1.175868	0.512393	0.622416	0.070704	0	32	22	35	48	31	42	53	70	54	48
ENSMUSG00000024914	chr19	Drap1	5422805	5423025	1741	-0.12098	8.151024	0.512703	0.622738	0.040667	0	4092	4781	6017	4662	5148	6568	5230	6546	6121	6655
ENSMUSG00000044716	chr5	Dok7	35056813	35056988	4228	-0.11953	4.522464	0.512784	0.622782	0.037568	0	342	442	421	361	404	430	647	483	592	405
ENSMUSG00000059923	chr11	Grb2	1.16E+08	1.16E+08	2916	0.106901	6.364892	0.512908	0.622878	0.031304	0	1041	1202	1572	1219	1638	1640	2104	1596	2496	2168
ENSMUSG00000045534	chr6	Kcna5	1.27E+08	1.27E+08	2834	-0.16707	3.040958	0.513069	0.623019	0.069395	0	88	95	211	220	114	149	168	146	223	212
ENSMUSG00000028423	chr4	Nfx1	40970906	40971059	8564	-0.10532	5.050349	0.513298	0.623187	0.02942	0	506	495	663	547	657	526	692	915	881	726
ENSMUSG00000063787	chr14	Chchd1	20703027	20703197	587	-0.13759	5.77139	0.513282	0.623187	0.051748	0	782	1083	1244	777	840	1305	1322	1057	1108	1123
ENSMUSG00000016520	chr5	Lnx2	1.47E+08	1.47E+08	4557	-0.14151	2.70471	0.513424	0.623286	0.048594	0	85	100	114	118	151	72	149	138	215	160
ENSMUSG00000026828	chr2	Galnt5	57997884	57999813	4462	0.248594	1.779473	0.513557	0.623393	0.157233	0	47	31	79	20	84	42	167	62	107	52
ENSMUSG00000089875	chr13	Etohd2	59769965	59770133	3136	-0.20643	0.986066	0.514004	0.62388	0.079912	0	22	36	49	28	35	32	28	58	41	45
ENSMUSG00000067567	chrX	Hdac8	1.02E+08	1.02E+08	4839	0.156585	2.144882	0.514107	0.623951	0.053971	0	60	75	84	52	68	95	121	89	118	106
ENSMUSG00000025579	chr11	Gaa	1.19E+08	1.19E+08	4783	-0.13583	7.917386	0.51423	0.624046	0.051637	0	3476	3198	4986	4387	5348	3999	4184	8606	5299	4663
ENSMUSG00000070425	chr7	Trpc2	1.02E+08	1.02E+08	5673	0.154641	2.06784	0.514333	0.624115	0.05472	0	60	56	80	41	89	88	102	86	117	109
ENSMUSG00000035578	chr16	Iqcg	33015385	33017063	3462	-0.19462	1.757612	0.514512	0.624278	0.087943	0	53	58	62	76	40	84	64	54	101	52
ENSMUSG00000024112	chr17	Cacna1h	25374285	25376146	9763	-0.21559	1.902804	0.514597	0.624327	0.110159	0	40	45	89	93	65	36	142	50	89	85

ENSMUSG00000036282	chr14	Naa30	49172226	49172377	6970	-0.1195	4.535564	0.514765	0.624475	0.037831	0	367	357	450	393	439	370	514	729	574	403
ENSMUSG00000020883	chr11	Fbxl20	98082556	98089698	12106	-0.12869	4.40391	0.514909	0.624595	0.044131	0	341	275	410	389	433	258	401	683	502	533
ENSMUSG00000074121	chr7	Ntf5	45413695	45413788	1962	-0.19584	2.561676	0.515194	0.624886	0.095359	0	62	115	116	122	103	144	135	49	157	140
ENSMUSG00000044145	chr2	1810024B03Rik	1.27E+08	1.27E+08	3550	0.188717	0.460615	0.515348	0.625019	0.069032	0	15	11	28	21	26	29	23	37	39	30
ENSMUSG00000038446	chr10	Cdc40	40831626	40833356	3361	-0.11786	3.655115	0.515589	0.625256	0.035042	0	180	172	265	222	258	151	307	322	322	320
ENSMUSG00000002910	chr8	Arrdc2	70835155	70835994	2329	0.348522	4.408476	0.515768	0.625418	0.335466	0	261	216	792	245	51	402	219	1200	175	686
ENSMUSG00000032827	chr6	Ppp1r9a	4902917	4903031	14531	-0.15543	2.319408	0.515824	0.625432	0.053606	0	73	54	80	101	130	81	127	88	126	122
ENSMUSG00000021023	chr12	1110008L16Rik	55299577	55299666	4452	-0.12407	3.140811	0.515998	0.625588	0.038347	0	120	151	175	151	163	124	188	235	264	179
ENSMUSG00000022561	chr15	Gpaa1	76331231	76331463	2846	0.104712	4.870118	0.516048	0.625594	0.029243	0	380	422	539	436	584	614	683	569	877	785
ENSMUSG00000018509	chr11	Cenpv	62524946	62525287	1811	0.123541	3.761738	0.516114	0.625619	0.039353	0	164	216	264	220	210	339	307	306	312	343
ENSMUSG00000006014	chr1	Prg4	1.5E+08	1.5E+08	4280	0.2824	5.331414	0.516308	0.625799	0.223084	0	769	117	497	198	1603	549	1136	1498	1138	890
ENSMUSG00000001227	chr17	Sema6b	56123085	56124917	3977	0.14473	2.906096	0.51666	0.626171	0.051568	0	78	72	144	147	159	115	173	162	243	229
ENSMUSG00000022551	chr15	Cyc1	76343523	76343692	1194	-0.1227	9.064784	0.516771	0.626251	0.042812	0	7301	10437	10076	10447	7677	11238	11428	11097	14765	11010
ENSMUSG00000070002	chr8	Ell	70539675	70539841	3085	0.128058	3.868609	0.517029	0.626509	0.042927	0	205	161	242	238	327	236	296	509	365	367
ENSMUSG00000078580	chr7	E430018J23Rik	1.27E+08	1.27E+08	3334	0.18076	1.273192	0.517221	0.626687	0.062142	0	31	25	37	39	51	32	52	69	86	54
ENSMUSG00000030120	chr6	Mlf2	1.25E+08	1.25E+08	1533	0.102923	7.677364	0.517365	0.626806	0.030032	0	2672	2916	3676	3353	3943	4287	4330	5080	5751	5207
ENSMUSG00000029710	chr5	Ephb4	1.37E+08	1.37E+08	4640	0.109794	4.734237	0.517492	0.626905	0.032174	0	309	354	446	555	478	472	622	707	834	607
ENSMUSG00000074922	chr19	Fam122a	24476502	24477356	855	0.137349	2.819138	0.517621	0.627006	0.044975	0	92	105	136	106	114	140	146	126	238	208
ENSMUSG00000035027	chr10	Map2k2	81105915	81106238	3722	-0.10946	7.23602	0.517847	0.627225	0.033886	0	2034	2459	3027	2650	2924	3289	3334	2842	3871	3421
ENSMUSG00000032571	chr9	Pik3r4	1.06E+08	1.06E+08	9660	-0.10015	3.977197	0.518029	0.62739	0.025196	0	237	212	309	285	318	253	361	352	459	358
ENSMUSG00000020863	chr11	Luc7l3	94287890	94291578	7278	0.103703	5.518039	0.518085	0.627404	0.0295	0	681	674	868	638	816	896	1202	1030	1167	1219
ENSMUSG00000071648	chr19	Rom1	8927382	8927887	1526	0.129462	3.024724	0.518523	0.627879	0.040759	0	113	125	169	98	136	168	171	181	250	212
ENSMUSG00000020412	chr11	Ascc2	4637747	4637822	4964	-0.10288	4.927158	0.518661	0.627991	0.02851	0	411	455	548	553	677	512	778	570	876	710
ENSMUSG00000032062	chr9	2310030G06Rik	50739691	50740749	1242	0.204704	1.093279	0.519338	0.628756	0.085432	0	27	23	51	33	24	30	48	76	60	42
ENSMUSG00000010097	chr19	Nxf1	8757073	8757259	5980	0.105825	6.299772	0.519462	0.628816	0.031629	0	1080	1185	1518	1152	1400	1737	1948	1708	2076	1977
ENSMUSG00000031576	chr8	Kcnu1	25849623	25849850	3659	-0.25296	0.071175	0.519478	0.628816	0.099758	0	13	15	27	14	19	27	9	20	22	22
ENSMUSG00000019806	chr10	Aig1	13647054	13647706	9196	-0.1183	3.777321	0.519823	0.629178	0.035804	0	192	184	284	239	299	236	398	239	414	253
ENSMUSG00000006024	chr7	Napa	16098458	16098774	3786	0.123338	6.920995	0.519916	0.629181	0.043473	0	2010	1502	2143	1708	2327	2022	2560	4257	3231	2719
ENSMUSG00000090386	chr16	Mir99ahg	77236317	77236335	14045	0.191941	1.105696	0.519892	0.629181	0.075472	0	29	32	31	30	37	30	55	46	44	81
ENSMUSG00000024793	chr4	Tnfrsf25	1.52E+08	1.52E+08	2277	0.217181	0.237877	0.52007	0.629257	0.091188	0	11	11	23	12	28	22	30	15	29	39
ENSMUSG00000050966	chr4	Lin28a	1.34E+08	1.34E+08	3996	-0.24827	0.466966	0.520068	0.629257	0.111002	0	10	24	33	14	39	28	18	23	28	39
ENSMUSG00000004895	chr3	Prcc	87858903	87859346	2099	0.111387	5.267812	0.520183	0.629283	0.034461	0	500	523	721	671	684	723	855	1243	991	834
ENSMUSG00000033594	chr8	Spata2l	1.23E+08	1.23E+08	2683	-0.18767	0.756333	0.520182	0.629283	0.066581	0	26	22	20	30	45	27	34	31	42	41
ENSMUSG00000038893	chr11	Fam117a	95337018	95337261	3029	0.142624	2.707388	0.520545	0.629666	0.046676	0	94	77	86	121	134	104	146	169	180	195
ENSMUSG00000023089	chr6	Ndufa5	24518666	24518824	1032	0.132875	7.220414	0.520922	0.629988	0.050868	0	2126	2575	2783	2382	1804	3925	3435	3262	3698	3490
ENSMUSG00000025212	chr19	Sfxn3	45047576	45047890	2966	-0.09979	5.123109	0.520993	0.629988	0.02743	0	591	498	669	572	669	597	717	793	953	878
ENSMUSG00000030035	chr6	Wbp1	83119044	83119720	2079	-0.1034	4.213459	0.520966	0.629988	0.027777	0	258	236	389	363	367	301	433	383	520	460
ENSMUSG00000030528	chr7	Blm	80454993	80455436	4946	0.165528	1.55209	0.520938	0.629988	0.057331	0	37	33	52	38	66	46	64	91	84	67
ENSMUSG00000028687	chr4	Mutyh	1.17E+08	1.17E+08	2612	0.194291	0.915058	0.521304	0.630309	0.066827	0	23	31	31	25	28	35	53	28	61	47
ENSMUSG00000029290	chr5	Zfp326	1.06E+08	1.06E+08	7217	-0.12888	3.08508	0.521368	0.630332	0.041593	0	118	128	175	132	186	108	161	228	234	220
ENSMUSG00000025086	chr19	Trub1	57452906	57453196	6395	-0.1252	3.005449	0.521632	0.630595	0.03718	0	127	125	160	109	173	142	175	185	184	198
ENSMUSG00000086765	chr4	Gm11827	11122805	11122915	1368	0.315023	0.753547	0.521838	0.630754	0.238727	0	23	28	30	21	13	18	18	110	25	33
ENSMUSG00000091471	chr19	Gm20538	44543722	44543812	225	0.123727	7.663799	0.521854	0.630754	0.044384	0	2767	3563	3957	2971	2742	4997	4462	4414	5433	5021
ENSMUSG00000030562	chr7	Nox4	87246096	87246219	8471	0.200508	1.950008	0.521925	0.630785	0.097774	0	60	56	55	62	55	43	117	157	97	61
ENSMUSG00000028016	chr3	Ints12	1.33E+08	1.33E+08	7257	0.11351	3.351437	0.522109	0.630952	0.031344	0	150	139	177	141	207	179	252	280	296	226
ENSMUSG00000033707	chr15	Lrrc24	76715276	76716306	3912	-0.10498	4.730978	0.522751	0.631673	0.030053	0	366	439	491	490	502	501	483	644	700	645
ENSMUSG00000029815	chr6	Malsu1	49073795	49074103	3079	-0.12615	4.720947	0.523111	0.632052	0.044242	0	378	479	525	440	454	512	491	816	531	542
ENSMUSG00000020717	chr11	Pecam1	1.07E+08	1.07E+08	6228	-0.12996	6.481144	0.523637	0.632601	0.049138	0	998	1476	1746	2233	1316	1340	1752	2165	2766	2090
ENSMUSG00000078937	chr15	Cpt1b	89416405	89416979	3372	-0.12646	7.963499	0.523656	0.632601	0.046873	0	3724	4361	4661	4919	3838	4440	4688	7843	5999	4765
ENSMUSG00000029328	chr5	Hnrnpdl	1E+08	1E+08	4818	-0.11112	6.307027	0.523756	0.632666	0.035664	0	1232	1310	1829	1121	1352	1396	1766	1990	1906	1803
ENSMUSG00000023267	chr4	Gabrr2	33062999	33063366	2105	0.370548	2.076265	0.523854	0.632729	0.376495	0	23	86	50	42	101	44	16	326	47	102
ENSMUSG00000038210	chr6	Hoxa11	52242106	52243592	2287	-0.28567	0.24124	0.524259	0.633163	0.162371	0	12	27	21	22	18	40	13	16	13	27
ENSMUSG00000035754	chr10	Wdr18	79960152	79960372	2954	0.097728	4.969065	0.524496	0.633394	0.026292	0	404	439	532	542	615	568	699	783	964	783
ENSMUSG00000043953	chr9	Ccrl2	1.11E+08	1.11E+08	2110	-0.19343	2.626209	0.524707	0.633594	0.099495	0	82	71	131	161	101	76	86	234	113	154
ENSMUSG00000027030	chr2	Stk39	68210445	68211993	4955	0.136873	2.582256	0.524853	0.633659	0.043267	0	80	68	104	94	128	96	147	122	182	182
ENSMUSG00000098374	chr17	Gm28043	29614876	29615078	6521	-0.11171	5.910038	0.524813	0.633659	0.035956	0	840	915	1196	1072	1211	982	1155	1830	1542	1248
ENSMUSG00000021271	chr12	Zfp839	1.11E+08	1.11E+08	3725	0.161868	3.089304	0.525025	0.633812	0.068898	0	108	114	155	142	146	97	185	357	212	198
ENSMUSG00000027932	chr3	Slc27a3	90385239	90385533	2569	0.210405	1.433021	0.525132	0.633851	0.111251	0	39	23	44	17	84	50	68	49	97	65
ENSMUSG00000039960	chr8	Rhou	1.24E+08	1.24E+08	3806	0.224564	4.392062	0.525149	0.633851	0.145389	0	281	264	365	347	356	247	288	1352	391	346
ENSMUSG00000020659	chr12	Cbll1	31484829	31487461	4007	-0.1311	3.279285	0.525368	0.634005	0.045398	0	140	146	165	186	205	125	187	311	263	200
ENSMUSG00000026388	chr1	3110009E18Rik	1.2E+08	1.2E+08	2428	0.222655	0.173077	0.52535	0.634005	0.104242	0	10	18	14	19	18	35	30	17	19	24
ENSMUSG00000097121	chr12	D130020L05Rik	1.01E+08	1.01E+08	2431	0.236351	0.095418	0.525513	0.634124	0.080592	0	15	14	12	21	11	20	24	31	21	25
ENSMUSG00000016503	chr5	Gtf3a	1.47E+08	1.47E+08	2548	0.107071	4.655706	0.525974	0.634625	0.031298	0	333	432	443	382	415	495	553	523	801	686
ENSMUSG00000030846	chr7	Tial1	1.28E+08	1.28E+08	5861	-0.10404	5.267096	0.526242	0.634893	0.030776	0	596	602	760	615	751	634	835	1041	874	935
ENSMUSG00000038416	chr8	Cdc16	13757676	13757854	3103	-0.09745	5.112104	0.526654	0.635335	0.026691	0	552	510	657	533	735	619	847	730	934	772
ENSMUSG00000025856	chr5	Pdgfa	1.39E+08	1.39E+08	3119	0.107346	4.624096	0.527636	0.636464	0.032225	0	358	336	456	435	383	572	608	503	659	602

ENSMUSG00000025728	chr17	Pigq	25926427	25926515	5769	0.107171	5.042812	0.52786	0.636679	0.032506	0	429	458	525	603	636	579	823	612	1063	953
ENSMUSG00000030881	chr7	Arfip2	1.06E+08	1.06E+08	4902	0.126389	3.553891	0.528026	0.636823	0.042393	0	197	126	192	145	280	171	312	278	360	321
ENSMUSG00000039754	chr5	Alkbh4	1.36E+08	1.36E+08	2117	0.141427	2.309701	0.528464	0.637297	0.047834	0	79	63	88	63	93	115	119	95	135	126
ENSMUSG00000028251	chr4	Tstd3	21757382	21758475	1588	-0.13343	4.138436	0.528758	0.637596	0.050497	0	248	367	371	276	246	365	456	269	492	364
ENSMUSG00000048277	chr11	Syngr2	1.18E+08	1.18E+08	1776	0.109478	7.492646	0.529525	0.638465	0.03604	0	2518	2421	3227	3100	3225	3947	3789	5317	4398	4091
ENSMUSG00000035923	chr10	Myf6	1.07E+08	1.07E+08	1248	0.133136	6.026517	0.530184	0.6392	0.05299	0	817	947	1322	1067	1043	1348	1242	2451	1426	1368
ENSMUSG00000042032	chr11	Mat2b	40679314	40680194	5001	-0.10746	5.889378	0.530227	0.6392	0.034209	0	882	1015	1200	993	1008	1014	1233	1643	1510	1259
ENSMUSG00000019792	chr10	Trmt11	30534225	30535244	2359	-0.14983	2.231351	0.530686	0.639698	0.057584	0	86	75	98	60	83	73	134	80	139	90
ENSMUSG00000059743	chr3	Fdps	89093592	89093843	1241	0.137657	4.831218	0.530789	0.639766	0.05588	0	343	328	501	465	664	589	693	349	917	944
ENSMUSG00000036718	chr5	Micall2	1.4E+08	1.4E+08	4147	0.209305	1.278153	0.531109	0.640095	0.104726	0	21	19	41	43	61	31	64	34	103	68
ENSMUSG00000056952	chr6	Tatdn2	1.14E+08	1.14E+08	3548	-0.10326	4.536184	0.531242	0.640201	0.030329	0	332	371	453	404	440	342	467	628	604	583
ENSMUSG00000026197	chr1	Zfand2b	75168646	75168707	1772	0.111728	3.569983	0.531443	0.640387	0.033458	0	146	169	261	161	217	223	264	336	327	279
ENSMUSG00000018604	chr5	Tbx3	1.2E+08	1.2E+08	5365	0.167247	2.405818	0.53157	0.640438	0.069815	0	72	64	72	103	98	55	129	159	209	112
ENSMUSG00000049858	chr10	Suox	1.29E+08	1.29E+08	2349	-0.10042	5.115614	0.531578	0.640438	0.029183	0	474	575	702	589	651	603	708	909	906	777
ENSMUSG00000104011	chr1	RP24-272N10.3	1.64E+08	1.64E+08	540	0.232006	0.643308	0.531716	0.640549	0.100792	0	20	29	15	31	14	29	45	38	48	25
ENSMUSG00000004040	chr11	Stat3	1.01E+08	1.01E+08	9527	0.107949	6.549756	0.532219	0.641099	0.035206	0	1410	1241	1818	1143	1975	2011	2245	1896	2870	2311
ENSMUSG00000002055	chr11	Spag5	78301529	78301710	5624	-0.12423	3.194	0.532434	0.641302	0.041147	0	123	138	221	158	153	178	199	150	272	217
ENSMUSG00000014313	chr15	Cox6c	35925886	35926368	3567	0.131483	8.593277	0.532663	0.641522	0.052998	0	5232	7135	7722	5689	4462	9282	8769	10093	9146	8993
ENSMUSG00000075592	chr14	Nynrin	55854036	55854059	7436	-0.13456	2.782147	0.532844	0.641685	0.048189	0	103	88	113	112	186	84	169	150	203	165
ENSMUSG00000029009	chr4	Mthfr	1.48E+08	1.48E+08	7315	0.111435	3.50791	0.533101	0.641938	0.033724	0	143	137	200	182	257	197	298	269	276	329
ENSMUSG00000035649	chr4	Zcchc7	44755877	44756034	9612	0.117577	3.35047	0.533154	0.641946	0.036251	0	174	127	154	147	206	197	227	253	261	286
ENSMUSG00000049562	chr19	Ap5b1	5568074	5568607	3092	0.189609	1.301651	0.533275	0.642035	0.07884	0	42	22	44	32	45	42	41	55	108	55
ENSMUSG00000028029	chr3	Aimp1	1.33E+08	1.33E+08	1122	-0.11142	6.306457	0.533429	0.642165	0.0375	0	1187	1322	1737	1246	1344	1666	1711	1959	1743	1664
ENSMUSG00000023980	chr17	Taf8	47488050	47489896	2779	0.125269	3.975201	0.533575	0.64227	0.044616	0	222	215	285	253	274	294	317	585	354	338
ENSMUSG00000028955	chr4	Vamp3	1.51E+08	1.51E+08	2889	-0.10092	6.044084	0.533609	0.64227	0.03061	0	956	1021	1338	1150	1239	1243	1534	1187	1906	1583
ENSMUSG00000020092	chr10	Pald1	61319657	61321242	4274	0.105461	4.042042	0.533788	0.642318	0.030296	0	199	225	294	291	319	252	440	338	555	435
ENSMUSG00000022972	chr16	1110004E09Rik	90925809	90926082	1360	-0.10024	4.008902	0.53371	0.642318	0.0274	0	228	279	303	262	308	310	334	365	438	355
ENSMUSG00000024232	chr18	Bambi	3507957	3508285	5040	0.186878	1.696848	0.533788	0.642318	0.087017	0	60	27	56	28	77	48	68	75	102	103
ENSMUSG00000036552	chr17	Ermard	14978864	14978899	6352	0.139166	2.209022	0.533947	0.642454	0.046362	0	62	64	98	58	79	83	121	117	114	118
ENSMUSG00000021285	chr12	Ppp1r13b	1.12E+08	1.12E+08	4658	-0.11567	3.469337	0.534357	0.642863	0.036522	0	145	165	208	239	199	169	211	293	329	244
ENSMUSG00000030801	chr7	Kat8	1.28E+08	1.28E+08	1573	0.120497	3.905979	0.534427	0.642863	0.041018	0	193	236	292	212	259	296	278	499	360	364
ENSMUSG00000053581	chr5	Zfand2a	1.39E+08	1.39E+08	3407	0.157353	4.042373	0.534409	0.642863	0.07276	0	216	221	337	217	314	220	291	762	384	368
ENSMUSG00000024033	chr17	Rsph1	31255019	31255219	1164	-0.19029	1.281177	0.534687	0.643121	0.088728	0	40	36	35	43	54	39	57	21	76	66
ENSMUSG00000029385	chr5	Ccng2	93267257	93267797	5458	0.159563	4.183872	0.535024	0.643469	0.074807	0	304	252	320	289	241	247	402	814	363	400
ENSMUSG00000041303	chr1	Gtf3c3	54396004	54398002	4925	-0.10907	3.65602	0.53516	0.643578	0.032499	0	197	182	239	221	247	195	281	366	318	252
ENSMUSG00000032479	chr9	Map4	1.1E+08	1.1E+08	10576	-0.10671	8.739398	0.535873	0.644379	0.035468	0	6554	5680	8646	8226	8049	7398	8952	12372	10156	9046
ENSMUSG00000049439	chr1	Cyp20a1	60343323	60343457	2286	0.120874	3.237589	0.536004	0.64448	0.039375	0	125	103	191	123	220	169	245	219	313	202
ENSMUSG00000005378	chr5	Wbscr22	1.35E+08	1.35E+08	3386	0.108859	4.180679	0.536277	0.644752	0.03338	0	246	308	339	254	293	396	442	355	553	436
ENSMUSG00000032477	chr9	Cdc25a	1.1E+08	1.1E+08	3625	-0.12083	3.033359	0.536441	0.644894	0.038794	0	127	120	178	118	165	143	142	208	233	184
ENSMUSG00000013997	chr1	Nit1	1.71E+08	1.71E+08	4932	-0.10034	4.595061	0.536842	0.64519	0.029307	0	385	409	486	368	419	469	509	526	647	557
ENSMUSG00000018217	chr11	Pmp22	63128982	63129150	2354	0.108146	6.470894	0.536768	0.64519	0.036057	0	1310	946	1501	1450	2017	1482	2375	2002	3088	1973
ENSMUSG00000025933	chr1	Tmem14a	21218575	21218889	1351	-0.20226	0.388302	0.53692	0.64519	0.075412	0	24	25	20	19	19	18	33	19	30	33
ENSMUSG00000027487	chr2	Cdk5rap1	1.54E+08	1.54E+08	3434	0.136036	3.164399	0.536875	0.64519	0.052331	0	108	119	219	127	139	163	189	305	245	182
ENSMUSG00000039770	chr17	Ypel5	72836704	72836791	2869	0.114431	5.489933	0.536829	0.64519	0.039663	0	658	726	843	679	653	956	1021	1355	1027	1013
ENSMUSG00000062421	chr11	Arf2	1.04E+08	1.04E+08	2998	-0.09477	4.694178	0.537197	0.645467	0.026145	0	371	412	465	466	511	465	594	513	758	601
ENSMUSG00000006958	chr16	Chrd	20733127	20733295	5838	-0.15904	2.544887	0.537513	0.645734	0.067897	0	107	73	126	61	145	83	165	155	131	102
ENSMUSG00000031381	chrX	Piga	1.64E+08	1.64E+08	6379	0.170554	1.515685	0.537492	0.645734	0.067975	0	32	34	56	37	61	35	62	82	110	61
ENSMUSG00000058392	chr17	Rrp1b	32036100	32036604	7702	0.135421	2.854725	0.537595	0.645776	0.047695	0	101	106	113	80	172	135	176	138	242	190
ENSMUSG00000020785	chr11	Camkk1	73019008	73019127	3728	-0.28423	1.213157	0.537773	0.645935	0.220869	0	50	12	35	16	99	38	70	17	64	47
ENSMUSG00000058806	chr10	Col13a1	61838236	61838708	4605	-0.23898	1.872773	0.537844	0.645963	0.153993	0	68	28	73	45	118	49	147	50	108	35
ENSMUSG00000041119	chr17	Pde9a	31386234	31386356	2834	-0.21895	0.669091	0.538043	0.646146	0.100112	0	27	14	25	47	21	19	31	39	35	39
ENSMUSG00000001493	chr11	Meox1	1.02E+08	1.02E+08	2228	0.150905	3.347194	0.53816	0.646231	0.06526	0	186	100	170	133	212	184	391	176	312	185
ENSMUSG00000036564	chr8	Ndrg4	95676980	95677092	4887	0.17765	2.881168	0.538404	0.646468	0.093445	0	118	53	147	59	211	152	210	129	257	159
ENSMUSG00000009681	chr10	Bcr	75060896	75062310	6537	0.145158	2.848862	0.53846	0.646479	0.057457	0	107	57	104	132	173	130	184	138	238	191
ENSMUSG00000004980	chr6	Hnrnpa2b1	51460434	51463254	4086	0.107807	8.979063	0.538603	0.646489	0.036722	0	6521	7821	10018	7517	8741	11068	12679	8767	14794	13643
ENSMUSG00000017286	chr11	Glod4	76120987	76121596	6005	0.094435	4.987083	0.538648	0.646489	0.026387	0	408	470	615	482	591	621	751	705	972	779
ENSMUSG00000029394	chr5	Cdk2ap1	1.24E+08	1.24E+08	1945	-0.10234	5.207623	0.538656	0.646489	0.031373	0	513	568	739	650	731	757	849	638	971	918
ENSMUSG00000031889	chr8	D230025D16Rik	1.05E+08	1.05E+08	4704	0.193776	4.756298	0.538636	0.646489	0.115978	0	354	348	506	437	462	343	404	1566	501	531
ENSMUSG00000015747	chr3	Vps45	95999832	96000151	3991	0.116077	3.648289	0.538767	0.646539	0.038421	0	167	172	261	167	238	285	323	206	358	331
ENSMUSG00000048249	chr17	Crebrf	26715650	26715774	8564	-0.18193	3.816625	0.538791	0.646539	0.100024	0	210	231	273	270	255	156	192	647	227	308
ENSMUSG00000023307	chr19	March5	37207543	37207904	2396	-0.10043	5.9723	0.539062	0.646809	0.031106	0	926	1000	1269	1066	1153	1104	1253	1603	1547	1552
ENSMUSG00000033285	chr3	Wdr3	1E+08	1E+08	5218	0.100511	3.815423	0.539307	0.647046	0.02774	0	178	194	252	249	259	245	363	380	389	319
ENSMUSG00000098794	chr2	Gm28038	30281043	30281136	378	0.19989	2.094052	0.539478	0.647195	0.106895	0	34	94	62	77	51	69	69	156	105	122
ENSMUSG00000048756	chr10	Foxo3	42181841	42186295	7571	0.170244	5.110307	0.539701	0.647407	0.090223	0	571	346	485	531	798	506	728	1687	775	559
ENSMUSG00000024213	chr17	Nudt3	27579382	27580954	2985	-0.10708	7.049259	0.539829	0.647505	0.03606	0	1889	2325	2590	2289	2308	2897	2801	2887	3105	2980
ENSMUSG00000022433	chr15	Csnk1e	79417856	79419187	6406	-0.10849	5.571191	0.540059	0.647725	0.036341	0	659	783	865	845	964	742	1004	1490	1156	953

ENSMUSG00000002129	chr11	Sf3a1	4160350	4160550	6147	0.103212	4.850073	0.540377	0.648005	0.032403	0	355	361	492	467	678	590	805	577	846	660
ENSMUSG00000027340	chr2	Slc23a2	1.32E+08	1.32E+08	7951	-0.10371	3.885596	0.540387	0.648005	0.030943	0	228	190	272	262	330	202	326	315	482	365
ENSMUSG00000065124	chr2	Snora65	32963291	32963420	130	0.173541	0.818248	0.540457	0.648034	0.059802	0	20	26	32	20	33	40	41	36	45	42
ENSMUSG00000031877	chr8	Ces2g	1.05E+08	1.05E+08	2859	-0.22423	1.024092	0.540722	0.648238	0.118925	0	24	14	38	26	81	40	34	37	47	49
ENSMUSG00000035139	chr13	Secisbp2	51651697	51651820	4626	0.12755	3.717477	0.540712	0.648238	0.04738	0	180	168	246	211	243	218	263	505	318	286
ENSMUSG00000031483	chr8	Erlin2	27023799	27023906	3943	0.103703	4.250192	0.540799	0.64825	0.03082	0	273	225	314	349	372	301	500	389	639	502
ENSMUSG00000033065	chr15	Pfkm	98092589	98092665	2957	-0.10977	11.31912	0.540825	0.64825	0.038586	0	39254	41723	51333	45945	41775	56552	47070	61735	60859	56444
ENSMUSG00000033728	chr15	Lrrc14	76710623	76710927	5647	0.104744	3.949704	0.540917	0.648304	0.031742	0	201	206	319	205	320	313	367	293	461	428
ENSMUSG00000057751	chr4	Megf6	1.54E+08	1.54E+08	7877	-0.21039	1.566019	0.541381	0.648804	0.117972	0	27	44	55	60	76	43	105	30	99	40
ENSMUSG00000033595	chr14	Lgi3	70530821	70531270	3180	0.246295	-0.09433	0.541486	0.648874	0.110373	0	10	5	16	12	22	12	33	10	28	24
ENSMUSG00000021951	chr14	N6amt2	57549598	57549879	836	0.115747	4.065565	0.541943	0.649365	0.039488	0	210	269	330	254	269	389	427	269	484	440
ENSMUSG00000053093	chr14	Myh7	54970688	54970810	8586	0.563416	6.140511	0.542313	0.649696	0.971	0	14	1400	10	2094	1179	1323	130	4015	4018	642
ENSMUSG00000097239	chr11	Gm27029	1.01E+08	1.01E+08	2079	-0.12389	6.582676	0.542283	0.649696	0.048702	0	1282	1648	2096	1408	1949	2343	2221	1358	2413	2183
ENSMUSG00000054690	chr3	Emcn	1.37E+08	1.37E+08	5409	-0.12237	4.136971	0.54241	0.649728	0.045294	0	200	286	325	439	270	274	348	361	547	457
ENSMUSG00000086567	chr13	Gm2830	54499705	54500089	385	0.115102	4.575167	0.542434	0.649728	0.040811	0	330	323	522	340	397	621	507	563	534	588
ENSMUSG00000072969	chrX	Armcx5	1.36E+08	1.36E+08	4247	0.252706	2.404882	0.542528	0.649785	0.190084	0	62	61	76	96	104	61	67	357	92	79
ENSMUSG00000027176	chr2	Cstf3	1.05E+08	1.05E+08	5879	0.129462	3.384635	0.542832	0.650092	0.04864	0	113	156	216	137	214	196	308	158	297	309
ENSMUSG00000048776	chr6	Pthlh	1.47E+08	1.47E+08	1603	-0.27432	-0.06739	0.542909	0.650129	0.150467	0	10	15	4	26	24	14	31	14	18	14
ENSMUSG00000029776	chr6	Hibadh	52546228	52547062	2226	-0.11658	7.102051	0.543226	0.650452	0.043646	0	1954	2458	2616	2585	2207	2368	2532	4216	3242	2978
ENSMUSG00000018659	chr11	Pnpo	96937825	96939083	2925	-0.10306	4.061503	0.54362	0.650867	0.031656	0	246	307	322	285	261	275	367	398	445	394
ENSMUSG00000057130	chr18	Txnl4a	80206795	80206901	2185	0.096363	4.462911	0.543682	0.650886	0.027823	0	286	322	426	326	422	478	505	523	579	544
ENSMUSG00000043770	chr4	Gm12481	43664043	43664339	297	0.10527	5.320611	0.544806	0.652175	0.034871	0	483	608	847	636	643	949	942	855	1144	889
ENSMUSG00000029436	chr5	Mmp17	1.3E+08	1.3E+08	4395	-0.19562	0.57307	0.544857	0.65218	0.08163	0	20	17	23	36	29	27	28	20	54	25
ENSMUSG00000035969	chr4	Rusc2	43381979	43382199	7923	-0.11387	4.499338	0.545567	0.652973	0.039982	0	308	303	395	479	487	297	442	691	620	512
ENSMUSG00000089865	chr9	Dyx1c1Ccpg1	72958852	72958997	4383	-0.12644	6.032543	0.545707	0.653084	0.051453	0	1040	914	1242	1256	1250	1032	1348	2352	1359	1172
ENSMUSG00000035011	chr10	Zbtb7a	81135220	81135591	6808	-0.10486	5.041623	0.545924	0.653287	0.034307	0	458	446	569	655	741	501	630	931	931	741
ENSMUSG00000019851	chr10	Perp	18845071	18845406	1901	-0.18083	0.745914	0.546305	0.653686	0.0696	0	21	36	27	30	25	26	30	42	41	35
ENSMUSG00000029125	chr5	Stx18	38038742	38039499	4194	0.10026	3.795759	0.546377	0.653716	0.028289	0	189	215	268	209	228	262	333	324	377	371
ENSMUSG00000025451	chr13	Paip1	1.19E+08	1.19E+08	3456	-0.1012	5.584205	0.546465	0.653766	0.032455	0	693	794	1004	810	828	875	1109	1282	1087	1008
ENSMUSG00000028475	chr4	5430416O09Rik	43730034	43730164	4086	0.210871	1.008802	0.546793	0.654101	0.105277	0	24	26	36	37	24	21	35	84	51	51
ENSMUSG00000024240	chr18	Epc1	6435951	6437307	4475	-0.12465	4.27268	0.547001	0.654293	0.047959	0	310	277	334	328	433	288	389	690	405	373
ENSMUSG00000004565	chr8	Pnpla6	3515384	3515556	4496	0.117886	3.237623	0.547418	0.654736	0.038264	0	144	127	160	166	146	175	230	174	281	281
ENSMUSG00000039768	chr4	Dnajc11	1.52E+08	1.52E+08	10678	0.10756	5.741923	0.54749	0.654765	0.037254	0	610	861	1004	898	930	1239	1314	953	1556	1367
ENSMUSG00000030852	chr7	Tacc2	1.31E+08	1.31E+08	9537	0.214734	9.147442	0.54756	0.654792	0.151693	0	8856	7196	10635	8931	7918	7823	7871	36394	10738	7837
ENSMUSG00000042138	chr9	Msantd2	37489321	37489833	2289	0.164755	1.504728	0.547665	0.654862	0.06752	0	53	26	52	32	53	56	66	58	74	83
ENSMUSG00000027318	chr2	Adam33	1.31E+08	1.31E+08	5394	0.208583	1.990772	0.54794	0.655077	0.12103	0	89	31	60	33	87	54	91	128	75	137
ENSMUSG00000047238	chrX	Mageh1	1.53E+08	1.53E+08	1410	0.135146	2.476428	0.547906	0.655077	0.050718	0	83	64	120	67	105	128	146	110	148	130
ENSMUSG00000002728	chr2	Naa20	1.46E+08	1.46E+08	3705	-0.10202	5.251742	0.548731	0.655965	0.03303	0	540	665	822	583	669	789	819	737	1027	889
ENSMUSG00000087174	chrX	5530601H04Rik	1.05E+08	1.05E+08	9005	0.198296	1.328694	0.54906	0.656302	0.090582	0	39	33	50	31	33	22	64	84	65	71
ENSMUSG00000086610	chr5	Gm15408	1.49E+08	1.49E+08	1379	0.176356	1.291721	0.549112	0.656308	0.073288	0	32	33	50	34	35	68	39	52	69	58
ENSMUSG00000025666	chrX	Tmem47	81070698	81070817	4025	-0.1183	3.38382	0.549286	0.656321	0.040652	0	154	120	170	208	260	155	270	246	307	196
ENSMUSG00000028073	chr3	Pear1	87747890	87750297	6781	0.113177	3.803539	0.549278	0.656321	0.037426	0	196	163	251	272	234	190	304	376	463	385
ENSMUSG00000028975	chr4	Pex14	1.49E+08	1.49E+08	6272	0.09236	4.612463	0.54936	0.656321	0.026231	0	302	340	494	395	455	455	550	606	696	638
ENSMUSG00000031422	chrX	Morf4l2	1.37E+08	1.37E+08	3135	0.101174	7.019505	0.549317	0.656321	0.033778	0	1857	1790	2490	1691	2704	2549	3690	2654	3766	3041
ENSMUSG00000051950	chr5	B3glct	1.5E+08	1.5E+08	4798	0.136546	3.062243	0.549242	0.656321	0.055152	0	119	77	153	116	206	126	204	151	305	247
ENSMUSG00000034245	chr6	Hdac11	91156665	91156847	3849	-0.10985	3.561191	0.549474	0.6564	0.034344	0	188	145	223	201	268	224	312	256	314	208
ENSMUSG00000030706	chr7	Mrpl48	1.01E+08	1.01E+08	6119	0.108155	5.744657	0.549765	0.656691	0.0381	0	687	837	1089	803	888	1263	1400	932	1550	1289
ENSMUSG00000022412	chr15	Mief1	80234080	80234181	5541	-0.10151	4.589241	0.550159	0.657078	0.032175	0	373	382	477	406	428	415	531	690	591	471
ENSMUSG00000032480	chr9	Dhx30	1.1E+08	1.1E+08	3726	-0.0938	4.97428	0.550184	0.657078	0.027354	0	472	452	604	477	721	588	704	725	793	722
ENSMUSG00000028894	chr4	Inpp5b	1.25E+08	1.25E+08	4657	-0.10656	3.609317	0.550604	0.657523	0.033009	0	153	170	255	209	278	188	271	225	366	332
ENSMUSG00000039556	chrX	Ppp1r3f	7557296	7560886	5153	-0.16111	1.467856	0.550754	0.657646	0.066772	0	44	36	60	44	53	36	44	87	67	63
ENSMUSG00000028811	chr4	Yars	1.29E+08	1.29E+08	5943	-0.09449	5.468713	0.551266	0.6582	0.028647	0	624	702	955	695	850	868	1007	903	1139	1056
ENSMUSG00000073131	chrX	Vma21	71815924	71816334	7303	0.093972	5.068099	0.551389	0.65829	0.028211	0	441	439	631	561	653	632	869	904	903	723
ENSMUSG00000030245	chr6	Golt1b	1.42E+08	1.42E+08	2818	0.114836	4.304741	0.551514	0.658383	0.041403	0	279	253	382	279	398	387	548	278	674	526
ENSMUSG00000048833	chr12	Slc39a9	80644215	80644976	5229	-0.09899	4.294864	0.551728	0.658582	0.03029	0	317	231	380	352	423	288	488	401	581	479
ENSMUSG00000038393	chr3	Txnip	96557957	96558485	3031	0.188895	8.930952	0.55178	0.658587	0.120082	0	4589	5490	12909	8677	7267	5022	7243	24183	10403	14455
ENSMUSG00000031819	chr8	Emc8	1.21E+08	1.21E+08	6295	0.102311	4.119313	0.551862	0.658607	0.03171	0	225	247	307	293	325	320	410	319	519	536
ENSMUSG00000038759	chr6	Nup205	35177430	35177659	6406	-0.11871	3.946156	0.551892	0.658607	0.043416	0	208	186	319	256	392	233	372	222	493	429
ENSMUSG00000038861	chr3	Pi4kb	94974731	94975085	3880	0.094021	4.881178	0.552086	0.658782	0.028121	0	429	380	528	415	643	569	689	757	816	710
ENSMUSG00000020022	chr10	Ndufa12	94198955	94199130	1334	-0.1095	7.283392	0.55224	0.658909	0.040253	0	2244	2773	2872	3023	2437	3527	3307	3210	3872	3328
ENSMUSG00000029613	chr5	Eif2ak1	1.44E+08	1.44E+08	5675	-0.09364	5.846223	0.552564	0.659216	0.028698	0	839	842	1109	1029	1153	1062	1190	1438	1533	1264
ENSMUSG00000032942	chr7	Ucp3	1E+08	1E+08	3135	-0.15868	5.886172	0.552593	0.659216	0.084502	0	714	1332	1633	645	846	681	1124	1789	2013	1100
ENSMUSG00000009739	chr15	Pou6f1	1.01E+08	1.01E+08	6987	-0.11775	3.898425	0.55283	0.659371	0.042773	0	267	192	293	251	285	248	279	481	315	328
ENSMUSG00000036995	chr4	Asap3	1.36E+08	1.36E+08	4225	0.147419	2.953509	0.552866	0.659371	0.067985	0	105	69	115	101	234	146	217	131	266	189
ENSMUSG00000044348	chrX	Slc25a53	1.37E+08	1.37E+08	7963	-0.18107	0.571343	0.552852	0.659371	0.060682	0	24	17	29	19	36	19	30	31	38	36
ENSMUSG00000010392	chr11	Gosr1	76726602	76730233	4289	-0.09349	4.53716	0.553448	0.660008	0.027361	0	339	345	487	380	452	360	509	593	601	567

ENSMUSG00000020474	chr11	Polm	5827860	5829115	3658	0.144505	1.965292	0.553624	0.660047	0.056576	0	51	44	58	58	95	57	86	88	125	118
ENSMUSG00000034453	chr10	Polr3b	84622437	84622538	4829	0.094287	4.079776	0.553583	0.660047	0.026463	0	256	215	298	282	309	319	425	354	524	418
ENSMUSG00000073678	chr1	Pgap1	54472994	54480844	16611	-0.14461	2.413468	0.553559	0.660047	0.060513	0	84	59	108	94	120	67	149	82	186	113
ENSMUSG00000025269	chrX	Apex2	1.51E+08	1.51E+08	8744	0.121187	2.845318	0.554117	0.660521	0.040661	0	101	114	104	98	149	144	153	155	223	190
ENSMUSG00000030739	chr7	Myh14	44605803	44606363	7273	0.178997	4.926778	0.554164	0.660521	0.107159	0	358	382	517	605	527	432	457	1669	587	595
ENSMUSG00000086350	chr1	B230369F24Rik	1.78E+08	1.78E+08	2560	-0.20587	0.709104	0.554089	0.660521	0.102962	0	18	39	22	33	24	40	32	21	38	34
ENSMUSG00000030002	chr6	Dusp11	85942268	85947776	7639	-0.09741	5.295921	0.554446	0.660801	0.031046	0	649	543	772	568	873	604	1010	893	962	978
ENSMUSG00000036362	chr3	P2ry13	59207896	59210358	2524	0.239273	0.294361	0.554512	0.660822	0.124777	0	16	15	6	12	38	25	33	20	36	28
ENSMUSG00000003435	chr7	Supt5	28314898	28315270	3509	-0.10354	6.181259	0.554599	0.660868	0.035935	0	1065	996	1389	1306	1565	1136	1463	2201	1855	1541
ENSMUSG00000101556	chr17	Gm28869	15061069	15061182	811	0.193254	0.344154	0.554664	0.660889	0.063175	0	13	19	25	16	18	19	33	24	39	32
ENSMUSG00000020385	chr11	Clk4	51261730	51261793	5797	0.157202	4.53589	0.554807	0.661003	0.081496	0	380	351	400	273	405	337	432	1097	449	517
ENSMUSG00000069206	chr13	Zfp874a	67424549	67426365	5263	-0.158	2.577569	0.554883	0.661037	0.073793	0	87	89	133	106	104	79	105	226	113	125
ENSMUSG00000020774	chr11	Aspa	73304992	73305633	5954	0.184592	2.386149	0.555025	0.661149	0.102254	0	51	103	71	76	97	95	93	62	184	213
ENSMUSG00000036104	chr1	Rab3gap1	1.28E+08	1.28E+08	11718	-0.10065	5.166136	0.555315	0.661438	0.033298	0	570	543	688	597	695	585	733	1080	902	744
ENSMUSG00000031960	chr8	Aars	1.11E+08	1.11E+08	9282	-0.09484	6.687485	0.555503	0.661547	0.030354	0	1381	1494	2094	1806	2198	1888	2106	2637	2677	2309
ENSMUSG00000046658	chr5	Zfp316	1.43E+08	1.43E+08	6891	0.119411	2.732573	0.555472	0.661547	0.041021	0	94	73	107	114	141	114	153	190	188	155
ENSMUSG00000044442	chr16	N6amt1	87354185	87354386	6135	-0.10912	3.242057	0.555631	0.661643	0.035007	0	152	146	194	163	153	156	180	233	274	218
ENSMUSG00000021969	chr14	Zdhhc20	57832702	57836646	5173	0.114903	3.587604	0.555898	0.661904	0.040289	0	151	137	222	181	284	153	317	319	409	285
ENSMUSG00000037243	chr11	Zfp692	58307069	58307256	1963	0.144575	2.237382	0.556224	0.662235	0.057083	0	64	59	93	63	90	70	140	79	134	150
ENSMUSG00000032324	chr9	Tspan3	56135885	56136735	1728	-0.0937	7.144209	0.556477	0.662423	0.029998	0	2183	2136	2800	2230	2872	2630	3515	3186	3757	2876
ENSMUSG00000074215	chr8	Gm10643	84063561	84065137	1577	-0.1871	0.733539	0.556474	0.662423	0.088409	0	18	37	30	32	21	27	38	40	26	39
ENSMUSG00000021255	chr12	Esrrb	86361117	86361538	6047	-0.21187	1.627019	0.556601	0.662514	0.129517	0	27	48	42	113	37	60	52	77	79	55
ENSMUSG00000044231	chr13	Nhlrc1	47012558	47014850	2293	-0.12589	2.618526	0.556918	0.662834	0.042923	0	77	81	123	112	142	131	123	124	154	138
ENSMUSG00000000088	chr9	Cox5a	57521232	57521415	690	0.116366	9.036184	0.557063	0.662949	0.046921	0	6625	9389	9233	9213	7028	13524	11838	11578	13700	11937
ENSMUSG00000031353	chrX	Rbbp7	1.63E+08	1.63E+08	2909	0.09913	6.861225	0.557341	0.663166	0.033656	0	1578	1820	2137	1783	2032	2245	2637	3443	3113	2557
ENSMUSG00000042851	chr2	Zc3h6	1.29E+08	1.29E+08	5668	-0.28354	1.857471	0.557301	0.663166	0.259696	0	80	63	61	68	43	22	27	215	62	51
ENSMUSG00000090110	chrX	Mtcp1	75404846	75405218	1310	-0.14699	1.819326	0.557633	0.663456	0.054759	0	53	56	75	52	66	67	68	96	87	61
ENSMUSG00000020758	chr11	Itgb4	1.16E+08	1.16E+08	7015	-0.15101	2.509167	0.557939	0.663763	0.071844	0	80	69	85	153	106	67	122	154	192	101
ENSMUSG00000021368	chr13	Tbc1d7	43151744	43151980	1259	0.103296	3.971744	0.558008	0.663788	0.033697	0	199	242	283	251	281	385	364	293	456	369
ENSMUSG00000014329	chr10	Bicc1	70922832	70925378	7441	0.118689	4.715226	0.558443	0.664249	0.047385	0	387	230	486	356	693	425	757	711	776	544
ENSMUSG00000018548	chr11	Trim37	87127077	87127494	7214	-0.12327	2.948889	0.55883	0.664567	0.046722	0	128	95	168	101	181	98	179	198	205	185
ENSMUSG00000050503	chr9	Fbxl22	66508459	66512018	3935	0.265546	4.512753	0.558843	0.664567	0.242508	0	142	244	366	255	820	801	853	75	615	449
ENSMUSG00000078440	chr10	Dohh	81384428	81384578	3202	0.093703	5.15164	0.558855	0.664567	0.02905	0	459	567	686	549	600	744	784	828	1025	883
ENSMUSG00000003849	chr8	Nqo1	1.07E+08	1.07E+08	1553	-0.18142	3.04676	0.558942	0.664613	0.106758	0	118	166	167	140	126	150	96	340	126	164
ENSMUSG00000020471	chr11	Pold2	5872180	5872418	1896	-0.11873	4.66333	0.559243	0.664915	0.046983	0	360	374	497	466	509	378	428	902	592	532
ENSMUSG00000028960	chr4	Ube4b	1.49E+08	1.49E+08	7078	0.107739	5.422372	0.559529	0.665198	0.039473	0	586	535	775	658	927	688	886	1498	1178	963
ENSMUSG00000001053	chr11	N4bp3	51643063	51644148	2728	-0.16192	2.671525	0.559649	0.665226	0.08633	0	81	138	114	138	71	73	169	97	223	153
ENSMUSG00000035109	chr2	Shc4	1.26E+08	1.26E+08	8263	-0.1936	0.678843	0.559616	0.665226	0.075201	0	16	17	30	35	39	25	41	26	48	26
ENSMUSG00000066900	chr5	Suds3	1.17E+08	1.17E+08	2418	-0.09433	5.898988	0.559857	0.665361	0.030381	0	871	982	1195	1034	1039	1156	1343	1214	1571	1431
ENSMUSG00000074643	chr2	Cpne1	1.56E+08	1.56E+08	4507	-0.10158	4.329957	0.559858	0.665361	0.033976	0	338	270	370	302	462	264	419	458	646	520
ENSMUSG00000002109	chr2	Ddb2	91211572	91212012	2736	0.153926	1.623232	0.560109	0.665601	0.060208	0	41	44	53	40	58	47	61	105	80	75
ENSMUSG00000030532	chr7	Hddc3	80343137	80343249	860	0.152218	2.139809	0.560208	0.665622	0.067539	0	56	69	72	58	86	108	108	57	126	126
ENSMUSG00000036882	chr7	Arhgap33	30522226	30523846	4280	0.21384	0.403315	0.560222	0.665622	0.107791	0	22	10	15	15	33	11	42	27	45	32
ENSMUSG00000027428	chr2	Rbbp9	1.45E+08	1.45E+08	2362	-0.12033	3.108865	0.560993	0.666458	0.042723	0	140	90	181	143	200	118	199	181	244	228
ENSMUSG00000032194	chr9	Kank2	21766773	21769004	4853	-0.09889	5.4146	0.561112	0.666458	0.03307	0	625	510	750	768	1084	717	1132	843	1152	985
ENSMUSG00000043962	chr4	Thrap3	1.26E+08	1.26E+08	9234	-0.11136	5.976781	0.561119	0.666458	0.043026	0	1015	799	1201	1085	1401	867	1257	2071	1614	1316
ENSMUSG00000052033	chr2	Pfdn4	1.7E+08	1.7E+08	2520	0.116211	3.247256	0.561068	0.666458	0.040806	0	124	157	208	114	149	199	232	213	262	231
ENSMUSG00000038227	chr6	Hoxa9	52223100	52224482	5580	-0.11841	3.369903	0.561387	0.66672	0.042463	0	164	137	212	149	238	179	231	302	199	226
ENSMUSG00000042709	chr11	Atpaf2	60400626	60401538	2137	0.105557	4.738083	0.561838	0.667198	0.03704	0	345	427	473	455	429	555	524	492	873	790
ENSMUSG00000019590	chr11	Cyb561	1.06E+08	1.06E+08	3653	0.120192	3.094937	0.562145	0.667447	0.0425	0	122	121	171	132	128	161	192	151	301	235
ENSMUSG00000022414	chr15	Tab1	80133154	80133188	2931	-0.08938	4.392172	0.562125	0.667447	0.025904	0	293	316	396	382	420	327	467	477	585	533
ENSMUSG00000074794	chr13	Arrdc3	80883384	80883929	6259	0.215589	5.118943	0.562358	0.667586	0.162785	0	536	338	680	584	553	405	536	2296	556	530
ENSMUSG00000078681	chr7	Tm2d3	65691169	65691290	1489	-0.09993	4.255376	0.562327	0.667586	0.032355	0	277	339	416	271	334	381	428	390	482	450
ENSMUSG00000001100	chr11	Poldip2	78512193	78512472	3783	-0.10075	6.904783	0.562896	0.668117	0.035838	0	1665	1979	2311	2244	2123	2194	2315	3365	3076	2512
ENSMUSG00000023932	chr17	Cdc5l	45391892	45392304	2989	0.092699	5.549492	0.56295	0.668117	0.029601	0	564	733	903	711	886	998	1129	981	1341	1167
ENSMUSG00000027833	chr3	Shox2	66971727	66973907	3311	-0.15709	2.203641	0.562949	0.668117	0.072958	0	74	54	97	50	131	56	124	76	136	117
ENSMUSG00000084289	chrX	Gm6977	90744546	90744992	512	0.145235	1.783331	0.563258	0.668425	0.055652	0	47	53	56	55	52	72	60	84	93	99
ENSMUSG00000050234	chr4	Gja4	1.27E+08	1.27E+08	1685	0.10955	3.349716	0.563356	0.668485	0.037161	0	114	144	176	198	183	213	203	214	319	277
ENSMUSG00000031578	chr8	Mak16	31159468	31160577	1857	0.095331	3.855845	0.563608	0.668611	0.028762	0	158	223	273	231	286	276	372	343	419	329
ENSMUSG00000037013	chr18	Ss18	14624198	14627311	4523	0.091081	4.325072	0.563515	0.668611	0.026759	0	273	294	344	280	432	361	521	478	556	495
ENSMUSG00000057614	chr5	Gnai1	18265135	18267209	3193	-0.19333	2.530262	0.563601	0.668611	0.126362	0	113	50	105	97	148	46	77	96	183	241
ENSMUSG00000033157	chr16	Abhd10	45729725	45731959	3710	-0.10717	3.304231	0.563702	0.668665	0.034818	0	119	176	187	167	201	187	222	181	280	233
ENSMUSG00000053684	chr10	BC048403	1.22E+08	1.22E+08	3136	0.180222	1.025427	0.564368	0.669398	0.074785	0	31	34	29	19	37	24	55	45	68	53
ENSMUSG00000032398	chr9	Snapc5	64179297	64179420	757	-0.10478	4.454985	0.56467	0.669699	0.036815	0	320	368	472	390	328	448	498	387	541	567
ENSMUSG00000016252	chr2	Atp5e	1.74E+08	1.74E+08	1756	0.118346	8.340881	0.564854	0.669783	0.050421	0	4443	5979	6461	4422	4280	8360	7603	7576	7867	7144
ENSMUSG00000037296	chr8	Lsm1	25785591	25785717	2360	0.105956	3.30159	0.56487	0.669783	0.033321	0	141	164	173	140	161	200	231	236	270	241

ENSMUSG00000097882	chr8	0610038B21Rik	77517056	77518579	3071	-0.21063	0.525574	0.564886	0.669783	0.117828	0	22	19	19	29	32	18	18	59	30	21
ENSMUSG00000081128	chr2	Gm13328	20235045	20236064	1020	0.260917	-0.14129	0.565453	0.670398	0.108857	0	15	12	12	12	9	19	9	14	31	30
ENSMUSG00000033487	chr14	Fndc3a	72537946	72540481	9944	-0.11878	3.522966	0.565701	0.670635	0.045787	0	187	115	205	198	305	142	251	294	337	278
ENSMUSG00000024962	chr19	Vegfb	6982473	6982867	1605	-0.11612	6.052133	0.566092	0.670983	0.048281	0	916	1204	1080	1552	910	1262	1233	1374	2048	1550
ENSMUSG00000048076	chr11	Arf1	59211412	59212695	2089	0.088496	7.799427	0.566075	0.670983	0.028241	0	3138	3170	4107	3472	4186	4220	5170	5644	6286	5523
ENSMUSG00000007610	chr8	Gtpbp3	71488103	71488840	3984	0.104931	3.209872	0.566575	0.671393	0.031778	0	141	132	172	125	166	159	218	226	281	233
ENSMUSG00000019857	chr10	Asf1a	53596961	53597298	2180	-0.10753	3.344005	0.566576	0.671393	0.0362	0	146	175	210	166	171	182	221	274	249	202
ENSMUSG00000022681	chr16	Ntan1	13819251	13819436	2174	0.097717	4.464309	0.566583	0.671393	0.031708	0	319	341	449	338	314	450	499	542	615	540
ENSMUSG00000048967	chr8	Yjefn3	69887788	69888022	808	0.147734	1.963678	0.567172	0.672033	0.065469	0	57	48	61	72	62	100	97	57	110	97
ENSMUSG00000073775	chr4	Kti12	1.09E+08	1.09E+08	1629	0.09408	4.42139	0.567703	0.672604	0.030032	0	252	313	453	350	366	463	511	498	602	485
ENSMUSG00000044433	chr8	Camsap3	3587450	3587959	4295	0.216737	0.171269	0.567777	0.672635	0.100834	0	12	7	18	13	31	11	25	23	36	36
ENSMUSG00000014158	chr5	Trpv4	1.15E+08	1.15E+08	4076	0.151078	1.351816	0.56783	0.67264	0.055355	0	34	29	38	36	59	46	63	51	69	73
ENSMUSG00000021716	chr13	Srek1ip1	1.05E+08	1.05E+08	3254	-0.10679	3.789918	0.567921	0.672654	0.037617	0	205	224	273	254	228	267	350	207	377	345
ENSMUSG00000024050	chr17	Wiz	32354055	32355183	9204	0.095354	4.205847	0.567939	0.672654	0.029762	0	261	248	310	292	379	301	389	542	569	437
ENSMUSG00000032757	chr6	Bet1	4076899	4078036	3656	-0.09319	4.277463	0.568008	0.672679	0.028779	0	319	312	373	280	374	371	444	456	476	423
ENSMUSG00000014767	chr17	Tbp	15499888	15500024	13399	0.121469	2.805594	0.568208	0.6728	0.043202	0	113	95	116	95	131	108	165	214	195	163
ENSMUSG00000039910	chr10	Cited2	17723228	17723459	1968	-0.13428	5.409735	0.568204	0.6728	0.064823	0	583	548	554	1093	949	594	743	1427	1263	764
ENSMUSG00000003068	chr10	Stk11	80115803	80116907	4580	0.100201	6.376774	0.568683	0.673304	0.036261	0	1137	1245	1551	1337	1412	1539	1751	2646	2100	1963
ENSMUSG00000032523	chr9	Hhatl	1.22E+08	1.22E+08	1911	-0.09889	7.229298	0.568853	0.673449	0.035554	0	2011	1975	2833	2670	3682	3185	2902	3502	3707	3434
ENSMUSG00000033102	chr13	Cdc14b	64192545	64196675	6083	-0.17558	2.666656	0.569019	0.673587	0.100447	0	117	64	139	93	149	80	92	268	135	113
ENSMUSG00000020669	chr12	Sh3yl1	30911668	30912227	2555	0.245194	-0.12382	0.569238	0.673674	0.11222	0	3	14	19	11	16	8	27	17	26	27
ENSMUSG00000041765	chr14	Ubac2	1.22E+08	1.22E+08	2153	-0.09118	4.805067	0.569165	0.673674	0.028654	0	402	471	518	496	503	538	601	661	754	591
ENSMUSG00000050608	chr4	Minos1	1.39E+08	1.39E+08	2766	0.120707	6.856408	0.569232	0.673674	0.053283	0	1623	2056	2291	1678	1481	3085	2928	2117	2947	2714
ENSMUSG00000025377	chr11	Enthd2	1.2E+08	1.2E+08	3329	0.116921	2.92992	0.569613	0.67406	0.040855	0	126	86	145	117	129	150	191	142	236	199
ENSMUSG00000085151	chr2	1110018N20Rik	1.67E+08	1.67E+08	1579	-0.17119	1.489565	0.569916	0.674361	0.079107	0	23	56	58	48	57	53	59	37	84	67
ENSMUSG00000098530	chr12	Gm28051	1.03E+08	1.03E+08	445	-0.16108	1.199421	0.570058	0.674471	0.064524	0	25	41	51	38	40	43	56	33	59	52
ENSMUSG00000021189	chr12	Atxn3	1.02E+08	1.02E+08	5407	0.114052	3.144204	0.570449	0.674876	0.04001	0	141	111	153	136	160	118	202	223	295	246
ENSMUSG00000052915	chr11	Msl1	98795516	98796604	5433	-0.08866	6.291669	0.57059	0.674928	0.02844	0	1128	1078	1482	1455	1641	1448	1698	1780	2041	1884
ENSMUSG00000079363	chr5	Gbp4	1.05E+08	1.05E+08	4538	0.145216	2.133706	0.570571	0.674928	0.065119	0	57	57	82	85	58	110	90	88	98	130
ENSMUSG00000028439	chr4	Fam219a	41517691	41520395	3724	0.144548	5.151765	0.570669	0.674963	0.075805	0	486	438	595	642	665	491	666	1701	824	676
ENSMUSG00000020283	chr11	Pex13	23646479	23649590	4644	0.09417	4.427869	0.570849	0.675119	0.029928	0	278	328	376	379	367	394	433	595	612	557
ENSMUSG00000019295	chr5	Tmem129	33653216	33654614	2740	-0.10028	3.787287	0.570903	0.675125	0.033417	0	232	184	267	223	283	207	301	399	376	276
ENSMUSG00000028188	chr3	Spata1	1.46E+08	1.46E+08	4114	-0.18008	1.074358	0.571176	0.67539	0.079638	0	21	33	44	44	38	38	46	63	40	31
ENSMUSG00000040170	chr1	Fmo2	1.63E+08	1.63E+08	5609	0.233797	3.258571	0.571339	0.675524	0.193995	0	123	129	172	185	111	72	99	630	211	198
ENSMUSG00000039137	chr4	Whrn	63414910	63415666	7337	-0.18468	1.165372	0.571414	0.675556	0.094926	0	27	23	33	56	55	39	53	29	82	36
ENSMUSG00000078765	chr7	U2af1l4	30563301	30563349	3804	0.106048	4.663684	0.571519	0.675622	0.039428	0	376	401	465	387	383	593	639	422	689	685
ENSMUSG00000059022	chr6	Kcp	29473162	29473780	7806	0.12148	2.683983	0.571621	0.675685	0.046562	0	100	59	98	115	139	121	167	150	179	154
ENSMUSG00000041229	chrX	Phf8	1.52E+08	1.52E+08	9318	0.103459	3.738419	0.572077	0.676142	0.035675	0	190	163	220	192	315	207	305	384	348	369
ENSMUSG00000053553	chr5	3110082I17Rik	1.39E+08	1.39E+08	1429	0.128725	2.424422	0.572105	0.676142	0.049569	0	72	70	86	70	127	96	140	93	177	144
ENSMUSG00000031604	chr8	Msmo1	64718139	64719181	6144	0.167354	3.223885	0.572267	0.676275	0.101306	0	86	80	143	153	297	209	200	105	305	325
ENSMUSG00000037419	chr9	Endod1	14353990	14357887	4470	0.135455	3.2833	0.572424	0.676403	0.061476	0	140	120	133	170	207	184	294	117	367	236
ENSMUSG00000048696	chr10	Mex3d	80380355	80382621	3266	0.127087	2.568831	0.572493	0.676427	0.051028	0	68	62	98	106	141	83	158	163	181	137
ENSMUSG00000032425	chr9	Zfp949	88548020	88548508	4110	-0.16987	3.059836	0.572761	0.676686	0.099444	0	121	111	198	167	136	99	139	364	131	170
ENSMUSG00000031527	chr8	Eri1	35465265	35469370	5067	0.111763	3.343481	0.573363	0.67734	0.039512	0	138	152	194	154	168	176	263	169	369	264
ENSMUSG00000019975	chr10	Ikbip	91082940	91083296	4894	0.132041	3.975753	0.573439	0.677372	0.061914	0	278	169	292	158	362	327	491	216	499	384
ENSMUSG00000027357	chr2	Crls1	1.33E+08	1.33E+08	2082	-0.09589	4.070219	0.574053	0.678003	0.030861	0	237	251	339	296	324	314	360	321	401	484
ENSMUSG00000032377	chr9	Plscr4	92457373	92457925	3590	-0.14447	2.457544	0.574071	0.678003	0.069512	0	100	75	96	88	114	62	97	195	138	115
ENSMUSG00000037552	chr7	Plekhg2	28359604	28361261	6797	0.119246	3.437368	0.574144	0.678031	0.047064	0	156	115	174	200	222	139	354	225	370	250
ENSMUSG00000044502	chr11	Bod1	31665181	31665867	1644	-0.0983	6.856613	0.574336	0.6782	0.036108	0	1755	1931	2335	1823	2126	2460	2472	2917	2591	2427
ENSMUSG00000024858	chr19	Adrbk1	4286001	4287264	4476	0.087733	6.06523	0.574716	0.67859	0.028326	0	906	970	1169	1129	1249	1239	1548	1487	1990	1827
ENSMUSG00000034522	chr14	Zfp395	65358676	65358755	4229	-0.11283	4.234662	0.574984	0.678849	0.044806	0	257	230	340	361	465	258	338	597	443	480
ENSMUSG00000021318	chr13	Gli3	15463235	15463408	9589	0.156656	2.00723	0.575222	0.679072	0.077495	0	65	32	63	46	110	70	128	84	115	88
ENSMUSG00000012296	chr17	Tjap1	46257851	46259483	2595	0.103082	4.735896	0.575527	0.679375	0.038174	0	418	324	469	431	501	448	633	908	686	540
ENSMUSG00000048445	chr11	Ccdc57	1.21E+08	1.21E+08	3743	0.152181	1.894469	0.575764	0.679596	0.068036	0	46	50	66	60	65	54	57	131	115	93
ENSMUSG00000019278	chr8	Dpep1	1.23E+08	1.23E+08	2241	0.17138	5.033498	0.576022	0.679842	0.11014	0	587	306	557	460	671	490	587	1738	527	652
ENSMUSG00000033021	chr1	Gmppa	75435930	75436011	2395	-0.08708	4.977242	0.576099	0.679876	0.027093	0	493	444	614	489	678	571	660	660	880	799
ENSMUSG00000101013	chr5	A630072M18Rik	20950989	20956398	5410	0.147265	1.484224	0.576246	0.679991	0.064035	0	34	37	57	32	56	60	54	86	71	57
ENSMUSG00000033909	chr11	Usp36	1.18E+08	1.18E+08	7689	-0.09157	4.348297	0.576617	0.680371	0.029057	0	315	269	380	334	465	326	439	547	510	479
ENSMUSG00000061374	chr7	Fiz1	5007057	5009205	2834	0.105175	4.162408	0.576789	0.680516	0.038903	0	249	226	320	306	340	293	357	621	526	374
ENSMUSG00000022203	chr14	Efs	54916543	54917532	3571	0.152669	2.848544	0.576845	0.680524	0.080657	0	119	58	92	87	219	112	210	133	231	201
ENSMUSG00000007379	chr3	Dennd2c	1.03E+08	1.03E+08	6858	0.134803	2.944587	0.57706	0.680719	0.061918	0	88	84	158	125	162	102	212	280	192	150
ENSMUSG00000021737	chr14	Psmd6	14112184	14112386	2326	-0.10522	7.08196	0.577257	0.680894	0.042159	0	1773	2301	2974	2159	2553	2644	2746	4023	2909	2719
ENSMUSG00000059173	chr2	Pde1a	79834453	79836924	6012	-0.17702	1.656758	0.577424	0.681033	0.099266	0	51	30	56	67	70	23	49	86	102	87
ENSMUSG00000022114	chr14	Spry2	1.06E+08	1.06E+08	2085	0.096784	3.738567	0.577518	0.681044	0.03188	0	190	150	206	223	314	243	328	313	419	309
ENSMUSG00000029228	chr5	Lnx1	74592446	74592973	3988	-0.15612	1.420955	0.577532	0.681044	0.071781	0	35	35	63	60	35	35	51	53	76	75
ENSMUSG00000055653	chrX	Gpc3	52272426	52272954	2690	0.140281	4.551616	0.577654	0.68113	0.074096	0	309	192	281	312	838	443	600	585	654	581

ENSMUSG00000022684	chr16	Bfar	13671858	13672078	4451	-0.09262	5.82334	0.577752	0.681187	0.032085	0	917	834	1114	904	1105	1013	1191	1579	1396	1194
ENSMUSG00000035890	chr10	Rnf126	79758515	79759236	1639	0.088959	4.510196	0.577898	0.681301	0.027964	0	303	322	412	396	407	453	473	616	658	530
ENSMUSG00000022956	chr16	Atp5o	91684398	91684480	2259	0.09966	8.968776	0.578015	0.681362	0.038341	0	6222	8512	8642	9025	7660	11812	11128	11586	13638	11648
ENSMUSG00000040234	chr6	Tm7sf3	1.47E+08	1.47E+08	3438	0.113503	4.18075	0.578097	0.681362	0.046709	0	294	184	332	210	453	343	459	318	635	462
ENSMUSG00000044469	chr17	Tnfaip8l1	56162477	56162606	2379	-0.15374	1.43359	0.57805	0.681362	0.070129	0	33	39	61	58	39	47	53	38	81	72
ENSMUSG00000022179	chr14	4931414P19Rik	54583663	54584706	2585	0.145919	1.569145	0.578302	0.681486	0.051135	0	48	40	44	49	44	53	70	76	87	67
ENSMUSG00000024944	chr19	Arl2	6134374	6134801	2891	0.091146	5.075694	0.578269	0.681486	0.030435	0	458	510	613	542	594	696	694	890	854	888
ENSMUSG00000027470	chr2	Mylk2	1.53E+08	1.53E+08	2951	-0.16487	9.316632	0.57835	0.681486	0.104976	0	11100	8518	13760	12595	10094	8488	9416	30426	10489	10834
ENSMUSG00000036427	chr7	Gpi1	34202122	34202549	4497	0.098982	9.953806	0.578407	0.681495	0.037968	0	12221	15385	17734	16862	17883	21902	17645	27866	27371	24004
ENSMUSG00000038797	chr7	Zscan2	80860920	80861077	2712	0.170089	0.690961	0.578465	0.681505	0.060128	0	22	17	30	27	23	24	37	45	42	40
ENSMUSG00000024943	chr19	Smc5	23206441	23208968	5730	-0.10357	3.711222	0.578528	0.681522	0.036809	0	184	154	279	248	276	178	278	376	365	287
ENSMUSG00000028568	chr4	Btf3l4	1.09E+08	1.09E+08	4546	0.091927	4.448624	0.578923	0.681914	0.0301	0	303	309	433	354	359	444	474	614	600	477
ENSMUSG00000031714	chr8	Gab1	80764434	80766487	4859	-0.10956	4.277505	0.57896	0.681914	0.04391	0	263	345	368	318	377	266	389	655	509	370
ENSMUSG00000050697	chr15	Prkaa1	5143861	5143995	4655	-0.08924	4.259539	0.57916	0.682093	0.028271	0	290	260	347	339	416	269	474	467	553	426
ENSMUSG00000026333	chr1	Gin1	97770172	97770255	6048	0.147319	1.612337	0.57931	0.68221	0.063915	0	32	44	67	43	50	57	85	46	92	85
ENSMUSG00000041548	chr5	Hspb8	1.16E+08	1.16E+08	1950	0.108153	8.971305	0.579408	0.682225	0.04553	0	5541	7245	12113	6873	9179	10573	13300	14492	11069	10525
ENSMUSG00000048807	chr11	Slc35e4	3907021	3907984	3063	0.088536	5.036934	0.579421	0.682225	0.029006	0	416	420	691	552	598	636	728	865	911	798
ENSMUSG00000029094	chr5	Afap1	35893319	35893540	8543	-0.11362	3.348214	0.579485	0.682242	0.043152	0	152	104	206	165	269	151	286	208	273	226
ENSMUSG00000042873	chr6	Lhfpl4	1.13E+08	1.13E+08	4762	-0.23931	0.122636	0.579739	0.682483	0.139025	0	23	4	15	24	25	19	15	29	15	27
ENSMUSG00000026851	chr2	BC005624	30972177	30973301	3280	-0.09023	4.760595	0.580329	0.683004	0.029283	0	381	410	529	469	548	563	601	505	692	675
ENSMUSG00000053094	chr5	Tmem248	1.3E+08	1.3E+08	3845	-0.08874	5.613372	0.580309	0.683004	0.029548	0	683	759	964	799	1025	886	945	1315	1319	1069
ENSMUSG00000054619	chr15	Mettl7a1	1E+08	1E+08	1883	-0.12928	4.990039	0.580302	0.683004	0.063589	0	536	466	607	514	641	395	453	1219	743	754
ENSMUSG00000026860	chr2	Sh3glb2	30344809	30345427	3990	0.093852	4.817301	0.581354	0.684152	0.032324	0	390	392	485	450	563	506	622	527	899	871
ENSMUSG00000056167	chr9	Cnot10	1.15E+08	1.15E+08	2979	0.089556	4.458731	0.581549	0.684324	0.028647	0	322	304	405	355	385	391	500	641	574	531
ENSMUSG00000034826	chr5	Nup54	92415540	92416338	2867	0.108314	3.142856	0.581835	0.684602	0.037207	0	104	151	156	134	156	140	225	213	246	243
ENSMUSG00000037169	chr12	Mycn	12936096	12937610	3292	-0.24486	0.031277	0.582061	0.684798	0.141251	0	8	12	14	30	21	15	28	6	34	18
ENSMUSG00000043024	chr6	Gm16433	1.09E+08	1.09E+08	2248	0.173535	0.518717	0.5821	0.684798	0.069783	0	15	22	20	17	31	26	44	36	32	26
ENSMUSG00000025971	chr1	9430016H08Rik	57406328	57407222	7878	0.096996	4.179958	0.58251	0.685194	0.034127	0	215	270	349	335	287	375	399	509	445	429
ENSMUSG00000028549	chr4	Itgb3bp	99765402	99767576	4632	-0.13829	2.103454	0.582536	0.685194	0.065501	0	74	79	80	56	75	70	95	60	154	98
ENSMUSG00000022761	chr16	Lztr1	17508688	17509218	5445	-0.08595	4.971926	0.582615	0.685228	0.027686	0	498	452	632	530	580	485	705	801	882	707
ENSMUSG00000066150	chr4	Slc31a1	62360727	62360843	4280	-0.08557	4.851213	0.582679	0.685246	0.027076	0	419	437	540	502	583	512	732	566	851	622
ENSMUSG00000000884	chr16	Gnb1l	18498768	18498851	4164	-0.16727	1.16504	0.58312	0.685647	0.074656	0	37	27	53	27	48	32	61	43	39	61
ENSMUSG00000045886	chr10	Gm9803	43524102	43524617	516	0.159385	1.842437	0.58308	0.685647	0.076341	0	50	69	46	57	47	95	79	88	82	76
ENSMUSG00000090125	chr4	Pou3f1	1.25E+08	1.25E+08	3849	0.223908	0.036521	0.583221	0.685708	0.113818	0	18	8	10	15	20	12	32	36	17	19
ENSMUSG00000031487	chr8	Brf2	27123832	27124620	1383	0.106631	2.882994	0.584022	0.686592	0.037116	0	99	113	129	97	149	148	154	178	226	177
ENSMUSG00000006586	chr4	Runx1t1	13743436	13743729	7959	-0.15847	1.291312	0.58412	0.686648	0.075819	0	42	31	45	40	50	27	54	80	46	54
ENSMUSG00000018599	chr11	Mief2	60728398	60728567	2716	0.092171	6.406553	0.584232	0.686663	0.033352	0	1091	1258	1684	1387	1446	1950	2028	1745	2432	1980
ENSMUSG00000025949	chr1	Pikfyve	65186683	65186778	18504	0.107994	3.697133	0.584188	0.686663	0.042522	0	191	122	242	182	320	200	296	373	357	347
ENSMUSG00000024382	chr18	Ercc3	32240300	32240421	2835	0.08628	3.967965	0.584462	0.686873	0.026671	0	192	207	277	253	347	311	360	371	449	380
ENSMUSG00000085436	chr2	Zfp335os	1.65E+08	1.65E+08	1273	-0.16151	1.901879	0.584509	0.686873	0.084454	0	43	81	77	67	50	88	58	87	73	87
ENSMUSG00000029623	chr5	Pdap1	1.45E+08	1.45E+08	3201	0.085581	6.111015	0.584572	0.686888	0.028436	0	901	1039	1210	1148	1307	1286	1540	1733	2070	1711
ENSMUSG00000052504	chr16	Epha3	63543538	63546236	5659	-0.25224	0.741691	0.584812	0.687112	0.181655	0	11	37	18	34	45	45	16	17	33	53
ENSMUSG00000073599	chr18	Ecscr	35713086	35713434	1680	0.106765	3.281603	0.585272	0.687594	0.038251	0	107	164	161	183	156	184	209	221	314	246
ENSMUSG00000023050	chr15	Map3k12	1.02E+08	1.03E+08	8986	0.142543	2.187392	0.586198	0.688623	0.062658	0	73	56	78	66	80	52	110	93	186	124
ENSMUSG00000034121	chr11	Mks1	87853215	87853329	4044	0.159325	1.148033	0.58625	0.688626	0.070527	0	37	21	36	34	39	37	34	60	63	68
ENSMUSG00000038085	chr2	Cnbd2	1.56E+08	1.56E+08	3879	0.136641	1.987178	0.586441	0.688792	0.062675	0	41	59	92	47	72	83	84	80	101	122
ENSMUSG00000037503	chr1	Fam168b	34813219	34817404	5219	-0.08723	5.812954	0.58684	0.689202	0.029791	0	751	783	1061	969	1332	858	1381	1216	1638	1347
ENSMUSG00000036158	chr15	Prickle1	93499114	93501303	4345	-0.11735	2.860749	0.586963	0.689288	0.044521	0	99	104	106	143	176	126	164	193	181	139
ENSMUSG00000038542	chr8	Pcid2	13077189	13078289	3084	0.092603	3.604344	0.587038	0.689317	0.030167	0	131	182	231	197	244	223	277	318	355	287
ENSMUSG00000040370	chr6	Lyrm5	1.45E+08	1.45E+08	2682	-0.09248	5.141204	0.587189	0.689437	0.033119	0	541	617	665	627	549	730	767	784	895	771
ENSMUSG00000014232	chr16	Cluap1	3908801	3908864	2279	0.104281	3.070712	0.587267	0.68947	0.036734	0	136	105	165	133	127	159	206	211	233	196
ENSMUSG00000008958	chr3	Vps72	95111022	95111214	3639	-0.08707	4.694595	0.587444	0.689619	0.028396	0	319	434	532	459	483	473	564	568	682	637
ENSMUSG00000031059	chrX	Ndufb11	20615326	20615542	908	0.105199	7.949702	0.587534	0.689666	0.044799	0	3294	4384	4779	3838	3348	5866	5504	6397	5990	5648
ENSMUSG00000000171	chr9	Sdhd	50596338	50597250	1287	0.107357	8.368639	0.58783	0.68993	0.046793	0	4241	6290	6019	5131	4479	8132	7638	6582	9005	8126
ENSMUSG00000017713	chr11	Tha1	1.18E+08	1.18E+08	2910	-0.11987	3.006136	0.587909	0.68993	0.049038	0	88	161	162	138	140	164	166	148	198	207
ENSMUSG00000032175	chr9	Tyk2	21104069	21105183	4619	0.093831	3.803348	0.587859	0.68993	0.030846	0	197	177	262	238	251	224	343	280	430	417
ENSMUSG00000021752	chr14	Kctd6	8214148	8214342	3253	-0.10535	3.025063	0.588549	0.690565	0.038088	0	102	143	157	134	162	161	155	193	221	173
ENSMUSG00000028128	chr3	F3	1.22E+08	1.22E+08	1876	0.129997	2.968922	0.588517	0.690565	0.059834	0	136	63	97	141	185	150	210	179	212	192
ENSMUSG00000024079	chr17	Eif2ak2	78852564	78855261	5113	0.152717	3.297151	0.588628	0.690598	0.089983	0	132	105	200	151	193	278	222	86	264	323
ENSMUSG00000020364	chr11	Zfp354a	51059257	51059402	4318	-0.22717	2.553584	0.588808	0.690693	0.1948	0	105	96	122	99	94	69	86	333	82	46
ENSMUSG00000033722	chr1	BC034090	1.55E+08	1.55E+08	8222	0.174694	2.005601	0.588793	0.690693	0.109567	0	57	23	57	58	122	60	149	68	115	98
ENSMUSG00000058267	chr1	Mrps14	1.6E+08	1.6E+08	3258	0.095777	5.371877	0.588976	0.690832	0.03609	0	552	710	802	629	615	949	1016	936	1059	964
ENSMUSG00000024446	chr17	Rpp21	36255645	36255798	1218	0.11188	3.083579	0.589979	0.691949	0.041153	0	144	116	150	135	120	181	205	171	262	197
ENSMUSG00000056481	chr19	Cd248	5068078	5070637	2560	-0.1482	5.092594	0.590057	0.691982	0.087773	0	407	327	560	555	1276	660	838	367	1014	910
ENSMUSG00000063146	chr5	Clip2	1.34E+08	1.34E+08	4995	0.128091	3.255549	0.590356	0.692274	0.061892	0	120	85	138	152	282	161	262	164	337	249
ENSMUSG00000026696	chr1	Vamp4	1.63E+08	1.63E+08	4565	-0.09475	3.662625	0.590462	0.69234	0.032671	0	223	184	256	186	232	203	296	327	295	300

ENSMUSG00000027882	chr3	Stxbp3a	1.09E+08	1.09E+08	5340	0.086375	4.978899	0.590798	0.692531	0.029121	0	475	419	612	463	586	620	750	837	767	784
ENSMUSG00000030530	chr7	Furin	80388585	80391296	9178	0.094205	6.040813	0.590848	0.692531	0.035906	0	871	770	1167	1124	1459	985	1579	1995	1866	1590
ENSMUSG00000036446	chr10	Lum	97565501	97565885	2075	0.113862	6.638	0.590875	0.692531	0.053203	0	1320	1100	1617	1321	2841	1737	3297	2065	3242	1885
ENSMUSG00000062861	chr7	Zfp28	6383318	6383601	4142	0.151712	1.557126	0.590791	0.692531	0.062877	0	53	39	44	49	36	48	62	72	86	84
ENSMUSG00000097210	chr7	Fam160a2	1.05E+08	1.05E+08	2508	-0.18847	1.127978	0.590871	0.692531	0.112376	0	37	42	39	31	35	42	71	24	30	58
ENSMUSG00000030327	chr6	Necap1	1.23E+08	1.23E+08	2386	-0.08556	4.292962	0.591956	0.693681	0.026949	0	282	287	406	283	436	362	446	432	516	455
ENSMUSG00000040177	chr7	2310057M21Rik	1.31E+08	1.31E+08	2214	0.112761	3.573935	0.591942	0.693681	0.048275	0	123	186	230	222	189	261	265	379	288	221
ENSMUSG00000000142	chr11	Axin2	1.09E+08	1.09E+08	5506	-0.12449	2.79067	0.592185	0.693831	0.055294	0	110	101	128	143	109	126	118	215	173	128
ENSMUSG00000065265	chr9	Gm23455	15316489	15316588	100	0.241711	-0.1962	0.592165	0.693831	0.152599	0	16	7	4	9	23	13	18	11	21	35
ENSMUSG00000067787	chr2	Blcap	1.58E+08	1.58E+08	3043	0.102431	4.530558	0.59228	0.693883	0.040447	0	334	362	404	352	391	404	448	442	695	821
ENSMUSG00000020519	chr11	Sap30l	57801637	57802289	1151	-0.10582	3.95479	0.592412	0.693979	0.042283	0	252	220	303	285	271	296	276	492	332	318
ENSMUSG00000022111	chr14	Uchl3	1.02E+08	1.02E+08	929	-0.09617	4.125304	0.592538	0.694007	0.034937	0	226	335	315	283	332	373	387	327	457	401
ENSMUSG00000027860	chr3	Vangl1	1.02E+08	1.02E+08	4038	-0.1245	2.16155	0.592641	0.694007	0.049609	0	61	64	75	73	113	77	119	76	128	93
ENSMUSG00000028563	chr4	Tm2d1	98355370	98355680	1124	-0.09374	4.231983	0.592686	0.694007	0.033613	0	274	335	422	266	308	348	411	461	474	413
ENSMUSG00000038781	chr17	Stap2	55997081	55997361	1491	0.144956	2.316259	0.59252	0.694007	0.0697	0	64	91	85	79	62	105	102	74	168	153
ENSMUSG00000062995	chr6	Ica1	8630527	8630797	3243	0.161226	1.028007	0.592606	0.694007	0.069755	0	23	27	40	34	29	41	42	32	80	47
ENSMUSG00000039759	chr4	Thap3	1.52E+08	1.52E+08	1334	0.093342	5.023064	0.592871	0.694165	0.034857	0	431	493	684	477	538	727	805	855	771	695
ENSMUSG00000030725	chr7	Lipt2	1E+08	1E+08	1663	-0.11638	2.387938	0.592938	0.694184	0.042193	0	70	88	95	83	112	103	118	121	123	107
ENSMUSG00000026839	chr2	Upp2	58567298	58567528	7053	-0.20285	0.101261	0.593317	0.694511	0.108012	0	24	12	19	14	18	23	16	9	36	23
ENSMUSG00000051851	chrX	Cxx1c	53608032	53608432	401	0.132255	1.68095	0.593291	0.694511	0.052161	0	43	35	56	50	66	53	92	70	106	63
ENSMUSG00000064105	chr19	Cnnm2	46761596	46763393	3558	0.149126	1.669672	0.593458	0.694617	0.064149	0	53	35	52	52	51	40	77	71	89	107
ENSMUSG00000022983	chr16	Scaf4	90228957	90230244	4364	0.089741	3.758201	0.593575	0.694695	0.029152	0	170	187	226	221	293	239	286	323	459	331
ENSMUSG00000022994	chr15	Adcy6	98589994	98592475	6017	-0.09078	5.261774	0.59377	0.694865	0.033478	0	568	556	709	736	732	535	782	824	1136	1129
ENSMUSG00000037366	chr4	Pafah2	1.34E+08	1.34E+08	3616	-0.13194	2.16814	0.594475	0.695631	0.060163	0	63	73	95	78	75	75	95	59	140	128
ENSMUSG00000028647	chr4	Mycbp	1.24E+08	1.24E+08	2934	-0.09137	3.526872	0.59454	0.695649	0.02961	0	168	179	251	179	210	222	255	239	306	269
ENSMUSG00000067629	chr17	Syngap1	26941384	26941518	6267	0.141246	2.034442	0.594666	0.695731	0.070209	0	51	40	77	47	111	71	133	85	123	81
ENSMUSG00000073096	chr6	Lrrc61	48554796	48554982	2913	0.108931	4.114666	0.594711	0.695731	0.045758	0	287	240	294	274	277	281	344	631	421	411
ENSMUSG00000038260	chr7	Trpm4	45303155	45303692	4245	-0.09116	4.060058	0.594887	0.695878	0.031464	0	254	249	375	268	284	289	381	450	410	344
ENSMUSG00000026589	chr1	Sec16b	1.58E+08	1.58E+08	5410	-0.16073	2.187811	0.595056	0.695958	0.090585	0	81	33	100	49	143	61	116	95	119	107
ENSMUSG00000034520	chr11	Gjc1	1.03E+08	1.03E+08	5003	-0.11412	2.764264	0.595024	0.695958	0.04764	0	89	84	142	136	138	98	196	118	205	147
ENSMUSG00000036867	chr9	Smad6	63953076	63954056	3205	-0.14427	1.958526	0.595416	0.696321	0.064861	0	52	42	90	75	79	53	73	106	80	110
ENSMUSG00000029148	chr5	Nrbp1	31240864	31241002	3559	0.088043	6.145386	0.595669	0.696557	0.03216	0	886	1046	1402	1102	1323	1259	1693	2062	1842	1655
ENSMUSG00000066278	chr5	Vps37b	1.24E+08	1.24E+08	2512	0.110549	2.935208	0.595774	0.696621	0.043846	0	80	102	148	129	156	149	177	132	252	213
ENSMUSG00000003235	chr16	Eif2b5	20498817	20499096	3209	0.085734	5.917611	0.595868	0.696672	0.030469	0	773	838	1185	975	1159	1242	1295	1629	1638	1419
ENSMUSG00000021754	chr13	Map3k1	1.12E+08	1.12E+08	7447	0.103066	3.42858	0.595944	0.696702	0.038918	0	152	121	161	210	221	179	221	240	343	324
ENSMUSG00000031155	chrX	Pim2	7878262	7878556	2795	0.165855	0.556282	0.596133	0.696865	0.059042	0	17	19	27	22	23	26	34	24	43	43
ENSMUSG00000031090	chr7	Nadsyn1	1.44E+08	1.44E+08	3306	0.137828	1.6623	0.596345	0.697054	0.054946	0	40	43	41	50	71	60	65	63	105	85
ENSMUSG00000075394	chr15	Hoxc4	1.03E+08	1.03E+08	2568	-0.11695	2.162826	0.596582	0.697272	0.043952	0	68	68	86	82	76	78	101	102	130	83
ENSMUSG00000021670	chr13	Hmgcr	96648967	96650633	7275	0.11815	3.507367	0.596705	0.697347	0.054486	0	119	145	165	188	306	193	268	180	399	355
ENSMUSG00000046947	chr6	Adck2	39573873	39575206	4095	-0.1061	7.01022	0.596747	0.697347	0.047675	0	1845	2586	2734	2017	1810	2911	2675	2871	3142	2672
ENSMUSG00000019889	chr10	Ptprk	28074820	28075177	6177	-0.11363	3.117791	0.597412	0.698026	0.048851	0	105	160	143	194	137	152	205	185	270	160
ENSMUSG00000045294	chr5	Insig1	28071363	28071795	2697	-0.15528	4.280115	0.59743	0.698026	0.099511	0	265	161	301	405	628	193	290	400	543	769
ENSMUSG00000032263	chr9	Bckdhb	83925145	83925359	1805	0.096405	4.05549	0.597496	0.698045	0.0351	0	268	242	271	269	272	276	325	484	448	471
ENSMUSG00000039787	chr2	Cercam	29869164	29869345	3383	0.175043	3.597133	0.59781	0.698354	0.126289	0	251	60	184	97	375	217	423	213	385	263
ENSMUSG00000029670	chr6	Ing3	21949571	21949793	4806	0.126498	2.990461	0.598235	0.698791	0.059432	0	98	122	154	133	118	110	195	298	195	164
ENSMUSG00000021395	chr13	Spin1	51100880	51100990	4434	0.090958	4.454587	0.598616	0.699176	0.032529	0	319	305	344	352	449	340	556	672	605	477
ENSMUSG00000026510	chr1	Trp53bp2	1.82E+08	1.82E+08	4418	0.096149	3.681619	0.598808	0.699287	0.035809	0	157	153	254	201	281	209	267	401	368	303
ENSMUSG00000030678	chr7	Maz	1.27E+08	1.27E+08	2365	-0.08165	6.239856	0.598811	0.699287	0.028125	0	1116	1161	1385	1305	1524	1285	1642	1782	2030	1865
ENSMUSG00000044991	chr2	1110034G24Rik	1.33E+08	1.33E+08	2117	-0.13505	1.906681	0.599108	0.699574	0.06234	0	54	78	77	57	49	68	83	79	89	87
ENSMUSG00000026434	chr1	Nucks1	1.32E+08	1.32E+08	6779	0.085665	6.279845	0.599229	0.699657	0.031089	0	1162	1068	1585	1019	1486	1546	1903	1739	2208	1935
ENSMUSG00000003299	chr9	Mrpl4	21002737	21002997	1285	0.091356	5.493258	0.599379	0.699772	0.034672	0	520	761	775	850	710	912	1013	966	1430	1115
ENSMUSG00000032519	chr9	Slc25a38	1.2E+08	1.2E+08	2747	0.101575	3.778209	0.599547	0.69991	0.040651	0	193	196	268	206	235	280	315	440	276	311
ENSMUSG00000027937	chr3	Jtb	90231597	90232040	1531	0.089968	5.668131	0.599901	0.700045	0.034005	0	737	807	1020	741	775	1136	1229	1185	1280	1212
ENSMUSG00000045007	chr11	Tubg2	1.01E+08	1.01E+08	1754	-0.16224	0.942202	0.599743	0.700045	0.084494	0	33	29	16	40	42	32	34	38	62	38
ENSMUSG00000052406	chr2	Rexo4	26953563	26954596	3662	0.083112	4.218462	0.599768	0.700045	0.027053	0	259	233	354	277	396	328	479	414	510	504
ENSMUSG00000071369	chr10	Map3k5	19934472	19935074	6262	-0.10496	3.574625	0.599844	0.700045	0.041879	0	174	147	229	237	245	242	269	165	360	298
ENSMUSG00000079428	chrX	Tceal7	1.36E+08	1.36E+08	1217	-0.13713	6.761462	0.599915	0.700045	0.080867	0	1342	1169	2585	1303	3494	2264	3325	1420	3175	1860
ENSMUSG00000018740	chr11	Slc25a35	68968131	68969037	3677	0.207197	2.908402	0.600015	0.700102	0.174959	0	107	91	123	126	126	83	96	58	297	431
ENSMUSG00000032386	chr9	Trip4	65828930	65833448	8394	-0.08222	4.141632	0.600438	0.700537	0.025718	0	252	254	354	279	382	314	419	371	469	424
ENSMUSG00000073478	chr1	D730003I15Rik	1.91E+08	1.91E+08	1687	0.177267	0.375204	0.600634	0.700705	0.086529	0	13	21	18	15	27	21	25	25	27	50
ENSMUSG00000025575	chr11	Cant1	1.18E+08	1.18E+08	4358	0.0854	4.435761	0.600897	0.700954	0.02906	0	318	263	402	314	468	348	486	557	639	588
ENSMUSG00000006705	chr17	Pknox1	31564749	31564888	6892	-0.0985	3.505256	0.601135	0.701113	0.035663	0	161	135	194	210	288	211	289	244	305	222
ENSMUSG00000103235	chr9	DHX30	1.1E+08	1.1E+08	3585	-0.08214	4.964043	0.601126	0.701113	0.027302	0	464	447	598	472	716	586	702	723	793	718
ENSMUSG00000028426	chr4	Rad23b	55350043	55350427	5733	-0.1044	6.976963	0.601414	0.701379	0.047309	0	1822	1896	2526	2124	2582	2003	2540	4436	2808	2344
ENSMUSG00000057691	chr6	Zfp746	48062395	48064952	3651	0.0957	3.550114	0.601599	0.701536	0.035376	0	149	154	206	181	259	199	250	372	311	273
ENSMUSG00000063052	chr3	Lrrc40	1.58E+08	1.58E+08	4575	-0.0959	2.93784	0.601747	0.70165	0.033143	0	117	114	143	129	151	131	166	154	229	182

ENSMUSG00000029086	chr5	Prom1	43993625	43994496	4517	-0.2423	1.627038	0.602213	0.702133	0.225489	0	47	47	77	51	50	25	57	176	33	28
ENSMUSG00000027016	chr2	Zfp385b	77410634	77412140	8223	0.226002	2.21731	0.602306	0.702183	0.208455	0	120	16	69	31	116	53	192	101	175	69
ENSMUSG00000030929	chr7	Eri2	1.2E+08	1.2E+08	7170	0.162997	1.218978	0.602653	0.702529	0.079443	0	34	34	36	26	45	32	67	31	84	67
ENSMUSG00000024163	chr17	Mapk8ip3	24892153	24892683	14558	-0.08559	4.576885	0.602755	0.702588	0.030243	0	375	309	462	409	504	320	533	601	696	590
ENSMUSG00000028672	chr4	Hmgcl	1.36E+08	1.36E+08	2434	0.086366	5.510156	0.602816	0.7026	0.031392	0	633	746	805	779	686	924	1040	1017	1302	1182
ENSMUSG00000030207	chr6	8430419L09Rik	1.35E+08	1.35E+08	5776	0.124019	2.643002	0.602921	0.702637	0.055	0	108	82	113	72	115	115	176	99	216	152
ENSMUSG00000098907	chr9	Mir7082	21075497	21075588	92	0.132918	1.337354	0.602949	0.702637	0.050789	0	34	28	41	46	45	44	58	67	68	60
ENSMUSG00000038215	chr8	Cep44	56531522	56531732	2817	0.107573	2.519993	0.603103	0.702757	0.039193	0	70	78	106	89	114	91	144	144	152	156
ENSMUSG00000000753	chr11	Serpinf1	75409769	75410393	2359	-0.14251	7.793132	0.603477	0.703072	0.089581	0	4897	1623	4336	2281	6735	4446	6238	4257	5047	4375
ENSMUSG00000033335	chr9	Dnm2	21424908	21425256	5330	0.080537	5.62944	0.603526	0.703072	0.027496	0	659	651	908	885	933	847	1115	1126	1579	1336
ENSMUSG00000073968	chr7	Trim68	1.03E+08	1.03E+08	2389	-0.1182	2.334872	0.603463	0.703072	0.052241	0	99	72	83	77	96	92	99	85	142	139
ENSMUSG00000023764	chr11	Sfi1	3131850	3132131	7559	0.123195	2.601015	0.603629	0.703133	0.05367	0	93	66	104	91	127	74	186	147	158	172
ENSMUSG00000069808	chr11	Fam57a	76179671	76179986	6615	-0.13306	1.747448	0.603903	0.703393	0.060489	0	44	46	67	60	71	55	76	43	108	87
ENSMUSG00000038807	chr11	Rap1gap2	74383356	74387511	6632	-0.10811	4.421058	0.604124	0.703571	0.049346	0	280	329	400	472	366	332	745	343	575	426
ENSMUSG00000069917	chr11	Hba-a2	32296489	32296618	667	0.168607	2.94372	0.604158	0.703571	0.116871	0	49	137	80	173	160	127	141	105	321	271
ENSMUSG00000032370	chr9	Lactb	66955393	66956200	2031	-0.08901	4.292106	0.604631	0.704063	0.031844	0	243	338	414	335	351	408	393	417	528	449
ENSMUSG00000026049	chr1	Tex30	44086613	44087063	1926	-0.14523	1.557953	0.604922	0.704344	0.068778	0	50	50	58	29	63	43	57	82	66	69
ENSMUSG00000026193	chr1	Fn1	71585520	71586283	11685	0.200781	8.567842	0.605398	0.704838	0.179478	0	5227	1845	5374	3840	14967	4762	15420	3978	16492	8743
ENSMUSG00000003778	chr18	Brd8	34598615	34600241	10633	0.093461	4.106694	0.605515	0.704915	0.035194	0	290	180	278	267	380	260	438	423	525	449
ENSMUSG00000021500	chr13	Ddx46	55635027	55635195	5747	-0.09302	5.176005	0.605739	0.705117	0.037341	0	543	518	617	644	802	505	747	1141	955	768
ENSMUSG00000085180	chr4	Al838599	3242055	3242190	4243	-0.22345	-0.03882	0.605854	0.705191	0.155153	0	19	9	16	10	26	7	23	39	14	12
ENSMUSG00000025867	chr13	Cplx2	54371349	54371575	4928	-0.15144	1.663038	0.606011	0.705314	0.070393	0	41	27	51	67	91	55	73	64	84	65
ENSMUSG00000022314	chr15	Rad21	51962605	51964247	3604	-0.08176	6.104281	0.606315	0.70549	0.02937	0	1022	931	1310	1268	1405	1065	1633	1669	2029	1496
ENSMUSG00000035642	chr7	Aamdc	97550331	97550741	1615	0.096673	6.749611	0.606286	0.70549	0.041631	0	1538	1679	2159	1466	1816	2679	2862	2011	2694	2505
ENSMUSG00000089083	chr6	Rnu7	1.25E+08	1.25E+08	62	-0.20151	0.153646	0.606223	0.70549	0.108344	0	16	23	25	14	12	16	27	12	21	35
ENSMUSG00000051367	chr12	Six1	73040015	73040574	4383	-0.09727	5.860078	0.606548	0.705702	0.041485	0	724	847	1187	1153	1139	983	1244	1848	1330	1115
ENSMUSG00000073591	chr18	Pcdhb22	37517871	37524479	6609	-0.14582	1.68082	0.606981	0.706147	0.068807	0	49	33	47	50	100	52	76	72	72	73
ENSMUSG00000028745	chr4	Capzb	1.39E+08	1.39E+08	3299	-0.08368	8.45633	0.607354	0.706402	0.031587	0	4805	5444	7026	5903	7171	7554	7612	6962	9381	8006
ENSMUSG00000031755	chr8	Bbs2	94067954	94068382	3194	0.127513	1.945812	0.607321	0.706402	0.057663	0	61	37	70	64	69	84	93	107	90	78
ENSMUSG00000047921	chr15	Trappc9	72589621	72590162	6363	-0.08027	5.305107	0.607257	0.706402	0.027538	0	574	555	687	740	848	753	837	859	1080	949
ENSMUSG00000019951	chr10	Uhrf1bp1l	89744991	89745288	6446	0.116127	3.845993	0.607437	0.706433	0.055153	0	186	234	243	262	209	192	269	545	421	332
ENSMUSG00000027167	chr2	Elp4	1.06E+08	1.06E+08	3318	0.115096	2.481902	0.607581	0.706433	0.04828	0	68	63	106	89	121	100	109	171	144	142
ENSMUSG00000029486	chr5	Mrpl1	96209493	96209565	4295	-0.09826	5.02831	0.607505	0.706433	0.041835	0	482	631	661	517	481	734	712	724	744	695
ENSMUSG00000047989	chr18	Ino80c	24104757	24106658	2828	-0.07869	4.997031	0.607585	0.706433	0.026341	0	504	499	601	502	621	577	693	764	842	743
ENSMUSG00000001847	chr5	Rac1	1.44E+08	1.44E+08	2652	0.079842	7.388036	0.607849	0.706622	0.02864	0	2395	2366	3029	2638	3200	3073	3807	4390	4826	4069
ENSMUSG00000079018	chr15	Ly6c1	75044018	75044332	1677	0.102935	5.920263	0.607845	0.706622	0.047063	0	757	978	1282	1061	758	1172	1278	1820	1393	1592
ENSMUSG00000014980	chr1	Tsen15	1.52E+08	1.52E+08	4195	0.102353	3.460552	0.608016	0.706756	0.041196	0	179	169	202	155	164	259	284	200	300	263
ENSMUSG00000096458	chr12	Moap1	1.03E+08	1.03E+08	1328	-0.11123	2.842537	0.608171	0.706878	0.050041	0	111	140	135	112	107	128	201	155	178	132
ENSMUSG00000037705	chr9	Tecta	42329619	42330325	7411	-0.32061	0.154136	0.608865	0.707565	0.350503	0	8	23	10	48	4	33	18	4	27	22
ENSMUSG00000041187	chr7	Prkd2	16842902	16843033	3757	0.108649	3.11653	0.608844	0.707565	0.044088	0	117	134	130	168	134	142	212	166	315	224
ENSMUSG00000022109	chr14	Med4	73510049	73510185	1304	0.085845	4.173065	0.609004	0.707644	0.030352	0	276	257	357	256	305	379	462	414	442	442
ENSMUSG00000048170	chr7	Mcmbp	1.29E+08	1.29E+08	5107	-0.08177	4.396049	0.609035	0.707644	0.027381	0	279	278	434	352	486	345	460	463	624	512
ENSMUSG00000066829	chr9	Zfp810	22276748	22279280	3238	-0.14141	0.90487	0.609466	0.708086	0.062492	0	23	26	32	36	40	21	52	40	46	41
ENSMUSG00000061979	chr5	Wbscr16	1.34E+08	1.34E+08	2874	0.098754	4.403918	0.609525	0.708095	0.041592	0	298	317	380	336	364	384	409	755	511	474
ENSMUSG00000040270	chr4	Bach2	32238804	32239089	9940	-0.17019	1.454886	0.609905	0.708477	0.099805	0	43	33	46	59	54	37	54	107	57	36
ENSMUSG00000020895	chr11	Tmem107	69070806	69071033	1369	0.154263	1.361758	0.610204	0.708764	0.081688	0	38	33	42	22	62	50	74	36	78	67
ENSMUSG00000059013	chr2	Sh2d3c	32721055	32721195	5233	-0.12895	3.202074	0.610369	0.708896	0.071225	0	88	155	190	232	130	151	138	193	251	291
ENSMUSG00000034308	chr8	Sdr42e1	1.18E+08	1.18E+08	2957	0.213536	0.080397	0.611105	0.709692	0.134186	0	11	9	18	14	23	12	20	12	25	52
ENSMUSG00000001445	chr11	Mrpl10	97041560	97041652	1708	0.087029	5.276876	0.611388	0.709961	0.033323	0	491	649	748	666	556	778	944	913	1078	931
ENSMUSG00000078173	chr3	Lenep	89400988	89402793	1806	-0.11649	2.437276	0.611507	0.71004	0.049882	0	82	92	84	101	100	119	123	93	130	125
ENSMUSG00000038069	chr8	Cdkn2aip	47709344	47712294	3494	-0.11969	2.536077	0.611737	0.710209	0.053601	0	73	79	121	110	119	79	124	186	147	108
ENSMUSG00000078546	chr17	2210404O09Rik	21879570	21881094	3167	0.20914	-0.21162	0.611755	0.710209	0.106974	0	13	8	23	7	8	10	17	25	20	24
ENSMUSG00000021124	chr12	Vti1b	79156017	79156571	1612	-0.08985	5.520123	0.611945	0.710364	0.036173	0	685	746	937	756	809	971	1013	732	1245	1196
ENSMUSG00000028410	chr4	Dnaja1	40722150	40722435	8629	0.08522	5.63252	0.611991	0.710364	0.03269	0	630	783	953	666	1005	1026	1358	958	1356	1237
ENSMUSG00000017802	chr11	Fam134c	1.01E+08	1.01E+08	3589	-0.08399	6.049483	0.61227	0.710508	0.032036	0	960	1027	1375	1091	1243	1061	1390	1842	1679	1556
ENSMUSG00000048537	chr9	Phldb1	44686304	44687698	7179	0.099389	5.42314	0.612208	0.710508	0.044519	0	688	396	700	744	970	585	1107	1276	1262	1024
ENSMUSG00000054293	chrX	A630033H20Rik	1.07E+08	1.07E+08	3465	-0.1882	0.537734	0.612245	0.710508	0.122766	0	18	19	23	18	45	13	18	21	59	43
ENSMUSG00000037031	chr10	Tspan15	62185396	62188162	3605	0.098763	3.584194	0.612393	0.710592	0.039709	0	170	155	213	189	238	177	233	399	326	314
ENSMUSG00000057093	chr7	C030039L03Rik	27689340	27689486	5508	0.200745	0.11882	0.612495	0.71065	0.098286	0	15	14	22	13	12	21	35	12	38	18
ENSMUSG00000037822	chr5	Smim14	65446844	65450437	7460	0.081461	5.066468	0.612677	0.710802	0.029235	0	536	379	627	518	671	615	860	746	965	844
ENSMUSG00000040247	chr19	Tbc1d10c	4184358	4185073	1758	-0.1473	2.069766	0.612831	0.710921	0.078337	0	57	76	87	64	76	105	85	55	80	119
ENSMUSG00000034575	chr13	Papd7	69497959	69500110	3972	0.101846	3.450241	0.612921	0.710966	0.043757	0	173	116	147	174	272	239	277	264	290	229
ENSMUSG00000001785	chr10	Pwp1	85871831	85872014	2730	-0.08277	4.49116	0.613016	0.711017	0.029261	0	342	308	484	364	438	383	473	610	624	462
ENSMUSG00000032478	chr9	Nme6	1.1E+08	1.1E+08	1014	-0.09112	3.977366	0.613178	0.711145	0.035097	0	266	252	301	261	256	333	346	269	415	397
ENSMUSG00000021076	chr12	Actr10	70937857	70938031	4022	0.080277	5.717183	0.613488	0.711428	0.029138	0	719	791	971	800	990	1042	1169	1453	1386	1227
ENSMUSG00000059741	chr9	Myl3	1.11E+08	1.11E+08	1306	0.476423	5.703488	0.613525	0.711428	1.009656	0	15	1173	4	1830	487	1009	75	2821	2625	705

ENSMUSG00000026566	chr1	Mpzl1	1.66E+08	1.66E+08	3550	-0.09687	3.841522	0.613946	0.711857	0.039561	0	260	151	252	226	354	213	352	378	372	305
ENSMUSG00000022538	chr16	Lsg1	30560494	30561862	5555	0.08417	4.0098	0.614019	0.711882	0.029982	0	199	222	308	262	319	292	365	483	412	370
ENSMUSG00000026816	chr2	Gtf3c5	28566311	28567177	4560	0.099594	3.730855	0.614072	0.711883	0.041403	0	179	195	203	225	261	263	362	190	419	368
ENSMUSG00000015839	chr2	Nfe2l2	75675513	75677184	3796	0.092696	5.146177	0.61425	0.71203	0.038241	0	565	457	536	583	713	492	810	1117	1126	788
ENSMUSG00000022472	chr15	Desi1	81992523	81994845	3635	0.083711	4.200151	0.614431	0.71218	0.029778	0	228	280	348	293	339	377	482	340	545	455
ENSMUSG00000035671	chr8	Zswim4	84210942	84212805	4348	0.103752	3.543604	0.614586	0.7123	0.044593	0	151	163	178	203	240	164	275	411	323	240
ENSMUSG00000038070	chr4	Cntln	84884309	84884824	7102	0.114807	2.084043	0.614689	0.71236	0.048724	0	58	43	72	66	98	69	110	94	122	112
ENSMUSG00000007721	chr8	Ccdc124	70868227	70868645	911	0.085981	5.510606	0.614873	0.712514	0.033674	0	563	732	769	814	800	1055	933	992	1333	1118
ENSMUSG00000056724	chr9	Nbeal2	1.11E+08	1.11E+08	9554	-0.10941	2.621214	0.615119	0.712739	0.04567	0	75	82	146	107	123	91	114	138	180	167
ENSMUSG00000071454	chr12	Dtnb	3572381	3572647	9603	-0.13373	1.089052	0.61536	0.712958	0.055381	0	36	29	35	32	46	34	48	50	44	50
ENSMUSG00000003813	chr8	Rad23a	84834019	84834324	2577	-0.08241	6.690386	0.615607	0.71315	0.031666	0	1460	1648	1910	1896	1941	1983	2084	2600	2532	2441
ENSMUSG00000026259	chr1	Ngef	87476834	87477744	3905	-0.19579	0.022853	0.615628	0.71315	0.118324	0	27	9	17	6	23	13	20	17	30	22
ENSMUSG00000028125	chr3	Abca4	1.22E+08	1.22E+08	11829	-0.22305	1.067293	0.616049	0.713559	0.188546	0	29	21	43	41	50	33	16	101	24	37
ENSMUSG00000038291	chr8	Snx25	46033261	46033822	4440	-0.10029	2.841289	0.616085	0.713559	0.040229	0	106	113	137	108	149	104	176	197	176	149
ENSMUSG00000038042	chr13	Ptpdc1	48577873	48579843	4310	0.120113	2.176675	0.616203	0.713577	0.053064	0	66	64	76	48	102	69	120	121	124	108
ENSMUSG00000067916	chr4	Gm13139	1.47E+08	1.47E+08	2917	-0.1824	0.353471	0.616199	0.713577	0.102322	0	13	23	19	26	24	8	24	31	28	41
ENSMUSG00000018909	chr7	Arrb1	99535466	99535798	11175	-0.09261	4.539471	0.616287	0.713615	0.038264	0	336	280	419	458	528	365	530	370	742	657
ENSMUSG00000056459	chr12	Zbtb25	76347782	76350273	3131	0.124437	2.502082	0.616409	0.713696	0.06127	0	82	63	112	76	117	104	126	205	129	109
ENSMUSG00000022442	chr15	Ttll1	83483772	83484313	2918	0.111253	2.730551	0.616577	0.713771	0.050191	0	79	91	135	93	133	125	156	102	239	182
ENSMUSG00000054770	chr1	Kctd18	57955101	57956820	12973	-0.11045	2.444409	0.616544	0.713771	0.045399	0	91	73	116	90	94	81	116	150	142	116
ENSMUSG00000025265	chrX	Fgd1	1.51E+08	1.51E+08	4931	-0.13355	2.3031	0.616737	0.713897	0.067461	0	77	47	84	79	146	73	148	86	140	99
ENSMUSG00000000435	chr10	Myf5	1.07E+08	1.07E+08	2083	0.193209	0.790703	0.617068	0.71422	0.110739	0	21	19	16	27	45	16	63	38	59	32
ENSMUSG00000053411	chr15	Cbx7	79915807	79918050	6487	0.151616	3.88163	0.617209	0.714324	0.104491	0	245	183	284	231	207	198	223	780	297	298
ENSMUSG00000089739	chr2	Gm20431	1.68E+08	1.68E+08	2367	-0.07754	5.58819	0.617399	0.714484	0.027683	0	616	730	966	878	957	757	1070	1180	1415	1097
ENSMUSG00000021033	chr12	Gstz1	87147707	87147844	1665	0.117113	5.540242	0.617487	0.714526	0.064087	0	623	661	762	781	903	617	763	908	1436	2047
ENSMUSG00000024234	chr18	Mtpap	4375592	4375778	2651	-0.08801	4.111784	0.617547	0.714535	0.033677	0	242	295	354	251	340	296	351	495	466	344
ENSMUSG00000032392	chr9	Parp16	65214690	65214863	2483	-0.10296	2.789983	0.61798	0.714977	0.044113	0	103	102	161	107	119	104	124	159	215	178
ENSMUSG00000032051	chr9	Fdx1	51943307	51943649	861	-0.11147	4.383224	0.618384	0.715361	0.056985	0	267	473	374	378	271	490	411	372	561	470
ENSMUSG00000038604	chr8	Fam65a	1.06E+08	1.06E+08	4109	0.088691	4.587775	0.618452	0.715361	0.034823	0	329	307	382	482	443	354	536	704	768	568
ENSMUSG00000092187	chr7	Gm20457	64337550	64337933	682	0.149579	0.524946	0.618467	0.715361	0.07588	0	20	16	29	13	29	34	34	21	38	36
ENSMUSG00000024563	chr18	Smad2	76241580	76241979	3549	0.085286	3.667094	0.618672	0.715421	0.029766	0	187	165	193	204	278	220	284	290	392	344
ENSMUSG00000025199	chr19	Chuk	44073335	44074540	5087	-0.08704	4.052452	0.618707	0.715421	0.033603	0	228	260	385	274	276	232	421	338	469	437
ENSMUSG00000050668	chr17	Gpatch11	78835516	78835678	4198	-0.0915	3.897524	0.618655	0.715421	0.035761	0	206	250	308	261	247	315	370	260	347	365
ENSMUSG00000084514	chr18	Mir1893	6490564	6490646	83	-0.20789	0.775756	0.618726	0.715421	0.159538	0	23	34	30	35	21	19	42	73	24	17
ENSMUSG00000064307	chr7	Lrrc51	1.02E+08	1.02E+08	1210	0.163525	0.965364	0.618785	0.71543	0.082229	0	23	31	43	19	30	30	39	69	50	41
ENSMUSG00000021103	chr12	Mnat1	73123717	73123926	5385	0.085882	3.606408	0.618841	0.715434	0.029735	0	189	166	231	186	205	209	304	332	325	287
ENSMUSG00000003955	chr16	Fam162a	36043844	36044091	635	0.089657	5.443083	0.619268	0.715869	0.037662	0	509	747	840	706	701	1040	1056	856	1170	1041
ENSMUSG00000027012	chr2	Dync1i2	71211706	71211845	8280	0.077862	5.89637	0.619458	0.716028	0.028297	0	859	844	1141	956	1033	1044	1555	1467	1674	1428
ENSMUSG00000038593	chr5	Tctn1	1.22E+08	1.22E+08	4856	0.151525	1.215952	0.619989	0.716525	0.080714	0	37	21	47	31	41	29	58	83	57	48
ENSMUSG00000052752	chr17	Traf7	24508562	24509358	5872	0.074997	4.968651	0.619991	0.716525	0.025323	0	424	431	594	506	599	535	757	745	933	803
ENSMUSG00000049551	chr5	Fzd9	1.35E+08	1.35E+08	2293	-0.10746	4.074008	0.620471	0.71702	0.052031	0	215	242	312	408	274	368	318	244	470	474
ENSMUSG00000060376	chr7	Bckdha	25629852	25630433	1773	0.121857	6.853656	0.620581	0.717087	0.071839	0	1457	1796	2048	2261	1610	1845	1805	4864	2676	2855
ENSMUSG00000039205	chr2	Ciz1	32352327	32352527	8604	0.077779	4.652873	0.620826	0.71731	0.027296	0	339	333	395	443	541	465	571	615	697	664
ENSMUSG00000090035	chr10	Galnt4	99108159	99113247	5089	-0.12945	2.69517	0.620984	0.717433	0.070735	0	90	68	140	90	185	93	160	85	229	163
ENSMUSG00000025332	chrX	Kdm5c	1.52E+08	1.52E+08	7110	0.09163	5.089562	0.621136	0.717549	0.039071	0	480	455	578	539	711	472	676	1099	948	948
ENSMUSG00000079043	chr2	Fastkd5	1.31E+08	1.31E+08	3015	-0.09533	3.309105	0.621345	0.717731	0.036344	0	121	146	198	179	212	208	237	218	265	174
ENSMUSG00000020496	chr11	Rnf187	58932288	58933396	1949	0.079901	6.685965	0.621479	0.717825	0.030914	0	1326	1411	1802	1654	2250	2124	2239	2497	2759	2669
ENSMUSG00000024410	chr18	3110002H16Rik	12168717	12168902	5768	0.082888	3.836145	0.621579	0.717881	0.029885	0	176	180	312	220	279	253	340	298	434	394
ENSMUSG00000029198	chr5	Grpel1	36464998	36465255	3528	0.092213	6.249521	0.622372	0.718737	0.041024	0	1025	1276	1336	1326	1115	1519	1522	2332	2109	1645
ENSMUSG00000027575	chr2	Arfgap1	1.81E+08	1.81E+08	5367	0.082612	5.075527	0.622501	0.718826	0.031922	0	564	380	620	483	699	602	780	911	943	817
ENSMUSG00000024732	chr19	Ccdc86	10941481	10943289	5774	0.088084	4.665429	0.62277	0.719076	0.036609	0	252	376	512	412	526	540	712	551	734	496
ENSMUSG00000026024	chr1	Als2	59162926	59164215	9496	-0.10641	4.690698	0.623245	0.719565	0.053306	0	374	329	552	467	531	377	542	966	538	466
ENSMUSG00000035547	chr7	Capn5	98121559	98124055	5485	0.119407	2.441607	0.623329	0.719602	0.060338	0	78	51	86	75	146	86	161	138	162	108
ENSMUSG00000027746	chr3	Ufm1	53855212	53857995	4122	0.076913	4.736233	0.623516	0.719758	0.027169	0	354	367	556	425	469	486	717	623	720	644
ENSMUSG00000000563	chr3	Atp5f1	1.06E+08	1.06E+08	4105	-0.09154	9.367326	0.623642	0.719843	0.041612	0	9885	12351	12932	11419	9471	13978	14072	16070	16405	13335
ENSMUSG00000053483	chr1	Usp21	1.71E+08	1.71E+08	4756	0.082382	4.001846	0.623759	0.719918	0.030345	0	238	200	298	256	306	345	426	297	436	399
ENSMUSG00000084896	chr11	Gm11632	98084457	98085076	674	-0.15125	1.384406	0.623881	0.719998	0.094966	0	42	34	47	38	62	22	41	87	59	74
ENSMUSG00000024081	chr17	Cebpz	78919006	78920017	4074	0.089301	4.509845	0.623992	0.720067	0.036827	0	323	336	425	325	430	388	542	764	575	462
ENSMUSG00000021831	chr14	Ero1l	45283092	45286088	4413	-0.10087	2.753093	0.624176	0.720219	0.039624	0	104	99	131	96	148	119	144	125	214	155
ENSMUSG00000009876	chr2	Cox4i2	1.53E+08	1.53E+08	788	0.154134	1.436803	0.62443	0.720452	0.096062	0	26	47	45	41	47	62	74	25	89	71
ENSMUSG00000001334	chr4	Fndc5	1.29E+08	1.29E+08	2763	-0.12307	6.187177	0.624557	0.720478	0.074882	0	849	1442	1197	1916	805	1432	1792	1158	2348	1460
ENSMUSG00000002007	chrX	Srpk3	73774405	73774506	2784	0.094606	5.893062	0.624536	0.720478	0.043963	0	743	824	1159	887	1236	1429	1682	893	1635	1441
ENSMUSG00000034194	chr14	R3hcc1	69697305	69697602	2768	0.082743	3.993504	0.624619	0.72049	0.030846	0	183	237	302	291	276	326	366	410	389	396
ENSMUSG00000029632	chr6	Ndufa4	11900373	11900591	492	-0.09908	8.644382	0.625255	0.721164	0.049141	0	6220	7784	7914	6815	5139	8636	8389	10008	9127	8262
ENSMUSG00000039233	chr13	Tbce	13997949	13998181	4540	-0.08972	4.251157	0.625397	0.721267	0.036941	0	269	350	404	267	335	388	465	343	447	483
ENSMUSG00000040028	chr8	Elavl1	4284782	4289924	6030	0.078428	4.930059	0.625472	0.721293	0.028887	0	399	463	590	416	617	569	816	633	917	731

ENSMUSG00000071064	chr8	Zfp827	79028437	79028729	8944	0.118956	2.752388	0.625578	0.721356	0.061748	0	53	81	111	129	172	107	189	133	209	180
ENSMUSG00000029655	chr5	N4bp2l2	1.51E+08	1.51E+08	12262	-0.07809	4.07707	0.625883	0.72163	0.027328	0	251	263	322	273	332	275	388	449	435	367
ENSMUSG00000032419	chr9	Tbx18	87702800	87705945	4718	-0.14114	1.388126	0.62592	0.72163	0.070727	0	40	30	49	34	72	36	48	57	96	50
ENSMUSG00000057367	chr9	Birc2	7818227	7818943	4580	-0.08613	4.562476	0.626225	0.721861	0.034832	0	391	348	443	391	446	398	484	706	515	552
ENSMUSG00000066175	chr7	2510046G10Rik	1.27E+08	1.27E+08	1052	0.194754	-0.12414	0.626178	0.721861	0.070439	0	9	10	15	13	17	9	19	26	25	24
ENSMUSG00000025532	chr5	Crcp	1.3E+08	1.3E+08	1579	-0.08788	4.069377	0.626442	0.722051	0.035455	0	274	270	347	251	287	346	407	274	488	374
ENSMUSG00000029402	chr5	Snrnp35	1.24E+08	1.24E+08	1347	-0.09321	3.746416	0.626606	0.72218	0.038204	0	185	217	248	241	258	315	262	226	346	338
ENSMUSG00000013736	chr6	Trnt1	1.07E+08	1.07E+08	3869	-0.09811	4.012986	0.627017	0.722593	0.044902	0	222	270	337	256	303	239	350	557	368	299
ENSMUSG00000064372	chrMT	mt-Tp	15356	15422	67	-0.3505	0.409746	0.627072	0.722596	0.554388	0	31	16	4	43	17	12	4	2	93	29
ENSMUSG00000026121	chr1	Sema4c	36548639	36550368	4593	0.082662	3.756402	0.627221	0.722699	0.030236	0	157	173	235	247	291	221	357	304	422	328
ENSMUSG00000063281	chr18	Zfp35	23989632	23989731	3040	-0.08697	3.270518	0.627265	0.722699	0.031567	0	145	142	192	165	179	174	220	249	239	198
ENSMUSG00000014748	chr6	Tex261	83768885	83771303	4088	-0.07663	6.233969	0.627348	0.722735	0.029001	0	1145	1135	1472	1240	1460	1487	1593	1698	2009	1731
ENSMUSG00000067722	chr17	BC003965	25184561	25184640	3022	-0.08906	4.903306	0.627496	0.722845	0.038349	0	418	550	606	505	467	645	631	526	892	674
ENSMUSG00000005198	chr11	Polr2a	69733997	69735566	7067	0.08177	6.070691	0.627653	0.722966	0.033227	0	868	797	1135	1201	1529	1135	1434	1729	2046	1798
ENSMUSG00000031448	chr8	Adprhl1	13235655	13235988	1820	0.094633	4.658844	0.627753	0.723021	0.043299	0	243	346	436	590	433	519	536	569	847	580
ENSMUSG00000025047	chr19	Pdcd11	47090766	47090867	6041	0.079819	4.093876	0.627848	0.723069	0.028732	0	224	233	297	250	391	285	388	397	560	436
ENSMUSG00000029735	chr6	Tpk1	43345001	43346900	4329	-0.14768	0.753049	0.629043	0.724325	0.06673	0	24	28	26	32	29	24	50	26	44	34
ENSMUSG00000037316	chr8	Bag4	25764538	25768409	4798	-0.10167	2.839976	0.629007	0.724325	0.044014	0	116	95	127	126	149	97	131	158	219	206
ENSMUSG00000025555	chr14	Farp1	1.21E+08	1.21E+08	5524	0.102049	3.217494	0.62967	0.724987	0.046706	0	139	94	137	142	242	138	250	236	299	208
ENSMUSG00000004263	chr6	Atn1	1.25E+08	1.25E+08	5085	0.078492	6.573324	0.62992	0.725214	0.031211	0	1180	1472	1705	1642	1744	2041	2118	2292	2574	2312
ENSMUSG00000020802	chr11	Ube2o	1.17E+08	1.17E+08	5288	-0.10738	4.978091	0.630375	0.725678	0.057246	0	409	447	682	550	669	453	573	1227	698	584
ENSMUSG00000024487	chr18	Yipf5	40204865	40206400	2329	-0.09175	4.107348	0.630558	0.725708	0.039815	0	302	210	326	226	430	287	473	307	525	369
ENSMUSG00000031521	chr8	Aga	53511702	53511931	1289	0.095058	3.472543	0.630541	0.725708	0.041844	0	159	142	233	137	227	251	253	184	346	291
ENSMUSG00000056305	chr6	Usp39	72318678	72319239	2425	0.076043	4.344678	0.630499	0.725708	0.027509	0	261	268	425	314	394	423	447	475	599	477
ENSMUSG00000026154	chr1	1110058L19Rik	23995939	23996360	874	0.097405	4.319945	0.630727	0.725842	0.045232	0	268	369	359	316	267	472	507	362	637	411
ENSMUSG00000035521	chr17	Gnptg	25233331	25234722	2249	-0.08583	3.616039	0.630873	0.725842	0.032918	0	224	163	227	192	238	236	237	288	308	304
ENSMUSG00000052125	chr12	F730043M19Rik	33111711	33112137	4610	0.173963	0.204541	0.630868	0.725842	0.099032	0	9	13	24	13	25	18	33	11	40	30
ENSMUSG00000087413	chr4	Gm11266	82508016	82508229	1271	0.153161	2.008916	0.630884	0.725842	0.097178	0	67	60	66	68	43	65	70	117	72	156
ENSMUSG00000026755	chr2	Arpc5l	39008076	39008346	4438	-0.09657	6.456304	0.630968	0.725878	0.047547	0	1343	1547	1873	1419	1314	2223	1926	1650	2007	1856
ENSMUSG00000098132	chr7	Rassf10	1.13E+08	1.13E+08	3496	-0.18704	0.02012	0.631244	0.726135	0.105851	0	8	16	18	24	16	14	23	12	40	14
ENSMUSG00000082575	chr4	Gm13050	1.43E+08	1.43E+08	1345	0.14852	1.26466	0.632274	0.727259	0.071873	0	25	41	32	45	38	30	51	71	80	56
ENSMUSG00000007338	chr19	Mrpl49	6053630	6054982	1722	-0.08479	4.874563	0.632439	0.727389	0.035351	0	459	440	636	496	476	633	726	524	811	601
ENSMUSG00000083240	chr2	Gm13453	40127504	40127860	357	0.145888	1.462554	0.632666	0.72759	0.080923	0	38	32	39	64	36	60	42	77	71	73
ENSMUSG00000038646	chr7	Fam103a1	81762925	81763056	1741	-0.09337	3.606978	0.632726	0.727598	0.040812	0	172	200	211	225	232	186	276	391	284	231
ENSMUSG00000028797	chr4	Tmem234	1.3E+08	1.3E+08	4273	0.079127	5.437406	0.633226	0.728087	0.031305	0	597	626	902	681	710	716	984	1259	1235	1031
ENSMUSG00000097047	chr17	1110020A21Rik	84954967	84955308	853	-0.15259	1.049692	0.633257	0.728087	0.101205	0	38	43	31	36	21	43	27	53	56	39
ENSMUSG00000019478	chr8	Rab4a	1.24E+08	1.24E+08	1757	-0.07935	4.193746	0.633577	0.728335	0.029567	0	290	290	352	291	333	392	405	389	487	379
ENSMUSG00000045414	chr9	1190002N15Rik	94517864	94520646	3950	0.095631	3.694864	0.633564	0.728335	0.043227	0	163	160	201	219	310	212	426	249	432	256
ENSMUSG00000075528	chr11	Aarsd1	1.01E+08	1.01E+08	3052	0.076414	4.850744	0.63375	0.728473	0.028795	0	400	405	480	470	593	613	602	618	868	743
ENSMUSG00000029446	chr5	Psph	1.3E+08	1.3E+08	4010	-0.09042	3.262053	0.634213	0.728945	0.035348	0	131	143	199	167	182	194	210	174	233	257
ENSMUSG00000054387	chr1	Mdm4	1.33E+08	1.33E+08	14798	0.088911	4.860317	0.634277	0.728958	0.039535	0	509	341	552	346	608	466	687	823	736	788
ENSMUSG00000028436	chr4	Dcaf12	41291300	41293214	3442	0.080966	5.621656	0.634379	0.729015	0.03328	0	760	689	886	779	864	857	1098	1560	1307	1086
ENSMUSG00000010911	chr2	Apip	1.03E+08	1.03E+08	1000	-0.08435	4.567268	0.63473	0.729296	0.035024	0	345	425	484	383	376	505	515	473	573	583
ENSMUSG00000020515	chr11	Cnot8	58104153	58104208	2636	0.078137	5.490158	0.634698	0.729296	0.031253	0	620	627	904	670	844	997	1178	869	1211	1084
ENSMUSG00000028158	chr3	Mttp	1.38E+08	1.38E+08	4410	0.131723	1.759954	0.635026	0.729577	0.067915	0	41	47	52	56	67	62	118	50	82	89
ENSMUSG00000048755	chr15	Mcat	83546797	83547942	1893	0.080759	4.332706	0.635151	0.729659	0.030794	0	251	323	359	359	331	333	425	539	615	520
ENSMUSG00000042328	chr5	Hps4	1.12E+08	1.12E+08	3948	0.105875	2.442232	0.635548	0.730055	0.045853	0	77	67	95	103	87	97	138	99	165	152
ENSMUSG00000040034	chr10	Nup43	7667503	7667681	2560	0.096949	2.423347	0.636138	0.730672	0.041435	0	65	71	116	86	90	102	120	125	148	141
ENSMUSG00000062198	chr12	2700097O09Rik	55045661	55045943	4939	0.134189	2.187357	0.636469	0.730991	0.077045	0	68	74	98	55	56	106	122	62	122	128
ENSMUSG00000030978	chr7	Rrm1	1.02E+08	1.02E+08	3997	-0.08342	5.273157	0.636751	0.731254	0.036133	0	609	640	650	685	704	722	913	609	1266	910
ENSMUSG00000019804	chr10	Snx3	42502030	42502426	1413	0.083776	6.688529	0.636812	0.731262	0.037127	0	1286	1601	1938	1640	1919	2195	2462	1718	3179	2844
ENSMUSG00000097164	chr10	Cep83os	94673493	94677129	4135	0.133221	1.642635	0.636863	0.731262	0.076162	0	35	31	59	54	66	45	57	117	88	65
ENSMUSG00000030177	chr6	Ccdc77	1.2E+08	1.2E+08	6685	-0.16326	2.662859	0.637031	0.731395	0.133375	0	117	88	141	89	115	72	104	316	120	76
ENSMUSG00000005510	chr2	Ndufs3	90894634	90894877	2178	0.089148	7.860162	0.637347	0.731697	0.042558	0	3021	4163	4145	3857	3389	5484	4837	6047	6108	5095
ENSMUSG00000029165	chr5	Agbl5	30888694	30888842	7053	0.134826	1.369297	0.637624	0.731833	0.062766	0	41	29	40	45	42	50	44	53	96	64
ENSMUSG00000031955	chr8	Bcar1	1.12E+08	1.12E+08	3171	-0.08076	4.068274	0.637582	0.731833	0.031571	0	219	259	272	307	385	294	418	313	536	354
ENSMUSG00000036309	chr11	Skp1a	52231995	52232118	2211	-0.09106	7.585965	0.637599	0.731833	0.044399	0	2604	3364	3830	3200	3514	3640	3816	6060	4006	3929
ENSMUSG00000022000	chr14	Zc3h13	75284373	75284665	6151	-0.0765	4.07892	0.637942	0.732135	0.027981	0	217	233	328	312	368	249	385	408	482	411
ENSMUSG00000027208	chr2	Fgf7	1.26E+08	1.26E+08	3248	-0.13881	1.348084	0.637993	0.732135	0.073433	0	36	38	40	34	69	32	60	77	63	43
ENSMUSG00000011254	chr11	Thg1l	45946843	45948328	3015	0.121378	2.297618	0.638235	0.732266	0.066115	0	49	71	102	68	101	107	142	64	156	118
ENSMUSG00000025784	chr9	Clec3b	1.23E+08	1.23E+08	990	0.098471	6.300723	0.638266	0.732266	0.052063	0	1068	873	1372	931	2291	1793	2021	1420	2187	2017
ENSMUSG00000051169	chr6	Rpusd3	1.13E+08	1.13E+08	2161	0.096996	2.939221	0.63825	0.732266	0.040341	0	95	128	139	126	120	155	151	176	245	190
ENSMUSG00000021000	chr12	Ctage5	59129720	59129896	9323	-0.0914	5.766816	0.638481	0.732451	0.044146	0	850	798	1061	1015	947	916	1015	1842	1226	1121
ENSMUSG00000070720	chr4	Tmem200b	1.32E+08	1.32E+08	1370	0.153039	0.935169	0.638978	0.732961	0.089394	0	24	15	24	31	52	23	60	41	63	40
ENSMUSG00000026821	chr2	Ralgds	28513125	28513560	6159	-0.09551	4.841975	0.639133	0.733078	0.046934	0	284	435	474	481	857	466	542	620	864	775
ENSMUSG00000032012	chr9	Pvrl1	43744576	43744722	5054	0.117413	2.173482	0.639555	0.733501	0.058719	0	68	45	75	72	97	72	155	87	129	98

ENSMUSG00000040725	chr7	Hnrnpul1	25721498	25722363	3589	0.080374	5.95205	0.639835	0.733762	0.034404	0	825	760	1154	1065	1273	1006	1387	1925	1720	1430
ENSMUSG00000085287	chr17	4833418N02Rik	87274886	87275370	2762	0.186193	2.033287	0.639954	0.733837	0.172345	0	60	37	83	58	78	46	60	247	62	78
ENSMUSG00000037172	chr6	E330009J07Rik	40401375	40406934	7511	-0.13411	1.786761	0.640219	0.73408	0.079923	0	62	32	52	53	99	42	59	89	111	81
ENSMUSG00000024764	chr19	Naa40	7225668	7228091	3275	-0.07664	4.124888	0.640543	0.734391	0.028181	0	230	242	330	339	359	310	376	450	461	378
ENSMUSG00000053137	chr15	Mapk11	89142486	89143817	2440	0.127869	1.560698	0.640814	0.73464	0.059452	0	47	40	40	46	53	54	77	46	98	76
ENSMUSG00000031823	chr8	Zdhhc7	1.2E+08	1.2E+08	3472	0.072201	5.099043	0.641038	0.734837	0.026995	0	419	525	620	561	672	672	807	760	998	861
ENSMUSG00000042632	chr15	Pla2g6	79286228	79286895	4980	-0.08037	3.952564	0.641154	0.734909	0.031245	0	202	224	285	312	305	261	301	392	379	416
ENSMUSG00000022498	chr16	Txndc11	11074911	11075642	8835	0.080533	3.6464	0.641357	0.735081	0.03047	0	186	145	209	211	266	211	325	259	386	327
ENSMUSG00000049792	chr12	Bag5	1.12E+08	1.12E+08	2508	0.08276	3.99816	0.64141	0.735081	0.034014	0	216	205	262	275	341	276	365	508	443	322
ENSMUSG00000098802	chr7	Mir7046	24970010	24970075	66	0.148674	0.830462	0.641599	0.735236	0.078421	0	28	19	17	29	40	30	29	47	51	50
ENSMUSG00000028917	chr4	Plekhm2	1.42E+08	1.42E+08	5186	-0.08378	5.155637	0.641662	0.735248	0.037314	0	470	586	653	643	709	501	681	1103	961	829
ENSMUSG00000028150	chr3	Rorc	94372831	94372931	2098	0.171522	5.194141	0.641804	0.735289	0.159527	0	527	564	541	715	471	483	459	2308	572	652
ENSMUSG00000029767	chr6	Calu	29348069	29348208	4733	-0.08945	7.697108	0.641753	0.735289	0.043945	0	3138	2712	4000	3097	5184	3810	5787	2988	6319	4761
ENSMUSG00000000531	chr15	Grasp	1.01E+08	1.01E+08	2013	0.107417	2.613412	0.642024	0.73548	0.052653	0	81	80	115	121	86	88	141	194	175	139
ENSMUSG00000034379	chr16	Wdr5b	36041190	36042973	1784	-0.12485	1.490895	0.64222	0.735643	0.059978	0	37	44	59	50	47	58	75	44	71	54
ENSMUSG00000025354	chr10	Dnajc14	1.29E+08	1.29E+08	4229	0.070132	5.033553	0.642634	0.736012	0.025403	0	445	461	590	534	644	602	802	712	986	829
ENSMUSG00000029535	chr5	Triap1	1.15E+08	1.15E+08	1088	0.083985	4.181293	0.642648	0.736012	0.03568	0	240	308	377	253	278	413	430	412	493	400
ENSMUSG00000003868	chr7	Ruvbl2	45421852	45422005	2573	0.074706	4.626311	0.642947	0.736293	0.028392	0	339	341	453	418	457	477	574	465	805	650
ENSMUSG00000084819	chr11	Gm11967	5915315	5915396	480	0.204079	0.280693	0.643082	0.736387	0.14058	0	12	26	22	15	10	39	16	17	39	26
ENSMUSG00000024208	chr17	Uqcc2	27122663	27122840	837	-0.09241	6.944195	0.643727	0.737004	0.047183	0	1766	2278	2483	1893	2109	3115	2829	2157	2817	2662
ENSMUSG00000083396	chr7	Gm15542	1.41E+08	1.41E+08	1194	0.125238	1.245221	0.643695	0.737004	0.053836	0	22	34	47	37	43	42	51	58	70	57
ENSMUSG00000015980	chr7	Lrrc27	1.39E+08	1.39E+08	3637	0.142421	1.352454	0.644129	0.737356	0.085599	0	25	48	36	38	47	54	56	32	77	82
ENSMUSG00000029447	chr5	Cct6a	1.3E+08	1.3E+08	1599	0.074987	6.666413	0.644141	0.737356	0.031092	0	1239	1482	2059	1453	2122	2015	2568	2378	2880	2313
ENSMUSG00000079562	chr5	Maea	33335572	33335645	2128	0.073268	6.019828	0.644303	0.73748	0.029155	0	920	952	1231	999	1176	1196	1623	1711	1806	1436
ENSMUSG00000031171	chrX	Ftsj1	8238668	8240830	4760	-0.07845	3.697299	0.644374	0.737492	0.029504	0	220	181	266	193	245	247	302	294	333	283
ENSMUSG00000066491	chr12	Gm6265	56373593	56373823	231	-0.19332	0.284846	0.64442	0.737492	0.139154	0	16	31	19	22	10	33	22	28	18	18
ENSMUSG00000028926	chr5	Cdk14	4803391	4806731	15344	-0.09741	3.341719	0.644576	0.73761	0.046658	0	146	106	198	181	254	143	240	167	328	280
ENSMUSG00000029711	chr5	Epo	1.37E+08	1.37E+08	855	-0.16537	0.065	0.645056	0.738098	0.080826	0	13	12	16	28	15	16	22	15	32	21
ENSMUSG00000028683	chr4	Eif2b3	1.17E+08	1.17E+08	6520	0.084795	4.118591	0.645498	0.738543	0.03618	0	238	307	299	258	285	316	406	531	443	376
ENSMUSG00000015243	chr4	Abca1	53030787	53034083	10363	0.102472	4.870634	0.645681	0.73863	0.05681	0	427	337	547	567	476	358	617	1140	753	701
ENSMUSG00000050730	chr9	Arhgap42	8994329	8997685	7113	-0.10459	2.761768	0.645633	0.73863	0.050315	0	107	69	124	121	167	102	181	177	163	133
ENSMUSG00000027550	chr3	Lrrcc1	14533788	14534022	7475	0.101995	2.642318	0.645825	0.738734	0.04633	0	105	68	122	93	108	106	183	124	197	141
ENSMUSG00000023923	chr17	Tbc1d5	50733127	50736244	5613	-0.07924	3.613642	0.64599	0.738861	0.030009	0	155	171	235	205	292	196	288	247	356	308
ENSMUSG00000049232	chr6	Tigd2	59208870	59209181	3007	-0.09776	3.654409	0.646643	0.739547	0.049501	0	166	215	246	224	227	185	257	446	300	226
ENSMUSG00000032423	chr9	Syncrip	88449731	88454295	9575	-0.07266	5.901812	0.646939	0.739825	0.029135	0	833	846	1088	1026	1370	996	1407	1220	1830	1423
ENSMUSG00000015222	chr1	Map2	66175273	66175495	16449	-0.14586	1.535863	0.647208	0.740014	0.096442	0	70	28	49	32	67	40	86	65	80	44
ENSMUSG00000058444	chr9	Map2k5	63163769	63164190	2309	0.075067	4.15296	0.647211	0.740014	0.0285	0	226	267	293	302	356	339	362	453	564	414
ENSMUSG00000096255	chr17	Dynlt1b	6430112	6430238	768	0.182895	1.91902	0.647385	0.740151	0.169608	0	99	36	59	33	54	84	27	81	163	109
ENSMUSG00000028779	chr4	Pef1	1.3E+08	1.3E+08	1915	0.070456	5.069019	0.648184	0.741003	0.026508	0	485	497	636	502	607	639	761	775	997	847
ENSMUSG00000032656	chr18	March3	56761716	56762568	6006	0.152425	1.004621	0.648285	0.741058	0.097999	0	21	29	38	16	49	30	50	27	81	52
ENSMUSG00000021504	chr13	B4galt7	55599896	55600192	2896	0.100091	3.15118	0.648587	0.741342	0.048532	0	156	120	168	118	141	165	241	139	302	227
ENSMUSG00000060548	chr14	Tnfrsf19	60963834	60966465	4777	-0.11575	3.598037	0.648646	0.741348	0.072291	0	263	115	220	223	218	147	335	397	291	191
ENSMUSG00000023826	chr17	Park2	10840384	10840489	10101	-0.1134	2.270553	0.64891	0.741527	0.057692	0	57	65	96	101	96	74	92	150	102	112
ENSMUSG00000056899	chr12	Immp2l	41024090	41024145	1832	-0.10845	2.441124	0.648864	0.741527	0.060427	0	92	92	94	115	60	97	119	120	145	120
ENSMUSG00000032435	chr9	Dync1li1	1.15E+08	1.15E+08	2601	0.071717	5.489961	0.649116	0.741641	0.028524	0	544	685	910	686	853	878	1119	1102	1271	997
ENSMUSG00000083621	chrX	Gm14586	52772342	52772749	408	0.089638	3.234731	0.649116	0.741641	0.038103	0	161	131	141	149	165	198	214	184	308	221
ENSMUSG00000025745	chr5	Hadha	30118301	30119960	5341	0.090203	8.37614	0.649179	0.741651	0.046863	0	4113	5363	5280	6981	4886	5816	6138	10499	9828	7956
ENSMUSG00000073758	chr4	Sh3d21	1.26E+08	1.26E+08	2717	0.177046	0.811708	0.649304	0.741733	0.116878	0	29	29	27	27	14	15	36	62	55	42
ENSMUSG00000035125	chr6	Gcfc2	81923669	81923938	7571	0.123965	1.317405	0.649396	0.741776	0.057614	0	34	37	43	40	36	42	64	42	76	70
ENSMUSG00000057147	chr2	Dph6	1.15E+08	1.15E+08	7407	-0.13116	2.232135	0.64958	0.74191	0.088234	0	89	74	84	54	99	58	138	50	151	130
ENSMUSG00000071567	chr14	A830039N20Rik	23292291	23293643	1353	0.106361	2.233268	0.649621	0.74191	0.053369	0	62	69	74	71	95	109	128	77	116	121
ENSMUSG00000032384	chr9	Csnk1g1	65908974	65909168	11973	-0.08662	3.037992	0.649864	0.742127	0.035855	0	139	108	159	126	169	130	217	179	231	171
ENSMUSG00000023046	chr15	Igfbp6	1.02E+08	1.02E+08	1112	-0.10248	5.822625	0.649926	0.742137	0.059443	0	995	507	1241	763	1498	1002	1481	1602	1324	926
ENSMUSG00000037210	chr5	Fam193a	34369933	34370427	7418	-0.07745	3.907846	0.650234	0.742366	0.030621	0	217	192	293	259	333	220	333	421	408	330
ENSMUSG00000070509	chr7	Rgma	73375520	73375888	3782	0.085526	5.527816	0.650227	0.742366	0.041437	0	648	534	679	838	1076	987	1281	758	1456	1063
ENSMUSG00000034842	chr5	Art3	92331827	92331912	3932	-0.11933	7.441939	0.650799	0.74295	0.082697	0	2826	2658	3206	3237	3103	2588	2802	7649	2951	3269
ENSMUSG00000026519	chr1	Tmem63a	1.81E+08	1.81E+08	4492	0.071973	4.862511	0.651125	0.74326	0.028564	0	416	367	540	424	641	566	618	718	822	748
ENSMUSG00000079477	chr6	Rab7	87999106	88000530	2610	-0.07627	8.063152	0.651296	0.743395	0.033929	0	3952	4227	5462	4598	4628	4589	4940	7196	7280	6510
ENSMUSG00000025584	chr7	Pde8a	81213596	81214088	4045	0.109709	3.330567	0.651421	0.743476	0.06297	0	99	129	127	242	211	128	215	261	316	313
ENSMUSG00000043439	chr11	E130012A19Rik	97627389	97629702	2314	0.182907	0.952181	0.652029	0.744109	0.171573	0	19	17	31	28	53	38	27	96	22	38
ENSMUSG00000020305	chr11	Asb3	30954395	30954569	5275	-0.09355	2.962354	0.652495	0.744492	0.045087	0	147	128	148	102	131	126	186	201	199	161
ENSMUSG00000022889	chr16	Mrpl39	84717576	84718384	2533	-0.07843	4.960774	0.652526	0.744492	0.034576	0	418	543	620	583	482	605	702	572	942	720
ENSMUSG00000097081	chr12	Gm10425	1.11E+08	1.11E+08	3364	-0.23632	0.181977	0.652434	0.744492	0.219936	0	7	8	27	14	43	19	39	6	36	12
ENSMUSG00000035234	chr5	Fam175a	1.01E+08	1.01E+08	3011	0.10684	2.269441	0.652754	0.744691	0.051558	0	77	60	106	68	68	83	142	105	130	114
ENSMUSG00000015749	chr3	Anp32e	95929246	95929650	3566	-0.07266	6.350522	0.653224	0.745165	0.030507	0	1286	1114	1649	1232	1749	1531	1936	1598	2218	2006
ENSMUSG00000002588	chr6	Pon1	5168090	5168496	2898	-0.25337	0.051006	0.653397	0.745267	0.319624	0	26	8	5	22	23	4	13	5	38	46

ENSMUSG00000024151	chr17	Msh2	87672330	87672806	5518	-0.0753	3.609223	0.653421	0.745267	0.02876	0	193	185	246	198	213	225	257	272	320	303
ENSMUSG00000024527	chr18	Afg3l2	67404767	67405514	3085	-0.07843	6.393908	0.653732	0.745539	0.035968	0	1092	1494	1549	1620	1407	1533	1658	2178	2352	1841
ENSMUSG00000027800	chr3	Tm4sf1	57285611	57287770	3355	0.071099	4.731316	0.653767	0.745539	0.027202	0	351	407	429	480	485	451	645	636	781	680
ENSMUSG00000022503	chr16	Nubp1	10411948	10411995	3637	0.092266	3.6063	0.653848	0.74557	0.045029	0	173	175	256	141	238	224	329	185	366	363
ENSMUSG00000025545	chr14	Clybl	1.22E+08	1.22E+08	1239	0.082232	5.6946	0.654214	0.745926	0.038971	0	629	965	958	859	736	1135	1138	1207	1398	1283
ENSMUSG00000006315	chr7	Tmem147	30727701	30727903	868	-0.07301	6.485025	0.654335	0.746002	0.031092	0	1359	1352	1742	1568	1632	1903	1906	1907	2320	2065
ENSMUSG00000038605	chr2	Samd10	1.82E+08	1.82E+08	2448	0.138758	1.119524	0.654972	0.746667	0.072256	0	31	36	32	38	25	46	47	46	47	65
ENSMUSG00000027620	chr2	Rbm39	1.56E+08	1.56E+08	6946	0.078272	6.167558	0.65555	0.747264	0.035888	0	1083	1034	1269	1012	1445	1118	1749	2219	1825	1743
ENSMUSG00000031548	chr8	Sfrp1	23411502	23412328	4372	-0.13225	3.09851	0.655701	0.747375	0.09603	0	173	77	127	87	293	94	177	232	241	220
ENSMUSG00000057388	chr17	Mrpl18	12911349	12911749	1398	0.084552	6.201195	0.656097	0.747764	0.042259	0	884	1339	1411	1194	1079	1695	1877	1438	2014	1726
ENSMUSG00000028037	chr3	Ifi44	1.52E+08	1.52E+08	6116	0.195459	1.218024	0.656708	0.748397	0.197326	0	22	35	63	27	28	73	48	13	44	90
ENSMUSG00000072946	chr12	Ptgr2	84285232	84285476	5929	-0.07996	6.045811	0.65676	0.748397	0.037891	0	929	1091	1295	1234	1086	1332	1539	1059	1976	1600
ENSMUSG00000053965	chr3	Pde5a	1.23E+08	1.23E+08	6728	0.10426	2.475297	0.657414	0.74908	0.054529	0	68	60	105	94	120	72	173	123	189	119
ENSMUSG00000017718	chr11	Afmid	1.18E+08	1.18E+08	3539	0.094402	2.331185	0.657505	0.749123	0.045059	0	75	61	103	68	94	110	120	98	153	113
ENSMUSG00000053644	chr18	Aldh7a1	56509687	56509982	5181	-0.07325	5.008822	0.657755	0.749345	0.030317	0	483	408	564	530	801	598	714	684	821	833
ENSMUSG00000026938	chr2	Fcna	25624666	25625088	1374	-0.16498	2.654861	0.657856	0.749399	0.146146	0	67	38	133	81	264	97	95	95	168	234
ENSMUSG00000081810	chr4	Gm11878	22519628	22520027	400	0.153106	0.905575	0.658118	0.749636	0.091454	0	23	38	21	19	38	47	50	36	40	41
ENSMUSG00000049536	chrX	Tceal1	1.37E+08	1.37E+08	2803	-0.11128	2.16369	0.658348	0.749836	0.06348	0	56	80	96	68	81	55	139	76	142	92
ENSMUSG00000026895	chr2	Ndufa8	36036326	36036641	861	0.08386	7.510116	0.658425	0.749862	0.042724	0	2280	3152	3179	3447	2550	4269	4000	3766	5167	4493
ENSMUSG00000032180	chr9	Tmed1	21507380	21508391	1487	0.073357	4.845958	0.658972	0.750423	0.030879	0	426	418	607	409	471	596	745	647	778	651
ENSMUSG00000028743	chr4	Akr7a5	1.39E+08	1.39E+08	1793	0.076162	4.725158	0.659473	0.750933	0.034043	0	281	393	488	465	539	592	527	577	751	692
ENSMUSG00000043411	chr4	Usp48	1.38E+08	1.38E+08	9686	-0.06761	4.479438	0.65963	0.75105	0.025252	0	334	311	421	372	472	408	484	476	621	552
ENSMUSG00000022793	chr16	B4galt4	38742264	38742368	3032	0.092683	2.476836	0.659963	0.751366	0.042286	0	74	72	102	100	95	125	135	114	150	130
ENSMUSG00000024498	chr18	Tcerg1	42511510	42511585	4246	-0.06928	4.875415	0.660064	0.75142	0.027416	0	382	445	574	452	679	496	669	665	845	686
ENSMUSG00000052928	chr18	Ctif	75431224	75435409	6173	-0.07113	4.294409	0.660135	0.751439	0.028116	0	252	279	374	347	439	289	502	465	542	452
ENSMUSG00000046491	chr11	C1qtnf2	43474276	43474387	1308	0.11978	3.260111	0.660376	0.751651	0.085303	0	153	80	137	108	303	232	247	139	251	270
ENSMUSG00000056598	chr11	Lrrc48	60353329	60353432	4519	-0.15365	0.942099	0.661035	0.75234	0.101069	0	19	48	38	28	26	48	38	38	40	34
ENSMUSG00000097974	chr7	Gm10605	99625936	99629133	3569	0.086553	3.62067	0.661533	0.752845	0.042169	0	136	209	227	212	203	295	265	249	291	344
ENSMUSG00000030619	chr7	Eed	89954656	89955063	2218	0.073742	4.21197	0.661619	0.752881	0.030413	0	237	305	347	285	324	358	452	513	482	395
ENSMUSG00000051351	chr4	Zfp46	1.36E+08	1.36E+08	5212	-0.08617	3.858256	0.661987	0.753238	0.04228	0	249	182	289	262	257	214	301	476	339	307
ENSMUSG00000074170	chr7	Plekhf1	38220654	38222158	1559	0.086452	3.371235	0.662279	0.753508	0.040644	0	165	123	199	168	176	189	223	325	232	256
ENSMUSG00000029528	chr5	Pxn	1.16E+08	1.16E+08	8195	-0.07465	6.309729	0.66275	0.753982	0.034147	0	1142	938	1542	1409	1869	1316	1692	2180	2069	1788
ENSMUSG00000026240	chr1	Cops7b	86582904	86583096	5515	0.075777	3.743017	0.663048	0.75416	0.030855	0	185	213	257	196	227	270	334	258	390	342
ENSMUSG00000090622	chr10	A930033H14Rik	69209762	69212384	2969	-0.16346	0.316004	0.66307	0.75416	0.129133	0	26	16	25	19	14	11	16	40	47	17
ENSMUSG00000090958	chr7	Lrrc32	98494222	98494308	3817	-0.10856	3.198579	0.663044	0.75416	0.066372	0	124	92	116	220	250	118	221	181	318	211
ENSMUSG00000040139	chr7	9430038I01Rik	1.37E+08	1.37E+08	5752	0.117402	1.54689	0.663149	0.754188	0.057505	0	32	49	46	52	46	49	59	75	77	84
ENSMUSG00000027523	chr2	Gnas	1.74E+08	1.74E+08	11186	-0.0681	9.946449	0.663809	0.754876	0.029368	0	13898	14253	18132	18418	20040	19152	22626	23561	25609	21115
ENSMUSG00000094483	chr11	Purb	6467599	6475917	8319	-0.07102	6.041046	0.66387	0.754884	0.031048	0	856	958	1211	1136	1534	1064	1699	1386	2026	1413
ENSMUSG00000079659	chr5	Tmem243	9100737	9100859	988	-0.11465	2.187789	0.664041	0.755016	0.072952	0	79	72	101	68	64	52	86	152	114	103
ENSMUSG00000004187	chr15	Kifc2	76660641	76660765	3143	-0.10545	1.709869	0.664349	0.755056	0.055963	0	48	48	62	66	50	47	87	83	76	66
ENSMUSG00000022816	chr16	Fstl1	37776873	37777152	4914	-0.11004	8.161502	0.664258	0.755056	0.076572	0	4366	3007	5146	4060	8979	5181	10003	3466	7893	5762
ENSMUSG00000028134	chr3	Ptbp2	1.2E+08	1.2E+08	3364	-0.09044	3.607612	0.664191	0.755056	0.046077	0	178	164	280	190	240	180	261	415	294	223
ENSMUSG00000028420	chr4	Tmem38b	53826045	53826220	3807	0.076768	5.94466	0.664151	0.755056	0.036486	0	767	919	1287	972	1080	1101	1417	1908	1469	1453
ENSMUSG00000034810	chr2	Scn7a	66673425	66676561	7338	0.096435	3.360965	0.664328	0.755056	0.051063	0	173	103	190	153	209	116	234	303	316	287
ENSMUSG00000049521	chr15	Cdc42ep1	78842647	78842725	2542	-0.07957	4.240242	0.664435	0.755091	0.036791	0	219	263	296	430	423	313	460	391	601	399
ENSMUSG00000080893	chr5	Gm15920	1.3E+08	1.3E+08	402	-0.09631	2.974425	0.664489	0.755091	0.048149	0	111	119	172	136	133	197	157	155	180	169
ENSMUSG00000005813	chr3	Metap1	1.38E+08	1.38E+08	2549	-0.07546	6.074318	0.664951	0.755492	0.035282	0	969	1023	1442	1081	1274	1273	1426	1938	1560	1396
ENSMUSG00000066553	chr12	Gm6969	24638669	24639010	342	0.155336	0.451837	0.664946	0.755492	0.081591	0	21	24	14	23	16	33	28	31	33	29
ENSMUSG00000031480	chr8	Thsd1	22227313	22227429	4422	-0.11648	2.148508	0.665046	0.755538	0.068071	0	40	58	99	111	74	76	95	109	127	82
ENSMUSG00000039470	chr8	Zdhhc2	40423815	40424169	5528	-0.13584	0.956404	0.665118	0.755558	0.089641	0	25	32	32	38	34	31	43	17	64	54
ENSMUSG00000021113	chr12	Snapc1	73964530	73964746	2125	0.083282	3.199401	0.665892	0.756375	0.036419	0	125	130	169	140	176	165	261	157	280	238
ENSMUSG00000027430	chr2	Dtd1	1.45E+08	1.45E+08	2353	0.083248	3.121849	0.666179	0.756639	0.035581	0	128	134	163	131	138	165	216	225	222	203
ENSMUSG00000025155	chr11	Dus1l	1.21E+08	1.21E+08	3758	0.078476	4.930406	0.666625	0.757084	0.037546	0	376	482	555	472	594	526	597	1016	848	671
ENSMUSG00000030965	chr7	Fam175b	1.33E+08	1.33E+08	5427	-0.07502	4.765551	0.666711	0.757119	0.033687	0	407	379	508	462	581	474	610	817	655	519
ENSMUSG00000042099	chr17	Kank3	33810520	33810565	3118	-0.08633	4.152527	0.666883	0.757253	0.045325	0	244	273	397	340	266	225	326	503	474	506
ENSMUSG00000005360	chr15	Slc1a3	8634124	8636339	8537	-0.16836	2.85543	0.666994	0.757316	0.177085	0	118	62	90	137	240	48	107	77	280	316
ENSMUSG00000020955	chr12	Ap4s1	51690966	51691314	1113	-0.08011	5.291959	0.667463	0.757786	0.03994	0	598	692	846	606	580	826	775	980	897	901
ENSMUSG00000035142	chr12	Nubpl	52097737	52097891	4954	-0.08698	2.522596	0.667799	0.758106	0.038901	0	87	77	111	103	110	95	113	146	153	136
ENSMUSG00000046574	chr7	Prr12	45027707	45028624	6879	-0.07641	4.406014	0.667952	0.758217	0.0344	0	307	219	400	387	534	341	468	490	650	481
ENSMUSG00000000384	chr11	Tbrg4	6615598	6615766	3696	0.074516	5.531239	0.668141	0.758334	0.034644	0	539	801	780	840	777	950	921	1099	1418	1146
ENSMUSG00000057594	chr11	Arl16	1.2E+08	1.2E+08	2742	-0.08836	2.308914	0.668164	0.758334	0.039722	0	70	68	103	85	95	90	110	100	151	103
ENSMUSG00000021108	chr12	Prkch	73584797	73585525	4519	-0.08525	3.297655	0.668312	0.758439	0.042153	0	114	147	194	218	168	133	219	213	328	236
ENSMUSG00000098557	chr14	Kctd12	1.03E+08	1.03E+08	6057	0.094856	4.923858	0.668375	0.758448	0.056721	0	476	272	469	407	883	468	916	596	1044	700
ENSMUSG00000025645	chr9	Ccdc51	1.09E+08	1.09E+08	1526	0.089902	2.881236	0.66852	0.758488	0.042368	0	101	124	129	128	99	143	165	172	205	190
ENSMUSG00000028430	chr4	Nol6	41114427	41115506	5242	0.068511	4.833696	0.668504	0.758488	0.028693	0	370	355	509	482	633	488	620	748	851	719
ENSMUSG00000021040	chr12	Slirp	87443896	87444026	3104	-0.07632	4.845639	0.668716	0.758649	0.036175	0	462	516	576	436	435	573	670	564	716	717

ENSMUSG00000046318	chr18	Ccbe1	66045302	66047469	9511	0.129626	1.649536	0.668799	0.758681	0.086519	0	61	30	58	51	40	48	82	83	55	101
ENSMUSG00000028293	chr4	Slc35a1	34663257	34664230	2293	0.074884	3.977764	0.669637	0.759507	0.032438	0	234	223	311	220	288	309	429	271	491	386
ENSMUSG00000078350	chr4	Smim1	1.54E+08	1.54E+08	5761	-0.1007	2.417121	0.6696	0.759507	0.050121	0	82	57	108	85	129	103	133	90	134	130
ENSMUSG00000039321	chr11	Uts2r	1.21E+08	1.21E+08	1703	-0.1721	1.04556	0.669879	0.759719	0.134515	0	40	15	26	32	65	51	51	49	35	24
ENSMUSG00000057143	chr7	Trim12c	1.04E+08	1.04E+08	3740	0.101229	3.058461	0.670157	0.759972	0.062054	0	116	109	152	129	161	212	180	117	189	278
ENSMUSG00000031922	chr9	Cep57	13807792	13808840	4180	-0.09676	2.504774	0.670336	0.760114	0.05363	0	96	78	104	91	113	69	126	178	154	112
ENSMUSG00000051124	chr6	Gimap9	48676129	48676254	1642	-0.14214	0.577765	0.670392	0.760115	0.087311	0	12	30	32	31	17	23	32	26	36	39
ENSMUSG00000026162	chr1	Nhej1	74967139	74967768	1118	0.092796	2.353032	0.670457	0.760126	0.04455	0	63	84	85	81	91	105	136	94	144	124
ENSMUSG00000017707	chr2	Serinc3	1.64E+08	1.64E+08	3840	0.084188	7.764	0.670602	0.760209	0.046583	0	3125	3271	4084	3527	3535	3322	5080	7864	4978	4896
ENSMUSG00000032135	chr9	Mcam	44134469	44134756	3350	-0.08455	5.541235	0.67064	0.760209	0.046261	0	607	762	805	962	851	753	1094	635	1558	1330
ENSMUSG00000020074	chr10	Ccar1	62743928	62744822	4478	-0.0696	5.129445	0.670848	0.760383	0.03044	0	478	537	678	608	698	527	882	967	883	744
ENSMUSG00000037531	chr3	Mrpl47	32725397	32727717	4419	-0.0829	4.52033	0.671752	0.761344	0.04297	0	289	422	498	410	332	447	482	640	596	414
ENSMUSG00000028013	chr3	Ppa2	1.33E+08	1.33E+08	2535	0.081244	5.239568	0.672054	0.761624	0.042699	0	478	595	763	588	637	969	943	614	1008	917
ENSMUSG00000031365	chrX	Zfp275	73342621	73342751	6745	-0.08496	3.868995	0.672139	0.761658	0.043783	0	254	171	254	198	388	198	416	357	393	303
ENSMUSG00000040591	chr2	1110051M20Rik	91275068	91277134	5202	0.071551	3.556371	0.672378	0.761866	0.028219	0	168	168	185	206	222	228	296	261	338	275
ENSMUSG00000019256	chr12	Ahr	35497974	35500700	6163	-0.13134	1.688349	0.672899	0.762395	0.100264	0	35	52	54	77	55	27	58	110	103	61
ENSMUSG00000024462	chr17	Gabbr1	37045966	37046289	7764	0.099173	3.223252	0.673447	0.762954	0.058008	0	129	129	169	119	206	123	230	350	207	211
ENSMUSG00000037458	chr15	Azin1	38487430	38490472	6231	-0.0874	6.210086	0.673602	0.763067	0.050458	0	779	1144	1595	1062	1937	1321	2093	1106	2349	1599
ENSMUSG00000020689	chr11	Itgb3	1.05E+08	1.05E+08	5901	0.132422	2.266456	0.673698	0.763112	0.105439	0	69	35	60	51	175	98	139	102	131	103
ENSMUSG00000025231	chr19	Sufu	46396896	46397284	6945	-0.07615	3.515638	0.674824	0.764325	0.032689	0	159	146	211	179	294	191	273	231	315	289
ENSMUSG00000030611	chr7	Mrps11	78783119	78783423	2172	0.082257	4.169979	0.674944	0.764399	0.041719	0	270	300	338	275	251	418	422	302	522	472
ENSMUSG00000032033	chr9	Barx2	31846044	31847055	1968	-0.17287	2.173476	0.675273	0.764709	0.190928	0	38	107	49	149	36	80	77	54	207	84
ENSMUSG00000022364	chr15	Tbc1d31	57912199	57912391	6366	-0.11561	2.277978	0.675404	0.764732	0.069467	0	60	50	94	69	154	71	118	137	114	95
ENSMUSG00000028223	chr4	Decr1	15917240	15919094	3879	0.086339	7.0041	0.675362	0.764732	0.05023	0	1634	2245	2231	2415	1730	2233	2197	3902	3533	3620
ENSMUSG00000020583	chr12	Matn3	8947929	8948251	3014	-0.27498	0.035609	0.675762	0.765075	0.384396	0	14	3	26	12	34	7	46	30	14	1
ENSMUSG00000047786	chr17	Lix1	17402672	17403026	3434	-0.14615	0.778299	0.675877	0.765143	0.093949	0	28	34	25	20	34	42	32	19	45	40
ENSMUSG00000035851	chr5	Ythdc1	86804221	86804591	10352	0.069745	4.891749	0.676236	0.765486	0.030945	0	466	443	528	429	535	542	725	844	738	681
ENSMUSG00000022180	chr14	Slc7a8	54722216	54724251	4033	0.083525	4.641508	0.676348	0.76555	0.045283	0	287	327	573	428	426	424	412	530	852	818
ENSMUSG00000020922	chr11	Lsm12	1.02E+08	1.02E+08	2388	-0.06762	5.220553	0.676557	0.765725	0.029701	0	541	588	717	656	671	781	827	734	1061	825
ENSMUSG00000019518	chr5	Ap4m1	1.38E+08	1.38E+08	3640	0.110522	2.453049	0.676725	0.76579	0.064952	0	90	74	96	68	103	60	121	186	151	145
ENSMUSG00000032952	chr3	Ap4b1	1.04E+08	1.04E+08	2907	-0.07144	3.974307	0.676682	0.76579	0.031524	0	235	235	326	284	254	251	385	428	387	333
ENSMUSG00000028107	chr3	Tars2	95739976	95740319	4438	-0.06504	4.854924	0.676813	0.765826	0.027123	0	424	446	536	530	522	552	651	595	821	679
ENSMUSG00000003992	chr13	Ssbp2	91460283	91460447	7961	-0.0694	3.661321	0.677129	0.766122	0.029435	0	206	184	231	224	225	198	338	267	342	298
ENSMUSG00000020752	chr11	Recql5	1.16E+08	1.16E+08	6986	0.076361	3.116098	0.677526	0.766508	0.033529	0	113	125	169	127	167	160	223	224	227	193
ENSMUSG00000020694	chr11	Tlk2	1.05E+08	1.05E+08	8070	-0.08462	5.505999	0.67769	0.766553	0.048118	0	677	683	855	784	907	712	930	1658	975	848
ENSMUSG00000029048	chr4	Rer1	1.55E+08	1.55E+08	1814	0.067052	6.25846	0.677732	0.766553	0.030342	0	1121	1174	1420	1090	1426	1552	1798	1698	2058	2001
ENSMUSG00000090000	chr18	Ier3ip1	76930017	76930216	1894	0.069791	5.444972	0.677703	0.766553	0.032208	0	590	717	855	669	694	931	1130	905	1212	996
ENSMUSG00000037656	chr8	Slc20a2	22476700	22476925	3649	0.08445	5.848812	0.678779	0.767549	0.048461	0	843	772	1055	1022	968	853	1248	2188	1465	1198
ENSMUSG00000048921	chr7	Zfp689	1.27E+08	1.27E+08	2005	-0.14852	0.163517	0.678777	0.767549	0.067706	0	10	15	20	23	23	16	26	18	34	21
ENSMUSG00000053886	chr8	Sh2d4a	68276567	68276872	2718	-0.09259	2.321386	0.678686	0.767549	0.046059	0	66	70	75	104	110	100	108	107	136	102
ENSMUSG00000025504	chr7	Eps8l2	1.41E+08	1.41E+08	4370	-0.12642	1.140429	0.678976	0.767673	0.07398	0	29	23	37	50	47	38	29	55	57	57
ENSMUSG00000089917	chr2	Uckl1	1.82E+08	1.82E+08	4629	-0.06885	4.19971	0.678999	0.767673	0.030135	0	325	249	388	283	314	327	425	374	518	450
ENSMUSG00000014873	chr2	Surf2	26916367	26916503	3408	0.073916	3.322404	0.679152	0.767783	0.031394	0	146	147	184	138	192	185	249	264	260	227
ENSMUSG00000047227	chr12	Gm527	64917911	64918191	1463	-0.14829	0.283008	0.679217	0.767794	0.074084	0	19	22	20	15	22	19	27	35	25	18
ENSMUSG00000091421	chr3	Gm4202	92689426	92690158	733	-0.14725	0.80946	0.680013	0.768631	0.094626	0	22	19	36	30	41	22	52	34	62	18
ENSMUSG00000085586	chr11	Gm11613	97644184	97644557	1971	0.099611	2.710837	0.680171	0.768746	0.056619	0	97	95	116	105	104	109	146	239	160	124
ENSMUSG00000028948	chr4	Nol9	1.52E+08	1.52E+08	4956	0.066717	3.936358	0.680391	0.768876	0.026631	0	241	200	277	234	291	268	355	403	453	350
ENSMUSG00000039725	chr2	2810408M09Rik	1.65E+08	1.65E+08	2118	-0.07715	3.213308	0.680452	0.768876	0.032777	0	130	133	176	142	214	188	197	189	254	213
ENSMUSG00000096474	chr1	Gm5561	1.8E+08	1.8E+08	480	0.159432	0.182704	0.680419	0.768876	0.093187	0	15	16	9	19	22	17	31	21	45	16
ENSMUSG00000021371	chr13	Mcur1	43538412	43541729	4350	-0.06792	5.47989	0.680703	0.769034	0.031296	0	640	684	805	876	792	803	843	1118	1169	1148
ENSMUSG00000039611	chr4	Tmem246	49584506	49587241	3325	-0.0934	5.102849	0.680694	0.769034	0.05953	0	430	676	826	484	526	752	938	444	925	788
ENSMUSG00000025422	chr10	Agap2	1.27E+08	1.27E+08	5633	-0.12653	1.568504	0.680896	0.769173	0.097973	0	44	45	54	72	32	27	69	89	89	55
ENSMUSG00000025795	chr10	Rassf3	1.21E+08	1.21E+08	3425	0.071283	5.872759	0.681085	0.769173	0.034796	0	746	899	1037	1113	957	1132	1689	1157	1744	1304
ENSMUSG00000029521	chr5	Chek2	1.11E+08	1.11E+08	2247	0.106661	1.687528	0.681236	0.769173	0.059827	0	40	48	76	45	42	62	86	68	96	67
ENSMUSG00000030298	chr6	Sec13	1.14E+08	1.14E+08	1663	0.065304	5.948752	0.681203	0.769173	0.029256	0	879	889	1100	926	1261	1232	1556	1253	1863	1480
ENSMUSG00000031221	chrX	Igbp1	1E+08	1E+08	5717	0.071436	5.171278	0.681157	0.769173	0.034171	0	497	582	649	595	586	659	814	1077	845	885
ENSMUSG00000036432	chr3	Siah2	58674938	58676443	2999	-0.07504	3.346235	0.681225	0.769173	0.034555	0	150	168	163	185	193	184	261	217	301	189
ENSMUSG00000075419	chr2	Dolk	30284231	30286334	2104	-0.06672	4.503099	0.68101	0.769173	0.028792	0	326	344	452	354	463	399	452	459	650	633
ENSMUSG00000082908	chr2	Gm13736	87526145	87526397	253	0.126017	1.12329	0.681271	0.769173	0.066009	0	28	31	42	38	26	39	50	51	46	66
ENSMUSG00000026942	chr2	Traf2	25517982	25519628	5101	0.06984	4.275005	0.681368	0.769221	0.03172	0	274	252	353	275	433	390	499	342	606	477
ENSMUSG00000028226	chr4	Mmp16	17852893	17853097	8667	-0.18543	0.442696	0.681425	0.769222	0.148947	0	21	7	29	18	41	22	52	14	31	19
ENSMUSG00000060121	chr12	Gemin2	59013393	59013613	2415	0.105444	2.590336	0.6816	0.769294	0.068408	0	76	112	129	65	92	158	121	112	154	159
ENSMUSG00000060260	chr7	Pwwp2b	1.39E+08	1.39E+08	2640	0.1091	2.033837	0.681581	0.769294	0.062634	0	46	58	56	88	73	73	85	72	137	123
ENSMUSG00000032570	chr9	Atp2c1	1.05E+08	1.05E+08	9689	-0.06896	4.712327	0.681887	0.769554	0.031667	0	386	384	452	443	580	389	638	747	693	535
ENSMUSG00000027080	chr2	Med19	84678402	84678661	2059	-0.07846	3.435567	0.681994	0.769613	0.03784	0	147	168	209	183	217	190	309	164	302	261
ENSMUSG00000012405	chr14	Rpl15	18267823	18269316	2397	0.064589	7.235925	0.682157	0.769734	0.029421	0	2108	2194	2952	2208	2891	2990	3854	3455	4253	3424

ENSMUSG00000027580	chr2	Helz2	1.81E+08	1.81E+08	11529	0.104815	3.44622	0.682333	0.76987	0.072987	0	134	132	207	203	202	243	239	120	277	419
ENSMUSG00000001761	chr6	Smo	29735694	29736353	3779	-0.08981	4.00228	0.682876	0.77042	0.052856	0	260	153	265	229	502	227	405	401	472	325
ENSMUSG00000009566	chr2	Fpgs	32682609	32683468	3802	0.086758	3.342634	0.68336	0.770893	0.048062	0	115	165	184	118	242	208	249	166	337	256
ENSMUSG00000030996	chr7	Art1	1.02E+08	1.02E+08	1417	0.095279	8.056622	0.683407	0.770893	0.065043	0	4472	3638	4601	4463	4103	4848	4903	11095	5874	5088
ENSMUSG00000032469	chr9	Dbr1	99575799	99576125	2488	0.090577	2.539073	0.68357	0.771014	0.049537	0	89	63	114	81	120	101	111	180	160	138
ENSMUSG00000028978	chr5	Nos3	24364810	24365001	4132	-0.0945	3.424127	0.683714	0.771114	0.060126	0	135	167	167	253	194	137	190	187	394	332
ENSMUSG00000022779	chr16	Top3b	16870736	16870829	8340	-0.06528	3.892662	0.683894	0.771254	0.026471	0	210	204	267	263	327	237	369	323	403	366
ENSMUSG00000020034	chr10	Tcp11l2	84576626	84577012	3438	-0.10224	5.763314	0.684138	0.771467	0.07416	0	784	795	1258	877	1004	755	968	2340	1118	917
ENSMUSG00000051451	chr7	Crebzf	90442729	90446104	4989	0.08374	3.527583	0.684294	0.77158	0.04287	0	182	146	225	153	226	135	260	311	387	317
ENSMUSG00000058388	chr3	Phtf1	1.04E+08	1.04E+08	7294	0.082736	2.97196	0.684571	0.771829	0.041713	0	96	102	151	131	155	144	240	136	223	192
ENSMUSG00000018651	chr11	Tada2a	84078920	84079777	2974	-0.07542	3.501577	0.684723	0.771937	0.034597	0	194	148	244	160	220	226	246	229	284	286
ENSMUSG00000027522	chr2	Stx16	1.74E+08	1.74E+08	3962	0.064666	5.060664	0.684894	0.772068	0.028382	0	491	481	609	503	636	605	930	733	853	854
ENSMUSG00000012422	chr13	Tmem167	90089123	90089783	10807	-0.06655	4.929147	0.685277	0.772373	0.030033	0	461	438	606	414	701	516	666	787	823	688
ENSMUSG00000079557	chr17	March2	33685692	33686398	5997	-0.07182	6.347618	0.685248	0.772373	0.036715	0	1182	1289	1638	1388	1458	1644	1526	2250	1859	1878
ENSMUSG00000009741	chr9	Ubp1	1.14E+08	1.14E+08	3850	-0.06237	4.738972	0.685644	0.772599	0.026454	0	381	424	495	432	543	421	670	578	728	670
ENSMUSG00000073198	chr12	Gm10480	18216555	18217757	1203	-0.15864	0.000928	0.685533	0.772599	0.137018	0	19	15	16	12	17	6	12	41	25	18
ENSMUSG00000091243	chr16	Vgll3	65815633	65815758	3322	-0.09357	2.664362	0.68563	0.772599	0.050438	0	74	83	121	112	159	92	188	118	192	127
ENSMUSG00000058076	chr1	Sdhc	1.71E+08	1.71E+08	3250	0.072973	8.023613	0.68589	0.772812	0.038752	0	3407	4440	4843	4496	3794	6029	5707	5678	6994	6397
ENSMUSG00000031828	chr8	Klhl36	1.2E+08	1.2E+08	2141	0.122744	1.068614	0.685995	0.772868	0.063822	0	24	30	42	24	41	34	55	35	59	62
ENSMUSG00000026785	chr2	Pkn3	30077684	30077799	4255	0.104878	2.665208	0.686226	0.772939	0.063452	0	78	111	112	129	64	118	152	125	191	174
ENSMUSG00000048503	chr9	Tmem136	43108653	43111858	3500	-0.11253	1.241772	0.686208	0.772939	0.066337	0	43	40	46	29	37	35	65	56	57	43
ENSMUSG00000099227	chr1	Mir8114	1.54E+08	1.54E+08	111	0.15763	4.079326	0.686215	0.772939	0.17554	0	362	135	280	219	329	120	246	1029	381	326
ENSMUSG00000024168	chr17	Tmem204	25057702	25058473	2022	-0.06998	3.790165	0.686329	0.772992	0.031481	0	201	200	260	269	245	255	348	314	408	247
ENSMUSG00000018102	chr13	Hist1h2bc	23684199	23684621	736	-0.06795	5.667902	0.686839	0.773429	0.032661	0	675	843	1100	879	837	1039	1254	1033	1329	1100
ENSMUSG00000020238	chr10	Ncln	81486249	81487605	3465	-0.06127	5.705791	0.686784	0.773429	0.026485	0	694	793	1041	878	1069	888	1123	1198	1551	1248
ENSMUSG00000025173	chr11	Wdr45b	1.21E+08	1.21E+08	4562	-0.06606	4.724949	0.686884	0.773429	0.030188	0	361	456	512	393	532	404	626	695	737	574
ENSMUSG00000024037	chr17	Wdr4	31494323	31496928	5432	-0.07381	3.169027	0.687022	0.773521	0.033298	0	131	123	173	145	197	161	185	176	287	214
ENSMUSG00000004347	chr6	Pde1c	56069821	56071041	12803	-0.13356	0.565131	0.687097	0.773543	0.083509	0	15	17	35	35	20	18	43	30	38	27
ENSMUSG00000036139	chr15	Hoxc9	1.03E+08	1.03E+08	2430	0.085053	3.090358	0.687168	0.77356	0.045729	0	122	125	155	137	141	184	188	259	175	189
ENSMUSG00000001349	chr9	Cnn1	22099281	22099418	2368	0.181435	1.012957	0.687428	0.77379	0.204879	0	15	22	26	59	28	35	58	10	102	41
ENSMUSG00000040195	chr10	Tmem194	1.28E+08	1.28E+08	7822	0.092911	2.344289	0.687597	0.773917	0.04774	0	82	61	75	93	90	97	127	130	155	93
ENSMUSG00000031556	chr8	Tm2d2	25017211	25017592	1280	0.068423	5.333521	0.687706	0.773977	0.033063	0	611	584	745	595	742	756	870	1231	979	949
ENSMUSG00000038668	chr4	Lpar1	58435255	58437634	4289	-0.08675	4.557693	0.687922	0.774156	0.051779	0	348	220	457	342	716	416	670	476	681	430
ENSMUSG00000025651	chr9	Uqcrc1	1.09E+08	1.09E+08	4135	-0.0748	9.660702	0.688017	0.774201	0.041518	0	10414	14927	14959	16339	11947	16418	15899	19527	22435	17440
ENSMUSG00000025407	chr10	Gli1	1.27E+08	1.27E+08	3665	-0.17471	0.474598	0.688285	0.774439	0.149515	0	22	13	14	20	48	10	32	51	31	20
ENSMUSG00000000826	chr2	Dnajc5	1.82E+08	1.82E+08	6953	-0.06201	6.055683	0.688388	0.774492	0.027682	0	938	989	1219	1177	1368	1195	1593	1560	1825	1437
ENSMUSG00000051224	chrX	Tceanc	1.66E+08	1.67E+08	4201	0.135156	1.550388	0.688505	0.774561	0.108085	0	31	41	52	46	57	36	51	138	67	55
ENSMUSG00000031661	chr8	Nkd1	88521344	88521531	4459	0.124335	1.369854	0.688842	0.774877	0.084274	0	30	40	25	42	62	40	86	48	85	48
ENSMUSG00000032584	chr9	Mst1r	1.08E+08	1.08E+08	5007	-0.1326	1.136201	0.688912	0.774894	0.093837	0	48	27	36	18	55	28	38	52	62	58
ENSMUSG00000027478	chr2	Dnmt3b	1.54E+08	1.54E+08	5106	0.13468	0.518437	0.688996	0.774925	0.071531	0	19	21	21	17	28	17	35	32	32	48
ENSMUSG00000019878	chr10	Hsf2	57486385	57486601	2613	0.08926	4.77148	0.689415	0.775137	0.057343	0	389	345	493	468	519	459	594	1124	611	471
ENSMUSG00000022840	chr16	Adcy5	35154877	35157235	7007	0.140534	2.302777	0.689521	0.775137	0.130428	0	61	38	65	98	131	42	89	87	176	220
ENSMUSG00000026307	chr1	Scly	91298338	91298448	4549	0.080164	3.665506	0.689496	0.775137	0.042595	0	170	183	212	234	222	280	277	187	406	363
ENSMUSG00000037972	chr16	Snn	11066298	11066447	2902	0.078854	3.333519	0.689435	0.775137	0.039924	0	96	155	173	201	192	170	219	249	293	276
ENSMUSG00000040877	chr12	Wdr25	1.09E+08	1.09E+08	4398	-0.09835	1.831627	0.68927	0.775137	0.050452	0	45	60	69	50	77	69	71	74	85	90
ENSMUSG00000042549	chr11	Map2k3os	60920917	60921905	1291	-0.12291	2.170926	0.689436	0.775137	0.089906	0	68	72	83	91	67	107	81	149	79	63
ENSMUSG00000036661	chr15	Dennd3	73512560	73512847	5703	-0.08902	2.143889	0.689591	0.775153	0.046892	0	60	57	79	90	89	59	103	100	134	102
ENSMUSG00000031068	chr7	Glrx3	1.37E+08	1.37E+08	1651	-0.06769	6.717511	0.689698	0.775211	0.033837	0	1489	1795	2068	1824	1762	2118	2129	2342	2678	2653
ENSMUSG00000025917	chr1	Cops5	10024601	10025063	3766	-0.07771	6.775718	0.689822	0.775287	0.044788	0	1727	1796	2123	1782	1900	2069	2151	3522	2257	2286
ENSMUSG00000015597	chr17	Zfp318	46383731	46384330	8594	0.079662	3.78909	0.690278	0.775676	0.04255	0	210	165	237	224	286	198	331	481	369	282
ENSMUSG00000098381	chr3	Mir7225	97690509	97690562	54	0.077768	7.679271	0.690281	0.775676	0.045382	0	2775	2812	3541	3668	3916	4480	3684	6678	4468	4838
ENSMUSG00000020142	chr11	Slc1a4	20302180	20304500	3926	-0.13848	1.944935	0.690368	0.775712	0.119871	0	68	38	45	46	140	65	132	54	99	69
ENSMUSG00000036572	chrX	Upf3b	37091678	37092661	3999	-0.07173	3.836633	0.690899	0.776245	0.033029	0	213	191	313	211	299	260	311	386	309	339
ENSMUSG00000054414	chr3	Slc30a7	1.16E+08	1.16E+08	9020	0.079685	3.57111	0.691391	0.776734	0.043025	0	198	107	226	164	278	202	311	243	392	286
ENSMUSG00000020549	chr11	Elac2	64979038	64979331	3479	0.068747	4.78066	0.691749	0.776944	0.033739	0	343	370	507	500	531	467	565	867	770	621
ENSMUSG00000021748	chr14	Pdhb	8165991	8166481	1485	0.074854	8.513817	0.691766	0.776944	0.042502	0	4614	6936	6625	6121	4997	8053	8178	8275	9853	9074
ENSMUSG00000037617	chr15	Spag1	36179368	36179582	3814	0.15637	-0.06785	0.691688	0.776944	0.082769	0	12	15	11	13	16	22	20	12	21	29
ENSMUSG00000039117	chr2	Taf4a	1.8E+08	1.8E+08	4627	0.073986	3.27912	0.691802	0.776944	0.034619	0	126	134	173	172	180	161	252	283	244	213
ENSMUSG00000026753	chr2	Ppp6c	39194354	39197589	4219	0.063456	5.891245	0.691988	0.777027	0.029683	0	831	910	1125	877	1100	1211	1304	1493	1619	1418
ENSMUSG00000039018	chr7	Mtg1	1.4E+08	1.4E+08	4019	0.074537	4.506147	0.691932	0.777027	0.039702	0	290	406	395	346	392	573	510	443	564	571
ENSMUSG00000007837	chr7	Prrg2	45053613	45054197	2091	0.081072	3.203925	0.692266	0.777276	0.044079	0	105	150	196	156	132	198	195	204	229	259
ENSMUSG00000006599	chr7	Gtf2h1	46796103	46796288	2984	0.064416	4.374307	0.692794	0.777806	0.028342	0	292	301	382	328	385	345	478	597	549	505
ENSMUSG00000024974	chr19	Smc3	53600398	53600554	5541	0.067662	4.91568	0.692999	0.777973	0.033367	0	405	349	521	537	677	507	727	893	840	648
ENSMUSG00000040463	chr11	Mybbp1a	72441355	72441575	5803	0.07629	6.121453	0.693155	0.778085	0.043882	0	882	921	1315	1139	1466	1106	1283	2461	1968	1576
ENSMUSG00000041459	chr4	Tardbp	1.49E+08	1.49E+08	7796	0.063435	6.62577	0.693234	0.778111	0.03034	0	1399	1460	2039	1400	1782	1861	2342	2441	2664	2467
ENSMUSG00000035757	chr15	Selo	89089084	89089665	3744	-0.08421	4.031932	0.693695	0.778565	0.051425	0	233	301	299	267	287	228	270	576	391	389

ENSMUSG00000051339	chr5	2900026A02Rik	1.13E+08	1.13E+08	5876	0.066935	5.750923	0.693793	0.778612	0.033662	0	683	630	922	1015	1203	970	1213	1491	1640	1150
ENSMUSG00000031816	chr8	Mthfsd	1.21E+08	1.21E+08	4894	-0.07542	3.34931	0.693886	0.778653	0.036423	0	140	149	217	167	198	200	236	164	275	273
ENSMUSG00000029030	chr4	Tprgl	1.54E+08	1.54E+08	2242	-0.0689	6.414026	0.694729	0.779536	0.036089	0	1247	1283	1585	1536	1638	1580	1690	2513	1922	1930
ENSMUSG00000001105	chr11	Ift20	78536361	78536576	1525	-0.07019	4.137995	0.694841	0.779586	0.034366	0	248	283	380	256	336	344	467	289	493	404
ENSMUSG00000033610	chr19	Pank1	34810894	34812387	3692	0.083055	3.727891	0.694942	0.779586	0.047097	0	191	185	231	234	223	194	243	479	405	279
ENSMUSG00000039474	chr5	Wfs1	36966104	36968678	3564	0.074563	6.313746	0.69492	0.779586	0.042267	0	1092	1067	1310	1737	1231	1470	2216	1438	2729	1787
ENSMUSG00000030814	chr7	Bcl7c	1.28E+08	1.28E+08	5331	0.065224	4.532812	0.695189	0.779736	0.031545	0	275	313	458	333	536	488	588	476	618	569
ENSMUSG00000038685	chr2	Rtel1	1.81E+08	1.81E+08	6616	0.078968	3.128583	0.695136	0.779736	0.039764	0	131	121	154	119	180	161	210	156	253	263
ENSMUSG00000033763	chr8	Mtss1l	1.11E+08	1.11E+08	5311	0.080265	5.862248	0.695292	0.779789	0.049164	0	746	666	1098	1208	1042	830	1400	2062	1385	1329
ENSMUSG00000002342	chr8	Tmem161a	70172356	70172440	3673	0.067881	6.17165	0.695427	0.779876	0.035181	0	1025	1030	1369	1164	1289	1443	1534	2193	1789	1580
ENSMUSG00000029659	chr5	Medag	1.49E+08	1.49E+08	3956	0.090024	4.411513	0.695508	0.779904	0.061273	0	313	201	389	285	570	397	783	511	472	371
ENSMUSG00000104300	chr9	DHX30	1.1E+08	1.1E+08	3672	-0.06208	4.948631	0.695593	0.779936	0.027622	0	451	445	595	455	705	585	695	719	790	720
ENSMUSG00000024091	chr17	Vapa	65580056	65580847	1640	-0.0643	6.845377	0.695672	0.779962	0.031772	0	1691	1819	2334	1767	2211	2253	2595	2920	2909	2367
ENSMUSG00000041840	chr18	Haus1	77757567	77757753	1004	0.076029	3.313181	0.695783	0.780023	0.039163	0	148	136	212	124	184	208	227	195	255	288
ENSMUSG00000033653	chr16	Vps8	21423118	21423225	8670	0.086473	3.434885	0.696143	0.780363	0.050992	0	149	157	190	149	228	187	270	142	413	305
ENSMUSG00000025089	chr19	Gfra1	58235604	58238546	5476	-0.09804	3.175903	0.696302	0.780479	0.063281	0	133	108	138	141	268	143	203	303	190	166
ENSMUSG00000058638	chr7	Zfp110	12834761	12835164	4116	0.065721	3.794125	0.696394	0.780518	0.028345	0	204	182	256	232	253	217	323	379	398	344
ENSMUSG00000019880	chr10	Rspo3	29453109	29454329	2394	-0.14025	0.269964	0.696572	0.780528	0.092992	0	14	14	18	19	34	16	17	41	30	20
ENSMUSG00000035572	chr4	Dcaf10	45342101	45342727	7305	-0.08072	4.237329	0.696517	0.780528	0.047543	0	265	261	363	335	401	260	368	691	440	381
ENSMUSG00000042579	chr3	4632404H12Rik	89767511	89769562	2791	-0.12012	1.234471	0.696519	0.780528	0.073542	0	36	32	56	29	45	53	36	61	60	40
ENSMUSG00000028631	chr4	Kcnq4	1.21E+08	1.21E+08	4024	0.065373	4.731313	0.696808	0.780729	0.031386	0	323	396	502	435	519	462	718	752	705	530
ENSMUSG00000018999	chr6	Slc35b4	34153380	34158626	9177	0.080651	3.647782	0.697016	0.780899	0.045614	0	183	144	220	182	295	207	281	197	460	380
ENSMUSG00000079316	chrX	Rab9	1.66E+08	1.66E+08	1749	0.077119	4.066756	0.697265	0.781115	0.042473	0	243	255	310	253	289	283	357	603	418	335
ENSMUSG00000007216	chr6	Zfp775	48613180	48613259	4083	-0.08372	2.791249	0.697345	0.78114	0.04553	0	111	98	128	122	127	112	123	210	188	145
ENSMUSG00000039621	chr2	Prex1	1.67E+08	1.67E+08	10266	0.079378	4.483484	0.6974	0.78114	0.047588	0	339	183	413	343	577	367	642	432	694	573
ENSMUSG00000030967	chr7	Zranb1	1.33E+08	1.33E+08	5431	0.112848	6.456365	0.698396	0.782193	0.100461	0	1345	1144	1521	1409	1623	1306	1368	4650	1738	1515
ENSMUSG00000027230	chr2	Creb3l1	91982328	91983007	2603	-0.13061	4.258037	0.698541	0.782291	0.12984	0	273	142	346	221	767	371	612	159	575	417
ENSMUSG00000027367	chr2	Stard7	1.27E+08	1.27E+08	5567	0.080968	7.163245	0.699328	0.78311	0.052056	0	1917	2220	2323	2832	2246	2300	3055	5351	3615	2908
ENSMUSG00000032458	chr9	Copb2	98563721	98563823	6351	0.060779	6.639861	0.699447	0.783146	0.029153	0	1421	1251	1783	1593	2186	1855	2462	2240	2822	2538
ENSMUSG00000070610	chr4	Gm13127	1.45E+08	1.45E+08	1389	0.1101	1.089498	0.699474	0.783146	0.0699	0	17	33	44	36	34	41	38	48	75	46
ENSMUSG00000029869	chr6	Ephb6	41605482	41605820	3773	0.130948	0.983364	0.699802	0.78345	0.084164	0	22	24	23	42	39	26	54	30	76	49
ENSMUSG00000055707	chr8	Klhl26	70450228	70453019	3069	-0.06907	3.548795	0.700127	0.783751	0.032636	0	153	179	219	203	245	180	260	332	277	278
ENSMUSG00000013646	chr11	Sh3bp5l	58330724	58330802	6352	-0.0609	4.804685	0.700235	0.783808	0.027711	0	403	421	533	472	553	479	565	710	726	712
ENSMUSG00000021815	chr14	Mss51	20482864	20483241	1829	0.1384	3.900701	0.700374	0.7839	0.149797	0	311	66	301	103	435	230	437	514	441	210
ENSMUSG00000016087	chr9	Fli1	32422204	32424305	3486	0.083476	3.164615	0.700704	0.784206	0.045606	0	109	141	132	182	152	116	225	217	280	249
ENSMUSG00000004897	chr3	Hdgf	87906321	87906714	2873	0.062633	7.873933	0.700832	0.784286	0.031621	0	3211	3412	4470	3878	4225	5040	4895	5814	6171	5834
ENSMUSG00000099881	chr8	2810013P06Rik	1.23E+08	1.23E+08	2137	0.089613	2.773751	0.701501	0.784971	0.054341	0	92	104	110	127	109	135	121	226	191	136
ENSMUSG00000001661	chr15	Hoxc6	1.03E+08	1.03E+08	2408	0.080053	3.039269	0.701855	0.78524	0.040962	0	131	115	148	116	148	148	230	146	280	183
ENSMUSG00000045519	chr9	Zfp560	20345136	20349159	4981	0.082363	2.535438	0.701817	0.78524	0.043236	0	83	92	93	87	105	125	124	143	137	148
ENSMUSG00000021054	chr12	Sgpp1	75714248	75716664	3324	-0.06367	4.637083	0.701984	0.785257	0.030426	0	348	411	475	336	558	449	614	589	694	493
ENSMUSG00000049811	chr11	Fam161a	23007531	23007608	4396	0.130187	0.80616	0.702032	0.785257	0.078744	0	28	28	27	19	28	22	36	35	49	62
ENSMUSG00000073471	chr17	Rsph3a	7945653	7946303	2189	0.079884	2.972788	0.70204	0.785257	0.040483	0	99	126	156	131	115	143	184	217	207	179
ENSMUSG00000019689	chr6	1110001J03Rik	38533502	38533711	689	-0.07335	5.092292	0.702182	0.785352	0.042144	0	540	612	707	542	471	769	676	797	848	728
ENSMUSG00000002249	chr17	Tead3	28331671	28332833	4398	0.075315	2.894206	0.702297	0.785417	0.035716	0	96	97	137	134	136	122	203	186	208	166
ENSMUSG00000026435	chr1	Slc45a3	1.32E+08	1.32E+08	3563	-0.10865	1.425903	0.70237	0.785436	0.065753	0	48	24	51	44	60	46	44	69	78	56
ENSMUSG00000018765	chr11	Fxr2	69632990	69633398	3766	0.080394	6.733716	0.702602	0.785632	0.052526	0	1398	1537	2074	1738	1920	1975	2041	4090	2260	2261
ENSMUSG00000054509	chr14	Parp4	56575619	56575730	6534	-0.07265	3.596486	0.702723	0.785703	0.037809	0	189	130	233	219	270	167	272	341	343	262
ENSMUSG00000030560	chr7	Ctsc	88278085	88278374	5801	0.066235	6.130042	0.702874	0.785746	0.035302	0	982	830	1283	1031	1680	1171	1945	1388	2132	1818
ENSMUSG00000040913	chr19	Fbxw4	45578254	45578925	3158	0.060526	4.458451	0.702832	0.785746	0.026891	0	309	337	367	346	430	419	457	536	627	575
ENSMUSG00000009545	chr7	Kcnq1	1.43E+08	1.43E+08	4093	0.167052	0.263994	0.703027	0.785853	0.101656	0	14	26	16	11	18	13	24	22	49	32
ENSMUSG00000016239	chrX	Lonrf3	36328353	36329399	3812	0.152767	0.267522	0.703675	0.786514	0.102332	0	13	15	14	16	30	12	16	32	36	42
ENSMUSG00000032298	chr9	Neil1	57142800	57143326	1871	-0.08402	2.775896	0.704176	0.786946	0.049225	0	96	131	116	101	133	118	170	105	210	171
ENSMUSG00000036622	chr4	Atp13a2	1.41E+08	1.41E+08	6000	-0.05846	5.052472	0.704121	0.786946	0.026495	0	469	462	699	556	656	552	802	711	976	782
ENSMUSG00000064120	chr17	Mocs1	49428362	49428564	3110	0.138571	4.040018	0.704319	0.787043	0.153791	0	223	203	283	268	334	158	207	1036	285	318
ENSMUSG00000013495	chr5	Tmem175	1.09E+08	1.09E+08	3875	0.081936	2.8472	0.704481	0.78716	0.044453	0	93	90	158	104	138	99	160	190	203	212
ENSMUSG00000029095	chr5	Ablim2	35757880	35758060	7047	-0.0583	5.561737	0.704764	0.787362	0.026879	0	703	696	859	781	992	869	1155	1136	1167	1052
ENSMUSG00000059486	chr6	Kbtbd2	56777524	56780413	4083	-0.06597	4.520624	0.704775	0.787362	0.033775	0	316	366	435	382	459	334	518	703	585	487
ENSMUSG00000042506	chr11	Usp22	61151785	61154513	4886	0.060482	4.558391	0.70529	0.787873	0.027567	0	336	307	387	391	512	380	600	583	727	542
ENSMUSG00000007603	chr17	Dus3l	56764751	56764941	2303	0.061027	4.170246	0.705375	0.787905	0.027333	0	271	237	346	294	318	321	431	487	484	416
ENSMUSG00000029627	chr5	Zkscan14	1.45E+08	1.45E+08	1967	-0.08216	3.224301	0.705849	0.788371	0.047543	0	146	143	205	139	161	157	185	306	213	185
ENSMUSG00000090136	chr9	Gm10177	37252922	37253365	444	0.090733	2.454708	0.706379	0.788899	0.058924	0	81	84	111	63	96	118	138	108	109	166
ENSMUSG00000032193	chr9	Ldlr	21723576	21723844	4531	-0.11443	4.497711	0.706757	0.789257	0.105513	0	247	188	261	397	966	434	436	347	751	579
ENSMUSG00000015656	chr9	Hspa8	40800984	40801348	4156	-0.06837	10.03943	0.707584	0.790053	0.03974	0	13036	17383	20459	16601	23275	23407	25677	16943	28053	24846
ENSMUSG00000025607	chr6	Copg2	30747554	30748987	4477	-0.06002	4.639681	0.707546	0.790053	0.02804	0	375	392	503	362	488	461	638	495	650	596
ENSMUSG00000042364	chr13	Snx18	1.14E+08	1.14E+08	4446	0.06302	4.386694	0.707705	0.790125	0.030786	0	288	241	372	345	481	311	540	531	626	512
ENSMUSG00000019998	chr10	Stx7	24149317	24149726	2500	0.063524	5.150966	0.708158	0.790345	0.032308	0	484	567	658	510	677	654	948	624	1121	921

ENSMUSG00000024901	chr19	Peli3	4930651	4932867	3786	-0.18917	0.896298	0.708016	0.790345	0.25159	0	27	35	42	27	25	13	15	108	21	36
ENSMUSG00000026837	chr2	Col5a1	27886425	27886924	8490	-0.11214	7.988045	0.708115	0.790345	0.106762	0	3497	2192	4546	3273	9565	4247	8284	2533	8324	5592
ENSMUSG00000028252	chr4	Ccnc	21727701	21727915	5115	-0.07103	3.220819	0.708187	0.790345	0.036461	0	151	146	191	136	163	166	240	165	272	215
ENSMUSG00000030189	chr6	Ybx3	1.31E+08	1.31E+08	1862	-0.08546	9.200323	0.708115	0.790345	0.062248	0	8686	8593	10799	11207	11350	9704	9432	23155	11852	11955
ENSMUSG00000020021	chr10	Fgd6	94036001	94036310	8241	-0.09159	2.470658	0.708432	0.790554	0.062784	0	90	70	105	98	108	58	112	102	190	174
ENSMUSG00000023939	chr17	Mrpl14	45686322	45686427	949	0.07123	5.175268	0.70937	0.791537	0.04143	0	474	640	620	689	467	793	753	875	1022	842
ENSMUSG00000059325	chr5	Hopx	77086988	77087816	1516	0.088109	2.684546	0.709545	0.791668	0.055765	0	75	92	111	80	163	120	141	108	195	203
ENSMUSG00000030889	chr7	Vwa3a	1.21E+08	1.21E+08	5821	-0.16927	0.201947	0.709755	0.791838	0.192264	0	20	18	18	26	9	3	19	25	26	47
ENSMUSG00000029686	chr6	Cul1	47453398	47453627	4058	-0.0825	6.354326	0.709931	0.791971	0.058013	0	1210	1202	1611	1394	1630	1182	1709	3200	1719	1448
ENSMUSG00000013593	chr1	Ndufs2	1.71E+08	1.71E+08	2313	-0.07327	9.719246	0.71022	0.792231	0.046519	0	11989	15957	16744	15111	11267	17574	17317	22403	19302	18064
ENSMUSG00000020311	chr11	Erlec1	30930774	30931848	3260	-0.06189	5.096089	0.710552	0.792537	0.031166	0	513	502	687	554	662	633	716	974	828	728
ENSMUSG00000045466	chr6	Zfp956	47953390	47953582	2968	0.091315	2.846661	0.710731	0.792672	0.061818	0	105	94	139	111	126	115	116	273	175	176
ENSMUSG00000038637	chr7	Lrrc56	1.41E+08	1.41E+08	6068	-0.13303	1.095626	0.71098	0.792887	0.105947	0	15	31	36	60	38	27	30	59	62	53
ENSMUSG00000055817	chr17	Mta3	83706163	83706285	5319	0.068236	3.219841	0.711162	0.792961	0.033646	0	137	114	164	139	205	142	221	235	279	239
ENSMUSG00000059534	chr11	Uqcr10	4701973	4702220	584	0.075117	8.105535	0.711124	0.792961	0.049015	0	3671	5197	5676	3971	3569	6634	6362	6408	6731	6283
ENSMUSG00000062691	chr17	Cebpzos	78916500	78916525	1131	-0.07287	4.026413	0.711248	0.792993	0.041321	0	249	268	363	258	240	392	355	355	378	328
ENSMUSG00000032495	chr9	Lrrc2	1.11E+08	1.11E+08	3657	0.152168	5.16593	0.711749	0.793454	0.198826	0	521	456	550	866	397	386	531	2435	620	418
ENSMUSG00000069171	chr13	Nr2f1	78188973	78190013	4752	0.135724	0.243065	0.711776	0.793454	0.08434	0	23	11	17	12	23	16	24	21	34	39
ENSMUSG00000048439	chr5	Nupl2	24164963	24165203	3768	-0.07655	2.647637	0.711882	0.793509	0.039628	0	101	80	132	110	107	104	130	136	178	159
ENSMUSG00000020178	chr10	Adora2a	75316943	75317147	2534	0.124841	1.181448	0.712018	0.793518	0.093898	0	21	29	39	56	28	25	53	50	65	76
ENSMUSG00000024158	chr17	Hagh	24840143	24840281	1908	-0.06395	5.684794	0.712062	0.793518	0.034575	0	716	848	1084	853	875	981	1063	1443	1186	1143
ENSMUSG00000066724	chr7	Gm10175	23946649	23947237	589	-0.11209	0.808267	0.71203	0.793518	0.085586	0	26	35	17	36	27	28	32	43	54	31
ENSMUSG00000061898	chr5	Rbak	1.43E+08	1.43E+08	3623	-0.09945	2.123603	0.712448	0.793884	0.070182	0	76	66	78	49	100	54	89	144	104	94
ENSMUSG00000054580	chr2	Pla2r1	60417543	60420302	9618	-0.09074	1.841836	0.712564	0.793949	0.05466	0	64	41	74	53	70	52	83	90	108	67
ENSMUSG00000038241	chr2	Cep250	1.56E+08	1.56E+08	10373	0.070554	3.449522	0.712924	0.794222	0.037811	0	140	130	191	211	219	199	209	218	375	311
ENSMUSG00000087090	chr7	Nctc1	1.43E+08	1.43E+08	3438	-0.07519	6.099328	0.712872	0.794222	0.048865	0	1193	867	1431	1038	1362	1150	1252	2244	1361	1722
ENSMUSG00000005533	chr7	Igf1r	67952859	67952952	4489	-0.09546	2.513375	0.713014	0.794259	0.069707	0	107	52	111	88	132	67	154	158	172	96
ENSMUSG00000024826	chr19	Dpf2	5896516	5898631	6501	-0.06018	5.718192	0.713313	0.794528	0.030754	0	788	742	1019	927	1018	990	1202	1439	1332	1022
ENSMUSG00000017309	chr11	Cd300lg	1.02E+08	1.02E+08	2737	0.091258	4.941112	0.713576	0.794694	0.070733	0	388	459	594	655	359	392	476	1090	904	891
ENSMUSG00000056204	chr8	Pgpep1	70646436	70650785	4882	0.062812	4.484828	0.713577	0.794694	0.032245	0	297	295	346	408	490	428	559	403	684	602
ENSMUSG00000026516	chr1	Nvl	1.81E+08	1.81E+08	13488	0.061067	3.964157	0.714004	0.794786	0.028503	0	236	186	290	271	291	252	350	425	458	382
ENSMUSG00000029012	chr5	Orc5	22486485	22487217	2825	-0.06298	3.540547	0.713974	0.794786	0.030889	0	184	185	235	182	194	192	264	299	309	260
ENSMUSG00000038256	chr3	Bcl9	97203662	97205977	8285	0.086462	2.620467	0.713872	0.794786	0.055987	0	106	59	77	120	129	100	143	139	182	171
ENSMUSG00000047909	chr2	Ankrd16	11777876	11778227	5926	0.067186	3.822368	0.71378	0.794786	0.035411	0	229	189	246	189	296	255	292	422	343	362
ENSMUSG00000051316	chr18	Taf7	37640491	37643532	3302	-0.13365	3.543229	0.713876	0.794786	0.150684	0	180	162	228	204	242	126	181	663	181	131
ENSMUSG00000058297	chr10	Spock2	60106219	60106656	5533	0.164665	3.852079	0.713958	0.794786	0.233215	0	312	91	181	180	376	123	219	996	253	184
ENSMUSG00000037214	chr8	Thap1	26158212	26158521	1328	-0.1069	1.101969	0.714627	0.795415	0.065187	0	40	33	43	29	31	29	47	43	54	60
ENSMUSG00000024940	chr19	Ltbp3	5740904	5740985	5190	0.066945	6.223614	0.714725	0.795461	0.039464	0	1083	760	1222	1204	1949	1237	1957	1729	2318	1786
ENSMUSG00000023393	chr2	Slc17a9	1.81E+08	1.81E+08	3200	0.243425	-0.45177	0.715308	0.795929	0.333332	0	10	1	9	1	29	6	7	12	25	31
ENSMUSG00000027313	chr2	Chac1	1.19E+08	1.19E+08	1637	0.183914	4.90047	0.715318	0.795929	0.297181	0	335	384	209	992	367	279	215	2101	399	689
ENSMUSG00000027324	chr2	Rpusd2	1.19E+08	1.19E+08	2706	-0.10829	1.389145	0.715232	0.795929	0.078796	0	36	35	51	48	50	33	57	93	65	38
ENSMUSG00000004837	chr11	Grap	61653265	61653424	1793	0.080716	2.944772	0.715663	0.796142	0.047288	0	79	118	146	151	125	162	156	147	247	203
ENSMUSG00000016386	chr2	Mpped2	1.07E+08	1.07E+08	3425	-0.18881	0.816935	0.715683	0.796142	0.242101	0	5	66	19	34	20	44	21	32	43	40
ENSMUSG00000042901	chr1	Aida	1.83E+08	1.83E+08	6175	-0.05741	4.757389	0.715647	0.796142	0.026905	0	384	386	560	412	575	510	614	554	744	667
ENSMUSG00000045822	chr2	Zswim3	1.65E+08	1.65E+08	2708	-0.10848	1.11594	0.715924	0.796331	0.064518	0	24	36	51	30	40	45	55	40	50	41
ENSMUSG00000085172	chr18	Gm6542	36609958	36610729	772	-0.11556	0.825773	0.715967	0.796331	0.069776	0	20	29	27	43	26	28	35	37	53	37
ENSMUSG00000001158	chr6	Snrnp27	86675221	86675580	1767	0.06112	5.485197	0.71631	0.796648	0.032518	0	608	734	853	679	768	1023	1105	954	1159	1028
ENSMUSG00000065529	chr11	Mir22	75463716	75463810	95	0.148082	2.156699	0.716766	0.797092	0.170299	0	83	40	76	55	93	45	71	262	97	63
ENSMUSG00000001054	chr11	Rmnd5b	51623671	51624146	2161	0.059852	3.811624	0.716898	0.797174	0.026804	0	219	179	255	237	251	237	341	324	425	351
ENSMUSG00000031750	chr8	Il34	1.11E+08	1.11E+08	1959	0.079601	2.825383	0.717302	0.797559	0.048072	0	107	75	152	128	108	134	188	135	240	150
ENSMUSG00000025868	chr13	Higd2a	54590207	54590419	648	0.066815	6.256222	0.717829	0.798081	0.040075	0	1011	1324	1349	1324	1157	1834	1666	1773	1883	1813
ENSMUSG00000090236	chr16	Car15	17835276	17835539	1283	0.147878	0.117241	0.718034	0.798245	0.079469	0	16	13	20	11	18	14	37	22	21	27
ENSMUSG00000015536	chr13	Mocs2	1.15E+08	1.15E+08	9054	-0.06929	5.501406	0.718388	0.798575	0.042709	0	681	781	919	687	775	830	857	1444	977	997
ENSMUSG00000099112	chr15	Gm27406	1.02E+08	1.02E+08	182	0.067106	4.044783	0.719508	0.799756	0.038552	0	234	166	301	287	373	276	335	519	468	374
ENSMUSG00000039328	chr8	Rnf122	31111820	31112172	7080	0.067888	3.737752	0.719661	0.799861	0.038899	0	133	215	222	249	268	300	345	261	366	299
ENSMUSG00000084093	chr1	Gm16418	1.66E+08	1.66E+08	171	0.105108	1.831721	0.719964	0.800133	0.07354	0	53	60	54	66	40	93	72	73	94	80
ENSMUSG00000032171	chr9	Pin1	20652130	20652197	3808	0.063314	5.394201	0.720846	0.80105	0.035708	0	631	737	771	605	639	940	965	925	1126	1006
ENSMUSG00000024511	chr18	Rab27b	69979131	69985377	10679	0.139404	1.46671	0.720919	0.801066	0.160624	0	42	19	73	17	67	38	112	51	95	36
ENSMUSG00000062963	chr1	Ufc1	1.71E+08	1.71E+08	2070	0.060982	5.781762	0.721149	0.801257	0.033911	0	746	855	1091	897	890	1244	1267	1254	1322	1372
ENSMUSG00000034781	chr10	Gna11	81528724	81530985	4097	-0.06163	5.407383	0.721226	0.801278	0.034008	0	553	591	803	819	879	667	925	1275	1041	946
ENSMUSG00000021661	chr13	Ankra2	98263158	98263476	3510	-0.06577	3.446051	0.721997	0.802006	0.034983	0	168	169	229	168	187	182	259	304	252	234
ENSMUSG00000050144	chr3	Slc25a44	88410498	88412897	3578	-0.07037	4.906677	0.721994	0.802006	0.044938	0	482	426	533	531	584	408	523	976	704	819
ENSMUSG00000024176	chr17	Sox8	25565892	25568081	3118	-0.11989	1.726702	0.722441	0.802436	0.098994	0	46	25	45	58	115	61	85	53	102	61
ENSMUSG00000026254	chr1	Eif4e2	87213914	87214019	7497	-0.05641	6.035	0.72253	0.802469	0.029355	0	942	1048	1299	1022	1272	1131	1734	1375	1811	1487
ENSMUSG00000020719	chr11	Ddx5	1.07E+08	1.07E+08	5775	-0.05625	8.127435	0.722606	0.80249	0.029886	0	4143	4133	5479	4220	5975	4513	7102	6849	7341	6389
ENSMUSG00000024260	chr18	Sap130	31634371	31634489	4050	-0.06609	3.601872	0.7227	0.802529	0.037053	0	204	147	204	210	270	167	238	329	369	295

ENSMUSG00000068184	chr13	Ndufaf2	1.08E+08	1.08E+08	679	0.080648	3.131175	0.72315	0.802966	0.054744	0	119	141	193	125	122	208	211	132	258	224
ENSMUSG00000015337	chr2	Endog	30171493	30172066	1063	-0.0739	4.890495	0.723265	0.803028	0.049691	0	345	584	586	572	420	695	615	514	840	668
ENSMUSG00000034413	chr17	Neurl1b	26414829	26414995	6331	0.090394	2.328155	0.723359	0.803054	0.061382	0	58	63	91	94	96	68	148	86	202	107
ENSMUSG00000041849	chr15	Card6	5095981	5101095	6101	-0.08958	1.696955	0.723404	0.803054	0.059084	0	49	46	61	71	42	52	81	62	90	74
ENSMUSG00000051359	chr15	Ncald	37366175	37368925	6987	0.079065	3.195339	0.723496	0.803091	0.052407	0	113	92	141	166	241	174	277	156	256	227
ENSMUSG00000001891	chr11	Ugp2	21321138	21322129	3069	-0.07307	9.078656	0.724252	0.803802	0.051239	0	6981	10807	10987	8887	8111	12925	10811	13823	12940	9789
ENSMUSG00000020743	chr11	Mif4gd	1.16E+08	1.16E+08	2010	-0.06352	5.008791	0.724244	0.803802	0.036313	0	414	508	615	572	644	681	722	501	870	876
ENSMUSG00000042396	chr9	Rbm7	48488709	48489988	1798	0.074655	3.578719	0.72481	0.804356	0.045867	0	168	185	177	205	225	166	290	413	339	228
ENSMUSG00000029390	chr5	Tmed2	1.25E+08	1.25E+08	2199	0.054666	6.561871	0.725475	0.804966	0.028334	0	1387	1345	1810	1439	1768	1759	2259	2321	2540	2357
ENSMUSG00000061306	chr11	Slc38a10	1.2E+08	1.2E+08	6421	-0.06492	6.196755	0.725463	0.804966	0.040056	0	1041	979	1371	1312	1617	1277	1642	1100	2497	1984
ENSMUSG00000024454	chr18	Hdac3	37935844	37937683	4026	-0.05942	5.874719	0.725621	0.804998	0.033281	0	860	989	1114	1004	994	1111	1201	1507	1401	1442
ENSMUSG00000039220	chr17	Ppp1r10	35916434	35916598	5623	-0.06162	4.352601	0.725593	0.804998	0.033672	0	311	263	317	328	538	309	515	439	595	497
ENSMUSG00000035152	chr11	Ap2b1	83299024	83299053	8755	-0.05429	5.79039	0.72574	0.805066	0.027632	0	792	784	980	982	1193	908	1231	1297	1657	1306
ENSMUSG00000029001	chr4	Fbxo44	1.48E+08	1.48E+08	3024	-0.09731	2.251098	0.725818	0.805088	0.07583	0	73	80	103	87	55	84	82	158	117	84
ENSMUSG00000052684	chr4	Jun	95049034	95052222	3189	0.087622	5.936285	0.726042	0.805268	0.073905	0	717	512	769	1373	1728	903	1427	2013	1876	1240
ENSMUSG00000059713	chr4	Rcan3	1.35E+08	1.35E+08	5111	0.077397	2.872592	0.726096	0.805268	0.045293	0	97	90	145	126	134	114	180	124	263	204
ENSMUSG00000023106	chr5	Denr	1.24E+08	1.24E+08	2844	-0.05754	5.604426	0.726182	0.805299	0.03093	0	658	853	992	768	854	979	1166	1031	1245	1106
ENSMUSG00000004462	chr16	Tbccd1	22813215	22813956	2702	0.066312	3.056231	0.726479	0.805522	0.034352	0	129	99	159	130	157	142	226	190	235	195
ENSMUSG00000044864	chr3	Ankrd50	38449261	38452505	8488	-0.06079	4.026363	0.7265	0.805522	0.032124	0	221	203	294	310	372	229	456	360	467	368
ENSMUSG00000024011	chr17	Pi16	29318877	29319391	3987	0.08878	5.335608	0.727196	0.806225	0.076568	0	457	350	485	727	1374	814	903	732	1132	1268
ENSMUSG00000071291	chr13	Zfp58	67490167	67492150	2435	-0.09851	1.805277	0.727251	0.806225	0.073657	0	60	56	57	64	53	80	82	55	63	96
ENSMUSG00000036225	chr18	Kctd1	14968685	14969695	3587	-0.09275	1.276858	0.727348	0.806268	0.055127	0	33	35	33	49	51	39	57	57	61	50
ENSMUSG00000025129	chr11	Ppp1r27	1.21E+08	1.21E+08	771	0.102547	6.653971	0.727767	0.806663	0.103246	0	739	1877	1507	1980	2049	3599	2359	1529	2402	1703
ENSMUSG00000028970	chr5	Abcb1b	8798147	8798289	4344	0.110168	2.523569	0.72782	0.806663	0.103122	0	86	87	98	100	77	64	91	270	146	122
ENSMUSG00000024335	chr17	Brd2	34112023	34112708	7285	-0.05608	6.509182	0.727881	0.806666	0.030446	0	1328	1411	1603	1584	1823	1625	1889	2436	2428	2053
ENSMUSG00000025809	chr8	Itgb1	1.29E+08	1.29E+08	4081	0.055071	8.301019	0.728104	0.806783	0.029887	0	4279	4286	6162	5096	6217	5550	8817	7420	9003	6947
ENSMUSG00000055371	chr2	Stam2	52691664	52694937	6007	-0.05688	3.967644	0.728063	0.806783	0.027799	0	200	227	306	281	322	236	413	364	407	375
ENSMUSG00000019873	chr10	Reep3	67009189	67013786	5473	-0.05949	4.748207	0.728194	0.806818	0.032663	0	427	298	475	477	635	417	608	566	852	670
ENSMUSG00000027243	chr2	Harbi1	91710852	91710975	5588	-0.08233	2.421037	0.728657	0.807202	0.051229	0	67	101	105	74	105	82	111	154	131	121
ENSMUSG00000057897	chr11	Camk2b	5969644	5971826	9125	-0.05913	7.340951	0.728605	0.807202	0.03427	0	2304	2194	2934	3080	3395	3542	3560	3653	4565	3083
ENSMUSG00000020258	chr9	Glyctk	1.06E+08	1.06E+08	4229	-0.12056	-0.0255	0.728903	0.80741	0.076758	0	16	13	22	13	13	10	26	15	28	22
ENSMUSG00000022471	chr15	Xrcc6	81987835	81987952	4476	-0.0624	4.680712	0.728976	0.807427	0.035831	0	409	377	522	379	496	558	572	406	715	654
ENSMUSG00000030058	chr6	Copg1	87887814	87888072	10905	0.061139	5.972018	0.729264	0.807498	0.036551	0	851	746	1190	957	1471	1173	1750	1102	1959	1551
ENSMUSG00000040859	chr4	Bsdc1	1.29E+08	1.29E+08	5630	0.091137	5.457331	0.729192	0.807498	0.08094	0	655	624	827	675	759	584	822	2129	943	809
ENSMUSG00000044072	chr11	Eml6	29743048	29744610	9279	0.11945	0.907288	0.729274	0.807498	0.087311	0	26	19	34	23	42	28	73	42	41	32
ENSMUSG00000052854	chrX	Nrk	1.39E+08	1.39E+08	9210	-0.12991	2.648206	0.729109	0.807498	0.144996	0	73	41	86	88	283	112	204	108	182	85
ENSMUSG00000058173	chr9	Smco4	15505487	15505641	988	-0.08316	3.44519	0.729688	0.807892	0.061404	0	156	164	207	185	219	261	204	117	352	287
ENSMUSG00000034501	chr12	Pcnxl4	72536357	72536539	4420	0.072808	2.859428	0.729831	0.80792	0.041763	0	91	119	123	122	126	133	219	170	184	150
ENSMUSG00000034714	chr11	Ttyh2	1.15E+08	1.15E+08	3739	0.07605	4.908738	0.729782	0.80792	0.056756	0	291	365	450	471	943	587	831	509	950	735
ENSMUSG00000047632	chr19	Fgfbp3	36917550	36919277	1772	-0.11851	0.025255	0.73002	0.808066	0.07099	0	12	13	21	14	21	10	21	27	30	17
ENSMUSG00000014813	chr14	Stc1	69029289	69029507	3743	0.130275	0.283272	0.730571	0.80861	0.097207	0	16	6	17	27	24	14	35	23	33	33
ENSMUSG00000025732	chr17	Fam195a	25863698	25864039	816	0.073371	4.922041	0.730714	0.808704	0.051751	0	358	517	650	576	335	672	572	672	902	786
ENSMUSG00000036278	chr19	Macrod1	7056768	7057182	1274	-0.06273	7.294556	0.731033	0.808993	0.039425	0	2269	2633	2989	2867	2530	3462	2951	3970	3718	3558
ENSMUSG00000052712	chr17	BC004004	29268788	29269002	6017	0.055713	6.37769	0.73112	0.809024	0.030736	0	1162	1268	1581	1330	1454	1749	1926	1853	2144	2146
ENSMUSG00000053604	chr6	Rpia	70765720	70766648	5359	-0.06045	4.097635	0.731271	0.809062	0.033175	0	256	269	337	279	308	342	347	301	472	483
ENSMUSG00000055067	chr1	Smyd3	1.79E+08	1.79E+08	9184	-0.07868	2.523978	0.731246	0.809062	0.048725	0	97	61	105	98	129	85	152	111	145	155
ENSMUSG00000045302	chr5	Preb	30950853	30955737	7176	0.056416	5.89911	0.731431	0.809109	0.031246	0	842	838	1200	875	1153	1100	1418	1170	1735	1710
ENSMUSG00000049643	chr7	2310022A10Rik	27553233	27553353	4780	0.057961	6.295627	0.731431	0.809109	0.033555	0	1030	1151	1360	1323	1588	1848	1677	1644	2116	1953
ENSMUSG00000005897	chr10	Nr2c1	94148023	94148102	4607	0.070644	2.987793	0.731551	0.809178	0.039912	0	105	116	162	126	130	148	169	235	218	167
ENSMUSG00000032590	chr9	Apeh	1.08E+08	1.08E+08	5651	-0.054	5.127127	0.731637	0.809209	0.027598	0	468	517	643	606	754	656	802	667	1000	883
ENSMUSG00000038793	chr1	Lefty1	1.81E+08	1.81E+08	1758	-0.13877	0.271344	0.732468	0.810063	0.099312	0	22	8	25	14	30	21	33	15	24	30
ENSMUSG00000082691	chr6	Dynlt1-ps1	1.35E+08	1.35E+08	342	0.085695	2.399562	0.732855	0.810426	0.069525	0	66	78	106	74	98	153	93	81	143	139
ENSMUSG00000040888	chr17	Gfer	24693191	24694442	1775	-0.06327	4.515852	0.733055	0.810582	0.037514	0	311	378	535	350	371	495	440	517	541	577
ENSMUSG00000001017	chr3	Chtop	90498956	90500107	3637	-0.05583	6.614258	0.73321	0.810689	0.031316	0	1388	1421	2097	1495	2002	1983	2296	1895	2668	2335
ENSMUSG00000045777	chr7	Ifitm10	1.42E+08	1.42E+08	4789	0.089689	1.851077	0.733529	0.810977	0.058	0	44	50	70	73	46	68	72	89	116	80
ENSMUSG00000029675	chr5	Eln	1.35E+08	1.35E+08	2583	0.081351	7.002543	0.733632	0.811026	0.067987	0	1638	1104	1738	2293	3983	2112	3453	2151	4317	3629
ENSMUSG00000029780	chr6	Nt5c3	56882400	56883058	4250	-0.0829	5.882859	0.733721	0.81106	0.069663	0	854	1045	1251	954	920	1138	953	2275	1127	1072
ENSMUSG00000026239	chr1	Pde6d	86542994	86543583	2178	0.05823	4.295183	0.733876	0.811101	0.030618	0	293	301	385	313	296	385	448	407	638	464
ENSMUSG00000058447	chr7	Gm26920	30056034	30057519	2374	0.09007	1.217116	0.733855	0.811101	0.053778	0	25	30	42	37	48	38	57	61	54	58
ENSMUSG00000029569	chr6	Tmem168	13580687	13583334	5825	0.058209	3.919909	0.734239	0.811438	0.030332	0	176	215	289	245	321	215	369	387	467	384
ENSMUSG00000096768	chrY	Erdr1	90784738	90784822	1124	0.182617	2.309799	0.734573	0.811743	0.327971	0	56	53	88	106	81	102	97	132	5	244
ENSMUSG00000049107	chr6	Ntf3	1.26E+08	1.26E+08	1427	-0.10577	0.838909	0.734963	0.812108	0.065377	0	20	27	33	37	30	31	47	26	45	42
ENSMUSG00000031832	chr8	Taf1c	1.2E+08	1.2E+08	3386	-0.06998	2.859437	0.735121	0.812218	0.040928	0	105	116	134	109	150	122	132	202	214	152
ENSMUSG00000046329	chr17	Slc25a23	57043711	57045663	5294	0.060672	4.397928	0.735968	0.813089	0.035477	0	307	244	350	393	435	394	447	378	697	613
ENSMUSG00000071477	chr6	Zfp777	48024188	48025818	3588	-0.07062	3.925341	0.736271	0.813359	0.047493	0	229	182	290	278	326	221	295	546	369	296
ENSMUSG00000054874	chr19	Pcnxl3	5664635	5665247	8757	-0.05707	4.352935	0.736376	0.81341	0.030573	0	290	249	371	337	515	315	522	473	554	486

ENSMUSG00000030695	chr7	Aldoa	1.27E+08	1.27E+08	2754	-0.06184	13.91456	0.736547	0.813534	0.040497	0	209788	253356	297555	281352	272671	342911	266060	397062	357162	372999
ENSMUSG00000062906	chr15	Hdac10	89123307	89123479	3379	-0.07541	3.013765	0.736634	0.813565	0.051096	0	142	101	171	101	174	119	147	227	197	223
ENSMUSG00000022241	chr15	Tars	11383663	11384159	2636	0.051177	5.593781	0.73738	0.814324	0.026875	0	650	669	935	717	1023	954	1122	1173	1320	1149
ENSMUSG00000026797	chr2	Stxbp1	32787602	32789637	4991	0.075204	2.705683	0.737504	0.814375	0.049271	0	77	77	106	124	146	132	152	111	230	152
ENSMUSG00000084235	chr5	Gm15421	22528321	22528719	399	0.114722	0.385818	0.737544	0.814375	0.058978	0	14	17	27	21	18	21	30	30	34	32
ENSMUSG00000086596	chr9	Susd5	1.14E+08	1.14E+08	3874	0.120942	1.7153	0.738329	0.815177	0.139049	0	45	22	37	62	95	65	108	28	115	75
ENSMUSG00000020628	chr12	Trappc12	28690629	28691557	4257	0.060328	3.818539	0.738784	0.815566	0.034438	0	203	179	232	253	284	243	301	445	353	328
ENSMUSG00000024067	chr17	Dpy30	74299474	74299824	974	0.05394	4.408596	0.738799	0.815566	0.028818	0	304	275	435	339	390	444	474	446	565	574
ENSMUSG00000016552	chr15	Foxred2	77940522	77943392	5939	0.111337	1.80433	0.738957	0.815675	0.11196	0	52	22	54	39	115	55	80	120	90	67
ENSMUSG00000033075	chr15	Senp1	98038744	98042952	11873	-0.06041	3.454358	0.739262	0.815817	0.033297	0	187	137	182	171	255	178	242	276	296	258
ENSMUSG00000051390	chr17	Zbtb22	33915904	33915964	2672	0.057738	4.145632	0.739226	0.815817	0.032125	0	228	241	346	304	332	284	357	521	473	474
ENSMUSG00000102827	chr18	RP23-56B11.5	37652433	37652907	1740	0.133133	0.326749	0.739211	0.815817	0.096113	0	16	25	16	21	12	30	34	20	26	29
ENSMUSG00000006289	chr14	Osgep	50906478	50907357	4933	0.05329	5.024044	0.739371	0.815872	0.028677	0	448	516	599	521	568	694	742	723	871	804
ENSMUSG00000021687	chr13	Scamp1	94201310	94204163	4582	-0.05538	5.053106	0.739718	0.81616	0.031264	0	506	498	683	483	657	558	711	939	836	753
ENSMUSG00000071151	chr10	Gm4799	82954344	82955000	657	0.113701	0.71388	0.739809	0.81616	0.065449	0	20	24	26	29	24	31	31	27	51	48
ENSMUSG00000091957	chr18	Rps2-ps10	61259008	61259972	965	0.088955	2.249641	0.739754	0.81616	0.062042	0	67	89	89	66	60	101	92	91	161	118
ENSMUSG00000026971	chr2	Itgb6	60598292	60600583	7111	-0.08204	4.890027	0.74013	0.816449	0.07065	0	440	479	521	593	485	665	938	290	861	585
ENSMUSG00000053110	chr9	Yap1	7931999	7934732	9257	-0.05685	6.134899	0.740274	0.816543	0.03393	0	921	966	1355	1136	1695	1290	1671	1887	1774	1391
ENSMUSG00000002771	chr7	Grin2d	45831883	45834087	5862	0.139239	0.046054	0.740725	0.816976	0.122158	0	15	4	16	10	31	15	30	14	30	26
ENSMUSG00000039048	chr9	Foxred1	35204206	35205123	4064	0.053898	5.001247	0.741062	0.817281	0.029084	0	424	532	569	539	540	563	685	777	952	849
ENSMUSG00000022354	chr15	Ndufb9	58933810	58933938	651	0.064294	8.549778	0.741373	0.817546	0.045261	0	5363	6749	7080	6014	4889	8895	8324	9077	9289	8414
ENSMUSG00000039850	chr11	Endov	1.19E+08	1.19E+08	6138	-0.07151	2.653749	0.741419	0.817546	0.043909	0	81	83	134	110	129	83	141	175	177	140
ENSMUSG00000027463	chr2	Slc52a3	1.52E+08	1.52E+08	2767	0.104418	0.424108	0.742537	0.818713	0.084596	0	19	12	27	18	25	32	26	16	35	40
ENSMUSG00000020175	chr10	Rab36	75037058	75037321	6175	0.131266	-0.00491	0.743231	0.819352	0.089956	0	17	6	20	11	18	15	33	16	26	20
ENSMUSG00000020777	chr11	Acox1	1.16E+08	1.16E+08	5082	0.064658	6.952524	0.743278	0.819352	0.046022	0	1743	1733	2271	2263	2085	1901	2312	4399	3209	3035
ENSMUSG00000054823	chr8	Whsc1l1	25601601	25601993	16513	-0.05721	4.197501	0.743294	0.819352	0.033501	0	305	227	317	302	414	244	458	477	494	445
ENSMUSG00000029592	chr5	Usp30	1.14E+08	1.14E+08	3372	0.062505	3.528121	0.743396	0.819399	0.036581	0	147	170	210	229	176	199	266	340	304	258
ENSMUSG00000039166	chr10	Akap7	25169090	25171248	4375	0.072497	3.277975	0.743705	0.819644	0.048534	0	144	136	130	215	148	162	199	294	276	225
ENSMUSG00000042487	chr9	Leo1	75441524	75441635	2192	0.064682	4.496443	0.743737	0.819644	0.045319	0	241	264	471	389	515	482	617	333	654	594
ENSMUSG00000024603	chr18	Dctn4	60526221	60526365	3714	0.070495	5.263264	0.743978	0.81978	0.053682	0	570	511	708	630	709	551	798	1556	940	758
ENSMUSG00000034022	chr15	Cpsf1	76595809	76595932	4515	0.05595	4.558776	0.743949	0.81978	0.032238	0	309	297	406	449	478	395	477	687	725	537
ENSMUSG00000041571	chr7	Sepw1	15917208	15917539	736	-0.06227	9.683494	0.744221	0.819919	0.043547	0	12432	13578	17513	12876	13387	19851	16387	17561	17435	20514
ENSMUSG00000090523	chr18	Gypc	32528322	32530201	2331	0.053535	4.917742	0.744223	0.819919	0.030879	0	379	415	604	469	633	656	660	617	812	816
ENSMUSG00000028849	chr4	Map7d1	1.26E+08	1.26E+08	3652	-0.05452	7.887925	0.744362	0.820006	0.033186	0	2884	3568	4824	4691	4296	4606	5845	4872	6486	5296
ENSMUSG00000036646	chr2	Man1b1	25332338	25332582	5391	-0.05338	4.838916	0.744541	0.820138	0.030033	0	430	387	558	475	593	466	720	512	856	756
ENSMUSG00000060380	chr9	C030014I23Rik	44477924	44479733	2446	-0.12312	0.321077	0.744897	0.820466	0.072853	0	17	15	22	24	23	27	20	34	23	23
ENSMUSG00000028700	chr4	Pomgnt1	1.16E+08	1.16E+08	5463	0.053336	6.090816	0.74519	0.820723	0.031207	0	976	1024	1234	1103	1235	1302	1476	1930	1873	1506
ENSMUSG00000054474	chr6	Thnsl2	71128166	71128852	2071	0.077152	3.022894	0.74526	0.820735	0.057452	0	128	112	121	118	174	135	139	295	198	195
ENSMUSG00000044906	chr18	4930503L19Rik	70453140	70453388	2291	0.104631	1.169423	0.745528	0.820964	0.08085	0	41	24	35	20	54	34	65	43	74	48
ENSMUSG00000007805	chr1	Twist2	91801461	91802149	3174	0.121675	0.743358	0.745653	0.820972	0.11025	0	29	7	33	25	34	35	37	42	27	47
ENSMUSG00000037347	chrX	Chst7	20059560	20061208	2206	-0.08299	1.623626	0.745602	0.820972	0.062658	0	34	58	58	61	44	45	62	64	96	77
ENSMUSG00000016933	chr2	Plcg1	1.61E+08	1.61E+08	7857	-0.05463	5.035488	0.745829	0.821097	0.032238	0	438	464	573	649	676	462	766	896	888	779
ENSMUSG00000042628	chr12	Zfyve1	83546941	83548115	3869	-0.10537	4.689405	0.745886	0.821097	0.123122	0	383	362	548	457	486	225	384	1378	499	431
ENSMUSG00000068732	chr3	Tmem167b	1.09E+08	1.09E+08	2948	-0.05062	4.690863	0.746186	0.821362	0.026714	0	375	364	477	413	576	406	644	630	680	613
ENSMUSG00000018405	chr11	Mrm1	84813061	84814511	2868	-0.07109	3.082248	0.746256	0.821374	0.050264	0	115	146	184	149	118	175	229	141	239	168
ENSMUSG00000007812	chr5	Zfp655	1.45E+08	1.45E+08	4514	-0.0841	3.628869	0.746549	0.821631	0.075618	0	200	161	238	186	279	114	256	507	285	251
ENSMUSG00000031451	chr8	Gas6	13465374	13465900	2593	0.052447	7.035492	0.746758	0.821796	0.031228	0	1646	1864	2194	2293	2850	2638	3088	2957	3485	3366
ENSMUSG00000023484	chr15	Prph	99055174	99055763	1865	0.146268	0.463237	0.747293	0.822086	0.181711	0	26	8	23	9	37	19	62	26	38	13
ENSMUSG00000027358	chr2	Bmp2	1.34E+08	1.34E+08	3555	-0.11024	1.142499	0.747253	0.822086	0.101666	0	28	16	29	56	58	37	66	48	45	40
ENSMUSG00000030057	chr6	Cnbp	87842615	87844156	2536	-0.06228	8.917164	0.747318	0.822086	0.044608	0	7023	7402	10877	7367	8695	8699	9918	15858	10320	9936
ENSMUSG00000054034	chrX	Tceal5	1.36E+08	1.36E+08	1263	-0.06453	5.917507	0.747253	0.822086	0.046229	0	752	801	1368	836	1522	1322	1575	964	1794	1213
ENSMUSG00000097993	chr1	Ptprv	1.35E+08	1.35E+08	6987	-0.26659	-0.30701	0.747297	0.822086	0.626098	0	31	3	15	1	13	0	39	3	31	8
ENSMUSG00000029557	chr5	Ftsj2	1.4E+08	1.4E+08	1443	0.070457	2.826929	0.747453	0.822169	0.048235	0	80	109	146	121	116	162	172	117	201	180
ENSMUSG00000040268	chr7	Plekha1	1.31E+08	1.31E+08	8527	-0.04886	4.926459	0.747897	0.822591	0.025401	0	437	416	593	543	601	545	720	679	876	678
ENSMUSG00000031024	chr7	St5	1.1E+08	1.1E+08	4526	0.055426	3.839117	0.748221	0.822883	0.030772	0	187	184	243	277	281	257	388	270	437	354
ENSMUSG00000028104	chr3	Polr3gl	96577872	96578588	1597	-0.05829	5.135578	0.748345	0.822888	0.03725	0	568	552	703	554	592	753	697	909	731	853
ENSMUSG00000031158	chrX	Timm17b	7899357	7899469	2557	-0.05208	4.603635	0.748301	0.822888	0.028513	0	345	382	526	366	445	482	566	486	666	573
ENSMUSG00000040136	chr7	Abcc8	46104523	46104761	4952	-0.09486	1.923795	0.748446	0.822901	0.075438	0	69	30	61	58	107	65	84	95	109	67
ENSMUSG00000062580	chr1	Timm17a	1.35E+08	1.35E+08	7893	-0.055	6.613915	0.748475	0.822901	0.034546	0	1357	1659	1998	1710	1560	2049	2175	2202	2525	2171
ENSMUSG00000091931	chr12	AK010878	1.03E+08	1.03E+08	1417	-0.0736	2.452928	0.748882	0.823282	0.049453	0	81	91	119	75	94	115	142	100	138	113
ENSMUSG00000032232	chr9	Cgnl1	71626509	71629392	7844	-0.06908	4.290512	0.749289	0.823665	0.052615	0	308	228	346	315	493	279	390	288	681	640
ENSMUSG00000055725	chr5	Paqr3	97082329	97082608	7566	-0.08174	1.030254	0.750417	0.824839	0.055559	0	32	35	35	30	34	34	39	42	55	52
ENSMUSG00000020329	chr10	Polrmt	79736123	79736283	4685	-0.05634	4.506089	0.75075	0.825117	0.034392	0	294	322	477	436	410	375	485	683	595	461
ENSMUSG00000022704	chr16	Qtrtd1	43861407	43863301	4629	-0.06889	2.349877	0.750933	0.825117	0.044157	0	87	83	95	69	91	77	120	106	148	126
ENSMUSG00000040152	chr2	Thbs1	1.18E+08	1.18E+08	6073	0.083117	5.905822	0.750797	0.825117	0.080459	0	1109	419	1122	1021	1244	616	1289	2151	1786	1524
ENSMUSG00000041268	chr9	Dmxl2	54365158	54366627	13419	0.082422	2.571193	0.750968	0.825117	0.063716	0	94	63	105	92	124	63	113	174	205	167

ENSMUSG00000086427	chr6	Hoxa11os	52244393	52245656	3073	-0.17083	-0.06703	0.750893	0.825117	0.210916	0	10	21	19	15	11	30	8	15	6	31
ENSMUSG00000018841	chr11	Rad51d	82876434	82879023	3714	0.081253	2.599341	0.751283	0.825397	0.061143	0	92	94	96	82	118	76	129	133	162	227
ENSMUSG00000031485	chr8	Prosc	27042555	27042713	4534	-0.0491	5.129637	0.752262	0.826408	0.027223	0	493	538	653	599	689	593	775	935	964	760
ENSMUSG00000102426	chrX	RP23-330G24.3	1.52E+08	1.52E+08	1477	0.119052	0.070318	0.753255	0.827433	0.08895	0	13	17	16	9	21	10	18	31	27	31
ENSMUSG00000031708	chr8	Tecr	83571700	83571935	1334	-0.0607	8.153158	0.754043	0.828233	0.044628	0	3229	4854	5700	5481	5060	6884	5557	5361	7040	7123
ENSMUSG00000029098	chr5	Acox3	35583040	35583134	9093	0.049459	4.651114	0.754689	0.828876	0.026773	0	396	344	456	432	418	471	617	580	683	624
ENSMUSG00000025104	chr7	Hdgfrp3	81881251	81886083	9575	0.08264	2.112077	0.754844	0.828981	0.066817	0	64	49	70	52	113	54	102	119	155	90
ENSMUSG00000060470	chr8	Gpr97	95017692	95017820	2436	0.107115	-0.01687	0.75494	0.829021	0.107791	0	5	12	20	15	21	24	10	27	24	21
ENSMUSG00000071528	chr19	Usmg5	47083471	47083569	341	-0.06821	7.38474	0.75525	0.829295	0.056912	0	2430	3458	3422	2650	2020	3851	3798	3955	3657	3399
ENSMUSG00000030754	chr7	Copb1	1.14E+08	1.14E+08	3315	0.051024	5.477314	0.755966	0.830015	0.030912	0	615	593	804	634	1050	740	1235	1098	1272	980
ENSMUSG00000032212	chr9	Sltm	70542920	70543081	3646	0.047635	4.983625	0.756556	0.830597	0.026135	0	438	477	568	506	605	617	701	765	865	792
ENSMUSG00000005262	chr16	Ufd1l	18811779	18811883	4336	-0.06145	5.617112	0.756799	0.830733	0.045669	0	759	801	924	792	880	872	929	1690	1013	1041
ENSMUSG00000027552	chr3	E2f5	14578641	14579023	1782	-0.08836	1.27661	0.75674	0.830733	0.075582	0	35	41	45	40	38	25	58	37	80	71
ENSMUSG00000031878	chr8	Nae1	1.05E+08	1.05E+08	7792	-0.05656	4.651945	0.757202	0.831109	0.037236	0	386	424	526	357	429	475	598	716	566	488
ENSMUSG00000031783	chr8	Polr2c	94857450	94857641	1580	0.053858	5.510428	0.7577	0.831523	0.035012	0	666	722	905	633	792	922	964	1317	1086	1072
ENSMUSG00000049502	chr16	Dtx3l	35926511	35929368	5724	0.067026	3.854392	0.757674	0.831523	0.052941	0	175	180	254	305	267	358	369	189	400	381
ENSMUSG00000049659	chr11	Aftph	20685084	20686198	6979	0.048653	4.602144	0.757847	0.83162	0.027245	0	335	367	458	355	478	472	550	641	639	562
ENSMUSG00000003848	chr8	Nob1	1.07E+08	1.07E+08	3486	0.059164	4.157177	0.758011	0.831733	0.0399	0	221	299	322	264	348	304	429	590	461	332
ENSMUSG00000021967	chr14	Mrpl57	57826239	57826322	2321	0.050545	4.422158	0.758091	0.831755	0.029709	0	274	329	423	349	380	479	488	505	577	464
ENSMUSG00000070327	chr11	Rnf213	1.19E+08	1.19E+08	16888	0.084093	4.892566	0.758176	0.831782	0.087837	0	369	329	588	542	615	867	612	281	706	994
ENSMUSG00000053641	chr9	Dennd4a	64811340	64811586	8645	-0.07016	3.028283	0.758635	0.83222	0.051478	0	130	71	160	134	210	115	194	171	256	200
ENSMUSG00000047473	chr7	Zfp30	29783998	29784901	6078	-0.06596	2.450681	0.758742	0.832271	0.045268	0	73	82	92	117	94	91	142	122	154	108
ENSMUSG00000034911	chr8	Ushbp1	71384274	71385793	3549	-0.05888	3.786292	0.758857	0.832332	0.04176	0	197	233	253	266	208	170	294	337	392	404
ENSMUSG00000050627	chr9	Gpd1l	1.15E+08	1.15E+08	5077	0.047268	5.306188	0.759227	0.832672	0.02673	0	607	525	727	646	743	757	937	982	1127	887
ENSMUSG00000042340	chr7	Ctf1	1.28E+08	1.28E+08	1345	0.065665	3.007383	0.759644	0.833063	0.044174	0	116	124	130	144	129	165	150	229	193	203
ENSMUSG00000008859	chr13	Rala	17880575	17882501	2684	-0.05384	5.175251	0.759802	0.83312	0.03568	0	505	640	705	626	564	678	861	624	1022	959
ENSMUSG00000030683	chr7	Sez6l2	1.27E+08	1.27E+08	4210	0.114728	1.287671	0.759877	0.83312	0.107647	0	20	50	39	48	28	37	61	33	99	62
ENSMUSG00000041278	chr11	Ttc1	43729512	43730607	2032	0.057121	5.092354	0.759847	0.83312	0.039583	0	442	576	687	527	542	640	715	1093	835	747
ENSMUSG00000020260	chr10	Pofut2	77259300	77259453	2219	-0.05708	4.975335	0.76013	0.833267	0.039311	0	430	447	599	483	747	577	902	465	974	704
ENSMUSG00000059288	chr13	Cdyl	35659862	35659993	4018	-0.07188	2.448999	0.760131	0.833267	0.055742	0	85	79	97	69	133	72	115	168	146	117
ENSMUSG00000080746	chr4	Rpsa-ps12	1.49E+08	1.49E+08	892	0.101644	0.979629	0.760208	0.833286	0.068436	0	24	32	38	30	26	34	59	35	44	54
ENSMUSG00000029388	chr5	Eif2b1	1.25E+08	1.25E+08	2577	0.052317	5.276635	0.760452	0.833487	0.033807	0	532	582	781	595	686	815	799	1099	917	915
ENSMUSG00000059183	chr9	Mtfmt	65435782	65436007	3655	-0.06388	2.501304	0.760699	0.833691	0.042728	0	84	87	95	109	98	99	128	102	177	136
ENSMUSG00000015759	chr14	Cnih1	46775582	46776549	1570	0.049761	5.79675	0.760825	0.833763	0.03075	0	798	833	1036	856	1033	1156	1344	1041	1641	1409
ENSMUSG00000016984	chr11	Etaa1	17938756	17940350	4185	0.092415	1.496355	0.760908	0.833789	0.06623	0	50	29	53	40	48	46	54	55	111	69
ENSMUSG00000024899	chr19	Papss2	32620005	32620186	3635	0.066814	3.666783	0.761164	0.833885	0.049363	0	183	156	234	238	220	155	261	248	450	437
ENSMUSG00000027573	chr2	Gid8	1.81E+08	1.81E+08	2464	-0.04784	4.969775	0.761176	0.833885	0.0271	0	438	458	647	529	593	610	759	725	823	660
ENSMUSG00000030718	chr7	Ppme1	1E+08	1E+08	2361	-0.04794	5.122693	0.761079	0.833885	0.02781	0	447	532	698	612	679	609	836	845	1028	699
ENSMUSG00000041995	chr13	Zbed3	95325237	95325344	1894	-0.0619	2.519662	0.761316	0.833972	0.041812	0	82	84	94	118	102	93	120	123	177	139
ENSMUSG00000025158	chr11	Rfng	1.21E+08	1.21E+08	2489	0.052942	3.856464	0.761379	0.833975	0.030586	0	214	212	269	237	244	282	354	260	430	391
ENSMUSG00000027474	chr2	Ccm2l	1.53E+08	1.53E+08	2407	0.083861	2.069606	0.761562	0.834043	0.061452	0	52	52	73	89	67	50	98	99	124	131
ENSMUSG00000031613	chr8	Hpgd	56294552	56294712	1719	0.078819	2.152142	0.761523	0.834043	0.066805	0	64	45	90	73	85	83	106	154	93	80
ENSMUSG00000030770	chr7	Parva	1.12E+08	1.12E+08	10157	-0.05138	5.088307	0.761789	0.834187	0.032231	0	497	420	560	634	806	581	887	646	1013	802
ENSMUSG00000083774	chr7	Gm7180	81222362	81222874	513	-0.1088	0.421133	0.761814	0.834187	0.074823	0	23	20	26	20	18	33	21	26	33	25
ENSMUSG00000039990	chr7	Edrf1	1.34E+08	1.34E+08	5992	0.061067	3.716547	0.762293	0.83458	0.042505	0	195	206	221	192	249	227	258	455	310	301
ENSMUSG00000047710	chr8	Champ1	13869641	13869811	4040	0.051827	3.602353	0.762251	0.83458	0.029183	0	176	170	193	180	275	222	267	285	361	305
ENSMUSG00000039670	chr11	Oxld1	1.2E+08	1.2E+08	813	-0.07097	3.428453	0.762392	0.834622	0.060375	0	157	227	212	174	123	223	213	296	280	194
ENSMUSG00000042831	chr7	Alkbh6	30308717	30308834	3123	0.060385	3.483523	0.762527	0.834703	0.040385	0	178	170	214	166	171	244	291	188	295	295
ENSMUSG00000063576	chr17	Klhdc3	46674550	46675152	2126	0.053866	7.200533	0.762615	0.834733	0.037601	0	2120	2088	2449	2736	2627	2828	2846	4509	4073	3203
ENSMUSG00000027223	chr2	Mapk8ip1	92383676	92384421	4644	0.06057	4.279988	0.762912	0.834993	0.046111	0	270	180	328	286	563	335	432	537	593	427
ENSMUSG00000039480	chr10	Nt5dc1	34288288	34288562	3192	-0.08712	2.424763	0.763138	0.835133	0.082499	0	76	73	109	87	113	63	91	215	103	127
ENSMUSG00000049411	chr18	Tmem241	11981303	11983593	3336	-0.08217	1.430652	0.76316	0.835133	0.062853	0	54	38	39	34	57	52	51	54	73	65
ENSMUSG00000085704	chr2	4921531C22Rik	1.8E+08	1.8E+08	1967	0.084344	1.039619	0.763307	0.835227	0.06417	0	20	34	40	31	34	39	51	33	68	46
ENSMUSG00000020381	chr11	3010026O09Rik	50174444	50174547	2039	0.086043	1.456571	0.763721	0.835548	0.073181	0	33	36	62	32	54	50	55	41	109	69
ENSMUSG00000032330	chr9	Cox7a2	79755241	79755605	754	0.055776	7.417171	0.76366	0.835548	0.040736	0	2360	3136	3216	2668	2418	3871	4010	3713	4732	3832
ENSMUSG00000035314	chr7	Gdpd5	99381549	99382208	3582	0.064474	2.643727	0.764234	0.836043	0.039248	0	83	82	107	105	129	90	149	145	193	169
ENSMUSG00000046668	chr18	Cxxc5	35829818	35829986	2271	-0.05428	4.80123	0.764529	0.8363	0.03565	0	459	291	570	427	655	543	713	625	704	585
ENSMUSG00000021876	chr14	Rnase4	51091077	51091253	1996	0.06889	6.011329	0.76499	0.836606	0.062539	0	1166	625	1205	830	1489	1019	1576	2384	1531	1193
ENSMUSG00000029918	chr6	Mrps33	39801804	39802544	1236	0.057227	3.889808	0.764935	0.836606	0.039067	0	187	254	321	230	207	335	370	312	382	336
ENSMUSG00000092558	chr17	Med20	47611582	47611692	7324	-0.05343	4.354611	0.764918	0.836606	0.034576	0	317	325	454	294	337	405	488	523	501	400
ENSMUSG00000031431	chrX	Tsc22d3	1.41E+08	1.41E+08	4341	0.079239	7.16586	0.765525	0.837125	0.083804	0	2596	1954	3323	2008	1625	2655	2749	5845	2640	3069
ENSMUSG00000041842	chr3	Fhdc1	84442198	84446530	6270	-0.14478	-0.06185	0.766309	0.83785	0.19753	0	14	8	14	11	30	11	29	3	42	14
ENSMUSG00000083327	chrX	Vcp-rs	1.04E+08	1.04E+08	2406	-0.05184	5.067781	0.766269	0.83785	0.033941	0	458	489	604	586	727	595	660	1016	825	730
ENSMUSG00000000827	chr2	Tpd52l2	1.81E+08	1.81E+08	4982	-0.04758	5.607486	0.766434	0.83792	0.029424	0	752	738	984	759	896	838	1178	1301	1189	1080
ENSMUSG00000051344	chr1	Plekhm3	64785983	64786587	10921	0.070849	2.965794	0.766575	0.838008	0.053889	0	123	82	135	123	172	98	156	179	256	256
ENSMUSG00000087259	chr11	2610035D17Rik	1.13E+08	1.13E+08	2121	0.107611	2.087712	0.766721	0.838102	0.130402	0	76	44	71	86	53	50	79	192	62	118

ENSMUSG00000020841	chr11	Cpd	76778424	76782410	8332	-0.04872	6.428098	0.767366	0.838741	0.031557	0	1180	1075	1615	1646	1881	1448	1837	2188	2310	2139
ENSMUSG00000042207	chr1	Kdm5b	1.35E+08	1.35E+08	16555	0.055286	4.069224	0.767577	0.838905	0.037234	0	240	206	303	256	379	234	426	511	514	333
ENSMUSG00000032178	chr9	Ilf3	21368019	21368099	4754	-0.0462	4.678126	0.767972	0.839256	0.026857	0	395	335	511	406	534	421	594	616	779	553
ENSMUSG00000076275	chr7	Mir675	1.43E+08	1.43E+08	84	0.061487	8.902095	0.76802	0.839256	0.051936	0	3587	7053	11083	9105	9116	7449	12720	12230	14115	11229
ENSMUSG00000041012	chr9	Cmtm8	1.15E+08	1.15E+08	1064	-0.11103	1.354496	0.768536	0.839755	0.120996	0	12	44	55	59	47	65	47	36	66	58
ENSMUSG00000029617	chr5	Ccz1	1.44E+08	1.44E+08	1762	-0.04542	5.012766	0.768656	0.839819	0.026668	0	477	518	614	518	598	595	731	702	855	819
ENSMUSG00000027187	chr2	Cat	1.03E+08	1.03E+08	2613	0.081426	6.247375	0.76873	0.839833	0.090122	0	1086	1076	1336	1436	1193	645	1139	3147	2235	2196
ENSMUSG00000026941	chr2	Mamdc4	25563115	25563369	4630	-0.05041	5.582973	0.768869	0.839919	0.033704	0	679	826	970	791	774	1001	1046	1179	1131	1070
ENSMUSG00000024197	chr17	Plin3	56278962	56280073	2159	0.058964	5.262936	0.769049	0.84005	0.04529	0	573	664	631	654	562	591	738	1289	1110	880
ENSMUSG00000009863	chr4	Sdhb	1.41E+08	1.41E+08	2239	0.056703	8.655379	0.76918	0.84006	0.044534	0	5175	7336	7166	7488	5358	9281	8703	9632	10711	9109
ENSMUSG00000051159	chrX	Cited1	1.02E+08	1.02E+08	1754	0.093061	0.737098	0.76914	0.84006	0.066338	0	22	21	27	18	40	38	37	31	48	34
ENSMUSG00000066595	chr1	Mfsd7b	1.91E+08	1.91E+08	5177	0.063255	3.619175	0.769456	0.840295	0.049032	0	147	166	177	229	288	164	225	395	358	335
ENSMUSG00000021681	chr13	Aggf1	95350683	95351702	3697	-0.04644	4.877624	0.769674	0.840437	0.028403	0	405	495	597	460	527	494	682	625	864	733
ENSMUSG00000037921	chr8	Ddx60	61928087	61928276	6931	-0.10634	1.10213	0.769707	0.840437	0.096594	0	19	22	46	33	64	45	47	33	39	63
ENSMUSG00000082045	chr11	Gm11585	1.02E+08	1.02E+08	569	0.128315	-0.07915	0.769926	0.84061	0.093263	0	16	7	20	8	17	13	32	16	25	18
ENSMUSG00000025969	chr1	Nrp2	62703285	62704277	11842	-0.05426	4.904223	0.770225	0.840839	0.039685	0	365	444	516	686	533	460	663	564	1048	761
ENSMUSG00000032036	chr9	Kirrel3	34485894	34486184	6454	0.113112	0.157474	0.770258	0.840839	0.095367	0	12	9	19	16	27	14	40	27	28	15
ENSMUSG00000028069	chr3	Gpatch4	88043108	88043179	2447	0.052368	4.32469	0.770352	0.840875	0.036262	0	226	306	415	320	383	473	392	388	588	512
ENSMUSG00000057156	chr14	Homez	54852736	54858281	5907	-0.07353	2.054361	0.770761	0.841255	0.054374	0	55	43	93	73	90	67	112	75	103	107
ENSMUSG00000039577	chr4	Nphp4	1.52E+08	1.52E+08	6044	-0.12128	-0.1755	0.770917	0.84136	0.111258	0	11	13	22	10	13	15	29	8	26	11
ENSMUSG00000028385	chr4	Snx30	59805840	59806225	7795	0.075718	3.112356	0.771033	0.84142	0.071322	0	157	73	136	108	233	116	186	176	298	274
ENSMUSG00000002280	chr17	Narfl	25773776	25773887	3826	-0.04748	4.943629	0.771221	0.841515	0.029899	0	422	509	618	552	492	588	672	687	830	744
ENSMUSG00000007097	chr1	Atp1a2	1.72E+08	1.72E+08	7038	0.069265	10.72954	0.771242	0.841515	0.067883	0	24753	23451	30443	29350	30390	27984	30789	74574	38511	30236
ENSMUSG00000040459	chr8	Arglu1	8666577	8667416	1711	0.044575	5.014134	0.771984	0.842258	0.026435	0	453	471	613	478	647	639	751	714	886	826
ENSMUSG00000031070	chr7	Mrgprf	1.45E+08	1.45E+08	2214	0.077753	2.593793	0.772351	0.842593	0.081227	0	86	45	83	91	193	120	177	116	179	121
ENSMUSG00000003208	chr17	Ccdc94	55959187	55959261	1311	-0.06927	2.550888	0.772514	0.842704	0.049395	0	63	93	96	116	129	125	120	112	147	148
ENSMUSG00000020886	chr11	Dlg4	70017085	70017233	4982	-0.07492	2.639729	0.773189	0.843305	0.061342	0	95	62	105	101	174	117	180	99	148	152
ENSMUSG00000029916	chr6	Agk	40325478	40325530	2225	-0.06048	2.902811	0.773203	0.843305	0.041174	0	108	110	143	122	149	132	166	117	239	200
ENSMUSG00000033768	chr19	Nrxn2	6418731	6418972	13812	-0.11836	-0.03238	0.773248	0.843305	0.089159	0	12	9	25	12	20	8	20	29	23	20
ENSMUSG00000017478	chr8	Zc3h18	1.22E+08	1.22E+08	9190	-0.04787	4.688195	0.773433	0.84344	0.030754	0	329	393	474	454	547	378	566	727	746	570
ENSMUSG00000038217	chr11	Tlcd2	75461715	75461755	1936	-0.06753	3.871397	0.774109	0.844111	0.059532	0	245	127	249	210	445	210	330	438	409	290
ENSMUSG00000033565	chr15	Rbfox2	77078990	77084206	7358	0.050982	6.487701	0.774763	0.844758	0.037478	0	1237	1028	1434	1487	2307	1574	2558	2115	2483	1972
ENSMUSG00000024785	chr19	Rcl1	29101375	29101640	1803	-0.05759	3.225903	0.774922	0.844865	0.039747	0	125	116	183	163	214	132	199	182	290	277
ENSMUSG00000046605	chr11	B3gntl1	1.22E+08	1.22E+08	3518	-0.07621	1.432653	0.775747	0.845698	0.05969	0	53	34	50	39	46	39	67	66	60	65
ENSMUSG00000001924	chrX	Uba1	20658326	20658526	4819	0.045093	7.378489	0.775914	0.845755	0.029714	0	2185	2283	2935	2881	3509	3201	3866	3508	5152	4106
ENSMUSG00000028102	chr3	Pex11b	96635376	96635500	5615	0.056776	4.543055	0.775939	0.845755	0.043977	0	357	353	487	320	377	393	520	813	562	472
ENSMUSG00000039164	chr2	Naif1	32450457	32452949	4650	-0.05853	2.376936	0.775983	0.845755	0.03922	0	79	73	86	86	112	84	129	122	141	111
ENSMUSG00000048965	chr7	Mrgpre	1.44E+08	1.44E+08	3759	0.120389	0.740177	0.776308	0.846043	0.126442	0	25	15	17	31	38	21	48	17	77	35
ENSMUSG00000097867	chr16	1110054M08Rik	24391612	24393107	1603	-0.06035	3.766159	0.7766	0.846294	0.04633	0	207	197	199	256	293	357	299	225	339	292
ENSMUSG00000061950	chr17	Ppp4r1	65782573	65782683	5449	0.043991	4.622052	0.776944	0.846602	0.026451	0	338	313	458	385	549	419	615	579	701	615
ENSMUSG00000039130	chr6	Zc3hc1	30366380	30366745	4601	0.051426	4.136439	0.777271	0.846892	0.035554	0	205	303	335	306	281	388	414	341	481	441
ENSMUSG00000037514	chr2	Pank2	1.31E+08	1.31E+08	4912	0.047065	4.533416	0.777419	0.846987	0.030005	0	333	336	433	402	386	439	498	613	559	615
ENSMUSG00000048930	chr6	Tada3	1.13E+08	1.13E+08	3883	-0.04797	3.797269	0.777519	0.847029	0.030249	0	203	222	241	247	255	264	343	246	403	335
ENSMUSG00000098253	chr18	Mir7219	68260920	68260973	54	-0.06592	2.109418	0.777629	0.847082	0.053492	0	68	82	70	68	67	89	87	94	113	96
ENSMUSG00000020709	chr11	Adap2	80154105	80154309	1785	0.076594	1.677019	0.777851	0.847258	0.059811	0	44	33	64	50	64	43	68	63	113	93
ENSMUSG00000021596	chr13	Mctp1	76384535	76385251	8193	0.116869	0.427181	0.777934	0.847281	0.094509	0	22	9	20	24	25	12	27	29	53	35
ENSMUSG00000029635	chr5	Cdk8	1.46E+08	1.46E+08	3881	-0.0491	3.631109	0.778129	0.847427	0.031293	0	219	171	231	183	238	228	257	313	355	262
ENSMUSG00000079941	chr13	Gm11273	21501029	21501418	390	0.06486	3.388109	0.778272	0.847515	0.05349	0	144	189	168	205	124	240	253	224	320	195
ENSMUSG00000019813	chr10	Cep57l1	41718840	41719907	7526	0.077384	1.507225	0.778643	0.847852	0.055119	0	45	30	58	42	49	48	60	79	84	60
ENSMUSG00000023055	chr15	Calcoco1	1.03E+08	1.03E+08	3963	0.074162	6.551267	0.778703	0.847852	0.082322	0	1434	1303	1655	1636	1561	1351	1673	4489	1918	1756
ENSMUSG00000032437	chr9	Stt3b	1.15E+08	1.15E+08	4195	-0.04933	6.683293	0.779061	0.848175	0.036416	0	1484	1536	2098	1658	1978	1572	2134	3163	2574	2400
ENSMUSG00000026848	chr2	Tor1b	30952959	30953223	5327	-0.04485	5.149453	0.779547	0.848637	0.028595	0	550	548	711	515	678	707	805	802	884	847
ENSMUSG00000023909	chr17	Paqr4	23736186	23737999	2507	-0.0601	3.306688	0.779653	0.84866	0.047834	0	136	137	186	165	220	172	277	132	348	211
ENSMUSG00000090330	chr7	9130221H12Rik	25228687	25228773	1577	0.056906	2.458229	0.77969	0.84866	0.040632	0	76	74	95	82	118	107	110	136	170	122
ENSMUSG00000022103	chr14	Gfra2	70890130	70890894	3462	-0.06476	2.613646	0.77982	0.848734	0.048652	0	86	64	110	111	153	101	170	138	167	116
ENSMUSG00000000301	chr11	Pemt	59970614	59970875	2104	0.079229	1.346774	0.78003	0.848817	0.059362	0	39	31	49	35	45	38	64	42	83	71
ENSMUSG00000052395	chr14	Rft1	30654360	30654475	4355	0.059987	2.875323	0.78008	0.848817	0.039127	0	120	93	135	106	139	111	158	173	238	197
ENSMUSG00000082935	chr1	Gm7658	21511933	21513056	1124	-0.09495	1.051848	0.77997	0.848817	0.095685	0	27	26	35	48	35	36	20	65	58	45
ENSMUSG00000021764	chr13	Ndufs4	1.14E+08	1.14E+08	1534	-0.05459	7.366188	0.78029	0.848979	0.045481	0	2324	3155	3308	2850	2176	3608	3706	3751	4039	3551
ENSMUSG00000024587	chr18	Nars	64499665	64500649	2632	-0.04466	6.79368	0.780396	0.849027	0.030115	0	1574	1686	2276	1786	2111	1960	2498	2927	2892	2478
ENSMUSG00000022791	chr16	Tnk2	32643874	32643942	5496	-0.04921	5.820401	0.780597	0.849179	0.035868	0	786	703	1012	1085	1264	1010	1195	1064	1522	1710
ENSMUSG00000043866	chr7	Taf10	1.06E+08	1.06E+08	4584	0.046466	4.882323	0.780879	0.849419	0.030762	0	418	428	589	476	506	573	697	540	878	814
ENSMUSG00000031636	chr8	Pdlim3	45885485	45885672	1578	-0.04869	8.9693	0.781253	0.84976	0.036619	0	6916	6479	9809	8718	11221	11082	10157	12481	10923	11882
ENSMUSG00000026574	chr1	Dpt	1.65E+08	1.65E+08	1724	0.062686	6.807142	0.781881	0.850339	0.061075	0	1695	1088	1912	1494	3197	2571	3244	1694	2895	2807
ENSMUSG00000068479	chr2	Mfap1a	1.21E+08	1.21E+08	4198	0.05373	3.482672	0.781909	0.850339	0.037046	0	146	169	197	198	198	178	254	356	308	230
ENSMUSG00000030763	chr7	Lcmt1	1.23E+08	1.23E+08	1369	0.044893	4.443894	0.781975	0.850344	0.02884	0	311	322	403	332	416	490	490	447	596	526

ENSMUSG00000087385	chr4	AA415398	1.2E+08	1.2E+08	2760	0.078967	1.30252	0.782131	0.850447	0.065308	0	32	30	51	35	46	44	45	77	51	65
ENSMUSG00000040605	chr16	Bace2	97356728	97357101	3736	-0.07493	2.416841	0.782259	0.850482	0.067178	0	93	63	92	84	120	113	145	63	167	110
ENSMUSG00000098488	chr2	Pla2g4b	1.2E+08	1.2E+08	5831	-0.08447	1.309198	0.782286	0.850482	0.079299	0	34	43	58	21	50	42	69	42	56	61
ENSMUSG00000013973	chr1	Dedd	1.71E+08	1.71E+08	5861	-0.04819	4.983972	0.78238	0.850517	0.033903	0	460	511	622	551	522	667	678	834	748	652
ENSMUSG00000020063	chr10	Sirt1	63319005	63320964	5331	-0.06246	2.869471	0.782465	0.850543	0.055645	0	102	127	115	130	138	97	125	240	199	173
ENSMUSG00000020088	chr10	Sar1a	61680310	61680413	2611	-0.04393	7.149076	0.782784	0.850822	0.029895	0	2200	2069	2737	2178	2876	2724	3270	3440	3589	3223
ENSMUSG00000080989	chr2	Gm14048	1.31E+08	1.31E+08	1268	-0.1151	0.210609	0.78286	0.850839	0.100315	0	13	14	23	23	20	18	16	44	20	20
ENSMUSG00000015850	chr3	Adamtsl4	95676201	95676969	4198	-0.05656	4.28315	0.783637	0.851061	0.047371	0	309	216	384	372	382	258	409	656	575	355
ENSMUSG00000025544	chr14	Tm9sf2	1.22E+08	1.22E+08	3107	0.043109	6.621999	0.783679	0.851061	0.028805	0	1452	1446	1869	1460	1881	1837	2397	2463	2705	2272
ENSMUSG00000031093	chrX	Dock11	35888832	35889032	9240	-0.06219	3.212776	0.783239	0.851061	0.053127	0	160	87	154	143	253	125	211	215	314	208
ENSMUSG00000033429	chr7	Mcee	64392645	64392843	824	-0.05362	4.955386	0.783365	0.851061	0.043529	0	442	605	633	500	410	635	637	791	742	705
ENSMUSG00000033961	chr7	Zfp446	12977848	12978112	5801	-0.07222	1.636058	0.783539	0.851061	0.057237	0	50	32	71	52	55	55	73	64	98	56
ENSMUSG00000049076	chr16	Acap2	31092413	31096446	6493	0.05628	4.24957	0.783657	0.851061	0.045002	0	317	219	298	288	439	226	441	590	598	449
ENSMUSG00000050567	chr11	Maml1	50255634	50258828	5528	-0.05654	3.510185	0.783413	0.851061	0.043253	0	127	167	213	191	281	151	248	351	295	263
ENSMUSG00000085793	chr12	Lin52	84451508	84451543	2144	-0.06656	3.290167	0.783453	0.851061	0.063521	0	178	154	185	161	137	153	211	350	179	204
ENSMUSG00000086914	chr9	Gm16124	53667246	53667355	516	-0.078	2.624474	0.783377	0.851061	0.080479	0	95	104	127	90	102	120	101	234	108	114
ENSMUSG00000099492	chr1	Gm5525	29484604	29485915	1312	-0.08312	0.917012	0.783417	0.851061	0.07854	0	15	35	27	43	34	29	42	36	59	40
ENSMUSG00000021007	chr12	Spata7	98628157	98628334	4642	-0.06995	1.475255	0.783843	0.851171	0.049764	0	36	44	57	45	48	53	58	67	70	57
ENSMUSG00000030074	chr6	Gxylt2	1.01E+08	1.01E+08	2678	0.098154	0.816627	0.784154	0.851377	0.094852	0	25	15	30	17	50	27	48	25	62	42
ENSMUSG00000051223	chr1	Bzw1	58392898	58393216	4033	0.043856	6.564575	0.784106	0.851377	0.02983	0	1447	1282	1713	1401	1973	1540	2191	2419	2849	2336
ENSMUSG00000028089	chr3	Chd1l	97560742	97561087	3008	-0.04732	3.812126	0.784224	0.851385	0.029971	0	200	210	276	241	259	273	271	376	364	312
ENSMUSG00000025428	chr18	Atp5a1	77773729	77774110	3135	-0.04772	11.17229	0.784381	0.851451	0.036444	0	30230	40976	41920	44275	36912	48028	48996	52391	63487	50820
ENSMUSG00000027175	chr2	Tcp11l1	1.05E+08	1.05E+08	6877	-0.07409	1.885485	0.784407	0.851451	0.072168	0	78	32	65	71	61	72	64	77	112	86
ENSMUSG00000027193	chr2	Api5	94411682	94413781	4545	-0.04502	5.15	0.784512	0.851497	0.03089	0	501	556	734	532	692	534	795	996	1007	783
ENSMUSG00000027335	chr2	Adra1d	1.32E+08	1.32E+08	1899	-0.14	0.065265	0.784589	0.851514	0.193939	0	9	15	26	17	17	9	26	3	27	43
ENSMUSG00000024598	chr18	Fbn2	58008623	58010632	10480	0.12435	2.886767	0.784829	0.851708	0.235793	0	94	26	103	42	363	119	285	130	250	117
ENSMUSG00000026037	chr1	Orc2	58462771	58464290	3857	-0.05123	3.953051	0.784981	0.851806	0.038176	0	233	247	309	231	287	246	321	502	408	296
ENSMUSG00000084691	chr12	Gm24895	1.1E+08	1.1E+08	74	-0.08936	1.957719	0.785487	0.852289	0.104319	0	62	52	71	33	114	53	133	81	119	50
ENSMUSG00000026042	chr1	Col5a2	45374321	45376230	9591	-0.06744	7.989536	0.785709	0.852396	0.073175	0	3647	2440	4712	3048	8740	3945	8244	4319	7549	5332
ENSMUSG00000079605	chr17	Zbtb9	26973167	26973314	2798	-0.06224	2.368618	0.785677	0.852396	0.044475	0	67	89	77	85	115	98	123	102	137	119
ENSMUSG00000039428	chr7	Tmem135	89139723	89141970	6104	0.056671	4.788519	0.785819	0.852448	0.049444	0	293	397	478	486	636	452	543	459	894	986
ENSMUSG00000005268	chr15	Prlr	10177238	10177871	15339	-0.1593	0.245971	0.786065	0.852565	0.253897	0	11	4	9	17	61	15	14	31	20	39
ENSMUSG00000037971	chr9	1110032A03Rik	50762828	50764016	5293	-0.05194	3.357685	0.786112	0.852565	0.035927	0	169	137	201	166	191	181	219	282	221	255
ENSMUSG00000097101	chr13	1810034E14Rik	64248700	64249203	1805	0.111741	0.158544	0.786054	0.852565	0.118166	0	18	8	23	6	28	15	28	15	35	32
ENSMUSG00000035171	chr19	1110059E24Rik	21581202	21581630	3067	-0.05021	3.206549	0.786365	0.852773	0.035007	0	139	149	183	147	155	172	219	171	290	204
ENSMUSG00000059401	chrX	Mamld1	71050256	71050349	4796	-0.07856	1.843663	0.78705	0.853449	0.079668	0	38	42	52	83	90	45	64	110	90	92
ENSMUSG00000020380	chr11	Rad50	53649519	53650655	5375	-0.05867	3.047894	0.787309	0.853663	0.048253	0	148	108	125	136	179	120	157	163	258	254
ENSMUSG00000000811	chr6	Txnrd3	89643988	89644402	2836	-0.05458	2.945237	0.787463	0.853697	0.03816	0	98	114	143	137	160	135	135	196	227	184
ENSMUSG00000024613	chr18	Tcof1	60813755	60814188	5266	-0.043	4.637726	0.78741	0.853697	0.027704	0	339	342	447	468	522	420	494	601	767	601
ENSMUSG00000003198	chr17	Zfp959	55892120	55892186	2028	-0.08103	1.482974	0.787703	0.85389	0.063843	0	34	42	55	36	68	48	61	83	61	52
ENSMUSG00000041889	chr1	Shisa4	1.35E+08	1.35E+08	2418	0.045737	7.541415	0.787946	0.854086	0.034444	0	2592	2368	3511	2989	4026	4273	4447	4043	5447	3715
ENSMUSG00000029387	chr5	Gtf2h3	1.25E+08	1.25E+08	3840	-0.04807	3.524629	0.788281	0.854382	0.033379	0	151	196	223	209	186	215	272	224	356	252
ENSMUSG00000021495	chr13	Fam193b	55539319	55539712	4338	0.05684	3.581032	0.788517	0.854571	0.043822	0	197	174	186	201	205	161	242	338	307	381
ENSMUSG00000006057	chr11	Atp5g1	96068852	96073218	4912	-0.0537	8.631139	0.788769	0.854778	0.047979	0	5451	7668	6754	7913	5298	8802	8348	8748	11267	7924
ENSMUSG00000052914	chr4	Cyp2j6	96516138	96518205	3605	0.059119	2.693832	0.78901	0.854968	0.0433	0	84	96	105	113	124	93	144	194	179	157
ENSMUSG00000055065	chr15	Ddx17	79527707	79530517	4761	-0.04725	6.603397	0.789069	0.854968	0.036457	0	1350	1272	1705	1708	2321	1761	2713	1677	2570	2465
ENSMUSG00000042992	chr6	Loh12cr1	1.35E+08	1.35E+08	1822	-0.05205	3.907107	0.789792	0.855685	0.039101	0	173	275	307	254	257	341	334	295	349	365
ENSMUSG00000004631	chr6	Sgce	4674350	4674632	3086	0.046494	3.847527	0.790312	0.856176	0.031962	0	215	166	274	198	340	233	372	320	443	350
ENSMUSG00000029231	chr5	Pdgfra	75152291	75152457	6737	-0.05941	5.8756	0.790446	0.856176	0.058249	0	1118	514	1048	872	1524	878	1206	1872	1453	1329
ENSMUSG00000032583	chr9	Mon1a	1.08E+08	1.08E+08	2826	-0.04705	3.451078	0.790562	0.856176	0.03236	0	160	193	207	172	181	196	252	261	273	262
ENSMUSG00000034563	chr9	Ccpg1	72985429	72985673	7497	-0.0551	6.089683	0.790834	0.856176	0.05047	0	1052	922	1255	1284	1282	1117	1432	2479	1446	1273
ENSMUSG00000034674	chr10	Tdg	82629828	82629939	5374	0.041176	3.965102	0.790821	0.856176	0.025452	0	200	211	286	255	340	292	368	365	434	383
ENSMUSG00000035048	chr9	Anapc13	1.03E+08	1.03E+08	2377	0.045616	5.053689	0.790661	0.856176	0.033868	0	452	496	665	542	569	770	719	797	765	811
ENSMUSG00000038721	chr11	Hoxb7	96286623	96287127	1544	0.115466	0.156726	0.790863	0.856176	0.078503	0	20	15	11	19	15	16	27	18	36	28
ENSMUSG00000038762	chr17	Abcf1	35956819	35957589	4410	0.041886	6.647805	0.790805	0.856176	0.029231	0	1248	1493	1793	1703	2068	1878	2187	2429	3005	2425
ENSMUSG00000047731	chr19	Wbp1l	46599084	46599293	4463	-0.05043	6.260223	0.790758	0.856176	0.042436	0	1146	1138	1567	1407	1227	1232	1568	2520	1887	1589
ENSMUSG00000062761	chr5	Zfp512	31452436	31452577	3293	-0.04348	3.958541	0.790776	0.856176	0.028031	0	245	236	257	267	300	288	371	320	386	409
ENSMUSG00000072837	chr10	Mir546	1.27E+08	1.27E+08	121	0.063374	3.914403	0.791182	0.856454	0.063653	0	190	191	257	274	326	208	326	640	341	277
ENSMUSG00000032744	chr4	Heyl	1.23E+08	1.23E+08	5113	0.061059	4.253371	0.791386	0.856608	0.059367	0	217	240	317	461	324	310	714	308	543	411
ENSMUSG00000093273	chr11	Mir3064	1.07E+08	1.07E+08	67	0.047455	4.274236	0.791485	0.856648	0.034245	0	260	292	399	264	376	282	586	490	489	457
ENSMUSG00000045092	chr3	S1pr1	1.16E+08	1.16E+08	3029	-0.05748	4.884713	0.791725	0.856841	0.053975	0	326	410	658	741	380	469	684	743	685	796
ENSMUSG00000027316	chr2	Gfra4	1.31E+08	1.31E+08	2165	-0.07957	1.200325	0.791919	0.856844	0.069696	0	19	39	48	47	37	39	40	50	68	55
ENSMUSG00000029578	chr5	Wipi2	1.43E+08	1.43E+08	8041	0.054476	5.453847	0.791976	0.856844	0.049161	0	636	598	853	737	765	655	897	1693	1033	936
ENSMUSG00000047187	chr4	Rab2a	8535644	8535908	2133	0.052352	7.199835	0.791885	0.856844	0.046587	0	2412	2190	2839	2053	2480	2697	2960	5069	3332	3283
ENSMUSG00000051355	chr11	Commd1	22896136	22900057	5936	0.04815	5.669195	0.79192	0.856844	0.038541	0	736	858	981	762	799	1247	1208	1003	1271	1199
ENSMUSG00000018189	chr1	Uchl5	1.44E+08	1.44E+08	2921	-0.04445	4.870627	0.792201	0.856979	0.031913	0	426	525	574	426	505	567	628	707	740	696

ENSMUSG00000028221	chr4	Tmem55a	14864076	14864437	2339	-0.04293	5.053279	0.792225	0.856979	0.029646	0	484	529	669	492	635	652	829	710	958	662
ENSMUSG00000076281	chr9	Gm24270	56223715	56223771	57	0.08203	3.866993	0.792538	0.857251	0.111572	0	158	271	291	129	340	301	188	351	227	640
ENSMUSG00000039826	chr2	Trub2	29761224	29761688	6316	0.045928	4.740644	0.792697	0.857289	0.033461	0	360	447	496	431	444	522	520	771	716	621
ENSMUSG00000040003	chr5	Magi2	19227046	19227589	7239	-0.0854	0.925711	0.792635	0.857289	0.064981	0	27	21	31	32	46	30	54	45	39	36
ENSMUSG00000028124	chr3	Gclm	1.22E+08	1.22E+08	5543	0.088103	4.008493	0.792797	0.857331	0.128545	0	208	240	300	243	310	198	225	937	266	288
ENSMUSG00000020241	chr10	Col6a2	76595762	76596811	8326	0.07801	8.630468	0.793053	0.857541	0.105502	0	5757	3030	7007	4938	12771	7919	14213	4086	13576	8223
ENSMUSG00000016528	chr1	Mapkapk2	1.31E+08	1.31E+08	3041	-0.04293	7.80701	0.793237	0.857673	0.03184	0	2893	3667	4164	4186	4052	4451	4689	5022	6325	5239
ENSMUSG00000022403	chr15	St13	81363669	81365578	3457	0.041324	6.264591	0.793447	0.857698	0.02881	0	1014	1072	1435	1286	1566	1236	1946	1743	2388	1907
ENSMUSG00000030806	chr7	Stx1b	1.28E+08	1.28E+08	4802	0.094006	1.048309	0.793405	0.857698	0.114903	0	31	13	32	34	52	20	46	50	44	80
ENSMUSG00000031565	chr8	Fgfr1	25513654	25513714	8120	0.051948	6.489542	0.793433	0.857698	0.046543	0	1413	865	1818	1384	2012	1404	2289	2856	2081	2055
ENSMUSG00000022617	chr15	Chkb	89416405	89416979	5805	-0.05128	8.066398	0.793948	0.858173	0.045957	0	3913	4546	4899	5134	4030	4793	5166	8680	6610	5380
ENSMUSG00000016181	chr1	Diexf	1.93E+08	1.93E+08	6530	-0.05061	3.081959	0.794344	0.858497	0.033549	0	129	123	164	120	179	150	203	205	223	181
ENSMUSG00000023886	chr17	Smoc2	14279506	14279799	2832	-0.05029	7.141965	0.794372	0.858497	0.043838	0	2290	1612	2743	2434	3034	3215	3639	2166	3722	3287
ENSMUSG00000022350	chr15	E430025E21Rik	59331998	59332359	4032	-0.04067	4.952428	0.79448	0.858547	0.027172	0	438	440	628	541	579	505	652	786	884	757
ENSMUSG00000026229	chr1	Psmd1	86064387	86064805	7265	0.05068	7.504839	0.795015	0.859058	0.04522	0	2415	2686	3506	2983	3357	3287	3453	6462	4193	4041
ENSMUSG00000021072	chr12	Tmx1	70453095	70453320	3299	0.048744	4.079074	0.795166	0.859087	0.036872	0	236	220	315	232	396	233	342	429	600	441
ENSMUSG00000021365	chr13	Nedd9	41309916	41312170	4712	-0.06239	3.475665	0.795141	0.859087	0.060561	0	122	131	155	266	285	168	352	189	320	248
ENSMUSG00000019738	chr7	Polr2i	30231948	30232404	1212	0.046861	4.330662	0.795482	0.859362	0.034681	0	290	324	411	323	284	422	471	388	568	521
ENSMUSG00000019848	chr10	Popdc3	45178098	45178192	2083	-0.04544	4.879954	0.795724	0.859488	0.033615	0	409	411	619	495	575	561	711	829	717	535
ENSMUSG00000030865	chr7	Chp2	1.22E+08	1.22E+08	1603	-0.06685	2.560301	0.79569	0.859488	0.062749	0	87	64	116	110	125	88	115	204	117	136
ENSMUSG00000024533	chr18	Spire1	67488209	67491549	5178	0.044672	3.668846	0.795954	0.859603	0.030846	0	164	161	215	221	290	227	352	268	383	278
ENSMUSG00000090019	chr6	Gimap1	48739054	48739156	1872	0.076562	1.752267	0.795899	0.859603	0.065764	0	40	52	57	70	45	53	66	67	104	107
ENSMUSG00000017858	chr2	Ift52	1.63E+08	1.63E+08	2802	-0.04012	3.936904	0.79652	0.860097	0.025513	0	236	211	285	273	285	253	348	355	458	356
ENSMUSG00000037916	chr19	Ndufv1	4007497	4007665	2521	-0.04832	8.386054	0.796536	0.860097	0.0419	0	4266	6084	6152	6553	5072	6415	6307	9245	9117	7244
ENSMUSG00000019842	chr10	Traf3ip2	39612934	39613346	3687	0.064647	2.008382	0.7968	0.860248	0.051824	0	50	60	70	67	74	83	85	115	87	93
ENSMUSG00000049488	chr4	Tmem67	12039355	12039892	7744	-0.068	1.218559	0.796781	0.860248	0.055867	0	32	29	40	36	56	30	56	58	59	54
ENSMUSG00000103974	chr13	AL589742.1	21500953	21501352	475	0.05926	3.391746	0.796897	0.860286	0.053035	0	144	190	168	206	126	240	253	224	321	195
ENSMUSG00000043415	chr2	Otud1	19657752	19660583	2832	-0.07104	4.135501	0.797116	0.860455	0.085649	0	184	222	226	496	384	304	607	360	521	214
ENSMUSG00000020682	chr11	Mmp28	83440768	83442945	3874	-0.08848	1.73551	0.797393	0.860671	0.119734	0	54	34	47	76	68	20	57	110	98	93
ENSMUSG00000039159	chr6	Ube2h	30211289	30215083	4780	0.042542	6.172626	0.79744	0.860671	0.03214	0	1003	861	1221	1284	1635	1255	1891	1818	1932	1669
ENSMUSG00000079669	chr9	Gm17396	1.17E+08	1.17E+08	1655	0.068913	1.375636	0.797578	0.860753	0.055994	0	37	37	42	34	54	42	51	76	65	65
ENSMUSG00000006611	chr13	Hfe	23702034	23704426	3572	0.046514	4.986308	0.797691	0.860799	0.037947	0	354	512	688	478	585	727	683	599	855	851
ENSMUSG00000042659	chr7	Arrdc4	68737045	68739533	3989	0.048176	3.205433	0.797745	0.860799	0.036977	0	108	129	176	152	193	164	202	249	210	255
ENSMUSG00000020107	chr10	Anapc16	59987409	59988838	4890	0.047531	5.29864	0.798125	0.861141	0.039651	0	548	642	788	581	655	834	859	1199	891	812
ENSMUSG00000097915	chr15	A330009N23Rik	1.01E+08	1.01E+08	1392	0.110633	0.208395	0.798186	0.861141	0.077716	0	19	21	17	15	11	21	25	22	29	31
ENSMUSG00000023066	chr18	Rttn	88971790	88972078	7268	-0.06225	1.272917	0.798355	0.861255	0.051842	0	33	34	52	37	43	34	60	48	73	54
ENSMUSG00000030019	chr6	Fbxl14	1.19E+08	1.19E+08	2963	0.043854	3.730783	0.79877	0.861636	0.029855	0	159	192	271	221	250	238	286	276	422	356
ENSMUSG00000040586	chrX	Ofd1	1.66E+08	1.66E+08	4453	0.056353	2.828941	0.799045	0.861865	0.051993	0	98	96	159	85	142	120	143	234	182	156
ENSMUSG00000030647	chr7	Ndufc2	97400003	97400357	754	-0.05015	6.809503	0.799206	0.861971	0.045993	0	1604	2250	2164	1779	1560	2541	2487	2218	2968	2506
ENSMUSG00000032239	chr9	Rp9	22448311	22448854	1142	0.046828	4.562297	0.79943	0.862146	0.037728	0	295	411	476	387	353	553	531	493	607	572
ENSMUSG00000023800	chr17	Tiam2	3326573	3326726	6281	0.075152	1.770238	0.799637	0.862302	0.067017	0	49	46	64	42	70	42	101	101	100	59
ENSMUSG00000038290	chr11	Smg6	74925823	74926003	8453	0.045109	4.48737	0.799707	0.862311	0.034844	0	324	260	408	395	468	349	506	704	568	534
ENSMUSG00000097577	chr14	6230400D17Rik	20687236	20688613	1554	0.106805	0.814567	0.799796	0.86234	0.145129	0	31	16	45	25	16	30	28	76	42	24
ENSMUSG00000029428	chr5	Stx2	1.29E+08	1.29E+08	4164	0.04545	3.536826	0.799917	0.862403	0.032076	0	180	140	209	162	265	199	303	245	357	275
ENSMUSG00000015944	chr5	Gatsl2	1.34E+08	1.34E+08	7560	0.048275	6.820098	0.800871	0.863229	0.043288	0	1686	1312	2082	2029	2236	1841	2243	3852	2721	2754
ENSMUSG00000044317	chr7	Gpr4	19212538	19212634	2884	-0.06922	1.899999	0.800901	0.863229	0.07482	0	52	60	51	91	53	55	70	77	142	81
ENSMUSG00000055932	chr8	Fto	91313532	91313620	13026	-0.04127	6.679388	0.800933	0.863229	0.031296	0	1583	1361	1803	1756	2223	1941	2189	2685	2774	2184
ENSMUSG00000064337	chrMT	mt-Rnr1	70	1024	955	0.075374	8.816906	0.800885	0.863229	0.106456	0	5185	8721	8217	9247	4572	7497	6394	20033	8686	10905
ENSMUSG00000002963	chr7	Pnkp	44857139	44857302	3133	-0.04365	4.375629	0.801075	0.863315	0.032516	0	282	324	443	301	413	336	392	581	581	504
ENSMUSG00000002103	chr2	Acp2	91202885	91203048	5186	-0.03991	4.972029	0.801279	0.863468	0.028287	0	502	417	613	510	617	525	696	632	956	836
ENSMUSG00000031723	chr8	Txnl4b	1.1E+08	1.1E+08	1892	-0.0467	3.469411	0.801415	0.863524	0.034688	0	166	160	237	185	184	217	244	193	325	286
ENSMUSG00000048796	chr3	Cyb561d1	1.08E+08	1.08E+08	5086	-0.05092	3.008921	0.801559	0.863524	0.037435	0	99	127	149	115	194	145	176	191	208	193
ENSMUSG00000059669	chr12	Taf1b	24498581	24498649	2019	0.060485	2.526399	0.801538	0.863524	0.047329	0	77	82	118	98	88	92	175	126	177	113
ENSMUSG00000085037	chr4	4933421O10Rik	33027142	33030521	3847	0.072504	1.464368	0.801581	0.863524	0.078685	0	43	24	53	37	63	42	61	90	52	72
ENSMUSG00000091803	chr12	Cox16	81359026	81359344	3751	-0.046	5.211655	0.802557	0.864508	0.038472	0	565	655	797	512	581	781	802	882	858	873
ENSMUSG00000058454	chr7	Dhcr7	1.44E+08	1.44E+08	3784	-0.06921	3.518821	0.802767	0.864667	0.08279	0	131	167	196	183	315	221	268	94	410	322
ENSMUSG00000027198	chr2	Ext2	93661028	93661681	7328	0.039606	5.086133	0.803023	0.864876	0.028857	0	471	431	641	564	712	649	880	812	798	849
ENSMUSG00000027809	chr3	Etfdh	79603788	79604165	7505	-0.05876	7.136869	0.803489	0.865254	0.066315	0	1908	2635	2631	2785	1838	2217	2513	5259	3336	2761
ENSMUSG00000097350	chr17	4732491K20Rik	12318885	12319172	3142	-0.07138	1.384677	0.803499	0.865254	0.074385	0	42	40	43	58	29	56	57	59	64	48
ENSMUSG00000027981	chr3	Rnpc3	1.14E+08	1.14E+08	6627	0.055445	2.537019	0.80365	0.865349	0.047816	0	70	87	133	84	96	98	141	168	141	131
ENSMUSG00000019854	chr10	Reps1	18055861	18056115	5301	-0.0392	4.376515	0.803822	0.865467	0.026232	0	322	273	403	325	440	350	488	510	571	476
ENSMUSG00000006675	chr9	P4htm	1.09E+08	1.09E+08	3890	0.077619	1.286938	0.804096	0.865695	0.070883	0	46	25	37	27	56	41	53	70	62	55
ENSMUSG00000017428	chr11	Psmd11	80428615	80428755	6383	0.059239	6.749249	0.805225	0.866775	0.068267	0	1509	1696	2074	1724	1752	1854	2138	4605	2266	1833
ENSMUSG00000033233	chr3	Trim45	1.01E+08	1.01E+08	6005	0.070716	1.468323	0.805203	0.866775	0.053185	0	31	49	49	40	48	47	74	63	72	64
ENSMUSG00000042828	chr7	Trim72	1.28E+08	1.28E+08	2553	0.04499	8.166395	0.805415	0.866837	0.039801	0	3733	4033	5689	4495	5906	6438	7850	4506	8358	6753
ENSMUSG00000062908	chr3	Acadm	1.54E+08	1.54E+08	2932	0.053631	7.972242	0.805422	0.866837	0.056293	0	3268	4524	4239	5046	3143	4149	4415	8090	6716	6619

ENSMUSG00000075271	chr2	Ttc30a1	75978247	75981967	3721	-0.07186	0.794854	0.80547	0.866837	0.070899	0	31	20	36	19	35	26	45	26	52	40
ENSMUSG00000042804	chr4	Gpr153	1.52E+08	1.52E+08	3909	-0.06865	4.307709	0.805607	0.866917	0.086602	0	331	157	346	306	593	383	721	241	544	360
ENSMUSG00000020527	chr11	Myo19	84880148	84880511	7113	-0.06691	1.653161	0.805812	0.867055	0.073927	0	34	44	65	62	58	35	79	47	101	95
ENSMUSG00000038534	chr11	Osbpl7	97050628	97050953	5920	0.062702	2.256956	0.80586	0.867055	0.052473	0	72	57	102	61	94	76	100	92	155	144
ENSMUSG00000028300	chr4	3110043O21Rik	35191285	35193294	4603	0.043339	4.034662	0.806226	0.867196	0.03111	0	248	227	332	253	281	257	334	386	495	484
ENSMUSG00000033105	chr10	Lss	76531588	76531621	10787	-0.09911	1.896117	0.806242	0.867196	0.159978	0	47	26	47	59	148	33	59	69	108	151
ENSMUSG00000033857	chr11	Engase	1.18E+08	1.18E+08	5184	-0.0652	3.48376	0.806156	0.867196	0.071451	0	176	111	210	109	373	242	261	200	279	272
ENSMUSG00000049670	chr19	Morn4	42074939	42076255	1816	0.068965	1.264599	0.806211	0.867196	0.058669	0	29	38	46	41	33	47	44	63	66	55
ENSMUSG00000065399	chr18	Mir133a-1	10782899	10782985	87	-0.07426	1.524268	0.806332	0.867226	0.075049	0	43	57	59	32	45	61	62	55	56	78
ENSMUSG00000021904	chr14	Sema3g	31217860	31218025	4538	-0.04773	3.928791	0.806477	0.867309	0.042159	0	201	261	231	340	238	259	272	385	426	406
ENSMUSG00000023990	chr17	Tfeb	47737030	47737316	5669	-0.04282	5.793948	0.806535	0.867309	0.034581	0	719	746	1129	1021	1133	1151	1022	1459	1376	1305
ENSMUSG00000040950	chr11	Mgl2	70130329	70130442	2094	0.05689	3.438464	0.806873	0.867604	0.061114	0	157	111	191	153	287	247	309	141	281	290
ENSMUSG00000046679	chr6	C87436	86438374	86438487	4092	0.048773	3.08394	0.80697	0.867642	0.038912	0	123	117	158	150	139	149	174	252	216	204
ENSMUSG00000074030	chr8	Exoc8	1.25E+08	1.25E+08	7406	-0.04317	3.475721	0.807076	0.867688	0.032238	0	170	169	204	157	238	186	277	206	352	264
ENSMUSG00000024769	chr19	Cdc42bpg	6306456	6306875	6099	0.05092	2.899911	0.807148	0.867698	0.03917	0	112	106	124	131	129	118	157	216	204	186
ENSMUSG00000022710	chr16	Usp7	8689595	8690886	7766	-0.04126	6.159847	0.807466	0.867777	0.03315	0	998	1040	1340	1173	1544	1240	1538	2097	1802	1540
ENSMUSG00000029433	chr5	Diablo	1.24E+08	1.24E+08	6155	0.039596	5.646129	0.807332	0.867777	0.029982	0	739	793	955	738	877	1010	1055	1297	1361	1172
ENSMUSG00000030732	chr7	Chrdl2	1E+08	1E+08	1728	-0.09156	0.616575	0.807472	0.867777	0.067947	0	19	20	24	27	35	32	41	22	32	34
ENSMUSG00000089718	chr9	2310075C17Rik	1.12E+08	1.12E+08	326	-0.07492	2.479397	0.807423	0.867777	0.103519	0	106	106	73	89	83	74	151	198	147	60
ENSMUSG00000036009	chr10	Mettl25	1.06E+08	1.06E+08	2688	0.065287	1.589022	0.807556	0.8678	0.056724	0	38	38	49	47	68	53	73	57	112	58
ENSMUSG00000030584	chr7	Dpf1	29303951	29304112	3529	-0.08345	0.747716	0.807742	0.867932	0.08039	0	16	19	36	20	49	25	33	29	53	42
ENSMUSG00000034908	chr9	Sidt2	45937857	45939316	5135	-0.05144	6.112774	0.807874	0.86794	0.052428	0	998	927	1196	1283	1516	976	1306	2597	1693	1398
ENSMUSG00000055632	chr2	Hmcn2	31314415	31314676	16073	-0.04751	6.212404	0.807842	0.86794	0.044399	0	1287	680	1414	1264	1738	1220	2127	1738	1909	1548
ENSMUSG00000085419	chr11	Gm11734	1.18E+08	1.18E+08	728	0.09751	0.143725	0.808036	0.868046	0.105563	0	15	7	25	10	26	20	37	20	19	24
ENSMUSG00000032534	chr9	Cep63	1.03E+08	1.03E+08	9588	0.040481	4.074483	0.808112	0.868061	0.029557	0	198	249	326	286	332	303	441	343	435	465
ENSMUSG00000059447	chr5	Hadhb	30155248	30155339	6595	0.046978	8.090691	0.808238	0.868129	0.044463	0	3779	4871	4864	4885	3637	4725	5337	8187	7672	6566
ENSMUSG00000022371	chr15	Col14a1	55307750	55307984	7013	-0.07988	6.432536	0.80859	0.868439	0.128014	0	1200	621	1306	1080	3604	1725	2764	860	2566	1915
ENSMUSG00000028266	chr3	Lmo4	1.44E+08	1.44E+08	3295	0.041131	4.265495	0.808858	0.868592	0.030067	0	263	282	315	349	367	321	420	564	512	458
ENSMUSG00000030505	chr7	Prmt3	49778346	49778501	3361	-0.0418	3.954245	0.808855	0.868592	0.029163	0	240	218	282	226	347	320	364	338	374	362
ENSMUSG00000028243	chr4	Ubxn2b	6191098	6191213	6642	-0.07694	1.427038	0.80922	0.868906	0.092171	0	49	36	60	30	47	21	69	52	97	67
ENSMUSG00000034445	chr19	Cyb561a3	10577454	10578083	1474	0.054876	2.259104	0.809275	0.868906	0.040848	0	68	65	79	86	86	84	119	100	130	127
ENSMUSG00000025135	chr11	Anapc11	1.21E+08	1.21E+08	5057	-0.03907	4.556235	0.80945	0.869025	0.02851	0	333	377	443	394	434	469	554	434	690	556
ENSMUSG00000062944	chr7	9130023H24Rik	1.28E+08	1.28E+08	3581	-0.06568	1.617096	0.80984	0.869376	0.055817	0	40	46	47	48	75	43	84	57	82	77
ENSMUSG00000033326	chr4	Kdm4a	1.18E+08	1.18E+08	5782	-0.03958	5.035601	0.809953	0.869431	0.029641	0	414	450	591	584	769	544	722	848	876	796
ENSMUSG00000014786	chr8	Slc9a5	1.05E+08	1.05E+08	5222	0.079006	1.162529	0.810116	0.869539	0.074442	0	24	35	52	25	39	26	55	44	78	60
ENSMUSG00000068966	chr2	Zbtb34	33406108	33412495	6604	-0.04981	2.833017	0.810587	0.869976	0.041018	0	109	78	128	130	159	115	145	169	190	193
ENSMUSG00000051107	chr13	Gm15440	51685529	51686246	1231	0.04141	5.790155	0.811041	0.870396	0.035132	0	698	824	950	955	1148	1248	1045	1405	1382	1379
ENSMUSG00000024620	chr18	Pdgfrb	61045150	61045572	5478	0.04336	5.933186	0.811354	0.870665	0.038403	0	799	669	1099	1205	1327	875	1541	1736	1763	1416
ENSMUSG00000026201	chr1	Stk16	75210838	75211052	4518	-0.0415	4.387589	0.811655	0.87092	0.032684	0	308	315	411	341	392	414	543	333	595	516
ENSMUSG00000041716	chr12	Gm20604	1.03E+08	1.03E+08	2795	-0.04456	3.481917	0.81187	0.871083	0.037199	0	162	207	212	170	179	208	305	222	311	230
ENSMUSG00000026353	chr1	Ubxn4	1.28E+08	1.28E+08	4659	0.061667	6.179984	0.81214	0.871103	0.079204	0	1000	1063	1428	1203	1225	986	1451	3394	1575	1238
ENSMUSG00000035722	chr10	Abca7	79996494	79996588	6752	0.043188	3.869548	0.812083	0.871103	0.031368	0	202	242	230	264	247	242	345	313	427	410
ENSMUSG00000036781	chr9	Rps27l	66946086	66946180	816	0.040394	5.79139	0.81206	0.871103	0.033443	0	804	865	1135	760	987	1229	1276	1313	1434	1226
ENSMUSG00000091478	chr11	Gm10039	1E+08	1E+08	411	0.047211	5.297921	0.812134	0.871103	0.044732	0	496	744	650	749	532	903	927	848	1129	813
ENSMUSG00000047342	chr11	Zfp286	62753377	62753682	4735	0.083113	0.402267	0.812246	0.871149	0.06947	0	14	17	32	16	21	21	35	21	38	33
ENSMUSG00000053470	chr6	Kdm3a	71588974	71589715	4921	0.049788	3.894583	0.812396	0.871242	0.048338	0	191	187	292	235	326	215	338	554	338	314
ENSMUSG00000038690	chr5	Atp5j2	1.45E+08	1.45E+08	1231	0.046684	8.329639	0.812631	0.871426	0.046186	0	4299	6159	6170	5180	4190	7549	7189	7201	8549	7193
ENSMUSG00000026335	chr1	Pam	97795114	97795392	11892	0.044674	6.069015	0.812793	0.871533	0.041825	0	1048	711	1162	964	1730	1212	2001	1423	1954	1405
ENSMUSG00000032607	chr9	Amt	1.08E+08	1.08E+08	2437	0.105705	0.135714	0.812938	0.871597	0.116815	0	19	8	9	23	21	10	18	34	31	30
ENSMUSG00000058503	chr5	Fam133b	3543844	3543947	1555	-0.05064	2.949761	0.812978	0.871597	0.046958	0	115	139	130	108	153	115	172	237	194	162
ENSMUSG00000031425	chrX	Plp1	1.37E+08	1.37E+08	5551	0.062313	2.653761	0.81342	0.872002	0.067414	0	110	75	92	103	125	88	154	232	162	108
ENSMUSG00000044715	chr12	Gskip	1.06E+08	1.06E+08	2776	-0.04378	3.504563	0.81361	0.872072	0.03429	0	159	174	229	185	209	225	288	186	332	266
ENSMUSG00000097944	chr8	A130014A01Rik	1.2E+08	1.2E+08	2323	0.080034	0.836936	0.813565	0.872072	0.073372	0	25	31	24	31	24	33	45	52	38	33
ENSMUSG00000031349	chrX	Nsdhl	72918557	72918693	2853	-0.05667	3.244048	0.81377	0.872175	0.060099	0	135	117	166	161	231	149	220	115	289	318
ENSMUSG00000001039	chr11	B9d1	61505144	61505271	1593	-0.08604	1.043006	0.81388	0.872212	0.094085	0	20	33	43	40	34	50	49	20	59	43
ENSMUSG00000020149	chr11	Rab1	20201432	20201652	3799	-0.03639	7.12886	0.81393	0.872212	0.028139	0	2036	1975	2668	2293	2935	2482	3119	3114	4130	3394
ENSMUSG00000093574	chr5	Gm20671	32737230	32737454	1731	-0.04016	3.885442	0.814151	0.872381	0.03312	0	214	235	265	236	294	192	365	300	501	376
ENSMUSG00000078154	chr11	Gm12184	48825346	48826655	1310	0.065703	1.361198	0.814386	0.872565	0.0563	0	30	35	57	38	43	55	59	56	58	64
ENSMUSG00000002845	chr16	Tmem39a	38558698	38558762	4094	0.045195	3.443149	0.814938	0.873032	0.038402	0	170	129	187	135	278	181	277	259	301	269
ENSMUSG00000058761	chr7	Rnf169	99920257	99926483	7647	-0.0464	3.404149	0.814948	0.873032	0.038141	0	130	182	170	155	260	213	250	209	309	225
ENSMUSG00000014551	chr6	Mrps25	92169525	92175208	6576	-0.04661	4.774108	0.815532	0.873591	0.044945	0	390	477	552	468	406	638	586	414	796	676
ENSMUSG00000039804	chr2	Ncoa5	1.65E+08	1.65E+08	4383	-0.04023	3.995789	0.815738	0.873675	0.030398	0	246	226	258	243	378	307	400	301	450	371
ENSMUSG00000085322	chr2	Gm14261	1.69E+08	1.69E+08	1429	-0.09735	0.649065	0.815693	0.873675	0.104042	0	21	24	28	23	32	48	18	35	26	33
ENSMUSG00000018239	chr11	Zcchc10	53324679	53324741	1391	0.049861	2.790853	0.81688	0.874831	0.038257	0	99	112	121	100	126	118	171	172	170	180
ENSMUSG00000041775	chr7	Mapk1ip1	1.39E+08	1.39E+08	1883	0.050344	3.902047	0.817028	0.874922	0.050331	0	224	232	286	249	217	272	268	536	326	348
ENSMUSG00000004268	chr6	Emg1	1.25E+08	1.25E+08	1404	0.040204	5.645813	0.817604	0.875471	0.035048	0	692	823	1036	691	868	1125	1259	962	1344	1175

ENSMUSG00000020472	chr11	Zkscan17	59485520	59487817	4573	0.060728	4.571706	0.817974	0.875799	0.079968	0	290	311	458	403	501	312	449	1130	517	421
ENSMUSG00000027878	chr3	Notch2	98013538	98013771	10506	-0.05097	4.614602	0.818167	0.875939	0.054154	0	417	227	399	324	761	383	612	584	607	628
ENSMUSG00000032641	chr6	Gpr19	1.35E+08	1.35E+08	2637	0.074238	1.724629	0.818326	0.876042	0.077648	0	36	51	62	53	60	39	64	126	84	75
ENSMUSG00000064090	chr11	Vrk2	26471322	26471786	6591	0.049849	2.844832	0.818439	0.876095	0.044516	0	87	118	107	135	133	144	174	129	197	197
ENSMUSG00000005682	chr10	Pan2	1.28E+08	1.28E+08	4450	-0.04402	3.374478	0.819596	0.877197	0.03628	0	165	136	206	141	231	168	225	236	254	303
ENSMUSG00000073485	chr1	H3f3aos	1.81E+08	1.81E+08	3044	0.097098	0.168469	0.819571	0.877197	0.120499	0	17	10	18	18	20	16	12	48	21	26
ENSMUSG00000029199	chr5	Lias	65391497	65391673	4570	0.043558	5.57473	0.819725	0.877199	0.041591	0	664	855	839	784	721	918	929	1511	1232	1022
ENSMUSG00000039318	chr1	Rab3gap2	1.85E+08	1.85E+08	10800	-0.03676	4.76192	0.819666	0.877199	0.028877	0	388	355	520	469	577	394	602	630	819	723
ENSMUSG00000031060	chrX	Rbm10	20617503	20618082	3714	0.037926	4.147606	0.81981	0.877223	0.028418	0	268	258	341	232	359	329	404	382	544	440
ENSMUSG00000039509	chr8	Nup133	1.24E+08	1.24E+08	5808	0.038138	4.291196	0.820027	0.877387	0.028547	0	324	276	332	308	358	365	407	511	579	451
ENSMUSG00000078786	chr7	BC024978	27195781	27196107	2756	-0.04838	2.607502	0.820589	0.877921	0.041989	0	85	97	109	86	135	93	139	155	189	122
ENSMUSG00000021892	chr14	Sh3bp5	31359880	31359966	3194	0.037553	5.012497	0.820928	0.878176	0.030817	0	380	428	569	600	713	516	727	736	983	895
ENSMUSG00000022330	chr15	Osr2	35296098	35296467	1723	-0.08254	1.05224	0.821208	0.878176	0.103047	0	18	45	21	43	42	43	32	47	44	56
ENSMUSG00000027219	chr2	Slc28a2	1.22E+08	1.22E+08	4208	-0.05238	2.937552	0.821151	0.878176	0.052946	0	113	108	133	172	113	154	171	125	193	221
ENSMUSG00000038160	chr10	Atg5	44268358	44268584	2352	-0.03573	3.930117	0.821133	0.878176	0.025535	0	217	228	315	252	271	273	352	339	440	352
ENSMUSG00000054302	chr12	Eapp	54670340	54673850	4448	-0.04317	4.211716	0.821153	0.878176	0.037952	0	279	251	402	288	352	344	392	579	394	391
ENSMUSG00000066037	chr4	Hnrnpr	1.36E+08	1.36E+08	8733	-0.0392	4.661652	0.821123	0.878176	0.033743	0	366	319	507	395	578	329	619	575	856	600
ENSMUSG00000009418	chr1	Nav1	1.35E+08	1.35E+08	17303	0.047036	4.598434	0.821416	0.878262	0.047952	0	394	216	373	490	530	308	608	588	749	673
ENSMUSG00000099966	chr14	2810402E24Rik	20641009	20644048	3040	0.051965	2.057761	0.821372	0.878262	0.047572	0	53	58	81	67	76	89	76	103	109	103
ENSMUSG00000064158	chr7	Izumo1	45621811	45622000	2992	-0.0857	0.070171	0.821728	0.878528	0.087929	0	15	10	18	24	15	12	23	18	41	17
ENSMUSG00000040694	chr17	Apobec2	48419231	48419633	1218	0.040234	8.650739	0.822771	0.879576	0.038483	0	5752	6504	7647	6714	6224	8804	8947	11154	10002	8081
ENSMUSG00000098413	chr19	Mir6990	6914196	6914286	91	0.094427	0.416569	0.822954	0.879703	0.080137	0	23	21	22	10	23	22	34	24	30	39
ENSMUSG00000070934	chr4	Rraga	86575668	86577285	1618	-0.03534	5.363805	0.82303	0.879716	0.028205	0	630	611	774	639	825	734	927	1101	1127	860
ENSMUSG00000020439	chr11	Smtn	3517523	3517827	4380	0.044418	6.671985	0.823494	0.880144	0.046877	0	1320	1430	1781	1809	2099	2220	2999	1369	2998	2471
ENSMUSG00000050796	chr4	B3galt6	1.56E+08	1.56E+08	3184	-0.05869	1.811709	0.823813	0.880417	0.0608	0	42	60	70	53	67	49	97	55	118	80
ENSMUSG00000035285	chr7	Nat14	4922251	4922639	1612	0.082409	0.898161	0.823901	0.880443	0.107024	0	14	35	32	26	37	46	47	18	59	41
ENSMUSG00000006651	chr7	Aplp1	30434981	30435391	2391	-0.07471	0.733584	0.824157	0.880649	0.071776	0	16	23	27	39	30	28	42	28	52	30
ENSMUSG00000003934	chr11	Efnb3	69554092	69556269	3183	-0.10792	-0.03642	0.824454	0.88083	0.11263	0	13	6	19	22	17	10	24	30	26	10
ENSMUSG00000043998	chr12	Mgat2	69184157	69186770	2614	-0.04068	3.91867	0.824417	0.88083	0.036584	0	212	204	285	224	366	194	366	351	542	326
ENSMUSG00000058886	chr7	Deaf1	1.41E+08	1.41E+08	2192	-0.04104	3.601046	0.824571	0.880887	0.030964	0	171	145	228	210	280	249	275	250	326	281
ENSMUSG00000028702	chr4	Rad54l	1.16E+08	1.16E+08	7706	0.090767	1.099609	0.824958	0.881233	0.128645	0	37	24	37	21	47	36	49	15	79	72
ENSMUSG00000025049	chr19	Taf5	47067748	47068326	3258	0.056358	1.992764	0.825409	0.881479	0.055894	0	56	55	72	65	70	71	72	130	106	83
ENSMUSG00000025902	chr1	Sox17	4490931	4492668	4772	-0.06014	2.389866	0.825407	0.881479	0.070259	0	66	81	94	123	72	79	83	168	137	125
ENSMUSG00000031378	chrX	Abcd1	73716597	73717930	4192	-0.03633	5.314648	0.825502	0.881479	0.03017	0	498	601	704	756	819	795	814	841	1106	1016
ENSMUSG00000056665	chr15	Them6	74721204	74721807	1784	-0.04602	2.825517	0.825507	0.881479	0.040687	0	109	103	129	112	141	151	148	126	186	188
ENSMUSG00000058239	chr7	Usf2	30945252	30946669	2647	0.038462	5.613114	0.825471	0.881479	0.034655	0	724	802	972	778	711	1077	1085	1091	1284	1191
ENSMUSG00000060073	chr12	Psma3	70974621	70974767	3894	0.03767	7.250557	0.825726	0.881645	0.034704	0	2170	2320	2959	2218	2901	3234	3476	4161	3598	3315
ENSMUSG00000005442	chr7	Cic	25267704	25267756	10294	0.040095	5.303557	0.825986	0.881719	0.037916	0	558	418	650	707	970	590	880	897	1321	1071
ENSMUSG00000018401	chr11	Mtmr4	87592162	87592250	6240	-0.0542	4.054108	0.825965	0.881719	0.067694	0	275	217	273	285	359	208	344	693	338	314
ENSMUSG00000050619	chr2	Zscan29	1.21E+08	1.21E+08	7169	-0.04866	2.930078	0.825901	0.881719	0.043182	0	107	98	120	143	177	129	159	215	172	187
ENSMUSG00000022340	chr15	Sybu	44671859	44673648	3599	-0.05964	1.074487	0.826212	0.881824	0.059521	0	38	26	40	31	36	27	44	45	66	52
ENSMUSG00000075330	chr16	A930003A15Rik	19876570	19877110	746	0.062315	4.717703	0.826169	0.881824	0.094847	0	325	286	497	360	741	702	868	242	812	465
ENSMUSG00000027583	chr2	Zbtb46	1.81E+08	1.81E+08	8508	-0.04399	2.639648	0.826301	0.88185	0.037951	0	87	81	109	111	137	102	141	130	199	143
ENSMUSG00000069255	chr13	Dusp22	30659999	30660146	1743	0.041947	4.901256	0.826371	0.881858	0.040123	0	398	539	507	544	430	623	795	530	854	721
ENSMUSG00000011096	chr7	Akt1s1	44848991	44849348	3201	0.039611	6.495109	0.826727	0.881898	0.038437	0	1323	1397	1780	1388	1508	1909	1743	2624	2139	2123
ENSMUSG00000020788	chr11	Atp2a3	72961169	72961471	5281	-0.04751	3.952274	0.826707	0.881898	0.050345	0	217	161	231	323	397	244	261	320	502	470
ENSMUSG00000025007	chr19	Aldh18a1	40550257	40551329	4072	-0.05645	3.98018	0.826657	0.881898	0.073547	0	222	224	279	210	422	276	450	141	551	411
ENSMUSG00000032750	chrX	Gab3	74966843	74967985	3891	0.087274	-0.22706	0.826675	0.881898	0.085695	0	10	6	10	14	22	11	19	13	26	23
ENSMUSG00000072115	chr14	Ang	51091077	51091253	1273	-0.05552	3.074827	0.826701	0.881898	0.063909	0	142	76	161	121	224	110	178	274	209	192
ENSMUSG00000020495	chr11	Smg8	87077732	87078150	3218	-0.04582	3.250434	0.826936	0.882026	0.047348	0	156	152	161	142	184	128	215	316	247	187
ENSMUSG00000051669	chr16	AU021092	5211828	5212212	1363	0.101507	0.43625	0.827039	0.882026	0.12789	0	14	25	22	27	11	17	45	17	54	23
ENSMUSG00000064284	chr15	Cdpf1	85806972	85807538	1215	0.043456	3.927109	0.827013	0.882026	0.042531	0	214	233	333	239	220	328	287	461	366	327
ENSMUSG00000044709	chr7	Gemin7	19564946	19565676	1519	-0.04139	5.245517	0.827261	0.882103	0.040228	0	514	622	809	588	676	911	784	639	995	967
ENSMUSG00000067713	chr15	Prkag1	98812798	98813480	1638	0.036327	5.733662	0.827303	0.882103	0.031697	0	749	868	1002	848	891	1155	1186	1106	1466	1330
ENSMUSG00000068921	chr3	Dap3	88920803	88923913	6483	-0.03592	5.75461	0.827268	0.882103	0.030952	0	746	879	1006	937	980	1107	1054	1315	1436	1269
ENSMUSG00000037808	chr9	Fam76b	13827716	13828061	4325	-0.04709	2.816177	0.827401	0.882141	0.047341	0	120	90	126	105	151	92	171	205	202	140
ENSMUSG00000016995	chr2	Matn4	1.64E+08	1.64E+08	5174	-0.11045	2.357811	0.827615	0.882233	0.282839	0	128	20	72	39	189	58	282	70	115	47
ENSMUSG00000025076	chr19	Casp7	56397129	56397317	2350	-0.05074	2.442295	0.827614	0.882233	0.052402	0	63	86	118	108	79	92	125	101	146	152
ENSMUSG00000092072	chr3	Gm4540	1.06E+08	1.06E+08	395	0.068293	0.671923	0.827893	0.882461	0.085421	0	19	23	34	16	31	46	31	27	41	30
ENSMUSG00000022336	chr15	Eif3e	43250040	43250237	1541	0.041691	6.630996	0.828108	0.882622	0.043447	0	1348	1539	1880	1537	1858	1817	2201	3403	2153	2053
ENSMUSG00000078784	chr3	1810022K09Rik	14606284	14606408	1753	0.039911	3.619861	0.828386	0.882851	0.032875	0	184	197	244	186	186	247	282	283	310	314
ENSMUSG00000032380	chr9	Dapk2	66158223	66158340	3512	0.056358	3.063973	0.828457	0.882858	0.06638	0	125	105	158	150	139	113	261	291	195	129
ENSMUSG00000020216	chr10	Jsrp1	80808496	80809039	1333	0.036578	8.387118	0.828566	0.882896	0.03407	0	4630	5010	6681	5112	6257	7643	7268	7990	7915	8150
ENSMUSG00000038296	chr7	Galnt18	1.11E+08	1.11E+08	2575	-0.0476	3.035169	0.828626	0.882896	0.046355	0	118	79	182	132	192	116	205	213	228	180
ENSMUSG00000048406	chr4	B330016D10Rik	1.42E+08	1.42E+08	1701	0.057277	2.775722	0.82869	0.882896	0.074164	0	70	123	118	121	120	141	125	256	142	127
ENSMUSG00000092310	chr9	Gm20509	73102470	73102675	1016	-0.0483	2.951166	0.828747	0.882896	0.047853	0	98	122	184	134	111	143	198	196	170	164

ENSMUSG00000020075	chr10	Ddx21	62580248	62582607	4742	-0.04266	5.70444	0.829091	0.883177	0.044894	0	632	759	1059	820	1213	785	1031	1810	1379	1022
ENSMUSG00000026280	chr1	Atg4b	93751500	93751581	8278	0.035572	4.804524	0.829139	0.883177	0.029668	0	433	402	565	424	468	576	682	577	764	682
ENSMUSG00000001119	chr10	Col6a1	76708792	76710181	4380	0.058443	8.49569	0.829442	0.883296	0.087871	0	5383	2843	5909	4662	11871	6527	12590	5088	12097	7276
ENSMUSG00000040771	chr17	Oard1	48410014	48410372	1336	0.039829	3.624306	0.829421	0.883296	0.033574	0	176	184	263	186	198	216	280	356	318	279
ENSMUSG00000053113	chr11	Socs3	1.18E+08	1.18E+08	2891	0.087736	4.388889	0.829432	0.883296	0.192209	0	545	97	121	382	534	582	546	330	772	259
ENSMUSG00000045598	chr7	Zfp553	1.27E+08	1.27E+08	3373	0.043327	2.975932	0.829615	0.883401	0.042402	0	125	81	151	124	165	151	163	207	246	158
ENSMUSG00000097277	chr7	2900076A07Rik	81523550	81523676	1993	0.073766	1.042218	0.829668	0.883401	0.067015	0	37	25	34	33	29	29	45	45	78	43
ENSMUSG00000021650	chr13	Ptcd2	99319649	99320393	1675	0.03697	4.862028	0.829891	0.88357	0.03251	0	388	498	542	483	462	633	680	607	797	689
ENSMUSG00000001855	chr2	Nup214	31974436	31974608	9659	0.037048	4.084013	0.830217	0.883849	0.0305	0	231	201	295	322	356	251	410	419	537	411
ENSMUSG00000056214	chr18	Pard6g	80046895	80047142	3143	-0.06469	1.850699	0.830593	0.884182	0.075843	0	53	33	70	52	99	41	93	95	116	65
ENSMUSG00000003604	chr2	Aven	1.12E+08	1.12E+08	5001	-0.04159	4.104352	0.831046	0.884595	0.039175	0	214	286	347	269	340	385	373	269	464	463
ENSMUSG00000052656	chr6	Rnf103	71493894	71494888	4348	-0.04029	4.524235	0.831196	0.884687	0.039608	0	353	319	447	395	430	346	508	779	556	458
ENSMUSG00000059810	chr4	Rgs3	62559847	62559882	10801	0.047122	3.612195	0.831271	0.8847	0.047214	0	180	145	222	248	203	129	325	303	399	325
ENSMUSG00000033717	chr19	Adra2a	54045182	54048982	3801	0.124163	-0.17616	0.831409	0.884778	0.165739	0	10	17	4	12	19	20	16	6	38	17
ENSMUSG00000075327	chr10	Zbtb2	4367074	4369851	3338	-0.05123	2.547674	0.831544	0.884854	0.053468	0	96	81	100	93	119	97	107	194	147	115
ENSMUSG00000001280	chr15	Sp1	1.02E+08	1.02E+08	8325	-0.03624	5.016472	0.831902	0.885099	0.031948	0	440	409	608	539	778	505	675	893	877	801
ENSMUSG00000075000	chr10	Nrbf2	67266689	67268166	1860	0.051433	3.280124	0.831898	0.885099	0.057462	0	130	153	191	167	144	125	202	364	247	216
ENSMUSG00000021619	chr13	Atg10	90935349	90936245	1609	-0.04421	3.050911	0.832041	0.885179	0.043147	0	125	139	126	164	132	175	197	180	215	168
ENSMUSG00000090031	chr1	4732440D04Rik	6209866	6215293	5428	0.100938	0.352182	0.832128	0.885203	0.106067	0	21	19	20	12	22	8	28	42	32	35
ENSMUSG00000021840	chr14	Mapk1ip1l	47298314	47298405	4608	0.034335	4.832473	0.832337	0.885357	0.028387	0	432	377	538	419	593	476	773	605	876	664
ENSMUSG00000073600	chr18	Prob1	35650351	35655240	4890	-0.04442	6.212052	0.832695	0.885671	0.051649	0	954	1104	1503	1446	1292	1247	1530	2687	1593	1403
ENSMUSG00000028927	chr4	Padi2	1.41E+08	1.41E+08	5013	-0.04635	7.377316	0.833055	0.885982	0.057474	0	2359	2609	2438	3604	2993	3318	5150	2864	5451	2426
ENSMUSG00000053460	chr6	Ggcx	72414308	72414449	3244	-0.06166	3.625082	0.833116	0.885982	0.093	0	203	136	243	175	304	238	381	86	379	326
ENSMUSG00000023460	chr17	Rab12	66494512	66495803	3021	0.055708	7.339929	0.833464	0.886284	0.083278	0	2260	2846	3039	2791	2133	2791	2893	7230	3178	2964
ENSMUSG00000041945	chr1	Mfsd9	40772038	40774546	5125	0.064088	0.645582	0.833972	0.886756	0.064307	0	17	18	34	24	28	28	46	25	39	37
ENSMUSG00000030785	chr7	Cox6a2	1.28E+08	1.28E+08	658	-0.03621	9.305546	0.834135	0.886793	0.035693	0	9393	9243	10751	12030	12016	14373	13295	15584	15411	13170
ENSMUSG00000051515	chr7	Fam181b	93079879	93080983	1836	-0.08347	0.793994	0.834087	0.886793	0.14575	0	12	37	34	41	15	19	22	53	47	48
ENSMUSG00000052794	chr8	1700030K09Rik	72443880	72443989	2970	-0.05648	1.864754	0.83439	0.886917	0.053287	0	57	45	74	55	73	63	76	105	78	82
ENSMUSG00000053279	chr19	Aldh1a1	20601961	20602077	2053	0.065584	6.114047	0.83433	0.886917	0.11546	0	1285	875	1028	1320	1052	834	1190	3664	1613	1008
ENSMUSG00000089824	chr2	Rbm12	1.56E+08	1.56E+08	6689	0.040647	3.349866	0.834444	0.886917	0.038986	0	131	116	172	169	260	173	249	240	346	205
ENSMUSG00000038351	chr11	Sgsm2	74849261	74850895	6884	0.049886	2.581076	0.835201	0.887654	0.060423	0	89	52	108	89	156	101	173	101	184	148
ENSMUSG00000036160	chr2	Surf6	26888628	26889378	4071	-0.03707	3.437195	0.835792	0.888213	0.031547	0	162	144	237	169	202	183	224	268	341	235
ENSMUSG00000026176	chr1	Ctdsp1	74391509	74391964	3334	-0.03292	6.494726	0.836077	0.888448	0.029353	0	1322	1216	1627	1683	1794	1685	2018	2250	2337	2092
ENSMUSG00000041629	chr11	Fam104a	1.14E+08	1.14E+08	2619	0.034204	5.179815	0.836274	0.888533	0.030917	0	481	582	723	590	602	784	819	868	943	820
ENSMUSG00000096952	chr8	Gm26572	1.21E+08	1.21E+08	3231	-0.06932	0.808777	0.836285	0.888533	0.076883	0	29	27	38	21	26	40	43	24	43	37
ENSMUSG00000097842	chr7	9330104G04Rik	16871354	16872913	2235	-0.08793	0.024031	0.836609	0.888809	0.124731	0	10	14	14	26	15	6	32	17	20	31
ENSMUSG00000026245	chr1	Farsb	78417975	78418222	2620	-0.03403	5.667855	0.836698	0.888835	0.030975	0	744	793	943	852	950	1099	1178	922	1427	1201
ENSMUSG00000048109	chr3	Rbm15	1.07E+08	1.07E+08	3270	0.042793	3.244486	0.836989	0.889076	0.045209	0	142	117	175	150	193	182	193	318	218	191
ENSMUSG00000019846	chr10	Lama4	38965515	38966149	12068	-0.04033	5.859187	0.837681	0.889743	0.044852	0	830	673	1003	1026	1462	964	1590	862	1933	1440
ENSMUSG00000050605	chr7	Zfp61	24291039	24292504	3431	-0.06121	1.290168	0.838203	0.890229	0.069757	0	31	32	55	34	51	27	47	76	69	54
ENSMUSG00000036356	chr8	Csgalnact1	68356781	68358713	4774	-0.05171	2.437304	0.838416	0.890318	0.061822	0	76	59	114	71	143	64	143	112	186	122
ENSMUSG00000050244	chr13	Heatr1	12395398	12395470	6537	-0.03427	3.783516	0.838368	0.890318	0.02759	0	190	185	268	221	305	240	310	281	433	331
ENSMUSG00000061143	chr3	Maml3	51685907	51690854	10486	-0.064	2.486955	0.838672	0.890522	0.099252	0	103	47	85	130	106	59	128	215	126	108
ENSMUSG00000026782	chr1	Abi2	60409619	60409919	8543	0.038624	3.410849	0.83883	0.890622	0.032347	0	155	154	222	159	179	174	263	253	347	227
ENSMUSG00000024132	chr17	Eci1	24426683	24426742	1091	-0.04048	6.366511	0.83919	0.890935	0.047091	0	1207	1554	1457	1475	1166	1489	1445	2489	2184	1878
ENSMUSG00000018733	chr11	Pex12	83294642	83296440	3536	-0.04655	3.34464	0.839399	0.891089	0.056516	0	158	163	168	176	183	147	239	371	231	170
ENSMUSG00000029701	chr6	Rbm28	29123573	29125524	5666	0.035845	4.856215	0.839527	0.891102	0.034665	0	429	421	576	429	529	587	751	467	842	770
ENSMUSG00000030662	chr14	Ipo5	1.21E+08	1.21E+08	4591	-0.03438	7.10074	0.83954	0.891102	0.033945	0	1847	2095	2444	2454	2796	2407	2765	3996	3543	3120
ENSMUSG00000024381	chr18	Bin1	32377217	32377490	2451	0.034456	9.510039	0.839696	0.891167	0.034714	0	8994	11427	14591	11879	13559	16347	17034	13998	19319	18667
ENSMUSG00000029364	chr5	Wsb2	1.17E+08	1.17E+08	5857	-0.03178	6.740881	0.83973	0.891167	0.028913	0	1541	1586	2099	1771	2052	1979	2715	2198	3121	2385
ENSMUSG00000020448	chr11	Rnf185	3415982	3418087	2906	-0.0321	4.933555	0.839896	0.891275	0.027503	0	411	475	608	528	555	605	652	712	871	676
ENSMUSG00000036782	chrX	Klhl13	23219271	23220852	4253	0.04422	3.788245	0.839963	0.891278	0.053133	0	176	160	210	187	427	213	428	317	417	273
ENSMUSG00000048852	chr11	Gm12185	48904656	48908479	5587	-0.10699	0.597993	0.840256	0.89152	0.222684	0	18	11	35	7	58	33	39	8	50	29
ENSMUSG00000034105	chr8	Tldc1	1.2E+08	1.2E+08	2574	0.04519	2.493607	0.840343	0.891544	0.044072	0	69	87	90	105	104	89	132	156	170	116
ENSMUSG00000050017	chr5	Pitpnb	1.11E+08	1.11E+08	2761	-0.03117	4.939332	0.840829	0.891923	0.026082	0	419	439	549	508	691	531	699	722	866	736
ENSMUSG00000070972	chr4	Dnajc25	58995062	58995105	4542	-0.03694	3.598194	0.840813	0.891923	0.030607	0	157	170	253	197	250	254	287	234	339	267
ENSMUSG00000030421	chr7	Uri1	37960002	37961697	3431	-0.04486	4.653605	0.841194	0.892174	0.056053	0	334	348	492	474	495	370	473	999	558	482
ENSMUSG00000036504	chr2	Phpt1	25573430	25573699	1074	-0.03461	5.575345	0.841158	0.892174	0.033919	0	661	823	954	789	771	1000	1035	1197	1130	1066
ENSMUSG00000083044	chr4	Gm12416	84104895	84105902	1008	-0.06988	0.214679	0.841414	0.892338	0.093313	0	13	24	17	21	15	28	22	26	30	14
ENSMUSG00000028759	chr4	Hp1bp3	1.38E+08	1.38E+08	8433	0.037993	6.330563	0.841523	0.892386	0.041945	0	1249	1104	1494	1305	1472	1181	1831	2782	2076	1706
ENSMUSG00000100214	chr7	6230415J03Rik	39571672	39576231	4560	0.07177	0.435973	0.841804	0.892616	0.062718	0	20	14	20	17	32	23	33	34	33	27
ENSMUSG00000062329	chr5	Cytl1	37735519	37735709	974	-0.07062	1.43943	0.842321	0.893095	0.117995	0	24	51	24	59	66	34	45	56	117	57
ENSMUSG00000021902	chr14	Phf7	31237696	31238153	1984	-0.05058	2.538534	0.842514	0.893163	0.063512	0	97	92	102	82	110	82	93	201	140	143
ENSMUSG00000068699	chr6	Flnc	29433153	29433813	9543	-0.03591	9.136628	0.842451	0.893163	0.038951	0	7722	6633	10387	11679	11727	9907	14287	15429	15556	9904
ENSMUSG00000086003	chr11	B230206L02Rik	94133485	94133555	1042	0.072485	0.498494	0.842828	0.893427	0.097236	0	18	21	33	17	18	31	39	41	22	21
ENSMUSG00000033554	chr3	Dph5	1.16E+08	1.16E+08	4086	0.044224	2.584204	0.84312	0.893668	0.046267	0	58	97	116	103	115	128	135	128	177	130

ENSMUSG00000017774	chr11	Myo1c	75650504	75650764	6585	0.031805	6.422207	0.843634	0.894067	0.030024	0	1107	1283	1614	1387	1731	1346	2253	1910	2650	2102
ENSMUSG00000019428	chr8	Fkbp8	70527724	70527836	4529	0.031115	6.90178	0.843654	0.894067	0.029212	0	1620	1771	2285	1918	2321	2281	2505	2854	3444	3050
ENSMUSG00000022438	chr15	Parvb	84232043	84232186	4416	0.034439	6.317713	0.84369	0.894067	0.035439	0	1071	1172	1596	1426	1312	1625	1944	1408	2604	1886
ENSMUSG00000007656	chr9	Arpp19	75037614	75037719	4957	-0.03273	5.71978	0.844033	0.894363	0.03166	0	724	878	1004	948	866	1100	1162	1161	1396	1217
ENSMUSG00000047735	chr6	Samd9l	3372257	3377281	5425	-0.04359	3.263726	0.844117	0.894383	0.044199	0	135	117	205	179	177	221	187	177	224	269
ENSMUSG00000009090	chr11	Ap1b1	4986824	4987051	4957	0.031794	5.795816	0.844694	0.894926	0.030393	0	676	839	1000	915	1192	1070	1229	1136	1650	1488
ENSMUSG00000042870	chr8	Tom1	75033686	75033827	2358	0.034633	4.821406	0.844881	0.89505	0.03437	0	407	390	509	498	525	472	607	910	733	615
ENSMUSG00000085028	chr2	Slc2a4rg-ps	1.81E+08	1.81E+08	2976	0.082218	0.66174	0.844941	0.89505	0.115147	0	34	16	32	17	20	19	53	27	29	51
ENSMUSG00000081476	chr2	Itpa-ps1	94384502	94385098	597	-0.07564	0.178241	0.84539	0.895457	0.108098	0	22	13	30	14	9	19	19	27	37	17
ENSMUSG00000078816	chr7	Prkcg	3303532	3303959	3112	0.094713	0.060808	0.84546	0.895464	0.068545	0	13	15	14	16	18	12	18	29	28	28
ENSMUSG00000046032	chrX	Snx12	1.01E+08	1.01E+08	2953	0.030019	4.876039	0.845659	0.895605	0.026328	0	379	413	572	454	628	535	683	659	876	722
ENSMUSG00000024400	chr18	Wdr33	31804057	31804254	6413	-0.03109	5.032151	0.846039	0.895871	0.028215	0	458	500	628	548	626	588	720	893	839	726
ENSMUSG00000090084	chrX	Srpx	10037977	10039100	2652	-0.04838	4.263432	0.845979	0.895871	0.06565	0	311	174	371	194	629	374	480	452	475	401
ENSMUSG00000031546	chr8	Gins4	23226610	23227175	1364	0.035125	3.623192	0.846132	0.895901	0.031707	0	165	207	211	185	239	245	260	252	348	340
ENSMUSG00000021411	chr13	Pxdc1	34627840	34628888	2103	0.046682	2.268206	0.846248	0.895955	0.049726	0	57	77	82	77	96	103	140	93	116	103
ENSMUSG00000045257	chr17	Morn2	80290212	80290337	644	0.054412	1.976942	0.846333	0.895976	0.065633	0	63	56	69	71	52	88	105	57	114	91
ENSMUSG00000026825	chr2	Dnm1	32308471	32309064	5240	-0.05705	3.768005	0.846409	0.895988	0.091984	0	216	88	236	176	485	217	453	231	359	300
ENSMUSG00000023191	chr6	Leprel2	1.25E+08	1.25E+08	3930	-0.05034	4.300239	0.846483	0.895998	0.07444	0	375	164	356	211	602	328	625	345	570	403
ENSMUSG00000032305	chr9	Fam219b	57537528	57537834	3055	0.038741	3.483594	0.846823	0.89629	0.039479	0	163	155	246	166	186	206	304	178	332	301
ENSMUSG00000021248	chr12	Tmed10	85340614	85343549	3526	-0.03035	6.819974	0.847122	0.896498	0.028876	0	1621	1488	2155	1846	2527	1973	2561	2724	3160	2691
ENSMUSG00000033216	chr6	Eefsec	88257334	88258391	2679	0.046788	2.477435	0.84715	0.896498	0.050174	0	70	89	90	78	125	111	127	90	178	147
ENSMUSG00000015488	chr2	Cacfd1	27009926	27010105	4693	0.03277	5.717245	0.847616	0.896837	0.03341	0	776	773	960	810	1022	995	1151	1610	1300	1114
ENSMUSG00000025980	chr1	Hspd1	55077835	55078440	2642	-0.03245	7.882286	0.847664	0.896837	0.033871	0	3031	4085	4720	3939	4108	4690	5298	4677	6552	5990
ENSMUSG00000044468	chr3	Fam46c	1E+08	1E+08	6097	0.056098	2.381768	0.847578	0.896837	0.086936	0	70	50	79	99	128	78	97	70	179	198
ENSMUSG00000026489	chr1	Adck3	1.8E+08	1.8E+08	5293	0.048929	9.099204	0.847818	0.896931	0.077525	0	7115	9111	7405	13656	6890	8912	10388	20837	15304	9997
ENSMUSG00000073700	chr4	Klhl21	1.52E+08	1.52E+08	3986	-0.05462	6.974111	0.847994	0.897049	0.096402	0	1882	2325	2302	2209	1800	1911	2056	5902	2477	1943
ENSMUSG00000022362	chr15	9130401M01Rik	58028243	58029044	1732	-0.03313	3.795631	0.848631	0.897646	0.028784	0	194	179	293	227	285	236	300	319	360	383
ENSMUSG00000038299	chr18	Wdr36	32837225	32837558	3281	0.029895	4.59193	0.848688	0.897646	0.026141	0	293	366	443	420	475	434	570	575	715	557
ENSMUSG00000041477	chr6	Dcp1b	1.19E+08	1.19E+08	6339	-0.04825	1.762452	0.848763	0.897657	0.050073	0	49	36	61	57	81	60	69	78	94	79
ENSMUSG00000030287	chr6	Itpr2	1.46E+08	1.46E+08	13484	0.037163	3.62439	0.848997	0.897718	0.037021	0	178	140	252	202	249	165	255	307	411	342
ENSMUSG00000057606	chr14	Colq	31523082	31524479	3803	0.034996	3.625794	0.849015	0.897718	0.032032	0	219	158	228	188	213	225	318	274	314	316
ENSMUSG00000059689	chr6	Zfp637	1.18E+08	1.18E+08	2565	-0.03318	4.462677	0.848917	0.897718	0.032927	0	342	324	406	396	379	393	485	653	520	473
ENSMUSG00000011877	chr11	Git1	77493562	77493634	4838	-0.03086	5.255942	0.849202	0.897778	0.030117	0	538	522	692	745	733	572	926	995	1141	830
ENSMUSG00000022244	chr15	Amacr	10981756	10982053	2575	0.03422	4.262513	0.849177	0.897778	0.034236	0	260	324	384	289	312	414	491	348	522	469
ENSMUSG00000031639	chr8	Tlr3	45395665	45397141	4396	0.056788	1.949133	0.849361	0.897877	0.085047	0	47	68	68	71	51	105	102	49	101	83
ENSMUSG00000059890	chr9	Ube4a	44923131	44925975	8635	0.067056	5.693932	0.849607	0.898069	0.146776	0	914	619	808	872	988	602	749	3138	806	843
ENSMUSG00000061313	chr8	Ddhd2	25725324	25727363	4267	-0.03599	3.995997	0.849896	0.898306	0.039235	0	237	240	335	226	308	264	352	249	492	497
ENSMUSG00000004535	chr6	Tax1bp1	52713729	52713855	6609	-0.04379	6.448657	0.850066	0.898416	0.063335	0	1271	1343	1729	1446	1611	1147	1547	3589	1962	1834
ENSMUSG00000022106	chr14	Rcbtb2	73123037	73123132	9489	0.032884	4.863303	0.85019	0.898469	0.033725	0	359	453	504	442	659	526	784	518	821	796
ENSMUSG00000027669	chr3	Gnb4	32580332	32585226	12692	-0.03278	3.729191	0.850245	0.898469	0.029541	0	217	166	233	232	267	240	313	340	347	280
ENSMUSG00000034663	chr5	Bmp2k	96997689	96998096	8480	-0.03323	3.695095	0.850376	0.898539	0.032134	0	197	173	213	224	285	189	275	329	351	356
ENSMUSG00000102805	chr3	RP24-559D1.1	84496426	84497891	2913	-0.03006	4.549973	0.850542	0.898645	0.02671	0	350	303	432	389	512	387	585	576	610	550
ENSMUSG00000037379	chr5	Spon2	33213518	33214652	2237	-0.10008	4.084406	0.850805	0.898855	0.320504	0	148	51	257	155	995	314	799	118	447	224
ENSMUSG00000046897	chr15	Zfp740	1.02E+08	1.02E+08	4822	0.032009	5.268416	0.850941	0.89893	0.032546	0	596	505	722	591	777	622	854	1156	962	959
ENSMUSG00000071180	chr13	Smim15	1.08E+08	1.08E+08	1852	0.032515	4.046344	0.851146	0.899078	0.029375	0	231	240	346	245	300	245	426	437	475	380
ENSMUSG00000044548	chr12	Dact1	71309884	71310307	3761	0.03845	2.780675	0.851232	0.8991	0.038843	0	98	88	118	113	145	130	160	188	187	136
ENSMUSG00000002814	chr11	Top3a	60740058	60740701	4599	0.039813	2.528602	0.85132	0.899125	0.042524	0	84	59	111	99	120	96	154	132	154	139
ENSMUSG00000022120	chr14	Rnf219	1.04E+08	1.04E+08	3456	-0.04629	2.199818	0.85151	0.899147	0.050507	0	56	60	80	70	123	76	105	86	135	120
ENSMUSG00000025139	chr7	Tollip	1.42E+08	1.42E+08	4333	0.034772	5.736885	0.851537	0.899147	0.039485	0	777	766	1004	862	989	851	1035	1826	1424	1186
ENSMUSG00000032403	chr9	2300009A05Rik	63394447	63394675	2000	0.042983	3.053941	0.851476	0.899147	0.046744	0	121	132	139	159	116	196	172	166	237	193
ENSMUSG00000037784	chr9	Dzip1l	99629496	99629669	7984	0.050343	1.784981	0.851806	0.899294	0.065066	0	47	45	74	32	81	50	95	78	103	77
ENSMUSG00000046756	chr11	Mrps7	1.16E+08	1.16E+08	2072	0.032892	6.140636	0.851771	0.899294	0.035692	0	979	1200	1336	1203	1043	1510	1550	1557	1968	1694
ENSMUSG00000031347	chrX	Cetn2	72913532	72914293	1646	-0.03587	4.651949	0.851963	0.899392	0.039942	0	356	433	568	364	387	557	587	571	532	591
ENSMUSG00000029782	chr6	Tmem209	30479053	30481137	8130	-0.03279	3.578389	0.852214	0.899588	0.031372	0	202	149	234	170	252	184	285	284	342	288
ENSMUSG00000042962	chr12	Gm5436	84258332	84258973	642	-0.05035	2.909232	0.852389	0.899704	0.077742	0	97	154	87	178	99	171	141	140	231	165
ENSMUSG00000021772	chr14	Nkiras1	18271136	18271323	5430	-0.03472	4.991119	0.852675	0.899868	0.038482	0	505	494	662	492	512	750	631	793	765	654
ENSMUSG00000052293	chr13	Taf9	1.01E+08	1.01E+08	2120	-0.03197	4.919938	0.852653	0.899868	0.03315	0	410	505	603	479	550	522	689	878	819	586
ENSMUSG00000015994	chr8	Fnta	25998729	25999564	1874	0.031259	5.795828	0.853116	0.900197	0.03286	0	743	917	1118	817	984	1192	1319	1144	1444	1398
ENSMUSG00000072594	chr14	Gm16439	44596665	44597228	564	-0.09805	0.734673	0.853113	0.900197	0.214038	0	13	26	38	32	28	15	29	93	22	17
ENSMUSG00000027865	chr3	Gdap2	1E+08	1E+08	3507	0.042743	2.950773	0.853275	0.900296	0.050497	0	126	89	143	128	144	112	165	265	202	167
ENSMUSG00000045316	chr17	Fahd1	24848896	24850302	1407	-0.03388	5.122203	0.853516	0.900482	0.037469	0	484	633	647	558	589	830	715	782	876	740
ENSMUSG00000008734	chr7	Gprc5b	1.19E+08	1.19E+08	4525	0.030833	5.27065	0.853599	0.900501	0.03095	0	537	515	645	724	776	612	866	1106	1121	884
ENSMUSG00000019868	chr10	Vta1	14654755	14655845	2263	0.029136	4.170419	0.853943	0.900795	0.025984	0	252	267	343	287	334	366	413	407	491	429
ENSMUSG00000051243	chr9	Islr2	58196298	58199983	4933	0.056377	1.729548	0.854141	0.900935	0.090693	0	48	29	43	53	96	52	118	56	97	64
ENSMUSG00000025855	chr5	Prkar1b	1.39E+08	1.39E+08	3810	-0.0578	1.317212	0.85424	0.900956	0.087739	0	31	22	56	40	60	22	72	57	82	49
ENSMUSG00000026585	chr1	Kifap3	1.64E+08	1.64E+08	4012	-0.02908	4.785091	0.854486	0.900956	0.028079	0	432	419	472	471	514	480	692	701	730	580

ENSMUSG00000031776	chr8	Arl2bp	94666755	94666901	1905	0.030201	6.253513	0.854317	0.900956	0.031445	0	1040	1148	1551	1223	1348	1471	1656	2077	1995	1764
ENSMUSG00000032422	chr9	Snx14	88376750	88376939	6107	-0.03253	4.003481	0.854437	0.900956	0.030853	0	221	239	290	224	387	296	436	326	415	368
ENSMUSG00000036964	chr11	Trim17	58954685	58955392	3736	0.035266	3.51758	0.854391	0.900956	0.041152	0	146	161	231	191	214	279	322	217	260	239
ENSMUSG00000024346	chr18	Pfdn1	36403679	36404460	1077	-0.03238	6.579529	0.854568	0.900973	0.036236	0	1328	1589	1926	1534	1675	2219	2214	1959	2333	2137
ENSMUSG00000022261	chr15	Sdc2	32920723	32921305	3322	-0.03553	5.490771	0.854926	0.901149	0.042128	0	705	444	745	773	1203	903	1179	880	1255	951
ENSMUSG00000028608	chr4	0610037L13Rik	1.08E+08	1.08E+08	5633	-0.03317	4.825352	0.854966	0.901149	0.036257	0	442	459	588	388	502	608	726	495	737	672
ENSMUSG00000034163	chr10	Zfc3h1	1.15E+08	1.15E+08	7848	0.031686	4.173506	0.854882	0.901149	0.032786	0	250	209	387	300	356	307	545	400	451	421
ENSMUSG00000035799	chr12	Twist1	33957671	33958638	1616	-0.07498	1.77823	0.854995	0.901149	0.163036	0	79	21	50	19	124	55	88	81	92	65
ENSMUSG00000021692	chr13	Dimt1	1.07E+08	1.07E+08	2545	-0.04707	1.957447	0.855137	0.901231	0.051975	0	69	48	77	54	74	62	97	102	94	81
ENSMUSG00000000942	chr6	Hoxa4	52189671	52190688	1594	0.056607	1.580154	0.855494	0.90147	0.075805	0	40	29	53	47	72	43	58	108	70	66
ENSMUSG00000042569	chr11	Dhrs7b	60830631	60830731	3325	0.036982	4.530975	0.855459	0.90147	0.044213	0	329	404	394	353	402	471	484	345	703	729
ENSMUSG00000026021	chr1	Sumo1	59586558	59586694	2076	0.032589	5.268518	0.856215	0.902161	0.036377	0	513	669	805	564	609	746	921	1071	929	844
ENSMUSG00000050222	chr14	Il17d	57524829	57524921	1221	0.055445	1.049375	0.856459	0.902349	0.074235	0	36	17	32	30	48	45	50	33	60	46
ENSMUSG00000092541	chr9	Gm20537	88407432	88407482	1009	0.031172	3.702691	0.856705	0.90254	0.028838	0	173	175	230	212	289	213	341	281	414	297
ENSMUSG00000025203	chr19	Scd2	44293676	44294411	5453	-0.05716	6.448365	0.856828	0.9026	0.117704	0	913	640	1066	1534	3719	1535	2383	1168	2470	2506
ENSMUSG00000042978	chr7	Sbk1	1.26E+08	1.26E+08	4092	-0.02944	5.596298	0.857067	0.902783	0.030518	0	799	567	955	838	936	776	1107	1278	1363	1104
ENSMUSG00000039263	chr2	Npepl1	1.74E+08	1.74E+08	2998	-0.02912	5.996268	0.857221	0.902877	0.029984	0	900	965	1260	1125	1128	1279	1346	1458	1690	1566
ENSMUSG00000027353	chr2	Mcm8	1.33E+08	1.33E+08	3718	-0.05838	0.591037	0.857371	0.902879	0.065034	0	25	20	25	22	28	24	24	33	55	28
ENSMUSG00000028345	chr4	Tex10	48430858	48431083	4382	0.036829	3.730131	0.857479	0.902879	0.03973	0	191	224	206	215	242	201	285	431	377	278
ENSMUSG00000046191	chr18	Pcdhb20	37504264	37507822	3559	0.058758	0.751079	0.857484	0.902879	0.082786	0	23	18	30	17	44	43	41	33	36	32
ENSMUSG00000048581	chr3	E130311K13Rik	63914684	63915738	2398	-0.05248	1.659869	0.85741	0.902879	0.068833	0	58	34	62	49	58	57	80	40	94	83
ENSMUSG00000035597	chr12	Prpf39	65036333	65036468	4401	0.036436	3.696505	0.857622	0.902956	0.040192	0	190	188	253	186	247	173	285	427	340	313
ENSMUSG00000022051	chr14	Bnip3l	66985239	66987775	3859	-0.04359	5.709705	0.85775	0.903022	0.069252	0	854	726	1075	861	907	688	845	2223	1226	1059
ENSMUSG00000025147	chr7	Mob2	1.42E+08	1.42E+08	1456	-0.03389	5.489906	0.857969	0.903184	0.041053	0	758	701	854	708	732	914	845	1358	1005	987
ENSMUSG00000062376	chr19	2010012O05Rik	46689906	46690085	2176	-0.03283	3.469693	0.858094	0.903247	0.033265	0	147	181	217	165	221	187	233	311	314	230
ENSMUSG00000029708	chr6	Gcc1	28416091	28419300	5287	-0.03757	3.464255	0.859443	0.904598	0.043652	0	163	138	223	157	258	176	236	357	295	203
ENSMUSG00000040855	chrX	Reps2	1.62E+08	1.62E+08	8296	0.042931	2.514384	0.859524	0.904614	0.066657	0	72	53	117	79	155	111	176	137	141	97
ENSMUSG00000036898	chr5	Zfp157	1.38E+08	1.38E+08	8782	0.044492	1.685392	0.859758	0.904654	0.052757	0	50	35	58	44	72	60	82	61	85	82
ENSMUSG00000041438	chr8	Cirh1a	1.07E+08	1.07E+08	2248	0.031861	4.474352	0.859715	0.904654	0.03566	0	267	334	463	373	403	387	488	706	565	466
ENSMUSG00000042570	chr10	Mier2	79540245	79541199	4497	-0.03079	3.883889	0.859672	0.904654	0.028487	0	231	177	303	219	322	275	345	342	400	334
ENSMUSG00000050908	chr16	Tvp23a	10420557	10422885	3971	-0.09466	0.323201	0.859962	0.9048	0.181986	0	19	9	17	16	41	19	40	5	46	23
ENSMUSG00000022552	chr15	Sharpin	76347040	76347185	3765	0.027523	4.52331	0.860101	0.904875	0.026671	0	331	305	418	393	457	477	499	504	632	578
ENSMUSG00000039497	chr10	Dse	34151394	34153974	4224	0.038002	4.055167	0.860164	0.904875	0.050652	0	285	144	285	224	453	236	419	389	544	407
ENSMUSG00000032803	chr9	Cdv3	1.03E+08	1.03E+08	7403	-0.02882	7.342301	0.860234	0.90488	0.031724	0	2284	2612	2923	2984	2816	2997	4089	3897	4433	3352
ENSMUSG00000057554	chr13	Lgals8	12439415	12440994	3688	0.028848	4.828845	0.860324	0.904905	0.028757	0	431	391	563	473	483	501	671	774	772	631
ENSMUSG00000031711	chr8	Zfp330	82763621	82764491	1675	0.030313	4.328831	0.860461	0.904981	0.033247	0	246	274	428	333	391	359	473	600	464	454
ENSMUSG00000034487	chr9	Kdelc2	53384023	53384286	3644	0.036775	3.690222	0.860973	0.905451	0.050197	0	192	108	271	179	336	239	373	243	372	295
ENSMUSG00000030880	chr7	Polr3e	1.21E+08	1.21E+08	4234	0.040595	3.982885	0.861135	0.905552	0.059051	0	205	203	299	266	337	232	297	649	421	273
ENSMUSG00000028060	chr3	2810403A07Rik	88685794	88685887	2999	-0.03465	4.641848	0.861252	0.905606	0.044405	0	393	411	467	360	460	379	538	873	563	517
ENSMUSG00000060044	chr10	Tmem26	68723746	68724090	5052	-0.07526	0.385181	0.86145	0.905746	0.104216	0	23	11	32	11	28	14	21	24	45	37
ENSMUSG00000004815	chr5	Dgkq	1.09E+08	1.09E+08	7189	0.044766	2.245538	0.861607	0.905842	0.045988	0	72	58	85	80	88	66	101	127	151	115
ENSMUSG00000032615	chr11	Nt5m	59839447	59839756	3361	0.03081	4.078602	0.861736	0.90591	0.030589	0	260	268	280	292	274	352	361	358	484	423
ENSMUSG00000027678	chr2	Ncoa3	1.66E+08	1.66E+08	7895	-0.03125	4.511636	0.861802	0.90591	0.035524	0	309	280	480	432	438	297	487	581	658	648
ENSMUSG00000021621	chr13	Zcchc9	91796533	91797254	3422	0.029808	3.685691	0.861993	0.905973	0.029187	0	184	169	248	205	257	221	302	365	344	279
ENSMUSG00000022510	chr16	Trp63	25683763	25684351	8391	-0.04053	2.914304	0.861968	0.905973	0.048895	0	106	125	132	116	151	137	125	239	200	155
ENSMUSG00000071014	chr4	Ndufb6	40270591	40270847	659	0.035392	6.793744	0.862585	0.906527	0.049084	0	1600	2125	2089	1741	1414	2691	2418	2525	2831	2422
ENSMUSG00000023072	chr7	Cep89	35397035	35397206	5087	-0.03549	2.842046	0.862747	0.906628	0.037117	0	90	114	119	129	148	128	152	163	186	188
ENSMUSG00000029049	chr4	Morn1	1.55E+08	1.55E+08	4320	0.083881	0.114948	0.863203	0.907038	0.092187	0	21	9	13	20	16	10	27	31	29	23
ENSMUSG00000009828	chr9	Ick	78109192	78109481	11524	-0.03875	3.383518	0.863709	0.907501	0.052635	0	177	117	189	159	242	126	242	348	250	238
ENSMUSG00000027014	chr2	Cwc22	77881159	77881490	6822	-0.03563	3.509946	0.863845	0.907575	0.045765	0	142	168	208	211	233	140	221	376	327	261
ENSMUSG00000002064	chr11	Sdf2	78245746	78246170	1515	0.030442	5.788732	0.864199	0.907877	0.036356	0	895	861	1093	699	993	1126	1233	1498	1348	1251
ENSMUSG00000039081	chr14	Zfp503	21983962	21986516	4213	0.04364	3.690645	0.864389	0.908009	0.06892	0	289	118	164	193	285	216	237	421	321	325
ENSMUSG00000040219	chr9	Ttc12	49436963	49438456	4545	0.056934	1.479511	0.864598	0.908159	0.079908	0	36	61	47	30	43	63	71	47	81	57
ENSMUSG00000021559	chr13	Dapk1	60601947	60602110	5934	-0.05244	4.008621	0.864889	0.908396	0.102463	0	216	131	258	178	647	213	274	535	405	425
ENSMUSG00000020648	chr12	Dus4l	31640055	31640944	1768	0.05661	1.906357	0.865202	0.908642	0.082364	0	52	78	62	64	35	68	67	102	106	93
ENSMUSG00000027673	chr3	Ndufb5	32736990	32737205	4995	-0.03428	8.094188	0.865254	0.908642	0.04859	0	3839	5265	5386	4656	3554	6484	6138	5715	6708	5943
ENSMUSG00000045573	chr4	Penk	4133531	4134507	1634	0.045085	3.850024	0.865416	0.908742	0.080559	0	249	140	298	177	332	283	215	591	329	260
ENSMUSG00000031153	chrX	Gripap1	7789765	7790068	5502	0.029924	4.508304	0.865525	0.908788	0.031804	0	314	360	404	380	411	396	537	402	722	649
ENSMUSG00000027998	chr3	Plrg1	83055522	83055654	2816	0.027088	4.695509	0.865793	0.908868	0.026985	0	393	381	513	393	453	497	635	609	749	558
ENSMUSG00000042251	chr1	Pm20d1	1.32E+08	1.32E+08	7028	-0.08771	0.144269	0.865693	0.908868	0.174514	0	12	8	13	36	18	12	20	8	43	35
ENSMUSG00000070420	chr5	Zscan25	1.45E+08	1.45E+08	1996	0.049165	2.617782	0.865798	0.908868	0.081076	0	73	89	97	105	136	77	125	261	153	107
ENSMUSG00000006920	chr11	Ezh1	1.01E+08	1.01E+08	7440	0.049312	5.058905	0.866147	0.908977	0.098258	0	536	439	574	612	553	398	511	1696	699	657
ENSMUSG00000026814	chr2	Eng	32646595	32647024	4048	0.031352	5.726623	0.86623	0.908977	0.039916	0	572	731	838	1239	1018	963	1130	1192	1692	1321
ENSMUSG00000027305	chr2	Ndufaf1	1.2E+08	1.2E+08	1501	0.033411	5.574189	0.866167	0.908977	0.044952	0	597	918	877	821	657	1138	1177	956	1251	1017
ENSMUSG00000038346	chr6	Zfp384	1.25E+08	1.25E+08	6421	0.027148	4.629955	0.866012	0.908977	0.027624	0	362	306	463	429	496	409	549	672	698	600
ENSMUSG00000064181	chr10	Rab3ip	1.17E+08	1.17E+08	2690	0.032512	4.048581	0.866048	0.908977	0.037645	0	204	319	292	282	245	341	373	411	416	387

ENSMUSG00000028464	chr4	Tpm2	43514711	43514861	2909	-0.02662	13.10372	0.866419	0.909106	0.030026	0	125525	122393	158963	156813	182687	173852	191268	224075	234033	191271
ENSMUSG00000057110	chr2	Cntrl	35109492	35109629	10334	-0.03273	3.323839	0.866701	0.909333	0.035315	0	163	115	192	172	201	182	195	218	272	281
ENSMUSG00000022105	chr14	Rb1	73183673	73184055	6015	0.037449	4.230738	0.866986	0.909468	0.052754	0	259	268	337	322	358	213	489	694	494	353
ENSMUSG00000023153	chr4	Tmem52	1.55E+08	1.55E+08	1157	-0.02993	6.561323	0.86701	0.909468	0.037234	0	1500	1466	1506	1565	1888	2063	1767	2505	2355	2079
ENSMUSG00000037608	chr10	Bclaf1	20312469	20312604	8426	0.037816	5.521644	0.867092	0.909468	0.059148	0	711	585	843	647	1028	673	922	1884	1097	861
ENSMUSG00000043969	chr19	Emx2	59458372	59459624	3002	0.06446	0.482236	0.867057	0.909468	0.098229	0	19	12	21	18	38	21	23	50	26	34
ENSMUSG00000022553	chr15	Maf1	76351294	76351659	2412	0.036257	6.214437	0.867312	0.909567	0.055231	0	1130	1043	1335	1258	1341	1334	1425	2872	1467	1569
ENSMUSG00000025978	chr1	Rftn2	55170159	55172082	5871	-0.03838	2.798625	0.867384	0.909567	0.049641	0	111	81	122	103	171	96	210	147	209	142
ENSMUSG00000070942	chr1	Il1rl2	40324610	40327606	6812	-0.04034	2.87076	0.86733	0.909567	0.050624	0	107	80	124	104	210	108	157	178	206	192
ENSMUSG00000021276	chr12	Cinp	1.11E+08	1.11E+08	2029	0.027095	4.249431	0.867558	0.909681	0.028205	0	283	280	358	265	384	404	442	401	505	465
ENSMUSG00000001441	chr11	Npepps	97205842	97206091	7206	-0.02691	6.244781	0.867913	0.909686	0.030324	0	1059	1219	1387	1358	1341	1489	1755	1800	1987	1699
ENSMUSG00000020198	chr10	Ap3d1	80706978	80707983	4730	-0.02758	5.557847	0.867652	0.909686	0.030974	0	636	608	794	848	1133	730	1032	1156	1447	1150
ENSMUSG00000023232	chr4	Serinc2	1.3E+08	1.3E+08	2319	0.027897	6.236799	0.867764	0.909686	0.033337	0	979	972	1523	1211	1639	1662	1735	1492	2038	1888
ENSMUSG00000026270	chr1	Capn10	92934376	92935014	4346	0.040364	2.751854	0.867702	0.909686	0.053422	0	99	89	146	110	103	99	148	203	144	193
ENSMUSG00000037355	chr5	Uvssa	33378549	33379325	8666	-0.05551	2.245118	0.867957	0.909686	0.100079	0	78	48	65	81	129	61	89	196	94	92
ENSMUSG00000053293	chr5	Pom121	1.35E+08	1.35E+08	5581	0.029263	4.323029	0.867862	0.909686	0.034156	0	247	243	378	322	491	314	419	572	607	466
ENSMUSG00000042389	chr6	Tsen2	1.16E+08	1.16E+08	6437	0.033146	2.927592	0.868248	0.909921	0.035906	0	100	125	140	107	149	146	173	159	218	193
ENSMUSG00000002803	chr12	Btbd6	1.13E+08	1.13E+08	2088	0.033948	3.515324	0.869135	0.910662	0.041265	0	153	161	210	231	179	225	327	186	354	254
ENSMUSG00000038742	chr9	Angptl6	20873809	20874072	1581	0.048933	1.633066	0.869152	0.910662	0.068505	0	49	49	47	42	58	73	84	42	86	69
ENSMUSG00000041124	chr9	Msantd4	4383535	4384142	2731	0.032665	5.092775	0.869089	0.910662	0.044371	0	456	525	604	621	599	614	744	1205	791	640
ENSMUSG00000034175	chr11	Rhbdd3	5098926	5099566	2790	-0.03012	4.496692	0.869432	0.910839	0.035164	0	324	341	435	371	429	434	441	677	490	529
ENSMUSG00000047789	chr13	Slc38a9	1.13E+08	1.13E+08	8904	0.031079	3.229323	0.869452	0.910839	0.034519	0	132	121	187	136	199	152	233	260	242	213
ENSMUSG00000038425	chr18	Poli	70508680	70509744	3863	0.059975	0.785652	0.869989	0.911333	0.060551	0	19	21	34	21	40	26	39	35	53	43
ENSMUSG00000041479	chr14	Syt15	34219595	34220180	5165	-0.04806	1.119632	0.870101	0.911381	0.056465	0	27	28	39	38	46	27	43	54	62	56
ENSMUSG00000031530	chr8	Dusp4	34807297	34808173	2740	-0.06186	1.244929	0.870697	0.911936	0.131559	0	25	25	27	58	62	17	40	80	79	52
ENSMUSG00000097828	chr13	6430562O15Rik	99396924	99398535	5693	-0.07208	0.108706	0.870765	0.911938	0.10957	0	13	17	13	19	22	21	30	8	38	16
ENSMUSG00000026718	chr2	Stam	14074098	14074336	8386	-0.0313	4.115573	0.870843	0.911951	0.039001	0	238	223	336	299	377	246	460	526	477	304
ENSMUSG00000004356	chr10	Utp20	88746607	88747059	8831	-0.03227	3.640886	0.871133	0.912186	0.038406	0	159	151	245	209	302	189	217	326	388	331
ENSMUSG00000027122	chr2	Arl14ep	1.07E+08	1.07E+08	5313	0.033884	2.904122	0.87169	0.9127	0.039629	0	93	93	133	127	173	111	207	188	207	169
ENSMUSG00000024896	chr19	Minpp1	32485769	32486559	2619	0.02691	4.283715	0.872146	0.912825	0.028945	0	255	281	354	327	397	370	501	368	642	424
ENSMUSG00000030322	chr6	Mbd4	1.16E+08	1.16E+08	5059	-0.04931	1.331209	0.871988	0.912825	0.062636	0	40	24	52	32	61	43	60	47	75	55
ENSMUSG00000038412	chr9	Higd1a	1.22E+08	1.22E+08	1873	0.029939	6.258903	0.872033	0.912825	0.040407	0	1053	1330	1524	1131	1245	1861	1834	1508	1938	1737
ENSMUSG00000043644	chr11	0610009L18Rik	1.2E+08	1.2E+08	619	0.032477	3.298593	0.872205	0.912825	0.043207	0	140	147	195	158	163	240	202	260	211	212
ENSMUSG00000045930	chr12	Clec14a	58264720	58269258	4539	0.04341	3.245494	0.872147	0.912825	0.071145	0	127	153	168	171	148	119	211	393	235	164
ENSMUSG00000050530	chr2	Fam171a1	3114224	3114265	4442	0.030075	3.623053	0.872174	0.912825	0.032966	0	182	151	206	237	238	188	345	314	329	278
ENSMUSG00000034848	chr2	Ttc21b	66184327	66184843	9282	-0.04432	1.902808	0.872694	0.913264	0.061965	0	62	36	77	49	90	68	81	75	88	106
ENSMUSG00000040658	chr17	Dnph1	46496789	46496972	1106	0.041192	2.441085	0.872756	0.913264	0.050298	0	72	96	93	71	106	98	122	97	155	163
ENSMUSG00000026694	chr1	Mettl13	1.63E+08	1.63E+08	9740	0.030711	3.362697	0.873007	0.913457	0.036086	0	148	144	181	164	208	191	206	317	269	217
ENSMUSG00000026664	chr2	Phyh	4919019	4919144	1893	-0.03482	7.318525	0.873291	0.913547	0.056766	0	2138	3131	2888	3299	1728	3162	3148	4132	4262	3628
ENSMUSG00000062563	chr12	Cys1	24665838	24666252	2646	-0.05356	1.703651	0.873238	0.913547	0.106884	0	59	35	57	44	76	41	87	124	74	38
ENSMUSG00000067547	chr15	Gm7666	6653923	6654741	819	-0.03022	3.531022	0.873205	0.913547	0.036938	0	153	203	204	197	206	234	216	263	389	230
ENSMUSG00000045725	chr6	Prr15	54327012	54327310	1381	-0.06571	0.996487	0.873811	0.914022	0.112716	0	12	38	41	33	40	31	35	28	49	75
ENSMUSG00000028292	chr4	Rars2	34614957	34615026	2771	0.028004	4.068348	0.873953	0.914102	0.030741	0	221	291	305	260	297	306	423	358	417	461
ENSMUSG00000023988	chr17	Bysl	47599331	47601898	3854	0.025296	4.895707	0.874588	0.914696	0.028806	0	390	390	587	485	636	576	679	580	940	743
ENSMUSG00000014907	chr8	Naf1	66860217	66861046	2990	-0.03619	2.174187	0.875205	0.915063	0.042289	0	59	65	92	79	80	88	98	92	122	109
ENSMUSG00000025236	chr9	Adpgk	59291572	59291866	2470	0.031913	3.333007	0.875202	0.915063	0.034859	0	155	142	176	149	204	156	208	215	348	274
ENSMUSG00000028996	chr4	Rbp7	1.49E+08	1.49E+08	718	0.048778	1.750868	0.87523	0.915063	0.063881	0	49	53	68	59	36	52	69	79	105	88
ENSMUSG00000034867	chr7	Ankrd27	35586244	35586369	5258	0.026168	4.039747	0.875062	0.915063	0.026223	0	257	211	289	282	317	279	363	384	498	421
ENSMUSG00000059439	chr11	Bcas3	85353167	85353233	6085	-0.02776	4.668872	0.875269	0.915063	0.03381	0	367	358	470	437	515	409	571	802	614	538
ENSMUSG00000026170	chr1	Cyp27a1	74713574	74713891	2173	-0.04654	5.105531	0.875963	0.915669	0.103307	0	531	563	642	616	532	442	492	1691	561	736
ENSMUSG00000045730	chr18	Adrb2	62177817	62179959	2143	-0.02911	3.986667	0.875981	0.915669	0.035726	0	223	245	265	316	274	307	326	465	380	330
ENSMUSG00000052456	chr8	Asna1	85017934	85018255	1250	0.02495	5.248178	0.876394	0.916031	0.028712	0	502	565	764	644	673	758	868	766	1098	979
ENSMUSG00000022820	chr16	Ndufb4	37647170	37647719	1170	-0.03279	6.130826	0.876702	0.91625	0.052057	0	1041	1375	1473	975	952	1705	1527	1484	1583	1608
ENSMUSG00000050248	chr5	Evc2	37338499	37338727	5837	-0.03054	3.376449	0.876801	0.91625	0.037609	0	156	116	190	180	238	146	240	289	305	226
ENSMUSG00000091586	chr17	Cyp4f17	32506462	32506578	1693	-0.06418	0.726313	0.876798	0.91625	0.077969	0	22	22	30	26	34	30	25	56	31	34
ENSMUSG00000020492	chr11	Ska2	87109234	87109304	3272	-0.03814	2.515647	0.877022	0.916411	0.057794	0	94	84	109	87	100	112	151	71	172	145
ENSMUSG00000024002	chr17	Brd4	32196274	32197820	8402	-0.02808	5.210356	0.877511	0.916841	0.037458	0	480	494	609	696	875	534	790	1092	1140	782
ENSMUSG00000038086	chr9	Hspb2	50751072	50751733	840	0.029486	6.230475	0.877566	0.916841	0.04275	0	974	1342	1478	1201	1158	1757	1802	1382	1829	1947
ENSMUSG00000014470	chr8	Rnf166	1.22E+08	1.22E+08	1985	0.028749	4.758167	0.877857	0.917006	0.037311	0	448	413	477	424	446	504	589	848	692	536
ENSMUSG00000026499	chr1	Acbd3	1.81E+08	1.81E+08	6780	-0.02873	4.217442	0.877922	0.917006	0.036305	0	288	212	330	264	496	275	461	416	548	471
ENSMUSG00000036208	chr16	BC027231	44724301	44724468	5741	0.052636	2.085919	0.877912	0.917006	0.095294	0	62	53	78	65	84	50	84	190	83	87
ENSMUSG00000036977	chr8	Anapc10	79711820	79711844	2802	-0.03695	2.294245	0.878133	0.917018	0.047022	0	61	81	102	87	75	95	116	118	116	106
ENSMUSG00000059482	chr4	2610301B20Rik	10874498	10874772	2391	-0.03249	2.556385	0.878027	0.917018	0.04667	0	95	77	103	89	127	84	143	158	187	107
ENSMUSG00000064369	chrMT	mt-Te	14071	14139	69	0.134281	2.094141	0.878117	0.917018	0.797532	0	21	38	28	208	31	4	13	13	440	116
ENSMUSG00000097162	chr7	2310010J17Rik	90124858	90125032	451	0.047372	0.8377	0.878382	0.91721	0.066416	0	25	24	36	24	30	30	36	58	42	34
ENSMUSG00000053646	chr9	Plxnb1	1.09E+08	1.09E+08	9545	-0.04331	1.93271	0.878856	0.917634	0.083636	0	77	29	66	72	72	45	116	70	119	88

ENSMUSG00000040187	chr6	Arntl2	1.47E+08	1.47E+08	3032	-0.05929	0.471235	0.879023	0.91774	0.067987	0	18	24	20	18	30	23	32	20	34	39
ENSMUSG00000029600	chr5	Rita1	1.21E+08	1.21E+08	2836	-0.03414	2.203572	0.879103	0.917755	0.043765	0	69	68	80	76	88	81	116	80	141	107
ENSMUSG00000013833	chr10	Med16	79894708	79895410	4663	-0.0268	4.801906	0.87929	0.91788	0.03357	0	353	375	540	560	535	483	498	748	794	711
ENSMUSG00000018001	chr5	Cyth3	1.44E+08	1.44E+08	4682	0.027335	4.574705	0.880182	0.918705	0.034696	0	361	290	487	358	487	327	592	696	706	521
ENSMUSG00000035062	chrX	Zc4h2	95639193	95640651	2257	0.04131	0.950597	0.880213	0.918705	0.056914	0	28	25	37	22	40	35	49	40	55	39
ENSMUSG00000024191	chr17	Bnip1	26781079	26781176	5097	-0.0294	4.050593	0.880315	0.918743	0.04072	0	250	259	339	268	268	345	419	232	500	411
ENSMUSG00000027671	chr3	Actl6a	32706298	32706428	3886	-0.02538	4.092628	0.880621	0.918992	0.028398	0	225	215	335	304	370	284	370	394	556	387
ENSMUSG00000033365	chr4	Ipo13	1.18E+08	1.18E+08	4207	-0.04181	7.557475	0.880802	0.919112	0.092279	0	2879	2629	3420	3600	3407	2818	2639	8952	3550	3544
ENSMUSG00000008690	chr15	Ncaph2	89355719	89355850	4198	-0.02356	5.792477	0.881418	0.919252	0.028494	0	842	761	1138	862	1080	966	1188	1224	1646	1437
ENSMUSG00000024099	chr17	Ndufv2	66078795	66079587	1990	-0.02998	8.358646	0.881404	0.919252	0.048129	0	4498	6372	5729	6114	4479	7865	7082	7187	8164	6968
ENSMUSG00000026276	chr1	Sept2	93478964	93479068	7979	0.023569	6.660683	0.881398	0.919252	0.029035	0	1384	1437	1955	1581	2082	1747	2710	2270	2991	2280
ENSMUSG00000032251	chr9	Irak1bp1	82829540	82830339	2158	0.059142	1.164926	0.881299	0.919252	0.067033	0	40	32	32	28	42	31	43	66	70	49
ENSMUSG00000032261	chr9	Sh3bgrl2	83548327	83548503	7865	0.048108	1.409936	0.881534	0.919252	0.067338	0	29	34	40	53	56	40	55	44	88	82
ENSMUSG00000037606	chr7	Osbpl5	1.44E+08	1.44E+08	4915	-0.02677	4.717124	0.881229	0.919252	0.033838	0	393	295	499	416	645	414	681	688	724	550
ENSMUSG00000039756	chr3	Dnttip2	1.22E+08	1.22E+08	2401	0.035338	4.605624	0.881523	0.919252	0.061878	0	355	380	462	385	410	354	499	1024	575	420
ENSMUSG00000053897	chr3	Slc39a8	1.36E+08	1.36E+08	7664	-0.06715	0.268445	0.881033	0.919252	0.104807	0	14	15	9	29	28	14	19	35	33	27
ENSMUSG00000097404	chr19	Gm10814	6012620	6012684	1933	-0.07952	0.223483	0.881325	0.919252	0.112928	0	22	16	23	8	23	21	12	38	26	24
ENSMUSG00000040265	chr1	Dnm3	1.62E+08	1.62E+08	24452	0.048862	2.440989	0.882502	0.920193	0.110268	0	90	52	75	125	95	79	100	247	118	88
ENSMUSG00000022843	chr16	Clcn2	20702964	20703437	6022	-0.05008	1.503534	0.882693	0.920323	0.109253	0	62	31	56	22	62	30	57	94	72	66
ENSMUSG00000073437	chr17	D330041H03Rik	24404649	24405338	3749	-0.05177	-0.04632	0.883942	0.921555	0.086647	0	14	8	22	12	19	8	25	21	20	27
ENSMUSG00000030246	chr6	Ldhb	1.42E+08	1.42E+08	1570	0.048503	6.242467	0.884506	0.922017	0.130148	0	782	1447	766	2456	553	1162	1630	1778	2862	1774
ENSMUSG00000089902	chr2	Gm13625	69871412	69871842	480	0.050278	1.054023	0.884518	0.922017	0.086578	0	23	40	38	24	37	51	40	27	58	57
ENSMUSG00000044950	chr11	Pwwp2a	43681998	43682616	5508	-0.03263	2.375361	0.88459	0.922022	0.047295	0	84	82	78	80	104	70	132	136	148	110
ENSMUSG00000033373	chr12	Fntb	76765589	76765638	3987	0.024519	5.364465	0.884726	0.922095	0.03248	0	587	653	879	569	715	875	973	990	1042	917
ENSMUSG00000031343	chrX	Gabra3	72432681	72434984	3924	0.057286	0.958729	0.884941	0.922249	0.151426	0	25	10	19	28	75	31	49	27	55	59
ENSMUSG00000006205	chr7	Htra1	1.31E+08	1.31E+08	2879	-0.03257	5.707293	0.88502	0.922262	0.056971	0	787	594	945	708	1473	1235	1405	723	1286	1285
ENSMUSG00000035958	chr13	Tdp2	24831679	24831929	2095	0.028778	3.016249	0.885431	0.922621	0.037516	0	118	119	179	115	130	150	188	195	210	199
ENSMUSG00000041734	chr3	Kirrel	87078593	87083620	7463	0.032222	4.142742	0.885558	0.922684	0.05607	0	272	163	301	238	516	255	492	497	535	326
ENSMUSG00000078429	chr10	Ctdsp2	1.27E+08	1.27E+08	5065	-0.03024	7.270239	0.885767	0.922832	0.052371	0	2351	1978	2592	2869	3305	2382	2939	5766	3496	3232
ENSMUSG00000022771	chr16	Ppil2	17086555	17087115	6171	-0.0219	4.929907	0.885944	0.922947	0.025421	0	450	465	567	482	595	552	701	707	827	742
ENSMUSG00000038055	chr16	Dexi	10502531	10503914	3353	-0.02726	4.774873	0.886107	0.923048	0.03693	0	351	419	580	431	536	671	536	579	652	657
ENSMUSG00000003809	chr8	Gcdh	84886393	84887053	2754	0.030137	5.293241	0.886319	0.923199	0.050864	0	614	536	705	647	729	697	744	1487	816	828
ENSMUSG00000025612	chr16	Bach1	87698945	87699056	6179	-0.03695	4.610424	0.886982	0.92382	0.077839	0	366	389	438	419	436	267	472	1100	544	447
ENSMUSG00000053198	chr7	Prx	27499324	27499365	5579	-0.0306	3.710914	0.887389	0.924174	0.050364	0	187	144	200	278	301	171	297	354	484	238
ENSMUSG00000056832	chr6	Ttc26	38381469	38381593	4673	-0.05117	0.905641	0.887485	0.924205	0.073998	0	26	23	49	27	27	33	48	26	53	45
ENSMUSG00000002741	chr11	Ykt6	5955693	5956004	2984	0.023179	6.288931	0.888165	0.924773	0.031324	0	1024	1196	1628	1192	1464	1441	1952	1507	2380	1980
ENSMUSG00000032604	chr9	Qars	1.09E+08	1.09E+08	7267	0.022952	6.433949	0.888119	0.924773	0.030751	0	1235	1303	1642	1335	1653	1543	1893	2440	2340	1967
ENSMUSG00000029153	chr5	Ociad2	73322199	73323847	2509	0.027299	4.756493	0.888352	0.924899	0.042087	0	443	387	496	453	432	633	455	626	639	770
ENSMUSG00000030878	chr7	Cdr2	1.21E+08	1.21E+08	2782	-0.04009	2.906407	0.888501	0.924985	0.079883	0	126	81	112	93	227	135	209	88	239	191
ENSMUSG00000026750	chr2	Psmb7	38588036	38588288	1214	0.02681	7.826266	0.888672	0.925093	0.04354	0	3180	3866	4423	3566	3599	4748	4629	6968	5033	4977
ENSMUSG00000074001	chr9	Klhl40	1.22E+08	1.22E+08	2455	0.025708	7.189804	0.889043	0.92534	0.040595	0	1829	2006	3220	2201	2997	3482	3837	2625	3797	3213
ENSMUSG00000087644	chrX	Gm14703	7651106	7652711	1820	-0.06005	0.227823	0.889018	0.92534	0.135894	0	15	15	14	23	25	14	16	52	16	24
ENSMUSG00000030533	chr7	Unc45a	80325292	80325877	3991	0.024791	3.558732	0.889635	0.925886	0.03057	0	158	172	210	178	257	220	310	221	357	277
ENSMUSG00000064037	chr5	Gpn1	31494741	31494883	7845	-0.02365	4.323551	0.889728	0.925914	0.030055	0	263	327	380	335	374	407	483	357	585	477
ENSMUSG00000056493	chr5	Foxk1	1.42E+08	1.42E+08	7445	-0.03608	4.550305	0.889916	0.926039	0.077067	0	297	348	412	404	532	244	420	1033	580	452
ENSMUSG00000029840	chr6	Mtpn	35508906	35512317	3960	0.023501	5.480746	0.890089	0.92615	0.031607	0	642	589	833	739	916	678	1137	877	1588	1087
ENSMUSG00000061100	chr16	Retnla	48842552	48842628	598	-0.05333	3.359008	0.890521	0.92653	0.162658	0	190	63	157	136	346	132	98	152	352	465
ENSMUSG00000056569	chr1	Mpz	1.71E+08	1.71E+08	2111	0.029082	6.267081	0.890815	0.926766	0.051788	0	1163	862	1185	1651	1527	1171	1949	1748	3177	1303
ENSMUSG00000040151	chr3	Hs2st1	1.44E+08	1.44E+08	4916	0.023112	4.452448	0.891145	0.92704	0.029428	0	311	296	442	319	455	330	614	535	612	503
ENSMUSG00000031532	chr8	Saraf	34154563	34154836	1897	0.023661	7.279266	0.89135	0.927184	0.035454	0	2225	2302	3023	2442	2890	3005	3211	4684	3805	3453
ENSMUSG00000022892	chr16	App	84954440	84955432	3128	0.024871	7.333753	0.891682	0.927454	0.039463	0	2304	1661	3160	2656	3851	2356	4048	3962	5414	3605
ENSMUSG00000081434	chr2	Gm14165	1.52E+08	1.52E+08	952	-0.04817	1.018957	0.891744	0.927454	0.108195	0	37	30	14	44	36	41	35	32	72	44
ENSMUSG00000027651	chr2	Rprd1b	1.58E+08	1.58E+08	6499	-0.02485	5.320629	0.891922	0.92757	0.036836	0	588	532	745	667	853	716	836	1285	971	790
ENSMUSG00000009293	chr10	Ube2g2	77622275	77622416	2431	0.023974	6.507797	0.892133	0.92769	0.036424	0	1185	1530	1921	1395	1484	1760	2043	2520	2214	2101
ENSMUSG00000020072	chr10	Pbld1	63024315	63024465	4889	0.045239	0.970153	0.892172	0.92769	0.073862	0	28	26	37	30	32	40	29	63	41	45
ENSMUSG00000027361	chr2	Gabpb1	1.27E+08	1.27E+08	7752	-0.02688	3.184606	0.892649	0.928116	0.033884	0	110	121	204	158	175	163	207	188	270	220
ENSMUSG00000025036	chr19	Sfxn2	46573365	46573459	3210	0.036774	2.379419	0.892818	0.928222	0.082361	0	86	37	77	74	158	94	115	106	126	162
ENSMUSG00000030417	chr7	Pdcd5	35641982	35642185	2486	0.022957	5.641335	0.893051	0.928262	0.032486	0	713	866	934	796	778	1043	1092	1153	1346	1198
ENSMUSG00000047905	chr6	Gm8566	67205619	67206083	465	0.065419	0.177898	0.892991	0.928262	0.071913	0	13	14	17	25	15	17	19	31	31	26
ENSMUSG00000079658	chr1	Tceb1	16641725	16643478	3026	-0.02342	6.101786	0.893058	0.928262	0.03463	0	941	1160	1336	1101	1221	1550	1538	1383	1765	1617
ENSMUSG00000030790	chr7	Adm	1.11E+08	1.11E+08	1619	-0.03968	1.91398	0.893272	0.928415	0.072165	0	46	59	79	76	50	71	58	114	86	91
ENSMUSG00000023027	chr15	Atf1	1E+08	1E+08	3060	0.024279	5.170914	0.893638	0.928517	0.036945	0	500	512	672	579	730	582	777	1208	876	792
ENSMUSG00000023087	chr3	Ccrn4l	51224447	51225287	10658	-0.03371	4.576172	0.893614	0.928517	0.071778	0	325	421	611	382	249	541	585	303	738	569
ENSMUSG00000042535	chr15	Gtpbp1	79690895	79691098	3398	0.022261	4.922632	0.893635	0.928517	0.030622	0	410	413	578	543	576	547	607	877	804	724
ENSMUSG00000061848	chr15	Gm5805	81972390	81972845	456	0.035668	1.955126	0.893521	0.928517	0.051085	0	62	53	63	74	57	73	81	99	108	86
ENSMUSG00000096929	chr1	A330023F24Rik	1.95E+08	1.95E+08	9354	0.05179	1.490204	0.893771	0.928585	0.140592	0	39	29	60	40	58	47	43	121	28	76

ENSMUSG00000004936	chr9	Map2k1	64185770	64186798	3391	-0.02156	5.932593	0.894001	0.928643	0.02979	0	868	859	1263	981	1195	1044	1390	1652	1694	1322
ENSMUSG00000032024	chr9	Clmp	40685962	40686359	4591	-0.03304	3.879194	0.894036	0.928643	0.059651	0	217	124	255	235	442	284	449	240	399	316
ENSMUSG00000060180	chr11	Myh13	67321658	67321806	6180	0.042384	3.311481	0.894095	0.928643	0.099328	0	123	136	170	233	144	85	334	293	372	126
ENSMUSG00000061607	chr17	Mdc1	35841515	35841679	7421	-0.029	3.009685	0.89395	0.928643	0.045375	0	115	112	144	125	181	124	209	122	257	224
ENSMUSG00000044026	chr19	Slc35g1	38395980	38396301	3471	-0.04999	1.074416	0.894291	0.928777	0.065528	0	24	20	38	42	50	34	44	39	56	59
ENSMUSG00000029108	chr5	Pcdh7	57718021	57722278	10478	-0.03265	3.292746	0.894543	0.928969	0.058489	0	144	95	201	132	270	122	315	210	284	211
ENSMUSG00000053012	chr6	Krcc1	71272019	71272059	1748	-0.02135	4.592016	0.894687	0.929049	0.029609	0	354	392	485	378	404	383	512	604	681	630
ENSMUSG00000020823	chr11	Sec14l1	1.17E+08	1.17E+08	7176	0.022133	6.134134	0.894816	0.929102	0.032642	0	928	979	1222	1111	1644	1312	1942	1363	2021	1649
ENSMUSG00000078495	chr4	Gm13157	1.48E+08	1.48E+08	2912	-0.03243	1.643843	0.894872	0.929102	0.062449	0	43	49	58	61	43	37	65	84	92	78
ENSMUSG00000033628	chr18	Pik3c3	30272747	30273018	4466	0.0224	4.286707	0.895674	0.929865	0.030481	0	270	272	386	309	383	331	404	586	511	459
ENSMUSG00000019761	chr11	Krt10	99385254	99385636	2094	0.04471	1.293594	0.895806	0.929932	0.075946	0	30	36	53	37	38	57	74	33	60	52
ENSMUSG00000000915	chr5	Hip1r	1.24E+08	1.24E+08	5022	0.033316	2.891201	0.896408	0.930459	0.057052	0	77	144	153	133	92	123	178	199	201	168
ENSMUSG00000031310	chrX	Zmym3	1.01E+08	1.01E+08	8021	0.02516	3.734023	0.896448	0.930459	0.033278	0	196	175	236	208	287	197	341	268	482	305
ENSMUSG00000040749	chrX	Siah1b	1.64E+08	1.64E+08	2119	-0.03911	1.3778	0.897007	0.930969	0.068448	0	23	45	57	45	43	42	58	62	86	44
ENSMUSG00000001948	chr9	Spa17	37603295	37603486	689	0.047815	1.048988	0.897482	0.931322	0.073888	0	30	24	38	45	24	46	49	41	45	50
ENSMUSG00000051444	chr3	Bbs12	37312554	37312585	2436	0.060692	0.185991	0.897476	0.931322	0.080684	0	19	17	15	15	18	18	14	24	43	27
ENSMUSG00000027641	chr2	Rbl1	1.57E+08	1.57E+08	5993	0.034188	2.185876	0.897828	0.931612	0.052702	0	64	63	60	90	90	77	105	81	149	121
ENSMUSG00000009633	chr1	G0s2	1.93E+08	1.93E+08	871	0.03977	4.279879	0.898023	0.931744	0.107451	0	250	295	311	418	309	395	300	171	550	879
ENSMUSG00000004394	chr11	Tmed4	6270369	6271800	2178	-0.02041	5.572941	0.898397	0.931923	0.027931	0	721	650	916	766	963	906	1151	1192	1126	1101
ENSMUSG00000034101	chr2	Ctnnd1	84600071	84602903	7319	-0.02199	6.060591	0.898392	0.931923	0.033756	0	896	833	1162	1168	1644	1120	1747	1344	2094	1517
ENSMUSG00000100254	chr7	TRPC2	1.02E+08	1.02E+08	2874	-0.06277	0.236569	0.898264	0.931923	0.074842	0	17	16	24	11	25	23	16	22	36	27
ENSMUSG00000097729	chr12	2310015A10Rik	80120548	80125126	4843	0.027985	3.92266	0.898554	0.932016	0.049155	0	232	231	271	264	238	267	274	546	323	353
ENSMUSG00000026260	chr1	Ndufa10	92439010	92439907	3331	-0.02533	8.206191	0.898754	0.932154	0.047174	0	3636	5543	5101	6139	4113	6415	6165	7289	7919	6083
ENSMUSG00000038732	chr13	Mboat1	30136498	30136762	3474	0.038662	1.99206	0.899276	0.932625	0.094137	0	59	40	49	72	104	72	123	43	107	116
ENSMUSG00000068394	chr2	Cep152	1.26E+08	1.26E+08	5768	0.034457	1.234095	0.899612	0.932903	0.057549	0	35	21	43	41	48	39	54	45	72	59
ENSMUSG00000001419	chr3	Mef2d	88142372	88142674	5985	0.024031	7.681553	0.899791	0.932996	0.043237	0	2991	2586	3667	3867	3970	3659	4333	7025	5012	4045
ENSMUSG00000073125	chrX	Xlr3b	73192207	73192249	3780	-0.11754	-0.01212	0.898836	0.932996	0.661051	0	4	19	49	5	2	4	37	15	1	43
ENSMUSG00000032314	chr9	Etfa	55454508	55454762	1835	0.024486	7.32585	0.900278	0.933309	0.044638	0	2127	2853	2758	3111	2245	2695	3187	4821	4646	3665
ENSMUSG00000052056	chr2	Zfp217	1.7E+08	1.7E+08	6139	0.023338	3.454223	0.90034	0.933309	0.036022	0	162	115	196	171	272	180	266	262	295	284
ENSMUSG00000093242	chr2	Gm24574	75659244	75659317	74	-0.06362	2.249888	0.900227	0.933309	0.26162	0	16	83	101	84	126	28	183	34	89	211
ENSMUSG00000027189	chr2	Trim44	1.02E+08	1.02E+08	5645	-0.0223	4.756199	0.900677	0.933588	0.035217	0	417	330	456	437	653	367	592	734	772	704
ENSMUSG00000027341	chr2	Tmem230	1.32E+08	1.32E+08	3267	-0.02159	4.227591	0.900813	0.933659	0.02899	0	259	273	391	313	338	388	462	354	500	447
ENSMUSG00000022722	chr16	Arl6	59612949	59613844	2098	0.037204	1.553782	0.901484	0.934252	0.057553	0	42	41	59	51	40	56	68	49	94	71
ENSMUSG00000029714	chr5	Gigyf1	1.38E+08	1.38E+08	5437	-0.0237	4.371578	0.901587	0.934252	0.041521	0	369	251	376	345	393	276	399	644	565	534
ENSMUSG00000075012	chr2	Fjx1	1.02E+08	1.02E+08	3134	0.037557	1.123842	0.901526	0.934252	0.073221	0	19	24	45	33	55	31	68	46	56	47
ENSMUSG00000017421	chr11	Zfp207	80383279	80383495	6658	0.024156	5.917782	0.901815	0.934418	0.043976	0	904	817	1138	948	1218	902	1238	2168	1570	1273
ENSMUSG00000021518	chr13	Ptdss1	66932830	66933686	3424	0.020224	5.171462	0.901896	0.934432	0.029137	0	467	519	677	617	722	625	904	673	1163	916
ENSMUSG00000040264	chr3	Gbp5	1.42E+08	1.42E+08	5844	0.037303	1.770523	0.902049	0.93452	0.083364	0	37	56	61	71	47	93	61	54	84	92
ENSMUSG00000032290	chr9	Ptpn9	56994968	56995656	4054	-0.02264	3.657679	0.902221	0.934629	0.032594	0	192	152	226	206	290	213	323	230	401	303
ENSMUSG00000038152	chr13	5033430I15Rik	45965253	45965383	952	0.047778	1.351325	0.902416	0.934751	0.118725	0	43	31	60	40	26	56	66	21	81	68
ENSMUSG00000043924	chr4	Ncmap	1.35E+08	1.35E+08	2227	0.040011	2.218003	0.902474	0.934751	0.089197	0	69	47	61	91	111	65	106	177	130	66
ENSMUSG00000006378	chr15	Gcat	79030874	79031120	3851	-0.0282	2.856232	0.902643	0.934856	0.041663	0	103	99	131	136	135	140	124	156	203	204
ENSMUSG00000048285	chr12	Frmd6	70825514	70825573	4660	-0.02248	4.853705	0.902876	0.935027	0.035216	0	433	335	527	446	726	516	822	665	778	566
ENSMUSG00000040841	chr7	Six5	19094594	19095418	3007	0.038993	2.149114	0.903232	0.935326	0.081288	0	74	47	65	57	119	53	79	102	133	157
ENSMUSG00000030008	chr6	Pradc1	85446810	85447297	1594	-0.02371	3.251572	0.90358	0.935546	0.032385	0	136	141	201	140	179	186	198	234	252	219
ENSMUSG00000041769	chr7	Ppp2r2d	1.39E+08	1.39E+08	5903	-0.02163	4.936923	0.903553	0.935546	0.034528	0	421	466	584	551	548	571	619	936	773	626
ENSMUSG00000031715	chr8	Smarca5	80698507	80701128	7777	-0.01973	5.362663	0.90384	0.935745	0.029266	0	547	584	736	679	944	682	994	1093	1167	859
ENSMUSG00000037007	chr5	Zfp113	1.38E+08	1.38E+08	6754	0.033359	2.235925	0.904313	0.936165	0.057051	0	72	66	80	83	78	71	106	159	105	104
ENSMUSG00000003382	chr3	Etv3	87525407	87525659	10274	0.024099	3.908203	0.90465	0.936444	0.03955	0	210	218	261	245	306	214	313	516	382	344
ENSMUSG00000087578	chr6	Ccdc142os	83106608	83107190	1083	-0.04981	0.36545	0.905015	0.936752	0.072255	0	17	25	21	12	26	25	28	23	37	24
ENSMUSG00000010054	chr9	Tusc2	1.08E+08	1.08E+08	1785	-0.02265	5.166875	0.90538	0.93706	0.040625	0	496	624	734	625	509	736	732	1004	826	805
ENSMUSG00000031398	chrX	Plxna3	74329066	74329215	7880	-0.05751	1.461261	0.905521	0.937135	0.191407	0	50	19	51	25	88	50	106	15	75	59
ENSMUSG00000018822	chr19	Sfrp5	42197971	42199031	1900	0.034561	2.612083	0.906135	0.937701	0.078482	0	94	60	70	151	122	80	152	128	246	128
ENSMUSG00000017764	chr2	Zswim1	1.65E+08	1.65E+08	2781	0.023398	3.054546	0.906264	0.937706	0.040607	0	102	103	145	162	176	167	171	231	212	180
ENSMUSG00000066058	chr4	Cldn19	1.19E+08	1.19E+08	4263	0.035047	1.723485	0.906275	0.937706	0.073376	0	45	31	56	64	72	60	73	97	106	45
ENSMUSG00000033703	chr8	Fuk	1.11E+08	1.11E+08	3838	-0.02914	2.390408	0.906482	0.937849	0.047498	0	65	71	106	83	115	88	142	86	142	141
ENSMUSG00000066306	chr7	Numa1	1.02E+08	1.02E+08	7195	-0.02108	5.886005	0.90657	0.937871	0.037008	0	864	746	1050	1040	1318	862	1200	1801	1617	1436
ENSMUSG00000035759	chr10	Bbs10	1.11E+08	1.11E+08	2753	0.036686	0.942197	0.906659	0.937893	0.063005	0	18	24	44	27	40	32	39	51	49	45
ENSMUSG00000017417	chr11	Plxdc1	97923238	97924607	4836	-0.03237	2.561255	0.906836	0.937962	0.059009	0	58	76	102	127	136	127	112	118	202	114
ENSMUSG00000028248	chr4	Pnisr	21847583	21848139	10187	0.022428	4.926075	0.906905	0.937962	0.038464	0	531	428	575	406	562	425	789	823	719	837
ENSMUSG00000050930	chr8	Map10	1.26E+08	1.26E+08	3542	0.034842	1.8747	0.906929	0.937962	0.080638	0	40	55	72	46	86	53	92	133	68	74
ENSMUSG00000027496	chr2	Aurka	1.72E+08	1.72E+08	2531	0.035806	2.941448	0.907113	0.938014	0.088488	0	113	116	176	101	119	174	173	66	254	232
ENSMUSG00000031516	chr8	Dctn6	34090420	34090842	2853	0.019146	4.856923	0.907115	0.938014	0.028519	0	399	462	500	486	545	537	684	762	712	689
ENSMUSG00000006127	chr11	Inpp5k	75630988	75631197	5728	-0.02377	4.897795	0.908174	0.939039	0.047738	0	464	413	520	515	593	429	588	1106	699	631
ENSMUSG00000048232	chr4	Fbxo10	45034247	45036082	4691	0.024316	2.960157	0.908258	0.939055	0.040898	0	101	91	152	115	190	120	198	161	232	206
ENSMUSG00000033174	chr6	Mgll	88724412	88724571	4868	0.03282	5.937607	0.908597	0.939336	0.094316	0	715	848	973	1421	1113	635	968	996	2174	2732

ENSMUSG00000035226	chr2	Rims4	1.64E+08	1.64E+08	4962	-0.04865	1.055032	0.908884	0.939562	0.100375	0	18	27	34	31	63	41	37	70	41	35
ENSMUSG00000022234	chr15	Cct5	31590800	31591055	2809	0.018866	7.481289	0.909248	0.939869	0.032589	0	2320	2475	3705	2665	3857	3528	4487	3418	4984	4577
ENSMUSG00000029059	chr4	Fam213b	1.55E+08	1.55E+08	1027	-0.02367	6.861043	0.909405	0.939961	0.050315	0	1405	2102	2493	1791	1983	3041	2370	1965	2984	2815
ENSMUSG00000036097	chr19	Fam178a	44931119	44931450	6880	-0.02109	4.639987	0.909748	0.940245	0.036492	0	362	299	474	429	552	357	606	776	611	548
ENSMUSG00000026277	chr1	Stk25	93619751	93622526	5812	0.019236	6.229052	0.909928	0.940361	0.033101	0	1077	1122	1478	1196	1345	1276	1874	2160	1838	1659
ENSMUSG00000022125	chr14	Cln5	1.03E+08	1.03E+08	2396	-0.01825	3.97864	0.910078	0.940445	0.031301	0	240	269	279	275	238	258	362	378	483	357
ENSMUSG00000003346	chr10	Abhd17a	80583654	80584063	1547	0.01808	5.547036	0.910312	0.94048	0.028812	0	667	658	921	842	785	950	981	1082	1344	1119
ENSMUSG00000026442	chr1	Nfasc	1.33E+08	1.33E+08	14145	0.042845	0.342517	0.910263	0.94048	0.091785	0	12	10	17	19	41	20	29	24	41	26
ENSMUSG00000062184	chrX	Hs6st2	51387212	51390361	7807	-0.02317	3.1676	0.910315	0.94048	0.044887	0	146	126	137	149	190	126	263	241	250	162
ENSMUSG00000021903	chr14	Galnt15	32028989	32030031	6326	0.044362	4.657132	0.910873	0.940986	0.178513	0	429	306	432	437	458	171	270	1580	505	493
ENSMUSG00000022329	chr15	Stk3	34875496	34876820	3237	0.02613	2.670808	0.911483	0.941546	0.045155	0	108	79	109	94	130	99	169	116	214	154
ENSMUSG00000079184	chr14	Mphosph8	56668248	56668564	3586	0.02018	4.086441	0.911617	0.941614	0.033424	0	231	241	351	264	323	280	362	533	460	360
ENSMUSG00000022377	chr15	Asap1	64086857	64089521	7482	0.021325	4.129901	0.912204	0.942106	0.035989	0	292	185	307	298	373	241	405	453	556	433
ENSMUSG00000051502	chr5	Ufsp1	1.37E+08	1.37E+08	1037	0.018432	4.524739	0.912229	0.942106	0.028893	0	366	326	452	355	399	453	608	535	581	504
ENSMUSG00000000751	chr11	Rpa1	75298166	75301403	5578	0.018165	6.114793	0.912674	0.942354	0.032437	0	1008	918	1292	1092	1483	1500	1462	1760	1729	1593
ENSMUSG00000018395	chr11	Kif3a	53567379	53567531	3586	-0.01978	3.035923	0.912622	0.942354	0.033302	0	108	126	155	131	165	127	201	204	225	191
ENSMUSG00000056019	chr8	Zfp709	71882068	71882208	4234	-0.03587	1.097149	0.91254	0.942354	0.057299	0	29	30	35	31	49	27	57	51	54	49
ENSMUSG00000026109	chr1	Tmeff2	50900647	50900782	6707	-0.03729	2.379805	0.912774	0.942387	0.090389	0	79	34	78	76	181	79	126	116	162	114
ENSMUSG00000031671	chr8	Setd6	95715915	95715963	1869	0.027804	2.944762	0.913069	0.942622	0.047381	0	93	144	98	140	149	142	189	152	228	190
ENSMUSG00000037526	chr14	Atg14	47540894	47543143	3450	0.031431	3.135312	0.913277	0.942766	0.077539	0	123	119	165	147	167	109	163	389	198	172
ENSMUSG00000035781	chr10	R3hdm4	79910053	79911139	1897	-0.01872	6.918486	0.913612	0.942974	0.034611	0	1842	1853	2220	1953	2271	2487	2482	3245	2762	2883
ENSMUSG00000048138	chr19	Dmrt2	25672420	25672758	2347	-0.02948	2.223274	0.913614	0.942974	0.056253	0	82	52	74	67	114	65	113	109	114	132
ENSMUSG00000041417	chr13	Pik3r1	1.02E+08	1.02E+08	10079	0.031517	5.715052	0.91376	0.943053	0.097646	0	801	748	853	809	1131	529	788	2607	1338	1022
ENSMUSG00000000093	chr11	Tbx2	85832551	85833501	3626	-0.02317	2.592962	0.913835	0.943061	0.054179	0	86	79	128	94	117	62	148	136	213	151
ENSMUSG00000096917	chr8	2500002B13Rik	57488054	57488193	2618	0.028583	2.489353	0.913957	0.943116	0.063316	0	81	84	132	70	90	135	157	118	108	118
ENSMUSG00000060441	chr7	Trim5	1.04E+08	1.04E+08	3690	0.055703	0.457136	0.914073	0.943166	0.182711	0	9	9	32	24	34	22	31	6	58	38
ENSMUSG00000020877	chr11	Scrn2	97029938	97030055	2050	0.024203	3.114273	0.914478	0.943513	0.045732	0	134	125	163	142	142	201	166	145	265	227
ENSMUSG00000072964	chrX	Bhlhb9	1.36E+08	1.36E+08	2978	0.02279	3.095217	0.914782	0.943757	0.04753	0	126	95	150	107	237	141	218	217	225	198
ENSMUSG00000049823	chr17	Zbtb12	34879483	34879524	2020	0.022038	2.625146	0.915262	0.944181	0.041858	0	85	79	96	104	144	124	124	143	162	159
ENSMUSG00000043885	chr9	Slc36a4	15709738	15709837	5563	-0.02534	3.130594	0.915351	0.944203	0.062815	0	159	83	157	127	213	93	226	180	303	233
ENSMUSG00000083626	chr7	Gm4459	1.4E+08	1.4E+08	468	0.033383	2.112101	0.915517	0.944304	0.070034	0	51	84	61	90	57	98	86	101	105	103
ENSMUSG00000029524	chr5	Sirt4	1.15E+08	1.15E+08	2398	-0.02401	2.954612	0.915948	0.944624	0.041277	0	107	128	144	144	117	165	177	167	214	159
ENSMUSG00000039043	chr7	2610034B18Rik	79925361	79926850	2277	-0.02466	2.798571	0.915964	0.944624	0.041972	0	89	100	157	101	137	133	177	136	217	136
ENSMUSG00000054863	chr15	Fam19a5	87625230	87625486	2575	0.032214	1.907193	0.916144	0.944739	0.049061	0	55	56	52	69	68	65	94	74	108	93
ENSMUSG00000021890	chr14	Eaf1	31495079	31495371	4238	0.017411	4.839291	0.9163	0.94476	0.028697	0	358	432	534	490	569	488	780	568	852	696
ENSMUSG00000028163	chr3	Nfkb1	1.36E+08	1.36E+08	4779	0.017324	4.902227	0.916291	0.94476	0.027131	0	411	444	538	540	542	487	725	742	910	677
ENSMUSG00000034300	chr18	Fam53c	34758906	34759144	4517	-0.01656	5.132211	0.916877	0.945284	0.027391	0	511	511	628	593	702	629	795	943	968	735
ENSMUSG00000018372	chr11	Cep95	1.07E+08	1.07E+08	4199	0.028054	2.382323	0.917312	0.945662	0.048694	0	80	61	94	97	92	76	124	157	132	118
ENSMUSG00000025525	chrX	Apool	1.12E+08	1.12E+08	3486	-0.01985	5.250038	0.917943	0.945806	0.042765	0	550	736	682	649	516	810	952	882	978	741
ENSMUSG00000030411	chr7	Nova2	18925888	18926164	8372	-0.03692	1.611019	0.917624	0.945806	0.082077	0	28	48	44	81	49	62	59	59	102	61
ENSMUSG00000032485	chr9	Scap	1.1E+08	1.1E+08	4275	0.018192	4.524176	0.917734	0.945806	0.031179	0	322	302	403	386	507	345	456	616	733	587
ENSMUSG00000032786	chr9	Alas1	1.06E+08	1.06E+08	4310	-0.02033	7.16453	0.917859	0.945806	0.046176	0	1793	2621	2470	3087	1915	2844	3023	3018	4399	3393
ENSMUSG00000037257	chr9	Aagab	63602655	63602771	2600	0.01688	4.420021	0.917931	0.945806	0.029153	0	271	304	418	345	450	412	579	398	609	511
ENSMUSG00000038866	chr1	Zcchc2	1.06E+08	1.06E+08	6774	0.022347	3.582661	0.917533	0.945806	0.046974	0	158	149	201	217	272	184	189	385	325	326
ENSMUSG00000084384	chr11	Gm12251	58392769	58393560	792	-0.02375	2.993279	0.917998	0.945806	0.050298	0	86	145	154	152	123	173	144	193	220	175
ENSMUSG00000100551	chr1	Gm19503	1.52E+08	1.52E+08	241	0.044617	0.962764	0.917712	0.945806	0.147992	0	17	31	66	27	12	39	45	55	35	42
ENSMUSG00000033099	chr15	Nol12	78934933	78935075	4317	0.020097	4.308667	0.91823	0.945974	0.042814	0	267	278	357	311	438	455	482	267	602	505
ENSMUSG00000001029	chr11	Icam2	1.06E+08	1.06E+08	1904	0.029646	3.136769	0.918456	0.946137	0.06732	0	111	170	130	199	92	182	210	170	253	210
ENSMUSG00000041890	chr5	Git2	1.15E+08	1.15E+08	7233	0.018545	4.472138	0.91869	0.946307	0.034654	0	316	274	373	413	473	350	513	687	603	461
ENSMUSG00000000805	chr11	Car4	84957786	84958050	1966	-0.03776	2.992401	0.918931	0.946415	0.154061	0	84	155	158	196	59	78	93	306	188	256
ENSMUSG00000095690	chr19	Rab11b-ps2	7398421	7399077	657	0.030955	2.150323	0.918864	0.946415	0.072738	0	61	49	73	93	85	60	100	162	92	99
ENSMUSG00000025495	chr7	Ptdss2	1.41E+08	1.41E+08	4875	-0.01727	4.227276	0.919184	0.946605	0.030554	0	258	286	361	323	339	321	373	533	563	389
ENSMUSG00000014959	chr2	Gorasp2	70661576	70661760	4145	0.01581	6.39053	0.919461	0.946722	0.02848	0	1107	1144	1651	1418	1710	1592	1837	1897	2470	2079
ENSMUSG00000027954	chr3	Efna1	89271733	89272604	1830	-0.01864	3.568994	0.919498	0.946722	0.040019	0	163	213	211	212	180	188	254	318	398	229
ENSMUSG00000028982	chr4	Slc25a33	1.5E+08	1.5E+08	1887	-0.02029	3.747768	0.919503	0.946722	0.04255	0	200	231	250	240	186	244	277	389	289	336
ENSMUSG00000054418	chr11	2900041M22Rik	1.18E+08	1.18E+08	1784	-0.06144	-0.12198	0.920006	0.94717	0.090149	0	17	12	20	6	15	9	23	20	21	22
ENSMUSG00000028614	chr4	Ndc1	1.07E+08	1.07E+08	4924	-0.01992	4.014084	0.920438	0.947439	0.03591	0	191	232	323	281	340	340	326	270	475	451
ENSMUSG00000033917	chr7	Gde1	1.19E+08	1.19E+08	1692	0.016013	5.392305	0.920542	0.947439	0.027816	0	645	594	751	679	813	804	925	850	1250	1112
ENSMUSG00000038957	chr9	Edc3	57708540	57708699	5804	-0.01785	4.057649	0.920339	0.947439	0.031342	0	250	226	362	257	303	278	332	443	424	450
ENSMUSG00000049904	chr11	Tmem17	22512088	22512583	1568	-0.02837	1.292099	0.92052	0.947439	0.053721	0	33	40	42	39	44	40	51	60	79	45
ENSMUSG00000053841	chr4	Txlna	1.3E+08	1.3E+08	5348	0.016182	4.815573	0.920643	0.947473	0.028093	0	408	381	511	408	647	494	682	601	855	693
ENSMUSG00000058301	chr8	Upf1	70331522	70332479	4616	-0.01601	5.520062	0.92087	0.947636	0.028247	0	654	619	845	734	1034	852	1144	976	1419	963
ENSMUSG00000030243	chr6	Recql	1.42E+08	1.42E+08	7510	-0.02649	2.785743	0.921116	0.947819	0.061628	0	94	93	145	100	148	109	146	89	244	216
ENSMUSG00000002343	chr8	Armc6	70220172	70220877	3262	0.020418	3.529433	0.921423	0.947899	0.043449	0	151	179	249	152	225	248	297	169	346	286
ENSMUSG00000027349	chr2	Fam98b	1.17E+08	1.17E+08	3390	-0.0164	4.466632	0.921466	0.947899	0.02903	0	290	350	434	387	389	423	541	417	672	516
ENSMUSG00000054252	chr5	Fgfr3	33721724	33721928	6907	0.039543	1.183543	0.921467	0.947899	0.066564	0	33	28	36	49	32	34	56	48	81	43

ENSMUSG00000097290	chr16	1300002E11Rik	21794347	21794446	3955	-0.028	2.197208	0.921323	0.947899	0.072517	0	70	70	99	76	61	97	94	56	145	129
ENSMUSG00000036040	chr2	Adamtsl2	27079379	27079573	7993	-0.02397	3.19145	0.922229	0.948612	0.050446	0	144	108	157	163	194	205	282	182	206	156
ENSMUSG00000021028	chr12	Mbip	56328306	56328799	1509	-0.02101	2.085938	0.923048	0.949326	0.045683	0	75	59	66	68	79	68	96	100	122	99
ENSMUSG00000062353	chr5	Gm15772	3236431	3236868	438	0.024866	2.331549	0.923061	0.949326	0.045397	0	66	79	74	98	90	96	116	95	152	125
ENSMUSG00000034614	chr11	Pik3ip1	3330401	3331004	4272	-0.04215	4.557827	0.923498	0.949493	0.220268	0	458	277	527	444	256	253	238	1527	249	399
ENSMUSG00000038195	chr11	Rilp	75510094	75510372	1583	0.016588	5.111466	0.923482	0.949493	0.034176	0	460	541	661	509	706	799	780	618	963	854
ENSMUSG00000069237	chr13	C78339	46669522	46670255	3827	-0.01592	4.964556	0.923447	0.949493	0.030375	0	487	430	587	517	597	498	762	895	829	651
ENSMUSG00000088609	chr13	Gm24187	9834469	9834525	57	0.032301	3.484352	0.923341	0.949493	0.126962	0	131	192	268	73	269	229	154	256	169	476
ENSMUSG00000074071	chr7	Fam169b	68273839	68273891	3074	0.048969	0.424977	0.923641	0.94957	0.12254	0	14	19	22	12	37	26	46	11	31	33
ENSMUSG00000032411	chr9	Tfdp2	96196275	96196560	14029	0.040898	5.593887	0.924839	0.950731	0.218944	0	733	697	826	761	951	454	509	3472	658	583
ENSMUSG00000079179	chr12	Rab10os	3235504	3235929	6144	0.02603	2.400832	0.925193	0.951025	0.060145	0	56	81	95	97	103	71	101	131	131	183
ENSMUSG00000029334	chr5	Prkg2	98929773	98932105	5369	-0.03988	0.879333	0.925554	0.951324	0.058619	0	22	26	35	26	40	38	35	40	41	45
ENSMUSG00000018995	chr7	Nars2	96951505	96951944	4213	-0.0211	2.85474	0.926063	0.951636	0.040622	0	82	130	142	110	138	135	172	164	210	149
ENSMUSG00000020042	chr10	Btbd11	85386814	85388478	10033	-0.03704	0.77542	0.925979	0.951636	0.072384	0	28	14	27	30	39	25	48	28	47	40
ENSMUSG00000024065	chr17	Ehd3	73804841	73805469	3658	-0.0305	2.532432	0.926002	0.951636	0.083891	0	51	54	144	125	121	96	97	198	151	116
ENSMUSG00000001435	chr10	Col18a1	77052178	77053407	7021	-0.02373	5.533217	0.926324	0.951816	0.074247	0	679	419	1020	629	1269	756	1568	593	1641	908
ENSMUSG00000097059	chr13	Fam120aos	48968287	48968604	1780	0.032555	1.853757	0.926376	0.951816	0.073502	0	59	53	67	68	39	62	71	116	83	82
ENSMUSG00000029279	chr5	Brdt	1.07E+08	1.07E+08	5115	0.029756	1.377222	0.926599	0.951975	0.057604	0	26	39	46	40	58	37	71	66	66	57
ENSMUSG00000037119	chr15	D15Ertd621e	58415468	58415777	5621	-0.01837	4.08138	0.926818	0.95213	0.041192	0	251	180	303	277	431	211	404	379	524	480
ENSMUSG00000044068	chr11	Zrsr1	22973215	22976496	3282	0.03572	3.379027	0.926913	0.952156	0.160797	0	168	158	164	173	179	136	152	632	142	141
ENSMUSG00000014353	chr2	Tmem87b	1.29E+08	1.29E+08	8395	-0.01924	4.322258	0.927239	0.95237	0.047606	0	299	261	382	336	407	254	424	730	464	455
ENSMUSG00000021868	chr14	Ppif	25694154	25694423	3641	0.018879	5.628835	0.927322	0.95237	0.048174	0	638	914	877	952	655	1219	1003	971	1481	1070
ENSMUSG00000037709	chr6	Fam13a	58932090	58935711	6328	-0.02506	3.860213	0.927534	0.95237	0.084516	0	218	135	296	296	287	134	195	362	530	515
ENSMUSG00000047412	chr9	Zbtb44	31030644	31030958	8857	-0.0204	5.095167	0.927513	0.95237	0.055778	0	524	491	602	589	660	589	626	1344	739	624
ENSMUSG00000052783	chr5	Grk4	34660379	34661004	4830	0.042824	0.162157	0.927357	0.95237	0.068912	0	12	16	18	20	18	24	29	24	27	16
ENSMUSG00000061118	chr5	Dnajc30	1.35E+08	1.35E+08	1661	0.016191	4.243651	0.927449	0.95237	0.029947	0	279	284	317	351	326	376	385	498	544	408
ENSMUSG00000024529	chr18	Lox	52516069	52519233	4810	-0.02875	6.419973	0.928239	0.952725	0.119147	0	1888	493	1853	828	2319	1044	2299	3060	2100	1495
ENSMUSG00000024975	chr19	Pdcd4	53892231	53892456	2556	0.017974	3.896113	0.928081	0.952725	0.033147	0	268	194	251	248	258	244	325	351	395	433
ENSMUSG00000053536	chr19	Cstf2t	31082841	31086590	3750	0.014556	4.712774	0.9283	0.952725	0.026671	0	356	409	472	412	528	489	670	604	763	551
ENSMUSG00000054737	chrX	Zfp182	21028939	21031652	5733	0.031954	0.96321	0.928115	0.952725	0.055742	0	27	26	38	23	40	30	47	49	53	41
ENSMUSG00000056131	chr9	Pgm3	86554377	86555403	4487	-0.02811	2.247437	0.928334	0.952725	0.083565	0	79	45	87	67	121	85	138	50	151	120
ENSMUSG00000072847	chr11	A530017D24Rik	61864568	61866225	2614	0.029038	2.144539	0.928336	0.952725	0.04981	0	61	72	71	72	80	69	87	127	139	94
ENSMUSG00000103041	chr3	RP24-372I24.4	65957758	65962036	4279	-0.03808	0.666116	0.928362	0.952725	0.095702	0	25	20	20	28	33	17	26	60	35	35
ENSMUSG00000028799	chr4	Zfp362	1.29E+08	1.29E+08	3052	-0.01664	3.698948	0.928548	0.952846	0.03176	0	202	152	224	246	265	227	314	327	382	256
ENSMUSG00000021606	chr13	Ndufs6	73319874	73320060	629	-0.01777	7.139751	0.92883	0.952853	0.046446	0	2026	2589	2910	2209	1957	3352	3002	3065	3259	3367
ENSMUSG00000025170	chr11	Rab40b	1.21E+08	1.21E+08	2008	0.015451	4.493603	0.928762	0.952853	0.029275	0	331	322	493	335	387	390	602	522	652	485
ENSMUSG00000047067	chr1	Dusp28	92906981	92907423	1314	0.017758	4.327117	0.928821	0.952853	0.043144	0	286	339	382	315	324	470	407	578	411	428
ENSMUSG00000051510	chr11	Mafg	1.21E+08	1.21E+08	5613	-0.01936	6.102362	0.928715	0.952853	0.054139	0	962	1093	1379	1124	1205	1120	1257	2628	1518	1403
ENSMUSG00000045854	chr4	Lyrm2	32800253	32800335	1140	0.017218	3.626477	0.929353	0.953319	0.030929	0	191	190	242	193	195	243	311	252	352	282
ENSMUSG00000026939	chr2	Tmem141	25620067	25620530	1122	-0.01675	3.445705	0.929739	0.953503	0.034277	0	155	186	211	175	174	220	236	221	286	286
ENSMUSG00000036188	chr12	Ankmy2	36157124	36157423	2446	-0.01947	3.28124	0.929714	0.953503	0.042424	0	113	131	187	195	192	174	237	149	303	265
ENSMUSG00000056820	chr8	Tsnax	1.25E+08	1.25E+08	2391	-0.01632	6.554406	0.929621	0.953503	0.039327	0	1412	1432	1833	1515	1680	1826	1964	2921	2053	2016
ENSMUSG00000020477	chr11	Mrps24	5703983	5704732	1466	-0.01527	5.374645	0.929902	0.953599	0.033372	0	599	674	787	749	639	913	910	887	1117	941
ENSMUSG00000085095	chr7	Gm15635	99661439	99661661	1056	0.038619	0.645906	0.93002	0.953649	0.105217	0	12	26	22	27	35	30	20	51	27	43
ENSMUSG00000046768	chr12	Rhoj	75308322	75309001	6484	-0.01728	4.796142	0.930145	0.953707	0.040313	0	442	303	493	480	636	462	670	860	720	509
ENSMUSG00000081219	chr2	Bambi-ps1	1.22E+08	1.22E+08	592	0.044414	0.193629	0.93067	0.954175	0.07645	0	24	13	17	14	17	14	24	27	28	32
ENSMUSG00000027351	chr2	Spred1	1.17E+08	1.17E+08	6784	-0.01659	4.356562	0.931033	0.954405	0.038222	0	332	234	348	307	515	339	506	368	711	487
ENSMUSG00000031982	chr8	Arv1	1.25E+08	1.25E+08	1165	0.038153	0.846329	0.930979	0.954405	0.077177	0	31	20	31	26	32	32	27	36	43	63
ENSMUSG00000027884	chr3	Clcc1	1.09E+08	1.09E+08	4368	-0.02127	4.958062	0.931132	0.954436	0.068559	0	482	465	595	505	553	428	629	1344	652	538
ENSMUSG00000025825	chr5	Iscu	1.14E+08	1.14E+08	2176	0.016435	5.99632	0.931298	0.954536	0.040903	0	960	1072	1181	1096	916	1299	1270	1832	1533	1480
ENSMUSG00000027835	chr3	Pdcd10	75516490	75517601	2939	-0.01471	3.459048	0.931949	0.955132	0.034475	0	180	186	205	159	175	181	252	283	311	248
ENSMUSG00000025821	chr6	Zfp282	47877204	47877836	7663	-0.0185	3.763062	0.9324	0.955524	0.046138	0	200	183	243	261	247	221	295	480	295	267
ENSMUSG00000075514	chr2	Gm13375	20969054	20969383	854	-0.03081	1.023768	0.932719	0.95578	0.060854	0	20	30	41	35	39	35	39	55	45	49
ENSMUSG00000020078	chr10	Vps26a	62454843	62456858	3252	-0.01332	5.438033	0.93286	0.955853	0.027277	0	633	654	787	707	852	813	901	1078	1142	1089
ENSMUSG00000074218	chr7	Cox7a1	30184171	30184245	364	-0.01816	7.863034	0.932983	0.955909	0.055333	0	3114	4643	4508	4097	2827	5720	4995	5295	5761	4713
ENSMUSG00000021537	chr13	Cetn3	81783292	81783357	999	-0.01375	4.169192	0.933078	0.955935	0.031485	0	286	301	305	266	332	274	450	480	474	417
ENSMUSG00000046792	chr7	Zfp787	6131489	6133171	1899	-0.01401	4.38288	0.933222	0.956012	0.026793	0	282	306	409	376	374	394	488	519	545	463
ENSMUSG00000009630	chr8	Ppp2cb	33599621	33600018	1826	-0.01347	4.950731	0.933915	0.95651	0.028182	0	452	431	602	579	522	580	663	705	847	792
ENSMUSG00000020462	chr11	Cfap36	29221532	29221985	2744	0.01686	3.139332	0.933788	0.95651	0.034129	0	125	116	172	128	190	133	225	213	257	208
ENSMUSG00000062081	chr14	Gm6055	48079375	48079752	378	0.032282	1.97627	0.933897	0.95651	0.111327	0	57	63	68	67	59	63	50	180	80	77
ENSMUSG00000013629	chr5	Cad	31054780	31055036	8164	0.019555	3.917155	0.934351	0.956814	0.059243	0	213	144	289	219	415	222	372	221	597	407
ENSMUSG00000042167	chr13	Papd4	93147400	93147665	1873	0.017833	3.31681	0.934293	0.956814	0.037503	0	157	123	158	181	202	152	241	292	275	209
ENSMUSG00000030064	chr6	Frmd4b	97286867	97288480	11521	-0.01631	4.218855	0.934467	0.956862	0.034941	0	248	213	387	261	486	295	469	421	520	467
ENSMUSG00000029103	chr5	Lrpap1	35091490	35093386	4127	-0.01343	5.824371	0.934841	0.957175	0.030069	0	887	726	1102	810	1270	955	1359	1297	1632	1386
ENSMUSG00000003923	chr10	Tfam	71225464	71228699	4438	0.015156	5.244669	0.935351	0.957626	0.038726	0	522	572	790	617	644	717	831	1200	989	686
ENSMUSG00000038383	chr2	Pigu	1.55E+08	1.55E+08	9326	0.014148	4.563474	0.935613	0.957753	0.029354	0	336	383	474	387	366	460	556	537	668	543

ENSMUSG00000062397	chr15	Zfp706	36997031	37000923	4413	0.013035	5.950786	0.93556	0.957753	0.030126	0	873	865	1140	943	1359	1269	1487	1232	1772	1476
ENSMUSG00000031095	chrX	Cul4b	38533274	38533728	3873	-0.01971	3.84646	0.93593	0.957936	0.063512	0	214	199	289	233	271	171	292	596	328	283
ENSMUSG00000045969	chr8	Ing1	11556066	11557045	2813	0.019276	3.897378	0.935895	0.957936	0.057475	0	222	204	256	225	329	216	274	596	403	264
ENSMUSG00000024600	chr18	Slc27a6	58556257	58556944	2485	-0.05347	-0.28093	0.936148	0.958088	0.231285	0	25	5	12	2	17	10	30	10	26	9
ENSMUSG00000045968	chr1	Teddm2	1.54E+08	1.54E+08	4905	-0.03739	1.709332	0.936952	0.95884	0.183268	0	64	43	63	51	44	32	45	184	46	58
ENSMUSG00000021037	chr12	Ahsa1	87266746	87266921	1347	0.013052	6.900731	0.937304	0.959129	0.03239	0	1552	1803	2666	1854	2108	2436	2743	2769	3242	2761
ENSMUSG00000025453	chr13	Nnt	1.19E+08	1.19E+08	7037	-0.01805	6.215671	0.937427	0.959184	0.062022	0	988	1131	1101	1725	1254	1096	1343	2798	1939	1491
ENSMUSG00000038860	chr2	Garnl3	32986224	32986830	12352	0.035453	0.345881	0.938327	0.960034	0.083187	0	20	8	18	21	31	17	30	29	27	36
ENSMUSG00000024069	chr17	Slc30a6	74395608	74395668	2171	0.018765	2.736287	0.938693	0.960338	0.04192	0	100	106	126	87	125	122	148	128	189	188
ENSMUSG00000029920	chr6	Smarcad1	65042667	65042961	5099	-0.01537	3.172714	0.939114	0.960698	0.039433	0	134	103	172	159	189	120	240	236	257	199
ENSMUSG00000037787	chr12	Apopt1	1.12E+08	1.12E+08	3945	-0.01332	4.889112	0.93926	0.960776	0.032077	0	406	497	566	504	493	643	608	636	803	719
ENSMUSG00000035765	chr18	Dym	75018772	75018984	2471	-0.01679	5.687494	0.939864	0.961271	0.055681	0	738	723	931	1023	904	929	847	1935	1059	1138
ENSMUSG00000086298	chr11	Gm11716	1.07E+08	1.07E+08	470	0.019542	3.580284	0.939883	0.961271	0.061123	0	199	177	187	260	142	243	225	390	271	249
ENSMUSG00000054733	chr14	Msra	64122623	64123353	1862	0.013724	4.314854	0.940849	0.962187	0.033794	0	254	295	384	387	327	393	448	354	579	555
ENSMUSG00000045377	chr11	Tmem88	69396519	69397881	1582	-0.01888	3.321377	0.940922	0.962192	0.063092	0	103	154	188	260	124	188	252	168	286	259
ENSMUSG00000006471	chr2	Ndor1	25244821	25247854	5835	-0.02024	2.991571	0.941232	0.962366	0.056019	0	124	85	179	112	171	96	163	251	215	200
ENSMUSG00000018481	chr11	Appbp2	85187262	85191899	6463	-0.01267	4.332523	0.941195	0.962366	0.026183	0	285	257	374	332	454	363	498	439	577	466
ENSMUSG00000002661	chr17	Alkbh7	56997339	56997567	1029	0.015798	3.563351	0.941415	0.962483	0.04292	0	159	204	229	187	189	275	271	186	327	306
ENSMUSG00000030663	chr7	1110004F10Rik	1.16E+08	1.16E+08	1495	0.011358	5.419996	0.94162	0.96262	0.025701	0	604	618	847	676	825	776	1003	1005	1264	988
ENSMUSG00000035443	chr9	Thyn1	26999677	26999765	959	0.014076	3.93086	0.942106	0.962976	0.036242	0	192	247	299	234	292	305	406	234	451	387
ENSMUSG00000039908	chr11	Slc26a11	1.19E+08	1.19E+08	3610	0.02113	2.584655	0.942056	0.962976	0.06032	0	98	82	123	63	126	72	156	178	158	140
ENSMUSG00000096199	chr12	Ptrhd1	4234027	4234278	4013	-0.01545	3.024451	0.9422	0.963	0.042392	0	104	154	144	130	138	157	215	174	188	194
ENSMUSG00000033126	chr10	Ybey	76459569	76463319	4520	0.01649	3.001889	0.942741	0.963482	0.044761	0	130	129	136	124	131	179	180	211	182	163
ENSMUSG00000018287	chr11	Spag7	70663771	70664220	1480	-0.01211	6.476627	0.943893	0.964242	0.033061	0	1124	1409	1759	1489	1715	1853	1877	2327	2214	1978
ENSMUSG00000021356	chr13	Irf4	30749226	30749295	4715	0.022457	1.595272	0.943972	0.964242	0.080812	0	48	21	52	50	76	43	57	87	74	85
ENSMUSG00000021567	chr13	Nkd2	73818534	73821537	4728	0.034016	1.41949	0.943685	0.964242	0.175671	0	47	18	53	26	74	36	110	82	54	22
ENSMUSG00000024360	chr18	Etf1	34902785	34905070	3709	0.011658	6.813041	0.943582	0.964242	0.031374	0	1485	1785	2250	1802	2039	2077	2451	3015	2952	2667
ENSMUSG00000026110	chr1	Mgat4a	37439340	37444685	12881	-0.01455	3.062062	0.9438	0.964242	0.042739	0	102	115	162	182	134	123	215	177	261	199
ENSMUSG00000055720	chr9	Ubl7	57910986	57911059	1364	0.011896	5.554111	0.943755	0.964242	0.03126	0	662	727	837	802	866	905	1003	1355	1195	1014
ENSMUSG00000092241	chr17	Gm20522	35122738	35123238	784	0.024905	1.240564	0.943918	0.964242	0.068687	0	32	38	45	41	30	47	43	69	65	42
ENSMUSG00000031209	chrX	Heph	96455359	96455713	7662	-0.02321	1.365727	0.944321	0.964527	0.118011	0	33	30	21	55	72	26	44	56	83	86
ENSMUSG00000009535	chr18	Rnmt	68300355	68300425	7339	-0.01559	4.988102	0.944998	0.965148	0.055691	0	500	457	609	480	613	509	603	1255	657	630
ENSMUSG00000024982	chr19	Zdhhc6	55298301	55298888	2284	0.010899	4.582822	0.94508	0.96516	0.024391	0	338	341	434	403	478	433	567	557	672	579
ENSMUSG00000020585	chr12	Laptm4a	8921664	8922294	1773	-0.01128	8.484506	0.945261	0.965273	0.031918	0	5707	5133	7182	5038	7030	7196	9214	7822	9459	7788
ENSMUSG00000011427	chr7	Zfp790	29816072	29816289	4525	0.021795	3.184317	0.945714	0.965665	0.093358	0	123	151	153	140	177	105	165	432	217	148
ENSMUSG00000045435	chr5	Tmem60	20882191	20882655	1147	-0.01205	3.84284	0.945884	0.965767	0.031818	0	233	222	272	243	213	286	327	333	361	341
ENSMUSG00000022421	chr15	Nptxr	79786352	79789916	5169	-0.02575	1.860599	0.946231	0.96605	0.099762	0	60	35	50	39	121	51	64	71	139	95
ENSMUSG00000043572	chr4	Pars2	1.07E+08	1.07E+08	3094	-0.01789	1.874602	0.946374	0.966125	0.057496	0	48	68	63	50	70	51	83	71	131	88
ENSMUSG00000075704	chr16	Txnrd2	18426417	18426559	3359	-0.01321	4.075027	0.946786	0.966474	0.038401	0	181	314	333	264	317	327	351	307	523	451
ENSMUSG00000002372	chr17	Ranbp3	56673225	56673411	2511	0.010337	5.52307	0.94688	0.966499	0.02723	0	578	704	903	728	935	900	1023	1076	1294	1084
ENSMUSG00000052605	chr7	Isoc2b	4844959	4845365	1297	-0.02415	2.345769	0.947057	0.966608	0.104456	0	82	107	113	53	56	118	122	57	135	141
ENSMUSG00000030051	chr6	Aplf	87628429	87630175	3278	-0.01774	2.048053	0.947142	0.966624	0.045147	0	59	57	78	59	89	65	87	110	120	91
ENSMUSG00000024991	chr19	Eif3a	60761116	60762304	5176	-0.01478	7.241295	0.947251	0.966664	0.058653	0	1975	2108	2869	2565	3326	1958	3067	6019	3874	2823
ENSMUSG00000041476	chrX	Smpx	1.58E+08	1.58E+08	2275	0.011556	8.283787	0.947417	0.966762	0.036417	0	4321	5024	6648	4992	4844	6544	7617	7604	7454	6919
ENSMUSG00000079511	chr6	Ccdc142	83101617	83102638	3763	-0.01198	5.722364	0.947535	0.966811	0.035958	0	690	917	1043	870	882	1225	1163	1136	1349	1172
ENSMUSG00000022220	chr14	Adcy4	55769058	55769287	3500	-0.01374	3.07542	0.948046	0.967261	0.049999	0	114	123	120	199	139	116	182	217	251	218
ENSMUSG00000039046	chr2	Usp6nl	6322667	6322954	8059	0.016923	3.014724	0.948704	0.967842	0.056414	0	142	80	119	132	196	103	169	229	261	196
ENSMUSG00000045757	chr7	Zfp764	1.27E+08	1.27E+08	2508	-0.02112	1.408277	0.948755	0.967842	0.066249	0	43	29	38	42	65	44	76	64	52	59
ENSMUSG00000014077	chr2	Chp1	1.2E+08	1.2E+08	3499	0.011722	6.556814	0.94883	0.967847	0.037874	0	1315	1382	1717	1636	1788	1472	1710	2849	2510	2563
ENSMUSG00000031505	chr8	Carkd	11497506	11497626	3694	-0.0111	4.694724	0.949049	0.967999	0.029638	0	343	387	545	451	443	470	572	695	642	616
ENSMUSG00000004771	chr9	Rab11a	64715299	64716988	2992	-0.00982	5.636167	0.949433	0.96814	0.026725	0	730	731	961	794	953	896	1073	1067	1459	1318
ENSMUSG00000028099	chr3	Polr3c	96711490	96712060	3386	-0.01115	4.438568	0.94933	0.96814	0.02779	0	267	309	481	361	411	402	489	465	659	512
ENSMUSG00000032462	chr9	Pik3cb	99036654	99039850	7193	-0.0124	3.100408	0.949435	0.96814	0.051252	0	109	120	161	184	138	109	168	192	270	269
ENSMUSG00000036206	chr1	Sh3bp4	89070415	89070597	5112	0.013199	2.86058	0.949467	0.96814	0.038081	0	93	92	129	135	153	105	184	181	206	175
ENSMUSG00000038982	chr13	Bloc1s5	38602709	38604028	1766	0.01473	3.49886	0.949543	0.968146	0.044175	0	170	195	199	177	180	249	277	169	315	299
ENSMUSG00000003228	chr19	Grk5	60889749	60890631	3165	0.018125	3.005625	0.949683	0.968218	0.059675	0	92	123	139	138	172	124	170	110	287	263
ENSMUSG00000051413	chr2	Plagl2	1.53E+08	1.53E+08	5735	-0.0168	3.122757	0.949872	0.968323	0.065604	0	100	104	136	122	285	111	176	222	297	219
ENSMUSG00000099647	chr7	Gm5776	54412158	54412478	321	-0.01843	1.55727	0.949926	0.968323	0.055165	0	36	51	44	49	59	48	71	68	94	53
ENSMUSG00000034928	chr13	Rnf44	54679399	54681811	5202	-0.01028	4.996354	0.950073	0.968401	0.029685	0	418	455	521	612	678	495	793	774	995	700
ENSMUSG00000018848	chr11	Rars	35808381	35808591	3228	-0.01	5.943456	0.950813	0.969084	0.028326	0	841	913	1158	1021	1243	1235	1415	1309	1682	1493
ENSMUSG00000022837	chr16	Iqcb1	36828385	36828492	5387	0.017654	1.992724	0.951096	0.969256	0.05974	0	59	56	81	55	72	60	89	132	87	88
ENSMUSG00000030087	chr6	Klf15	90462576	90462725	2527	-0.02514	4.557611	0.951127	0.969256	0.188774	0	355	291	475	473	385	193	222	1474	342	487
ENSMUSG00000037750	chr11	Fam222b	78094660	78094791	3490	-0.01207	3.14416	0.951191	0.969256	0.038403	0	135	117	165	171	144	157	212	174	301	186
ENSMUSG00000028576	chr4	Ift74	94614491	94614651	2656	0.018147	2.802954	0.951578	0.969579	0.065062	0	98	105	128	119	120	107	163	265	133	136
ENSMUSG00000026425	chr1	Srgap2	1.31E+08	1.31E+08	12560	0.010411	4.503884	0.951772	0.969633	0.031032	0	270	308	390	413	526	382	577	447	667	601
ENSMUSG00000033208	chr10	S100b	76253853	76253958	1484	0.027701	1.18901	0.951738	0.969633	0.111149	0	31	21	42	32	58	37	44	22	103	59

ENSMUSG00000074264	chr3	Amy1	1.14E+08	1.14E+08	3446	-0.02088	3.631112	0.952286	0.970085	0.134692	0	159	194	238	245	195	119	127	199	349	674
ENSMUSG00000052934	chr8	Fbxo31	1.22E+08	1.22E+08	5482	0.018439	6.879384	0.953136	0.97088	0.116013	0	1618	1582	2207	2025	2412	1611	1685	6401	1942	2064
ENSMUSG00000024800	chr19	Rpp30	36083716	36083818	1155	0.013506	3.213008	0.953258	0.970933	0.038285	0	130	147	202	138	144	188	198	241	251	194
ENSMUSG00000015711	chr3	Prune	95253674	95255427	3618	-0.0126	6.349333	0.953683	0.971294	0.053999	0	1128	1187	1593	1635	1272	1410	1576	2989	1716	1703
ENSMUSG00000032192	chr9	Gnb5	75311395	75311520	1188	0.013414	3.644245	0.953918	0.971462	0.040606	0	170	199	224	243	188	232	311	197	379	347
ENSMUSG00000023047	chr15	Amhr2	1.02E+08	1.02E+08	2002	0.021804	2.236653	0.954613	0.972098	0.122674	0	42	103	95	78	61	140	62	62	171	102
ENSMUSG00000051065	chr16	Mb21d2	28826176	28829009	3080	0.017317	3.067437	0.955126	0.972549	0.069942	0	123	101	167	136	167	116	173	341	218	132
ENSMUSG00000016534	chrX	Lamp2	38401357	38402281	9552	0.011051	6.88725	0.955249	0.972603	0.044533	0	1872	1466	2163	1776	2657	1571	2534	3940	3429	2609
ENSMUSG00000028138	chr3	Adh5	1.38E+08	1.38E+08	2801	-0.00909	5.899045	0.955835	0.973128	0.0305	0	801	979	1076	1012	1118	1069	1237	1572	1628	1445
ENSMUSG00000093571	chr7	Gm24757	30311525	30311895	371	0.020791	1.833095	0.956062	0.973288	0.049252	0	52	58	67	50	59	61	91	67	100	91
ENSMUSG00000078851	chr11	Hist3h2a	58954685	58956830	2146	0.010429	3.933767	0.956407	0.973567	0.043925	0	198	229	312	246	285	384	443	275	336	302
ENSMUSG00000048897	chr7	Zfp710	80024814	80024986	4803	-0.01096	4.42331	0.956556	0.973647	0.039111	0	271	291	343	410	496	387	504	332	684	606
ENSMUSG00000034850	chr2	Tmem127	1.27E+08	1.27E+08	4811	-0.00895	5.817635	0.956651	0.973672	0.03051	0	860	763	974	982	1153	901	1316	1564	1478	1332
ENSMUSG00000033809	chr16	Alg3	20605451	20605717	1451	0.011954	3.775572	0.956938	0.973894	0.05165	0	173	189	254	229	299	311	328	160	454	344
ENSMUSG00000057649	chr13	Brd9	73937838	73937945	2406	0.010982	3.763226	0.957018	0.973902	0.036384	0	183	197	251	228	268	246	422	219	380	321
ENSMUSG00000001930	chr6	Vwf	1.26E+08	1.26E+08	16064	-0.01103	4.985626	0.957874	0.974702	0.052517	0	386	462	565	709	528	417	586	618	1318	874
ENSMUSG00000060279	chr7	Ap2a1	44900373	44900815	4301	0.008284	6.281845	0.958206	0.974968	0.028516	0	1031	1082	1391	1401	1617	1476	1782	1810	2322	1746
ENSMUSG00000002052	chr11	Supt6	78206746	78207769	7095	-0.00976	5.801841	0.95847	0.974982	0.038197	0	783	671	1137	954	1187	835	1256	1773	1527	1148
ENSMUSG00000026578	chr1	Ccdc181	1.64E+08	1.64E+08	1909	-0.01335	2.81131	0.958291	0.974982	0.04196	0	109	122	135	94	116	128	164	176	175	160
ENSMUSG00000027582	chr2	Zgpat	1.81E+08	1.81E+08	5624	-0.00877	4.312181	0.958501	0.974982	0.027194	0	273	301	391	278	426	325	465	455	572	506
ENSMUSG00000037958	chr11	Ccdc55	77044292	77046754	3628	0.010015	3.891218	0.958428	0.974982	0.033193	0	222	211	268	226	304	260	307	461	375	323
ENSMUSG00000040269	chr3	Mrps28	8802146	8802414	783	-0.01041	5.718509	0.959012	0.97543	0.042837	0	747	890	1082	754	920	1352	1203	1065	1157	1184
ENSMUSG00000036918	chr17	Ttc7	87282886	87283410	6315	-0.0115	4.849935	0.959214	0.975564	0.050348	0	312	379	591	511	669	489	695	388	900	918
ENSMUSG00000021520	chr13	Uqcrb	66900617	66900826	876	0.009547	8.121346	0.960287	0.976583	0.043239	0	3939	5128	5181	4728	3839	6437	6230	6309	6874	6278
ENSMUSG00000037845	chr9	Fdxacb1	50768236	50768455	3256	-0.01068	2.537022	0.960725	0.976885	0.043469	0	77	102	101	88	109	108	150	107	150	149
ENSMUSG00000097039	chr15	Pvt1	62037986	62038201	6996	0.015655	1.207085	0.960684	0.976885	0.064409	0	27	29	53	33	44	45	44	41	58	71
ENSMUSG00000031950	chr8	Gabarapl2	1.12E+08	1.12E+08	2325	0.008629	5.804656	0.961238	0.977199	0.035945	0	770	850	1157	863	1020	1067	1248	1664	1236	1260
ENSMUSG00000057177	chr7	Gsk3a	25228258	25228918	2260	-0.00804	6.362584	0.961245	0.977199	0.031285	0	1217	1199	1475	1506	1473	1516	1631	2155	2261	2020
ENSMUSG00000094686	chr4	Ccl21a	42772860	42773283	870	-0.01382	3.909639	0.96115	0.977199	0.064911	0	197	237	341	223	260	448	196	321	425	299
ENSMUSG00000022468	chr15	Endou	97711019	97712169	2718	-0.01873	-0.19978	0.962106	0.977858	0.124689	0	11	12	13	22	6	7	14	27	20	23
ENSMUSG00000023026	chr15	Dip2b	1E+08	1E+08	9553	0.008057	3.872887	0.962064	0.977858	0.029232	0	170	193	288	256	325	244	384	315	418	358
ENSMUSG00000047261	chr16	Gap43	42248442	42249114	1523	0.025388	-0.22078	0.962067	0.977858	0.132851	0	11	6	10	13	24	17	24	5	29	15
ENSMUSG00000031681	chr8	Smad1	79338395	79339792	5814	0.009336	4.134785	0.962467	0.97813	0.033013	0	194	302	307	304	353	315	412	391	591	362
ENSMUSG00000032415	chr9	Ube2cbp	86307306	86307876	1790	-0.02181	1.235529	0.962797	0.97813	0.07077	0	24	34	48	33	54	47	72	36	54	51
ENSMUSG00000034442	chr12	Trmt5	73280410	73280632	1669	-0.01231	2.615925	0.962775	0.97813	0.043755	0	91	87	118	91	121	104	154	99	192	161
ENSMUSG00000044982	chr18	Sft2d3	31909094	31911903	2810	-0.01731	1.212104	0.962554	0.97813	0.071797	0	33	39	46	36	31	42	52	72	51	39
ENSMUSG00000054967	chr15	Zfp647	76910851	76912175	1608	-0.03339	-0.07946	0.962659	0.97813	0.104402	0	8	14	10	20	20	8	21	32	21	17
ENSMUSG00000081600	chr11	Gm12286	63312310	63313311	1002	0.024726	1.038142	0.962753	0.97813	0.096032	0	32	46	26	26	28	52	38	40	43	53
ENSMUSG00000035459	chr10	Stab2	86841198	86841658	8757	0.025355	1.882888	0.962883	0.978145	0.213727	0	64	69	61	56	39	42	37	224	55	63
ENSMUSG00000031536	chr8	Polb	22628119	22628369	1227	0.008442	5.328901	0.962992	0.978184	0.034481	0	544	696	848	601	634	790	999	1018	996	865
ENSMUSG00000015474	chr17	Ppt2	34616662	34617487	2614	0.007411	5.211472	0.963336	0.97839	0.026725	0	565	523	710	569	719	707	819	884	1019	898
ENSMUSG00000062591	chr17	Tubb4a	57080066	57081747	2228	0.013741	1.519822	0.963318	0.97839	0.125486	0	39	17	36	45	102	64	66	38	82	73
ENSMUSG00000074622	chr2	Mafb	1.6E+08	1.6E+08	3363	0.012027	5.534395	0.963744	0.978733	0.072817	0	815	559	482	1143	795	756	1112	713	1921	1083
ENSMUSG00000025204	chr19	Ndufb8	44548572	44550220	3146	0.008522	8.424934	0.963947	0.978868	0.041979	0	4689	6133	6976	5733	4768	7916	7466	7317	8956	8092
ENSMUSG00000033039	chr15	Micall1	79108972	79109429	6701	0.008135	4.771709	0.964108	0.978959	0.029064	0	370	363	497	494	562	393	683	626	820	718
ENSMUSG00000050295	chr13	Foxc1	31806691	31810643	3953	0.054804	0.027427	0.964567	0.979353	0.100011	0	13	11	15	23	13	10	19	32	36	15
ENSMUSG00000028681	chr4	Ptch2	1.17E+08	1.17E+08	5974	-0.02689	0.856444	0.964662	0.979378	0.152337	0	17	14	16	45	56	12	42	44	57	49
ENSMUSG00000069793	chr11	Slfn9	82979629	82981986	4726	0.026104	0.698957	0.964798	0.979444	0.196853	0	10	20	31	18	52	34	46	6	61	34
ENSMUSG00000021377	chr13	Dek	47084775	47086079	3089	0.007603	5.049342	0.965132	0.979496	0.031061	0	438	479	632	561	658	556	763	983	889	689
ENSMUSG00000034206	chr16	Polq	37011786	37012059	9685	0.027477	0.051265	0.965117	0.979496	0.099272	0	15	7	11	24	21	18	25	12	28	28
ENSMUSG00000054203	chr1	Ifi205	1.74E+08	1.74E+08	4177	0.009012	2.69504	0.96508	0.979496	0.074662	0	110	77	161	72	115	179	108	146	143	150
ENSMUSG00000097493	chr15	9930014A18Rik	60822271	60824783	7043	-0.02293	-0.02847	0.964938	0.979496	0.11245	0	15	16	9	20	13	7	18	33	23	23
ENSMUSG00000038324	chr2	Trpc4ap	1.56E+08	1.56E+08	8753	-0.00779	6.958157	0.96529	0.979584	0.037079	0	1747	1826	2268	2235	2344	2108	2430	3917	3284	2764
ENSMUSG00000073236	chr2	2500004C02Rik	1.53E+08	1.53E+08	2147	0.024731	-0.02476	0.965449	0.979674	0.120865	0	3	17	23	16	15	9	26	25	20	25
ENSMUSG00000001440	chr11	Kpnb1	97159714	97162681	6590	0.007022	7.078259	0.96554	0.979695	0.030749	0	1703	1908	2483	2168	3148	2321	3065	3043	4109	3427
ENSMUSG00000014243	chr11	Zswim7	62267224	62267606	732	-0.00925	3.932693	0.965703	0.979788	0.040169	0	231	250	273	264	241	328	285	442	335	349
ENSMUSG00000095115	chr7	Itpripl2	1.18E+08	1.18E+08	6862	-0.00799	5.099481	0.965933	0.97995	0.036789	0	545	376	559	587	833	506	959	747	1037	796
ENSMUSG00000031217	chrX	Efnb1	99136130	99137013	3452	0.010847	3.421743	0.966116	0.980063	0.056729	0	101	131	169	277	218	152	266	223	316	308
ENSMUSG00000035495	chr4	Tstd2	46114746	46117083	5570	-0.00746	3.820042	0.966383	0.98019	0.030864	0	172	205	254	270	282	224	324	304	492	321
ENSMUSG00000035863	chr10	Palm	79793572	79793740	2651	-0.00971	4.254421	0.966327	0.98019	0.050663	0	269	216	312	387	426	246	368	657	464	496
ENSMUSG00000067719	chr5	Gm10221	24581458	24581879	422	-0.00835	4.61833	0.966507	0.980244	0.04683	0	342	492	362	468	340	478	503	688	663	508
ENSMUSG00000004561	chr14	Mettl17	51884842	51885023	3970	0.013509	3.192206	0.966672	0.980328	0.059484	0	143	150	158	156	135	183	237	110	260	273
ENSMUSG00000023051	chr15	Tarbp2	1.03E+08	1.03E+08	4549	0.007726	4.419434	0.966731	0.980328	0.029253	0	297	358	419	333	360	429	531	442	592	496
ENSMUSG00000039959	chr5	Hip1	1.35E+08	1.35E+08	7850	-0.00715	5.622348	0.966821	0.980347	0.032373	0	694	605	830	895	1144	708	1142	1268	1529	1180
ENSMUSG00000024169	chr17	Ift140	25016091	25016136	7572	-0.00727	2.302656	0.966893	0.980349	0.047223	0	92	61	88	83	78	78	107	114	151	120
ENSMUSG00000029442	chr5	Wdr66	1.23E+08	1.23E+08	7583	0.022583	1.40865	0.967527	0.980894	0.075152	0	46	39	36	47	41	46	73	36	67	80

ENSMUSG00000030735	chr8	Gm9755	67514000	67515606	1607	0.011975	3.277344	0.967573	0.980894	0.060396	0	116	195	153	188	133	229	209	167	328	191
ENSMUSG00000030930	chr7	Chst15	1.32E+08	1.32E+08	5388	-0.00914	3.325025	0.96766	0.98091	0.054213	0	120	156	171	206	179	146	262	137	340	297
ENSMUSG00000019891	chr10	Dcbld1	52233619	52233835	7282	-0.01778	1.657011	0.968104	0.98111	0.052437	0	36	46	61	60	55	69	72	65	81	65
ENSMUSG00000028633	chr4	Ctps	1.21E+08	1.21E+08	3316	0.006378	4.694519	0.967992	0.98111	0.028448	0	324	352	548	395	564	447	690	601	690	603
ENSMUSG00000038984	chr15	Tspyl5	33683876	33687883	4008	-0.03475	0.294232	0.968091	0.98111	0.083088	0	10	15	23	21	28	11	33	30	38	21
ENSMUSG00000098661	chr7	Mir7052	44470347	44470411	65	0.038033	0.233704	0.96814	0.98111	0.091625	0	19	17	17	16	19	11	25	40	37	17
ENSMUSG00000031924	chr8	Cyb5b	1.07E+08	1.07E+08	4294	0.007721	6.185445	0.968596	0.9815	0.042747	0	925	1033	1325	1311	1513	1188	1534	1261	2096	2531
ENSMUSG00000019978	chr10	Epb4.1l2	25359798	25359981	4464	0.008271	5.544072	0.968748	0.981511	0.048758	0	718	476	768	775	1214	663	1253	795	1395	1449
ENSMUSG00000020918	chr11	Kat2a	1.01E+08	1.01E+08	3480	0.006421	4.384581	0.968723	0.981511	0.025541	0	271	295	403	339	442	380	489	468	640	474
ENSMUSG00000043432	chr7	Leng9	4147915	4150374	2460	-0.01433	1.701935	0.96914	0.981835	0.053404	0	43	49	74	45	55	58	69	65	110	69
ENSMUSG00000027435	chr2	Cd93	1.48E+08	1.48E+08	6677	0.008838	6.349023	0.969313	0.981939	0.05781	0	825	1314	1372	1998	1257	1305	1740	1432	3123	2184
ENSMUSG00000026564	chr1	Dusp27	1.66E+08	1.66E+08	4049	-0.00721	6.637134	0.969521	0.982079	0.038556	0	1153	1518	1742	1739	2272	2041	2627	2409	2734	1720
ENSMUSG00000056220	chr1	Pla2g4a	1.5E+08	1.5E+08	6391	0.015202	1.877567	0.969672	0.982159	0.112065	0	63	24	65	39	115	57	119	54	117	79
ENSMUSG00000041530	chr4	Ago1	1.26E+08	1.26E+08	8120	0.00754	4.164839	0.970064	0.982342	0.03451	0	293	199	305	286	419	280	371	433	534	497
ENSMUSG00000061130	chr17	Ppm1b	84956741	84956887	4971	-0.00695	7.015511	0.970065	0.982342	0.039394	0	1755	1916	2509	2363	2298	2244	2660	4187	3245	2710
ENSMUSG00000090083	chr17	Rnf8	29614790	29615078	3178	-0.00686	4.430837	0.969959	0.982342	0.026834	0	278	330	412	354	434	424	447	505	641	489
ENSMUSG00000036120	chr8	Rfxank	70130812	70133463	3676	-0.00888	3.255433	0.970305	0.982513	0.034764	0	138	129	188	134	211	155	216	232	233	268
ENSMUSG00000080717	chr16	B230307C23Rik	97997323	97997436	3657	0.040257	0.110279	0.970595	0.982735	0.142562	0	12	28	15	10	14	16	9	36	28	28
ENSMUSG00000027597	chr2	Ahcy	1.55E+08	1.55E+08	2805	0.008006	4.91758	0.970737	0.982806	0.048263	0	383	445	642	510	545	457	551	1116	808	618
ENSMUSG00000056091	chr6	St3gal5	72097592	72097782	2618	-0.00757	5.888119	0.970926	0.982926	0.050937	0	737	1029	988	1362	767	974	1465	1703	1601	1178
ENSMUSG00000029864	chr6	Gstk1	42245935	42246093	930	-0.00644	4.503769	0.971541	0.98345	0.030319	0	361	313	374	416	421	424	486	576	539	595
ENSMUSG00000039693	chr4	Msantd3	48539935	48539997	1973	-0.00683	3.644543	0.971595	0.98345	0.028158	0	181	175	234	230	219	238	314	274	355	267
ENSMUSG00000045078	chr5	Rnf216	1.43E+08	1.43E+08	4671	-0.00688	4.764494	0.971657	0.98345	0.032946	0	370	347	556	426	602	424	653	798	747	558
ENSMUSG00000006050	chr18	Sra1	36666681	36667659	4684	-0.00611	5.229312	0.97182	0.983543	0.029111	0	500	572	804	597	671	733	903	758	1076	896
ENSMUSG00000089698	chr16	Gm2541	85553233	85553943	711	-0.01069	0.546854	0.971941	0.983593	0.074775	0	19	21	24	27	23	17	33	49	36	25
ENSMUSG00000074797	chr2	Itpa	1.31E+08	1.31E+08	1963	-0.00614	4.650864	0.972521	0.984109	0.032472	0	378	403	543	366	395	483	673	541	687	531
ENSMUSG00000034570	chr11	Inpp5j	3494375	3495166	5092	-0.01506	1.824654	0.972593	0.98411	0.150803	0	29	64	63	96	34	69	95	32	148	65
ENSMUSG00000018932	chr11	Map2k3	60932033	60932271	3314	-0.00741	7.684088	0.972736	0.984182	0.054887	0	3170	2969	3581	3604	3853	3647	3892	7875	4351	3953
ENSMUSG00000023919	chr17	Cenpq	40923051	40923616	2604	0.011982	1.933451	0.972884	0.98426	0.050938	0	47	57	72	63	72	65	90	102	118	65
ENSMUSG00000056310	chr5	Tyw1	1.3E+08	1.3E+08	7388	0.00792	3.610476	0.973397	0.984707	0.032045	0	188	166	217	225	211	199	253	340	326	308
ENSMUSG00000005899	chr16	Smpd4	17619354	17619434	8926	0.008269	3.572415	0.973814	0.985057	0.029389	0	193	161	191	211	224	200	280	267	372	278
ENSMUSG00000087367	chr19	Gm15491	45749508	45749677	751	0.021886	0.651624	0.973895	0.985067	0.076116	0	22	25	22	20	33	36	37	19	48	33
ENSMUSG00000024570	chr18	Rbfa	80192265	80192882	1377	0.005549	5.025114	0.974113	0.985212	0.031033	0	426	493	574	612	604	672	648	834	826	790
ENSMUSG00000101856	chr5	1700096K18Rik	25530013	25531466	1454	-0.018	0.738169	0.974181	0.985212	0.067809	0	22	24	25	30	31	26	27	53	44	33
ENSMUSG00000084799	chr1	Ino80dos	63113078	63113219	2880	-0.02331	0.437301	0.974363	0.985324	0.118375	0	12	25	14	30	24	16	15	34	55	30
ENSMUSG00000021614	chr13	Vcan	89655312	89657358	14462	0.010464	4.860319	0.974783	0.985677	0.123271	0	461	215	496	336	997	478	938	238	1079	743
ENSMUSG00000030653	chr7	Pde2a	1.01E+08	1.01E+08	4220	0.00584	5.735694	0.975198	0.985934	0.038752	0	514	796	1108	1038	1040	862	1361	1047	1598	1435
ENSMUSG00000040532	chr5	Abhd11	1.35E+08	1.35E+08	2172	0.005592	5.490813	0.975322	0.985934	0.036029	0	575	751	852	774	781	1043	1036	809	1185	1118
ENSMUSG00000041133	chrX	Smc1a	1.52E+08	1.52E+08	5769	-0.00496	5.701826	0.975278	0.985934	0.026522	0	693	742	1003	872	1073	892	1294	1089	1562	1278
ENSMUSG00000090210	chr3	Itga10	96645584	96645686	5186	-0.01518	2.148983	0.975118	0.985934	0.212952	0	95	34	83	31	128	46	110	224	85	40
ENSMUSG00000020303	chr11	Stc2	31357307	31360528	5175	-0.01316	2.71114	0.975411	0.985952	0.096514	0	112	38	79	126	200	139	158	156	147	140
ENSMUSG00000015357	chr9	Clpx	65294260	65294565	3494	-0.00772	6.253753	0.976029	0.986433	0.075076	0	1073	1152	1408	1416	1320	1110	1333	3415	1633	1368
ENSMUSG00000060126	chr14	Tpt1	75845093	75845456	2380	0.005035	10.22221	0.976023	0.986433	0.033542	0	15765	19501	24962	18478	20961	24808	28309	28779	28817	27659
ENSMUSG00000042133	chr2	Ppig	69722545	69722957	8122	0.005974	4.843701	0.976178	0.986511	0.034243	0	396	425	555	485	530	428	653	904	750	638
ENSMUSG00000030722	chr7	Nfatc2ip	1.26E+08	1.26E+08	3388	-0.00866	2.190522	0.976286	0.986517	0.047313	0	73	66	75	74	85	72	99	134	123	95
ENSMUSG00000095403	chr8	Gm21092	20550331	20550428	4132	0.011726	2.021309	0.976326	0.986517	0.062132	0	63	39	74	53	107	63	98	114	106	86
ENSMUSG00000055835	chr8	Zfp1	1.12E+08	1.12E+08	1871	0.006552	2.813827	0.976409	0.986528	0.048004	0	86	108	155	103	130	120	153	222	180	137
ENSMUSG00000002221	chr5	Paxip1	27740667	27742503	5052	0.007232	3.419851	0.976673	0.986724	0.038094	0	150	146	219	172	202	153	264	333	267	233
ENSMUSG00000027931	chr3	Npr1	90450591	90451182	4783	0.006031	4.309442	0.977211	0.987194	0.032294	0	273	263	338	363	420	290	389	518	591	555
ENSMUSG00000018398	chr11	Sept8	53519257	53519451	6087	-0.00602	5.128182	0.977332	0.987245	0.042205	0	533	358	597	586	901	551	924	610	1063	977
ENSMUSG00000001052	chr3	Sec24b	1.3E+08	1.3E+08	6020	-0.00584	4.660604	0.978041	0.987817	0.041312	0	351	304	444	427	617	343	503	810	750	577
ENSMUSG00000022426	chr15	Josd1	79674250	79676179	3394	0.006214	4.823114	0.978031	0.987817	0.043105	0	443	412	457	511	516	437	626	990	689	567
ENSMUSG00000097343	chr7	9030407P20Rik	1.21E+08	1.21E+08	2347	0.014558	0.918751	0.97817	0.987875	0.078943	0	26	31	28	23	41	26	28	49	47	62
ENSMUSG00000085622	chr12	3110056K07Rik	70991615	70992055	1504	0.017253	1.034749	0.978252	0.987887	0.064913	0	28	31	36	37	29	39	40	35	52	63
ENSMUSG00000039607	chr9	Rbms3	1.17E+08	1.17E+08	10413	-0.00886	3.461918	0.978712	0.988278	0.069537	0	176	96	163	176	326	187	365	162	317	252
ENSMUSG00000058145	chr7	Adamts17	66839735	66839911	7218	-0.01661	1.586328	0.97886	0.988356	0.157006	0	46	26	40	51	86	62	112	19	98	48
ENSMUSG00000028893	chr4	Sesn2	1.32E+08	1.32E+08	3475	-0.00753	2.110669	0.979593	0.989024	0.076555	0	66	60	61	72	95	54	66	145	102	129
ENSMUSG00000019777	chr10	Hdac2	36974544	36974803	4474	-0.00437	6.005743	0.979836	0.989053	0.031169	0	933	973	1203	1095	1155	1303	1716	1283	1688	1459
ENSMUSG00000026725	chr1	Tnn	1.6E+08	1.6E+08	5817	-0.05269	-0.49109	0.979772	0.989053	1.048056	0	0	6	0	0	50	3	10	1	37	22
ENSMUSG00000033430	chr8	Terf2ip	1.12E+08	1.12E+08	3599	-0.00515	4.208557	0.979703	0.989053	0.033754	0	267	288	376	275	333	330	423	556	478	355
ENSMUSG00000041147	chr5	Brca2	1.51E+08	1.51E+08	10724	-0.00828	0.91524	0.97995	0.989096	0.100024	0	33	17	31	26	44	24	37	23	78	53
ENSMUSG00000012428	chr5	Steap4	7960472	7960541	3140	-0.00474	5.816275	0.980115	0.98919	0.041468	0	798	740	982	996	1232	855	1020	1093	2138	1631
ENSMUSG00000057706	chr7	Mex3b	82867333	82867927	3403	0.016995	0.952977	0.980246	0.98925	0.098696	0	17	22	39	31	47	18	60	46	69	29
ENSMUSG00000032265	chr9	Fam46a	85320439	85325233	5703	0.006967	3.76208	0.980331	0.989263	0.078233	0	286	92	228	149	389	232	322	275	376	382
ENSMUSG00000027628	chr2	Aar2	1.57E+08	1.57E+08	3615	0.004486	4.809134	0.980489	0.989351	0.026834	0	383	447	546	423	535	517	648	658	830	630
ENSMUSG00000001524	chr17	Gtf2h4	35667730	35668002	3313	0.004988	3.686228	0.980678	0.989406	0.028909	0	169	203	237	201	259	249	299	251	358	339

ENSMUSG00000021392	chr13	Nol8	49653350	49653397	4242	-0.00505	3.232318	0.980686	0.989406	0.051182	0	155	124	145	183	167	125	182	313	280	201
ENSMUSG00000049305	chr9	Ccdc71	1.08E+08	1.08E+08	3267	0.004241	4.213392	0.980773	0.989422	0.027412	0	241	272	316	318	403	337	419	492	497	415
ENSMUSG00000051149	chr2	Adnp	1.68E+08	1.68E+08	5350	-0.00444	5.260317	0.981273	0.989854	0.029278	0	496	509	686	639	917	664	901	968	1118	837
ENSMUSG00000093677	chr15	Gm20712	58780461	58781951	1491	0.011488	1.367706	0.981885	0.990399	0.060708	0	33	42	47	49	34	54	49	53	77	58
ENSMUSG00000027959	chr3	Sass6	1.17E+08	1.17E+08	4241	-0.01236	1.310782	0.982329	0.990774	0.071356	0	39	33	47	37	44	57	57	30	79	54
ENSMUSG00000045934	chr3	Mtmr11	96162004	96162258	3780	0.004988	2.414742	0.982488	0.990863	0.068711	0	83	41	115	65	145	82	140	125	142	128
ENSMUSG00000025220	chr19	Mgea5	45750261	45752280	5024	-0.0045	5.761185	0.982677	0.990982	0.044585	0	796	762	1097	853	1042	824	1214	1940	1259	1083
ENSMUSG00000048087	chr16	Gm4737	46152997	46155077	2081	-0.01591	1.140236	0.982906	0.991117	0.103387	0	19	28	39	37	58	25	37	86	56	43
ENSMUSG00000057406	chr5	Whsc1	33820725	33820877	15898	0.006263	3.994093	0.982955	0.991117	0.036191	0	265	207	307	241	302	212	417	302	533	435
ENSMUSG00000010517	chr4	Faf1	1.1E+08	1.1E+08	5093	-0.00386	5.624977	0.983692	0.991788	0.031452	0	712	714	948	801	958	980	1012	1419	1229	1063
ENSMUSG00000020321	chr11	Mdh1	21556787	21557568	2567	0.004143	9.381501	0.984042	0.992068	0.050271	0	8779	12870	12129	13002	7726	14096	14771	15428	18794	14543
ENSMUSG00000009076	chr11	Zmat5	4704678	4704721	1248	-0.00421	3.92419	0.984241	0.992125	0.032714	0	197	251	296	282	229	317	323	343	430	340
ENSMUSG00000024299	chr17	Adamts10	33524204	33524258	5453	0.005977	3.770034	0.984183	0.992125	0.057342	0	274	122	201	193	349	178	366	348	392	328
ENSMUSG00000038132	chr13	Rbm24	46418300	46419198	3215	-0.00472	6.968373	0.984639	0.992454	0.067353	0	1941	1679	2575	2100	2188	2043	2845	5121	2460	1994
ENSMUSG00000026712	chr2	Mrc1	14229392	14229573	6371	-0.00474	5.648449	0.984949	0.992654	0.057628	0	774	483	869	685	1495	940	1257	735	1684	1291
ENSMUSG00000084830	chrX	Gm14539	20581141	20581314	174	-0.00462	4.390599	0.984981	0.992654	0.04927	0	280	423	374	350	289	519	494	459	468	440
ENSMUSG00000022440	chr15	C1qtnf6	78523346	78525398	2402	0.005086	5.537041	0.985147	0.992677	0.082798	0	815	404	838	583	1316	821	1659	560	1501	951
ENSMUSG00000055436	chr3	Srsf11	1.58E+08	1.58E+08	7135	-0.0033	5.28311	0.985118	0.992677	0.035028	0	625	549	737	546	800	549	890	1162	1061	921
ENSMUSG00000000552	chr15	Zfp385a	1.03E+08	1.03E+08	2291	0.007094	4.881656	0.985487	0.992687	0.179401	0	191	210	265	534	1433	433	511	520	915	1125
ENSMUSG00000024845	chr19	Tmem134	4125934	4126200	4601	0.003326	5.854419	0.985516	0.992687	0.032852	0	835	931	1104	975	946	1200	1239	1292	1449	1522
ENSMUSG00000028341	chr4	Nr4a3	48045153	48045716	5987	-0.01309	1.955735	0.985449	0.992687	0.201089	0	37	95	45	84	48	64	210	42	74	49
ENSMUSG00000030714	chr7	Ccdc101	1.27E+08	1.27E+08	1802	-0.00513	3.555017	0.98549	0.992687	0.029942	0	162	168	232	198	219	234	238	277	295	308
ENSMUSG00000041729	chr9	Coro2b	62419492	62421413	5919	-0.00766	3.108819	0.985488	0.992687	0.037041	0	119	101	146	143	217	159	197	199	246	196
ENSMUSG00000036985	chrX	Zdhhc9	48171969	48173641	6733	-0.00399	3.952995	0.985788	0.992889	0.035716	0	238	189	268	250	355	262	402	250	503	404
ENSMUSG00000029310	chr5	Nudt9	1.04E+08	1.04E+08	2392	-0.00307	5.608189	0.986159	0.99319	0.029255	0	675	793	930	825	833	987	1156	1106	1213	1179
ENSMUSG00000021039	chr12	Snw1	87449936	87450716	2231	-0.00343	5.83089	0.986252	0.993212	0.040293	0	808	896	1133	898	1013	997	1274	1871	1397	1072
ENSMUSG00000100680	chr6	1810044D09Rik	91440987	91441158	486	-0.01259	1.62435	0.986347	0.993235	0.081353	0	55	45	52	54	41	68	52	94	54	72
ENSMUSG00000021532	chr13	Fastkd3	68582248	68582350	2362	0.004163	3.07174	0.98642	0.993237	0.045537	0	110	140	177	128	137	199	204	149	231	179
ENSMUSG00000010936	chr8	Vac14	1.11E+08	1.11E+08	3028	-0.00302	4.643976	0.987221	0.993882	0.031005	0	313	371	460	505	437	451	523	513	764	678
ENSMUSG00000027395	chr2	Polr1b	1.29E+08	1.29E+08	5805	0.002795	3.899421	0.98715	0.993882	0.030187	0	184	186	318	245	326	241	372	391	419	324
ENSMUSG00000097061	chr12	9330151L19Rik	69197211	69197615	2546	0.012945	1.832346	0.987276	0.993882	0.07003	0	57	46	64	62	58	46	56	118	96	95
ENSMUSG00000033955	chr2	Tnks1bp1	85048022	85048135	6184	0.003267	5.008599	0.987401	0.993935	0.03916	0	463	361	521	553	827	534	813	571	1117	787
ENSMUSG00000028565	chr4	Nfia	97772734	97772911	10891	-0.00304	5.163728	0.9877	0.994163	0.034376	0	613	464	583	525	815	682	846	653	1044	962
ENSMUSG00000045216	chr1	Hs6st1	36068400	36069184	5542	0.002745	5.329523	0.98802	0.994414	0.036826	0	574	493	739	656	932	679	937	1265	1027	786
ENSMUSG00000031465	chr8	Angpt2	18690263	18692208	3690	0.00543	2.020831	0.988542	0.994866	0.067358	0	42	39	102	77	78	55	89	88	121	118
ENSMUSG00000020782	chr11	Llgl2	1.16E+08	1.16E+08	4844	0.005275	2.831544	0.988911	0.995134	0.101085	0	78	105	120	130	159	90	114	339	153	127
ENSMUSG00000040016	chr3	Ptger3	1.58E+08	1.58E+08	2107	0.014098	0.872792	0.988952	0.995134	0.422527	0	28	5	7	39	69	14	15	11	73	99
ENSMUSG00000030037	chr6	Mrpl53	83109095	83109203	735	-0.00285	5.680129	0.989189	0.9953	0.036817	0	662	899	1012	848	837	1213	1127	1099	1309	1134
ENSMUSG00000030213	chr6	Atf7ip	1.37E+08	1.37E+08	19678	0.002398	5.215934	0.99002	0.996064	0.037171	0	494	440	653	699	855	590	754	1141	1021	857
ENSMUSG00000020577	chr12	Tspan13	36014557	36015772	2474	-0.00232	5.220102	0.990531	0.996506	0.039518	0	435	630	737	772	516	691	795	878	1142	858
ENSMUSG00000030894	chr7	Tpp1	1.06E+08	1.06E+08	3494	-0.00192	6.00959	0.991017	0.996922	0.030553	0	978	849	1225	1014	1349	1060	1419	1355	2076	1709
ENSMUSG00000035325	chr5	Sec31a	1E+08	1E+08	7884	0.001836	6.228135	0.991196	0.99703	0.032476	0	1069	893	1333	1214	1845	1378	1862	1641	2214	1700
ENSMUSG00000063684	chr2	Gm13910	1.09E+08	1.09E+08	1428	-0.00201	4.821228	0.991319	0.997081	0.046535	0	374	530	503	524	389	456	516	876	789	673
ENSMUSG00000045409	chr17	Trim39	36258873	36260921	7223	0.003525	3.214227	0.991553	0.997244	0.038523	0	156	116	175	133	189	161	208	274	237	194
ENSMUSG00000003559	chr19	As3mt	46707443	46707536	1751	-0.00232	4.970446	0.991649	0.997268	0.031708	0	455	447	618	525	573	649	744	735	969	551
ENSMUSG00000029291	chr5	Rufy3	88583574	88584317	3986	-0.00491	2.637858	0.992218	0.997723	0.06397	0	96	79	133	83	126	96	142	226	130	118
ENSMUSG00000039157	chr2	Fam102a	32535332	32536232	6066	0.0034	2.875862	0.992246	0.997723	0.045207	0	119	91	97	119	182	134	163	160	234	163
ENSMUSG00000033423	chr4	Eri3	1.18E+08	1.18E+08	3007	0.001631	6.028566	0.992319	0.997724	0.030884	0	933	979	1176	1086	1274	1400	1375	1614	1655	1498
ENSMUSG00000043323	chr5	Fbrsl1	1.1E+08	1.1E+08	4947	0.002858	3.824982	0.992397	0.99773	0.037481	0	185	204	234	283	271	235	297	453	355	307
ENSMUSG00000045664	chr19	Cdc42ep2	5917556	5918993	1491	0.002312	4.761835	0.992689	0.997952	0.052411	0	354	408	508	555	425	655	742	359	806	572
ENSMUSG00000004843	chr16	Chmp2b	65539133	65540250	1838	-0.00182	5.002849	0.993377	0.998332	0.03575	0	437	498	615	530	595	527	627	1033	813	738
ENSMUSG00000022663	chr16	Atg3	45158785	45159171	3154	0.00196	4.648009	0.993152	0.998332	0.026363	0	342	382	503	380	487	429	580	642	667	611
ENSMUSG00000024084	chr17	Qpct	79051906	79052388	1924	-0.00604	2.545875	0.9934	0.998332	0.106157	0	100	45	91	75	182	55	110	122	239	172
ENSMUSG00000024528	chr18	Srfbp1	52465693	52465785	1463	-0.00383	2.93186	0.993385	0.998332	0.05947	0	95	122	144	120	152	123	150	284	190	132
ENSMUSG00000051456	chr13	Hspb3	1.14E+08	1.14E+08	781	0.00156	5.011161	0.993428	0.998332	0.036923	0	515	429	597	529	617	751	875	545	833	707
ENSMUSG00000030688	chr7	Stard10	1.01E+08	1.01E+08	2383	-0.00171	4.889919	0.993761	0.998522	0.034457	0	436	501	503	515	490	660	628	584	790	757
ENSMUSG00000033712	chr14	Ccar2	70138177	70138947	3716	0.00224	4.490629	0.993735	0.998522	0.02589	0	306	331	424	383	431	382	480	553	691	536
ENSMUSG00000001288	chr15	Rarg	1.02E+08	1.02E+08	4109	-0.00322	4.171206	0.994083	0.998773	0.059151	0	294	139	291	329	478	274	473	552	425	372
ENSMUSG00000015672	chr13	Mrpl32	14610301	14610740	768	0.00172	4.482005	0.994305	0.998923	0.036649	0	299	363	422	403	362	459	500	643	492	472
ENSMUSG00000032582	chr9	Rbm6	1.08E+08	1.08E+08	13944	-0.00109	4.820185	0.994851	0.999399	0.026622	0	398	425	534	500	493	479	660	695	794	679
ENSMUSG00000062077	chr5	Trim54	31116712	31117077	1436	-0.00158	7.865381	0.995035	0.999512	0.068672	0	2845	3749	4529	4382	3984	4259	3815	9422	4465	4860
ENSMUSG00000021235	chr12	Coq6	84361657	84361819	3142	0.00194	4.71935	0.995309	0.999642	0.027401	0	373	405	459	474	474	469	546	666	765	637
ENSMUSG00000028343	chr4	Erp44	48193323	48194709	3418	-0.00177	5.370511	0.995268	0.999642	0.033755	0	636	546	866	557	877	880	1041	778	1087	1000
ENSMUSG00000043192	chr8	Gm1840	5639584	5640996	1413	0.002089	3.774721	0.99568	0.999942	0.038979	0	199	220	233	255	217	317	241	299	362	351
ENSMUSG00000003464	chr1	Pex19	1.72E+08	1.72E+08	3815	0.000702	6.907019	0.997051	1	0.032366	0	1583	1864	2307	2083	2192	2303	2476	3254	3090	2833
ENSMUSG00000004788	chr12	Eif2b2	85219481	85219724	1885	-0.00025	5.268646	1	1	0.028841	0	475	563	780	661	762	780	907	927	1056	805

ENSMUSG00000005873	chr18	Reep5	34344889	34347168	2894	0.000418	7.668962	0.998275	1	0.030059	0	2946	3168	3698	3306	3850	4169	4429	4325	5683	5092
ENSMUSG00000014592	chr4	Camta1	1.51E+08	1.51E+08	14570	0.001702	4.137022	0.998274	1	0.046393	0	241	292	329	339	245	325	357	577	449	329
ENSMUSG00000017550	chr11	Atad5	80089400	80089836	7532	-0.00878	0.952705	1	1	0.069752	0	26	38	27	23	39	31	48	34	64	40
ENSMUSG00000019845	chr10	Tube1	39134023	39134107	2929	0.025975	0.250062	1	1	0.08084	0	21	17	17	19	15	16	29	15	40	31
ENSMUSG00000020696	chr11	Rffl	82802449	82806189	5922	0.002093	2.83561	1	1	0.058157	0	88	99	149	128	128	105	113	246	184	180
ENSMUSG00000020780	chr11	Srp68	1.16E+08	1.16E+08	2737	-0.00036	6.403761	0.99978	1	0.034896	0	1186	1163	1633	1401	1737	1580	1704	2555	2075	1914
ENSMUSG00000021809	chr14	Nudt13	20294690	20294792	2523	0.002653	4.053415	0.996011	1	0.03576	0	244	288	303	296	227	338	359	352	451	423
ENSMUSG00000022378	chr15	Fam49b	63929097	63931679	3869	0.001258	5.448983	0.996145	1	0.031539	0	590	676	793	722	868	799	1155	744	1317	1116
ENSMUSG00000022847	chr16	Thpo	20725158	20726082	1837	0.000503	1.615762	1	1	0.138652	0	26	79	48	60	28	51	86	34	110	73
ENSMUSG00000022887	chr16	Masp1	23451785	23452572	2752	0.001914	1.26674	1	1	0.101566	0	28	29	23	64	49	34	74	38	80	49
ENSMUSG00000025184	chr19	R3hcc1l	42518759	42518857	7397	-0.00091	3.624742	0.999623	1	0.033821	0	194	165	241	198	226	206	242	371	331	284
ENSMUSG00000025870	chr13	Arl10	54575015	54575277	1729	-0.00022	0.954057	1	1	0.083493	0	25	18	40	32	41	17	51	39	73	42
ENSMUSG00000026189	chr1	Pecr	72259167	72259433	1516	0.001006	4.206564	0.996346	1	0.035748	0	248	316	316	267	387	409	355	485	440	427
ENSMUSG00000027820	chr3	Mme	63241537	63241566	11542	0.000124	3.060825	1	1	0.060474	0	138	77	117	142	226	134	163	237	200	231
ENSMUSG00000028018	chr3	Gstcd	1.33E+08	1.33E+08	4731	0.006573	1.405918	1	1	0.081758	0	44	38	37	30	64	39	60	36	99	72
ENSMUSG00000028684	chr4	Urod	1.17E+08	1.17E+08	2591	-0.00069	5.639013	0.998509	1	0.031519	0	687	767	935	853	914	997	934	1353	1312	1182
ENSMUSG00000028713	chr4	Cyp4b1	1.16E+08	1.16E+08	2256	-0.00042	2.107012	1	1	0.089937	0	76	69	59	77	64	49	56	129	134	135
ENSMUSG00000028862	chr4	Map3k6	1.33E+08	1.33E+08	4604	0.008158	1.480884	1	1	0.177054	0	44	49	68	31	29	21	41	141	67	51
ENSMUSG00000028909	chr4	Ptpru	1.32E+08	1.32E+08	7113	-0.01889	0.586174	1	1	0.201657	0	23	10	23	12	54	12	30	71	26	24
ENSMUSG00000029127	chr5	Zbtb49	38189735	38192137	7715	-0.01246	0.847517	1	1	0.073649	0	29	18	34	25	38	19	43	54	50	35
ENSMUSG00000029629	chr6	Phf14	11907809	11908017	4547	-0.00154	4.327079	0.996831	1	0.026262	0	272	304	390	330	378	367	479	506	500	475
ENSMUSG00000030691	chr7	Fchsd2	1.01E+08	1.01E+08	9199	-0.00061	3.099952	1	1	0.042991	0	125	121	162	122	183	139	253	139	271	202
ENSMUSG00000030825	chr7	Hsd17b14	45554893	45555066	2046	-0.01404	0.17743	1	1	0.087167	0	16	9	17	18	28	17	25	31	16	30
ENSMUSG00000031382	chrX	Asb11	1.64E+08	1.64E+08	2847	-0.00029	6.258682	0.999744	1	0.117611	0	1137	1388	1254	1420	1070	1448	1012	3719	1068	1455
ENSMUSG00000033128	chr15	Gga1	78877190	78877617	3034	-0.00017	5.550914	1	1	0.026791	0	657	649	869	839	912	784	1026	1117	1338	1242
ENSMUSG00000033906	chrX	Zdhhc15	1.05E+08	1.05E+08	5509	-0.00033	0.497325	1	1	0.08972	0	9	22	20	20	41	26	36	23	42	27
ENSMUSG00000034387	chr6	Ssu2	1.12E+08	1.12E+08	2543	0.012816	0.983013	1	1	0.124821	0	21	33	26	58	15	23	50	46	60	46
ENSMUSG00000035478	chr10	Mbd3	80392539	80393018	1987	0.000253	6.361058	0.999668	1	0.035965	0	1145	1273	1420	1408	1613	1734	1845	1358	2511	2149
ENSMUSG00000036435	chr5	Exoc1	76529311	76529462	9158	-0.00061	3.801637	0.997478	1	0.038722	0	204	241	271	201	232	270	342	220	461	338
ENSMUSG00000036580	chr3	Spg20	55112108	55112217	5362	0.000556	5.053331	0.998201	1	0.027372	0	435	478	639	539	699	602	855	798	929	695
ENSMUSG00000037710	chr10	Cisd1	71330480	71331126	1084	-0.00073	6.861306	0.99764	1	0.043993	0	1561	2114	2422	1822	1699	2787	2501	2496	2849	2696
ENSMUSG00000037813	chr2	D630003M21Rik	1.58E+08	1.58E+08	5104	-0.00451	1.820592	1	1	0.096706	0	67	23	63	64	73	59	112	89	96	46
ENSMUSG00000038546	chr13	Ranbp9	43402673	43403689	3064	-0.00144	5.419401	0.996352	1	0.076068	0	584	658	774	697	867	534	824	1957	940	750
ENSMUSG00000039958	chr6	Mettl20	1.49E+08	1.49E+08	2496	0.001719	3.445671	0.99918	1	0.065746	0	149	168	243	167	175	156	212	439	218	234
ENSMUSG00000041354	chr17	Rgl2	33929543	33930044	4625	0.000732	4.860161	1	1	0.028179	0	434	456	548	473	495	469	696	649	824	775
ENSMUSG00000041870	chr5	Ankrd13a	1.15E+08	1.15E+08	4098	0.000311	4.861619	1	1	0.030058	0	362	392	503	550	641	479	669	604	907	770
ENSMUSG00000041912	chr3	Tdrkh	94413296	94413362	3806	0.009154	1.427126	1	1	0.052709	0	40	34	50	39	54	34	60	63	83	69
ENSMUSG00000042197	chr1	Zfp451	33761545	33762209	15839	0.002588	3.617825	0.996465	1	0.038078	0	203	156	211	184	267	185	314	363	345	230
ENSMUSG00000044636	chr15	Csrnp2	1E+08	1E+08	4126	-0.00457	2.050434	1	1	0.04437	0	63	55	79	66	76	80	104	99	98	88
ENSMUSG00000045287	chr11	Rtn4rl1	75193783	75194294	3525	0.003956	1.540536	1	1	0.130013	0	31	23	42	50	97	35	49	44	92	116
ENSMUSG00000046167	chr9	Gldn	54286486	54286886	4658	0.004386	0.596288	1	1	0.06318	0	19	17	28	25	30	22	46	36	36	26
ENSMUSG00000051022	chr5	Hs3st1	39613935	39615404	2230	0.00722	0.730164	1	1	0.085909	0	20	25	28	38	18	40	42	31	37	30
ENSMUSG00000052468	chr3	Pmp2	10179851	10180800	1408	0.024872	-0.13726	1	1	0.245135	0	8	9	20	20	10	10	21	1	48	20
ENSMUSG00000055963	chr4	Triqk	12906838	12906938	3568	-0.02034	0.443847	1	1	0.089824	0	12	14	23	21	39	29	37	19	39	22
ENSMUSG00000057572	chr4	Zbtb8os	1.29E+08	1.29E+08	4500	-0.0015	3.728224	0.997311	1	0.036646	0	199	205	286	218	184	267	306	283	320	349
ENSMUSG00000067344	chr6	Rps25-ps1	1.45E+08	1.45E+08	378	0.002725	1.221658	1	1	0.067241	0	40	39	31	34	40	38	50	39	85	54
ENSMUSG00000072762	chr5	4930522L14Rik	1.1E+08	1.1E+08	2409	-0.01362	0.027254	1	1	0.073128	0	10	11	17	21	19	13	31	20	26	18
ENSMUSG00000074876	chr2	Spata5l1	1.23E+08	1.23E+08	1547	0.005432	1.808094	1	1	0.11112	0	46	49	80	49	62	55	49	156	60	74
ENSMUSG00000082029	chr2	H3f3c	1.2E+08	1.2E+08	411	0.013121	-0.00381	1	1	0.077379	0	21	12	15	11	15	17	19	25	29	16
ENSMUSG00000083022	chr11	Rps15a-ps6	6172644	6173036	393	0.006934	0.216273	1	1	0.137619	0	34	11	7	18	16	19	31	27	27	21
ENSMUSG00000086606	chr4	Gm13205	1.49E+08	1.49E+08	562	0.004555	-0.10214	1	1	0.098613	0	7	17	23	9	14	19	23	23	15	16
ENSMUSG00000090439	chr10	Gm17455	60399726	60399976	855	-0.00547	-0.19564	1	1	0.400964	0	22	0	16	2	26	8	39	6	25	14
ENSMUSG00000092118	chr7	Fancf	51860577	51862267	1691	-0.00026	0.352452	1	1	0.080701	0	10	19	23	18	30	32	24	26	34	20
ENSMUSG00000098954	chr4	Mir7658	1.56E+08	1.56E+08	57	0.007217	0.129258	1	1	0.080001	0	10	20	18	15	20	12	27	18	27	34
ENSMUSG00000103124	chr3	RP24-137C19.6	10179852	10180800	1568	0.008529	-0.16566	1	1	0.232768	0	8	9	20	19	10	10	21	1	45	20
ENSMUSG00000103393	chr1	RP24-499I2.1	1.62E+08	1.62E+08	600	0.000654	0.410243	1	1	0.134044	0	13	26	33	12	19	21	33	50	19	19
ENSMUSG00000103715	chr9	RP23-58N8.6	85749078	85750429	1352	0.000684	1.138029	1	1	0.077134	0	31	28	45	30	43	37	45	76	37	48

Table S6. RNA sequencing analysis and differential expression data of B10-mdx vs B10-WT mice at 6 months of age. Raw reads were mapped to chromosomes and gene identifiers and subsequent differential analysis was completed (n = 5 per group).

Ensembl ID	Chromosome	Gene Name	Start	End	Length	logFC_B10-*mdx*.6mo_B10-WT.6mo	logCPM_B10-*mdx*.6mo_B10-WT.6mo	PValue_B10-*mdx*.6mo_B10-WT.6mo	FDR_B10-*mdx*.6mo_B10-WT.6mo	Tgw.Disp	UpDown.Tgw	B10-WT.6mo_Rep1_raw	B10-WT.6mo_Rep2_raw	B10-WT.6mo_Rep3_raw	B10-WT.6mo_Rep4_raw	B10-WT.6mo_Rep5_raw	B10-*mdx*.6mo_Rep1_raw	B10-*mdx*.6mo_Rep2_raw	B10-*mdx*.6mo_Rep3_raw	B10-*mdx*.6mo_Rep4_raw	B10-*mdx*.6mo_Rep5_raw
ENSMUSG00000044303	chr4	Cdkn2a	89274471	89274774	1172	6.748858	3.328126	5.26E-88	6.97E-84	0.051085	1	8	2	4	0	0	332	446	238	409	351
ENSMUSG00000050335	chr14	Lgals3	47367751	47367852	1858	4.250201	6.163676	2.64E-70	1.75E-66	0.050505	1	101	73	126	155	114	2328	2725	3288	2344	1573
ENSMUSG00000045103	chrX	Dmd	82948870	82949147	23801	-3.63655	6.080686	2.17E-57	9.58E-54	0.048779	-1	1191	995	3956	2067	2580	121	269	162	206	174
ENSMUSG00000046805	chr19	Mpeg1	12460779	12460861	4335	2.965132	4.843893	1.54E-56	5.11E-53	0.032802	1	91	60	150	100	131	864	1087	1093	848	677
ENSMUSG00000038642	chr3	Ctss	95526786	95526925	1358	3.321494	5.836426	8.5E-56	2.26E-52	0.042616	1	149	109	236	161	188	2025	1969	2321	1564	1329
ENSMUSG00000072812	chr12	Ahnak2	1.13E+08	1.13E+08	14163	3.594627	4.913361	4.13E-49	9.14E-46	0.054419	1	44	29	109	89	115	809	882	794	1633	965
ENSMUSG00000025473	chr7	Adam8	1.4E+08	1.4E+08	4638	3.931626	2.547108	6.52E-47	1.24E-43	0.050074	1	10	3	23	6	16	153	221	235	199	162
ENSMUSG00000044320	chr2	1700001O22Rik	30794769	30795009	2788	-6.01398	3.707128	3.31E-45	5.49E-42	0.119146	-1	585	335	534	181	377	10	3	2	17	4
ENSMUSG00000060512	chr5	0610040J01Rik	63812495	63812595	1870	-4.11728	3.047592	9.3E-44	1.37E-40	0.066183	-1	189	144	273	308	351	17	31	19	10	5
ENSMUSG00000056888	chr10	Glipr1	1.12E+08	1.12E+08	1543	4.730287	1.647097	1.25E-39	1.65E-36	0.063993	1	2	0	4	7	4	69	139	132	125	66
ENSMUSG00000001131	chrX	Timp1	20870166	20870324	888	4.417208	3.031434	2.04E-38	2.11E-35	0.085419	1	5	8	7	15	22	224	486	133	341	247
ENSMUSG00000024803	chr19	Ankrd1	36111965	36112817	1765	4.231917	6.215019	2.07E-38	2.11E-35	0.095781	1	61	67	90	194	193	1719	5041	1906	2321	2236
ENSMUSG00000042607	chr6	Asb4	5383386	5383405	3932	-2.17387	3.508791	1.96E-38	2.11E-35	0.024364	-1	280	206	407	271	336	52	94	68	93	71
ENSMUSG00000038453	chr11	Srcin1	97509340	97512648	8386	-3.4863	1.768044	2.21E-36	2.09E-33	0.046226	-1	82	64	149	99	109	2	11	10	14	13
ENSMUSG00000018774	chr11	Cd68	69664213	69664504	1257	2.943547	4.551185	2.88E-36	2.55E-33	0.052651	1	73	48	147	52	130	587	755	1088	752	546
ENSMUSG00000102573	chr9	RP23-296I6.8	72691549	72695050	3502	-3.55253	3.362058	2.89E-35	2.4E-32	0.069693	-1	183	188	679	214	360	20	46	16	30	35
ENSMUSG00000001020	chr3	S100a4	90603770	90603806	587	2.447211	5.181595	5.33E-35	4.16E-32	0.040646	1	121	105	202	237	247	1135	1140	938	1503	841
ENSMUSG00000023992	chr17	Trem2	48346401	48346595	4946	3.964453	2.99439	3.62E-34	2.67E-31	0.08397	1	5	7	24	21	21	191	254	447	235	194
ENSMUSG00000044734	chr13	Serpinb1a	32842092	32843222	1943	2.899637	4.516986	9.52E-34	6.64E-31	0.054839	1	87	80	98	63	93	543	1170	448	1200	468
ENSMUSG00000013033	chr8	Lphn1	83900105	83900924	8587	-1.98319	4.498708	1.11E-33	7.34E-31	0.026716	-1	480	345	956	540	669	119	172	151	229	164
ENSMUSG00000091996	chr9	BC049352	45182007	45182315	2404	-4.48306	0.964302	8.78E-33	5.54E-30	0.058625	-1	45	37	66	58	87	3	1	6	2	2
ENSMUSG00000021190	chr12	Lgmn	1.02E+08	1.02E+08	2323	1.882138	6.300583	1.21E-31	7.26E-29	0.02823	1	489	334	649	574	669	2090	2776	2141	2516	1759
ENSMUSG00000054958	chr4	Nt5c1a	1.23E+08	1.23E+08	1220	-4.05015	2.593913	2.81E-31	1.62E-28	0.092558	-1	106	68	440	149	231	8	14	8	20	12
ENSMUSG00000036390	chr6	Gadd45a	67035096	67035772	1764	2.16648	5.566656	4.92E-31	2.72E-28	0.037108	1	288	175	308	260	348	1052	2031	1695	1259	1056
ENSMUSG00000044811	chr11	AF251705	1.15E+08	1.15E+08	1275	3.472877	1.60319	7.17E-31	3.8E-28	0.051672	1	9	4	10	8	7	79	113	121	88	78
ENSMUSG00000026459	chr1	Myog	1.34E+08	1.34E+08	1495	2.774699	3.846509	1.49E-30	7.6E-28	0.053821	1	47	56	55	68	56	436	359	565	562	310
ENSMUSG00000084883	chr12	Ccdc85c	1.08E+08	1.08E+08	1547	-3.16319	3.086713	1.64E-30	8.07E-28	0.065208	-1	181	122	362	255	349	16	42	20	26	49
ENSMUSG00000069806	chr7	Cacng7	3332955	3333036	2207	-2.20892	3.805518	2.54E-30	1.2E-27	0.035298	-1	327	239	543	281	494	72	83	67	134	96
ENSMUSG00000037406	chr8	Htra4	25025451	25025734	1795	-4.64731	2.998885	6.1E-30	2.79E-27	0.127034	-1	133	351	397	104	217	10	9	11	19	7
ENSMUSG00000091754	chr14	Gm3636	6735685	6736817	1746	4.129099	1.594969	1.52E-29	6.73E-27	0.076508	1	0	5	3	13	3	86	132	88	104	84
ENSMUSG00000040552	chr6	C3ar1	1.23E+08	1.23E+08	4305	2.329671	3.070674	3.11E-29	1.33E-26	0.03716	1	33	32	79	37	44	229	249	264	255	237
ENSMUSG00000079523	chr6	Tmsb10	72957347	72957652	1276	2.221974	5.065773	3.43E-29	1.42E-26	0.040978	1	153	147	188	214	230	1034	802	1000	1274	810
ENSMUSG00000028581	chr4	Laptm5	1.31E+08	1.31E+08	3788	2.241798	4.411206	7.78E-29	3.13E-26	0.0406	1	111	64	207	101	130	553	592	839	677	480
ENSMUSG00000046841	chr10	Ckap4	84526305	84528777	2954	1.783356	4.137132	9.38E-29	3.66E-26	0.024753	1	83	100	167	124	163	370	634	423	603	459
ENSMUSG00000033624	chr8	Pdpr	1.11E+08	1.11E+08	5028	-3.82221	6.004732	1.33E-28	5.03E-26	0.111178	-1	864	593	3784	2355	2990	87	253	108	143	190
ENSMUSG00000061086	chr11	Myl4	1.05E+08	1.05E+08	4637	3.287421	5.841081	1.45E-28	5.35E-26	0.086085	1	97	110	129	338	159	1634	2083	1455	2270	1956
ENSMUSG00000022003	chr14	Slc25a30	75761999	75762690	1706	-2.6479	2.278184	2.29E-28	8.21E-26	0.043851	-1	120	69	197	113	186	13	30	28	29	21
ENSMUSG00000031827	chr8	Cotl1	1.2E+08	1.2E+08	1628	2.191591	4.098337	2.57E-28	8.98E-26	0.038809	1	93	51	152	80	129	491	480	620	527	381
ENSMUSG00000001473	chr18	Tubb6	67390717	67390814	1757	2.318298	5.302537	2.83E-28	9.64E-26	0.046548	1	120	125	218	266	347	1138	1347	1057	1554	894
ENSMUSG00000062760	chr15	1810041L15Rik	84379203	84384392	6551	2.951099	2.465444	6.16E-28	2.04E-25	0.05595	1	31	12	25	16	13	125	205	186	175	171
ENSMUSG00000027346	chr2	Gpcpd1	1.33E+08	1.33E+08	7289	-1.88866	7.891385	9.18E-28	2.9E-25	0.033327	-1	4861	4375	10744	5035	5858	1290	2540	1537	2446	1599
ENSMUSG00000028843	chr4	Sh3bgrl3	1.34E+08	1.34E+08	821	1.924608	4.216009	9.04E-28	2.9E-25	0.030535	1	108	86	147	126	151	407	509	682	616	433
ENSMUSG00000053205	chr14	Styx	45351473	45351529	672	-3.72173	2.637184	1.68E-27	5.18E-25	0.094931	-1	105	107	433	126	223	3	21	14	22	20
ENSMUSG00000031838	chr8	Ifi30	70762774	70763040	980	1.972178	4.040419	2.02E-27	5.95E-25	0.032046	1	91	86	154	96	106	489	436	454	552	398
ENSMUSG00000040659	chr4	Efhd2	1.42E+08	1.42E+08	2381	1.729728	4.172571	2.02E-27	5.95E-25	0.02466	1	123	88	158	128	171	426	537	549	553	425
ENSMUSG00000020634	chr12	Ubxn2a	4879032	4880771	2820	-2.07629	6.467503	3.35E-27	9.46E-25	0.040279	-1	1567	1352	4147	2137	2888	450	1024	487	643	549
ENSMUSG00000044378	chr6	Slc15a5	1.38E+08	1.38E+08	3088	-6.03575	2.548791	3.32E-27	9.46E-25	0.194093	-1	169	66	82	299	296	7	0	1	6	1
ENSMUSG00000024300	chr17	Myo1f	33555719	33555856	4914	2.56292	2.824826	6.62E-27	1.83E-24	0.048197	1	33	19	45	26	40	181	213	300	226	152
ENSMUSG00000036377	chr5	C530008M17Rik	76656512	76658355	12305	-4.3536	0.82759	8.21E-27	2.22E-24	0.078238	-1	27	35	67	66	71	1	3	0	5	5
ENSMUSG00000026796	chr2	Fam129b	32876114	32876404	4672	2.026285	4.577486	1.29E-26	3.42E-24	0.036966	1	105	75	226	187	184	487	726	853	921	523
ENSMUSG00000032231	chr9	Anxa2	69453620	69453739	3731	1.827467	6.771098	2.42E-26	6.18E-24	0.032746	1	754	560	816	791	872	2792	2982	3193	3571	2786
ENSMUSG00000104217	chr1	RP24-426M1.3	4807892	4807982	825	-2.02305	4.528723	2.39E-26	6.18E-24	0.037212	-1	421	390	944	624	676	121	290	128	149	154
ENSMUSG00000029762	chr6	Akr1b8	34354119	34354296	1499	2.455692	2.903134	2.72E-26	6.81E-24	0.044913	1	45	34	44	23	31	195	245	228	286	176
ENSMUSG00000005087	chr2	Cd44	1.03E+08	1.03E+08	6776	1.948137	4.090388	3.65E-26	8.96E-24	0.033471	1	92	60	128	124	163	310	691	497	522	457
ENSMUSG00000031112	chrX	Stk26	50841047	50841546	5271	-4.16441	1.929803	4.12E-26	9.94E-24	0.109585	-1	88	101	258	47	100	6	8	4	12	6
ENSMUSG00000025268	chrX	Maged2	1.51E+08	1.51E+08	3239	1.788909	5.123856	5.37E-26	1.27E-23	0.030584	1	215	204	337	244	245	763	1040	744	1495	925

ENSMUSG00000061436	chr6	Hipk2	38694390	38698596	8836	-3.7855	5.444264	5.55E-26	1.29E-23	0.120405	-1	606	348	3134	1133	2149	79	89	80	166	121
ENSMUSG00000009013	chr5	Dynll1	1.15E+08	1.15E+08	2926	1.664862	4.778692	5.83E-26	1.33E-23	0.025983	1	196	159	234	201	252	633	864	828	924	553
ENSMUSG00000059149	chr1	Mfsd4	1.32E+08	1.32E+08	7187	-2.15959	3.493775	6.42E-26	1.44E-23	0.039399	-1	218	155	451	343	354	80	76	77	89	49
ENSMUSG00000029822	chr6	Osbpl3	50293330	50297161	9023	2.627228	2.17606	1.15E-25	2.54E-23	0.047389	1	12	9	22	26	30	100	165	107	191	131
ENSMUSG00000035133	chr12	Arhgap5	52516077	52519967	5197	-2.75762	4.303511	1.25E-25	2.72E-23	0.068651	-1	303	292	1013	576	750	32	150	100	99	94
ENSMUSG00000039316	chr17	Rftn1	49992257	49994481	4504	3.172367	2.687367	1.33E-25	2.84E-23	0.07774	1	11	5	16	31	40	141	230	206	253	205
ENSMUSG00000087410	chr11	2310065F04Rik	67112461	67114117	2916	-2.411	6.181105	1.79E-25	3.76E-23	0.056874	-1	1643	1673	2725	1392	2398	508	454	304	612	222
ENSMUSG00000042363	chr11	Lgalsl	20823576	20826515	4115	-1.82568	6.13266	2.15E-25	4.45E-23	0.033819	-1	1468	933	2795	1908	1989	386	762	433	766	526
ENSMUSG00000022952	chr16	Runx1	92601466	92606124	11827	2.131841	3.06957	2.39E-25	4.88E-23	0.036661	1	35	32	62	60	59	195	370	248	276	158
ENSMUSG00000007617	chr13	Homer1	93303757	93305302	10502	-1.90998	5.542542	2.74E-25	5.51E-23	0.036644	-1	981	853	2278	827	1189	234	444	325	503	315
ENSMUSG00000021998	chr14	Lcp1	75131101	75131204	9504	1.763195	4.595899	3.72E-25	7.36E-23	0.030265	1	152	112	291	138	212	542	858	803	645	535
ENSMUSG00000006731	chr10	B4galnt1	1.27E+08	1.27E+08	2474	2.717551	1.649253	4.59E-25	8.95E-23	0.044067	1	12	5	18	13	16	70	121	113	101	71
ENSMUSG00000002489	chr16	Tiam1	89787111	89789591	9911	-3.00673	3.155396	5.11E-25	9.82E-23	0.07614	-1	140	119	585	199	336	26	31	47	36	35
ENSMUSG00000090118	chr8	Gm16163	1.25E+08	1.25E+08	1119	-2.14279	3.05029	6.61E-25	1.25E-22	0.038605	-1	158	108	316	246	288	35	71	49	71	54
ENSMUSG00000036902	chr8	Neto2	85636588	85641116	5610	-3.46328	2.307835	9.3E-25	1.74E-22	0.090126	-1	199	77	217	84	153	16	9	13	27	9
ENSMUSG00000040751	chr5	Lat2	1.35E+08	1.35E+08	1505	2.918169	2.240746	1.01E-24	1.86E-22	0.06296	1	17	10	20	15	24	119	194	208	133	84
ENSMUSG00000032717	chr17	Mdfi	47815328	47816164	3092	4.157284	2.587686	1.11E-24	2.01E-22	0.125434	1	10	10	8	9	11	274	127	159	361	83
ENSMUSG00000036905	chr4	C1qb	1.37E+08	1.37E+08	1088	1.964179	5.685691	1.13E-24	2.02E-22	0.039727	1	308	241	525	250	388	1636	1425	1540	1342	1281
ENSMUSG00000024294	chr18	Mib1	10725548	10726533	10369	-1.89942	6.710469	1.22E-24	2.16E-22	0.037944	-1	1675	1963	4366	2416	3272	675	707	684	1150	804
ENSMUSG00000025777	chr1	Gdap1	17145362	17145588	7731	-2.39459	4.252034	1.38E-24	2.41E-22	0.054706	-1	484	367	931	279	585	114	103	81	122	121
ENSMUSG00000006519	chr8	Cyba	1.22E+08	1.22E+08	758	2.134997	4.01165	1.42E-24	2.44E-22	0.043195	1	90	47	123	100	125	438	497	632	470	312
ENSMUSG00000023067	chr17	Cdkn1a	29090979	29091101	2223	2.459132	5.217663	1.76E-24	2.99E-22	0.060703	1	112	93	209	329	181	809	1618	1198	1283	902
ENSMUSG00000027520	chr1	Zdbf2	63273265	63273472	12659	2.439464	2.1241	1.78E-24	2.99E-22	0.041726	1	14	15	33	26	18	82	152	127	186	112
ENSMUSG00000033685	chr7	Ucp2	1E+08	1E+08	6989	1.925351	4.809837	1.88E-24	3.12E-22	0.037663	1	126	114	246	222	246	681	753	1040	884	627
ENSMUSG00000039661	chr8	Dusp26	31089471	31089895	2305	-3.31437	4.513243	2.29E-24	3.75E-22	0.100813	-1	288	335	651	1142	985	60	79	69	58	102
ENSMUSG00000022292	chr15	Rrm2b	37923952	37927397	6437	-1.65925	4.503273	3.44E-24	5.56E-22	0.027879	-1	397	400	825	571	615	126	269	164	236	209
ENSMUSG00000005580	chr16	Adcy9	4287529	4289089	5197	-3.01591	4.553873	4.63E-24	7.34E-22	0.087148	-1	361	206	1474	709	949	65	145	65	101	99
ENSMUSG00000030579	chr7	Tyrobp	30413788	30413899	564	2.384607	4.027884	4.65E-24	7.34E-22	0.054556	1	111	56	97	59	88	516	557	587	422	344
ENSMUSG00000038147	chr1	Cd84	1.72E+08	1.72E+08	6272	3.033499	2.534949	5.34E-24	8.33E-22	0.073699	1	20	16	29	16	17	131	245	286	145	110
ENSMUSG00000050503	chr9	Fbxl22	66508459	66512018	3935	2.01545	3.134728	5.59E-24	8.62E-22	0.03556	1	50	27	66	59	77	202	314	236	368	169
ENSMUSG00000102869	chr2	RP24-114E18.7	1.56E+08	1.56E+08	1149	-1.95377	4.406751	6.25E-24	9.53E-22	0.038466	-1	406	393	992	407	602	115	233	114	168	168
ENSMUSG00000000682	chr4	Cd52	1.34E+08	1.34E+08	1187	2.916923	2.019353	8.64E-24	1.3E-21	0.062319	1	17	8	17	15	16	146	151	131	108	82
ENSMUSG00000024789	chr19	Jak2	29251828	29252118	5030	-1.46495	5.583691	1.03E-23	1.54E-21	0.023317	-1	948	762	1764	1003	1304	337	584	401	641	401
ENSMUSG00000029994	chr6	Anxa4	86736840	86737823	4545	1.515731	4.93578	1.06E-23	1.57E-21	0.024084	1	261	169	330	225	286	684	944	749	1128	653
ENSMUSG00000089929	chr9	Bcl2a1b	89199209	89199779	817	4.205637	0.832696	1.12E-23	1.64E-21	0.082898	1	1	1	1	6	4	57	80	62	44	38
ENSMUSG00000024672	chr19	Ms4a7	11321039	11321582	4453	2.561449	2.518445	1.17E-23	1.68E-21	0.05304	1	31	20	30	21	26	184	174	186	152	151
ENSMUSG00000030122	chr6	Ptms	1.25E+08	1.25E+08	1554	1.785417	6.626663	2.06E-23	2.93E-21	0.035559	1	653	495	790	688	930	2110	2441	3332	3461	2511
ENSMUSG00000002603	chr7	Tgfb1	25687002	25688223	2558	1.964659	3.372678	2.23E-23	3.15E-21	0.036064	1	54	43	94	71	77	252	242	335	356	276
ENSMUSG00000053063	chr6	Clec12a	1.29E+08	1.29E+08	5139	2.547299	2.429346	2.72E-23	3.79E-21	0.053378	1	24	18	34	22	25	190	169	169	140	126
ENSMUSG00000063142	chr14	Kcnma1	23289431	23289452	6513	-1.90207	4.069644	2.88E-23	3.98E-21	0.036803	-1	290	220	731	455	531	111	194	95	146	106
ENSMUSG00000028238	chr4	Atp6v0d2	19876841	19878380	2716	5.842526	2.206132	3.02E-23	4.13E-21	0.211388	1	1	2	6	2	1	64	217	369	90	63
ENSMUSG00000102049	chr1	Zbed6	1.34E+08	1.34E+08	5007	-3.31437	3.86467	5.18E-23	7.01E-21	0.105541	-1	258	172	1163	265	511	27	93	41	43	43
ENSMUSG00000043613	chr9	Mmp3	7445822	7446008	1798	3.851747	3.752201	5.5E-23	7.37E-21	0.131986	1	28	44	31	7	18	356	833	462	478	215
ENSMUSG00000064280	chr5	Ccdc146	21292961	21293495	4366	-2.45411	1.926864	5.82E-23	7.72E-21	0.045492	-1	99	85	146	76	101	14	24	19	24	24
ENSMUSG00000058715	chr1	Fcer1g	1.71E+08	1.71E+08	874	2.33558	3.838748	6.01E-23	7.89E-21	0.054778	1	88	54	120	47	69	511	466	424	444	273
ENSMUSG00000026480	chr1	Ncf2	1.53E+08	1.53E+08	8478	2.411495	2.570711	8.52E-23	1.11E-20	0.050098	1	26	19	33	33	36	177	199	220	177	108
ENSMUSG00000069516	chr10	Lyz2	1.17E+08	1.17E+08	1266	1.736552	7.564502	8.97E-23	1.16E-20	0.035072	1	1303	975	1993	1284	1518	5670	5376	5381	5288	4251
ENSMUSG00000000957	chr14	Mmp14	54431604	54431973	2597	1.643115	4.778556	9.79E-23	1.25E-20	0.029555	1	194	176	321	154	223	587	890	629	894	772
ENSMUSG00000027009	chr2	Itga4	79255426	79256064	13978	-2.6698	4.241861	1.12E-22	1.42E-20	0.073541	-1	434	382	1146	280	509	88	67	116	86	94
ENSMUSG00000038024	chr4	Dennd4c	86748555	86748912	8482	-2.4197	4.376071	1.63E-22	2.04E-20	0.062549	-1	383	244	1214	499	695	58	187	117	127	118
ENSMUSG00000023043	chr15	Krt18	1.02E+08	1.02E+08	1400	5.315776	1.765816	1.66E-22	2.06E-20	0.178429	1	2	2	2	5	1	61	56	244	141	69
ENSMUSG00000022500	chr16	Litaf	10959275	10961051	2642	2.086553	3.859316	1.86E-22	2.29E-20	0.045319	1	94	46	119	69	120	388	622	476	389	257
ENSMUSG00000034652	chr11	Cd300a	1.15E+08	1.15E+08	4738	2.704356	2.387107	2.46E-22	3E-20	0.06333	1	25	15	30	19	19	159	175	218	144	96
ENSMUSG00000034708	chr11	Grn	1.02E+08	1.02E+08	3474	1.842851	6.3869	2.77E-22	3.34E-20	0.039791	1	520	397	857	516	683	2113	2007	2992	2277	2210
ENSMUSG00000043091	chr15	Tuba1c	99029891	99030424	1977	2.139967	2.869635	3.42E-22	4.08E-20	0.042195	1	50	32	52	28	49	197	296	191	208	171
ENSMUSG00000054342	chr7	Kcnn4	24370263	24370595	2034	3.085642	1.128893	3.71E-22	4.39E-20	0.055338	1	8	6	7	2	11	54	72	53	102	55
ENSMUSG00000078532	chr4	Nkain1	1.31E+08	1.31E+08	1426	-1.66815	4.003378	4.23E-22	4.97E-20	0.029429	-1	309	252	596	377	466	148	135	137	174	98
ENSMUSG00000071076	chr8	Jund	70697739	70700616	2878	1.55881	5.099466	5.54E-22	6.44E-20	0.028011	1	234	209	314	318	301	632	992	965	1254	846
ENSMUSG00000025887	chr9	Casp12	5345430	5345525	3840	-1.59701	3.770447	6.66E-22	7.68E-20	0.02668	-1	234	246	447	314	422	88	145	132	174	87
ENSMUSG00000024074	chr17	Crim1	78200248	78201099	5995	-1.87554	5.507126	6.74E-22	7.71E-20	0.041428	-1	719	685	1726	1362	1443	216	398	271	529	388
ENSMUSG00000042826	chr11	Fgf11	69796068	69797879	3044	1.77939	2.947181	8.25E-22	9.35E-20	0.029302	1	41	35	81	58	64	142	260	221	256	199
ENSMUSG00000034584	chr9	Exph5	53301670	53301851	10519	-6.51935	-0.0932	8.75E-22	9.84E-20	0.104673	-1	21	14	61	15	31	0	0	0	0	1
ENSMUSG00000026547	chr1	Tagln2	1.73E+08	1.73E+08	2082	1.596612	5.482859	1.02E-21	1.14E-19	0.030359	1	288	247	389	321	548	920	1394	1312	1326	1142
ENSMUSG00000030789	chr7	Itgax	1.28E+08	1.28E+08	4045	4.767181	3.101037	1.03E-21	1.14E-19	0.193658	1	7	6	12	9	14	85	391	715	201	111
ENSMUSG00000018983	chr4	E2f2	1.36E+08	1.36E+08	4882	2.803617	2.013547	1.29E-21	1.41E-19	0.06585	1	22	10	22	8	16	117	97	105	170	123

ENSMUSG00000021185	chr12	9030617O03Rik	1.01E+08	1.01E+08	4434	-1.60162	4.422325	1.47E-21	1.6E-19	0.029013	-1	350	354	738	579	613	120	233	195	224	200
ENSMUSG00000028583	chr4	Pdpn	1.43E+08	1.43E+08	1817	1.877108	3.34839	1.54E-21	1.66E-19	0.036322	1	59	38	100	67	89	235	432	315	278	195
ENSMUSG00000026100	chr1	Mstn	53061640	53062141	2705	-2.93089	5.282232	2.05E-21	2.19E-19	0.095952	-1	1213	986	2193	396	796	93	223	179	173	163
ENSMUSG00000029304	chr5	Spp1	1.04E+08	1.04E+08	1648	3.054078	4.482527	2.19E-21	2.33E-19	0.101624	1	31	29	126	110	112	475	1024	1081	450	570
ENSMUSG00000049723	chr9	Mmp12	7344381	7344437	7237	6.238949	4.806853	3.14E-21	3.3E-19	0.317687	1	3	2	40	8	14	209	1651	2352	507	423
ENSMUSG00000018920	chr11	Cxcl16	70453983	70455444	3021	2.237128	2.662793	4.06E-21	4.24E-19	0.04866	1	21	23	49	40	44	208	190	166	172	171
ENSMUSG00000001025	chr3	S100a6	90612894	90613226	719	1.555408	6.241692	4.68E-21	4.85E-19	0.030384	1	515	453	652	642	799	1791	2074	1936	2583	1846
ENSMUSG00000020577	chr12	Tspan13	36014557	36015772	2474	1.404158	5.69028	5.35E-21	5.5E-19	0.024497	1	373	330	507	486	565	990	1822	1292	1691	1131
ENSMUSG00000042485	chr14	Mustn1	30879257	30879615	1177	2.033403	6.915537	6.05E-21	6.17E-19	0.051582	1	524	398	838	1003	1122	3254	4357	2360	5263	2733
ENSMUSG00000029816	chr6	Gpnmb	49036518	49036792	3798	4.235243	6.508799	8.09E-21	8.19E-19	0.185635	1	78	82	223	176	211	1147	3288	8077	2037	1229
ENSMUSG00000003949	chr11	Hlf	90336536	90340974	6681	-1.81075	4.180077	1.4E-20	1.41E-18	0.03875	-1	375	414	671	352	437	109	122	178	187	131
ENSMUSG00000095362	chr2	Gm14325	1.78E+08	1.78E+08	1616	-1.91183	2.930642	1.52E-20	1.51E-18	0.03827	-1	177	125	306	175	195	47	99	43	59	46
ENSMUSG00000024726	chr19	2410127L17Rik	18670780	18671202	2090	-1.52663	6.078454	1.68E-20	1.66E-18	0.030216	-1	1299	1204	2567	1481	1632	429	910	587	875	468
ENSMUSG00000022441	chr15	Efcab6	83866712	83867171	6408	-3.70336	3.093707	1.74E-20	1.71E-18	0.137698	-1	125	133	320	340	394	36	5	14	33	17
ENSMUSG00000081194	chrX	Gm8424	1.51E+08	1.51E+08	988	-3.06318	3.188083	1.84E-20	1.79E-18	0.100856	-1	155	121	421	319	351	26	67	11	27	46
ENSMUSG00000059493	chrX	Nhs	1.62E+08	1.62E+08	8805	-2.71767	2.302777	1.97E-20	1.9E-18	0.072971	-1	107	96	285	73	151	22	22	31	27	14
ENSMUSG00000026956	chr2	Uap1l1	25359889	25361739	4071	1.707567	3.417898	2.09E-20	2.01E-18	0.031475	1	62	60	91	80	104	269	272	289	358	267
ENSMUSG00000000290	chr10	Itgb2	77530252	77530459	3052	2.613735	3.783357	2.12E-20	2.02E-18	0.078196	1	53	35	99	56	73	279	454	794	379	225
ENSMUSG00000005054	chr10	Cstb	78425670	78425857	599	1.75437	3.70281	2.27E-20	2.15E-18	0.034471	1	94	81	107	89	92	336	424	405	382	255
ENSMUSG00000021728	chr13	Emb	1.17E+08	1.17E+08	2253	2.130759	2.599853	2.88E-20	2.71E-18	0.045176	1	28	31	54	30	34	137	219	229	173	121
ENSMUSG00000031760	chr8	Mt3	94152607	94152830	538	3.51293	1.932198	3.6E-20	3.36E-18	0.110831	1	9	5	8	11	14	179	104	89	178	56
ENSMUSG00000027712	chr3	Anxa5	36448926	36449406	1721	1.524291	5.954681	3.85E-20	3.57E-18	0.030476	1	436	418	602	454	636	1255	1737	1921	1849	1560
ENSMUSG00000042045	chr9	Sln	53850251	53850326	515	4.760207	5.106528	4.07E-20	3.75E-18	0.2275	1	22	12	22	97	41	1722	758	1224	1897	341
ENSMUSG00000068614	chr2	Actc1	1.14E+08	1.14E+08	1618	3.129117	9.268359	4.57E-20	4.18E-18	0.117968	1	3269	862	3138	1456	1479	17163	17990	32581	22900	9833
ENSMUSG00000020098	chr10	Pcbd1	61089343	61089416	809	3.406876	1.85851	7.44E-20	6.76E-18	0.103255	1	16	10	11	4	5	125	83	119	172	74
ENSMUSG00000030144	chr6	Clec4d	1.23E+08	1.23E+08	1336	4.467682	0.937031	8.85E-20	7.98E-18	0.139112	1	0	1	3	2	6	34	99	102	50	28
ENSMUSG00000027797	chr3	Dclk1	55242526	55242751	12991	2.475561	3.282435	1.35E-19	1.21E-17	0.071384	1	28	28	66	71	45	296	178	291	438	254
ENSMUSG00000099906	chr1	Gm28653	20679023	20684298	5276	4.778299	0.393597	1.67E-19	1.49E-17	0.118178	1	0	0	0	6	0	22	31	46	67	41
ENSMUSG00000006360	chr12	Crip1	1.13E+08	1.13E+08	445	1.408699	5.463174	1.88E-19	1.66E-17	0.026625	1	310	331	431	388	444	948	1294	1224	1323	1019
ENSMUSG00000096764	chr2	Gm21985	1.12E+08	1.12E+08	4532	-2.41468	3.323253	2.1E-19	1.85E-17	0.069459	-1	174	135	561	232	341	30	94	48	47	69
ENSMUSG00000046223	chr7	Plaur	24462500	24462567	1396	2.647816	1.333966	2.17E-19	1.89E-17	0.056606	1	11	2	14	13	13	46	106	75	77	73
ENSMUSG00000073982	chr7	Rhog	1.02E+08	1.02E+08	1356	1.487881	4.250512	2.49E-19	2.16E-17	0.02779	1	144	94	206	181	180	415	489	528	704	412
ENSMUSG00000062593	chr10	Lilrb4	51480640	51480753	1491	2.460455	2.179113	2.98E-19	2.56E-17	0.061872	1	16	14	34	20	26	93	223	166	99	101
ENSMUSG00000025429	chr18	Pstpip2	77794545	77794750	1395	-1.58148	4.641557	3.03E-19	2.59E-17	0.033266	-1	495	417	1081	445	665	168	298	168	331	197
ENSMUSG00000031010	chrX	Usp9x	13071498	13071733	15051	-2.07648	5.963402	3.45E-19	2.93E-17	0.058555	-1	1064	770	3593	1289	2090	357	623	413	371	408
ENSMUSG00000036908	chr19	Unc93b1	3935186	3935352	2841	1.735886	4.528401	3.6E-19	3.04E-17	0.039537	1	155	104	278	139	199	627	543	793	655	523
ENSMUSG00000038594	chr10	Cep85l	53278081	53278244	2691	-4.37267	3.458323	3.85E-19	3.23E-17	0.20102	-1	80	98	855	393	463	12	25	13	8	30
ENSMUSG00000049866	chr1	Arl4c	88673125	88674468	5492	2.328247	1.69269	4.09E-19	3.41E-17	0.047564	1	12	11	25	20	15	100	98	84	96	84
ENSMUSG00000018008	chr15	Cyth4	78597047	78597219	2791	1.77477	3.217659	4.32E-19	3.58E-17	0.036944	1	71	34	104	50	82	257	304	241	273	208
ENSMUSG00000021091	chr12	Serpina3n	1.04E+08	1.04E+08	2064	3.057584	4.782277	4.63E-19	3.82E-17	0.1157	1	129	93	116	34	79	932	1080	465	1589	510
ENSMUSG00000042254	chr9	Cilp	65265180	65265223	4252	2.677889	6.600132	4.87E-19	3.98E-17	0.094703	1	147	170	589	616	719	2092	3354	3947	3131	2705
ENSMUSG00000030707	chr7	Coro1a	1.27E+08	1.27E+08	2783	1.691268	3.482164	5.2E-19	4.23E-17	0.034099	1	87	62	106	64	99	312	372	296	337	213
ENSMUSG00000037902	chr2	Sirpa	1.3E+08	1.3E+08	4911	1.50562	4.914183	5.81E-19	4.7E-17	0.030866	1	194	175	380	227	307	698	891	1013	763	638
ENSMUSG00000037280	chr15	Galnt6	1.01E+08	1.01E+08	3871	3.871932	0.619142	6.38E-19	5.13E-17	0.101657	1	0	2	4	2	6	22	73	69	48	30
ENSMUSG00000020091	chr10	Eif4ebp2	61432497	61433828	1786	-1.7308	5.702395	8.83E-19	7.06E-17	0.042205	-1	979	731	2784	968	1392	316	515	378	575	431
ENSMUSG00000038068	chr13	Rnf144b	47122720	47122873	4694	-1.46616	4.595421	9.21E-19	7.31E-17	0.0291	-1	549	351	926	447	647	196	277	268	238	186
ENSMUSG00000002233	chr3	Rhoc	1.05E+08	1.05E+08	1292	1.334768	5.207139	9.94E-19	7.85E-17	0.024629	1	317	258	380	331	371	729	1118	974	1274	766
ENSMUSG00000055782	chr15	Abcd2	91145884	91149205	5527	-1.47143	5.754396	1.21E-18	9.53E-17	0.03093	-1	1170	884	1938	1082	1388	431	534	661	541	416
ENSMUSG00000062542	chr7	Syt9	1.07E+08	1.07E+08	3979	-4.53658	-0.07181	1.27E-18	9.92E-17	0.096564	-1	34	20	42	13	26	0	2	1	1	2
ENSMUSG00000036887	chr4	C1qa	1.37E+08	1.37E+08	1040	1.815185	5.427087	1.36E-18	1.06E-16	0.046442	1	290	223	447	234	345	1353	953	1402	1160	1006
ENSMUSG00000048583	chr7	Igf2	1.43E+08	1.43E+08	5723	2.145883	5.563871	1.43E-18	1.1E-16	0.064213	1	156	155	291	488	315	901	1765	1128	1999	1367
ENSMUSG00000051627	chr13	Hist1h1e	23621755	23622502	748	-2.93837	0.856857	1.45E-18	1.12E-16	0.066602	-1	33	29	59	57	73	2	6	9	9	10
ENSMUSG00000022488	chr15	Nckap1l	1.03E+08	1.03E+08	4717	1.807069	3.113863	1.59E-18	1.21E-16	0.039594	1	59	32	104	44	75	206	260	287	240	203
ENSMUSG00000032575	chr9	Manf	1.07E+08	1.07E+08	3524	1.4103	4.494327	1.68E-18	1.27E-16	0.026871	1	187	150	243	178	220	519	677	679	679	415
ENSMUSG00000074519	chr2	Etohi1	1.78E+08	1.78E+08	2145	-2.5458	2.11173	1.88E-18	1.41E-16	0.071051	-1	52	71	194	122	173	23	36	20	19	15
ENSMUSG00000041189	chr11	Chrnb1	69784036	69784761	2531	1.510406	5.74623	1.89E-18	1.42E-16	0.032794	1	445	399	564	382	392	1260	1792	1169	1759	1274
ENSMUSG00000027107	chr2	Chrna1	73563215	73566307	4386	1.517056	4.974004	2.37E-18	1.76E-16	0.032525	1	167	201	316	325	292	689	921	671	1147	816
ENSMUSG00000039168	chr15	Dap	31224314	31224583	1925	1.577456	3.814821	2.37E-18	1.76E-16	0.032124	1	80	88	142	108	147	327	366	450	390	340
ENSMUSG00000037405	chr9	Icam1	21015960	21016101	2540	1.995941	2.805321	2.87E-18	2.11E-16	0.047125	1	29	34	49	45	64	184	297	208	179	133
ENSMUSG00000019996	chr10	Map7	20148471	20149080	4351	-2.20969	2.169834	3.01E-18	2.21E-16	0.053632	-1	66	68	164	152	152	21	27	32	41	23
ENSMUSG00000038451	chr6	Spsb2	1.25E+08	1.25E+08	1658	2.115803	2.114069	3.1E-18	2.26E-16	0.044939	1	25	25	27	21	25	92	137	108	194	98
ENSMUSG00000026600	chr1	Soat1	1.56E+08	1.56E+08	9791	1.951825	3.048535	3.12E-18	2.26E-16	0.04656	1	56	40	87	33	55	195	225	300	246	197
ENSMUSG00000028111	chr3	Ctsk	95499286	95499336	1482	2.287303	4.698918	3.38E-18	2.43E-16	0.072086	1	107	103	201	112	196	398	1086	1316	815	393
ENSMUSG00000033220	chr15	Rac2	78559169	78561485	3036	2.266068	2.531567	3.4E-18	2.43E-16	0.060638	1	29	13	52	29	38	152	188	236	137	125
ENSMUSG00000027533	chr3	Fabp5	10012548	10012718	3567	1.889648	4.164533	3.69E-18	2.63E-16	0.048615	1	100	87	118	131	167	448	626	695	509	279

ENSMUSG00000023004	chr15	Tuba1b	98931425	98932562	1875	1.578323	5.554838	3.82E-18	2.71E-16	0.036284	1	390	300	354	367	424	1198	1308	1377	1570	924
ENSMUSG00000003363	chr7	Pld3	27532000	27532485	2924	1.475592	5.019584	3.97E-18	2.8E-16	0.031378	1	248	159	396	263	337	646	838	1115	1017	704
ENSMUSG00000029810	chr6	Tmem176b	48833811	48834139	2049	1.684235	4.978996	4.12E-18	2.89E-16	0.04073	1	189	206	364	210	231	926	816	1000	1014	553
ENSMUSG00000045838	chr2	A430105I19Rik	1.19E+08	1.19E+08	4779	-1.54242	4.517077	4.18E-18	2.92E-16	0.033714	-1	410	295	712	697	678	145	277	168	297	198
ENSMUSG00000090122	chrX	Kcne1l	1.42E+08	1.42E+08	1543	3.46556	0.287462	4.62E-18	3.2E-16	0.062715	1	1	3	5	4	1	28	53	30	33	37
ENSMUSG00000025647	chr9	Shisa5	1.09E+08	1.09E+08	1955	1.41924	4.561134	5.02E-18	3.46E-16	0.028398	1	166	130	253	224	264	479	718	769	645	499
ENSMUSG00000034993	chr11	Vat1	1.01E+08	1.01E+08	2766	1.541102	5.199202	5.04E-18	3.46E-16	0.034715	1	216	200	466	292	372	696	888	1289	1181	886
ENSMUSG00000057913	chr14	Gm10032	66784529	66784653	1838	-5.50471	0.375951	5.22E-18	3.57E-16	0.173733	-1	11	11	57	57	65	1	0	0	1	2
ENSMUSG00000036242	chr14	3632451O06Rik	49681560	49682416	3663	2.031796	3.621902	5.8E-18	3.95E-16	0.055214	1	32	57	130	92	85	267	433	258	390	426
ENSMUSG00000042359	chr2	Osbpl6	76406508	76406689	10063	-1.32612	5.850781	5.89E-18	3.98E-16	0.02634	-1	1061	882	2243	1168	1477	475	751	531	836	459
ENSMUSG00000033713	chr12	Foxn3	99194980	99196813	4651	-2.30611	3.922428	6.57E-18	4.38E-16	0.072698	-1	198	166	827	408	600	59	117	63	136	96
ENSMUSG00000042734	chr12	Ttc9	81631369	81631801	2042	2.749874	3.576868	6.55E-18	4.38E-16	0.099015	1	21	21	31	85	90	271	498	300	481	347
ENSMUSG00000048373	chr5	Fgfbp1	43978865	43979968	1154	-2.11111	2.694916	6.53E-18	4.38E-16	0.054186	-1	92	147	228	190	182	35	62	40	33	48
ENSMUSG00000024907	chr19	Gal	3409919	3410165	712	5.274297	0.574614	6.86E-18	4.55E-16	0.176782	1	1	1	1	1	1	78	17	42	52	40
ENSMUSG00000021699	chr13	Pde4d	1.08E+08	1.08E+08	12006	-1.91649	5.885084	7.56E-18	4.99E-16	0.05444	-1	982	949	2872	1317	1786	434	599	243	464	495
ENSMUSG00000023905	chr17	Tnfrsf12a	23675447	23676046	963	1.83115	4.006742	9.09E-18	5.97E-16	0.046617	1	111	46	126	157	126	443	475	381	574	383
ENSMUSG00000019913	chr10	Sim1	50895651	50896071	7355	-4.16405	-0.2265	1.12E-17	7.3E-16	0.084498	-1	14	15	32	33	25	0	2	0	5	0
ENSMUSG00000010461	chr10	Eya4	23104168	23106288	4192	-1.68654	4.468108	1.49E-17	9.69E-16	0.041248	-1	415	352	1085	372	624	132	207	165	241	210
ENSMUSG00000037989	chr13	Wnk2	49036303	49036505	8481	-1.46908	6.277949	1.8E-17	1.16E-15	0.033559	-1	1381	1070	3262	1695	2173	557	754	736	1115	634
ENSMUSG00000040410	chr4	Fbxl4	22357543	22357681	3798	-1.41273	4.851851	1.9E-17	1.22E-15	0.029806	-1	664	486	1107	481	680	239	355	251	342	254
ENSMUSG00000034361	chr8	Cpne2	94532990	94533193	3198	1.56246	3.930755	2.35E-17	1.5E-15	0.03414	1	116	74	145	128	154	399	409	485	457	287
ENSMUSG00000042312	chr3	S100a13	90514435	90514465	715	1.735856	4.401867	2.58E-17	1.65E-15	0.043558	1	159	158	151	125	152	567	587	572	748	453
ENSMUSG00000016256	chr2	Ctsz	1.74E+08	1.74E+08	1441	1.436071	5.74373	2.72E-17	1.73E-15	0.031995	1	443	350	581	430	497	1163	1463	1833	1524	1086
ENSMUSG00000035199	chr6	Arl6ip5	97210689	97210996	1442	1.36389	7.457503	2.97E-17	1.87E-15	0.029778	1	1387	1253	1749	1623	1763	3611	5675	3972	6436	3761
ENSMUSG00000041762	chr2	Gpr155	73341506	73343757	6679	-1.5313	4.407884	2.97E-17	1.87E-15	0.034928	-1	426	379	915	384	488	129	282	170	228	197
ENSMUSG00000039062	chr7	Anpep	79821803	79822376	3879	1.929594	4.770427	3.04E-17	1.9E-15	0.056172	1	153	105	286	160	233	438	795	1299	788	601
ENSMUSG00000038618	chr7	Rassf7	1.41E+08	1.41E+08	1803	3.063976	0.617416	3.35E-17	2.08E-15	0.063171	1	2	7	4	7	3	42	48	46	61	30
ENSMUSG00000015094	chr2	Npdc1	25399351	25399536	3906	1.406681	4.971614	3.42E-17	2.12E-15	0.029989	1	293	215	349	217	285	719	845	870	1077	629
ENSMUSG00000084169	chr11	Gm12240	56262855	56263083	229	-4.85966	-0.56411	3.54E-17	2.18E-15	0.083922	-1	25	12	20	17	17	1	0	0	2	0
ENSMUSG00000094786	chr2	Gm14403	1.77E+08	1.77E+08	1656	-2.16969	1.582815	5.92E-17	3.63E-15	0.04834	-1	52	43	125	84	93	15	31	14	18	19
ENSMUSG00000024912	chr19	Fosl1	5447703	5448055	1707	4.804467	-0.36606	6.45E-17	3.94E-15	0.07772	1	2	0	0	1	0	25	29	14	27	18
ENSMUSG00000003812	chr8	Dnase2a	84908560	84908874	5389	1.539769	3.452684	6.49E-17	3.95E-15	0.032412	1	91	47	103	88	119	260	351	308	306	236
ENSMUSG00000029070	chr4	Mxra8	1.56E+08	1.56E+08	2918	1.313773	5.511211	6.76E-17	4.09E-15	0.027371	1	325	290	640	404	480	910	1336	1220	1154	1230
ENSMUSG00000079547	chr17	H2-DMb1	34153072	34153453	1485	1.943915	2.876149	7.19E-17	4.34E-15	0.049442	1	47	39	62	38	51	234	183	221	247	139
ENSMUSG00000031146	chrX	Plp2	7667941	7668506	1334	1.73527	5.225039	7.57E-17	4.55E-15	0.04727	1	341	195	414	172	259	897	1137	889	1649	745
ENSMUSG00000028599	chr4	Tnfrsf1b	1.45E+08	1.45E+08	3818	1.518653	3.511643	8.62E-17	5.15E-15	0.031995	1	58	78	137	88	113	277	331	330	311	257
ENSMUSG00000097296	chr8	Gm26532	84208920	84209609	690	2.591596	1.073295	9.01E-17	5.36E-15	0.059251	1	5	8	18	9	5	35	70	57	89	60
ENSMUSG00000039477	chr5	Tnrc18	1.43E+08	1.43E+08	6880	-2.08788	3.596526	9.32E-17	5.52E-15	0.06359	-1	196	115	593	320	464	51	118	70	95	88
ENSMUSG00000031443	chr8	F7	13026034	13026131	1859	6.287458	-0.15643	9.66E-17	5.69E-15	0.151543	1	0	0	0	1	0	29	15	48	24	18
ENSMUSG00000007041	chr17	Clic1	35049966	35050486	1799	1.289003	4.453056	1.05E-16	6.13E-15	0.025009	1	159	166	240	200	245	509	729	532	596	450
ENSMUSG00000022871	chr16	Fetub	22918382	22918590	1913	4.080621	0.648111	1.07E-16	6.24E-15	0.131817	1	5	2	2	0	3	50	41	47	92	18
ENSMUSG00000000305	chr2	Cdh4	1.79E+08	1.79E+08	7257	-4.22676	2.972418	1.37E-16	7.96E-15	0.220214	-1	241	194	671	47	105	11	12	23	12	12
ENSMUSG00000090691	chr14	Gm3667	6868502	6869647	2053	4.319814	-0.21796	1.37E-16	7.96E-15	0.081244	1	1	1	0	1	2	22	41	17	21	25
ENSMUSG00000025355	chr10	Mmp19	1.29E+08	1.29E+08	3410	1.933755	3.09912	1.41E-16	8.12E-15	0.05193	1	49	46	90	42	56	149	273	356	226	209
ENSMUSG00000076036	chr7	Gm22133	45458089	45458197	109	1.833965	7.1091	1.53E-16	8.77E-15	0.055022	1	1088	804	1159	794	879	3527	3249	5361	4517	2723
ENSMUSG00000006356	chr12	Crip2	1.13E+08	1.13E+08	1437	1.376727	5.397624	1.55E-16	8.88E-15	0.030682	1	287	246	422	449	481	865	1051	1132	1458	1018
ENSMUSG00000031304	chrX	Il2rg	1.01E+08	1.01E+08	2387	2.221315	1.914971	1.69E-16	9.63E-15	0.056	1	13	21	21	24	22	118	129	93	100	95
ENSMUSG00000025283	chrX	Sat1	1.55E+08	1.55E+08	2774	1.423784	4.303829	1.71E-16	9.72E-15	0.03111	1	144	132	209	162	207	452	819	503	491	367
ENSMUSG00000014496	chr14	Ankrd28	31700015	31702306	5229	-1.51439	5.867517	1.73E-16	9.77E-15	0.037769	-1	975	761	2620	1301	1688	387	768	411	719	526
ENSMUSG00000002111	chr2	Spi1	91082390	91082523	2695	2.168924	2.285673	1.86E-16	1.05E-14	0.060345	1	34	8	45	25	30	149	148	144	154	103
ENSMUSG00000030218	chr6	Mgp	1.37E+08	1.37E+08	598	2.194243	6.028764	2.2E-16	1.23E-14	0.077374	1	161	224	369	580	576	1115	2791	2203	2018	1775
ENSMUSG00000057280	chr4	Musk	58285960	58286190	3776	-2.18548	3.236489	2.45E-16	1.36E-14	0.069884	-1	227	156	514	140	257	66	75	35	94	41
ENSMUSG00000044795	chr11	Cyb5d1	69391925	69392129	1605	-1.40937	3.235187	2.7E-16	1.5E-14	0.027231	-1	184	141	332	201	257	72	139	88	96	76
ENSMUSG00000009687	chr7	Fxyd5	31032722	31033018	4185	1.633472	3.845879	2.77E-16	1.52E-14	0.040452	1	76	66	112	146	162	364	503	397	397	298
ENSMUSG00000030047	chr6	Arhgap25	87458545	87460133	4250	2.657355	1.80447	2.76E-16	1.52E-14	0.085611	1	11	11	28	9	16	71	147	164	96	54
ENSMUSG00000073016	chrX	Uprt	1.04E+08	1.04E+08	2304	-2.87396	1.071973	2.82E-16	1.54E-14	0.085859	-1	27	33	120	45	79	5	10	12	12	5
ENSMUSG00000060063	chr5	Alox5ap	1.49E+08	1.49E+08	852	1.771587	3.031023	3.03E-16	1.65E-14	0.043333	1	57	46	62	50	74	243	229	244	241	158
ENSMUSG00000026012	chr1	Cd28	60716800	60717001	6122	-3.0982	2.393997	3.05E-16	1.65E-14	0.126993	-1	147	163	297	62	78	16	16	21	24	21
ENSMUSG00000050721	chr9	Plekho2	65554386	65557079	3271	1.383998	3.742932	3.06E-16	1.65E-14	0.028099	1	108	68	175	100	153	280	435	400	395	250
ENSMUSG00000060675	chr19	Pla2g16	7557459	7557564	6396	-1.27377	7.713155	3.07E-16	1.65E-14	0.027968	-1	3771	3606	5795	5140	5469	2002	2649	2058	2890	1677
ENSMUSG00000053199	chr9	Arhgap20	51765337	51765611	12685	-1.44265	4.243025	3.34E-16	1.79E-14	0.03248	-1	346	291	801	392	467	152	227	124	248	182
ENSMUSG00000021423	chr13	Ly86	37345345	37345574	997	2.261561	2.55917	3.39E-16	1.81E-14	0.069945	1	33	20	54	26	29	234	204	146	149	113
ENSMUSG00000034765	chr19	Dusp5	53529109	53529696	2473	3.166088	0.981528	4.16E-16	2.22E-14	0.099177	1	5	2	5	9	8	62	101	27	74	41
ENSMUSG00000033458	chr7	Fan1	64346758	64346895	5289	-1.6967	2.809949	4.3E-16	2.28E-14	0.039311	-1	141	96	300	136	216	40	73	68	63	55
ENSMUSG00000026469	chr1	Xpr1	1.55E+08	1.55E+08	17880	-1.56472	6.72008	4.45E-16	2.35E-14	0.041861	-1	2126	2073	4682	1611	2466	784	1024	844	1365	870

ENSMUSG00000049130	chr7	C5ar1	16246743	16249090	2570	1.828271	2.647718	4.81E-16	2.53E-14	0.045296	1	42	32	74	25	47	168	186	166	172	165
ENSMUSG00000040907	chr7	Atp1a3	24978167	24978576	5972	4.041815	1.876004	5.2E-16	2.73E-14	0.19531	1	9	0	10	5	9	50	95	277	106	72
ENSMUSG00000026360	chr1	Rgs2	1.44E+08	1.44E+08	3627	1.725851	3.494384	5.87E-16	3.07E-14	0.044833	1	53	54	85	113	111	253	473	319	298	230
ENSMUSG00000033825	chr17	Tpsb2	25366550	25366621	1081	1.884247	3.242804	6.52E-16	3.39E-14	0.053091	1	70	33	102	54	67	192	364	315	191	264
ENSMUSG00000031765	chr8	Mt1	94179089	94179338	540	3.427703	5.573984	7.45E-16	3.86E-14	0.175681	1	109	85	106	118	230	1468	4441	689	1463	428
ENSMUSG00000041959	chr3	S100a10	93555080	93555211	1212	1.302788	5.103398	8.3E-16	4.28E-14	0.028434	1	275	263	350	316	357	823	959	914	930	763
ENSMUSG00000093327	chr18	Mir5107	60812076	60812163	88	1.935509	5.12339	8.85E-16	4.55E-14	0.062737	1	266	187	331	147	213	1205	782	1052	1201	656
ENSMUSG00000022629	chr15	Kif21a	90933276	90934543	6475	-1.31048	4.498365	8.9E-16	4.56E-14	0.028293	-1	410	316	787	547	587	150	274	214	376	197
ENSMUSG00000036896	chr4	C1qc	1.37E+08	1.37E+08	1931	1.633988	5.377137	9.03E-16	4.61E-14	0.045577	1	328	206	482	240	396	1242	938	1316	1100	934
ENSMUSG00000078716	chr4	Tmem8b	43668971	43669172	5553	-1.65863	4.597127	9.21E-16	4.68E-14	0.04601	-1	357	312	683	808	862	148	245	178	289	210
ENSMUSG00000060572	chr4	Mfap2	1.41E+08	1.41E+08	1211	1.759832	2.580285	9.43E-16	4.77E-14	0.04185	1	39	31	63	33	50	123	143	181	192	173
ENSMUSG00000033777	chrX	Tlr13	1.06E+08	1.06E+08	4086	2.540084	1.227938	9.89E-16	4.97E-14	0.06988	1	7	4	16	9	17	54	99	89	67	37
ENSMUSG00000040433	chr9	Zbtb38	96682770	96689029	11733	-1.37959	5.079182	9.86E-16	4.97E-14	0.03232	-1	533	448	1257	828	1014	237	359	318	423	370
ENSMUSG00000099023	chr11	Gm27456	1.02E+08	1.02E+08	63	-2.30941	1.0047	1.04E-15	5.21E-14	0.051354	-1	32	38	82	48	64	6	16	8	14	15
ENSMUSG00000039704	chr15	Lmbrd2	9140621	9140740	3863	-3.33545	2.179836	1.08E-15	5.37E-14	0.148691	-1	49	45	347	105	182	8	25	13	9	17
ENSMUSG00000040345	chr10	Arhgap9	1.27E+08	1.27E+08	1811	2.328193	1.56192	1.08E-15	5.37E-14	0.06226	1	16	12	23	10	14	91	86	103	73	65
ENSMUSG00000027457	chr2	Snph	1.52E+08	1.52E+08	7861	-3.31278	0.390993	1.14E-15	5.65E-14	0.096623	-1	17	15	53	42	60	4	8	2	4	2
ENSMUSG00000072620	chr11	Slfn2	83065112	83065343	1664	1.956882	2.736566	1.15E-15	5.66E-14	0.054307	1	46	34	47	31	54	198	275	164	149	150
ENSMUSG00000017724	chr11	Etv4	1.02E+08	1.02E+08	3104	2.057956	2.124534	1.19E-15	5.84E-14	0.056004	1	19	15	45	24	32	85	141	81	159	155
ENSMUSG00000024965	chr19	Fermt3	6998958	6999520	2587	2.057979	2.209601	1.2E-15	5.86E-14	0.057141	1	24	16	52	21	31	132	124	168	126	97
ENSMUSG00000020312	chr10	Shc2	79617940	79620099	5537	-1.81103	3.249672	1.25E-15	6.08E-14	0.049716	-1	210	152	404	159	296	63	75	87	60	87
ENSMUSG00000027386	chr2	Fbln7	1.29E+08	1.29E+08	3228	2.005994	3.87639	1.26E-15	6.12E-14	0.065131	1	38	58	136	82	176	335	367	493	455	435
ENSMUSG00000031762	chr8	Mt2	94172618	94172875	556	4.712533	5.930839	1.26E-15	6.12E-14	0.29902	1	51	33	50	39	202	2102	6255	747	2045	380
ENSMUSG00000037416	chr18	Dmxl1	49832670	49833176	21860	-1.6481	4.813393	1.39E-15	6.73E-14	0.046457	-1	464	410	1399	564	792	125	346	233	313	249
ENSMUSG00000004707	chr1	Ly9	1.72E+08	1.72E+08	3307	3.103687	1.33608	1.41E-15	6.75E-14	0.115289	1	11	2	16	3	9	77	97	105	44	58
ENSMUSG00000066232	chr7	Ipo7	1.1E+08	1.1E+08	3117	-1.2368	6.188549	1.46E-15	6.99E-14	0.027175	-1	1279	1194	2605	1494	1822	556	1135	698	962	685
ENSMUSG00000022788	chr16	Fgd4	16416917	16422820	17517	-1.6425	3.994937	1.5E-15	7.15E-14	0.043841	-1	308	223	816	269	435	122	163	106	185	129
ENSMUSG00000034653	chr18	Ythdc2	44828665	44828918	6299	-1.82661	2.647837	1.51E-15	7.19E-14	0.047645	-1	108	82	244	148	229	26	62	48	58	56
ENSMUSG00000036257	chr12	Pnpla8	44221370	44221460	3947	-1.17661	6.838567	1.56E-15	7.37E-14	0.024928	-1	2098	1666	3532	2632	3014	951	1586	1189	1774	1018
ENSMUSG00000020623	chr11	Map2k6	1.1E+08	1.1E+08	3444	-1.51404	4.69296	1.56E-15	7.37E-14	0.038963	-1	429	316	1031	589	870	223	267	174	294	253
ENSMUSG00000038179	chr1	Slamf7	1.72E+08	1.72E+08	4577	2.236217	1.428304	1.57E-15	7.37E-14	0.05517	1	12	10	21	14	15	60	86	109	74	53
ENSMUSG00000025326	chr7	Ube3a	59228752	59229271	5097	-1.55712	4.893874	1.63E-15	7.61E-14	0.04177	-1	416	397	1376	647	961	188	395	227	344	246
ENSMUSG00000038023	chr5	Atp6v0a2	1.25E+08	1.25E+08	3019	-1.46857	4.100771	1.62E-15	7.61E-14	0.035163	-1	286	187	641	444	559	135	217	137	199	146
ENSMUSG00000059422	chr9	Gm8116	78820638	78821838	1201	-1.50205	3.560049	1.65E-15	7.7E-14	0.03532	-1	218	229	411	246	298	93	189	81	121	85
ENSMUSG00000059456	chr14	Ptk2b	66153257	66154269	7398	2.142619	1.877674	1.71E-15	7.94E-14	0.056725	1	18	18	29	21	18	85	113	149	105	70
ENSMUSG00000063506	chr14	Arhgap22	33214026	33214293	3876	2.182715	1.193206	1.79E-15	8.29E-14	0.047238	1	10	7	16	9	21	48	67	70	69	65
ENSMUSG00000026177	chr1	Slc11a1	74375195	74375321	3705	2.088069	2.457207	1.88E-15	8.65E-14	0.062068	1	21	25	63	22	38	129	170	228	158	101
ENSMUSG00000024610	chr18	Cd74	60803848	60804010	1410	1.852033	7.512198	1.91E-15	8.75E-14	0.060638	1	1314	1058	1977	857	1131	5807	3871	5707	6260	3774
ENSMUSG00000030772	chr7	Dkk3	1.12E+08	1.12E+08	3357	-3.5781	5.247925	1.92E-15	8.8E-14	0.193692	-1	308	539	3220	625	1751	80	94	115	50	165
ENSMUSG00000026728	chr2	Vim	13573927	13574060	4743	1.393439	7.534829	1.96E-15	8.92E-14	0.035197	1	1201	1209	2037	1794	2006	3554	4688	5711	5410	4868
ENSMUSG00000040613	chr6	Apobec1	1.23E+08	1.23E+08	2391	1.673941	2.587454	2.02E-15	9.18E-14	0.039035	1	35	25	80	38	55	150	192	165	154	146
ENSMUSG00000060961	chr5	Slc4a4	88886818	88887324	10815	-1.64651	3.562957	2.05E-15	9.29E-14	0.043347	-1	212	152	562	224	370	62	127	99	149	92
ENSMUSG00000015745	chr3	Plekho1	95988429	95989633	2172	1.486276	4.740929	2.29E-15	1.03E-13	0.038088	1	176	154	293	220	296	665	574	581	1155	604
ENSMUSG00000025402	chr10	Nab2	1.28E+08	1.28E+08	2941	1.991628	3.607652	2.48E-15	1.12E-13	0.064061	1	56	55	97	80	105	272	330	212	371	525
ENSMUSG00000076138	chr9	Gm26377	78478528	78478635	108	1.497176	5.839136	2.77E-15	1.24E-13	0.040032	1	426	434	609	427	459	1249	1260	1905	1974	1245
ENSMUSG00000029202	chr5	Pds5a	65615260	65615604	4146	-1.52267	3.949771	3.52E-15	1.57E-13	0.038485	-1	258	184	697	341	466	100	195	130	158	146
ENSMUSG00000086825	chr1	Gm15675	1.3E+08	1.3E+08	3681	1.643495	3.179619	3.69E-15	1.64E-13	0.041207	1	74	61	106	39	66	174	317	255	304	198
ENSMUSG00000004098	chr9	Col5a3	20770050	20770978	6809	1.515666	5.713815	3.93E-15	1.74E-13	0.041461	1	458	309	599	319	502	1184	1151	1256	1702	1636
ENSMUSG00000067924	chrX	Cxx1b	53669177	53670408	1232	1.229092	4.689959	4.15E-15	1.83E-13	0.025991	1	249	182	323	229	243	495	681	675	856	585
ENSMUSG00000021760	chr13	Gpx8	1.13E+08	1.13E+08	1016	1.687299	3.313307	4.24E-15	1.87E-13	0.044434	1	53	74	78	61	101	194	346	337	266	222
ENSMUSG00000040212	chr7	Emp3	45918023	45918235	972	1.438328	3.756201	4.52E-15	1.98E-13	0.033815	1	82	65	154	128	165	279	347	415	392	332
ENSMUSG00000027499	chr3	Pkia	7366669	7366752	3721	-1.26395	9.007363	4.59E-15	2E-13	0.030127	-1	8633	7590	18729	11601	13647	4018	7416	4497	6683	5317
ENSMUSG00000039476	chr2	Prrx2	30834972	30835252	1961	2.229175	1.119799	4.6E-15	2E-13	0.048807	1	14	7	11	8	17	50	66	52	72	64
ENSMUSG00000059498	chr1	Fcgr3	1.71E+08	1.71E+08	1736	1.733373	3.839232	4.59E-15	2E-13	0.049937	1	107	84	147	75	112	385	451	533	348	244
ENSMUSG00000001750	chr19	Tcirg1	3896050	3896192	4470	1.699771	3.446397	4.67E-15	2.02E-13	0.046666	1	67	51	107	81	107	289	272	409	273	223
ENSMUSG00000046230	chr19	Vps13a	16616763	16616915	9656	-1.44147	4.190258	4.78E-15	2.06E-13	0.035392	-1	256	249	796	391	570	135	245	158	220	148
ENSMUSG00000022048	chr14	Dpysl2	66802864	66805436	4520	1.462984	3.467266	5.08E-15	2.19E-13	0.033753	1	78	64	112	107	106	278	260	307	373	230
ENSMUSG00000019796	chr10	Lrp11	7589800	7590613	3418	1.694194	2.076287	5.48E-15	2.35E-13	0.034592	1	30	26	38	29	30	89	149	105	147	85
ENSMUSG00000025492	chr7	Ifitm3	1.41E+08	1.41E+08	678	1.270397	5.462968	5.68E-15	2.43E-13	0.029352	1	359	269	551	385	537	936	1430	1354	1044	885
ENSMUSG00000047141	chr16	Zfp654	64780351	64783276	4741	-1.31292	3.779268	5.8E-15	2.47E-13	0.027997	-1	216	235	536	271	352	99	183	140	170	130
ENSMUSG00000020437	chr11	Myo1g	6506548	6506832	6957	2.122627	1.809916	6.31E-15	2.68E-13	0.059541	1	21	9	30	16	27	87	92	137	99	77
ENSMUSG00000050310	chr15	Rictor	6708381	6708451	9311	-1.46775	3.900168	6.47E-15	2.74E-13	0.036242	-1	304	285	623	229	347	119	155	150	176	120
ENSMUSG00000050199	chr2	Lgr4	1.1E+08	1.1E+08	5884	-1.2392	4.938879	6.66E-15	2.81E-13	0.027543	-1	538	406	1164	656	827	209	422	309	439	311
ENSMUSG00000020388	chr11	Pdlim4	54054928	54055239	2560	1.519883	2.88176	6.71E-15	2.83E-13	0.034083	1	47	43	84	55	75	176	177	177	245	192
ENSMUSG00000063193	chr11	Cd300lb	1.15E+08	1.15E+08	2917	1.964402	1.501598	6.76E-15	2.84E-13	0.043525	1	14	11	25	17	22	50	114	90	86	57

ENSMUSG00000044951	chr13	Mylk4	32700827	32705215	6128	-1.54808	11.13988	6.81E-15	2.85E-13	0.045218	-1	42590	39256	91222	39752	65803	15473	19847	15688	36238	19530
ENSMUSG00000099088	chr10	Gm27920	1.23E+08	1.23E+08	96	-2.53733	0.672423	6.92E-15	2.89E-13	0.061143	-1	28	26	75	31	55	7	8	4	12	9
ENSMUSG00000031402	chrX	Mpp1	75109733	75110843	5343	1.262698	4.902551	6.98E-15	2.9E-13	0.028408	1	271	221	395	219	301	651	850	883	832	600
ENSMUSG00000044499	chr10	Hs3st5	36506814	36507615	4340	-1.72744	2.43237	7.62E-15	3.15E-13	0.043297	-1	94	73	191	159	158	26	61	36	61	45
ENSMUSG00000052336	chr9	Cx3cr1	1.2E+08	1.2E+08	3742	2.994019	0.443483	7.64E-15	3.15E-13	0.080238	1	2	2	6	5	7	44	26	39	46	39
ENSMUSG00000103319	chrX	AC055766.1	68821093	68821490	1019	-2.95571	0.510108	7.64E-15	3.15E-13	0.09012	-1	30	22	81	25	42	0	11	5	7	5
ENSMUSG00000035232	chrX	Pdk3	93764607	93765255	2561	2.212972	1.033172	7.95E-15	3.27E-13	0.046535	1	10	9	13	9	13	61	60	49	69	45
ENSMUSG00000067851	chr1	Arfgef1	10137571	10138996	11318	-1.1785	6.834725	8.15E-15	3.34E-13	0.026369	-1	2101	1609	4225	2312	2874	939	1547	1180	1605	1165
ENSMUSG00000079592	chr9	C1qtnf5	44107245	44107344	1398	1.56461	2.629655	8.24E-15	3.36E-13	0.035028	1	36	33	68	50	62	115	173	165	190	178
ENSMUSG00000056201	chr19	Cfl1	5490485	5490602	1148	1.205574	6.157655	9.14E-15	3.72E-13	0.027321	1	601	486	853	675	860	1629	1917	1950	2122	1407
ENSMUSG00000024695	chr19	Zfp91	12763660	12764380	10046	-1.14005	7.87732	9.22E-15	3.74E-13	0.025064	-1	4294	3631	7693	5022	5740	2122	3432	2286	3533	2211
ENSMUSG00000024420	chr18	Zfp521	13687013	13689024	6152	-1.32318	3.577036	9.28E-15	3.75E-13	0.028006	-1	221	181	453	224	323	109	138	113	133	120
ENSMUSG00000025534	chr5	Gusb	1.3E+08	1.3E+08	4548	1.301062	4.215215	9.69E-15	3.91E-13	0.029404	1	140	116	219	162	228	368	517	619	503	376
ENSMUSG00000053175	chr7	Bcl3	19808462	19809056	2485	2.872528	2.061087	1.12E-14	4.49E-13	0.12023	1	8	10	18	12	31	112	292	106	90	64
ENSMUSG00000022357	chr15	Klhl38	58314573	58315116	2212	-1.3671	4.990257	1.12E-14	4.5E-13	0.034342	-1	493	447	1245	711	940	224	489	295	306	316
ENSMUSG00000044501	chr17	Zfp758	22361453	22361707	2974	-1.62029	2.420415	1.15E-14	4.58E-13	0.037869	-1	93	96	187	112	164	25	54	50	68	43
ENSMUSG00000003882	chr15	Il7r	9506161	9508358	3208	4.071693	0.802028	1.21E-14	4.81E-13	0.171816	1	2	3	6	3	0	32	68	108	26	38
ENSMUSG00000050919	chr13	Zfp366	99184823	99184864	2763	-4.23373	-0.28786	1.23E-14	4.87E-13	0.117117	-1	10	7	41	22	37	0	2	1	1	2
ENSMUSG00000024737	chr19	Slc15a3	10839727	10839998	5491	2.607788	1.914697	1.24E-14	4.91E-13	0.098958	1	7	6	24	23	25	77	113	193	113	70
ENSMUSG00000024105	chr17	Themis3	66555252	66556264	1797	-6.0727	-0.45868	1.26E-14	4.97E-13	0.173634	-1	15	8	39	5	39	0	0	0	0	1
ENSMUSG00000047036	chr9	Zfp445	1.23E+08	1.23E+08	2961	-1.89646	3.050943	1.34E-14	5.28E-13	0.059145	-1	141	121	363	199	265	39	109	46	49	76
ENSMUSG00000040253	chr3	Gbp7	1.43E+08	1.43E+08	5552	-1.72174	3.28111	1.47E-14	5.76E-13	0.049637	-1	160	152	405	148	387	64	100	92	96	60
ENSMUSG00000001270	chr12	Ckb	1.12E+08	1.12E+08	1478	1.89358	3.73447	1.63E-14	6.39E-13	0.062239	1	64	78	110	76	120	227	346	636	417	264
ENSMUSG00000024924	chr19	Vldlr	27216484	27216948	10068	-1.53514	8.068742	1.74E-14	6.79E-13	0.045701	-1	4920	4056	11136	5718	7522	2215	2514	1587	4307	2138
ENSMUSG00000060591	chr7	Ifitm2	1.41E+08	1.41E+08	627	1.187083	5.409244	1.77E-14	6.86E-13	0.026504	1	348	271	527	457	490	987	1356	1120	1171	746
ENSMUSG00000103866	chr18	Setbp1	78755215	78755825	4749	-3.3311	0.98897	1.77E-14	6.86E-13	0.132338	-1	23	18	139	45	79	6	7	6	6	5
ENSMUSG00000028572	chr4	Hook1	95967240	95967556	8318	-1.39398	4.92253	1.91E-14	7.39E-13	0.036372	-1	580	546	1265	481	746	192	362	264	434	296
ENSMUSG00000020961	chr12	Ston2	91638542	91639805	6915	-2.3971	4.179498	1.99E-14	7.66E-13	0.101313	-1	216	145	1036	501	808	69	128	77	122	128
ENSMUSG00000058672	chr13	Tubb2a	34074301	34075528	1584	1.652787	3.728763	2E-14	7.68E-13	0.04757	1	67	59	97	145	143	299	329	384	466	326
ENSMUSG00000033684	chr1	Qsox1	1.56E+08	1.56E+08	8291	1.283817	4.834878	2.04E-14	7.83E-13	0.030423	1	213	202	308	301	295	556	671	705	1002	730
ENSMUSG00000021668	chr13	Polk	96480689	96482254	4289	-1.68434	3.793408	2.1E-14	8.01E-13	0.0504	-1	305	271	635	193	330	91	178	89	168	88
ENSMUSG00000025899	chr9	Alkbh8	3335478	3335594	3581	-1.68526	2.595002	2.14E-14	8.16E-13	0.044176	-1	110	84	261	120	191	32	82	43	68	40
ENSMUSG00000017754	chr2	Pltp	1.65E+08	1.65E+08	2562	1.383328	5.389863	2.18E-14	8.28E-13	0.036388	1	327	258	525	356	413	1077	898	1353	1193	867
ENSMUSG00000034739	chr9	Mfrp	44101738	44101946	4325	1.538491	2.641357	2.19E-14	8.29E-13	0.035105	1	37	33	70	50	65	116	173	165	191	179
ENSMUSG00000028710	chr4	Atpaf1	1.16E+08	1.16E+08	3609	-1.21014	5.390588	2.34E-14	8.82E-13	0.027942	-1	817	573	1179	1022	1161	353	704	355	555	386
ENSMUSG00000068335	chr6	Dok1	83030934	83032060	1977	1.715099	2.142584	2.33E-14	8.82E-13	0.039725	1	31	25	40	25	39	122	146	96	131	99
ENSMUSG00000015947	chr3	Fcgr1	96282909	96284619	2589	2.32258	1.773885	2.48E-14	9.33E-13	0.075059	1	19	12	23	13	21	128	107	83	72	91
ENSMUSG00000028874	chr4	Fgr	1.33E+08	1.33E+08	3863	2.719658	0.727933	2.56E-14	9.61E-13	0.082785	1	2	2	10	5	14	53	65	44	52	27
ENSMUSG00000019990	chr10	Pde7b	20398004	20400632	7232	-1.16018	4.726087	2.59E-14	9.67E-13	0.024902	-1	446	387	869	594	701	194	423	262	359	277
ENSMUSG00000049173	chr18	Myoz3	60576316	60576518	870	-1.36971	5.565423	2.82E-14	1.05E-12	0.036204	-1	887	560	1857	983	1466	375	657	362	511	507
ENSMUSG00000015659	chr17	Serac1	6042196	6044250	4576	-1.83288	2.95298	2.94E-14	1.09E-12	0.056094	-1	154	98	387	167	211	40	86	43	63	75
ENSMUSG00000060096	chr18	Amd-ps3	64448519	64450014	1496	-2.88978	2.921297	3.29E-14	1.22E-12	0.1371	-1	285	116	360	116	209	55	27	15	50	13
ENSMUSG00000056069	chr15	Fam105a	27655071	27657071	2830	2.047787	1.761895	3.43E-14	1.27E-12	0.056176	1	19	17	32	15	19	105	80	99	113	72
ENSMUSG00000030577	chr7	Cd22	30865402	30866662	4987	4.641	-0.49515	3.45E-14	1.27E-12	0.085732	1	1	1	0	1	0	12	15	26	28	20
ENSMUSG00000037379	chr5	Spon2	33213518	33214652	2237	2.251028	1.975768	3.62E-14	1.33E-12	0.074931	1	18	17	31	10	31	67	91	114	149	145
ENSMUSG00000040133	chr2	Gpr176	1.18E+08	1.18E+08	3899	3.073215	0.291849	4.02E-14	1.47E-12	0.080794	1	2	2	0	4	10	18	41	39	48	33
ENSMUSG00000049382	chr15	Krt8	1.02E+08	1.02E+08	1805	4.356834	0.46673	4.13E-14	1.51E-12	0.194126	1	1	0	4	2	2	19	18	75	81	25
ENSMUSG00000046541	chr7	Zfp526	25221451	25221504	3354	-2.03032	1.511051	4.15E-14	1.51E-12	0.054316	-1	42	45	123	77	84	10	29	14	28	20
ENSMUSG00000026771	chr2	Spopl	23506220	23511460	10280	-1.20061	4.094904	4.34E-14	1.58E-12	0.025751	-1	292	266	648	316	443	125	236	192	245	158
ENSMUSG00000032334	chr9	Loxl1	58287723	58288917	3338	1.290869	4.945135	4.59E-14	1.66E-12	0.031955	1	276	197	421	244	306	623	659	862	1019	770
ENSMUSG00000022339	chr15	Ebag9	44619641	44619942	1561	-1.13507	3.910269	4.62E-14	1.67E-12	0.022265	-1	284	241	494	279	377	120	218	163	205	156
ENSMUSG00000027827	chr3	Kcnab1	65109384	65109992	8593	-3.17359	2.738335	5.05E-14	1.82E-12	0.162935	-1	151	225	430	53	111	28	21	18	25	25
ENSMUSG00000024978	chr19	Gpam	55069734	55071046	3832	-1.86954	6.725039	5.74E-14	2.06E-12	0.068903	-1	1347	1475	3861	3522	3707	370	1253	759	913	938
ENSMUSG00000059182	chr6	Skap2	51859166	51859570	1638	1.377015	3.154356	5.91E-14	2.12E-12	0.030891	1	62	60	105	65	103	186	323	249	225	177
ENSMUSG00000035314	chr7	Gdpd5	99381549	99382208	3582	-1.86464	2.646311	5.99E-14	2.14E-12	0.057501	-1	102	129	318	102	160	40	49	42	74	40
ENSMUSG00000103268	chr9	AC161246.1	1.1E+08	1.1E+08	3165	-1.55783	7.299236	6.29E-14	2.24E-12	0.048968	-1	2473	2085	6874	3823	4699	901	2142	1026	1720	1617
ENSMUSG00000001525	chr17	Tubb5	35833921	35836039	3327	1.19275	5.866253	6.83E-14	2.43E-12	0.028453	1	454	451	640	559	724	1276	1516	1597	1658	1273
ENSMUSG00000001864	chr2	Aif1l	31950139	31950381	4032	1.66471	3.36917	6.96E-14	2.47E-12	0.049386	1	59	43	114	100	85	290	208	298	364	228
ENSMUSG00000030748	chr7	Il4ra	1.26E+08	1.26E+08	5092	1.828126	3.943058	7.07E-14	2.5E-12	0.062245	1	79	70	128	87	186	397	673	533	325	246
ENSMUSG00000042717	chr6	Ppp1r3a	14713822	14719941	7120	-1.48505	8.209392	7.58E-14	2.67E-12	0.045127	-1	5051	4855	12328	6205	7877	1496	3225	2353	4249	3168
ENSMUSG00000042460	chr6	C1galt1	7844842	7845394	2452	-2.06766	2.348241	7.78E-14	2.74E-12	0.069327	-1	110	59	267	102	153	30	60	31	25	30
ENSMUSG00000067925	chrX	Cxx1a	53642488	53643682	1195	1.11274	4.129524	8.46E-14	2.97E-12	0.02241	1	157	123	235	163	211	347	457	415	614	352
ENSMUSG00000036745	chr3	Ttll7	1.47E+08	1.47E+08	8105	-1.67977	7.520409	1.03E-13	3.62E-12	0.057616	-1	4403	3379	8886	2442	4049	1475	1936	1164	2098	1341
ENSMUSG00000060716	chr12	Plekhh1	79029163	79029420	6432	2.898143	1.303443	1.04E-13	3.63E-12	0.114477	1	7	9	14	7	7	59	55	118	46	82
ENSMUSG00000068740	chr3	Celsr2	1.08E+08	1.08E+08	11513	-1.69273	3.5633	1.08E-13	3.76E-12	0.05311	-1	178	147	550	285	374	55	106	133	134	84

ENSMUSG00000027907	chr3	S100a11	93520488	93520553	511	1.373874	4.894487	1.12E-13	3.89E-12	0.037266	1	291	193	279	258	275	616	836	1006	814	603
ENSMUSG00000050708	chr7	Ftl1	45457944	45458283	1340	1.542563	8.351518	1.13E-13	3.91E-12	0.049217	1	2802	2240	3396	2131	2583	7736	7661	12081	9744	6486
ENSMUSG00000024601	chr18	Isoc1	58659482	58659797	2563	-1.15451	4.626236	1.14E-13	3.93E-12	0.025833	-1	426	369	851	509	643	181	363	309	289	259
ENSMUSG00000041702	chr12	Btbd7	1.03E+08	1.03E+08	4298	-1.97607	2.847777	1.17E-13	4.01E-12	0.068446	-1	103	84	392	161	247	36	63	36	73	57
ENSMUSG00000054520	chr5	Sh3bp2	34525838	34525901	4277	1.903892	3.158342	1.16E-13	4.01E-12	0.065022	1	50	43	80	49	78	216	504	221	252	115
ENSMUSG00000017400	chr11	Stac2	98036623	98038070	3139	3.705906	0.525283	1.34E-13	4.61E-12	0.163559	1	1	0	7	4	3	12	45	82	45	37
ENSMUSG00000041650	chr14	Pcca	1.23E+08	1.23E+08	5210	-1.08356	5.807778	1.43E-13	4.87E-12	0.024138	-1	915	1001	1696	1140	1380	465	830	666	812	543
ENSMUSG00000018507	chr11	Trpv2	62574486	62574600	4485	1.725548	1.720655	1.44E-13	4.92E-12	0.039474	1	16	14	32	30	27	66	96	100	106	75
ENSMUSG00000052026	chr18	Slc6a7	60995381	60996831	3342	3.831332	-0.43517	1.5E-13	5.09E-12	0.091561	1	0	0	2	2	2	13	15	18	34	24
ENSMUSG00000048865	chr1	Arhgap30	1.71E+08	1.71E+08	8591	1.688173	2.309683	1.52E-13	5.15E-12	0.044755	1	32	23	53	26	53	120	174	151	118	104
ENSMUSG00000045319	chr2	Proser2	6097607	6101360	9563	2.48334	0.740045	1.55E-13	5.24E-12	0.066562	1	6	5	7	7	12	39	40	35	79	45
ENSMUSG00000021339	chr13	Mrs2	24992483	24993188	2035	-1.64763	3.067562	1.68E-13	5.65E-12	0.048357	-1	132	85	342	235	275	58	88	70	81	69
ENSMUSG00000094439	chr4	Gm21969	1.4E+08	1.4E+08	4402	-1.35558	5.826124	1.68E-13	5.65E-12	0.038051	-1	914	597	2163	1454	1783	412	719	546	674	569
ENSMUSG00000040446	chr18	Rprd1a	24484962	24488331	4297	-1.20428	4.124442	1.71E-13	5.74E-12	0.027392	-1	337	239	644	327	462	141	266	169	199	189
ENSMUSG00000027365	chr2	Trpm7	1.27E+08	1.27E+08	11315	-1.23906	4.966417	1.72E-13	5.77E-12	0.031014	-1	537	401	1277	651	824	209	437	339	408	323
ENSMUSG00000021280	chr12	Exoc3l4	1.11E+08	1.11E+08	2922	2.107774	2.895538	1.89E-13	6.31E-12	0.077936	1	57	48	49	23	33	228	239	151	293	167
ENSMUSG00000026656	chr1	Fcgr2b	1.71E+08	1.71E+08	5790	1.589234	3.59571	1.99E-13	6.63E-12	0.047552	1	84	71	161	61	113	372	378	337	305	217
ENSMUSG00000063524	chr4	Eno1	1.5E+08	1.5E+08	5379	1.259354	6.765827	2.13E-13	7.08E-12	0.033656	1	989	618	1311	1058	1214	2270	2455	3250	3588	2344
ENSMUSG00000031433	chrX	Rbm41	1.4E+08	1.4E+08	6638	-2.18101	1.002431	2.19E-13	7.27E-12	0.058422	-1	41	24	78	59	58	10	21	8	10	14
ENSMUSG00000042599	chr6	Kdm7a	39136623	39143305	10057	-1.1862	5.432553	2.21E-13	7.3E-12	0.029134	-1	677	549	1660	944	1213	324	598	470	610	432
ENSMUSG00000049625	chr13	Tifab	56173703	56176633	3498	2.302934	1.005637	2.29E-13	7.56E-12	0.066883	1	9	6	23	6	8	62	51	55	62	49
ENSMUSG00000059089	chr1	Fcgr4	1.71E+08	1.71E+08	1256	3.643186	0.327924	2.38E-13	7.84E-12	0.14105	1	2	2	4	2	3	42	52	57	18	17
ENSMUSG00000014846	chr8	Tppp3	1.05E+08	1.05E+08	1848	1.930054	6.025419	2.47E-13	8.11E-12	0.076697	1	324	219	446	577	641	1116	1700	1484	2049	2849
ENSMUSG00000074093	chr7	Svip	51997165	51999777	3059	-1.05124	5.087692	2.62E-13	8.57E-12	0.02254	-1	624	575	1026	673	789	284	529	360	495	372
ENSMUSG00000030116	chr6	Mfap5	1.23E+08	1.23E+08	3589	1.223335	4.526392	2.65E-13	8.67E-12	0.029852	1	187	165	320	211	228	471	583	726	585	521
ENSMUSG00000102351	chr16	AC107830.1	49913193	49913570	1815	1.320805	3.910001	2.7E-13	8.79E-12	0.03286	1	127	124	171	107	145	334	502	436	398	273
ENSMUSG00000051146	chr16	Camk2n2	20619215	20620243	1291	2.573725	0.624624	2.72E-13	8.84E-12	0.069341	1	5	6	8	3	10	27	49	32	79	37
ENSMUSG00000032383	chr9	Ppib	66060169	66060400	960	1.063587	5.285795	2.77E-13	8.97E-12	0.023194	1	365	300	479	404	461	859	1100	930	1116	782
ENSMUSG00000019988	chr10	Nedd1	92684746	92686295	3534	-1.15206	4.297329	2.85E-13	9.21E-12	0.026093	-1	373	291	737	369	460	148	290	197	277	212
ENSMUSG00000022358	chr15	Fbxo32	58175879	58181555	6936	-1.34884	8.272679	2.87E-13	9.25E-12	0.039322	-1	6822	5017	13015	5069	6703	2521	3579	2623	4512	2839
ENSMUSG00000048163	chr5	Selplg	1.14E+08	1.14E+08	2604	1.912049	2.6757	2.9E-13	9.33E-12	0.065455	1	42	21	84	28	45	198	155	213	179	133
ENSMUSG00000038844	chr2	Kif16b	1.43E+08	1.43E+08	6635	-1.38654	5.467364	3.03E-13	9.73E-12	0.040406	-1	673	512	1597	1227	1364	272	546	398	564	474
ENSMUSG00000026278	chr1	Bok	93685660	93685854	1775	1.950944	1.348199	3.1E-13	9.95E-12	0.049346	1	15	10	25	16	14	64	57	69	98	59
ENSMUSG00000060586	chr17	H2-Eb1	34305877	34306047	1184	1.834215	6.002701	3.18E-13	1.01E-11	0.070133	1	475	418	684	269	372	2128	1445	2015	2096	1202
ENSMUSG00000005958	chr16	Ephb3	21204755	21205263	6289	1.938588	1.403161	3.28E-13	1.05E-11	0.049959	1	14	9	22	19	20	52	64	87	82	74
ENSMUSG00000020644	chr12	Id2	25093801	25094576	1270	1.667855	2.409376	3.41E-13	1.08E-11	0.045411	1	38	30	50	37	43	125	213	155	117	107
ENSMUSG00000025877	chr13	Hk3	55005985	55006315	3682	2.449635	2.092721	3.4E-13	1.08E-11	0.101131	1	16	14	37	16	22	103	141	228	85	69
ENSMUSG00000020773	chr11	Trim47	1.16E+08	1.16E+08	2735	1.376244	3.707029	3.59E-13	1.14E-11	0.035987	1	99	80	137	109	155	219	330	318	430	398
ENSMUSG00000042439	chr18	Zfp532	65580230	65580510	11192	-1.18081	4.047134	3.6E-13	1.14E-11	0.026849	-1	298	201	607	336	468	155	213	184	233	140
ENSMUSG00000075470	chr15	Alg10b	90224311	90224608	3727	-1.66982	3.335166	3.89E-13	1.22E-11	0.053496	-1	167	164	427	221	294	37	154	76	94	89
ENSMUSG00000036594	chr17	H2-Aa	34282744	34283023	1874	1.755054	6.399339	4.03E-13	1.27E-11	0.065309	1	652	566	959	401	472	2652	1987	2611	2758	1602
ENSMUSG00000045382	chr1	Cxcr4	1.29E+08	1.29E+08	1808	1.862986	1.96553	4.26E-13	1.34E-11	0.054514	1	16	14	30	37	35	111	102	110	117	90
ENSMUSG00000063659	chr1	Zbtb18	1.77E+08	1.77E+08	6138	-1.12279	6.880856	4.64E-13	1.45E-11	0.027687	-1	2077	1785	4043	2423	2934	912	1538	1244	1952	1228
ENSMUSG00000044788	chr11	Fads6	1.15E+08	1.15E+08	6653	-2.05634	3.591839	4.77E-13	1.49E-11	0.083453	-1	171	116	321	480	523	59	102	65	123	81
ENSMUSG00000089672	chr10	Gp49a	51480632	51480753	2107	2.44403	1.951993	4.77E-13	1.49E-11	0.102166	1	16	3	25	24	28	90	181	152	77	75
ENSMUSG00000029675	chr5	Eln	1.35E+08	1.35E+08	2583	1.528026	4.366033	4.84E-13	1.5E-11	0.047565	1	150	137	222	135	202	348	418	589	981	482
ENSMUSG00000053347	chr17	Zfp943	21962552	21962819	5277	-1.2367	4.101596	4.88E-13	1.51E-11	0.030348	-1	305	349	602	316	358	150	247	156	221	163
ENSMUSG00000008475	chr1	Arpc5	1.53E+08	1.53E+08	2276	1.174554	4.620804	5.12E-13	1.58E-11	0.028221	1	217	191	300	197	299	527	787	700	599	473
ENSMUSG00000030329	chr6	Pianp	1.25E+08	1.25E+08	2753	3.381741	0.775754	5.16E-13	1.59E-11	0.149907	1	3	3	9	4	3	20	47	108	56	31
ENSMUSG00000049103	chr9	Ccr2	1.24E+08	1.24E+08	6393	1.44053	3.091926	5.62E-13	1.73E-11	0.037428	1	65	52	99	77	70	241	267	182	279	149
ENSMUSG00000034595	chr17	Ppp1r18	35865593	35865694	4317	1.28635	3.353992	5.64E-13	1.73E-11	0.030461	1	75	64	147	85	110	245	281	293	277	198
ENSMUSG00000015396	chr13	Cd83	43785107	43785250	2143	1.885171	1.586145	6.49E-13	1.99E-11	0.050888	1	12	18	23	16	29	86	105	61	89	68
ENSMUSG00000023904	chr17	Hcfc1r1	23673596	23673703	958	1.191244	6.735554	7.22E-13	2.21E-11	0.031502	1	1032	884	1187	927	1053	2237	3098	2337	3736	2231
ENSMUSG00000015340	chrX	Cybb	9435252	9438343	5808	1.665724	3.642752	7.36E-13	2.24E-11	0.055611	1	79	65	162	77	105	226	408	544	290	241
ENSMUSG00000073421	chr17	H2-Ab1	34263209	34263405	1637	1.830756	6.13684	7.44E-13	2.26E-11	0.072282	1	530	463	793	273	386	2294	1697	2133	2270	1374
ENSMUSG00000044934	chr13	Zfp367	64133022	64135536	5454	-1.11323	4.815597	7.68E-13	2.33E-11	0.026157	-1	532	501	804	507	739	231	367	275	448	315
ENSMUSG00000026411	chr1	Tmem9	1.36E+08	1.36E+08	2726	1.323284	3.926611	7.95E-13	2.41E-11	0.034925	1	123	95	184	154	136	315	364	315	496	452
ENSMUSG00000039208	chr11	Metrnl	1.22E+08	1.22E+08	1586	1.700654	3.258182	8.14E-13	2.46E-11	0.056732	1	40	32	79	103	112	204	320	260	262	262
ENSMUSG00000047246	chr13	Hist1h2be	23583742	23585970	4374	-1.34406	3.516541	8.45E-13	2.55E-11	0.034878	-1	205	138	328	293	379	97	130	95	144	119
ENSMUSG00000024679	chr19	Ms4a6d	11586604	11587181	1735	1.960402	1.868586	9.2E-13	2.77E-11	0.063345	1	16	16	47	18	22	101	135	120	88	63
ENSMUSG00000024349	chr18	Tmem173	35733678	35734698	2302	1.715496	2.861402	9.37E-13	2.81E-11	0.05533	1	40	37	72	49	73	180	344	206	169	111
ENSMUSG00000103779	chr17	RP24-490B17.7	51766643	51771443	4801	-1.49388	2.435725	9.38E-13	2.81E-11	0.037867	-1	100	85	187	104	172	35	72	36	63	52
ENSMUSG00000079465	chr1	Col4a3	82586921	82587431	9967	-2.51037	0.971192	1E-12	3E-11	0.088582	-1	30	22	121	42	60	10	10	9	13	8
ENSMUSG00000039496	chr2	Cdnf	3513030	3513096	3111	-1.26468	5.424186	1.02E-12	3.04E-11	0.035223	-1	653	595	1315	1104	1328	305	637	337	577	479
ENSMUSG00000062901	chr16	Klhl24	20097554	20097671	6683	-1.39798	6.268162	1.11E-12	3.3E-11	0.043799	-1	1171	1009	3336	1731	2246	468	1198	628	892	765

ENSMUSG00000057101	chr7	Zfp180	24081924	24082238	3886	-1.09523	4.41842	1.14E-12	3.39E-11	0.024918	-1	381	293	715	420	589	185	307	208	287	256
ENSMUSG00000004266	chr6	Ptpn6	1.25E+08	1.25E+08	2802	1.749723	2.192614	1.15E-12	3.41E-11	0.053092	1	21	20	50	29	48	138	144	132	125	78
ENSMUSG00000034641	chr11	Cd300ld	1.15E+08	1.15E+08	2645	1.876899	2.079442	1.21E-12	3.58E-11	0.06048	1	26	17	48	20	33	108	131	160	94	84
ENSMUSG00000032431	chr9	Crtap	1.14E+08	1.14E+08	1772	1.229461	3.824011	1.22E-12	3.6E-11	0.029988	1	109	107	168	116	175	319	337	407	401	306
ENSMUSG00000095538	chr7	Gm21983	27168430	27168804	1690	1.259392	2.922786	1.22E-12	3.6E-11	0.027337	1	68	48	92	63	83	170	219	170	231	167
ENSMUSG00000021203	chr12	Otub2	1.03E+08	1.03E+08	3695	-1.37472	3.042484	1.23E-12	3.61E-11	0.034903	-1	164	114	325	154	222	66	88	95	85	77
ENSMUSG00000028063	chr3	Lmna	88481148	88482100	4252	1.145859	6.479279	1.24E-12	3.63E-11	0.029744	1	711	585	1169	993	1047	1807	2239	1875	3146	2153
ENSMUSG00000045763	chr15	Basp1	25363285	25364918	1847	1.945497	1.822707	1.25E-12	3.64E-11	0.062626	1	9	16	40	24	27	84	105	128	85	83
ENSMUSG00000053291	chr7	Rab4b	27168424	27168804	1970	1.258364	2.93487	1.26E-12	3.66E-11	0.027431	1	70	50	92	64	80	171	221	174	229	169
ENSMUSG00000047945	chr4	Marcksl1	1.3E+08	1.3E+08	1605	1.864297	1.567305	1.27E-12	3.69E-11	0.05183	1	13	11	22	21	32	86	105	68	89	56
ENSMUSG00000068663	chr16	Clec16a	10545339	10545642	8368	-1.09469	6.034416	1.32E-12	3.83E-11	0.027008	-1	1142	857	2248	1427	1721	552	893	686	1061	672
ENSMUSG00000038370	chr1	Pcp4l1	1.71E+08	1.71E+08	1577	-1.56167	3.702114	1.43E-12	4.13E-11	0.050579	-1	288	160	310	457	332	83	163	96	174	97
ENSMUSG00000084516	chr2	Mir1902	1.04E+08	1.04E+08	80	-1.32853	3.781415	1.64E-12	4.73E-11	0.036253	-1	290	236	495	231	342	83	201	118	163	155
ENSMUSG00000046311	chr11	Zfp62	49203292	49203538	6060	-1.14238	3.970747	1.67E-12	4.82E-11	0.026593	-1	270	231	490	367	395	104	242	174	206	174
ENSMUSG00000033192	chr8	Lpcat2	92855350	92855625	3377	2.308499	0.644484	1.81E-12	5.2E-11	0.064079	1	5	4	10	6	14	37	53	42	34	48
ENSMUSG00000035357	chr6	Pdzrn3	1.01E+08	1.01E+08	7256	-1.19439	6.534472	1.89E-12	5.43E-11	0.032935	-1	1627	1378	3254	2058	2295	824	1356	731	1596	775
ENSMUSG00000026043	chr1	Col3a1	45311538	45311832	9816	1.252704	8.882608	1.92E-12	5.51E-11	0.036705	1	3617	2924	7724	3506	5507	9286	12611	10293	14420	13566
ENSMUSG00000024659	chr19	Anxa1	20373428	20373770	2608	1.542099	5.701501	1.97E-12	5.64E-11	0.053598	1	375	433	500	343	412	932	1843	2032	1251	1019
ENSMUSG00000070577	chr4	Gm572	1.49E+08	1.49E+08	1385	-1.62465	2.718983	2.1E-12	5.99E-11	0.05018	-1	126	69	191	185	242	50	78	46	63	54
ENSMUSG00000045246	chr8	Kcng4	1.2E+08	1.2E+08	3806	-2.41284	5.25795	2.14E-12	6.08E-11	0.125296	-1	750	434	1178	1206	1807	343	193	170	310	67
ENSMUSG00000057551	chr9	Zfp317	19641224	19641254	1824	-1.41772	2.779233	2.16E-12	6.12E-11	0.037437	-1	130	105	250	133	197	44	110	53	72	64
ENSMUSG00000021486	chr13	Prelid1	55322055	55322281	1088	1.147516	4.382995	2.3E-12	6.51E-11	0.02824	1	212	128	257	200	242	470	502	553	636	425
ENSMUSG00000079293	chr6	Clec7a	1.29E+08	1.29E+08	2287	1.990314	2.033631	2.34E-12	6.6E-11	0.069869	1	24	18	33	20	33	88	165	168	96	62
ENSMUSG00000020736	chr11	Nt5c	1.15E+08	1.15E+08	1140	1.420615	2.60684	2.47E-12	6.98E-11	0.03501	1	43	48	56	49	60	139	178	166	178	126
ENSMUSG00000053687	chr8	Dpep2	1.06E+08	1.06E+08	4540	2.915998	1.0767	2.49E-12	7E-11	0.130494	1	11	1	11	8	6	43	73	115	53	32
ENSMUSG00000052496	chr15	Pkdrej	85814676	85821733	7058	-3.07478	-0.25415	2.51E-12	7.06E-11	0.084146	-1	16	9	24	33	27	2	4	2	3	3
ENSMUSG00000024087	chr17	Cyp1b1	79706953	79710681	5128	2.11621	2.134687	2.6E-12	7.28E-11	0.082068	1	32	14	31	18	33	114	200	157	83	75
ENSMUSG00000041245	chrX	Wnk3	1.51E+08	1.51E+08	10589	-2.66789	0.517221	2.64E-12	7.38E-11	0.093987	-1	16	27	84	25	45	4	9	5	9	6
ENSMUSG00000069917	chr11	Hba-a2	32296489	32296618	667	1.547615	2.672919	2.76E-12	7.71E-11	0.044914	1	33	35	83	55	55	116	179	129	285	156
ENSMUSG00000040711	chr11	Sh3pxd2b	32347820	32347968	9709	1.239657	3.503161	2.78E-12	7.75E-11	0.031074	1	97	58	179	92	127	215	294	313	336	273
ENSMUSG00000052430	chr3	Bmpr1b	1.42E+08	1.42E+08	5962	-1.76814	2.815948	2.79E-12	7.76E-11	0.062565	-1	140	83	360	137	201	32	73	39	88	62
ENSMUSG00000041736	chr15	Tspo	83563573	83563644	854	1.828249	5.373494	2.81E-12	7.8E-11	0.075089	1	426	269	249	187	231	978	1229	1418	1368	873
ENSMUSG00000098404	chr7	Gm8086	15288251	15289190	940	-2.6598	0.150496	2.85E-12	7.88E-11	0.074646	-1	15	13	46	34	39	5	8	5	5	2
ENSMUSG00000020024	chr10	Cep83	94688790	94689046	2986	-1.10626	3.831156	3.17E-12	8.76E-11	0.025058	-1	230	243	394	320	370	117	232	139	196	147
ENSMUSG00000027782	chr3	Kpna4	69067149	69074187	8940	-1.16403	7.270343	3.24E-12	8.93E-11	0.032223	-1	2818	2124	6142	2887	3881	1188	2046	1597	2422	1572
ENSMUSG00000021065	chr12	Fut8	77238104	77238199	3543	-0.99607	4.131916	3.36E-12	9.24E-11	0.020776	-1	322	270	515	365	408	153	283	207	271	167
ENSMUSG00000094441	chr17	Zfp955a	33241519	33242950	1638	-2.3348	0.885359	3.36E-12	9.24E-11	0.078672	-1	24	36	74	54	54	5	19	9	6	14
ENSMUSG00000053560	chr8	Ier2	84661331	84662852	1522	1.453202	3.067105	3.39E-12	9.28E-11	0.04147	1	49	60	85	60	101	146	368	179	261	178
ENSMUSG00000033991	chr13	Ttc37	76098734	76098829	5381	-1.31664	3.796726	3.53E-12	9.65E-11	0.036759	-1	230	190	606	254	389	104	209	118	159	140
ENSMUSG00000003484	chr8	Cyp4f18	71988482	71988737	1855	2.738247	0.814951	3.55E-12	9.69E-11	0.101002	1	7	9	9	3	5	63	37	58	63	31
ENSMUSG00000029581	chr5	Fscn1	1.43E+08	1.43E+08	3012	1.466868	3.637867	3.78E-12	1.03E-10	0.045894	1	71	52	117	142	154	269	302	318	464	296
ENSMUSG00000027035	chr2	Cers6	68861441	68861805	8875	1.701516	1.831692	3.86E-12	1.05E-10	0.048006	1	14	18	34	22	44	87	112	90	94	90
ENSMUSG00000039879	chr10	Heca	17900466	17902377	3667	-1.63158	3.672842	3.86E-12	1.05E-10	0.057305	-1	208	139	556	299	438	71	151	82	117	143
ENSMUSG00000025903	chr1	Lypla1	4807788	4807982	7145	-1.39516	5.953813	4.08E-12	1.1E-10	0.045788	-1	1003	1109	2140	1489	1563	290	648	642	862	708
ENSMUSG00000038663	chr7	Fsd2	81533308	81535248	3985	-1.16017	8.043442	4.19E-12	1.13E-10	0.032506	-1	4564	3047	9745	5734	7593	2357	3699	2476	3920	2601
ENSMUSG00000051984	chr19	Sec31b	44516957	44517488	3950	-1.08114	4.51309	4.19E-12	1.13E-10	0.025815	-1	379	285	740	527	629	202	332	244	288	267
ENSMUSG00000008734	chr7	Gprc5b	1.19E+08	1.19E+08	4525	1.093308	5.244834	4.33E-12	1.16E-10	0.027593	1	331	269	645	304	439	727	1003	907	1386	736
ENSMUSG00000020516	chr11	Rps6kb1	86498871	86502962	8658	-1.00405	5.013627	4.54E-12	1.22E-10	0.02291	-1	555	476	1148	604	767	310	480	356	505	326
ENSMUSG00000079227	chr9	Ccr5	1.24E+08	1.24E+08	3704	1.932386	1.623421	4.59E-12	1.23E-10	0.063718	1	13	7	26	22	33	80	134	65	78	70
ENSMUSG00000004530	chr5	Coro1c	1.14E+08	1.14E+08	9664	1.091089	4.236215	4.66E-12	1.25E-10	0.025862	1	157	130	265	206	212	380	428	505	573	420
ENSMUSG00000022285	chr15	Ywhaz	36770770	36772777	3999	0.963797	5.710913	4.81E-12	1.28E-10	0.021673	1	505	430	737	512	663	1028	1490	1204	1619	1012
ENSMUSG00000034845	chr8	Plvap	71497754	71498405	2015	1.259863	4.494703	4.84E-12	1.29E-10	0.035636	1	214	164	277	198	196	415	642	706	809	362
ENSMUSG00000035373	chr11	Ccl7	82045712	82045859	801	3.078918	1.816117	4.9E-12	1.3E-10	0.173462	1	11	5	19	4	20	81	287	42	76	85
ENSMUSG00000049606	chr5	Zfp644	1.07E+08	1.07E+08	8803	-1.17876	3.785596	5.29E-12	1.4E-10	0.029507	-1	221	188	514	284	382	94	211	142	193	141
ENSMUSG00000085289	chr18	Gm15337	39367038	39370316	3888	2.537314	1.746488	5.36E-12	1.42E-10	0.11285	1	13	19	19	9	13	56	189	130	61	71
ENSMUSG00000035164	chr9	Zc3h12c	52111985	52116802	6133	-1.59351	2.400285	5.67E-12	1.5E-10	0.048018	-1	78	88	219	102	166	29	71	54	47	38
ENSMUSG00000023927	chr17	Satb1	51736187	51740413	19027	-1.14037	6.140298	5.78E-12	1.52E-10	0.03122	-1	1124	1067	2531	1428	1885	555	887	678	1072	845
ENSMUSG00000020668	chr12	Kif3c	3365132	3367531	6849	-1.17854	5.930681	5.89E-12	1.54E-10	0.033215	-1	1348	878	2073	1072	1543	680	715	545	918	543
ENSMUSG00000035614	chr12	Fam179b	64965742	64968028	6434	-1.52607	3.696238	5.9E-12	1.54E-10	0.050688	-1	189	133	476	369	453	122	125	110	133	107
ENSMUSG00000057191	chr9	AB124611	21526176	21526307	1447	2.021844	0.856507	5.89E-12	1.54E-10	0.050218	1	9	10	16	8	10	49	51	52	49	41
ENSMUSG00000070436	chr7	Serpinh1	99345375	99346422	2435	1.219765	6.595757	5.88E-12	1.54E-10	0.035951	1	754	594	1114	987	1267	1992	2354	3031	2474	2274
ENSMUSG00000032393	chr9	Dpp8	65032458	65032623	4968	-1.1242	6.845083	6.02E-12	1.57E-10	0.030732	-1	2036	1704	4521	2030	2833	983	1836	1136	1562	1168
ENSMUSG00000032353	chr9	Tmed3	89699205	89699979	2848	0.979118	4.559471	6.37E-12	1.66E-10	0.021275	1	207	171	326	256	321	465	617	582	683	489
ENSMUSG00000031740	chr8	Mmp2	92827328	92827777	3038	1.111821	7.021524	6.46E-12	1.68E-10	0.030215	1	948	917	2051	1165	1712	2690	3217	3226	3746	3147
ENSMUSG00000059326	chr19	Csf2ra	61224402	61225033	1849	1.867731	2.153508	6.65E-12	1.73E-10	0.065834	1	31	20	52	22	26	103	127	184	117	80

ENSMUSG00000061068	chr14	Mcpt4	56059744	56060100	990	1.557044	3.609564	6.75E-12	1.75E-10	0.052717	1	105	79	145	62	100	268	503	349	233	284
ENSMUSG00000023349	chr6	Clec4n	1.23E+08	1.23E+08	1420	2.489609	0.75331	7.24E-12	1.87E-10	0.089483	1	7	4	14	5	8	56	77	34	53	22
ENSMUSG00000026471	chr1	Mr1	1.55E+08	1.55E+08	5981	-0.98283	4.574698	7.52E-12	1.94E-10	0.021715	-1	380	338	679	558	616	241	351	257	369	248
ENSMUSG00000027078	chr2	Ube2l6	84798828	84798932	1996	1.368406	2.729624	7.54E-12	1.94E-10	0.035841	1	35	42	82	64	73	137	207	198	177	135
ENSMUSG00000096145	chr7	Vkorc1	1.28E+08	1.28E+08	767	1.107702	3.491861	8.1E-12	2.08E-10	0.024621	1	112	75	144	103	134	225	322	289	315	234
ENSMUSG00000022225	chr14	Cma1	55941453	55941797	1074	1.715471	2.91307	8.53E-12	2.19E-10	0.061218	1	54	46	76	40	60	150	330	223	129	198
ENSMUSG00000022490	chr15	Ppp1r1a	1.04E+08	1.04E+08	1295	-1.71407	5.230516	9.2E-12	2.35E-10	0.069899	-1	833	850	1219	825	792	214	359	504	193	295
ENSMUSG00000073684	chr4	2610002J02Rik	1.55E+08	1.55E+08	1743	1.595584	2.236812	9.24E-12	2.36E-10	0.04575	1	33	31	45	40	31	86	118	144	181	102
ENSMUSG00000021870	chr14	Slmap	26413168	26414988	8054	-1.00023	5.681365	9.83E-12	2.51E-10	0.024222	-1	788	711	1633	1141	1365	427	790	615	766	557
ENSMUSG00000041460	chr6	Cacna2d4	1.19E+08	1.19E+08	9478	-2.42685	3.067475	1.04E-11	2.64E-10	0.126248	-1	250	86	309	150	378	60	18	42	83	30
ENSMUSG00000018927	chr11	Ccl6	83587882	83588939	1795	1.796603	4.439344	1.1E-11	2.79E-10	0.075125	1	181	129	223	79	155	729	873	580	451	374
ENSMUSG00000030059	chr6	Tmf1	97155266	97155497	3465	-1.10606	4.096126	1.1E-11	2.79E-10	0.027562	-1	298	217	597	345	479	134	286	167	226	187
ENSMUSG00000036478	chr10	Btg1	96617001	96617472	5010	1.145599	4.533451	1.11E-11	2.81E-10	0.030352	1	240	188	311	176	225	499	667	638	642	441
ENSMUSG00000023243	chr14	Kcnk5	20140058	20142457	3364	1.779695	1.488609	1.12E-11	2.84E-10	0.051442	1	16	12	40	17	14	58	84	69	116	56
ENSMUSG00000018648	chr11	Dusp14	84048041	84049310	1945	1.48393	3.8597	1.14E-11	2.87E-10	0.049638	1	105	85	137	157	117	261	571	226	618	328
ENSMUSG00000032122	chr9	Slc37a2	37229149	37231656	5079	1.599309	2.346176	1.17E-11	2.93E-10	0.049844	1	40	16	48	38	59	114	144	164	136	114
ENSMUSG00000034947	chr11	Tmem106a	1.02E+08	1.02E+08	3138	1.577493	3.02606	1.22E-11	3.05E-10	0.052409	1	81	48	83	48	58	203	254	271	204	151
ENSMUSG00000022772	chr16	Senp5	31962506	31963537	4426	-1.57415	2.492834	1.23E-11	3.08E-10	0.049291	-1	98	74	235	122	169	30	82	47	46	52
ENSMUSG00000031934	chr9	Panx1	15005161	15006217	2997	1.378016	3.10279	1.26E-11	3.16E-10	0.039263	1	77	52	89	85	70	132	271	186	330	217
ENSMUSG00000078771	chr11	Evi2a	79526560	79527802	2297	1.316235	2.906938	1.29E-11	3.22E-10	0.034233	1	45	63	106	58	69	162	248	165	239	153
ENSMUSG00000100679	chr1	Gm28778	53297111	53297188	785	-1.31242	3.306127	1.29E-11	3.22E-10	0.037204	-1	170	137	352	229	271	73	180	76	118	81
ENSMUSG00000020590	chr12	Snx13	35047189	35047411	7387	-1.07373	5.97219	1.31E-11	3.27E-10	0.028567	-1	1008	876	2339	1270	1598	515	965	668	888	692
ENSMUSG00000015950	chr5	Ncf1	1.34E+08	1.34E+08	3663	1.652242	2.35144	1.34E-11	3.33E-10	0.053214	1	38	25	52	33	46	144	125	173	128	101
ENSMUSG00000100838	chr9	Gm29094	89199379	89199779	664	1.786008	1.635884	1.37E-11	3.4E-10	0.051621	1	20	22	22	16	25	84	109	84	80	60
ENSMUSG00000027750	chr3	Postn	54361109	54361267	7833	2.071675	4.529564	1.42E-11	3.52E-10	0.100461	1	102	94	153	168	195	234	992	543	515	1087
ENSMUSG00000072501	chr15	Phf20l1	66577572	66577847	6670	-1.15207	5.481678	1.53E-11	3.77E-10	0.032775	-1	746	725	1670	887	1042	290	575	467	711	522
ENSMUSG00000031983	chr8	2310022B05Rik	1.25E+08	1.25E+08	3297	1.260978	4.550622	1.56E-11	3.85E-10	0.038201	1	126	135	329	248	304	477	572	523	734	663
ENSMUSG00000067212	chr17	H2-T23	36029773	36030694	2889	1.549217	4.75878	1.72E-11	4.23E-10	0.057995	1	213	203	207	194	246	625	849	1076	605	468
ENSMUSG00000021238	chr12	Aldh6a1	84430723	84432548	3340	-1.24555	7.088676	1.75E-11	4.3E-10	0.039467	-1	1998	1935	4881	3424	3677	817	1885	1705	1651	1396
ENSMUSG00000020241	chr10	Col6a2	76595762	76596811	8326	1.304358	7.049015	1.76E-11	4.32E-10	0.043208	1	827	697	1790	1251	1811	2520	2952	3529	4083	3849
ENSMUSG00000021482	chr13	Aaed1	64291836	64292228	972	-1.29706	3.559494	1.83E-11	4.47E-10	0.037559	-1	186	160	497	259	298	95	187	109	117	114
ENSMUSG00000031444	chr8	F10	13037308	13037547	2731	3.830736	-0.4168	1.83E-11	4.47E-10	0.124494	1	1	1	1	0	3	14	37	31	13	11
ENSMUSG00000078862	chr2	Gm14326	1.78E+08	1.78E+08	2863	-1.44102	3.12096	1.84E-11	4.48E-10	0.045119	-1	133	166	293	166	272	63	112	53	95	101
ENSMUSG00000023845	chr17	Lnpep	17527723	17529880	5181	-2.02051	3.698687	1.88E-11	4.57E-10	0.09467	-1	152	121	830	293	461	48	130	88	117	91
ENSMUSG00000028859	chr4	Csf3r	1.26E+08	1.26E+08	3609	2.732942	0.421474	1.88E-11	4.57E-10	0.099537	1	5	5	9	2	4	42	60	42	26	20
ENSMUSG00000019122	chr11	Ccl9	83572919	83575495	3045	1.752088	3.974959	1.91E-11	4.63E-10	0.071729	1	110	113	169	64	110	526	609	408	304	300
ENSMUSG00000024477	chr18	Pggt1b	46239949	46241701	2736	-1.8171	2.15387	1.97E-11	4.77E-10	0.065621	-1	58	51	220	108	148	27	37	38	37	35
ENSMUSG00000057924	chr8	Gm10033	69372145	69372612	654	-2.01609	0.85432	1.99E-11	4.8E-10	0.058313	-1	34	21	77	47	51	13	20	10	11	8
ENSMUSG00000008384	chr7	Sertad1	27486910	27487078	1344	1.202184	3.641602	2.1E-11	5.05E-10	0.031648	1	91	110	135	106	152	292	415	280	354	234
ENSMUSG00000026739	chr2	Bmi1	18677018	18677469	3974	-1.07112	5.146127	2.14E-11	5.14E-10	0.028349	-1	583	592	1145	764	803	258	471	373	583	422
ENSMUSG00000029718	chr5	Pcolce	1.38E+08	1.38E+08	3823	1.138098	6.01065	2.2E-11	5.28E-10	0.032907	1	491	396	923	638	873	1366	1544	1722	1662	1627
ENSMUSG00000028289	chr4	Epha7	28813131	28813480	9884	-2.77209	0.152159	2.22E-11	5.33E-10	0.097788	-1	17	23	51	16	41	1	3	8	4	7
ENSMUSG00000034786	chr17	Gpsm3	34589806	34590260	1343	1.742584	2.10124	2.27E-11	5.44E-10	0.058691	1	34	22	39	23	35	115	81	131	151	95
ENSMUSG00000020810	chr11	Cygb	1.17E+08	1.17E+08	2331	1.198908	4.955785	2.32E-11	5.54E-10	0.035586	1	192	200	416	303	437	499	907	973	807	740
ENSMUSG00000033863	chr19	Klf9	23141226	23142259	3263	-1.44682	6.37302	2.44E-11	5.82E-10	0.053336	-1	1410	898	3519	2004	2507	474	1329	638	849	850
ENSMUSG00000079669	chr9	Gm17396	1.17E+08	1.17E+08	1655	2.744999	0.365472	2.46E-11	5.86E-10	0.092584	1	7	6	5	2	3	38	34	21	60	30
ENSMUSG00000064367	chrMT	mt-Nd5	11742	13565	1824	-1.97802	12.17101	2.53E-11	6.01E-10	0.097743	-1	42150	47168	172179	155291	219188	19474	47968	28709	48270	31269
ENSMUSG00000030739	chr7	Myh14	44605803	44606363	7273	-1.02511	5.483049	2.58E-11	6.11E-10	0.026422	-1	749	680	1228	1083	1093	354	595	561	659	527
ENSMUSG00000002265	chr7	Peg3	6703892	6711731	13314	2.174791	5.579705	2.6E-11	6.16E-10	0.115531	1	105	161	575	241	427	811	1361	1133	1144	2426
ENSMUSG00000044749	chr11	Abca6	1.1E+08	1.1E+08	5398	-2.17753	2.716535	2.68E-11	6.33E-10	0.104526	-1	67	69	371	154	278	45	45	35	36	46
ENSMUSG00000025754	chr7	Agbl1	76318072	76318143	4594	-4.47282	1.542039	2.69E-11	6.35E-10	0.350719	-1	15	7	81	171	190	4	7	2	7	2
ENSMUSG00000040747	chr3	Cd53	1.07E+08	1.07E+08	1742	1.55397	2.72661	2.78E-11	6.56E-10	0.05137	1	45	42	81	34	66	172	251	194	159	106
ENSMUSG00000008090	chr5	Fgfrl1	1.09E+08	1.09E+08	2656	1.211548	4.976353	2.81E-11	6.61E-10	0.036694	1	216	162	344	412	410	633	914	875	888	680
ENSMUSG00000030336	chr6	Cd27	1.25E+08	1.25E+08	2328	-2.46249	0.250559	2.82E-11	6.61E-10	0.079458	-1	22	18	34	35	43	8	8	2	12	1
ENSMUSG00000047466	chr18	8030462N17Rik	77633281	77635328	3418	-1.66681	3.400211	2.87E-11	6.74E-10	0.064954	-1	168	114	501	267	318	64	172	58	96	80
ENSMUSG00000068566	chr7	Myadm	3289038	3289325	3238	1.14744	5.812872	2.95E-11	6.88E-10	0.033767	1	378	321	739	635	814	958	1538	1384	1756	1435
ENSMUSG00000101152	chr9	Gm28305	1.04E+08	1.04E+08	365	-1.95046	2.110945	2.94E-11	6.88E-10	0.078542	-1	59	61	166	146	128	21	55	23	22	38
ENSMUSG00000031387	chrX	Renbp	73922121	73922263	2494	1.571362	2.093255	3.1E-11	7.21E-10	0.045873	1	36	25	40	33	31	96	114	141	115	91
ENSMUSG00000032997	chr1	Chpf	75474569	75476226	3856	1.376529	3.202758	3.15E-11	7.34E-10	0.042446	1	60	48	103	81	122	163	213	243	289	275
ENSMUSG00000034610	chr4	Zcchc11	1.08E+08	1.08E+08	8684	-1.22052	3.804969	3.33E-11	7.75E-10	0.034829	-1	201	189	570	301	379	95	214	151	174	139
ENSMUSG00000058818	chr7	Pirb	3711409	3712830	4471	1.705695	2.723728	3.36E-11	7.79E-10	0.064407	1	47	28	87	33	57	202	217	214	144	110
ENSMUSG00000036067	chr2	Slc2a6	27021363	27022069	3211	2.825051	0.219157	3.47E-11	8.04E-10	0.112858	1	1	0	11	8	1	33	28	36	44	23
ENSMUSG00000022102	chr14	Dok2	70766036	70766112	2902	1.821164	2.09173	3.52E-11	8.14E-10	0.065905	1	40	19	34	24	27	139	118	107	106	100
ENSMUSG00000052384	chr16	Nrros	32142785	32145005	4177	1.423531	2.831776	3.57E-11	8.24E-10	0.043178	1	63	36	83	64	60	179	210	222	189	121
ENSMUSG00000031626	chr8	Sorbs2	45507788	45507957	19432	-1.48235	5.912414	3.58E-11	8.25E-10	0.056582	-1	1228	1148	2972	785	1236	508	644	460	797	500

ENSMUSG00000026833	chr2	Olfm1	28192992	28193462	3553	1.245691	3.00844	3.67E-11	8.44E-10	0.032901	1	51	49	111	88	85	184	213	209	260	150
ENSMUSG00000003283	chr2	Hck	1.53E+08	1.53E+08	2092	2.073554	1.051857	3.71E-11	8.52E-10	0.06954	1	12	3	11	16	18	52	73	65	47	46
ENSMUSG00000025262	chrX	Fam120c	1.51E+08	1.51E+08	5823	-1.76756	2.508903	3.78E-11	8.65E-10	0.068147	-1	94	56	260	141	192	23	71	43	48	50
ENSMUSG00000037111	chr3	Setd7	51515319	51521487	10813	-1.14506	8.646068	3.9E-11	8.92E-10	0.034946	-1	6762	6810	15680	6213	10256	3580	5291	4070	5541	4325
ENSMUSG00000015342	chrX	Xk	9272756	9273234	5076	-1.35886	3.071049	3.96E-11	9.03E-10	0.040873	-1	126	111	350	196	225	57	88	77	113	92
ENSMUSG00000047963	chr5	Stbd1	92603051	92603337	1985	1.28619	6.473185	3.99E-11	9.09E-10	0.043238	1	1014	670	1071	551	747	1804	2952	1983	2925	1956
ENSMUSG00000011884	chr5	Gltp	1.15E+08	1.15E+08	1757	1.200255	4.130703	4.06E-11	9.23E-10	0.034658	1	152	105	200	173	223	404	409	554	493	323
ENSMUSG00000022200	chr15	Golph3	12321496	12321956	2606	-1.01136	5.922416	4.12E-11	9.36E-10	0.026628	-1	1218	845	1926	1165	1458	485	835	735	955	691
ENSMUSG00000015085	chr2	Entpd2	25395874	25396089	2128	1.038947	4.200805	4.16E-11	9.43E-10	0.025809	1	163	129	298	174	215	411	442	491	524	354
ENSMUSG00000044066	chr11	Cep68	20227037	20229481	5865	-1.22131	4.810772	4.21E-11	9.51E-10	0.037754	-1	370	348	932	760	867	212	395	271	356	310
ENSMUSG00000057762	chr13	Gm6169	97098237	97099296	1060	1.59435	1.59634	4.2E-11	9.51E-10	0.042074	1	16	21	33	16	30	55	88	73	118	67
ENSMUSG00000051236	chr10	Msrb3	1.21E+08	1.21E+08	4048	-1.06466	7.482124	4.22E-11	9.52E-10	0.030227	-1	3394	2812	6483	3084	4078	1600	2583	1795	2773	1916
ENSMUSG00000034898	chr9	Filip1	79815051	79815897	4888	-1.50535	5.281649	4.25E-11	9.55E-10	0.058221	-1	603	406	2095	686	1264	248	475	318	475	355
ENSMUSG00000050022	chr5	Amz1	1.41E+08	1.41E+08	6697	2.726861	0.63297	4.24E-11	9.55E-10	0.114483	1	7	3	5	9	5	36	35	78	50	23
ENSMUSG00000021556	chr13	Golm1	59634996	59637401	3693	-2.09454	4.665909	4.26E-11	9.56E-10	0.108343	-1	854	545	1184	308	390	186	266	137	230	78
ENSMUSG00000001983	chr11	Taco1	1.06E+08	1.06E+08	1383	-1.14786	5.318159	4.48E-11	1E-09	0.033944	-1	642	492	1041	1011	1327	376	594	374	492	427
ENSMUSG00000024298	chr17	Zfp871	32771236	32776008	5376	-2.72277	1.886087	4.58E-11	1.02E-09	0.156939	-1	59	26	268	71	138	7	35	12	26	10
ENSMUSG00000031434	chrX	Morc4	1.4E+08	1.4E+08	6051	1.114695	3.076071	4.57E-11	1.02E-09	0.025672	1	81	54	126	74	92	161	252	186	269	178
ENSMUSG00000040548	chr11	Tex2	1.07E+08	1.07E+08	5576	-1.09754	6.312711	4.7E-11	1.05E-09	0.031842	-1	1222	1010	2460	2102	2144	632	1097	962	1206	781
ENSMUSG00000049092	chr14	Gpr137c	45219719	45220418	3679	-2.5286	0.495216	4.7E-11	1.05E-09	0.096976	-1	17	22	50	47	50	3	10	3	6	13
ENSMUSG00000023367	chr6	Tmem176a	48841483	48841589	1119	1.41239	3.212776	4.72E-11	1.05E-09	0.045719	1	70	52	134	71	83	257	238	294	256	149
ENSMUSG00000034290	chr12	Nek9	85299514	85301926	5386	-1.07124	7.93865	4.77E-11	1.06E-09	0.030859	-1	4695	3167	8814	4909	5991	2360	3334	2339	4252	2364
ENSMUSG00000043019	chr1	Edem3	1.52E+08	1.52E+08	6381	-1.10927	5.020854	4.81E-11	1.06E-09	0.031427	-1	564	395	1325	581	882	262	461	381	444	339
ENSMUSG00000049775	chrX	Tmsb4x	1.67E+08	1.67E+08	1371	1.108328	7.519124	4.86E-11	1.07E-09	0.032895	1	1612	1534	1983	1907	2117	4343	5649	4296	4901	3578
ENSMUSG00000026358	chr1	Rgs1	1.44E+08	1.44E+08	6947	4.474376	0.629093	4.9E-11	1.08E-09	0.298779	1	2	1	2	2	2	4	90	101	28	27
ENSMUSG00000018363	chr11	Smurf2	1.07E+08	1.07E+08	6162	-1.02475	4.609174	5E-11	1.1E-09	0.026048	-1	376	328	910	489	625	225	378	292	312	261
ENSMUSG00000043157	chr14	Arl11	61309753	61309937	1482	2.528076	0.568479	5E-11	1.1E-09	0.095468	1	7	3	10	7	5	37	45	67	28	29
ENSMUSG00000032601	chr9	Prkar2a	1.09E+08	1.09E+08	6378	-1.09268	7.674845	5.33E-11	1.17E-09	0.032203	-1	3515	2829	7419	4267	5059	1500	2757	2097	3417	2331
ENSMUSG00000056737	chr6	Capg	72544391	72544466	2529	1.278643	4.823721	5.42E-11	1.19E-09	0.041644	1	238	267	354	184	250	553	768	880	756	653
ENSMUSG00000024781	chr19	Lipa	34492318	34494213	2969	1.500463	4.288762	5.45E-11	1.19E-09	0.056381	1	148	116	215	141	199	343	629	855	395	378
ENSMUSG00000026211	chr1	Obsl1	75479310	75479371	8467	1.084612	6.222237	5.47E-11	1.2E-09	0.031286	1	661	407	1156	762	980	1186	2140	1894	2343	1769
ENSMUSG00000094686	chr4	Ccl21a	42772860	42773283	870	1.590304	4.655775	5.78E-11	1.26E-09	0.064542	1	226	165	236	120	241	836	767	733	676	363
ENSMUSG00000031004	chr7	Mki67	1.36E+08	1.36E+08	10075	2.305963	1.183894	5.89E-11	1.28E-09	0.100181	1	6	4	17	14	19	84	51	67	49	60
ENSMUSG00000072235	chr15	Tuba1a	98949841	98951014	1647	1.00398	5.708177	5.94E-11	1.29E-09	0.02644	1	449	403	652	615	664	1024	1298	1393	1463	1131
ENSMUSG00000086503	chrX	Xist	1.03E+08	1.03E+08	17923	8.21023	4.593052	6.38E-11	1.39E-09	0.94012	1	2	4	4	0	2	3	1578	1506	13	1241
ENSMUSG00000018042	chr15	Cyb5r3	83153494	83154722	4298	1.045908	5.997874	6.63E-11	1.44E-09	0.029116	1	507	516	778	657	887	1237	1628	1549	2216	1275
ENSMUSG00000030306	chr6	Tmtc1	1.48E+08	1.48E+08	8578	-1.21919	6.842281	6.76E-11	1.46E-09	0.040105	-1	1522	1364	4521	2735	3524	1002	1526	1162	1366	1217
ENSMUSG00000032359	chr9	Ctsh	90054152	90054219	4499	1.283237	4.497276	6.77E-11	1.46E-09	0.041879	1	211	177	276	175	196	616	617	658	506	438
ENSMUSG00000000567	chr11	Sox9	1.13E+08	1.13E+08	4135	2.034206	1.743887	6.81E-11	1.47E-09	0.086658	1	10	7	29	18	42	70	171	81	88	70
ENSMUSG00000038658	chr19	Ric1	29522282	29522666	10727	-1.0571	4.677002	6.92E-11	1.49E-09	0.028527	-1	421	371	959	459	660	192	369	285	422	271
ENSMUSG00000032322	chr9	Pstpip1	56089962	56090444	3830	2.030178	1.31976	6.98E-11	1.5E-09	0.07284	1	16	15	18	9	15	56	86	99	60	43
ENSMUSG00000004591	chr3	Pkn2	1.43E+08	1.43E+08	7420	-1.11187	4.999582	7.05E-11	1.51E-09	0.032165	-1	563	478	1281	514	808	238	455	392	429	344
ENSMUSG00000029096	chr5	Htra3	35652041	35653122	3860	1.178955	5.64122	7.04E-11	1.51E-09	0.036945	1	394	326	702	446	635	1055	1106	1690	1243	1079
ENSMUSG00000029580	chr5	Actb	1.43E+08	1.43E+08	2679	0.982973	8.247207	7.05E-11	1.51E-09	0.026544	1	3090	2381	4293	2881	3770	6456	8556	7270	8662	5872
ENSMUSG00000101389	chr19	Ms4a4a	11375523	11375631	836	1.837601	2.099969	7.02E-11	1.51E-09	0.070303	1	26	25	35	21	38	143	108	138	128	63
ENSMUSG00000032307	chr9	Ube2q2	55148854	55149826	4305	-0.93628	5.399021	7.52E-11	1.6E-09	0.023018	-1	798	691	1249	770	945	377	675	498	689	441
ENSMUSG00000028630	chr10	Dyrk2	1.19E+08	1.19E+08	2137	-1.32691	4.065399	7.68E-11	1.63E-09	0.044133	-1	260	235	742	285	505	115	195	135	226	199
ENSMUSG00000020120	chr11	Plek	16971206	16974153	4486	1.685369	2.704813	8.17E-11	1.73E-09	0.06638	1	41	20	84	38	72	106	282	233	164	120
ENSMUSG00000060206	chr4	Zfp462	54945048	54945101	10702	-1.40029	3.495449	8.16E-11	1.73E-09	0.047589	-1	144	148	481	245	367	84	132	83	143	121
ENSMUSG00000024030	chr17	Abcg1	31057698	31057856	4066	2.33796	1.873246	8.21E-11	1.74E-09	0.119422	1	8	6	30	35	18	117	92	152	93	68
ENSMUSG00000091562	chr16	Gm9581	59558013	59560242	2870	-3.35019	1.324607	8.61E-11	1.82E-09	0.220479	-1	15	17	132	99	122	2	9	4	13	11
ENSMUSG00000018415	chr11	Gid4	60417145	60417844	4864	-1.0449	7.025329	8.65E-11	1.82E-09	0.029971	-1	2541	2100	4467	2170	3025	1194	1814	1408	1781	1550
ENSMUSG00000030323	chr6	Ift122	1.16E+08	1.16E+08	7953	1.195416	4.393763	8.64E-11	1.82E-09	0.036739	1	208	115	345	151	233	493	585	452	785	368
ENSMUSG00000041180	chr19	Hectd2	36554639	36554915	9066	-1.56711	2.69892	8.65E-11	1.82E-09	0.056644	-1	141	120	295	101	133	34	66	56	95	51
ENSMUSG00000102098	chr12	2310016D03Rik	30410559	30411950	1547	-4.05007	1.428488	8.66E-11	1.82E-09	0.316713	-1	14	11	72	134	191	2	10	2	7	6
ENSMUSG00000039891	chr10	Txlnb	17796226	17796421	5504	-1.15579	8.748016	8.85E-11	1.86E-09	0.036964	-1	6679	5115	15955	10595	11551	3419	6408	3841	6550	4533
ENSMUSG00000044676	chr8	Zfp612	1.1E+08	1.1E+08	2301	-2.18665	1.116722	8.9E-11	1.87E-09	0.091819	-1	44	38	82	47	70	5	33	4	15	14
ENSMUSG00000087006	chr2	Gm13889	93955810	93957049	1392	2.034078	2.381057	8.94E-11	1.87E-09	0.0938	1	32	11	31	37	50	106	316	113	160	80
ENSMUSG00000035385	chr11	Ccl2	82035571	82035737	1138	2.475477	1.598914	8.96E-11	1.87E-09	0.128238	1	7	8	21	10	27	93	165	29	108	61
ENSMUSG00000074238	chr3	Ap1ar	1.28E+08	1.28E+08	2391	-0.9557	4.933664	9.56E-11	1.99E-09	0.023779	-1	645	457	909	556	677	273	503	366	476	305
ENSMUSG00000044308	chr2	Ubr3	69897246	69897839	9719	-1.13055	8.292316	9.87E-11	2.06E-09	0.035534	-1	5212	4903	12963	5400	7478	2376	4273	3333	4848	3364
ENSMUSG00000046718	chr8	Bst2	71534264	71534480	764	1.379635	3.753017	9.89E-11	2.06E-09	0.046847	1	116	115	145	82	124	360	406	378	293	285
ENSMUSG00000020792	chr11	Exoc7	1.16E+08	1.16E+08	4367	-1.42442	6.521176	1.01E-10	2.1E-09	0.055265	-1	2268	1862	3644	1153	1827	815	924	909	1192	705
ENSMUSG00000020354	chr11	Sgcd	46896253	46897969	8257	-2.49007	3.181257	1.02E-10	2.1E-09	0.149547	-1	83	55	679	236	348	39	73	41	53	42
ENSMUSG00000004730	chr17	Emr1	57358686	57358756	3245	1.250425	3.632397	1.03E-10	2.12E-09	0.038328	1	99	77	202	89	134	310	275	306	336	311

ENSMUSG00000078680	chr4	Mup10	60578260	60578512	1391	6.741292	2.555234	1.06E-10	2.18E-09	0.688775	1	2	1	2	1	2	66	41	799	9	62
ENSMUSG00000020280	chr11	Pus10	23665674	23665748	4325	-1.01653	3.511405	1.06E-10	2.19E-09	0.02364	-1	220	170	317	250	263	104	170	116	173	126
ENSMUSG00000030786	chr7	Itgam	1.28E+08	1.28E+08	6377	1.468261	3.066738	1.06E-10	2.19E-09	0.051751	1	41	39	132	67	91	186	259	293	200	159
ENSMUSG00000029778	chr6	Adcyap1r1	55451978	55452368	6601	1.374831	2.450738	1.07E-10	2.2E-09	0.040253	1	36	32	86	34	58	92	155	140	205	121
ENSMUSG00000030677	chr7	Kif22	1.27E+08	1.27E+08	2063	2.955555	-0.29906	1.15E-10	2.36E-09	0.082324	1	3	3	2	2	2	24	17	20	22	25
ENSMUSG00000020901	chr11	Pik3r5	68432121	68432262	5550	2.090834	1.656444	1.16E-10	2.37E-09	0.092915	1	13	7	19	13	43	74	128	110	76	58
ENSMUSG00000031880	chr8	Rrad	1.05E+08	1.05E+08	1575	4.503697	5.573093	1.2E-10	2.45E-09	0.42835	1	30	20	28	63	198	751	6583	656	1137	263
ENSMUSG00000018585	chr11	Atox1	55446641	55446784	541	1.004656	4.207366	1.2E-10	2.46E-09	0.024991	1	204	140	223	190	212	338	547	468	560	344
ENSMUSG00000021477	chr13	Ctsl	64363214	64364200	1971	1.08656	7.650797	1.21E-10	2.46E-09	0.033036	1	1737	1819	2735	1756	2184	3499	6958	5620	5442	3767
ENSMUSG00000019942	chr10	Cdk1	69336635	69338596	3445	3.116373	0.161158	1.22E-10	2.48E-09	0.137064	1	1	3	1	5	6	42	22	22	27	42
ENSMUSG00000023150	chr1	Ivns1abp	1.51E+08	1.51E+08	5435	-0.96192	7.124405	1.22E-10	2.48E-09	0.025879	-1	2427	2072	4306	2976	3221	1307	2367	1468	2056	1543
ENSMUSG00000033557	chr1	Fam20b	1.57E+08	1.57E+08	8770	-1.14456	6.169701	1.24E-10	2.53E-09	0.036146	-1	1090	857	2013	1976	2247	679	949	719	1096	679
ENSMUSG00000022800	chr16	Fyttd1	32877500	32877670	6076	-0.98083	6.185204	1.26E-10	2.55E-09	0.026544	-1	1267	1058	2567	1383	1684	661	1100	778	1150	820
ENSMUSG00000022505	chr16	Emp2	10281749	10284615	3440	1.10835	3.776782	1.27E-10	2.57E-09	0.03	1	93	90	179	161	179	240	465	287	380	335
ENSMUSG00000021886	chr12	Gpr65	98268635	98268714	2049	2.418075	0.202811	1.29E-10	2.6E-09	0.080252	1	6	1	8	3	8	38	40	29	32	17
ENSMUSG00000025212	chr19	Sfxn3	45047576	45047890	2966	1.030044	5.315477	1.31E-10	2.65E-09	0.028524	1	413	342	589	299	447	817	1124	837	1249	854
ENSMUSG00000002204	chr7	Napsa	44572432	44572689	2158	2.305951	0.662851	1.32E-10	2.67E-09	0.079761	1	9	5	4	10	10	48	62	44	41	24
ENSMUSG00000068758	chr14	Il3ra	14346495	14346512	1394	1.717867	1.974826	1.33E-10	2.68E-09	0.060822	1	22	28	44	19	29	83	86	141	139	79
ENSMUSG00000050931	chr3	Sgms2	1.31E+08	1.31E+08	5873	1.788031	1.907988	1.42E-10	2.85E-09	0.068447	1	19	14	35	19	47	62	135	63	145	115
ENSMUSG00000051855	chr6	Mest	30723547	30723646	3935	1.842264	2.132794	1.42E-10	2.85E-09	0.074935	1	26	15	36	44	28	68	155	106	108	164
ENSMUSG00000091462	chr13	Gm17084	34033063	34037147	4085	1.505251	1.901817	1.48E-10	2.96E-09	0.043368	1	29	21	38	25	38	86	135	104	107	58
ENSMUSG00000028926	chr5	Cdk14	4803391	4806731	15344	1.353411	2.995766	1.51E-10	3.02E-09	0.043395	1	65	40	119	52	90	136	254	249	191	196
ENSMUSG00000028047	chr3	Thbs3	89215180	89215324	4823	1.249808	3.539117	1.56E-10	3.11E-09	0.038826	1	68	66	164	108	160	199	294	295	350	330
ENSMUSG00000015755	chr10	Tab2	7905653	7907577	6135	-0.94911	7.185718	1.61E-10	3.21E-09	0.025549	-1	2344	2203	4813	2866	3520	1369	2198	1682	2276	1614
ENSMUSG00000029622	chr5	Arpc1b	1.45E+08	1.45E+08	5103	1.005129	4.924515	1.63E-10	3.25E-09	0.02709	1	264	214	468	289	415	691	815	827	763	553
ENSMUSG00000034116	chr17	Vav1	57279100	57279401	3688	1.675051	1.454535	1.66E-10	3.29E-09	0.052472	1	15	9	35	18	26	62	105	82	67	48
ENSMUSG00000007872	chr4	Id3	1.36E+08	1.36E+08	1791	1.072188	4.382343	1.68E-10	3.34E-09	0.029784	1	194	167	228	233	233	386	550	608	576	435
ENSMUSG00000021738	chr14	Atxn7	14012491	14012750	6847	-0.98448	4.398924	1.72E-10	3.4E-09	0.025146	-1	344	301	769	370	539	192	324	245	336	209
ENSMUSG00000044033	chr2	Ccdc141	77009902	77015247	11717	1.64941	2.087768	1.73E-10	3.43E-09	0.057179	1	18	30	26	42	40	75	143	130	142	86
ENSMUSG00000040945	chr4	Rcc2	1.41E+08	1.41E+08	4155	1.073293	3.941579	1.81E-10	3.57E-09	0.028821	1	131	118	203	160	177	305	334	438	470	323
ENSMUSG00000025019	chr19	Lcor	41482645	41482783	7620	-2.41498	1.720503	1.83E-10	3.62E-09	0.128084	-1	32	32	213	70	133	14	22	11	23	21
ENSMUSG00000025898	chr9	Cwf19l2	3404085	3404190	3953	-1.12947	4.189747	1.86E-10	3.66E-09	0.033548	-1	261	301	680	362	461	120	297	180	257	207
ENSMUSG00000026288	chr1	Inpp5d	87620312	87620631	7602	1.588816	2.568026	1.86E-10	3.67E-09	0.059251	1	41	21	81	57	39	155	138	192	186	112
ENSMUSG00000037270	chr3	4932438A13Rik	36863106	36863348	26985	-1.15727	5.245252	1.89E-10	3.71E-09	0.036969	-1	565	443	1659	773	1036	328	605	374	527	342
ENSMUSG00000027272	chr2	Ubr1	1.21E+08	1.21E+08	9889	-1.0667	5.317844	1.91E-10	3.75E-09	0.031415	-1	674	568	1663	669	955	342	639	418	590	398
ENSMUSG00000064267	chr5	Hvcn1	1.22E+08	1.22E+08	3563	2.306807	2.034539	1.96E-10	3.84E-09	0.118702	1	16	24	26	21	16	62	134	228	127	55
ENSMUSG00000103229	chr3	Dcun1d1	35895620	35895699	780	-1.62896	3.248413	1.96E-10	3.84E-09	0.067377	-1	168	196	402	171	231	45	154	73	60	94
ENSMUSG00000039126	chr19	Prune2	16956118	16956292	12512	3.297868	4.324174	1.99E-10	3.9E-09	0.261706	1	14	16	37	163	66	427	662	459	1656	306
ENSMUSG00000049313	chr9	Sorl1	41964720	41968670	11321	-1.17972	6.034233	2.02E-10	3.95E-09	0.03922	-1	1079	754	2103	1609	2034	562	695	608	1126	695
ENSMUSG00000045767	chr13	B230219D22Rik	55693124	55693347	4651	-1.06108	5.351162	2.04E-10	3.97E-09	0.031241	-1	674	635	1386	769	1070	259	596	471	639	487
ENSMUSG00000063856	chr9	Gpx1	1.08E+08	1.08E+08	1441	1.265537	6.763421	2.08E-10	4.05E-09	0.045439	1	1217	792	1209	754	1039	2589	2701	3090	3748	1857
ENSMUSG00000000555	chr15	Itga5	1.03E+08	1.03E+08	4379	1.268006	3.854413	2.13E-10	4.13E-09	0.041882	1	87	64	183	157	211	223	491	361	446	355
ENSMUSG00000000278	chr11	Scpep1	88924020	88924724	2097	1.109233	4.208518	2.15E-10	4.17E-09	0.032365	1	167	124	258	169	228	353	448	597	444	413
ENSMUSG00000079471	chr17	Gm7325	45600967	45601685	976	3.665007	0.682774	2.28E-10	4.41E-09	0.243713	1	1	0	1	10	5	60	15	59	60	45
ENSMUSG00000040044	chr4	Orc3	34570796	34571018	6088	-0.94102	4.793277	2.32E-10	4.49E-09	0.023862	-1	522	410	929	491	623	255	477	310	423	290
ENSMUSG00000038506	chr8	Dcun1d2	13255963	13257976	3034	-0.95545	6.593945	2.33E-10	4.5E-09	0.026168	-1	1669	1409	3037	2051	2231	856	1705	1047	1398	1078
ENSMUSG00000042938	chr2	Gm14117	1.46E+08	1.46E+08	843	-1.76982	1.576593	2.35E-10	4.53E-09	0.064893	-1	46	42	99	86	97	8	36	18	35	26
ENSMUSG00000017057	chrX	Il13ra1	36112110	36112275	3712	1.31787	3.139316	2.38E-10	4.57E-09	0.042264	1	58	58	123	64	105	165	398	204	255	143
ENSMUSG00000033276	chr1	Stk36	74601445	74601613	6437	2.524231	0.476019	2.42E-10	4.66E-09	0.098573	1	9	5	4	4	7	38	26	55	36	35
ENSMUSG00000020859	chr11	Spag9	93996091	93996573	11209	-1.03374	7.762118	2.46E-10	4.71E-09	0.031053	-1	3495	2846	8151	4454	5477	1976	3493	2092	3525	2170
ENSMUSG00000040722	chr9	Scamp5	57441328	57443864	3190	1.385139	2.365388	2.5E-10	4.79E-09	0.042016	1	53	21	55	39	57	111	151	141	146	111
ENSMUSG00000026840	chr2	Lamc3	31887291	31887743	6091	-3.03931	0.593109	2.52E-10	4.82E-09	0.161565	-1	21	21	94	24	58	13	3	3	5	2
ENSMUSG00000022439	chr15	Parvg	84324026	84324127	3090	2.560127	0.180993	2.56E-10	4.9E-09	0.089081	1	6	2	4	2	9	32	36	39	35	14
ENSMUSG00000030798	chr7	Cd37	45233632	45233978	3538	1.679655	1.836412	2.57E-10	4.91E-09	0.059805	1	29	14	44	18	29	84	91	130	102	66
ENSMUSG00000085419	chr11	Gm11734	1.18E+08	1.18E+08	728	2.19065	0.448912	2.58E-10	4.92E-09	0.066327	1	7	7	11	5	5	19	57	41	35	34
ENSMUSG00000022831	chr16	Hcls1	36934983	36935074	2525	1.417861	2.813122	2.59E-10	4.93E-09	0.047479	1	54	50	67	49	79	186	173	217	210	118
ENSMUSG00000035621	chr10	Midn	80148272	80148349	4307	1.258928	5.175193	2.72E-10	5.16E-09	0.044545	1	238	184	426	430	468	646	1521	611	1182	814
ENSMUSG00000031662	chr8	Snx20	88626828	88627827	1434	2.265516	0.546708	2.74E-10	5.2E-09	0.07678	1	12	4	8	6	6	46	50	41	35	26
ENSMUSG00000009185	chr11	Ccl8	82115185	82115312	511	2.817652	3.577377	2.77E-10	5.24E-09	0.196959	1	61	62	63	9	25	524	460	408	284	158
ENSMUSG00000103888	chr1	AC123072.1	33908272	33908452	23154	-1.56293	8.121231	2.77E-10	5.25E-09	0.069869	-1	3713	2519	14321	6963	9136	1703	3032	2091	3426	2724
ENSMUSG00000006403	chr1	Adamts4	1.71E+08	1.71E+08	4810	3.32368	0.448722	2.79E-10	5.27E-09	0.202091	1	1	1	5	2	9	32	107	16	25	29
ENSMUSG00000022307	chr15	Oxr1	41447482	41447589	5165	-0.95981	5.915765	2.8E-10	5.28E-09	0.026282	-1	997	909	1965	1205	1451	483	995	714	892	704
ENSMUSG00000025813	chr7	Homer2	81600481	81610441	11149	-2.68979	3.682104	2.86E-10	5.39E-09	0.185236	-1	98	104	361	653	658	23	108	69	93	37
ENSMUSG00000068735	chr2	Trp53i11	93187548	93187747	3690	1.404882	2.658644	2.91E-10	5.47E-09	0.046843	1	40	21	67	62	91	126	204	157	206	134
ENSMUSG00000022587	chr15	Ly6e	74955051	74955335	3784	1.064807	6.579724	2.92E-10	5.48E-09	0.032814	1	851	703	1286	940	1217	2115	2438	2933	2403	1764

ENSMUSG00000021175	chr12	Cdca7l	1.18E+08	1.18E+08	3258	3.421539	-0.59646	2.97E-10	5.56E-09	0.120671	1	1	0	2	1	3	15	21	30	9	13
ENSMUSG00000104453	chr7	WI1-1616M8.3	81530309	81532521	2213	-1.09968	6.488061	3.05E-10	5.72E-09	0.035057	-1	1571	958	3019	2010	2705	840	1272	828	1499	855
ENSMUSG00000010751	chr7	Tnfrsf22	1.44E+08	1.44E+08	4289	1.455966	2.284251	3.14E-10	5.88E-09	0.046732	1	36	28	53	33	55	102	120	169	155	86
ENSMUSG00000025225	chr19	Nfkb2	46304737	46304820	3289	1.083741	4.123927	3.25E-10	6.08E-09	0.031061	1	131	150	218	158	234	381	478	396	636	283
ENSMUSG00000050010	chr5	Shisa3	67607883	67608684	4753	-2.07912	0.940146	3.3E-10	6.15E-09	0.079835	-1	25	20	62	62	78	12	14	11	14	12
ENSMUSG00000052812	chr12	Atad2b	4917404	4917921	4688	-1.84452	1.83212	3.43E-10	6.4E-09	0.075327	-1	55	41	183	79	108	25	32	18	25	35
ENSMUSG00000022440	chr15	C1qtnf6	78523346	78525398	2402	1.193543	3.108131	3.44E-10	6.4E-09	0.034961	1	57	49	124	68	132	191	228	196	264	195
ENSMUSG00000033792	chrX	Atp7a	1.06E+08	1.06E+08	8734	-2.39983	1.424027	3.45E-10	6.4E-09	0.126505	-1	38	25	151	68	97	10	34	15	8	9
ENSMUSG00000021636	chr13	Marveld2	1.01E+08	1.01E+08	3382	2.293134	0.903268	3.53E-10	6.55E-09	0.094165	1	6	12	10	4	14	31	72	28	78	58
ENSMUSG00000070462	chr7	Mesdc1	83879873	83884305	4433	1.232818	2.570406	3.56E-10	6.59E-09	0.033736	1	40	40	80	50	73	110	158	175	181	121
ENSMUSG00000024486	chr18	Hbegf	36504929	36506364	2373	1.114575	3.84572	3.65E-10	6.76E-09	0.032242	1	125	108	218	123	157	313	521	232	449	291
ENSMUSG00000028542	chr4	Slc6a9	1.18E+08	1.18E+08	5141	-1.36252	3.136144	3.66E-10	6.76E-09	0.047438	-1	151	140	393	164	201	45	108	96	139	70
ENSMUSG00000051439	chr18	Cd14	36725074	36726397	1572	1.441871	2.222154	3.85E-10	7.11E-09	0.04566	1	42	23	51	34	47	119	126	138	141	77
ENSMUSG00000030554	chr7	Synm	67730161	67736906	7866	-1.08918	9.875185	3.91E-10	7.19E-09	0.035428	-1	17024	16326	34874	14862	21578	9249	11908	9170	15039	9696
ENSMUSG00000049550	chr5	Clip1	1.24E+08	1.24E+08	9801	-1.09534	8.429807	3.91E-10	7.19E-09	0.035717	-1	5767	5718	13481	5969	7918	2760	4642	3402	5909	3702
ENSMUSG00000024696	chr19	Lpxn	12798606	12798679	1675	2.122887	0.939684	4.12E-10	7.56E-09	0.082071	1	5	8	11	17	12	54	64	67	51	27
ENSMUSG00000020300	chr11	Cpeb4	31872211	31873412	6369	-1.42625	5.732596	4.24E-10	7.77E-09	0.058989	-1	873	706	2243	1052	1699	207	614	518	728	612
ENSMUSG00000030148	chr6	Clec4a2	1.23E+08	1.23E+08	2860	1.69193	1.667835	4.24E-10	7.77E-09	0.058655	1	24	19	36	12	25	96	101	79	85	58
ENSMUSG00000047986	chr8	Palm3	84021471	84021528	3612	2.909587	0.211558	4.25E-10	7.77E-09	0.131076	1	6	1	3	3	6	34	22	15	47	44
ENSMUSG00000069792	chr11	Wfdc17	83703991	83704173	533	1.933878	2.33437	4.28E-10	7.81E-09	0.090036	1	50	27	38	16	27	170	183	118	143	88
ENSMUSG00000029333	chr5	Rasgef1b	99217426	99218798	3261	2.233281	0.255849	4.32E-10	7.88E-09	0.070335	1	2	3	5	7	13	28	42	34	27	28
ENSMUSG00000054428	chr4	Atpif1	1.33E+08	1.33E+08	1441	1.152123	4.774198	4.34E-10	7.9E-09	0.037154	1	269	245	262	275	254	643	891	608	778	515
ENSMUSG00000068373	chr2	D430041D05Rik	1.04E+08	1.04E+08	15851	-1.51666	2.682965	4.43E-10	8.06E-09	0.056435	-1	123	85	278	143	157	69	48	43	91	46
ENSMUSG00000034801	chr12	Sos2	69583762	69585632	8514	-1.1223	5.774591	4.5E-10	8.17E-09	0.036802	-1	875	682	2057	1211	1467	345	695	655	845	640
ENSMUSG00000044147	chr12	Arf6	69372150	69372223	3730	0.877666	4.752791	4.54E-10	8.23E-09	0.021043	1	260	227	400	281	357	511	715	656	785	515
ENSMUSG00000003233	chr16	Dvl3	20516982	20517355	4899	-1.17459	3.576037	4.56E-10	8.27E-09	0.036022	-1	212	123	441	260	347	89	176	118	159	129
ENSMUSG00000054659	chr4	Pm20d2	33174230	33174480	1834	-2.32599	2.51586	4.59E-10	8.31E-09	0.138404	-1	65	61	221	202	252	12	83	21	35	29
ENSMUSG00000031529	chr8	Tnks	34829179	34831721	6444	-1.27534	3.312459	4.69E-10	8.48E-09	0.042147	-1	144	115	428	208	296	74	146	95	134	86
ENSMUSG00000032089	chr9	Il10ra	45253837	45256441	3498	1.900481	1.985007	4.84E-10	8.73E-09	0.084727	1	11	26	53	14	30	113	104	130	97	92
ENSMUSG00000028132	chr3	Tmem56	1.21E+08	1.21E+08	7650	-1.07569	5.638848	4.85E-10	8.74E-09	0.033831	-1	944	778	1922	743	1200	372	774	633	671	511
ENSMUSG00000052837	chr8	Junb	84976909	84978748	1840	3.029395	5.116246	4.99E-10	8.98E-09	0.238718	1	73	77	120	92	261	610	4054	501	616	404
ENSMUSG00000052776	chr5	Oas1a	1.21E+08	1.21E+08	1885	2.225897	0.947793	5.08E-10	9.14E-09	0.095295	1	13	5	11	4	18	55	72	60	34	44
ENSMUSG00000021939	chr14	Ctsb	63122462	63122565	4739	1.096124	9.207211	5.17E-10	9.29E-09	0.036344	1	4653	3489	7689	7525	7434	12138	16067	17329	15611	11886
ENSMUSG00000017009	chr2	Sdc4	1.64E+08	1.64E+08	2547	0.97044	4.550758	5.22E-10	9.36E-09	0.026031	1	180	185	294	270	343	487	745	537	610	447
ENSMUSG00000015214	chrX	Mtmr1	71364760	71365072	5859	-0.9457	4.91197	5.3E-10	9.49E-09	0.025359	-1	487	409	1060	662	650	264	490	342	476	329
ENSMUSG00000031337	chrX	Mtm1	71210767	71210952	13935	-1.02372	3.512572	5.48E-10	9.8E-09	0.026413	-1	204	161	398	217	272	94	187	129	150	128
ENSMUSG00000021140	chr12	Pcnx	81860030	81860524	12139	-1.31082	6.148696	5.49E-10	9.81E-09	0.050881	-1	1081	633	2802	1884	2263	595	848	626	1067	626
ENSMUSG00000000392	chr2	Fap	62500943	62501288	5662	1.048495	3.695361	5.64E-10	1.01E-08	0.028365	1	123	98	200	111	146	225	395	346	311	298
ENSMUSG00000099329	chr17	Gm28052	29549799	29549994	380	-1.92763	1.736306	5.72E-10	1.02E-08	0.086378	-1	60	34	135	87	118	8	40	26	20	30
ENSMUSG00000025531	chrX	Chm	1.13E+08	1.13E+08	6780	-1.31459	4.260009	5.76E-10	1.02E-08	0.048977	-1	268	302	840	366	521	107	268	231	184	212
ENSMUSG00000056515	chr17	Rab31	65651726	65654503	3476	1.038437	3.561917	5.75E-10	1.02E-08	0.027773	1	94	67	190	121	163	258	325	284	332	232
ENSMUSG00000010830	chr15	Kdelr3	79516408	79516640	1414	1.231434	2.378783	5.78E-10	1.02E-08	0.03322	1	33	34	68	48	64	113	139	120	148	124
ENSMUSG00000021242	chr12	Npc2	84754560	84757212	3261	1.191416	6.158556	5.78E-10	1.02E-08	0.042115	1	707	625	798	606	646	1527	1890	2267	1778	1472
ENSMUSG00000038366	chr11	Lasp1	97799000	97799197	6495	0.974293	4.780203	5.78E-10	1.02E-08	0.02685	1	255	208	428	260	352	482	650	787	780	595
ENSMUSG00000022261	chr15	Sdc2	32920723	32921305	3322	0.925222	4.649676	5.85E-10	1.03E-08	0.023959	1	204	182	414	259	362	455	666	628	674	556
ENSMUSG00000031555	chr8	Adam9	24949611	24951010	4011	-0.94426	6.309486	5.9E-10	1.04E-08	0.026627	-1	1335	1182	2754	1461	1861	794	1227	858	1162	921
ENSMUSG00000061119	chr7	Prcp	92875253	92875500	2956	1.216783	3.264912	6.24E-10	1.1E-08	0.038232	1	86	59	158	85	79	224	255	280	254	184
ENSMUSG00000029470	chr5	P2rx4	1.23E+08	1.23E+08	3309	1.291596	3.298393	6.27E-10	1.1E-08	0.043757	1	90	66	148	58	97	234	284	302	235	187
ENSMUSG00000099703	chr18	Gm28285	35553404	35553469	1264	-0.95972	3.825852	6.42E-10	1.13E-08	0.023932	-1	231	227	431	286	337	137	234	142	196	169
ENSMUSG00000038481	chr10	Cdk19	40349308	40349721	5807	-1.63631	5.234211	6.48E-10	1.14E-08	0.078121	-1	1024	548	1589	525	1021	427	288	247	518	179
ENSMUSG00000010277	chr11	2610507B11Rik	78261752	78261917	8798	-1.07281	8.858125	6.51E-10	1.14E-08	0.035227	-1	7105	5203	16295	11362	12928	4189	6524	4779	7448	4697
ENSMUSG00000048126	chr1	Col6a3	90765923	90765933	11963	1.216431	6.738373	6.84E-10	1.2E-08	0.044756	1	768	550	1778	887	1456	2005	2470	2715	2965	3202
ENSMUSG00000032495	chr9	Lrrc2	1.11E+08	1.11E+08	3657	-1.25822	6.259045	6.87E-10	1.2E-08	0.047583	-1	1027	1099	2369	2295	2078	623	980	542	1341	729
ENSMUSG00000015501	chr10	Hivep2	13966075	13966220	13720	-1.10583	6.070946	6.88E-10	1.2E-08	0.036725	-1	1034	899	2853	1269	1717	516	903	705	1074	743
ENSMUSG00000069662	chr10	Marcks	37133375	37136935	4048	1.108248	5.735383	6.89E-10	1.2E-08	0.03646	1	512	511	652	404	561	943	1328	1376	1619	1335
ENSMUSG00000019539	chr7	Rcn3	45082913	45083363	1604	1.11391	4.335574	6.94E-10	1.21E-08	0.035124	1	142	148	256	191	296	387	479	563	496	532
ENSMUSG00000041261	chr4	Car8	8143362	8146216	3853	-1.473	2.199375	7.02E-10	1.22E-08	0.050965	-1	95	50	122	111	167	26	60	43	57	36
ENSMUSG00000000374	chr10	Trappc10	78186725	78188094	5048	-0.95477	5.699768	7.06E-10	1.22E-08	0.027095	-1	900	595	1616	1158	1409	484	766	539	883	590
ENSMUSG00000027248	chr2	Pdia3	1.21E+08	1.21E+08	3139	1.030484	6.450838	7.05E-10	1.22E-08	0.032051	1	787	797	1187	787	1011	1955	2462	2359	2094	1717
ENSMUSG00000031875	chr8	Cmtm3	1.04E+08	1.04E+08	1616	1.1276	3.429042	7.06E-10	1.22E-08	0.032758	1	85	90	171	91	104	245	290	290	271	220
ENSMUSG00000060216	chr11	Arrb2	70432635	70432753	2845	1.139907	3.32872	7.35E-10	1.27E-08	0.033365	1	92	71	126	79	132	256	248	234	288	202
ENSMUSG00000028656	chr4	Cap1	1.23E+08	1.23E+08	3494	0.899441	5.208402	7.52E-10	1.3E-08	0.023591	1	342	261	581	395	530	687	1051	959	921	754
ENSMUSG00000006740	chr18	Kif5b	6201002	6203707	7395	-1.03721	6.643931	7.56E-10	1.3E-08	0.032754	-1	1648	1465	3626	1800	2632	744	1542	1097	1393	1255
ENSMUSG00000034557	chr4	Zfyve9	1.09E+08	1.09E+08	6459	-0.95133	6.542057	7.56E-10	1.3E-08	0.027507	-1	1523	1319	3251	1849	2213	1006	1348	976	1580	933
ENSMUSG00000051985	chr1	Igfn1	1.36E+08	1.36E+08	8996	2.834433	6.520974	7.75E-10	1.33E-08	0.219444	1	242	225	644	167	658	1057	1077	2178	2926	6596

ENSMUSG00000036412	chr18	Arsi	60911780	60912550	2975	1.541821	2.39764	7.97E-10	1.37E-08	0.057721	1	47	31	45	21	66	92	152	137	173	144
ENSMUSG00000022770	chr16	Dlg1	31663443	31663488	8963	-0.92376	6.046861	8.04E-10	1.38E-08	0.025742	-1	1183	920	2212	1223	1585	688	1026	693	1038	741
ENSMUSG00000032066	chr9	Bco2	50533087	50533519	2118	2.60909	-0.40157	8.25E-10	1.41E-08	0.071198	1	2	0	3	3	6	13	22	26	23	15
ENSMUSG00000001229	chr17	Dpp9	56186682	56187461	3509	-0.93836	5.597964	8.33E-10	1.43E-08	0.026288	-1	790	558	1485	1124	1313	449	730	558	764	551
ENSMUSG00000083405	chr16	Gm15725	37882542	37883631	1090	-2.47189	1.314633	8.36E-10	1.43E-08	0.138821	-1	31	18	158	50	103	9	18	9	12	17
ENSMUSG00000022253	chr15	Nadk2	9071260	9071765	4345	-0.94748	5.041829	8.64E-10	1.48E-08	0.026395	-1	533	480	1009	715	801	255	606	350	528	362
ENSMUSG00000054640	chr17	Slc8a1	81388691	81389067	2934	-2.13497	2.216607	8.94E-10	1.52E-08	0.117169	-1	66	77	302	89	109	29	62	13	26	26
ENSMUSG00000071715	chr15	Ncf4	78244801	78245087	2021	2.081923	1.007937	9.13E-10	1.55E-08	0.085495	1	8	9	11	12	17	50	67	80	57	23
ENSMUSG00000042042	chr6	Csgalnact2	1.18E+08	1.18E+08	5438	-0.93414	5.36515	9.14E-10	1.55E-08	0.025995	-1	667	728	1321	713	949	400	640	429	668	468
ENSMUSG00000017716	chr11	Birc5	1.18E+08	1.18E+08	3402	2.610207	0.185813	9.22E-10	1.57E-08	0.111831	1	4	3	7	2	7	32	22	38	20	40
ENSMUSG00000000340	chr3	Dbt	1.17E+08	1.17E+08	3296	-1.14032	5.162916	9.54E-10	1.62E-08	0.03894	-1	513	472	1217	856	1045	228	561	468	402	396
ENSMUSG00000030838	chr7	Ush1c	46195350	46195734	3849	-2.37003	0.206661	9.68E-10	1.64E-08	0.091553	-1	29	23	49	12	33	6	6	2	9	8
ENSMUSG00000080741	chr13	Gm11398	23620730	23621049	320	-1.9196	1.183035	9.73E-10	1.65E-08	0.074812	-1	40	24	74	62	87	16	14	11	17	23
ENSMUSG00000028469	chr4	Npr2	43631935	43632851	4667	-1.30455	5.347656	9.77E-10	1.65E-08	0.051279	-1	522	474	1225	1300	1296	278	525	414	453	467
ENSMUSG00000076444	chr4	Mir761	1.09E+08	1.09E+08	76	-2.33537	-0.17389	9.87E-10	1.67E-08	0.071312	-1	15	20	31	13	29	2	9	4	6	3
ENSMUSG00000025937	chr1	Lactb2	13623330	13626904	4566	-0.92233	4.156485	1E-09	1.69E-08	0.023559	-1	271	248	520	393	473	152	303	207	271	202
ENSMUSG00000020097	chr10	Sgpl1	61098642	61101008	6143	0.956529	4.405639	1.05E-09	1.76E-08	0.026121	1	199	145	365	220	248	433	558	579	533	416
ENSMUSG00000039701	chr3	Usp53	1.23E+08	1.23E+08	4014	-1.93808	2.539745	1.09E-09	1.82E-08	0.100242	-1	71	60	255	172	223	22	81	25	44	49
ENSMUSG00000032766	chr6	Gng11	4003943	4004411	880	1.188476	4.253625	1.1E-09	1.84E-08	0.040644	1	156	154	161	212	220	312	761	390	616	395
ENSMUSG00000060036	chr15	Rpl3	80077794	80077894	3119	0.987497	6.085568	1.1E-09	1.85E-08	0.029911	1	604	598	844	741	819	1489	1883	1774	1739	1283
ENSMUSG00000071713	chr15	Csf2rb	78325990	78326098	4764	1.833202	2.921644	1.1E-09	1.85E-08	0.091524	1	60	34	90	35	46	179	395	255	156	94
ENSMUSG00000098265	chr11	Gm27517	3645286	3645521	236	-1.92095	0.503124	1.11E-09	1.86E-08	0.055994	-1	17	23	56	33	45	8	12	9	10	11
ENSMUSG00000000120	chr11	Ngfr	95568818	95571095	3446	1.641334	1.417604	1.12E-09	1.87E-08	0.052471	1	18	21	28	18	12	43	88	72	85	65
ENSMUSG00000071267	chr17	Zfp942	21926960	21929489	5259	-1.16228	2.791678	1.13E-09	1.89E-08	0.033316	-1	116	125	242	127	160	52	96	73	91	76
ENSMUSG00000057329	chr1	Bcl2	1.07E+08	1.07E+08	9157	-1.59684	2.193581	1.2E-09	2.01E-08	0.063311	-1	86	44	143	131	157	30	59	52	38	26
ENSMUSG00000079419	chr19	Ms4a6c	11469366	11469556	2050	1.589986	2.109015	1.21E-09	2.02E-08	0.060241	1	28	28	44	30	37	148	134	78	114	87
ENSMUSG00000092463	chrX	Gm20489	1.01E+08	1.01E+08	1350	2.02853	1.148619	1.23E-09	2.05E-08	0.082469	1	9	15	13	16	11	75	71	56	45	50
ENSMUSG00000030793	chr7	Pycard	1.28E+08	1.28E+08	1405	2.027818	1.08185	1.27E-09	2.1E-08	0.083204	1	16	10	24	4	9	66	66	54	65	37
ENSMUSG00000020865	chr11	Abcc3	94343295	94343775	5698	2.176911	0.48502	1.28E-09	2.11E-08	0.081074	1	5	5	7	5	15	38	29	50	40	29
ENSMUSG00000049988	chr8	Lrrc25	70616844	70617026	1273	1.858677	0.912667	1.28E-09	2.12E-08	0.064377	1	13	7	16	10	15	59	48	56	51	32
ENSMUSG00000027832	chr3	Ptx3	66219910	66220191	2682	1.508049	3.988646	1.29E-09	2.13E-08	0.066086	1	114	91	150	116	189	271	886	219	535	324
ENSMUSG00000094870	chr13	Zfp131	1.2E+08	1.2E+08	3067	-0.93103	4.479899	1.31E-09	2.16E-08	0.025074	-1	350	337	713	472	513	180	337	308	320	260
ENSMUSG00000021311	chr13	Mtr	12186542	12187091	4482	-1.22972	3.59087	1.33E-09	2.19E-08	0.042244	-1	186	137	500	257	347	90	147	101	181	139
ENSMUSG00000003178	chr6	Mical3	1.21E+08	1.21E+08	2893	-1.54842	2.62285	1.34E-09	2.21E-08	0.063689	-1	80	67	241	186	192	32	65	46	86	58
ENSMUSG00000009471	chr7	Myod1	46376474	46377299	1854	1.108192	4.781372	1.38E-09	2.27E-08	0.036937	1	233	157	358	344	320	453	601	748	991	636
ENSMUSG00000023025	chr15	Larp4	99970074	99970278	6731	-0.97601	4.898664	1.38E-09	2.28E-08	0.028563	-1	460	422	1036	616	734	221	500	373	410	350
ENSMUSG00000050105	chr4	Grrp1	1.34E+08	1.34E+08	1275	1.809989	2.040741	1.39E-09	2.28E-08	0.080355	1	27	25	40	20	29	141	145	120	102	50
ENSMUSG00000020948	chr12	Klhl28	64942440	64943613	2854	-1.86154	1.896426	1.4E-09	2.29E-08	0.086793	-1	38	51	194	89	119	23	50	18	31	23
ENSMUSG00000025151	chrX	Maged1	94535474	94535677	4351	0.939305	5.173798	1.41E-09	2.31E-08	0.026664	1	283	286	524	410	502	712	870	992	984	726
ENSMUSG00000005034	chr3	Prkacb	1.47E+08	1.47E+08	5451	-0.86034	5.5569	1.42E-09	2.32E-08	0.022594	-1	844	691	1522	825	1076	474	688	595	775	530
ENSMUSG00000031779	chr8	Ccl22	94745590	94745786	2325	3.109979	-0.52869	1.43E-09	2.34E-08	0.106422	1	4	0	0	0	5	20	19	23	14	15
ENSMUSG00000042532	chr19	Golga7b	42247574	42247636	2988	1.380323	4.208836	1.44E-09	2.35E-08	0.055989	1	177	146	282	84	128	405	550	426	720	355
ENSMUSG00000028139	chr3	Riiad1	94464983	94465095	813	1.307762	2.790732	1.48E-09	2.41E-08	0.042807	1	63	56	67	68	50	154	233	141	222	139
ENSMUSG00000042390	chr3	Gatad2b	90341654	90341994	1906	-1.83626	2.447283	1.48E-09	2.41E-08	0.08959	-1	62	64	318	120	171	27	47	34	49	55
ENSMUSG00000052974	chr7	Cyp2f2	27119909	27120015	2025	2.41525	3.361122	1.48E-09	2.41E-08	0.161799	1	78	44	53	25	45	219	212	679	216	184
ENSMUSG00000021665	chr13	Hexb	97176332	97176589	1904	1.013267	4.182928	1.48E-09	2.41E-08	0.029633	1	142	133	241	191	265	375	490	463	403	434
ENSMUSG00000039824	chr10	Myl6b	1.28E+08	1.28E+08	1026	1.239931	3.121716	1.5E-09	2.44E-08	0.040313	1	78	61	85	96	82	156	206	198	336	210
ENSMUSG00000020627	chr12	Klhl29	5077472	5081334	7041	-1.39878	1.88812	1.54E-09	2.5E-08	0.043359	-1	77	43	111	81	119	24	47	32	40	39
ENSMUSG00000044813	chr4	Shb	45423278	45424123	3199	1.340322	2.193721	1.55E-09	2.5E-08	0.041189	1	30	32	50	41	49	81	141	149	128	85
ENSMUSG00000055024	chr15	Ep300	81585351	81588344	13886	-1.21833	5.271889	1.57E-09	2.54E-08	0.045832	-1	549	437	1698	839	1111	255	437	455	542	435
ENSMUSG00000063011	chr17	Msln	25748614	25748830	2114	3.251308	0.875396	1.57E-09	2.54E-08	0.227959	1	3	0	1	16	5	62	38	37	101	41
ENSMUSG00000021712	chr13	Trim23	1.04E+08	1.04E+08	5747	-1.08055	4.864618	1.68E-09	2.7E-08	0.035685	-1	492	492	1018	528	699	179	472	300	417	366
ENSMUSG00000027338	chr2	Prnd	1.32E+08	1.32E+08	3211	2.091409	0.311538	1.7E-09	2.73E-08	0.066376	1	3	3	8	7	13	18	45	28	52	25
ENSMUSG00000040183	chr4	Ankrd6	32804035	32806642	5477	-1.93164	1.323983	1.7E-09	2.74E-08	0.086159	-1	58	24	59	75	97	11	23	10	29	20
ENSMUSG00000073411	chr17	H2-D1	35262730	35263186	2579	1.427966	7.69098	1.72E-09	2.76E-08	0.064387	1	2053	1561	2029	1251	1820	5024	5183	8043	4970	3705
ENSMUSG00000036202	chr2	Rif1	52072837	52072866	10527	-1.27615	3.583673	1.72E-09	2.76E-08	0.04679	-1	166	154	548	245	328	81	200	109	140	117
ENSMUSG00000027602	chr2	Map1lc3a	1.55E+08	1.55E+08	1181	0.978361	8.198423	1.81E-09	2.9E-08	0.030916	1	2709	2672	3757	3051	3462	6241	8238	5829	10007	5603
ENSMUSG00000022847	chr16	Thpo	20725158	20726082	1837	-1.49859	1.945895	1.81E-09	2.9E-08	0.052385	-1	68	41	133	96	126	40	37	35	42	24
ENSMUSG00000056124	chr18	B4galt6	20684599	20688468	5808	1.397036	2.09306	1.82E-09	2.91E-08	0.045709	1	23	28	57	34	44	90	98	110	118	121
ENSMUSG00000022969	chr16	Il10rb	91406164	91406391	3808	1.097752	3.488351	1.88E-09	2.99E-08	0.032889	1	108	84	147	94	135	202	284	349	294	241
ENSMUSG00000037206	chr9	Islr	58156265	58158230	2354	1.034635	5.232346	1.9E-09	3.02E-08	0.033213	1	274	271	558	446	459	594	972	1024	974	997
ENSMUSG00000064344	chrMT	mt-Tm	3845	3913	69	-2.85652	4.721695	1.93E-09	3.08E-08	0.230667	-1	170	139	531	1347	1775	84	182	94	153	86
ENSMUSG00000020399	chr11	Havcr2	46454935	46455058	2721	2.927077	-0.56228	1.96E-09	3.11E-08	0.097354	1	2	0	1	0	7	15	16	24	18	15
ENSMUSG00000003153	chr6	Slc2a3	1.23E+08	1.23E+08	7245	-2.11319	4.186949	1.99E-09	3.17E-08	0.132067	-1	425	430	946	206	414	185	104	48	192	82
ENSMUSG00000025823	chr6	Pdia4	47796142	47796903	2480	1.034598	4.245479	2.01E-09	3.19E-08	0.031762	1	170	126	297	188	232	354	465	602	458	404

ENSMUSG00000008036	chr7	Ap2s1	16738410	16738538	1333	0.944646	5.379673	2.02E-09	3.2E-08	0.027626	1	444	344	491	465	497	903	1087	988	1240	763
ENSMUSG00000049164	chr19	Zfp518a	40894705	40894790	6840	-1.40436	2.426411	2.04E-09	3.22E-08	0.051158	-1	103	82	197	89	165	27	82	46	53	60
ENSMUSG00000025962	chr1	Fastkd2	63730614	63730691	5873	-0.97403	4.526755	2.04E-09	3.23E-08	0.028441	-1	425	351	602	533	527	254	378	196	322	267
ENSMUSG00000032387	chr9	Rbpms2	65629648	65629722	2041	1.588817	1.94935	2.06E-09	3.26E-08	0.060875	1	27	23	39	28	32	64	89	149	101	100
ENSMUSG00000047180	chr1	Neurl3	36264597	36266553	3217	1.806157	2.161693	2.08E-09	3.28E-08	0.084172	1	32	25	36	28	32	166	98	145	96	84
ENSMUSG00000041058	chr4	Wwp1	19608303	19611813	6453	-1.0478	7.889486	2.11E-09	3.32E-08	0.035661	-1	3557	2723	8495	5814	6272	1963	3477	2404	3822	2650
ENSMUSG00000026672	chr2	Optn	5020642	5021228	3753	-1.012	5.741874	2.14E-09	3.36E-08	0.032449	-1	857	752	1501	1310	1401	600	788	426	894	552
ENSMUSG00000042724	chr12	Map3k9	81714950	81722523	10619	2.734684	0.093728	2.15E-09	3.38E-08	0.121072	1	3	2	1	4	9	32	29	18	56	15
ENSMUSG00000040462	chr10	Os9	1.27E+08	1.27E+08	4049	0.870028	4.840263	2.26E-09	3.55E-08	0.022841	1	257	230	415	333	397	511	707	716	829	601
ENSMUSG00000044177	chr11	Wfikkn2	94235956	94239118	3827	-0.98886	4.064999	2.29E-09	3.58E-08	0.028546	-1	262	248	509	373	417	146	260	156	232	227
ENSMUSG00000037712	chr14	Fermt2	45458792	45460023	3746	-0.90001	7.611832	2.29E-09	3.59E-08	0.026471	-1	3277	2638	6472	3835	4825	1910	3019	2147	3249	2250
ENSMUSG00000048939	chr16	Atp13a5	29231851	29232863	4661	-1.92031	2.211922	2.29E-09	3.59E-08	0.0985	-1	58	54	155	163	172	41	31	17	58	26
ENSMUSG00000054263	chr15	Lifr	7129559	7129826	10330	-0.97984	5.377855	2.32E-09	3.62E-08	0.030182	-1	666	441	1306	980	1210	407	578	500	669	414
ENSMUSG00000021068	chr12	Nin	70011435	70014956	10345	-0.9919	4.869233	2.34E-09	3.65E-08	0.030405	-1	511	489	1045	478	653	234	391	346	483	343
ENSMUSG00000035992	chr11	Fnip1	54438199	54438388	7119	-1.11502	5.759357	2.36E-09	3.69E-08	0.03971	-1	776	783	2096	1142	1403	335	738	560	840	690
ENSMUSG00000023861	chr17	Mpc1	8282904	8283017	2082	-1.03889	6.92525	2.38E-09	3.7E-08	0.035086	-1	2084	1708	2892	3219	3240	1084	2162	1130	1892	1171
ENSMUSG00000062040	chr7	Zfp27	29893333	29896426	4224	-1.17355	2.80071	2.39E-09	3.72E-08	0.035318	-1	127	96	188	168	195	75	105	59	78	68
ENSMUSG00000084899	chr10	Gm15344	86692119	86692202	421	1.189275	4.95729	2.39E-09	3.72E-08	0.044005	1	324	246	249	281	362	801	910	803	793	572
ENSMUSG00000038205	chr3	Prkab2	97658193	97658369	5096	-1.05742	9.02467	2.42E-09	3.75E-08	0.03672	-1	11015	7869	19325	8014	11576	5811	7641	5161	7349	4934
ENSMUSG00000043832	chr6	Clec4a3	1.23E+08	1.23E+08	1327	1.802973	1.769753	2.5E-09	3.87E-08	0.080541	1	18	19	43	14	26	123	113	83	72	62
ENSMUSG00000001687	chr5	Ubl3	1.49E+08	1.49E+08	2668	-0.9277	6.384071	2.5E-09	3.87E-08	0.027831	-1	1547	1403	2569	1511	1776	803	1175	1003	1236	1023
ENSMUSG00000063550	chr7	Nup98	1.02E+08	1.02E+08	4051	-1.33077	3.095179	2.53E-09	3.91E-08	0.049806	-1	118	100	383	168	271	63	128	73	98	82
ENSMUSG00000004849	chr5	Ap1s1	1.37E+08	1.37E+08	2198	0.984472	4.836457	2.54E-09	3.92E-08	0.029669	1	299	269	366	270	296	584	729	700	912	533
ENSMUSG00000078453	chr10	Abracl	18011263	18011816	807	1.50279	1.640731	2.54E-09	3.92E-08	0.047857	1	26	23	26	25	22	80	85	76	83	72
ENSMUSG00000050556	chr2	Kcnb1	1.67E+08	1.67E+08	4060	-1.23574	3.457472	2.64E-09	4.07E-08	0.044135	-1	180	143	478	170	332	76	137	126	142	115
ENSMUSG00000071083	chr8	Gm10311	69373528	69373914	387	-2.21143	-0.19626	2.74E-09	4.22E-08	0.058871	-1	19	12	34	20	20	5	5	3	9	3
ENSMUSG00000070802	chr7	Pnmal2	16944682	16948828	4147	2.01899	1.141734	2.85E-09	4.37E-08	0.092843	1	5	7	13	18	24	56	46	46	75	74
ENSMUSG00000026875	chr2	Traf1	34941750	34944091	5051	1.965348	0.439422	2.85E-09	4.38E-08	0.0564	1	9	7	6	9	8	32	34	30	54	28
ENSMUSG00000028378	chr4	Ptgr1	58965439	58966763	2296	1.646428	1.981711	2.87E-09	4.39E-08	0.067623	1	28	21	38	38	22	100	109	131	76	97
ENSMUSG00000090290	chr8	Gm17296	1.26E+08	1.26E+08	5060	-1.77998	2.124455	2.95E-09	4.52E-08	0.085672	-1	59	49	197	113	148	17	67	26	31	38
ENSMUSG00000048330	chr7	Ric3	1.09E+08	1.09E+08	8561	-1.56609	1.15511	2.97E-09	4.54E-08	0.049808	-1	39	37	88	41	59	8	30	20	23	19
ENSMUSG00000028152	chr3	Tspan5	1.39E+08	1.39E+08	3917	1.155371	2.543446	3E-09	4.58E-08	0.032424	1	51	42	73	45	74	114	161	161	164	117
ENSMUSG00000071379	chr12	Hpcal1	17690814	17691046	1561	1.335588	2.879747	3.07E-09	4.68E-08	0.050209	1	40	41	121	66	75	201	191	215	202	123
ENSMUSG00000045136	chr13	Tubb2b	34127008	34128531	1922	1.991459	1.854562	3.09E-09	4.71E-08	0.103352	1	15	9	15	46	26	93	85	98	148	81
ENSMUSG00000027109	chr2	Sp3	72936427	72938382	4933	-1.06755	4.181923	3.27E-09	4.98E-08	0.034831	-1	288	268	660	405	398	119	224	218	279	232
ENSMUSG00000070354	chr11	Gm21975	79513385	79516762	3944	1.353271	2.136725	3.33E-09	5.07E-08	0.0447	1	39	20	51	30	56	94	161	111	102	92
ENSMUSG00000039114	chr13	Nrn1	36725625	36726856	1766	1.80381	0.711364	3.35E-09	5.09E-08	0.055617	1	10	7	17	8	12	28	64	30	65	32
ENSMUSG00000039976	chr11	Tbc1d16	1.19E+08	1.19E+08	7119	-1.30457	5.574901	3.45E-09	5.23E-08	0.055263	-1	1030	917	2071	617	905	414	715	546	523	333
ENSMUSG00000049409	chr6	Prokr1	87578593	87581916	4055	-2.44544	0.123058	3.45E-09	5.23E-08	0.102764	-1	15	12	56	20	40	3	2	7	7	8
ENSMUSG00000027715	chr3	Ccna2	36564866	36566282	3510	2.329558	0.361878	3.55E-09	5.37E-08	0.102579	1	3	1	6	13	8	38	32	37	28	36
ENSMUSG00000037649	chr17	H2-DMa	34135182	34135758	1641	1.539587	2.895269	3.61E-09	5.45E-08	0.068125	1	72	41	92	38	59	248	157	196	218	143
ENSMUSG00000042063	chr12	Zfp386	1.16E+08	1.16E+08	8753	-0.97397	4.156238	3.6E-09	5.45E-08	0.028735	-1	322	328	531	344	351	187	309	175	244	186
ENSMUSG00000029925	chr6	Tbxas1	38875404	38875452	9094	1.652997	1.483406	3.62E-09	5.46E-08	0.06496	1	13	9	36	14	36	51	74	97	84	62
ENSMUSG00000021457	chr13	Syk	52583173	52583605	9362	1.385573	2.784558	3.71E-09	5.6E-08	0.054336	1	49	32	96	53	81	183	159	233	183	117
ENSMUSG00000033467	chr5	Crlf2	1.1E+08	1.1E+08	1325	1.543141	2.100458	3.72E-09	5.6E-08	0.059289	1	40	27	35	32	32	78	102	152	154	80
ENSMUSG00000030029	chr6	Lrig1	94604529	94604779	5585	-0.97013	6.392895	3.79E-09	5.69E-08	0.031179	-1	1308	1006	2975	1767	2277	828	1334	821	1331	923
ENSMUSG00000073155	chr6	1810058I24Rik	35252654	35252782	2784	0.954849	5.809994	3.79E-09	5.69E-08	0.029696	1	538	503	611	625	718	1015	1567	1164	1758	1280
ENSMUSG00000001998	chr2	Ap4e1	1.27E+08	1.27E+08	9810	-1.27781	2.914206	3.81E-09	5.71E-08	0.045722	-1	113	104	324	153	196	54	106	62	85	91
ENSMUSG00000025993	chr1	Slc40a1	45908068	45909719	9000	-1.23859	4.730001	3.81E-09	5.71E-08	0.049339	-1	472	277	812	722	805	173	440	267	455	171
ENSMUSG00000064493	chr12	Snora28	1.12E+08	1.12E+08	127	-1.89974	0.77689	3.99E-09	5.97E-08	0.07597	-1	27	38	70	37	37	8	26	6	13	11
ENSMUSG00000026812	chr2	Tsc1	28641228	28641319	11833	-1.03343	5.524365	4.05E-09	6.06E-08	0.034905	-1	625	538	1761	1055	1254	403	649	472	716	534
ENSMUSG00000001027	chr11	Scn4a	1.06E+08	1.06E+08	7041	-1.08474	8.726564	4.21E-09	6.29E-08	0.039787	-1	6451	4919	16744	8847	11990	3540	5694	3948	6882	4966
ENSMUSG00000045594	chr9	Glb1	1.14E+08	1.14E+08	2395	1.299159	2.410903	4.46E-09	6.65E-08	0.044334	1	34	25	68	61	58	122	128	155	157	105
ENSMUSG00000085711	chrX	Gm15163	1.57E+08	1.57E+08	1302	-1.87764	0.909796	4.49E-09	6.69E-08	0.07786	-1	32	32	57	59	48	2	23	12	20	15
ENSMUSG00000055172	chr6	C1ra	1.25E+08	1.25E+08	2751	0.968777	5.011852	4.59E-09	6.84E-08	0.030203	1	266	292	551	275	384	705	885	865	805	593
ENSMUSG00000043733	chr5	Ptpn11	1.21E+08	1.21E+08	7492	-0.92091	6.892311	4.63E-09	6.88E-08	0.028617	-1	2008	1369	3692	2641	3182	1226	1730	1334	2023	1244
ENSMUSG00000054178	chr19	Gm9938	23723279	23725034	1756	-3.32225	0.21852	4.64E-09	6.89E-08	0.224677	-1	8	12	89	24	38	0	9	3	1	4
ENSMUSG00000084349	chrX	Rpl3-ps1	13202571	13203780	1210	1.205088	2.278864	4.65E-09	6.9E-08	0.034174	1	39	41	56	36	56	107	137	112	146	98
ENSMUSG00000032845	chr18	Alpk2	65265529	65266290	7782	-1.33491	5.559999	4.72E-09	6.99E-08	0.058752	-1	579	438	1709	1383	1665	430	526	422	550	486
ENSMUSG00000020914	chr11	Top2a	98992943	98993413	9013	2.403702	1.00701	4.74E-09	7.02E-08	0.143437	1	3	1	11	17	18	63	40	65	49	60
ENSMUSG00000037685	chr5	Atp8a1	67618140	67622696	10962	-1.11974	6.437513	4.75E-09	7.02E-08	0.042072	-1	1520	1442	3686	1249	1989	803	994	923	1473	829
ENSMUSG00000026355	chr1	Mcm6	1.28E+08	1.28E+08	4666	1.347422	2.200417	4.84E-09	7.15E-08	0.045772	1	23	33	44	48	54	101	118	116	127	115
ENSMUSG00000027978	chr3	Prss12	1.23E+08	1.23E+08	2607	2.414109	1.057014	4.84E-09	7.15E-08	0.140434	1	4	4	6	14	22	35	64	77	39	77
ENSMUSG00000030341	chr6	Tnfrsf1a	1.25E+08	1.25E+08	2591	0.996168	5.282125	4.86E-09	7.16E-08	0.032482	1	329	262	491	454	569	839	1347	959	1041	586
ENSMUSG00000028017	chr3	Egf	1.3E+08	1.3E+08	4757	-1.29783	5.27422	4.86E-09	7.16E-08	0.055444	-1	864	784	1519	491	772	352	453	518	418	286

ENSMUSG00000087038	chr9	2900079G21Rik	1.12E+08	1.12E+08	6718	2.714228	-0.32619	4.89E-09	7.19E-08	0.109679	1	0	1	2	5	6	14	14	20	29	28
ENSMUSG00000095079	chr12	Igha	1.13E+08	1.13E+08	2668	3.57431	-0.04492	4.97E-09	7.3E-08	0.229321	1	1	2	2	2	3	26	46	35	3	28
ENSMUSG00000053158	chr7	Fes	80377758	80378074	2762	1.265993	2.409602	5.1E-09	7.49E-08	0.041936	1	39	30	70	41	70	126	149	157	130	99
ENSMUSG00000030804	chr7	Gm21974	1.28E+08	1.28E+08	2037	0.946347	3.662136	5.11E-09	7.49E-08	0.025653	1	139	90	174	117	171	254	355	303	326	262
ENSMUSG00000003348	chr10	Mob3a	80685256	80687173	2644	1.023974	2.923622	5.14E-09	7.53E-08	0.027535	1	72	49	123	73	85	158	211	182	219	144
ENSMUSG00000030609	chr7	Aen	78895854	78896014	5687	-0.8416	5.143129	5.18E-09	7.58E-08	0.022861	-1	594	525	976	752	810	416	576	404	587	341
ENSMUSG00000031168	chrX	Ebp	8185329	8185833	2310	1.059603	3.281078	5.21E-09	7.61E-08	0.031308	1	104	71	131	95	96	171	256	275	293	192
ENSMUSG00000020124	chr10	Usp15	1.23E+08	1.23E+08	3227	-0.89544	6.837631	5.23E-09	7.64E-08	0.027249	-1	1883	1767	3316	2413	2662	1165	2144	1169	1725	1209
ENSMUSG00000016637	chr15	Ift27	78159465	78159708	1012	0.893719	3.952526	5.25E-09	7.66E-08	0.023404	1	164	126	192	159	217	288	451	335	435	321
ENSMUSG00000064356	chrMT	mt-Atp8	7766	7969	204	-2.67675	2.859072	5.38E-09	7.84E-08	0.209558	-1	41	47	239	256	504	20	42	26	65	29
ENSMUSG00000016559	chr11	H3f3b	1.16E+08	1.16E+08	2976	0.868091	6.298332	5.46E-09	7.94E-08	0.025342	1	776	706	1152	824	994	1558	2409	1598	2255	1525
ENSMUSG00000025351	chr10	Cd63	1.29E+08	1.29E+08	1031	1.095127	7.253988	5.55E-09	8.06E-08	0.040847	1	1571	1509	1921	1206	1348	3290	4835	3402	4635	2948
ENSMUSG00000047686	chrX	Zcchc5	1.07E+08	1.07E+08	2948	1.688327	1.032959	5.55E-09	8.06E-08	0.057642	1	15	11	26	12	9	35	62	42	67	61
ENSMUSG00000024338	chr17	Psmb8	34197721	34197761	2736	1.359577	3.417913	5.59E-09	8.1E-08	0.055737	1	104	77	109	67	111	261	316	377	234	178
ENSMUSG00000048960	chr1	Prex2	10993465	10993909	16609	-1.58359	2.744591	5.59E-09	8.1E-08	0.074006	-1	73	74	316	139	262	37	78	55	80	56
ENSMUSG00000025738	chr17	Fbxl16	25809085	25809386	3478	1.294777	2.151354	5.75E-09	8.31E-08	0.04177	1	29	22	56	56	40	81	153	95	142	96
ENSMUSG00000026458	chr1	Ppfia4	1.34E+08	1.34E+08	6572	1.549319	1.722981	5.82E-09	8.41E-08	0.057903	1	27	17	36	31	18	87	74	91	90	79
ENSMUSG00000005057	chr5	Sh2b2	1.36E+08	1.36E+08	2848	1.583126	2.167487	5.85E-09	8.43E-08	0.067764	1	41	18	49	29	40	88	111	187	115	88
ENSMUSG00000061136	chr2	Prpf40a	53134704	53139270	10273	-0.89237	4.74605	5.85E-09	8.43E-08	0.025481	-1	472	422	893	462	589	239	396	342	402	335
ENSMUSG00000024339	chr17	Tap2	34203527	34204623	3781	0.952573	4.006926	5.86E-09	8.44E-08	0.027506	1	147	137	212	149	228	338	433	427	457	266
ENSMUSG00000035929	chr17	H2-Q4	35379617	35379707	2596	1.076745	4.331948	5.89E-09	8.47E-08	0.036782	1	184	175	241	168	255	464	588	596	437	361
ENSMUSG00000034910	chr9	Pygo1	72925645	72925960	7916	-0.97988	4.516114	5.9E-09	8.48E-08	0.030758	-1	327	267	802	546	595	198	373	241	379	237
ENSMUSG00000043531	chr19	Sorcs1	50143301	50144147	8317	-3.35512	0.44804	6.02E-09	8.64E-08	0.258834	-1	47	39	83	6	15	3	5	1	8	4
ENSMUSG00000042109	chr15	Csdc2	81936759	81936987	4623	1.793072	1.406134	6.05E-09	8.67E-08	0.077545	1	17	9	19	27	18	74	57	46	104	71
ENSMUSG00000025289	chrX	Prdx4	1.55E+08	1.55E+08	2106	1.082362	3.061524	6.13E-09	8.79E-08	0.032397	1	67	60	97	109	88	166	239	199	221	189
ENSMUSG00000034685	chr11	Fam171a2	1.02E+08	1.02E+08	3119	1.821211	1.369922	6.19E-09	8.85E-08	0.081808	1	8	8	15	26	31	70	61	60	89	64
ENSMUSG00000022221	chr14	Ripk3	55784996	55785351	1964	2.136773	0.192776	6.23E-09	8.91E-08	0.072892	1	2	4	10	11	3	21	40	37	30	23
ENSMUSG00000043241	chr2	Upf2	5951469	5951553	5474	-0.8212	5.182219	6.31E-09	9.01E-08	0.021978	-1	556	515	1136	721	874	399	551	456	610	387
ENSMUSG00000027288	chr2	Zfp106	1.21E+08	1.21E+08	10429	-1.07705	10.04625	6.36E-09	9.07E-08	0.040257	-1	14052	12485	36780	27609	29721	8797	16189	10438	16146	11459
ENSMUSG00000042821	chr2	Snai1	1.68E+08	1.68E+08	1621	1.537791	1.08795	6.45E-09	9.18E-08	0.045188	1	19	9	18	13	23	39	70	48	59	55
ENSMUSG00000037112	chr9	Sik2	50892801	50893389	9539	-1.26908	3.368217	6.52E-09	9.28E-08	0.048954	-1	202	157	394	178	266	69	96	162	116	100
ENSMUSG00000028337	chr4	Coro2a	46536937	46539267	6459	2.047042	0.531277	6.59E-09	9.35E-08	0.079142	1	13	3	11	6	8	40	50	40	27	33
ENSMUSG00000055447	chr16	Cd47	49855618	49855832	5277	0.883303	5.1959	6.59E-09	9.35E-08	0.025659	1	367	303	551	340	517	765	1089	910	881	668
ENSMUSG00000022634	chr15	Yaf2	93284278	93285622	1873	-0.93647	3.903149	6.61E-09	9.38E-08	0.026635	-1	302	235	418	270	345	134	206	176	288	145
ENSMUSG00000028822	chr4	Tmem50a	1.35E+08	1.35E+08	1270	0.869219	5.529649	6.83E-09	9.68E-08	0.025117	1	511	419	611	473	564	890	1209	1037	1357	947
ENSMUSG00000034210	chr4	Efcab14	1.16E+08	1.16E+08	8201	-0.84859	5.829156	6.86E-09	9.71E-08	0.024308	-1	943	731	1820	1108	1438	565	997	614	924	651
ENSMUSG00000087543	chr15	Gm16576	79742698	79742911	5404	-1.25408	2.788951	6.89E-09	9.74E-08	0.044778	-1	105	76	278	139	220	53	97	63	88	70
ENSMUSG00000022905	chr16	Kpna1	35978750	35978850	8486	-0.92638	7.625392	6.95E-09	9.81E-08	0.029864	-1	3657	2927	7048	3273	4395	1827	3085	2228	3224	2211
ENSMUSG00000037742	chr9	Eef1a1	78478449	78478858	2493	0.921822	9.101841	6.99E-09	9.86E-08	0.02977	1	4792	4698	8641	5798	6798	11334	13370	14582	14407	11236
ENSMUSG00000033182	chr6	Kbtbd12	88547340	88547915	7153	-1.08983	4.132209	7.05E-09	9.94E-08	0.037967	-1	295	216	745	343	408	179	292	141	228	185
ENSMUSG00000020649	chr12	Rrm2	24708241	24708445	2771	2.450162	1.467468	7.13E-09	1E-07	0.157155	1	6	10	11	27	9	90	62	46	167	45
ENSMUSG00000050390	chr4	C77080	1.29E+08	1.29E+08	5770	1.921892	2.21186	7.13E-09	1E-07	0.107593	1	16	10	37	40	54	66	106	103	199	175
ENSMUSG00000072294	chr14	Klf12	99874486	99875314	1856	-3.34955	0.306089	7.27E-09	1.02E-07	0.239661	-1	7	6	72	38	59	3	2	1	4	7
ENSMUSG00000021182	chr12	Ccdc88c	1.01E+08	1.01E+08	6313	-1.01125	4.799525	7.48E-09	1.05E-07	0.033794	-1	442	359	1149	466	730	245	445	275	425	313
ENSMUSG00000033526	chr2	Ppip5k1	1.21E+08	1.21E+08	12486	-1.72422	6.29976	7.59E-09	1.06E-07	0.099916	-1	795	719	2132	3386	3115	477	870	533	852	648
ENSMUSG00000022383	chr15	Ppara	85734983	85735145	3836	-3.07829	1.862575	7.61E-09	1.07E-07	0.260297	-1	21	14	125	224	158	10	20	8	15	15
ENSMUSG00000031637	chr8	Lrp2bp	45999303	45999505	4338	1.186667	4.007337	7.77E-09	1.09E-07	0.044716	1	165	132	226	110	142	281	498	517	355	360
ENSMUSG00000035673	chr10	Sbno2	80057416	80057864	4227	1.788337	4.055737	7.76E-09	1.09E-07	0.103992	1	92	51	200	98	189	365	1135	347	418	194
ENSMUSG00000056211	chr1	R3hdm1	1.28E+08	1.28E+08	31486	-0.88515	5.885942	7.8E-09	1.09E-07	0.026759	-1	957	889	1932	1166	1332	598	796	692	1127	618
ENSMUSG00000019461	chr11	Plscr3	69846376	69846522	3148	0.900885	3.881862	7.95E-09	1.11E-07	0.02428	1	123	129	209	167	192	289	359	366	437	284
ENSMUSG00000025789	chr7	St8sia2	73939119	73943464	5384	2.618718	-0.37784	8.01E-09	1.11E-07	0.091536	1	0	3	3	5	3	14	14	28	26	18
ENSMUSG00000029322	chr5	Plac8	1.01E+08	1.01E+08	1592	3.000768	1.925278	8.01E-09	1.11E-07	0.239911	1	12	25	9	2	10	122	209	152	75	37
ENSMUSG00000030680	chr7	Pagr1a	1.27E+08	1.27E+08	4405	0.835774	4.480683	8.02E-09	1.11E-07	0.022014	1	202	196	351	239	302	449	544	522	636	437
ENSMUSG00000022533	chr16	Atp13a3	30312423	30315901	9559	-1.20772	5.262116	8.04E-09	1.12E-07	0.049478	-1	612	633	1838	560	877	281	411	490	554	383
ENSMUSG00000046324	chr19	Ermp1	29608214	29612679	9338	-0.97194	4.193053	8.14E-09	1.13E-07	0.029973	-1	356	218	494	346	565	214	257	231	237	175
ENSMUSG00000039835	chr10	Nhsl1	18390322	18390510	11056	-1.12207	3.2791	8.25E-09	1.14E-07	0.037448	-1	156	130	373	175	272	73	126	103	125	125
ENSMUSG00000021929	chr14	Kpna3	61365186	61367729	4167	-0.8985	7.242677	8.29E-09	1.15E-07	0.02831	-1	2610	2361	4915	2753	3440	1363	2486	1610	2497	1826
ENSMUSG00000029233	chr5	Srd5a3	76140271	76140548	4648	1.356853	2.328383	8.28E-09	1.15E-07	0.049762	1	33	37	56	37	58	95	103	167	156	114
ENSMUSG00000012640	chr7	Zfp715	43296197	43296448	5119	-1.11851	3.174719	8.44E-09	1.17E-07	0.037141	-1	150	124	368	159	227	76	155	77	129	88
ENSMUSG00000056234	chr14	Ncoa4	32159865	32160010	4452	-0.97962	4.168278	8.51E-09	1.17E-07	0.030598	-1	291	220	627	342	508	163	312	229	203	196
ENSMUSG00000058230	chr7	Arhgap35	16493719	16498010	9147	-0.94405	5.21586	8.52E-09	1.17E-07	0.03	-1	626	418	1407	760	897	411	532	405	608	371
ENSMUSG00000009585	chr15	Apobec3	79891659	79891822	6083	1.41145	2.115412	8.59E-09	1.18E-07	0.053808	1	31	19	57	37	45	107	142	139	95	70
ENSMUSG00000000183	chr6	Fgf6	1.27E+08	1.27E+08	1232	-2.27991	0.313962	8.77E-09	1.21E-07	0.104243	-1	15	20	44	26	54	3	17	8	3	5
ENSMUSG00000027215	chr2	Cd82	93419111	93419942	3005	1.213041	4.432843	8.8E-09	1.21E-07	0.048545	1	246	175	268	127	203	542	620	535	717	334
ENSMUSG00000082519	chr2	Vamp7-ps	1.74E+08	1.74E+08	655	-1.51656	1.460991	8.81E-09	1.21E-07	0.053774	-1	48	47	101	54	74	23	40	26	14	22

ENSMUSG00000017831	chr17	Rab5a	53479234	53479608	2357	-0.87335	5.062666	8.85E-09	1.21E-07	0.025472	-1	538	572	1041	591	752	288	523	417	533	408
ENSMUSG00000076068	chr10	Mir678	76207326	76207409	84	2.179523	0.446784	8.9E-09	1.22E-07	0.084037	1	9	8	5	8	4	28	27	38	61	30
ENSMUSG00000020572	chr12	Nampt	32820335	32820626	4547	-0.93717	6.944376	9.11E-09	1.25E-07	0.03087	-1	1905	1591	3437	3045	3275	1218	2223	1282	1900	1226
ENSMUSG00000000094	chr11	Tbx4	85886422	85886562	3401	1.136849	2.467624	9.2E-09	1.26E-07	0.033427	1	46	34	62	62	68	97	187	122	178	106
ENSMUSG00000074899	chr2	Sptbn5	1.2E+08	1.2E+08	10292	-2.47125	-0.30582	9.26E-09	1.26E-07	0.102716	-1	15	8	23	19	35	1	11	2	4	2
ENSMUSG00000006728	chr10	Cdk4	1.27E+08	1.27E+08	3249	0.841586	4.997562	9.31E-09	1.27E-07	0.023376	1	341	252	430	383	418	664	869	698	887	608
ENSMUSG00000021180	chr12	Rps6ka5	1.01E+08	1.01E+08	4406	-1.46587	2.893009	9.33E-09	1.27E-07	0.065758	-1	114	80	232	238	232	31	95	61	98	79
ENSMUSG00000027843	chr3	Ptpn22	1.04E+08	1.04E+08	3064	2.19873	-0.01409	9.33E-09	1.27E-07	0.076081	1	2	1	10	7	5	22	40	25	31	13
ENSMUSG00000099312	chrX	Gm27733	1.03E+08	1.03E+08	68	8.692363	0.726537	9.33E-09	1.27E-07	0.925755	1	0	0	0	0	0	0	111	98	0	66
ENSMUSG00000049791	chr7	Fzd4	89404366	89404971	3685	-1.53227	5.110556	9.58E-09	1.3E-07	0.079978	-1	410	344	1299	999	1347	144	531	252	444	312
ENSMUSG00000087231	chr6	E230016M11Rik	67036599	67036935	3353	2.262515	-0.29432	9.6E-09	1.3E-07	0.064449	1	3	1	8	4	3	15	21	21	33	15
ENSMUSG00000039304	chr3	Tnfsf10	27317028	27317290	5266	-1.35182	2.988864	9.77E-09	1.32E-07	0.056249	-1	98	94	333	170	272	53	124	74	108	56
ENSMUSG00000066647	chr7	Gm5113	30169875	30170214	3002	-1.7852	2.538784	9.83E-09	1.33E-07	0.096374	-1	92	43	204	191	223	23	61	44	45	61
ENSMUSG00000025044	chr8	Msr1	39581700	39581865	3998	1.414035	1.57449	9.88E-09	1.34E-07	0.045373	1	18	24	38	18	27	49	107	76	77	71
ENSMUSG00000011256	chr11	Adam19	46055992	46056210	7115	1.176575	3.452171	9.95E-09	1.35E-07	0.043503	1	93	57	156	83	162	218	238	247	336	310
ENSMUSG00000100975	chr12	Gm28875	1.05E+08	1.05E+08	642	1.675672	0.909445	1E-08	1.36E-07	0.053809	1	12	13	16	11	14	33	45	62	56	45
ENSMUSG00000021579	chr13	Lrrc14b	74359578	74361399	2755	-0.8979	6.932605	1.03E-08	1.39E-07	0.02854	-1	2183	1424	3620	2760	3095	1171	2167	1341	1867	1349
ENSMUSG00000071253	chr10	Slc25a16	62920633	62920881	4799	-0.89636	4.904776	1.05E-08	1.41E-07	0.026963	-1	553	442	981	509	696	244	463	345	484	389
ENSMUSG00000038056	chr5	Kmt2c	25271798	25273758	20291	-1.07991	5.08987	1.07E-08	1.44E-07	0.039926	-1	537	439	1565	538	871	293	472	387	453	388
ENSMUSG00000030515	chr7	Tarsl2	65644898	65645214	4095	-0.86771	6.251495	1.07E-08	1.44E-07	0.026427	-1	1323	1221	2327	1436	1648	786	1332	813	1165	870
ENSMUSG00000046731	chr11	Kctd11	69878261	69881406	3146	1.192284	2.281722	1.1E-08	1.48E-07	0.03615	1	42	35	65	41	49	70	152	121	147	117
ENSMUSG00000021258	chr12	Ccnk	1.08E+08	1.08E+08	2627	-0.92906	6.421502	1.11E-08	1.49E-07	0.030492	-1	1457	1407	2860	1542	1884	793	1108	1002	1634	918
ENSMUSG00000020733	chr11	Slc9a3r1	1.15E+08	1.15E+08	1925	1.419527	2.004291	1.13E-08	1.51E-07	0.05247	1	19	32	40	40	37	88	106	130	107	79
ENSMUSG00000043336	chr16	Filip1l	57353093	57353458	5335	-0.93795	5.030778	1.13E-08	1.51E-07	0.02993	-1	543	368	1164	694	823	274	542	439	443	362
ENSMUSG00000024663	chr19	Rab3il1	10001669	10002217	4543	0.999314	3.586332	1.13E-08	1.52E-07	0.030999	1	95	77	229	106	156	243	354	297	288	257
ENSMUSG00000028150	chr3	Rorc	94372831	94372931	2098	-1.04784	6.102848	1.15E-08	1.53E-07	0.038716	-1	1148	1119	1857	1759	1522	721	1076	575	1264	554
ENSMUSG00000033382	chr18	Trappc8	20817224	20818311	5482	-0.87679	5.027115	1.15E-08	1.54E-07	0.026004	-1	532	415	1142	646	769	318	588	379	447	378
ENSMUSG00000025323	chr12	Sp4	1.18E+08	1.18E+08	5770	-1.38722	2.462602	1.16E-08	1.55E-07	0.055843	-1	71	72	248	126	150	33	62	50	66	63
ENSMUSG00000020186	chr10	Csrp2	1.11E+08	1.11E+08	973	1.51162	2.299617	1.16E-08	1.55E-07	0.064083	1	34	39	39	41	41	86	130	156	108	153
ENSMUSG00000028434	chr4	Epb4.1l4b	56991972	56995803	8858	-1.1821	3.347444	1.19E-08	1.58E-07	0.0433	-1	159	120	435	181	300	98	133	126	112	91
ENSMUSG00000034218	chr9	Atm	53439149	53439929	10338	-1.62344	2.772684	1.19E-08	1.59E-07	0.082142	-1	108	71	309	139	251	40	112	45	43	64
ENSMUSG00000062312	chr11	Erbb2	98412470	98412735	5210	1.276826	2.666647	1.22E-08	1.62E-07	0.047645	1	27	43	87	64	78	122	158	136	217	169
ENSMUSG00000040584	chr5	Abcb1a	8660077	8660222	5480	-1.12966	3.169627	1.24E-08	1.65E-07	0.039095	-1	132	122	299	224	235	62	172	83	122	86
ENSMUSG00000085334	chr4	Gm12940	1.27E+08	1.27E+08	2680	1.232057	2.767883	1.27E-08	1.68E-07	0.043864	1	56	57	84	45	77	158	194	201	196	105
ENSMUSG00000055541	chr7	Lair1	4007073	4009834	3760	1.77945	0.8659	1.28E-08	1.69E-07	0.066301	1	7	11	16	13	14	29	65	66	40	39
ENSMUSG00000022525	chr16	Hrasls	29209695	29209809	3286	-0.91788	6.077205	1.31E-08	1.73E-07	0.029867	-1	1339	1097	2128	1178	1364	734	1099	683	1067	714
ENSMUSG00000023169	chr15	Slc38a1	96571418	96576812	8391	1.79386	0.839889	1.31E-08	1.73E-07	0.067574	1	8	7	7	15	22	31	69	38	58	42
ENSMUSG00000034636	chr4	Zyg11b	1.08E+08	1.08E+08	9046	-1.18135	6.496228	1.33E-08	1.75E-07	0.049737	-1	1136	966	3562	2345	2699	638	1271	848	1392	983
ENSMUSG00000036256	chr5	Igfbp7	77349240	77349499	1213	0.882516	6.149666	1.32E-08	1.75E-07	0.027608	1	635	571	1116	772	963	1232	1955	2014	1869	1342
ENSMUSG00000059588	chr2	Calcrl	84330626	84333678	4882	-1.4624	3.705593	1.33E-08	1.75E-07	0.070956	-1	172	246	490	277	386	48	120	185	139	138
ENSMUSG00000061111	chr11	Fam195b	1.21E+08	1.21E+08	1282	0.863748	5.214854	1.33E-08	1.75E-07	0.025505	1	376	323	448	434	500	724	942	857	1071	759
ENSMUSG00000000901	chr10	Mmp11	75923222	75923490	2572	1.413741	2.006341	1.33E-08	1.75E-07	0.055685	1	28	13	54	31	51	68	104	85	147	114
ENSMUSG00000020101	chr10	4632428N05Rik	60346851	60347103	5014	1.012622	4.608696	1.35E-08	1.77E-07	0.034805	1	232	176	342	214	344	489	589	801	610	442
ENSMUSG00000096910	chr17	Zfp955b	33289649	33289669	1638	-2.21895	0.902695	1.35E-08	1.77E-07	0.124922	-1	15	27	97	37	76	7	22	5	14	10
ENSMUSG00000079434	chr1	Neu2	87509889	87510215	2590	1.103864	4.521625	1.35E-08	1.78E-07	0.041532	1	158	160	361	259	253	320	978	539	538	534
ENSMUSG00000021822	chr14	Plau	20836662	20836734	2343	0.932187	5.487061	1.37E-08	1.79E-07	0.030413	1	418	333	716	497	541	1094	948	1023	1369	852
ENSMUSG00000030102	chr6	Itpr1	1.08E+08	1.08E+08	9848	-1.36101	5.189444	1.38E-08	1.8E-07	0.064719	-1	950	634	1340	483	829	382	286	265	616	309
ENSMUSG00000024885	chr19	Aldh3b1	3913493	3914084	1875	1.359051	1.710059	1.39E-08	1.82E-07	0.045298	1	16	23	42	30	32	82	85	89	86	65
ENSMUSG00000039763	chr16	Dnajc28	91614257	91617379	3562	-1.02262	4.897811	1.39E-08	1.82E-07	0.03611	-1	445	393	703	829	864	293	512	320	365	310
ENSMUSG00000051674	chr5	Dcun1d4	73481002	73481094	5803	-1.04201	3.292253	1.4E-08	1.82E-07	0.033186	-1	193	149	346	154	231	76	147	132	140	92
ENSMUSG00000008845	chr6	Cd163	1.24E+08	1.24E+08	4492	-1.78017	3.419695	1.41E-08	1.83E-07	0.103468	-1	199	190	608	153	249	100	72	135	65	49
ENSMUSG00000025132	chr11	Arhgdia	1.21E+08	1.21E+08	2258	0.89519	6.896741	1.41E-08	1.84E-07	0.028883	1	1085	852	1635	1564	1603	2123	2989	2959	3630	2476
ENSMUSG00000091474	chr7	2610021A01Rik	41599261	41599400	4004	-1.17376	2.606108	1.41E-08	1.84E-07	0.038953	-1	103	113	181	123	149	48	95	63	58	72
ENSMUSG00000004933	chr10	Matk	81252935	81253278	4594	2.212211	0.303656	1.43E-08	1.86E-07	0.095268	1	5	4	6	7	9	28	37	51	38	12
ENSMUSG00000039512	chr17	Uhrf1bp1	27856490	27856794	8708	-1.00917	5.115447	1.44E-08	1.87E-07	0.0355	-1	492	372	1158	832	1039	313	543	333	566	374
ENSMUSG00000085022	chr4	Gm5860	82065431	82066040	2714	-0.97168	2.911906	1.44E-08	1.88E-07	0.026435	-1	128	118	197	160	191	73	113	79	121	77
ENSMUSG00000032020	chr9	Ubash3b	41011098	41015036	7326	1.83601	1.156067	1.45E-08	1.88E-07	0.083414	1	12	8	16	15	23	66	105	47	49	33
ENSMUSG00000000594	chr11	Gm2a	55098115	55098244	4127	1.05312	4.239105	1.48E-08	1.92E-07	0.037323	1	182	128	317	173	199	399	434	620	465	356
ENSMUSG00000025239	chr9	Limd1	1.23E+08	1.23E+08	4849	-0.89993	6.448411	1.53E-08	1.99E-07	0.029179	-1	1625	1298	2970	1419	2012	971	1428	946	1437	840
ENSMUSG00000017697	chr2	Ada	1.64E+08	1.64E+08	2002	1.703157	0.844544	1.54E-08	1.99E-07	0.056835	1	14	9	11	11	17	48	57	40	41	43
ENSMUSG00000024411	chr18	Aqp4	15389394	15393729	5082	-3.03464	3.735966	1.54E-08	1.99E-07	0.285085	-1	115	91	270	767	738	16	123	24	37	72
ENSMUSG00000047045	chrX	Tmem164	1.43E+08	1.43E+08	6851	1.2092	2.480405	1.54E-08	1.99E-07	0.041211	1	49	35	82	33	71	125	173	148	140	106
ENSMUSG00000029161	chr5	Cgref1	30933146	30933988	1328	1.810196	2.256704	1.55E-08	2E-07	0.096133	1	32	35	31	37	22	163	135	85	206	71
ENSMUSG00000041298	chr5	Katnal1	1.49E+08	1.49E+08	11881	-1.11033	3.207521	1.6E-08	2.06E-07	0.038117	-1	139	127	278	215	271	85	134	65	136	112
ENSMUSG00000025920	chr1	Stau2	16228674	16229866	6747	-0.94632	5.395837	1.6E-08	2.06E-07	0.031631	-1	699	548	1109	1083	1055	338	694	441	619	555

ENSMUSG00000030844	chr7	Rgs10	1.28E+08	1.28E+08	1711	1.385916	2.419115	1.63E-08	2.09E-07	0.056289	1	38	39	75	37	45	146	124	157	114	125
ENSMUSG00000025498	chr7	Irf7	1.41E+08	1.41E+08	3020	1.634926	2.669911	1.64E-08	2.1E-07	0.083096	1	44	40	69	38	53	190	233	200	80	132
ENSMUSG00000024675	chr19	Ms4a4c	11404770	11404797	1751	2.910509	-0.26607	1.67E-08	2.15E-07	0.145881	1	4	1	4	2	2	34	29	7	19	22
ENSMUSG00000058446	chr6	Znrf2	54816916	54817472	6176	-0.78711	5.363245	1.68E-08	2.16E-07	0.021585	-1	729	581	1115	791	998	481	630	545	681	422
ENSMUSG00000062382	chr13	Gm10116	74406396	74407317	922	1.471588	2.400057	1.69E-08	2.16E-07	0.063835	1	48	30	58	34	49	120	90	184	181	105
ENSMUSG00000096493	chr1	Gm10031	1.57E+08	1.57E+08	2568	-1.19993	1.976751	1.69E-08	2.16E-07	0.036424	-1	64	58	141	79	101	32	62	34	57	32
ENSMUSG00000101523	chr1	Csnk2a1	1.57E+08	1.57E+08	2653	-1.19993	1.976751	1.69E-08	2.16E-07	0.036424	-1	64	58	141	79	101	32	62	34	57	32
ENSMUSG00000030276	chr6	Ttll3	1.13E+08	1.13E+08	5059	0.988847	4.175833	1.7E-08	2.17E-07	0.032325	1	220	149	217	157	204	367	464	441	598	321
ENSMUSG00000026986	chr2	Hnmt	24002910	24003954	1769	-1.70021	1.757322	1.7E-08	2.17E-07	0.080936	-1	72	89	100	63	71	18	23	44	26	29
ENSMUSG00000042350	chr12	Arel1	84918148	84920580	6044	-0.82436	5.252014	1.72E-08	2.19E-07	0.023674	-1	575	510	1286	759	901	409	624	438	598	448
ENSMUSG00000002871	chr6	Tpra1	88902251	88902530	3026	0.914938	4.544514	1.72E-08	2.19E-07	0.028529	1	218	131	341	306	325	391	637	580	713	474
ENSMUSG00000021918	chr14	Nek4	30951486	30951718	2754	-1.30438	1.765058	1.75E-08	2.23E-07	0.041429	-1	51	60	126	65	85	29	42	35	33	34
ENSMUSG00000052155	chr2	Acvr2a	48814109	48814826	5686	-1.19035	5.190827	1.75E-08	2.23E-07	0.05042	-1	669	763	1419	515	736	223	446	420	561	406
ENSMUSG00000102947	chr2	AL772372.1	93956379	93956441	747	2.005714	1.486628	1.75E-08	2.23E-07	0.109928	1	20	7	14	20	23	70	164	54	77	36
ENSMUSG00000035352	chr11	Ccl12	82101845	82101972	537	3.071487	0.23519	1.77E-08	2.24E-07	0.200916	1	4	4	5	1	3	31	85	14	14	28
ENSMUSG00000055612	chr2	Cdca7	72476159	72476311	3202	2.338152	-0.12909	1.78E-08	2.25E-07	0.094721	1	4	0	7	5	5	30	31	24	22	12
ENSMUSG00000093938	chr11	Evi2b	79515056	79516762	1858	1.696706	1.322506	1.78E-08	2.26E-07	0.073389	1	24	4	20	13	30	52	86	69	66	57
ENSMUSG00000021262	chr12	Evl	1.09E+08	1.09E+08	2695	1.30353	2.753911	1.79E-08	2.26E-07	0.052023	1	50	28	69	85	78	138	197	220	175	126
ENSMUSG00000073409	chr17	H2-Q6	35424850	35424940	2085	1.407844	3.057825	1.8E-08	2.27E-07	0.06242	1	66	68	61	60	94	171	293	292	167	157
ENSMUSG00000021796	chr14	Bmpr1a	34410734	34414669	6351	-0.90499	6.215587	1.8E-08	2.28E-07	0.029695	-1	1178	1025	2473	1490	1839	574	1176	891	1217	929
ENSMUSG00000042759	chr7	Apobr	1.27E+08	1.27E+08	3779	1.545661	1.554786	1.81E-08	2.28E-07	0.060712	1	30	15	25	15	29	67	79	91	66	71
ENSMUSG00000034377	chr17	Tulp4	6106437	6106582	18054	-1.03205	6.444531	1.81E-08	2.28E-07	0.038755	-1	1344	1020	3379	1678	2507	863	1077	828	1581	916
ENSMUSG00000035181	chr12	Heatr5a	51875873	51877616	7761	-1.08659	4.326375	1.81E-08	2.28E-07	0.040618	-1	307	185	664	510	628	169	333	219	270	194
ENSMUSG00000057133	chr2	Chd6	1.61E+08	1.61E+08	19093	-1.23491	4.249017	1.82E-08	2.29E-07	0.052788	-1	264	178	910	463	491	151	240	206	287	161
ENSMUSG00000052144	chr6	Ppp4r2	1.01E+08	1.01E+08	3641	-0.81565	5.050743	1.83E-08	2.29E-07	0.023026	-1	559	483	1079	570	771	317	519	429	520	411
ENSMUSG00000063632	chr12	Sox11	27334264	27342574	8311	3.080402	-0.02424	1.84E-08	2.3E-07	0.189584	1	0	2	2	5	5	25	10	37	54	13
ENSMUSG00000028696	chr4	Ipp	1.17E+08	1.17E+08	2126	-0.9393	3.289229	1.86E-08	2.33E-07	0.026241	-1	173	132	297	204	235	104	163	93	142	108
ENSMUSG00000031903	chr8	Pla2g15	1.06E+08	1.06E+08	2704	1.077544	3.648151	1.86E-08	2.33E-07	0.037686	1	133	83	175	114	139	284	282	375	296	265
ENSMUSG00000071266	chr17	Zfp946	22424222	22424429	3504	-1.24932	2.331309	1.86E-08	2.33E-07	0.04441	-1	109	84	182	92	98	47	73	59	56	34
ENSMUSG00000024059	chr17	Clip4	71781947	71782069	4055	-1.82567	6.365695	1.88E-08	2.35E-07	0.117615	-1	766	782	3031	3225	3208	306	859	462	898	845
ENSMUSG00000022575	chr15	Gsdmd	75862339	75862481	1776	1.276363	2.40763	1.91E-08	2.38E-07	0.047514	1	45	23	68	51	61	124	157	164	122	95
ENSMUSG00000049225	chr4	Pdp1	11958184	11962233	4507	-1.1866	6.439751	1.91E-08	2.38E-07	0.051298	-1	1182	1210	2608	2271	2688	652	1197	568	1556	981
ENSMUSG00000031375	chrX	Bgn	73483602	73483762	6099	1.536905	6.749562	1.94E-08	2.41E-07	0.08509	1	372	420	1140	1191	1539	1806	2473	3425	3376	3323
ENSMUSG00000025533	chr5	Asl	1.3E+08	1.3E+08	4563	0.988096	3.276034	1.95E-08	2.43E-07	0.029451	1	91	77	138	88	123	184	236	265	249	214
ENSMUSG00000022372	chr15	Sla	66780819	66782755	9186	1.810663	1.386041	1.98E-08	2.47E-07	0.086802	1	22	9	23	14	21	95	65	77	59	45
ENSMUSG00000002222	chr6	Rmnd5a	71388634	71393188	6783	-0.85346	7.717808	1.99E-08	2.47E-07	0.027047	-1	3469	3010	7203	3792	4906	2113	3363	2383	3453	2487
ENSMUSG00000078578	chr3	Ube2d3	1.35E+08	1.35E+08	2675	-0.88695	7.732717	2.02E-08	2.51E-07	0.029243	-1	3895	3620	6580	3739	4367	1933	3381	2434	3722	2380
ENSMUSG00000042505	chr6	Acn9	6956004	6956200	5095	-0.93534	3.546626	2.02E-08	2.51E-07	0.027435	-1	199	200	338	251	232	111	154	151	183	129
ENSMUSG00000045071	chr4	E130308A19Rik	59626211	59626491	12617	-1.35668	2.871879	2.02E-08	2.51E-07	0.059034	-1	127	92	319	109	240	49	98	55	126	55
ENSMUSG00000038250	chr8	Usp38	80980734	80981980	4684	-0.93216	4.67848	2.03E-08	2.52E-07	0.030121	-1	479	330	984	422	581	249	394	285	367	310
ENSMUSG00000026628	chr1	Atf3	1.91E+08	1.91E+08	2154	2.05829	2.885006	2.09E-08	2.59E-07	0.137417	1	14	36	25	62	86	139	363	278	192	118
ENSMUSG00000036391	chr11	Sec24a	51692264	51695241	10683	-1.06666	4.308685	2.1E-08	2.6E-07	0.039373	-1	328	272	859	309	493	145	253	251	291	230
ENSMUSG00000035849	chr11	Krt222	99232761	99235147	3292	-1.67601	0.480611	2.11E-08	2.6E-07	0.051005	-1	34	25	40	21	40	8	13	11	16	9
ENSMUSG00000074994	chr2	Qser1	1.05E+08	1.05E+08	8973	-0.93415	6.540296	2.12E-08	2.62E-07	0.032139	-1	1504	1250	3634	1631	2235	780	1492	1089	1519	1048
ENSMUSG00000079065	chr5	BC005561	1.05E+08	1.05E+08	5181	-1.62626	1.27312	2.25E-08	2.77E-07	0.067073	-1	46	20	110	50	73	14	27	24	23	16
ENSMUSG00000029860	chr6	Zyx	42349828	42350119	3739	0.852841	4.849547	2.26E-08	2.79E-07	0.025505	1	279	183	493	329	407	533	698	737	815	583
ENSMUSG00000069919	chr11	Hba-a1	32283511	32283801	812	1.166991	4.910187	2.27E-08	2.79E-07	0.048764	1	210	181	391	417	299	624	768	561	1360	558
ENSMUSG00000037447	chr1	Arid5a	36307733	36307836	12540	1.914464	3.508142	2.27E-08	2.79E-07	0.123911	1	50	56	67	79	124	150	873	196	357	175
ENSMUSG00000039601	chr17	Rcan2	43801851	43802096	3744	-1.89746	5.626074	2.27E-08	2.79E-07	0.127457	-1	695	364	981	2251	2155	341	418	251	647	286
ENSMUSG00000021374	chr13	Nup153	46679905	46681242	6914	-0.88211	5.178586	2.28E-08	2.8E-07	0.027731	-1	627	453	1339	688	801	321	584	434	556	445
ENSMUSG00000037706	chr7	Cd81	1.43E+08	1.43E+08	2270	0.814032	6.744963	2.3E-08	2.81E-07	0.024538	1	1084	892	1676	1138	1501	1976	2645	2404	3269	2206
ENSMUSG00000030095	chr6	Tmem43	91473703	91473898	3741	0.858549	5.548122	2.31E-08	2.82E-07	0.026514	1	544	387	658	451	611	935	1111	1123	1340	951
ENSMUSG00000043483	chr12	Gm6863	96922420	96923061	642	1.016419	3.395913	2.34E-08	2.86E-07	0.032091	1	99	95	161	96	99	204	296	257	353	176
ENSMUSG00000030068	chr6	Gm20696	99257484	99260419	3994	-1.06034	2.880241	2.5E-08	3.05E-07	0.033446	-1	156	106	198	152	179	64	118	85	78	85
ENSMUSG00000002699	chr11	Lcp2	34046920	34047431	4459	1.514159	1.432002	2.53E-08	3.09E-07	0.057024	1	21	16	28	15	27	79	95	59	72	41
ENSMUSG00000027368	chr2	Dusp2	1.27E+08	1.27E+08	2003	1.957799	0.572773	2.58E-08	3.15E-07	0.084424	1	8	4	12	11	10	30	33	33	37	59
ENSMUSG00000031748	chr8	Gnao1	93809966	93810129	6785	-1.39302	2.30512	2.64E-08	3.22E-07	0.058895	-1	63	55	172	116	189	31	58	43	72	44
ENSMUSG00000039652	chr19	Cpeb3	37021291	37025087	7414	-1.03514	5.151584	2.64E-08	3.22E-07	0.039017	-1	582	517	1413	632	841	227	493	387	671	402
ENSMUSG00000024856	chr19	Cdk2ap2	4097182	4097507	1636	0.926883	4.330231	2.66E-08	3.23E-07	0.029401	1	222	166	266	203	239	355	526	593	575	352
ENSMUSG00000028530	chr4	Jak1	1.01E+08	1.01E+08	7227	-0.85299	7.122469	2.7E-08	3.28E-07	0.027399	-1	2399	2063	4602	2287	3392	1396	2336	1579	2233	1607
ENSMUSG00000079362	chr5	Gbp6	1.05E+08	1.05E+08	7842	-1.33209	2.50694	2.73E-08	3.31E-07	0.054065	-1	76	77	251	114	162	63	60	56	70	39
ENSMUSG00000028030	chr3	Tbck	1.33E+08	1.33E+08	4108	-1.47888	1.611288	2.75E-08	3.33E-07	0.059422	-1	40	39	113	74	100	16	49	25	28	27
ENSMUSG00000040022	chr19	Rab11fip2	59902884	59907143	6080	-1.01893	3.367107	2.75E-08	3.34E-07	0.032937	-1	167	153	397	179	243	97	130	115	145	127
ENSMUSG00000029862	chr6	Clcn1	42286685	42286946	5428	-0.90541	7.321788	2.79E-08	3.37E-07	0.030974	-1	2606	2030	5605	3011	4174	1477	2533	1674	2561	2005
ENSMUSG00000036667	chr6	Fam115a	42668002	42670323	9622	1.046186	3.278242	2.86E-08	3.46E-07	0.034738	1	95	71	140	102	94	180	257	266	221	237

ENSMUSG00000039968	chr5	Rsbn1l	20893028	20896704	5550	-1.04654	3.522922	2.87E-08	3.47E-07	0.036067	-1	173	202	412	218	253	93	142	167	145	129
ENSMUSG00000101904	chr1	Gm29427	1.31E+08	1.31E+08	1909	-1.74829	1.401194	2.87E-08	3.47E-07	0.085549	-1	28	36	87	72	106	12	41	17	21	18
ENSMUSG00000048967	chr8	Yjefn3	69887788	69888022	808	1.291962	3.026536	2.92E-08	3.52E-07	0.053079	1	65	75	69	77	73	217	196	181	294	146
ENSMUSG00000026414	chr1	Tnnt2	1.36E+08	1.36E+08	7752	2.358175	3.560965	2.93E-08	3.53E-07	0.1878	1	31	15	32	131	101	365	199	277	565	342
ENSMUSG00000032312	chr9	Csk	57626647	57627503	2748	1.043587	3.530172	2.94E-08	3.54E-07	0.035962	1	88	85	173	114	150	262	229	327	326	235
ENSMUSG00000019841	chr10	Rev3l	39732118	39732613	13293	-1.00556	4.970034	2.94E-08	3.54E-07	0.036703	-1	576	425	1271	528	691	252	488	464	379	323
ENSMUSG00000041134	chr16	Cyyr1	85421533	85422341	8894	-1.42755	2.707824	3.02E-08	3.63E-07	0.066288	-1	100	77	207	161	241	48	129	46	64	42
ENSMUSG00000041697	chr5	Cox6a1	1.15E+08	1.15E+08	702	1.089956	4.870459	3.03E-08	3.64E-07	0.04292	1	319	233	275	306	315	627	720	922	776	534
ENSMUSG00000023800	chr17	Tiam2	3326573	3326726	6281	1.648582	1.942589	3.05E-08	3.66E-07	0.08303	1	16	10	30	35	58	59	112	122	123	99
ENSMUSG00000037646	chr15	Vps13b	35371546	35371777	13370	-1.16325	3.726273	3.11E-08	3.73E-07	0.046471	-1	216	129	600	284	332	110	193	158	146	134
ENSMUSG00000074283	chr7	Zfp109	24228048	24229840	1935	-2.36223	0.027061	3.14E-08	3.77E-07	0.115565	-1	12	14	52	29	23	1	10	9	2	5
ENSMUSG00000020592	chr12	Sdc1	8771323	8771701	3809	1.219563	2.972405	3.15E-08	3.77E-07	0.047871	1	69	50	112	54	94	112	230	279	221	152
ENSMUSG00000049744	chr2	Arhgap15	43748824	43748899	8818	-1.60545	0.947282	3.23E-08	3.86E-07	0.058335	-1	22	33	64	44	65	16	18	11	24	14
ENSMUSG00000043895	chr9	S1pr2	20965952	20968570	2815	1.342908	2.215307	3.26E-08	3.89E-07	0.053788	1	21	30	61	39	59	86	124	163	131	86
ENSMUSG00000034075	chr2	Zdhhc5	84687970	84689444	5047	-0.8902	6.46332	3.28E-08	3.91E-07	0.02995	-1	1341	1005	2861	2023	2333	838	1338	1048	1496	983
ENSMUSG00000018819	chr7	Lsp1	1.42E+08	1.42E+08	5174	0.88427	5.446739	3.3E-08	3.94E-07	0.028823	1	455	371	787	345	534	880	1087	977	1261	923
ENSMUSG00000069763	chr11	Tmem100	90030348	90030743	1767	-1.90461	3.190823	3.3E-08	3.94E-07	0.124671	-1	265	319	211	112	146	60	70	97	68	52
ENSMUSG00000063065	chr7	Mapk3	1.27E+08	1.27E+08	2163	0.826774	5.089283	3.33E-08	3.97E-07	0.024604	1	349	287	487	405	430	628	794	861	1028	651
ENSMUSG00000034165	chr17	Ccnd3	47505051	47505266	8775	0.938349	4.716583	3.35E-08	3.99E-07	0.03168	1	196	197	354	343	366	546	584	694	768	520
ENSMUSG00000071748	chrX	Gm14698	68821093	68825318	4226	-1.62656	1.400181	3.37E-08	4E-07	0.072892	-1	52	58	107	35	62	10	31	18	31	26
ENSMUSG00000041161	chr4	Otud3	1.39E+08	1.39E+08	1668	-0.95434	3.6603	3.41E-08	4.05E-07	0.029998	-1	227	197	443	209	282	147	165	160	190	116
ENSMUSG00000022867	chr16	Usp25	77014069	77014140	4412	-0.95673	6.897941	3.42E-08	4.06E-07	0.034903	-1	1947	1782	4230	2116	2948	901	1994	1184	1896	1551
ENSMUSG00000030557	chr7	Mef2a	67231163	67235228	6283	-0.87824	7.038201	3.43E-08	4.06E-07	0.029461	-1	2258	1793	4612	2346	3100	1179	2130	1452	2125	1653
ENSMUSG00000053318	chr1	Slamf8	1.73E+08	1.73E+08	3079	2.345176	0.383378	3.43E-08	4.06E-07	0.125357	1	2	6	10	7	6	37	48	54	18	19
ENSMUSG00000001119	chr10	Col6a1	76708792	76710181	4380	1.056972	6.827337	3.45E-08	4.08E-07	0.042555	1	795	669	1843	1201	1673	1926	2516	2788	3350	3240
ENSMUSG00000027900	chr3	Dram2	1.07E+08	1.07E+08	3863	-0.81907	5.80483	3.46E-08	4.09E-07	0.025044	-1	912	956	1714	1002	1165	543	912	704	924	641
ENSMUSG00000075232	chr10	Amd1	40287458	40289469	3206	-2.28385	9.550146	3.46E-08	4.09E-07	0.185672	-1	26574	14842	31151	8503	18513	8060	3070	2217	7747	1658
ENSMUSG00000037151	chr10	Lrrc20	61475833	61475889	2619	-0.86334	7.723076	3.49E-08	4.12E-07	0.028678	-1	4058	2712	6315	4229	4958	2358	3314	2062	3684	2376
ENSMUSG00000031226	chrX	Pbdc1	1.05E+08	1.05E+08	6098	1.021991	3.507338	3.55E-08	4.18E-07	0.033953	1	117	95	128	111	135	197	388	308	263	226
ENSMUSG00000034342	chr9	Cbl	44149262	44151737	5083	-2.01873	0.976124	3.55E-08	4.18E-07	0.108274	-1	23	19	96	38	84	10	17	9	12	18
ENSMUSG00000024548	chr18	Setbp1	78750380	78755825	9953	-1.28744	2.829507	3.6E-08	4.23E-07	0.053733	-1	105	83	329	130	208	48	89	71	82	82
ENSMUSG00000035569	chr8	Ankrd11	1.23E+08	1.23E+08	11637	-1.00981	6.013647	3.6E-08	4.23E-07	0.038516	-1	894	715	2529	1458	1747	538	975	725	940	762
ENSMUSG00000045752	chr7	Tssc4	1.43E+08	1.43E+08	1760	0.986888	3.495257	3.61E-08	4.24E-07	0.0313	1	108	104	127	108	143	255	312	235	347	205
ENSMUSG00000038271	chr6	Iffo1	1.25E+08	1.25E+08	5691	0.908155	3.981053	3.61E-08	4.24E-07	0.027922	1	139	130	194	177	234	282	457	289	539	328
ENSMUSG00000058883	chr13	Zfp708	67069398	67071528	2450	-1.36065	1.658465	3.62E-08	4.24E-07	0.049339	-1	81	36	99	65	79	19	40	26	38	35
ENSMUSG00000042608	chr4	Stk40	1.26E+08	1.26E+08	4117	-0.82466	6.382662	3.62E-08	4.25E-07	0.02582	-1	1334	1157	2495	1851	1863	822	1372	977	1496	913
ENSMUSG00000000804	chr11	Usp32	84984442	84986583	7680	-0.92579	3.857608	3.65E-08	4.27E-07	0.028801	-1	212	199	533	291	338	145	190	202	213	155
ENSMUSG00000040322	chr3	Slc25a24	1.09E+08	1.09E+08	3431	1.185284	2.928151	3.65E-08	4.27E-07	0.04511	1	46	51	96	84	95	116	204	148	282	209
ENSMUSG00000048799	chr18	Cep120	53681724	53683464	4553	-0.82346	4.451198	3.68E-08	4.3E-07	0.023645	-1	324	300	624	498	529	223	357	260	321	277
ENSMUSG00000033004	chr14	Mycbp2	1.03E+08	1.03E+08	19248	-0.89579	5.490507	3.71E-08	4.33E-07	0.02993	-1	686	560	1731	846	1099	382	749	578	720	483
ENSMUSG00000032508	chr9	Myd88	1.19E+08	1.19E+08	2576	1.580555	3.444078	3.73E-08	4.35E-07	0.087251	1	64	63	98	82	127	217	702	213	280	136
ENSMUSG00000020230	chr10	Prmt2	76207222	76207793	3177	1.302027	2.52545	3.74E-08	4.35E-07	0.051638	1	55	48	59	37	56	128	120	163	199	115
ENSMUSG00000030657	chr7	Xylt1	1.17E+08	1.17E+08	3822	-2.80319	0.253637	3.74E-08	4.35E-07	0.176573	-1	13	7	79	27	42	7	3	2	4	7
ENSMUSG00000038037	chr16	Socs1	10783808	10784921	1220	1.834477	0.888862	3.81E-08	4.43E-07	0.079721	1	7	10	9	8	26	30	68	43	75	35
ENSMUSG00000028381	chr4	Ugcg	59189257	59189741	5212	1.039318	3.861179	3.81E-08	4.43E-07	0.037167	1	123	121	193	144	175	298	558	388	331	215
ENSMUSG00000020766	chr11	Galk1	1.16E+08	1.16E+08	1406	1.334691	2.103718	3.86E-08	4.48E-07	0.050665	1	40	33	37	30	46	87	94	115	127	113
ENSMUSG00000038894	chr8	Irs2	10986980	10987014	4024	-1.39019	2.800907	3.86E-08	4.48E-07	0.064161	-1	103	72	298	157	223	42	119	50	71	71
ENSMUSG00000043740	chr17	B430306N03Rik	48316141	48316485	6937	3.037607	-0.46713	3.86E-08	4.48E-07	0.151958	1	2	1	3	1	3	15	37	28	7	10
ENSMUSG00000078970	chr11	Wdr92	17182107	17182146	2497	-0.96497	5.148511	3.94E-08	4.57E-07	0.034663	-1	601	537	1269	630	825	290	712	340	457	429
ENSMUSG00000044827	chr5	Tlr1	64924811	64927298	2652	2.081488	0.031716	4.07E-08	4.72E-07	0.069681	1	5	3	3	7	9	27	30	21	24	28
ENSMUSG00000057469	chr12	E2f6	16810965	16811315	2421	-0.80364	7.207239	4.27E-08	4.94E-07	0.02507	-1	2724	1981	4111	3090	3315	1613	2433	1754	2456	1642
ENSMUSG00000087014	chr10	Gm16364	39556071	39557285	1313	-1.49486	1.337016	4.33E-08	5E-07	0.058416	-1	48	50	59	58	71	24	35	11	25	22
ENSMUSG00000051285	chr1	Pcmtd1	7088920	7089216	6654	-0.80381	6.412879	4.38E-08	5.05E-07	0.02483	-1	1402	1299	2607	1610	1890	820	1468	1025	1363	1041
ENSMUSG00000003762	chr7	Adck4	27233023	27233173	3175	1.062169	2.77294	4.51E-08	5.2E-07	0.033795	1	67	54	81	63	81	129	206	177	219	108
ENSMUSG00000045205	chr4	Dpy19l4	11261315	11265942	8101	-0.96069	4.566849	4.56E-08	5.26E-07	0.033784	-1	362	341	935	387	594	184	327	280	394	293
ENSMUSG00000046432	chrX	Ngfrap1	1.36E+08	1.36E+08	973	1.434109	1.299933	4.57E-08	5.26E-07	0.050883	1	20	8	20	21	33	55	74	50	73	58
ENSMUSG00000021196	chr13	Pfkp	6579768	6581592	9395	1.096829	3.059103	4.6E-08	5.29E-07	0.039454	1	46	59	128	90	108	181	261	227	195	153
ENSMUSG00000018965	chr5	Ywhah	33018816	33019154	2274	0.761275	5.207857	4.64E-08	5.33E-07	0.021291	1	409	304	573	401	520	653	1017	851	1055	688
ENSMUSG00000098503	chr11	Gm27937	3646942	3647029	88	-2.10785	-0.28573	4.66E-08	5.35E-07	0.070953	-1	15	10	32	21	19	1	8	2	9	5
ENSMUSG00000028478	chr4	Clta	44004452	44004700	1800	0.789323	5.653849	4.71E-08	5.4E-07	0.023427	1	524	468	711	570	657	975	1311	1145	1320	1032
ENSMUSG00000038059	chr18	Smim3	60474193	60475585	1984	1.518454	2.016973	4.73E-08	5.42E-07	0.071694	1	18	14	39	45	51	99	140	60	139	95
ENSMUSG00000071669	chr16	Snx29	11322908	11322978	6435	-1.61573	1.131298	4.73E-08	5.42E-07	0.066062	-1	38	22	110	41	59	14	20	19	25	16
ENSMUSG00000052160	chr12	Pld4	1.13E+08	1.13E+08	1978	1.279286	3.408272	4.76E-08	5.45E-07	0.057077	1	98	78	153	67	98	322	225	302	291	179
ENSMUSG00000006494	chr2	Pdk1	71873224	71873565	7779	-1.01151	5.85483	4.78E-08	5.47E-07	0.039309	-1	868	702	1548	1621	1596	423	1002	733	746	645
ENSMUSG00000044338	chr2	Aplnr	85136225	85139923	3699	0.967328	3.755822	4.8E-08	5.48E-07	0.032011	1	123	93	163	161	190	221	326	309	505	279

ENSMUSG00000042155	chr2	Klhl23	69821944	69822059	4925	-1.10987	4.364523	4.83E-08	5.51E-07	0.04536	-1	309	219	500	577	710	192	304	192	269	231
ENSMUSG00000043252	chr4	Tmem64	15265831	15266749	4670	-0.86426	7.026366	4.87E-08	5.55E-07	0.029189	-1	2437	1924	4366	2279	2739	1302	1878	1457	2248	1593
ENSMUSG00000066324	chr4	Impad1	4762484	4767972	6543	-0.90177	6.948382	4.87E-08	5.55E-07	0.031757	-1	1953	1763	4167	2265	3169	981	1804	1407	2235	1551
ENSMUSG00000028053	chr3	Ash1l	88950622	88950995	13076	-1.08218	5.301872	4.97E-08	5.65E-07	0.044618	-1	547	413	1686	838	1122	271	611	454	589	425
ENSMUSG00000035274	chr9	Tpbg	85842380	85842592	3828	2.865273	0.479114	4.97E-08	5.66E-07	0.22362	1	0	0	5	11	9	20	62	49	19	50
ENSMUSG00000078794	chr7	Dact3	16875317	16875673	2828	1.358965	1.769191	5.01E-08	5.7E-07	0.05231	1	15	17	43	31	46	53	90	85	129	79
ENSMUSG00000057181	chr11	5730455P16Rik	80360492	80364018	4842	-0.87691	6.11833	5.05E-08	5.74E-07	0.02974	-1	1299	1003	2358	1148	1572	653	1297	750	1072	773
ENSMUSG00000002897	chr6	Il17ra	1.2E+08	1.2E+08	3970	1.471521	2.492259	5.06E-08	5.74E-07	0.070269	1	44	37	64	45	42	119	186	223	145	67
ENSMUSG00000043262	chr7	Uevld	46923539	46926488	7226	-0.91128	3.406351	5.13E-08	5.81E-07	0.026863	-1	192	160	324	196	243	111	167	130	126	128
ENSMUSG00000023913	chr17	Pla2g7	43568098	43568170	2905	-1.47864	6.085466	5.14E-08	5.82E-07	0.083615	-1	1598	1796	2450	750	1188	723	713	666	620	482
ENSMUSG00000054675	chr5	Tmem119	1.14E+08	1.14E+08	2315	1.590396	2.562699	5.14E-08	5.82E-07	0.085906	1	31	27	77	34	73	101	94	214	173	188
ENSMUSG00000006390	chr4	Elovl1	1.18E+08	1.18E+08	2726	1.01446	3.39187	5.17E-08	5.85E-07	0.034624	1	101	65	127	95	171	218	296	268	318	174
ENSMUSG00000028341	chr4	Nr4a3	48045153	48045716	5987	2.090701	2.16517	5.28E-08	5.96E-07	0.144947	1	5	22	28	24	58	145	110	102	94	161
ENSMUSG00000028480	chr4	Glipr2	43957401	43957773	2320	1.090593	2.3837	5.28E-08	5.96E-07	0.033798	1	57	33	66	42	64	106	159	112	145	111
ENSMUSG00000091089	chr14	A930018M24Rik	50895942	50896709	1422	-1.26182	4.495759	5.37E-08	6.06E-07	0.059807	-1	311	293	714	576	751	177	446	207	162	227
ENSMUSG00000057230	chr6	Aak1	86849517	86850215	8272	-1.42123	2.259643	5.47E-08	6.16E-07	0.064312	-1	61	53	247	103	128	36	57	43	62	37
ENSMUSG00000022912	chr16	Pros1	62854307	62854504	4088	0.942677	4.155303	5.48E-08	6.17E-07	0.031996	1	141	140	280	180	250	302	604	500	373	353
ENSMUSG00000023892	chr17	Zfp51	21450352	21450421	2600	-1.10096	2.925111	5.56E-08	6.26E-07	0.039364	-1	131	143	239	142	169	78	132	70	77	79
ENSMUSG00000046402	chr9	Rbp1	98422961	98425051	2652	1.261586	2.071751	5.61E-08	6.3E-07	0.04622	1	25	30	42	39	57	70	127	122	103	101
ENSMUSG00000050737	chr2	Ptges	30889471	30892826	3931	1.449424	2.54634	5.63E-08	6.32E-07	0.069575	1	49	30	69	35	67	117	126	247	146	113
ENSMUSG00000024588	chr18	Fech	64456550	64458217	2901	-0.82381	7.12603	5.7E-08	6.4E-07	0.026834	-1	2304	1892	4126	2893	3392	1416	2654	1571	2066	1607
ENSMUSG00000071714	chr15	Csf2rb2	78282517	78285379	4612	1.702845	2.597667	5.74E-08	6.43E-07	0.098695	1	32	38	66	35	54	140	269	247	113	63
ENSMUSG00000028552	chr4	Eps15	1.09E+08	1.09E+08	6931	-0.98745	6.603665	5.77E-08	6.46E-07	0.038341	-1	1863	1771	3519	1366	1959	867	1366	1103	1577	1088
ENSMUSG00000030592	chr7	Ryr1	29003340	29003553	15371	-1.02863	11.42349	5.85E-08	6.55E-07	0.042216	-1	41033	32089	112365	55785	72956	22531	34775	28528	49348	31908
ENSMUSG00000098112	chr15	Bin2	1.01E+08	1.01E+08	2530	2.076459	-0.09147	5.9E-08	6.6E-07	0.073374	1	5	2	8	4	6	21	37	21	16	24
ENSMUSG00000002020	chr12	Ltbp2	84783212	84784395	8184	2.429621	0.921764	5.91E-08	6.61E-07	0.169604	1	6	4	18	8	10	18	44	110	35	58
ENSMUSG00000021390	chr13	Ogn	49608071	49608126	2540	-1.09131	5.625358	6.02E-08	6.72E-07	0.046227	-1	678	890	1996	836	1169	511	703	724	528	390
ENSMUSG00000032011	chr9	Thy1	44043384	44043476	1735	1.163073	4.11311	6.06E-08	6.76E-07	0.050295	1	134	79	242	175	256	294	404	553	399	474
ENSMUSG00000026365	chr1	Cfh	1.4E+08	1.4E+08	8383	-1.13485	4.58902	6.08E-08	6.77E-07	0.048754	-1	307	339	1085	420	670	159	342	336	293	250
ENSMUSG00000048895	chr11	Cdk5r1	80477023	80481184	4162	2.068191	-0.18349	6.08E-08	6.77E-07	0.059067	1	4	3	5	3	8	13	27	26	29	17
ENSMUSG00000075602	chr15	Ly6a	74994877	74995479	1205	0.980893	6.093151	6.14E-08	6.83E-07	0.037636	1	676	572	903	664	841	1608	2229	1826	1486	1071
ENSMUSG00000022139	chr14	Mbnl2	1.2E+08	1.2E+08	4552	-1.03551	6.69079	6.18E-08	6.87E-07	0.042368	-1	1363	1402	3675	2254	2949	639	1519	1341	1515	1252
ENSMUSG00000042208	chr11	0610010F05Rik	23564961	23565136	5226	-0.78568	4.218783	6.22E-08	6.91E-07	0.021819	-1	311	284	529	349	427	166	322	222	316	233
ENSMUSG00000041997	chr2	Tlk1	70712407	70714165	6474	-0.77824	5.529899	6.24E-08	6.93E-07	0.023231	-1	786	663	1497	783	1056	459	816	569	792	513
ENSMUSG00000059408	chr17	Mrgprh	12876034	12877842	1809	-1.51853	1.276821	6.44E-08	7.14E-07	0.062098	-1	44	49	94	40	55	18	30	31	17	14
ENSMUSG00000042249	chr5	Adrbk2	1.13E+08	1.13E+08	6537	-1.45303	3.094139	6.47E-08	7.17E-07	0.074995	-1	199	116	389	115	222	68	111	118	81	38
ENSMUSG00000020988	chr12	L2hgdh	69690436	69692496	3338	-0.81859	5.614752	6.54E-08	7.24E-07	0.025941	-1	748	597	1429	1122	1253	467	902	592	759	558
ENSMUSG00000038344	chrX	Txlng	1.63E+08	1.63E+08	7541	-1.08024	2.767357	6.58E-08	7.28E-07	0.037099	-1	100	113	213	138	181	57	86	98	76	74
ENSMUSG00000023827	chr17	Agpat4	12118704	12118840	2701	1.191305	2.21088	6.76E-08	7.47E-07	0.041474	1	37	32	43	37	71	90	133	123	130	95
ENSMUSG00000018672	chr11	Copz2	96849870	96849996	2208	0.873499	4.865451	6.77E-08	7.48E-07	0.028569	1	311	276	362	311	352	589	703	688	906	543
ENSMUSG00000020657	chr12	Dnajc27	4082574	4082873	4713	-1.08788	6.526125	6.81E-08	7.51E-07	0.046926	-1	1348	894	2691	2704	2829	795	1357	880	1364	1035
ENSMUSG00000031595	chr8	Pdgfrl	40926212	40926425	3126	1.766341	2.235051	7.01E-08	7.73E-07	0.10747	1	9	15	43	39	70	77	132	155	130	144
ENSMUSG00000027962	chr3	Vcam1	1.16E+08	1.16E+08	3398	1.052616	2.986591	7.11E-08	7.84E-07	0.036384	1	78	57	118	61	98	162	256	207	168	162
ENSMUSG00000038811	chr11	Gngt2	95837216	95837371	1877	1.504865	1.903908	7.16E-08	7.88E-07	0.067303	1	17	34	31	35	30	105	113	101	85	74
ENSMUSG00000030249	chr6	Abcc9	1.43E+08	1.43E+08	7538	-0.96654	7.756216	7.19E-08	7.91E-07	0.037614	-1	3202	2448	8879	4084	5850	2031	3232	2327	3383	2483
ENSMUSG00000019188	chr2	H13	1.53E+08	1.53E+08	8884	0.780786	5.479567	7.22E-08	7.93E-07	0.023474	1	489	358	716	542	534	799	1150	1056	1346	822
ENSMUSG00000021981	chr14	Cab39l	59440981	59441018	3037	-0.84777	4.672199	7.23E-08	7.94E-07	0.026824	-1	444	311	670	556	687	296	417	341	325	270
ENSMUSG00000027742	chr3	Cog6	52981875	52983191	4957	-0.89567	6.706066	7.3E-08	8E-07	0.0321	-1	1819	1792	3377	1805	2182	1089	1929	1018	1487	1200
ENSMUSG00000056529	chr4	Ptafr	1.33E+08	1.33E+08	3637	1.32246	2.468319	7.35E-08	8.05E-07	0.059151	1	47	19	101	35	60	117	150	171	143	117
ENSMUSG00000029512	chr5	Ulk1	1.11E+08	1.11E+08	5213	-0.82887	6.392687	7.52E-08	8.23E-07	0.027375	-1	1482	1007	2833	1613	1990	844	1388	960	1384	996
ENSMUSG00000028832	chr4	Stmn1	1.34E+08	1.34E+08	1922	1.637029	1.549594	7.56E-08	8.27E-07	0.079802	1	13	16	24	26	31	86	60	75	61	88
ENSMUSG00000027994	chr3	Ccdc109b	1.3E+08	1.3E+08	1318	1.556183	1.119253	7.59E-08	8.3E-07	0.064834	1	15	7	30	12	22	67	68	41	61	39
ENSMUSG00000034868	chr17	Myl12b	70973920	70974496	1711	0.870795	4.333672	7.6E-08	8.31E-07	0.027721	1	200	171	263	238	257	401	523	564	504	359
ENSMUSG00000038116	chr2	Phf20	1.56E+08	1.56E+08	9988	-0.83194	4.68582	7.61E-08	8.31E-07	0.025877	-1	394	317	872	503	655	286	436	291	370	304
ENSMUSG00000023074	chrX	Mospd1	53344598	53344906	2085	-0.94964	6.339756	7.69E-08	8.39E-07	0.036063	-1	1387	1406	2954	1310	1654	688	1247	833	1457	915
ENSMUSG00000037060	chr7	Prkcdbp	1.05E+08	1.05E+08	1035	1.069452	4.044436	7.7E-08	8.39E-07	0.041983	1	178	149	199	122	183	360	381	507	432	314
ENSMUSG00000044042	chr2	Fmn1	1.13E+08	1.13E+08	15397	2.186658	0.381949	7.73E-08	8.42E-07	0.123718	1	1	2	19	7	7	18	41	48	28	39
ENSMUSG00000028992	chr4	Nmnat1	1.49E+08	1.49E+08	3037	-0.86202	4.148862	7.83E-08	8.52E-07	0.027071	-1	259	236	456	443	460	170	285	241	284	177
ENSMUSG00000033313	chr8	Fbxl8	1.05E+08	1.05E+08	2103	1.664378	0.500477	7.84E-08	8.53E-07	0.051717	1	11	7	10	7	14	20	41	39	49	31
ENSMUSG00000042594	chr5	Sh2b3	1.22E+08	1.22E+08	4734	0.800827	4.991282	8.05E-08	8.74E-07	0.024577	1	322	203	613	365	417	599	917	676	880	625
ENSMUSG00000066687	chr9	Zbtb16	48654311	48657371	5100	-1.23804	5.032952	8.11E-08	8.8E-07	0.059955	-1	471	413	1317	737	950	277	367	570	299	238
ENSMUSG00000021213	chr13	Akr1c13	4191184	4191310	1400	2.183564	-0.24619	8.18E-08	8.87E-07	0.0678	1	5	5	4	4	2	20	22	26	22	16
ENSMUSG00000001493	chr11	Meox1	1.02E+08	1.02E+08	2228	1.511163	2.499822	8.22E-08	8.9E-07	0.079539	1	21	23	60	61	74	110	152	134	132	200
ENSMUSG00000091498	chr12	Mpc1-ps	1.11E+08	1.11E+08	330	-0.92266	5.015233	8.22E-08	8.9E-07	0.033118	-1	581	433	710	807	856	327	621	314	495	318
ENSMUSG00000038039	chr10	Gcc2	58255497	58255571	9630	-0.757	4.722578	8.25E-08	8.93E-07	0.021375	-1	428	370	802	498	609	280	458	299	464	307

ENSMUSG00000024887	chr19	Asah2	31984654	31986947	4682	-0.99991	2.903682	8.31E-08	8.98E-07	0.032375	-1	121	108	253	139	193	53	105	99	115	83
ENSMUSG00000023947	chr17	Nfkbie	45555716	45556314	2422	1.465448	1.103734	8.37E-08	9.03E-07	0.051314	1	18	11	24	9	25	44	69	63	61	35
ENSMUSG00000030208	chr6	Emp1	1.35E+08	1.35E+08	3046	1.023449	5.970469	8.37E-08	9.03E-07	0.041899	1	517	377	860	622	1041	1025	2240	1489	1339	1582
ENSMUSG00000086219	chr5	Srrm4os	1.16E+08	1.16E+08	3655	1.910798	3.223735	8.43E-08	9.09E-07	0.131858	1	84	70	90	16	37	259	219	299	258	252
ENSMUSG00000020326	chr11	Ccng1	40748552	40751059	3512	-0.8445	9.507195	8.5E-08	9.16E-07	0.029318	-1	12259	10762	25521	12798	15680	6970	11794	9138	11975	8179
ENSMUSG00000010095	chr19	Slc3a2	8706882	8708094	2958	0.786283	5.261471	8.57E-08	9.22E-07	0.023944	1	412	304	677	400	496	747	990	972	1042	669
ENSMUSG00000020782	chr11	Llgl2	1.16E+08	1.16E+08	4844	-1.07473	2.448399	8.61E-08	9.25E-07	0.035163	-1	87	94	184	89	142	56	74	64	74	48
ENSMUSG00000035840	chr13	Lysmd3	81657806	81657936	3124	-1.39113	1.689888	8.61E-08	9.25E-07	0.056393	-1	43	38	118	80	102	18	47	30	31	33
ENSMUSG00000021384	chr13	Susd3	49230690	49231331	2837	2.484806	-0.27061	8.65E-08	9.29E-07	0.115803	1	4	1	5	4	3	33	13	21	25	14
ENSMUSG00000039137	chr4	Whrn	63414910	63415666	7337	1.710141	1.126751	8.66E-08	9.29E-07	0.081223	1	17	9	33	10	10	34	55	59	64	72
ENSMUSG00000021245	chr12	Mlh3	85234529	85235729	5446	-0.88744	3.840004	8.69E-08	9.3E-07	0.027923	-1	218	214	455	275	355	140	272	152	181	173
ENSMUSG00000032690	chr5	Oas2	1.21E+08	1.21E+08	4451	1.611993	1.500807	8.68E-08	9.3E-07	0.075081	1	25	15	32	21	13	73	101	89	55	49
ENSMUSG00000054648	chr8	Zfp869	69706332	69707694	1590	-0.87033	3.461481	8.69E-08	9.3E-07	0.025632	-1	187	181	290	230	243	106	190	119	168	129
ENSMUSG00000078877	chr2	Gm14295	1.77E+08	1.77E+08	3527	-1.28683	2.280148	8.69E-08	9.3E-07	0.052784	-1	78	76	161	102	139	48	74	24	53	54
ENSMUSG00000044786	chr7	Zfp36	28376784	28378493	1792	1.728804	4.601963	8.81E-08	9.42E-07	0.115107	1	137	147	184	162	261	447	1887	386	476	400
ENSMUSG00000003623	chr5	Crot	8966033	8966972	5456	-0.88705	5.333848	8.82E-08	9.42E-07	0.030949	-1	811	644	1352	627	802	423	687	465	532	473
ENSMUSG00000022092	chr14	Ppp3cc	70217898	70218277	1948	-0.83551	4.173829	8.94E-08	9.54E-07	0.025601	-1	269	254	478	423	446	175	339	192	280	209
ENSMUSG00000085939	chr18	Cd63-ps	50134726	50135600	875	1.13858	3.164703	8.95E-08	9.54E-07	0.044372	1	109	79	93	58	90	177	277	208	265	187
ENSMUSG00000037852	chr8	Cpe	64592558	64593221	2087	0.834442	8.712069	9.08E-08	9.67E-07	0.028688	1	4495	3610	6879	4124	5200	8813	10742	9452	12685	7454
ENSMUSG00000032368	chr9	Zic1	91358058	91361766	5693	-3.08096	-0.17379	9.1E-08	9.69E-07	0.203646	-1	9	5	47	39	20	2	1	1	3	7
ENSMUSG00000039960	chr8	Rhou	1.24E+08	1.24E+08	3806	-1.84796	4.713026	9.51E-08	1.01E-06	0.131922	-1	299	211	571	1229	1093	170	258	289	165	146
ENSMUSG00000034390	chr8	Cmip	1.17E+08	1.17E+08	4732	0.926694	3.607755	9.54E-08	1.01E-06	0.030283	1	96	95	170	123	194	201	311	334	332	264
ENSMUSG00000034591	chr10	Slc41a2	83230848	83233750	5349	1.542803	1.312041	9.72E-08	1.03E-06	0.065598	1	11	15	26	22	23	32	79	84	58	66
ENSMUSG00000064358	chrMT	mt-Co3	8607	9390	784	-1.91347	4.79311	9.72E-08	1.03E-06	0.141546	-1	193	236	800	1118	1396	135	282	176	360	148
ENSMUSG00000031576	chr8	Kcnu1	25849623	25849850	3659	1.850861	0.42828	9.92E-08	1.05E-06	0.073976	1	12	5	12	5	8	28	62	27	29	29
ENSMUSG00000030220	chr6	Arhgdib	1.37E+08	1.37E+08	1839	0.956194	3.933365	9.94E-08	1.05E-06	0.033663	1	128	117	195	156	239	361	385	410	410	244
ENSMUSG00000043126	chr10	D830039M14Rik	61475245	61476937	1693	-0.99912	2.918973	9.97E-08	1.05E-06	0.033107	-1	148	87	192	175	209	71	118	76	120	76
ENSMUSG00000029246	chr5	Ppat	76913249	76915405	4421	-0.9309	4.771188	1.01E-07	1.06E-06	0.033886	-1	498	474	927	446	548	238	471	250	452	330
ENSMUSG00000054752	chr4	Fsd1l	53631471	53631612	9739	0.95172	3.739892	1.01E-07	1.06E-06	0.033034	1	125	73	206	144	198	205	354	287	419	338
ENSMUSG00000054008	chr18	Ndst1	60685978	60689364	6070	-1.16691	5.397544	1.01E-07	1.07E-06	0.05462	-1	549	401	1536	1120	1368	275	653	387	625	478
ENSMUSG00000089762	chr2	Ier5l	30471537	30474219	2683	1.223838	1.702447	1.01E-07	1.07E-06	0.039958	1	34	19	34	25	38	63	83	87	100	66
ENSMUSG00000037278	chr11	Tmem97	78541817	78542796	1375	1.265761	1.679795	1.02E-07	1.07E-06	0.042904	1	23	26	44	26	26	70	98	81	71	72
ENSMUSG00000024042	chr17	Sik1	31844248	31846643	4511	1.247574	3.683713	1.02E-07	1.08E-06	0.057711	1	75	147	136	82	147	258	514	272	376	245
ENSMUSG00000046982	chr18	Tshz1	84011627	84016241	5656	-0.90327	3.464651	1.04E-07	1.1E-06	0.028114	-1	166	146	368	214	291	107	140	142	184	125
ENSMUSG00000030782	chr7	Tgfb1i1	1.28E+08	1.28E+08	3598	1.138635	2.826833	1.06E-07	1.12E-06	0.044033	1	58	45	87	75	87	116	142	195	270	156
ENSMUSG00000030060	chr6	Hmces	87913935	87914011	2308	1.211924	2.264568	1.07E-07	1.13E-06	0.04526	1	35	40	56	48	45	101	120	149	147	78
ENSMUSG00000028284	chr4	Map3k7	31964097	31964382	6423	-0.77077	6.150431	1.09E-07	1.14E-06	0.024112	-1	1205	913	2071	1423	1722	787	1151	851	1240	797
ENSMUSG00000031506	chr1	Ptpn7	1.35E+08	1.35E+08	6102	1.617636	0.733441	1.13E-07	1.19E-06	0.056689	1	14	9	16	9	12	36	65	45	39	27
ENSMUSG00000006736	chr10	Tspan31	1.27E+08	1.27E+08	1516	0.739872	5.368229	1.15E-07	1.2E-06	0.021553	1	450	366	645	443	578	783	1091	948	1102	780
ENSMUSG00000005142	chr8	Man2b1	85083269	85083488	4325	0.96445	4.814854	1.15E-07	1.21E-06	0.036929	1	254	174	512	287	354	600	643	883	706	503
ENSMUSG00000048490	chr16	Nrip1	76287400	76295015	11457	-0.98276	5.131979	1.16E-07	1.21E-06	0.038675	-1	568	641	1348	528	724	405	521	446	471	300
ENSMUSG00000008226	chr2	Scrn3	73312601	73312713	4815	-0.81241	6.112028	1.18E-07	1.23E-06	0.027005	-1	1212	1070	2123	1252	1484	605	1176	844	1161	856
ENSMUSG00000031666	chr8	Rbl2	91070057	91070406	6963	-0.84299	5.841735	1.18E-07	1.24E-06	0.028906	-1	847	781	2048	1134	1314	521	1041	659	866	703
ENSMUSG00000064357	chrMT	mt-Atp6	7927	8607	681	-2.05464	4.683423	1.19E-07	1.24E-06	0.163379	-1	174	190	728	974	1508	111	245	157	312	121
ENSMUSG00000046138	chr19	9930021J03Rik	29714402	29719606	8134	-1.04965	4.068249	1.22E-07	1.27E-06	0.042423	-1	240	168	705	372	444	134	255	185	224	200
ENSMUSG00000037824	chr14	Tspan14	40906445	40908129	2475	0.901782	4.241031	1.23E-07	1.28E-06	0.031215	1	171	114	326	223	251	332	506	557	553	306
ENSMUSG00000005413	chr8	Hmox1	75093591	75093772	2161	0.976622	3.762034	1.24E-07	1.3E-06	0.03521	1	160	86	210	120	160	317	450	298	360	211
ENSMUSG00000020700	chr11	Map3k3	1.06E+08	1.06E+08	4023	-0.9358	4.520636	1.26E-07	1.31E-06	0.03422	-1	352	245	831	492	616	195	390	275	293	287
ENSMUSG00000042010	chr5	Acacb	1.14E+08	1.14E+08	9632	-1.17749	7.917504	1.27E-07	1.32E-06	0.057666	-1	3293	2305	7853	7598	7175	1843	3260	2483	4356	1995
ENSMUSG00000025287	chrX	Acot9	1.55E+08	1.55E+08	2273	0.845788	4.727308	1.29E-07	1.34E-06	0.027809	1	268	222	334	328	348	467	889	475	779	537
ENSMUSG00000066026	chr4	Dhrs3	1.45E+08	1.45E+08	2927	1.06614	4.753576	1.3E-07	1.35E-06	0.045327	1	266	228	319	213	353	790	673	631	586	532
ENSMUSG00000022811	chr16	Zfp148	33380775	33381027	9545	-0.83328	4.399798	1.3E-07	1.35E-06	0.02657	-1	306	304	748	358	526	199	333	272	337	249
ENSMUSG00000021952	chr14	Xpo4	57581002	57582468	7266	-1.3879	1.642958	1.31E-07	1.36E-06	0.057459	-1	47	34	137	69	85	20	42	22	37	33
ENSMUSG00000032131	chr9	Abcg4	44273188	44274857	5211	-2.39979	-0.00545	1.31E-07	1.36E-06	0.12616	-1	12	6	35	27	48	6	6	3	4	6
ENSMUSG00000062078	chr17	Qk	10206471	10209631	9879	-1.06483	7.030962	1.31E-07	1.36E-06	0.04726	-1	1737	1443	4246	3617	3796	886	1872	1435	2200	1487
ENSMUSG00000090171	chr1	Ugt1a2	88200601	88201500	2211	1.910776	1.363549	1.34E-07	1.38E-06	0.112803	1	27	9	20	11	14	57	53	118	65	51
ENSMUSG00000089960	chr1	Ugt1a1	88211959	88212871	2224	1.910776	1.363549	1.34E-07	1.38E-06	0.112813	1	27	9	20	11	14	57	53	118	65	51
ENSMUSG00000089943	chr1	Ugt1a5	88166012	88166903	2203	1.910773	1.363549	1.34E-07	1.39E-06	0.112851	1	27	9	20	11	14	57	53	118	65	51
ENSMUSG00000089675	chr1	Ugt1a8	88087813	88088721	2227	1.910772	1.363549	1.35E-07	1.39E-06	0.112869	1	27	9	20	11	14	57	53	118	65	51
ENSMUSG00000090175	chr1	Ugt1a9	88070800	88071678	2190	1.910772	1.363549	1.35E-07	1.39E-06	0.112878	1	27	9	20	11	14	57	53	118	65	51
ENSMUSG00000035783	chr19	Acta2	34241090	34241810	1781	1.043593	6.263552	1.35E-07	1.39E-06	0.045055	1	577	772	867	775	943	1082	1867	1890	2856	1869
ENSMUSG00000090165	chr1	Ugt1a10	88055388	88055664	2267	1.910771	1.363549	1.35E-07	1.39E-06	0.112892	1	27	9	20	11	14	57	53	118	65	51
ENSMUSG00000020220	chr4	Vps13d	1.45E+08	1.45E+08	24771	-0.97195	5.983595	1.37E-07	1.41E-06	0.03908	-1	880	657	2354	1436	1801	543	997	684	1018	712
ENSMUSG00000097971	chr17	Gm26917	39843013	39846341	3329	1.14816	4.565275	1.38E-07	1.42E-06	0.052684	1	272	131	258	261	243	412	498	452	931	674
ENSMUSG00000023274	chr6	Cd4	1.25E+08	1.25E+08	4032	2.447176	0.243421	1.38E-07	1.42E-06	0.147292	1	9	3	11	1	2	27	23	50	47	15

ENSMUSG00000001700	chr18	Gramd3	56432132	56432357	2605	-0.85597	3.593965	1.39E-07	1.43E-06	0.025797	-1	184	150	355	253	333	126	203	134	179	141
ENSMUSG00000021027	chr12	Ralgapa1	55602929	55604268	7874	-0.84446	5.248516	1.42E-07	1.46E-06	0.028835	-1	619	425	1380	734	943	339	612	467	636	454
ENSMUSG00000022516	chr16	Nudt16l1	4939111	4939293	1269	0.853553	4.01066	1.43E-07	1.47E-06	0.026833	1	173	151	192	172	210	327	426	371	462	294
ENSMUSG00000065460	chr2	Mir133a-2	1.8E+08	1.8E+08	104	1.521956	1.318216	1.45E-07	1.49E-06	0.067298	1	24	10	28	14	23	73	51	65	82	44
ENSMUSG00000034998	chr17	Foxn2	88440711	88440884	7357	-0.89191	3.607126	1.46E-07	1.5E-06	0.029063	-1	190	191	359	268	266	90	218	154	183	142
ENSMUSG00000001555	chr11	Fkbp10	1E+08	1E+08	2935	0.971066	3.301411	1.47E-07	1.5E-06	0.033506	1	78	68	130	114	145	184	231	220	275	254
ENSMUSG00000070814	chr7	6330408A02Rik	13258967	13261640	11662	-0.79138	4.366312	1.48E-07	1.51E-06	0.023942	-1	344	275	504	433	555	196	331	248	347	262
ENSMUSG00000034327	chr14	Kctd9	67715937	67716181	4746	-0.7843	5.907395	1.49E-07	1.52E-06	0.025422	-1	896	905	1750	1249	1370	619	1000	665	1125	676
ENSMUSG00000022014	chr14	Epsti1	77904239	77904664	2317	1.49486	1.261355	1.5E-07	1.53E-06	0.065363	1	19	9	40	12	19	68	63	59	60	50
ENSMUSG00000024811	chr19	Tnks2	36834232	36834736	10406	-0.80171	7.247704	1.51E-07	1.54E-06	0.027209	-1	2448	1916	4965	2989	3700	1467	2506	1818	2660	1793
ENSMUSG00000021624	chr13	Cd180	1.03E+08	1.03E+08	4509	1.78234	0.755466	1.52E-07	1.55E-06	0.09123	1	7	3	30	9	11	36	42	57	41	41
ENSMUSG00000097141	chr18	Gm10524	82692284	82694176	1893	-1.38402	2.168679	1.52E-07	1.55E-06	0.065396	-1	85	53	192	81	127	38	51	21	75	41
ENSMUSG00000005362	chr6	Crbn	1.07E+08	1.07E+08	5179	-0.75834	5.098169	1.53E-07	1.55E-06	0.023002	-1	533	475	1102	673	749	329	584	421	595	418
ENSMUSG00000026854	chr2	Usp20	30982279	30982398	9017	0.816187	4.377914	1.55E-07	1.57E-06	0.025754	1	195	169	389	192	288	394	493	434	659	432
ENSMUSG00000024397	chr17	Aif1	35170991	35171193	1532	1.922121	1.482628	1.56E-07	1.58E-06	0.118245	1	18	22	27	9	11	112	85	63	61	51
ENSMUSG00000063488	chr9	Zkscan7	1.23E+08	1.23E+08	2228	-1.40788	1.162603	1.56E-07	1.59E-06	0.052423	-1	38	31	70	58	58	16	39	17	16	20
ENSMUSG00000029054	chr4	Gabrd	1.55E+08	1.55E+08	2875	1.813	1.150602	1.57E-07	1.59E-06	0.09594	1	7	20	24	7	16	56	68	44	50	72
ENSMUSG00000026828	chr2	Galnt5	57997884	57999813	4462	1.939713	0.433976	1.67E-07	1.69E-06	0.095187	1	4	4	9	10	14	25	47	21	31	51
ENSMUSG00000000958	chr14	Slc7a7	54369444	54369886	2142	1.526723	1.075483	1.67E-07	1.69E-06	0.062562	1	13	10	14	15	30	37	63	47	55	64
ENSMUSG00000033209	chr5	Ttc28	1.11E+08	1.11E+08	12315	-1.15929	4.053448	1.67E-07	1.69E-06	0.053214	-1	222	160	809	317	489	143	225	174	242	157
ENSMUSG00000074676	chr2	Foxs1	1.53E+08	1.53E+08	1311	1.680375	0.602326	1.68E-07	1.7E-06	0.061541	1	7	11	10	10	14	22	58	27	50	39
ENSMUSG00000063439	chr7	B9d2	25681158	25681474	1021	1.104213	2.892321	1.71E-07	1.73E-06	0.043004	1	88	41	79	60	104	140	230	143	239	166
ENSMUSG00000022464	chr15	Slc38a4	96994823	96997091	3952	-1.31312	5.963358	1.74E-07	1.76E-06	0.072135	-1	1803	828	2411	800	1452	732	741	534	935	345
ENSMUSG00000040998	chr3	Npnt	1.33E+08	1.33E+08	5026	-1.45191	4.39373	1.74E-07	1.76E-06	0.085745	-1	565	283	665	328	663	268	180	111	352	113
ENSMUSG00000039988	chr3	Ankrd13c	1.58E+08	1.58E+08	2668	-0.8275	3.630741	1.77E-07	1.78E-06	0.024709	-1	207	156	396	233	309	128	214	141	217	123
ENSMUSG00000023328	chr5	Ache	1.37E+08	1.37E+08	4623	0.920051	5.922121	1.77E-07	1.79E-06	0.035659	1	616	350	1015	682	799	1217	1423	1189	1691	1605
ENSMUSG00000041598	chr11	Cdc42ep4	1.14E+08	1.14E+08	3643	0.80295	3.630347	1.78E-07	1.8E-06	0.0229	1	118	98	205	124	185	228	345	288	314	248
ENSMUSG00000064340	chrMT	mt-Tl1	2676	2750	75	-1.63916	6.302187	1.79E-07	1.8E-06	0.111196	-1	944	503	2330	3098	3311	649	965	566	937	444
ENSMUSG00000001418	chr3	Glmp	88325023	88325201	6291	0.772051	4.786166	1.81E-07	1.82E-06	0.023707	1	299	212	434	320	379	525	634	680	771	538
ENSMUSG00000002985	chr7	Apoe	19696109	19697103	1980	1.601137	8.080837	1.81E-07	1.82E-06	0.106891	1	2717	2338	2536	1151	1387	7179	5558	10677	7064	5537
ENSMUSG00000091712	chr16	Sec14l5	5147109	5147129	2337	-1.3154	2.992266	1.82E-07	1.83E-06	0.065527	-1	120	88	383	160	216	47	145	60	90	80
ENSMUSG00000035284	chr9	Vps13c	67840396	67840526	11523	-1.26547	4.374628	1.85E-07	1.86E-06	0.065361	-1	241	179	848	571	687	148	302	208	227	227
ENSMUSG00000063511	chr7	Snrnp70	45376462	45377278	1676	0.803201	5.654934	1.85E-07	1.86E-06	0.026792	1	555	460	717	531	651	1047	1142	1200	1428	970
ENSMUSG00000048779	chr7	P2ry6	1.01E+08	1.01E+08	1938	1.347901	1.863502	1.86E-07	1.86E-06	0.060617	1	22	14	56	24	51	96	82	91	117	69
ENSMUSG00000045896	chr6	Paip2b	83805401	83808892	6157	-0.85633	7.174199	1.87E-07	1.87E-06	0.031491	-1	2177	2002	3829	3477	3634	1460	2600	1421	2290	1725
ENSMUSG00000041431	chr13	Ccnb1	1.01E+08	1.01E+08	4217	2.865604	-0.75556	1.88E-07	1.88E-06	0.139293	1	2	0	3	0	4	16	6	20	13	18
ENSMUSG00000031600	chr8	Vps37a	40511783	40512233	6379	-0.96053	6.185045	1.91E-07	1.9E-06	0.039217	-1	1363	1295	2682	989	1497	742	1147	729	1142	785
ENSMUSG00000034412	chr11	Tbc1d10a	4186789	4187099	2733	1.135735	2.121539	1.91E-07	1.91E-06	0.038986	1	41	30	46	40	54	78	120	110	107	110
ENSMUSG00000034201	chr11	Gas2l1	5054132	5056689	6100	1.121443	2.720457	1.92E-07	1.91E-06	0.043685	1	62	41	70	65	89	128	138	178	181	169
ENSMUSG00000027201	chr2	Myef2	1.25E+08	1.25E+08	5936	1.168331	2.146318	1.94E-07	1.93E-06	0.04342	1	30	29	46	44	65	92	101	96	146	105
ENSMUSG00000020143	chr11	Dock2	34226815	34227730	11425	1.22473	2.107623	1.95E-07	1.94E-06	0.049158	1	39	21	70	32	45	75	123	143	113	81
ENSMUSG00000065947	chrMT	mt-Nd4l	9877	10173	297	-2.46376	1.896649	1.95E-07	1.94E-06	0.216785	-1	18	24	125	136	232	14	20	17	38	14
ENSMUSG00000039414	chr17	Heatr5b	78752906	78753336	6437	-0.98689	3.023396	1.96E-07	1.94E-06	0.034092	-1	124	106	305	155	204	82	127	99	95	88
ENSMUSG00000051579	chrX	Tceal8	1.36E+08	1.36E+08	2563	1.004019	3.444142	1.97E-07	1.96E-06	0.036978	1	98	115	134	91	124	173	334	225	330	261
ENSMUSG00000030451	chr7	Herc2	56050155	56050302	15440	-0.99039	6.35623	1.99E-07	1.97E-06	0.041887	-1	1069	905	3335	1728	2305	687	1189	923	1318	942
ENSMUSG00000035735	chr19	Dagla	10245265	10248624	5747	-0.96784	3.651556	1.99E-07	1.97E-06	0.035582	-1	256	129	473	211	319	122	198	141	196	123
ENSMUSG00000033453	chr9	Adamts15	30899155	30902789	5928	1.237282	2.04891	1.99E-07	1.98E-06	0.049246	1	33	23	46	42	49	67	90	115	120	116
ENSMUSG00000039599	chr14	Fam149b	20348162	20348394	3146	-0.76391	3.923688	2.01E-07	1.99E-06	0.02164	-1	267	192	406	311	370	149	256	212	247	167
ENSMUSG00000030654	chr7	Arl6ip1	1.18E+08	1.18E+08	2134	1.026947	4.166823	2.01E-07	1.99E-06	0.042013	1	163	175	242	149	201	398	424	578	412	330
ENSMUSG00000022971	chr16	Ifnar2	91372783	91373074	3329	0.985249	3.245729	2.03E-07	2E-06	0.035073	1	86	77	116	83	143	201	255	265	258	154
ENSMUSG00000045312	chr13	Lhfpl2	94057796	94057906	8276	1.506262	3.028471	2.03E-07	2.01E-06	0.086394	1	69	58	84	45	75	132	215	399	171	153
ENSMUSG00000044224	chr15	Dnajc21	10446756	10447226	4777	-0.82857	6.010161	2.06E-07	2.04E-06	0.029221	-1	1036	1115	1640	1289	1485	639	1151	653	1117	747
ENSMUSG00000038121	chr18	Fam210a	68260187	68268952	9813	-1.25654	6.657811	2.07E-07	2.04E-06	0.067403	-1	1215	917	3145	3333	3422	727	1601	882	1482	901
ENSMUSG00000021573	chr13	Tppp	74009407	74009509	5118	-1.08889	4.025687	2.07E-07	2.04E-06	0.047303	-1	245	178	751	322	399	136	187	164	251	206
ENSMUSG00000031601	chr8	Cnot7	40492540	40494115	5821	-0.73984	5.380025	2.08E-07	2.05E-06	0.022681	-1	701	597	1248	787	901	378	713	537	738	517
ENSMUSG00000040550	chr4	Otud6b	14809498	14811748	3387	-0.81536	5.939194	2.08E-07	2.05E-06	0.028239	-1	946	939	1710	1279	1458	530	1124	674	1005	789
ENSMUSG00000052414	chr15	Gm28047	1.03E+08	1.03E+08	1611	-1.67781	2.156187	2.08E-07	2.05E-06	0.102438	-1	63	36	260	92	136	31	65	30	48	20
ENSMUSG00000054589	chr18	Gm9949	62180126	62180603	962	-1.78684	0.069622	2.09E-07	2.05E-06	0.062086	-1	19	19	38	17	28	7	11	2	10	9
ENSMUSG00000035948	chr10	Acss3	1.07E+08	1.07E+08	4549	-1.76724	1.207571	2.11E-07	2.07E-06	0.096744	-1	47	40	117	37	45	16	10	28	17	18
ENSMUSG00000052397	chr17	Ezr	6738041	6739467	3290	1.393224	1.800905	2.12E-07	2.08E-06	0.06293	1	16	16	26	41	51	80	99	79	112	73
ENSMUSG00000030257	chr6	Srgap3	1.13E+08	1.13E+08	9852	1.542048	1.510088	2.13E-07	2.09E-06	0.078286	1	9	9	31	27	40	39	81	80	93	78
ENSMUSG00000036792	chr2	Mbd5	48949510	48949549	14221	-1.22917	3.38433	2.15E-07	2.1E-06	0.05895	-1	130	110	499	238	280	71	134	103	136	123
ENSMUSG00000039747	chr5	Orai2	1.36E+08	1.36E+08	3846	1.424885	0.896494	2.16E-07	2.11E-06	0.046544	1	16	10	25	11	14	38	61	46	59	29
ENSMUSG00000099858	chr1	Gm6652	1.54E+08	1.54E+08	1070	-1.27756	1.107393	2.16E-07	2.11E-06	0.038894	-1	36	35	61	51	53	17	29	16	24	24
ENSMUSG00000039523	chr4	Cep104	1.54E+08	1.54E+08	5279	-0.82234	5.50507	2.17E-07	2.13E-06	0.028413	-1	690	491	1422	1002	1235	443	748	534	736	554

ENSMUSG00000026131	chr1	Dst	33908225	33908452	38847	-1.16645	8.383762	2.2E-07	2.15E-06	0.058918	-1	4403	3076	15272	7626	9967	2632	4214	3154	5195	3769
ENSMUSG00000028701	chr4	Lurap1	1.16E+08	1.16E+08	5886	-0.9762	2.58481	2.23E-07	2.18E-06	0.031142	-1	107	88	201	104	143	62	80	64	101	59
ENSMUSG00000041685	chr13	Fcho2	98723407	98725776	5229	-0.9993	4.310071	2.23E-07	2.18E-06	0.040633	-1	260	275	734	447	485	133	264	243	288	277
ENSMUSG00000100235	chr13	Gm28557	67069399	67071528	5037	-1.12415	2.064437	2.25E-07	2.2E-06	0.039471	-1	93	49	130	83	104	32	59	40	55	50
ENSMUSG00000028007	chr3	Snx7	1.18E+08	1.18E+08	2171	1.115994	1.989974	2.26E-07	2.2E-06	0.036109	1	35	33	43	34	48	82	102	101	111	81
ENSMUSG00000005534	chr8	Insr	3150922	3156023	9633	-0.9395	5.986174	2.27E-07	2.21E-06	0.037831	-1	847	688	2390	1383	1783	594	1012	697	948	740
ENSMUSG00000029263	chr5	Pigg	1.08E+08	1.08E+08	4573	-1.11683	2.782694	2.3E-07	2.24E-06	0.044889	-1	84	95	222	173	197	52	95	64	95	87
ENSMUSG00000021690	chr13	Jmy	93430097	93435419	8780	-0.81454	5.128036	2.31E-07	2.25E-06	0.02754	-1	530	429	1274	662	838	354	557	437	517	444
ENSMUSG00000040687	chr2	Madd	91137360	91138401	9086	0.921114	3.045505	2.32E-07	2.25E-06	0.029314	1	69	72	134	72	110	155	199	188	261	170
ENSMUSG00000038095	chr5	Sbno1	1.24E+08	1.24E+08	10197	-0.78689	5.421594	2.32E-07	2.25E-06	0.025986	-1	682	581	1533	698	1022	449	689	517	717	512
ENSMUSG00000000420	chr18	Galnt1	24205344	24205518	5519	-0.75851	6.327217	2.34E-07	2.27E-06	0.024762	-1	1384	1054	2552	1477	1833	895	1288	1040	1360	889
ENSMUSG00000061577	chr8	Gpr114	94923694	94923757	3147	2.146638	-0.14903	2.34E-07	2.27E-06	0.093615	1	5	3	7	1	7	29	16	26	25	17
ENSMUSG00000006344	chr10	Ggt5	75589340	75589882	4736	1.170161	3.117206	2.35E-07	2.27E-06	0.05187	1	85	66	134	47	95	206	220	272	217	150
ENSMUSG00000037012	chr10	Hk1	62268855	62270056	8532	1.043942	3.837013	2.35E-07	2.27E-06	0.043826	1	98	67	218	165	230	246	354	350	402	377
ENSMUSG00000055632	chr2	Hmcn2	31314415	31314676	16073	1.434682	5.859211	2.35E-07	2.27E-06	0.08771	1	220	177	822	655	839	995	1295	1606	2295	1553
ENSMUSG00000072941	chr5	Sod3	52363946	52364052	3570	1.112021	4.48393	2.35E-07	2.27E-06	0.051273	1	205	155	287	209	281	361	426	846	565	526
ENSMUSG00000019947	chr10	Arid5b	68095593	68098669	4494	-1.3863	2.206463	2.36E-07	2.28E-06	0.068898	-1	57	49	163	120	165	23	64	37	70	41
ENSMUSG00000046058	chr7	Eid2	28267881	28269272	1392	1.199962	2.444077	2.37E-07	2.29E-06	0.049133	1	49	30	44	72	60	104	161	109	184	123
ENSMUSG00000047230	chrX	Cldn2	1.4E+08	1.4E+08	3325	2.6877	-0.57673	2.39E-07	2.31E-06	0.11302	1	1	1	0	7	2	11	23	8	28	17
ENSMUSG00000063895	chr14	Nupl1	60219204	60220158	2787	-0.95602	3.734412	2.39E-07	2.31E-06	0.035376	-1	221	170	498	247	323	116	248	134	160	169
ENSMUSG00000015355	chr1	Cd48	1.72E+08	1.72E+08	1189	1.218823	1.615447	2.41E-07	2.31E-06	0.041988	1	21	23	36	26	36	75	85	76	69	64
ENSMUSG00000018899	chr11	Irf1	53770014	53770278	3976	1.110506	4.004747	2.4E-07	2.31E-06	0.049374	1	141	131	173	167	184	288	776	363	352	265
ENSMUSG00000093575	chr16	Gm20695	3884648	3884806	1088	-0.97576	3.243819	2.4E-07	2.31E-06	0.035128	-1	143	106	312	215	263	81	156	105	121	117
ENSMUSG00000022255	chr15	Mtdh	34082694	34083413	12096	-0.84683	6.547376	2.41E-07	2.32E-06	0.031149	-1	1541	1264	3231	1671	2267	816	1643	974	1536	1219
ENSMUSG00000035963	chr10	Odf3l2	79639526	79640379	1248	-3.21167	2.647863	2.43E-07	2.33E-06	0.363809	-1	201	69	295	157	214	58	3	2	22	13
ENSMUSG00000058914	chr15	C1qtnf3	10952332	10952537	2557	1.802752	1.991438	2.48E-07	2.38E-06	0.118888	1	7	14	31	37	54	74	93	99	114	152
ENSMUSG00000048677	chr7	Tpcn2	1.45E+08	1.45E+08	2909	1.392114	1.382885	2.49E-07	2.39E-06	0.057809	1	18	10	34	19	32	67	77	78	63	40
ENSMUSG00000055660	chr17	Mettl4	94727080	94727395	2150	-1.28942	1.908608	2.49E-07	2.39E-06	0.055134	-1	47	64	146	76	99	23	62	27	47	39
ENSMUSG00000028557	chr4	Rnf11	1.09E+08	1.09E+08	4263	-0.8631	7.40171	2.52E-07	2.41E-06	0.032757	-1	3275	2891	4983	2830	3463	1514	2302	2259	2895	2038
ENSMUSG00000030729	chr7	Pgm2l1	1E+08	1E+08	7036	-0.9011	4.397707	2.52E-07	2.41E-06	0.033183	-1	370	312	786	332	464	177	345	320	294	214
ENSMUSG00000037966	chr13	Ninj1	49187485	49187637	1570	0.841285	4.193384	2.54E-07	2.43E-06	0.027925	1	211	150	275	198	207	411	442	436	510	315
ENSMUSG00000024556	chr18	Me2	73770040	73770808	2455	1.096295	2.621624	2.55E-07	2.43E-06	0.04141	1	53	46	65	65	77	151	154	162	179	98
ENSMUSG00000038204	chr5	Asb10	24532697	24533511	2806	-0.87859	6.892021	2.55E-07	2.44E-06	0.033825	-1	2628	1633	3766	2102	2328	1307	1926	1276	2140	1112
ENSMUSG00000093456	chr9	Gm20662	1.08E+08	1.08E+08	1853	-1.14933	2.204183	2.56E-07	2.44E-06	0.04425	-1	83	51	150	118	112	30	76	48	57	49
ENSMUSG00000049470	chr11	Aff4	53350833	53351129	13450	-0.84704	5.877914	2.58E-07	2.46E-06	0.03092	-1	941	716	2214	1037	1451	511	948	758	941	713
ENSMUSG00000037887	chr7	Dusp8	1.42E+08	1.42E+08	4870	-1.00511	4.870768	2.59E-07	2.47E-06	0.042731	-1	463	285	882	809	805	218	422	371	531	274
ENSMUSG00000004364	chr1	Cul3	80264923	80267287	4873	-0.78962	8.053828	2.62E-07	2.49E-06	0.02764	-1	5022	3896	8204	4461	5780	2742	4824	3105	4494	2897
ENSMUSG00000074829	chr9	2010315B03Rik	1.24E+08	1.24E+08	3914	-1.05105	2.855767	2.62E-07	2.49E-06	0.040588	-1	130	134	214	126	171	53	145	73	91	73
ENSMUSG00000034297	chr11	Med13	86267033	86271118	10840	-0.8528	5.281711	2.64E-07	2.51E-06	0.030872	-1	576	482	1514	716	933	353	576	491	693	444
ENSMUSG00000098926	chr1	Mir6904	1.81E+08	1.81E+08	67	-1.27917	1.446731	2.66E-07	2.53E-06	0.047896	-1	53	32	90	58	75	15	48	22	31	27
ENSMUSG00000048489	chr6	8430408G22Rik	1.17E+08	1.17E+08	1317	1.451194	2.413193	2.68E-07	2.55E-06	0.076711	1	48	29	40	53	48	86	263	162	116	85
ENSMUSG00000014547	chr14	Wdfy2	62837690	62838057	2011	-2.16879	0.658173	2.69E-07	2.55E-06	0.141774	-1	13	16	82	37	62	5	11	4	12	16
ENSMUSG00000025907	chr1	Rb1cc1	6206197	6206270	14690	-0.80232	6.37557	2.69E-07	2.55E-06	0.028068	-1	1148	1197	2589	1673	2085	816	1368	1008	1264	1080
ENSMUSG00000070034	chr1	Sp110	85576899	85577345	6781	1.43118	2.076743	2.7E-07	2.56E-06	0.070116	1	24	43	36	21	49	96	143	118	92	90
ENSMUSG00000098269	chr17	Mir8094	35251289	35251405	117	0.756362	4.057125	2.71E-07	2.56E-06	0.021869	1	168	140	281	179	231	311	472	320	521	297
ENSMUSG00000036676	chr10	Tmtc3	1E+08	1E+08	8939	-1.03676	3.023885	2.75E-07	2.6E-06	0.039716	-1	127	111	302	145	219	56	111	101	108	106
ENSMUSG00000097974	chr7	Gm10605	99625936	99629133	3569	1.005222	3.920949	2.78E-07	2.63E-06	0.040104	1	162	147	234	125	121	304	497	296	491	273
ENSMUSG00000038679	chr15	Trps1	50654752	50661736	13380	-0.94741	3.108533	2.79E-07	2.63E-06	0.032963	-1	121	122	303	158	233	66	148	101	133	94
ENSMUSG00000073412	chr17	Lst1	35185095	35185310	415	1.717943	0.282966	2.79E-07	2.63E-06	0.060667	1	7	7	15	3	9	29	45	28	31	20
ENSMUSG00000031993	chr9	Snx19	30427329	30429256	5541	-0.73615	5.434152	2.81E-07	2.65E-06	0.022971	-1	687	537	1354	826	1062	454	777	514	731	514
ENSMUSG00000006498	chr10	Ptbp1	79854427	79854721	4740	0.906014	4.233345	2.85E-07	2.69E-06	0.033641	1	182	107	301	228	254	319	515	573	445	367
ENSMUSG00000022548	chr16	Apod	31296192	31297576	2577	0.930077	6.571071	2.86E-07	2.69E-06	0.038045	1	642	904	1708	904	1195	2122	3116	2204	2337	1616
ENSMUSG00000035078	chr14	Mtmr9	63523616	63524217	2402	-0.98894	2.73482	2.87E-07	2.7E-06	0.033993	-1	107	78	215	139	187	64	111	84	90	57
ENSMUSG00000052889	chr7	Prkcb	1.22E+08	1.22E+08	4749	2.360299	0.677999	2.87E-07	2.7E-06	0.177988	1	5	4	18	5	8	33	39	96	41	13
ENSMUSG00000031157	chrX	Pqbp1	7894519	7894867	1636	0.759868	4.337604	2.89E-07	2.72E-06	0.022769	1	234	170	278	232	277	394	522	439	557	392
ENSMUSG00000034854	chr10	Mfsd12	81357491	81357886	3971	1.303756	3.013462	2.93E-07	2.75E-06	0.065923	1	66	56	107	72	67	129	214	347	172	159
ENSMUSG00000026096	chr1	Osgepl1	53313624	53313858	6147	-0.82537	4.77806	2.93E-07	2.75E-06	0.028567	-1	442	383	735	622	654	266	573	276	447	286
ENSMUSG00000059791	chr17	Nrm	35861318	35861517	1466	1.563322	0.710492	2.98E-07	2.79E-06	0.055901	1	16	8	10	12	14	37	52	44	38	33
ENSMUSG00000000031	chr7	H19	1.43E+08	1.43E+08	2372	1.668449	9.381016	2.98E-07	2.8E-06	0.119997	1	2969	3155	3519	9480	6053	7877	35565	14100	19491	19267
ENSMUSG00000037331	chr11	Larp1	58009064	58009547	6829	-0.81994	7.242487	2.99E-07	2.8E-06	0.0299	-1	2630	2008	5175	2709	3476	1426	2104	1942	2806	1805
ENSMUSG00000093989	chr11	Rnasek	70238124	70238470	885	0.796965	5.930173	3.03E-07	2.84E-06	0.027591	1	709	504	865	717	748	1108	1510	1334	1987	1173
ENSMUSG00000025572	chr11	Tmc6	1.18E+08	1.18E+08	4091	1.144404	2.260094	3.04E-07	2.85E-06	0.043844	1	43	27	44	51	68	102	121	99	165	100
ENSMUSG00000026977	chr2	March7	60209887	60210084	10391	-0.81096	4.550486	3.06E-07	2.86E-06	0.027103	-1	346	366	833	390	522	221	372	291	388	288
ENSMUSG00000024481	chr18	4833403I15Rik	46850039	46850877	3219	-1.96526	0.912004	3.07E-07	2.86E-06	0.120546	-1	21	30	102	36	54	13	8	23	16	5
ENSMUSG00000035275	chr4	Raver2	1.01E+08	1.01E+08	6342	-2.78691	2.310502	3.07E-07	2.86E-06	0.289009	-1	35	24	75	316	259	20	20	35	25	11

ENSMUSG00000028780	chr5	Sema3c	17574281	17574965	7140	-0.89599	5.540423	3.08E-07	2.87E-06	0.034789	-1	671	704	1698	769	1196	430	706	573	578	652
ENSMUSG00000030342	chr6	Cd9	1.25E+08	1.25E+08	2044	0.883677	4.853012	3.09E-07	2.88E-06	0.033113	1	216	219	423	341	459	461	834	786	657	659
ENSMUSG00000002804	chr12	Nudt14	1.13E+08	1.13E+08	793	1.055217	2.673497	3.13E-07	2.92E-06	0.038671	1	68	43	58	72	80	126	206	143	173	126
ENSMUSG00000005886	chr1	Ncoa2	13139105	13142772	15642	-0.9934	4.47068	3.14E-07	2.93E-06	0.041505	-1	304	242	943	439	597	183	279	286	353	253
ENSMUSG00000022090	chr14	Pdlim2	70164218	70164793	4486	1.155346	2.102855	3.16E-07	2.94E-06	0.044	1	38	26	65	42	39	69	112	105	114	121
ENSMUSG00000064147	chr17	Rab44	29135056	29136362	4109	2.164424	-0.13889	3.17E-07	2.94E-06	0.105719	1	5	2	6	0	10	28	33	21	21	13
ENSMUSG00000044244	chr9	Il20rb	1E+08	1E+08	4206	1.075303	2.094038	3.19E-07	2.96E-06	0.036484	1	37	24	72	43	43	91	113	109	117	81
ENSMUSG00000030753	chr7	Prkrir	98703103	98703478	4125	-0.78946	7.505961	3.29E-07	3.05E-06	0.027995	-1	3356	2711	5557	3178	3875	1970	3261	2003	3027	2047
ENSMUSG00000037242	chr4	Clic4	1.35E+08	1.35E+08	6572	0.823752	5.422307	3.32E-07	3.08E-06	0.029395	1	358	323	659	538	649	646	1380	1145	1063	819
ENSMUSG00000040097	chr17	Flywch1	23755423	23755944	2977	-0.6963	4.590367	3.33E-07	3.09E-06	0.019559	-1	390	328	706	455	547	270	388	309	418	294
ENSMUSG00000073664	chr1	Nbeal1	60180599	60180685	28441	-0.91688	4.54214	3.33E-07	3.09E-06	0.0354	-1	329	281	911	423	634	183	347	287	370	294
ENSMUSG00000036894	chr3	Rap2b	61361638	61368430	6793	0.96544	2.905308	3.36E-07	3.11E-06	0.033047	1	62	68	122	69	82	144	184	201	197	156
ENSMUSG00000024228	chr17	Nudt12	58999618	59002291	4401	-1.04322	2.461613	3.36E-07	3.11E-06	0.03708	-1	93	79	174	106	147	42	90	78	60	55
ENSMUSG00000024921	chr19	Smarca2	26605115	26605233	7854	-0.71614	5.63633	3.37E-07	3.11E-06	0.022175	-1	717	703	1459	979	1203	533	831	696	834	561
ENSMUSG00000030605	chr7	Mfge8	79133769	79134546	2125	1.701622	6.547049	3.38E-07	3.12E-06	0.12511	1	530	463	883	756	947	904	3041	5704	2325	1271
ENSMUSG00000038155	chr19	Gstp2	4040285	4040539	770	0.888874	5.184216	3.38E-07	3.12E-06	0.033914	1	412	361	547	335	346	692	899	843	1192	695
ENSMUSG00000036006	chr13	Fam65b	24582189	24582345	11662	-1.45043	2.84416	3.43E-07	3.16E-06	0.083081	-1	165	80	318	74	249	54	69	92	68	59
ENSMUSG00000036825	chr3	Ssx2ip	1.46E+08	1.46E+08	4195	-0.76435	5.284948	3.45E-07	3.18E-06	0.025125	-1	625	492	1033	881	964	422	589	465	764	425
ENSMUSG00000031824	chr8	6430548M08Rik	1.2E+08	1.2E+08	6626	1.095004	4.491541	3.48E-07	3.2E-06	0.051566	1	173	104	356	274	287	668	520	503	689	357
ENSMUSG00000027894	chr3	Slc6a17	1.07E+08	1.07E+08	10283	-1.72506	0.712613	3.49E-07	3.21E-06	0.086283	-1	22	25	57	43	49	8	12	5	30	12
ENSMUSG00000029763	chr6	Exoc4	33249085	33249238	12640	-0.77989	5.836486	3.49E-07	3.21E-06	0.026682	-1	910	671	2031	1102	1328	591	919	717	982	659
ENSMUSG00000004951	chr5	Hspb1	1.36E+08	1.36E+08	1031	0.916575	6.688981	3.5E-07	3.21E-06	0.037585	1	951	629	1291	1346	1601	2107	2308	2253	3561	2089
ENSMUSG00000032968	chr1	Inha	75507077	75507518	1475	1.347839	1.706126	3.5E-07	3.21E-06	0.058169	1	22	26	47	17	31	44	87	77	129	80
ENSMUSG00000026395	chr1	Ptprc	1.38E+08	1.38E+08	18313	1.244634	2.97698	3.57E-07	3.27E-06	0.060936	1	60	55	123	50	90	162	224	304	175	121
ENSMUSG00000037487	chr15	Ubr5	37967328	37968505	9790	-0.82755	6.81846	3.59E-07	3.29E-06	0.030729	-1	1761	1290	4158	2175	2788	1234	1783	1405	1882	1174
ENSMUSG00000001794	chr7	Capns1	30186942	30187533	2397	0.790503	7.69948	3.6E-07	3.3E-06	0.028267	1	2094	1897	3188	2365	2651	3854	4825	4802	6768	3920
ENSMUSG00000028402	chr4	Mpdz	81278500	81279769	12437	-0.94503	6.227253	3.61E-07	3.3E-06	0.0398	-1	1086	828	2479	1702	2191	548	1129	989	1082	956
ENSMUSG00000029561	chr5	Oasl2	1.15E+08	1.15E+08	3879	1.484395	2.455197	3.67E-07	3.36E-06	0.085717	1	41	26	81	30	57	114	203	190	71	129
ENSMUSG00000020521	chr11	Rnft1	86484657	86484799	4719	-0.75136	4.643578	3.68E-07	3.36E-06	0.023452	-1	437	363	795	410	551	263	434	306	389	311
ENSMUSG00000091955	chr7	Gm9844	24862213	24862697	485	2.221431	-0.10576	3.69E-07	3.37E-06	0.102292	1	8	5	7	1	1	20	17	28	31	23
ENSMUSG00000037674	chr9	Rfx7	72532240	72532980	15302	-0.88573	4.43594	3.75E-07	3.43E-06	0.033123	-1	355	255	824	422	495	167	379	307	335	222
ENSMUSG00000050761	chr16	Gp1bb	18620319	18621332	1881	1.609527	1.09742	3.76E-07	3.43E-06	0.075634	1	14	12	16	25	11	50	42	53	63	62
ENSMUSG00000049658	chr13	Bdp1	1E+08	1E+08	11005	-0.94595	3.625174	3.81E-07	3.47E-06	0.035645	-1	159	159	429	256	350	114	218	167	153	119
ENSMUSG00000052760	chr1	A630001G21Rik	85717083	85718368	2709	2.128757	-0.32736	3.83E-07	3.49E-06	0.082291	1	1	5	9	2	3	22	25	21	18	13
ENSMUSG00000063838	chr7	Cdc42ep5	4151260	4151787	1288	1.486356	0.857833	3.84E-07	3.49E-06	0.055386	1	17	10	13	13	17	35	39	53	54	43
ENSMUSG00000042404	chr3	Dennd4b	90265185	90265561	6031	-0.85126	6.966906	3.89E-07	3.54E-06	0.032784	-1	1920	1371	3858	2943	3309	1219	2020	1332	2218	1466
ENSMUSG00000024083	chr17	Pja2	64281005	64283538	4740	-0.78023	7.069171	3.91E-07	3.56E-06	0.027592	-1	2305	1780	4203	2477	3195	1238	2230	1550	2537	1627
ENSMUSG00000021096	chr12	Ppm1a	72761211	72761631	2789	-0.75404	7.501539	3.94E-07	3.58E-06	0.025891	-1	2957	2514	4882	3937	4141	1843	3201	2228	3153	2065
ENSMUSG00000040455	chr4	Usp45	21767156	21767244	6226	-0.89934	3.862164	3.96E-07	3.59E-06	0.032833	-1	224	184	541	274	355	111	249	154	251	176
ENSMUSG00000076617	chr12	Ighm	1.13E+08	1.13E+08	1886	-2.02627	7.339452	3.99E-07	3.63E-06	0.176028	-1	5662	3436	4847	2313	3919	1684	503	1673	1370	347
ENSMUSG00000007033	chr17	Hspa1l	34972703	34972862	2472	-1.16649	4.469571	4.01E-07	3.64E-06	0.059054	-1	283	295	460	714	724	163	298	190	331	272
ENSMUSG00000018654	chr11	Ikzf1	11685003	11685174	5777	1.352542	1.132056	4.02E-07	3.65E-06	0.052559	1	15	10	37	17	17	54	63	51	49	50
ENSMUSG00000032878	chr11	Ccdc85a	28385685	28388948	6971	-1.78847	2.737318	4.03E-07	3.65E-06	0.129205	-1	58	66	158	268	304	26	63	64	62	56
ENSMUSG00000060519	chr1	Tor3a	1.57E+08	1.57E+08	3892	0.836556	3.467063	4.03E-07	3.65E-06	0.026323	1	120	77	162	129	147	213	344	232	266	226
ENSMUSG00000026383	chr1	Epb4.1l5	1.2E+08	1.2E+08	14758	-1.10354	2.250821	4.05E-07	3.67E-06	0.042034	-1	82	79	174	69	121	42	63	63	64	40
ENSMUSG00000030539	chr7	Sema4b	80186841	80186991	5434	1.365846	1.74721	4.09E-07	3.7E-06	0.06395	1	17	18	46	31	37	79	75	119	76	66
ENSMUSG00000041992	chr12	Rapgef5	1.18E+08	1.18E+08	3987	-1.49068	0.618961	4.1E-07	3.7E-06	0.052267	-1	22	19	49	34	52	11	21	14	12	11
ENSMUSG00000027883	chr3	Gpsm2	1.09E+08	1.09E+08	3909	1.243762	2.058897	4.1E-07	3.7E-06	0.054155	1	23	24	56	43	51	64	94	94	142	123
ENSMUSG00000029135	chr5	Fosl2	32136472	32136805	5855	1.143088	4.242763	4.13E-07	3.73E-06	0.056272	1	148	134	316	147	223	370	932	471	377	275
ENSMUSG00000026253	chr1	Chrng	87204657	87204704	4163	3.278287	1.385262	4.14E-07	3.74E-06	0.36874	1	4	0	0	23	9	83	28	83	146	63
ENSMUSG00000095253	chr17	Zfp799	32815455	32821099	5833	-1.02139	2.412083	4.15E-07	3.74E-06	0.036432	-1	84	75	189	108	124	42	92	60	85	44
ENSMUSG00000001865	chr3	Cpa3	20215620	20215992	1517	1.285908	2.710243	4.17E-07	3.75E-06	0.063852	1	58	51	89	41	60	103	258	185	113	170
ENSMUSG00000030082	chr6	Sec61a1	88503601	88505293	6407	0.722164	4.680563	4.16E-07	3.75E-06	0.021792	1	283	193	432	299	363	455	697	597	650	505
ENSMUSG00000029817	chr6	Tra2a	49243921	49244731	1828	0.74676	4.245614	4.17E-07	3.75E-06	0.022416	1	201	167	283	220	258	361	509	458	465	356
ENSMUSG00000030790	chr7	Adm	1.11E+08	1.11E+08	1619	1.279273	2.34321	4.2E-07	3.77E-06	0.059918	1	42	36	74	36	46	147	101	145	148	84
ENSMUSG00000022799	chr16	Arhgap31	38598340	38603815	11141	-0.91163	4.526853	4.21E-07	3.78E-06	0.035552	-1	352	217	748	520	694	214	342	265	363	279
ENSMUSG00000040046	chr7	Tph1	46647130	46647600	3682	-2.07924	1.299421	4.21E-07	3.78E-06	0.151238	-1	79	54	85	18	72	28	16	11	17	9
ENSMUSG00000053931	chr3	Cnn3	1.21E+08	1.21E+08	2003	0.760861	4.83088	4.27E-07	3.83E-06	0.024737	1	225	238	481	352	428	545	818	646	685	556
ENSMUSG00000020571	chr12	Pdia6	17266545	17266651	3745	0.887064	6.212161	4.29E-07	3.85E-06	0.035429	1	873	674	1009	641	912	1599	1873	1963	1891	1360
ENSMUSG00000021255	chr12	Esrrb	86361117	86361538	6047	-3.76907	1.931582	4.32E-07	3.87E-06	0.493212	-1	14	18	47	303	192	2	20	1	15	11
ENSMUSG00000078763	chr11	Slfn1	83116849	83117062	1864	3.127647	-0.47781	4.33E-07	3.87E-06	0.203669	1	4	2	1	0	2	25	39	16	6	10
ENSMUSG00000028459	chr4	Cd72	43446462	43448036	3422	1.968301	0.209589	4.34E-07	3.88E-06	0.100535	1	4	2	9	12	7	31	28	43	21	23
ENSMUSG00000042129	chr6	Rassf4	1.17E+08	1.17E+08	6344	1.105803	2.928796	4.41E-07	3.94E-06	0.048045	1	77	41	136	53	88	168	156	207	223	165
ENSMUSG00000038582	chr5	Pptc7	1.22E+08	1.22E+08	4719	-1.18513	6.745686	4.48E-07	4E-06	0.063675	-1	1433	895	3155	3543	3522	874	1665	1024	1484	1034
ENSMUSG00000031540	chr8	Kat6a	22859535	22859632	9180	-0.91628	4.849564	4.49E-07	4.01E-06	0.036684	-1	434	341	1197	493	740	245	414	395	428	342

ENSMUSG00000002325	chr14	Irf9	55603571	55604243	5386	1.040253	3.27022	4.51E-07	4.02E-06	0.042723	1	86	67	125	91	136	173	401	250	219	150
ENSMUSG00000031242	chrX	2610002M06Rik	1.08E+08	1.08E+08	6337	-0.90573	3.303367	4.51E-07	4.02E-06	0.031786	-1	164	159	344	158	222	82	173	116	145	114
ENSMUSG00000048572	chr19	Tmem252	24674008	24674343	2462	2.261715	0.539646	4.53E-07	4.03E-06	0.156846	1	6	6	8	4	12	35	91	42	21	14
ENSMUSG00000038028	chr6	9630033F20Rik	1.27E+08	1.27E+08	3651	-0.93332	7.381235	4.55E-07	4.05E-06	0.040007	-1	3679	2863	4673	2763	3351	1538	2835	1573	3232	1603
ENSMUSG00000023348	chr5	Trip6	1.37E+08	1.37E+08	1760	1.135078	2.648324	4.55E-07	4.05E-06	0.047268	1	60	58	75	39	72	115	168	193	159	130
ENSMUSG00000002015	chrX	Bcap31	73686178	73686595	1219	0.869411	5.842213	4.61E-07	4.1E-06	0.033921	1	658	561	848	510	620	1078	1460	1574	1585	1053
ENSMUSG00000074457	chr3	S100a16	90537254	90537417	1617	0.802134	5.790358	4.63E-07	4.11E-06	0.028735	1	627	512	758	627	655	1094	1471	1112	1850	961
ENSMUSG00000020954	chr12	Strn3	51608541	51610272	4164	-0.86489	7.521201	4.68E-07	4.15E-06	0.034486	-1	3015	2738	6084	3413	4217	1383	3127	2016	3101	2472
ENSMUSG00000054871	chr9	Tmem158	1.23E+08	1.23E+08	1732	1.825272	1.097416	4.7E-07	4.17E-06	0.105495	1	6	15	15	20	13	24	64	91	70	40
ENSMUSG00000025558	chr14	Dock9	1.22E+08	1.22E+08	8199	-0.89778	4.672773	4.73E-07	4.19E-06	0.035116	-1	434	291	846	527	659	252	360	398	439	194
ENSMUSG00000032661	chr5	Oas3	1.21E+08	1.21E+08	5227	2.829778	-0.13851	4.73E-07	4.19E-06	0.206678	1	5	4	4	0	2	26	11	34	13	35
ENSMUSG00000020440	chr6	Arf5	28423560	28423755	1116	0.864702	5.966837	4.87E-07	4.31E-06	0.033765	1	700	602	704	634	817	1218	1679	1344	2050	1143
ENSMUSG00000004105	chr2	Angptl2	33216069	33216453	6286	0.98038	6.488189	4.88E-07	4.32E-06	0.044016	1	595	602	1396	1091	1322	1300	2421	2036	2440	2627
ENSMUSG00000070348	chr7	Ccnd1	1.45E+08	1.45E+08	3835	0.923252	3.451453	4.88E-07	4.32E-06	0.033572	1	89	82	143	149	138	209	259	279	274	254
ENSMUSG00000033799	chr13	Fam208b	3566036	3566667	8337	-1.01307	3.168388	4.91E-07	4.33E-06	0.04039	-1	126	117	338	185	233	61	154	100	117	113
ENSMUSG00000041779	chr1	Tram2	20996299	21001635	6661	1.117423	2.609043	5.09E-07	4.5E-06	0.047154	1	42	42	94	42	92	104	139	144	190	165
ENSMUSG00000096944	chr4	Gm26722	1.29E+08	1.29E+08	1048	0.84894	4.19626	5.09E-07	4.5E-06	0.030068	1	227	152	231	180	240	353	480	337	608	376
ENSMUSG00000028514	chr4	Usp24	1.06E+08	1.06E+08	12350	-0.89481	6.936602	5.18E-07	4.57E-06	0.037003	-1	1904	1235	4590	2666	3121	1104	1883	1406	2150	1391
ENSMUSG00000027366	chr2	Sppl2a	1.27E+08	1.27E+08	8665	-0.73484	6.185669	5.23E-07	4.61E-06	0.024618	-1	1252	1013	2290	1273	1617	760	1252	943	1186	877
ENSMUSG00000033186	chr14	Mzt1	99034544	99036510	2256	-0.78022	5.456466	5.31E-07	4.68E-06	0.027318	-1	734	709	1324	797	913	389	645	559	761	605
ENSMUSG00000031207	chrX	Msn	96096042	96096243	6327	0.802899	5.752176	5.38E-07	4.73E-06	0.029292	1	464	356	792	716	897	939	1569	1304	1470	1013
ENSMUSG00000047592	chr5	Nxpe5	1.38E+08	1.38E+08	4473	1.928576	0.662848	5.38E-07	4.73E-06	0.108909	1	14	7	15	4	8	39	70	51	28	22
ENSMUSG00000071042	chr17	Rasgrp3	75435905	75436168	4921	-0.86869	5.493469	5.41E-07	4.76E-06	0.034164	-1	776	487	1588	839	1200	464	838	412	779	475
ENSMUSG00000027339	chr2	Rassf2	1.32E+08	1.32E+08	11993	0.984399	3.263377	5.47E-07	4.81E-06	0.038605	1	85	79	179	73	106	239	244	219	245	185
ENSMUSG00000054206	chr10	Gzmm	79689020	79689465	1472	-0.87604	3.076219	5.53E-07	4.86E-06	0.028887	-1	160	112	257	147	209	79	158	90	140	82
ENSMUSG00000057637	chr4	Prdm2	1.43E+08	1.43E+08	7420	-0.78503	5.018954	5.54E-07	4.86E-06	0.027215	-1	428	436	1106	588	867	358	536	401	542	349
ENSMUSG00000026205	chr1	Slc23a3	75125541	75126018	2167	2.429056	1.173879	5.55E-07	4.87E-06	0.19869	1	10	21	13	0	5	60	54	78	83	48
ENSMUSG00000061455	chr4	Stx17	48124915	48124958	5935	-0.75849	4.897072	5.55E-07	4.87E-06	0.025212	-1	447	449	998	512	670	290	468	399	548	336
ENSMUSG00000035049	chr19	Rrp12	41862852	41863312	4319	-0.80571	5.067546	5.61E-07	4.91E-06	0.028861	-1	583	377	1138	641	812	318	468	409	652	401
ENSMUSG00000093402	chr3	Gm18588	68902267	68902758	492	-1.65682	0.962829	5.68E-07	4.97E-06	0.087843	-1	23	31	99	42	43	12	30	8	20	13
ENSMUSG00000090145	chr1	Ugt1a6b	88103252	88103378	2382	1.826274	1.419898	5.72E-07	5E-06	0.117717	1	30	11	22	11	14	61	53	120	65	54
ENSMUSG00000041378	chr16	Cldn5	18776847	18778260	1414	1.077656	3.224581	5.77E-07	5.04E-06	0.046227	1	98	99	113	60	91	178	271	229	310	167
ENSMUSG00000031101	chrX	Sash3	48146436	48146717	2677	1.759094	0.986648	5.84E-07	5.1E-06	0.099976	1	20	7	23	11	7	59	52	65	40	38
ENSMUSG00000021133	chr12	4933426M11Rik	80790532	80790815	5001	-0.7535	6.471954	5.9E-07	5.15E-06	0.026312	-1	1473	1123	2878	1579	2181	903	1644	1135	1385	1029
ENSMUSG00000013663	chr19	Pten	32757497	32758523	11507	-0.76606	4.926057	6.07E-07	5.28E-06	0.025963	-1	465	405	880	635	746	261	437	443	549	378
ENSMUSG00000022489	chr15	Pde1b	1.04E+08	1.04E+08	2954	1.558816	0.698707	6.07E-07	5.28E-06	0.066574	1	15	7	16	8	15	42	51	40	29	38
ENSMUSG00000040466	chr7	Blvrb	27447978	27448196	1414	1.114409	3.132294	6.07E-07	5.28E-06	0.050285	1	108	56	114	72	86	193	223	275	183	182
ENSMUSG00000048410	chr18	Zfp407	84128027	84128353	15167	-1.1717	2.545651	6.07E-07	5.28E-06	0.05278	-1	65	75	237	127	172	48	68	56	86	65
ENSMUSG00000047747	chr8	Rnf150	82863356	82864490	9685	-0.87018	6.228046	6.09E-07	5.3E-06	0.03515	-1	1231	1083	2812	1253	1673	728	1091	762	1506	836
ENSMUSG00000030774	chr7	Pak1	97842935	97843141	3065	1.013236	6.167449	6.13E-07	5.33E-06	0.047471	1	833	735	995	480	661	1582	2046	1576	2202	1377
ENSMUSG00000024654	chr19	Asrgl1	9109868	9113208	4297	-0.72579	6.137033	6.16E-07	5.35E-06	0.024295	-1	1229	1001	2098	1247	1561	781	1273	900	1121	799
ENSMUSG00000004798	chr11	Ulk2	61775649	61777839	5977	-0.75145	7.13935	6.26E-07	5.43E-06	0.026543	-1	2442	1973	4633	2410	3073	1463	2377	1774	2364	1688
ENSMUSG00000022361	chr15	Zhx1	58047003	58048785	6031	-0.72701	5.191266	6.3E-07	5.46E-06	0.023658	-1	576	587	1087	658	771	362	657	506	579	427
ENSMUSG00000032018	chr9	Sc5d	42254177	42255797	2328	-0.7921	4.071168	6.31E-07	5.47E-06	0.026278	-1	309	214	501	292	424	145	282	226	242	227
ENSMUSG00000023284	chr5	Zfp605	1.1E+08	1.1E+08	3497	-1.41106	1.119689	6.32E-07	5.47E-06	0.059626	-1	34	24	71	46	77	18	30	14	18	23
ENSMUSG00000031007	chrX	Atp6ap2	12587801	12587935	2618	0.779366	4.615118	6.34E-07	5.49E-06	0.026298	1	235	246	366	239	351	368	675	581	668	538
ENSMUSG00000053799	chr19	Exoc6	37550418	37550565	2729	-0.75484	5.772937	6.38E-07	5.52E-06	0.026139	-1	840	731	1489	1245	1278	586	1000	595	846	705
ENSMUSG00000026824	chr2	Kcnj3	55435970	55436510	5215	-2.405	-0.33898	6.47E-07	5.59E-06	0.136962	-1	8	19	40	21	8	4	6	2	6	2
ENSMUSG00000034295	chr18	Fhod3	24709445	24709773	5408	-0.95133	5.571664	6.47E-07	5.59E-06	0.041702	-1	648	503	1611	1145	1378	392	751	489	668	664
ENSMUSG00000005881	chr2	Ergic3	1.56E+08	1.56E+08	2121	0.765604	5.617258	6.53E-07	5.63E-06	0.026712	1	587	449	716	499	632	944	1171	1160	1437	915
ENSMUSG00000031609	chr8	Sap30	57482707	57483050	1178	1.17952	2.813215	6.53E-07	5.63E-06	0.055209	1	75	55	113	34	64	149	226	138	249	126
ENSMUSG00000022299	chr15	Slc25a32	39094191	39096108	2945	-1.07041	2.493035	6.6E-07	5.69E-06	0.042978	-1	103	75	221	82	147	44	82	58	89	58
ENSMUSG00000036890	chr2	Gtdc1	44564412	44565534	7928	-0.7387	4.056553	6.6E-07	5.69E-06	0.022731	-1	301	229	439	325	379	161	303	192	315	185
ENSMUSG00000026042	chr1	Col5a2	45374321	45376230	9591	0.890725	5.89916	6.64E-07	5.72E-06	0.036938	1	458	443	1078	530	984	1017	1651	1287	1478	1581
ENSMUSG00000026475	chr1	Rgs16	1.54E+08	1.54E+08	2339	2.108706	0.425736	6.65E-07	5.73E-06	0.134024	1	11	3	8	5	9	40	68	31	33	10
ENSMUSG00000047878	chr15	A4galt	83226726	83228594	2171	1.087601	1.960814	6.69E-07	5.76E-06	0.040387	1	27	23	66	32	52	91	107	91	103	73
ENSMUSG00000079104	chr12	Prps1l3	57230412	57230611	1720	-0.80967	3.763249	6.71E-07	5.77E-06	0.026853	-1	213	213	438	220	324	121	247	178	200	159
ENSMUSG00000038112	chr9	AW551984	39587396	39589125	6082	1.864614	1.221571	6.72E-07	5.77E-06	0.123083	1	4	15	31	13	15	35	99	84	36	60
ENSMUSG00000090100	chr2	Ttbk2	1.21E+08	1.21E+08	11406	-1.03927	3.129691	6.8E-07	5.84E-06	0.04368	-1	104	103	354	182	251	80	129	107	118	86
ENSMUSG00000040850	chr11	Psme4	30771726	30772224	8382	-0.81983	8.28649	6.89E-07	5.91E-06	0.03208	-1	5777	4515	10811	5142	6487	3618	5237	3338	5466	3195
ENSMUSG00000007682	chr12	Dio2	90724554	90729990	5813	1.682536	1.609727	6.9E-07	5.92E-06	0.107782	1	10	8	20	31	45	41	140	67	91	77
ENSMUSG00000007836	chr13	Hnrnpa0	58125879	58128556	2678	0.712659	5.153787	6.95E-07	5.95E-06	0.02275	1	351	303	609	411	516	582	838	815	1075	732
ENSMUSG00000040883	chr9	Tmem205	21921010	21921349	862	0.970978	3.695787	6.98E-07	5.97E-06	0.03928	1	144	121	173	127	115	245	323	376	319	271
ENSMUSG00000054545	chr1	Ugt1a6a	88134809	88134935	4312	1.807089	1.452897	6.98E-07	5.98E-06	0.118447	1	32	10	21	12	16	58	56	125	69	54
ENSMUSG00000033790	chr7	Tubgcp5	55794148	55794340	3681	-0.83139	3.151146	7.01E-07	5.99E-06	0.026124	-1	164	122	268	172	190	81	145	108	131	115

ENSMUSG00000022174	chr14	Dad1	54235479	54235713	3916	0.72929	5.342383	7.03E-07	6.01E-06	0.024039	1	472	344	585	475	558	745	990	873	1265	762
ENSMUSG00000024835	chr19	Coro1b	4148619	4148722	2372	0.811858	4.582842	7.08E-07	6.04E-06	0.029065	1	261	191	357	263	322	475	613	695	569	402
ENSMUSG00000029571	chr6	Tmem106b	13069759	13069795	6931	-0.76616	5.722456	7.12E-07	6.08E-06	0.027117	-1	776	592	1623	1154	1389	539	861	670	845	663
ENSMUSG00000056501	chr2	Cebpb	1.68E+08	1.68E+08	1504	0.974441	4.221966	7.16E-07	6.11E-06	0.041804	1	113	180	206	230	264	322	694	426	516	333
ENSMUSG00000028671	chr4	Gale	1.36E+08	1.36E+08	2370	2.319235	0.931295	7.26E-07	6.18E-06	0.187437	1	14	8	9	6	9	59	26	107	44	24
ENSMUSG00000040327	chr17	Cul9	46500572	46501071	12198	-0.71486	4.344639	7.29E-07	6.21E-06	0.021728	-1	295	285	591	420	464	226	349	237	351	246
ENSMUSG00000006398	chr4	Cdc20	1.18E+08	1.18E+08	1868	2.378382	-0.29628	7.34E-07	6.25E-06	0.120615	1	7	3	1	3	3	25	13	24	18	22
ENSMUSG00000026950	chr2	Neb	52136647	52137431	26369	-1.02031	11.83278	7.43E-07	6.32E-06	0.049867	-1	53967	38539	164827	71831	93153	26488	54205	40187	61424	42003
ENSMUSG00000033355	chr16	Rtp4	23609919	23610149	1573	1.522271	2.100286	7.49E-07	6.37E-06	0.089722	1	31	27	33	38	40	96	191	132	54	86
ENSMUSG00000027104	chr2	Atf2	73816509	73819148	8187	-0.772	3.996885	7.53E-07	6.4E-06	0.025075	-1	243	236	499	270	398	140	274	213	252	202
ENSMUSG00000029570	chr5	Lfng	1.41E+08	1.41E+08	2282	1.209	2.502547	7.56E-07	6.42E-06	0.05672	1	60	39	66	39	63	159	122	128	198	92
ENSMUSG00000042436	chr11	Mfap4	61485431	61485485	1922	1.541142	3.496587	7.57E-07	6.43E-06	0.104974	1	26	65	131	107	148	204	290	431	207	338
ENSMUSG00000040616	chr4	Tmem51	1.42E+08	1.42E+08	1875	1.249537	1.44271	7.7E-07	6.53E-06	0.048646	1	24	17	35	19	29	75	82	61	68	44
ENSMUSG00000050002	chr13	Idnk	58157649	58157736	1511	1.1592	2.034009	7.71E-07	6.54E-06	0.047154	1	35	22	39	55	45	89	121	105	101	81
ENSMUSG00000003402	chr9	Prkcsh	22003035	22003088	2013	0.772734	4.827843	7.83E-07	6.63E-06	0.026905	1	237	222	461	339	456	472	651	694	850	595
ENSMUSG00000060147	chr13	Serpinb6a	33917918	33918442	5409	1.259167	8.665337	7.88E-07	6.67E-06	0.07527	1	4496	3530	4606	2679	3181	10616	10218	6644	19014	6736
ENSMUSG00000098598	chr15	Pou6f1	1.01E+08	1.01E+08	906	-1.34001	1.517117	7.88E-07	6.67E-06	0.061817	-1	53	34	85	60	96	9	38	32	38	29
ENSMUSG00000063047	chr7	Zfp780b	27962708	27964869	3004	-1.86375	0.392568	7.89E-07	6.67E-06	0.103931	-1	16	10	57	38	41	4	19	8	8	9
ENSMUSG00000067203	chr17	H2-K2	33974831	33974877	1049	1.345631	1.29192	8.01E-07	6.76E-06	0.055436	1	25	17	24	13	25	62	69	64	55	49
ENSMUSG00000064345	chrMT	mt-Nd2	3914	4951	1038	-1.24776	12.83452	8.05E-07	6.8E-06	0.074253	-1	81183	79474	178325	225632	294740	46883	92564	74980	118911	71215
ENSMUSG00000078861	chr2	Zfp931	1.78E+08	1.78E+08	2299	-1.15381	2.030171	8.06E-07	6.8E-06	0.048075	-1	77	62	121	87	100	35	75	23	53	44
ENSMUSG00000093701	chr16	Gm21970	91391721	91391878	884	0.931669	2.972281	8.08E-07	6.81E-06	0.033442	1	73	58	99	79	120	154	216	218	198	137
ENSMUSG00000052316	chr16	Lrrc15	30269302	30274522	5310	3.077103	-0.64027	8.11E-07	6.83E-06	0.182645	1	1	3	0	1	3	2	24	21	13	24
ENSMUSG00000090272	chr1	Mndal	1.74E+08	1.74E+08	3443	1.106639	2.75961	8.19E-07	6.89E-06	0.049159	1	51	46	86	70	89	161	219	202	138	102
ENSMUSG00000025935	chr1	Tram1	13564698	13566396	3162	0.709622	4.321439	8.23E-07	6.93E-06	0.021491	1	186	180	338	225	297	336	499	478	547	396
ENSMUSG00000022401	chr15	Xpnpep3	81400138	81400287	6117	-1.0585	2.657065	8.29E-07	6.97E-06	0.043384	-1	109	77	215	136	159	51	100	58	69	89
ENSMUSG00000019338	chr3	Zfp687	95006590	95008213	5952	-0.82322	3.930613	8.31E-07	6.99E-06	0.028858	-1	249	212	536	272	333	193	205	169	269	162
ENSMUSG00000000794	chr3	Kcnn3	89520164	89521404	7391	1.620421	1.37969	8.34E-07	7E-06	0.094986	1	8	9	21	33	28	45	63	54	86	89
ENSMUSG00000030681	chr7	Mvp	1.27E+08	1.27E+08	2902	0.75686	5.421827	8.55E-07	7.18E-06	0.026549	1	444	353	669	529	570	813	962	892	1492	786
ENSMUSG00000020116	chr11	Pno1	17203198	17204001	1717	-0.70819	5.187255	8.57E-07	7.19E-06	0.023004	-1	629	577	941	645	822	370	697	474	603	413
ENSMUSG00000047454	chr12	Gphn	78226655	78226841	3397	-0.71481	5.353773	8.66E-07	7.26E-06	0.023567	-1	642	565	1319	719	937	408	721	516	661	535
ENSMUSG00000020640	chr12	Itsn2	4593008	4593232	5987	-0.95807	3.459032	8.7E-07	7.29E-06	0.038648	-1	145	122	404	234	315	104	172	144	138	119
ENSMUSG00000032300	chr9	1700017B05Rik	57252322	57254329	4934	1.051956	2.166066	8.74E-07	7.32E-06	0.038662	1	31	28	69	56	48	83	119	124	120	90
ENSMUSG00000085614	chr4	1700123M08Rik	11966565	11966683	1260	-0.88221	2.883948	8.79E-07	7.36E-06	0.029859	-1	117	110	217	148	179	62	137	83	127	71
ENSMUSG00000028367	chr4	Txn1	57943373	57943967	1051	1.040829	6.091459	8.82E-07	7.37E-06	0.051451	1	749	745	754	549	598	1425	2057	1799	2047	1108
ENSMUSG00000047497	chr15	Adamts12	11064790	11065157	6234	-1.86022	1.152277	8.82E-07	7.37E-06	0.125149	-1	29	22	134	32	76	7	15	24	22	15
ENSMUSG00000026981	chr2	Il1rn	24336853	24336992	5535	2.399044	0.701079	8.85E-07	7.39E-06	0.210731	1	1	0	12	8	20	34	88	41	24	42
ENSMUSG00000062785	chr7	Kcnc3	44590664	44591758	5344	-1.24954	2.516241	8.87E-07	7.4E-06	0.063187	-1	100	50	255	120	154	37	72	80	65	51
ENSMUSG00000050910	chr11	Cdr2l	1.15E+08	1.15E+08	3700	1.136567	1.500013	8.95E-07	7.46E-06	0.036704	1	20	22	33	23	38	49	96	63	81	54
ENSMUSG00000042473	chrX	Tbc1d8b	1.4E+08	1.4E+08	5211	-1.18262	2.430024	9E-07	7.5E-06	0.054859	-1	81	80	212	90	153	43	80	48	49	73
ENSMUSG00000023973	chr17	Cnpy3	46735705	46736908	2659	0.799699	3.731812	9.02E-07	7.52E-06	0.026511	1	152	98	205	144	178	240	311	349	378	247
ENSMUSG00000036707	chr1	Cab39	85793441	85793821	7077	-0.73565	7.747692	9.08E-07	7.56E-06	0.026361	-1	3631	3206	5961	4082	4819	2225	3835	2343	3957	2597
ENSMUSG00000025616	chr16	Usp16	87454703	87455102	9454	-0.73239	5.335785	9.1E-07	7.57E-06	0.024937	-1	758	644	1181	669	789	445	689	526	676	450
ENSMUSG00000006301	chr1	Tmbim1	74288247	74289518	12659	0.719279	6.266066	9.22E-07	7.66E-06	0.024683	1	856	658	1313	842	1033	1485	1981	1562	2279	1459
ENSMUSG00000002458	chr2	Rgs19	1.82E+08	1.82E+08	2230	1.171192	1.556559	9.28E-07	7.71E-06	0.043729	1	24	16	36	24	41	60	84	85	66	58
ENSMUSG00000085772	chr11	D630024D03Rik	31790113	31790425	1567	1.77962	-0.05771	9.28E-07	7.71E-06	0.060526	1	6	6	11	2	5	14	31	23	30	21
ENSMUSG00000029616	chr5	Erp29	1.21E+08	1.21E+08	9060	0.754303	5.166354	9.31E-07	7.72E-06	0.026219	1	387	315	510	438	476	796	868	814	948	639
ENSMUSG00000021902	chr14	Phf7	31237696	31238153	1984	-1.07466	3.011416	9.32E-07	7.73E-06	0.048538	-1	139	184	237	153	136	75	111	73	123	90
ENSMUSG00000046111	chr9	Cep295	15316915	15317113	11641	-1.05829	2.793135	9.36E-07	7.76E-06	0.04491	-1	86	92	270	139	193	75	112	78	86	56
ENSMUSG00000052688	chr1	5430435G22Rik	1.32E+08	1.32E+08	4624	1.013903	3.052361	9.37E-07	7.76E-06	0.042775	1	57	52	134	77	131	149	215	256	195	174
ENSMUSG00000058569	chr13	Tmed9	55593135	55593357	1420	0.758615	6.266445	9.38E-07	7.77E-06	0.027558	1	806	598	1067	988	1141	1614	2023	1673	2016	1454
ENSMUSG00000085457	chr13	1110046J04Rik	33935567	33938342	3487	1.727812	1.344741	9.4E-07	7.78E-06	0.105233	1	21	17	21	11	17	77	78	38	119	31
ENSMUSG00000095306	chr8	Gm21807	68099492	68099560	897	-2.27954	-0.20855	9.46E-07	7.82E-06	0.13038	-1	11	6	51	21	20	6	5	1	7	4
ENSMUSG00000028961	chr4	Pgd	1.49E+08	1.49E+08	6447	1.067888	4.64379	9.47E-07	7.83E-06	0.052936	1	271	175	310	253	271	492	539	963	663	386
ENSMUSG00000021302	chr13	Ggps1	14052449	14054455	2367	-0.96702	2.827931	9.5E-07	7.85E-06	0.037167	-1	131	112	239	126	148	60	142	77	90	72
ENSMUSG00000020484	chr11	Xbp1	5520659	5521200	3248	0.843348	6.401394	9.57E-07	7.9E-06	0.03424	1	1022	692	1398	834	905	1494	2774	2202	2121	1426
ENSMUSG00000055204	chr5	Ankrd17	90227190	90229341	10053	-0.86647	5.493414	9.64E-07	7.95E-06	0.035602	-1	570	528	1682	977	1166	373	713	562	779	528
ENSMUSG00000032076	chr9	Cadm1	47530173	47530505	9684	-1.34305	3.183832	9.69E-07	7.99E-06	0.079265	-1	223	201	355	93	160	100	99	92	95	72
ENSMUSG00000021256	chr12	Vash1	86678700	86680326	2599	-1.54241	0.922016	9.79E-07	8.07E-06	0.074012	-1	18	27	72	50	57	11	16	23	17	16
ENSMUSG00000030465	chr8	Psd3	67689082	67697187	15304	-0.87795	4.547439	9.82E-07	8.08E-06	0.035417	-1	456	267	852	358	596	244	361	258	456	211
ENSMUSG00000034006	chr18	Pqlc1	80253292	80253393	6100	0.951341	3.869003	9.88E-07	8.13E-06	0.040099	1	111	81	177	228	208	271	429	367	403	282
ENSMUSG00000021200	chr12	Asb2	1.03E+08	1.03E+08	3542	-0.80065	8.862585	9.98E-07	8.2E-06	0.031586	-1	10007	6608	14097	7712	9324	5211	7111	5574	7531	5562
ENSMUSG00000040351	chr5	Ankib1	3690000	3693496	6610	-0.83479	3.720416	1.01E-06	8.27E-06	0.029608	-1	190	169	469	255	319	116	202	196	204	147
ENSMUSG00000078920	chr11	Ifi47	49076587	49076662	2317	1.683126	1.947742	1.01E-06	8.27E-06	0.112044	1	32	23	26	23	34	90	205	106	46	73
ENSMUSG00000073490	chr1	AI607873	1.74E+08	1.74E+08	3481	1.304498	3.35497	1.02E-06	8.33E-06	0.076413	1	79	50	178	62	124	270	397	305	159	166

ENSMUSG00000054277	chr15	Arfgap3	83299740	83300702	2618	0.846755	3.25984	1.03E-06	8.46E-06	0.028859	1	104	74	166	82	125	182	233	201	293	201
ENSMUSG00000087370	chr13	Tmem170b	41606216	41606312	7160	-0.73795	4.995417	1.03E-06	8.46E-06	0.02512	-1	564	370	1023	589	750	301	519	445	508	414
ENSMUSG00000074165	chr7	Zfp788	41633203	41633694	4350	-0.9225	2.937936	1.04E-06	8.54E-06	0.034113	-1	135	133	237	129	167	58	121	83	133	91
ENSMUSG00000026162	chr1	Nhej1	74967139	74967768	1118	0.984905	2.361396	1.05E-06	8.59E-06	0.034127	1	50	40	59	62	56	105	140	119	149	95
ENSMUSG00000042228	chr4	Lyn	3678115	3678364	4073	0.962114	3.055191	1.06E-06	8.64E-06	0.037681	1	58	66	97	97	130	163	235	220	195	168
ENSMUSG00000052949	chr11	Rnf157	1.16E+08	1.16E+08	9537	-0.85628	4.560056	1.06E-06	8.66E-06	0.033783	-1	514	383	648	386	477	267	372	359	298	224
ENSMUSG00000000275	chr11	Trim25	88999376	89000082	5754	0.809683	3.919574	1.09E-06	8.9E-06	0.028703	1	142	112	248	153	241	287	457	402	339	261
ENSMUSG00000021786	chr14	Oxsm	16238656	16241070	4082	-0.81601	3.985127	1.09E-06	8.92E-06	0.02944	-1	249	216	412	315	448	126	311	199	228	195
ENSMUSG00000003873	chr7	Bax	45461695	45461966	869	0.836563	3.761335	1.11E-06	9.05E-06	0.02965	1	168	118	178	144	153	270	338	332	359	263
ENSMUSG00000031887	chr8	Tradd	1.05E+08	1.05E+08	1866	1.195581	1.874818	1.11E-06	9.06E-06	0.049507	1	28	33	32	34	42	90	84	85	103	80
ENSMUSG00000029434	chr5	Vps33a	1.24E+08	1.24E+08	4107	-0.68887	5.702071	1.11E-06	9.08E-06	0.022631	-1	791	718	1617	977	1172	555	960	671	936	570
ENSMUSG00000033538	chr9	Casp4	5308828	5308914	3710	1.730469	1.242099	1.13E-06	9.2E-06	0.110815	1	9	10	23	18	24	45	148	44	60	29
ENSMUSG00000070498	chr5	Tmem132b	1.26E+08	1.26E+08	8238	-2.95179	2.429274	1.14E-06	9.26E-06	0.356418	-1	189	72	310	46	180	39	5	5	56	5
ENSMUSG00000000902	chr10	Smarcb1	75896769	75897088	7930	0.742224	4.139317	1.15E-06	9.34E-06	0.023874	1	188	164	270	191	236	322	419	354	569	347
ENSMUSG00000051790	chr11	Nlgn2	69823122	69826079	5785	0.907232	2.745725	1.15E-06	9.36E-06	0.031438	1	60	51	101	74	85	111	169	163	173	163
ENSMUSG00000027408	chr2	Cpxm1	1.3E+08	1.3E+08	2432	1.112371	4.046836	1.17E-06	9.5E-06	0.056966	1	133	155	283	98	173	426	311	465	442	344
ENSMUSG00000032523	chr9	Hhatl	1.22E+08	1.22E+08	1911	0.774238	7.084482	1.17E-06	9.5E-06	0.029646	1	1358	868	2385	1678	2002	2331	3380	2954	4140	2896
ENSMUSG00000092470	chr16	Gm20518	17835277	17835539	3811	-0.86221	3.488771	1.17E-06	9.52E-06	0.031246	-1	175	119	356	232	319	115	167	137	162	139
ENSMUSG00000030351	chr6	Tspan11	1.28E+08	1.28E+08	4380	1.297671	1.256593	1.18E-06	9.53E-06	0.054011	1	9	13	25	32	27	46	66	56	70	55
ENSMUSG00000040524	chr9	Zfp609	65692391	65695694	8268	-0.96361	4.238394	1.18E-06	9.56E-06	0.042901	-1	262	183	754	399	533	164	235	261	301	205
ENSMUSG00000021061	chr12	Sptb	76580488	76583392	12147	-0.84999	7.886544	1.2E-06	9.7E-06	0.035953	-1	3256	2897	8907	4945	5680	2173	3455	2678	4318	2956
ENSMUSG00000046722	chr3	Cdc42se1	95228732	95228865	3258	0.685093	4.69104	1.2E-06	9.73E-06	0.021126	1	288	237	414	290	355	461	716	526	744	475
ENSMUSG00000038517	chr11	Tbkbp1	97136171	97137675	3975	-1.05645	2.905802	1.21E-06	9.77E-06	0.046856	-1	166	134	235	116	149	84	82	80	133	62
ENSMUSG00000038342	chr5	Mlxip	1.23E+08	1.23E+08	8206	-0.84998	6.55293	1.21E-06	9.8E-06	0.035588	-1	1503	1027	3696	1615	2440	871	1569	1200	1494	1052
ENSMUSG00000018924	chr11	Alox15	70344152	70344722	2454	2.902816	0.277045	1.21E-06	9.82E-06	0.252322	1	15	1	0	1	1	25	43	27	60	22
ENSMUSG00000040940	chr7	Arhgef1	24902912	24903128	7495	0.724026	5.186593	1.22E-06	9.83E-06	0.024759	1	431	264	608	386	546	687	934	877	985	650
ENSMUSG00000027239	chr2	Mdk	91929805	91930115	1324	1.464439	1.006482	1.22E-06	9.86E-06	0.065594	1	13	19	21	11	15	45	47	55	45	54
ENSMUSG00000042851	chr2	Zc3h6	1.29E+08	1.29E+08	5668	-1.4866	2.346886	1.22E-06	9.86E-06	0.094959	-1	63	102	222	93	133	13	80	39	60	56
ENSMUSG00000020821	chr11	Kif1c	70700548	70700709	7276	-0.7386	10.15828	1.22E-06	9.86E-06	0.027448	-1	18467	15528	31963	23426	27136	12098	17824	13242	21924	13934
ENSMUSG00000022853	chr16	Ehhadh	21761287	21763336	3018	-0.9387	2.804398	1.22E-06	9.86E-06	0.035018	-1	132	88	220	148	154	49	105	99	103	80
ENSMUSG00000004846	chr5	Plod3	1.37E+08	1.37E+08	4519	0.790009	4.7475	1.23E-06	9.88E-06	0.029136	1	255	197	418	360	364	450	580	698	756	591
ENSMUSG00000049339	chr1	Fam134a	75142778	75143128	2999	0.778071	4.215296	1.25E-06	1E-05	0.026907	1	205	174	261	190	252	337	440	497	527	327
ENSMUSG00000040663	chr19	Clcf1	4214238	4214500	3713	1.7697	0.141961	1.25E-06	1.01E-05	0.07005	1	7	6	10	5	7	19	39	27	44	12
ENSMUSG00000015143	chr12	Actn1	80167542	80168480	3805	0.956262	3.464385	1.26E-06	1.01E-05	0.039898	1	73	82	153	135	163	151	289	315	324	245
ENSMUSG00000016757	chr15	Ttll12	83575119	83577048	4010	0.786887	3.812482	1.26E-06	1.01E-05	0.026886	1	162	84	231	150	213	272	379	299	378	282
ENSMUSG00000042447	chr6	Mios	8209222	8209411	6552	-0.71284	4.077213	1.26E-06	1.01E-05	0.02224	-1	296	233	448	320	392	155	310	202	302	212
ENSMUSG00000037486	chr12	Asxl2	3426857	3427212	14574	-0.93004	3.800786	1.26E-06	1.01E-05	0.03872	-1	200	155	593	265	339	148	223	141	221	145
ENSMUSG00000038774	chr10	Ascc3	50592669	50592897	7477	-0.79358	4.085297	1.29E-06	1.04E-05	0.028121	-1	282	194	589	291	439	181	312	195	248	200
ENSMUSG00000021112	chr12	Mpp5	78748947	78749106	5512	-0.69753	4.868568	1.3E-06	1.04E-05	0.022581	-1	427	384	896	555	715	307	501	361	527	355
ENSMUSG00000100131	chr1	Gm28439	24611535	24612410	876	-1.4104	2.668244	1.3E-06	1.04E-05	0.087443	-1	50	79	188	182	269	40	86	55	85	53
ENSMUSG00000022789	chr16	Dnm1l	16312235	16314043	4107	-0.7518	5.993152	1.3E-06	1.04E-05	0.027664	-1	981	800	1718	1347	1706	642	1124	713	1066	825
ENSMUSG00000038418	chr18	Egr1	34859823	34861786	4484	1.95579	4.261227	1.3E-06	1.04E-05	0.177599	1	63	83	108	53	347	345	1227	229	643	463
ENSMUSG00000030659	chr7	Nucb2	1.17E+08	1.17E+08	2301	0.912075	2.545965	1.31E-06	1.05E-05	0.030937	1	47	46	85	61	83	121	157	140	145	114
ENSMUSG00000078779	chr7	Zfp59	27842855	27842887	1962	-1.85469	0.341399	1.31E-06	1.05E-05	0.105505	-1	25	23	53	22	28	4	22	3	6	12
ENSMUSG00000017760	chr2	Ctsa	1.65E+08	1.65E+08	4715	0.703691	6.515866	1.32E-06	1.05E-05	0.024453	1	1016	769	1510	1074	1253	1657	2390	2208	2403	1694
ENSMUSG00000031502	chr8	Col4a1	11198423	11199882	6818	0.815454	7.440171	1.33E-06	1.06E-05	0.033331	1	1625	1051	2745	2005	3037	3134	4569	3759	5046	3749
ENSMUSG00000020620	chr11	Abca8b	1.1E+08	1.1E+08	7423	-0.84733	5.055727	1.33E-06	1.06E-05	0.034394	-1	439	429	1228	607	898	325	513	341	534	456
ENSMUSG00000026222	chr1	Sp100	85649988	85650127	7556	0.893668	3.755424	1.34E-06	1.07E-05	0.035618	1	145	97	210	125	185	273	395	371	252	275
ENSMUSG00000022812	chr16	Gsk3b	38089001	38090613	9831	-0.7914	5.995611	1.34E-06	1.07E-05	0.030802	-1	1102	799	2292	1066	1486	591	969	792	1171	787
ENSMUSG00000068284	chr16	Gm608	44173246	44173510	13050	-0.8328	6.087108	1.36E-06	1.09E-05	0.03426	-1	1027	826	2639	1277	1576	689	1047	730	1288	769
ENSMUSG00000087042	chr11	Gm11611	97519612	97520173	1326	-2.03202	0.022379	1.37E-06	1.09E-05	0.109498	-1	30	15	36	18	21	5	3	15	4	5
ENSMUSG00000046157	chr12	Tmem229b	78961795	78965176	4732	1.18306	2.468487	1.37E-06	1.09E-05	0.058389	1	36	26	76	74	60	100	163	180	113	122
ENSMUSG00000030223	chr6	Ptpro	1.37E+08	1.37E+08	6744	1.37361	1.053599	1.38E-06	1.09E-05	0.058403	1	13	14	31	16	14	30	52	64	55	54
ENSMUSG00000026775	chr2	Yme1l1	23156369	23156731	8009	-0.70972	5.80947	1.38E-06	1.1E-05	0.024615	-1	837	880	1592	1038	1289	527	1015	744	914	721
ENSMUSG00000047407	chr17	Tgif1	70844205	70845272	5625	1.177838	2.489108	1.39E-06	1.1E-05	0.055851	1	52	54	80	42	37	102	204	152	133	108
ENSMUSG00000034761	chr12	Map4k5	69803750	69805351	8614	-0.7332	4.913159	1.41E-06	1.12E-05	0.025379	-1	446	371	921	562	819	278	506	394	523	383
ENSMUSG00000022816	chr16	Fstl1	37776873	37777152	4914	0.738019	6.479152	1.42E-06	1.13E-05	0.027139	1	805	725	1626	1008	1341	1652	2261	2125	2140	1904
ENSMUSG00000023942	chr17	Slc29a1	45585200	45585782	4008	0.714783	5.44439	1.42E-06	1.13E-05	0.02469	1	501	326	709	508	629	843	1001	1039	1206	816
ENSMUSG00000034664	chr11	Itga2b	1.02E+08	1.02E+08	5454	1.512385	0.631428	1.42E-06	1.13E-05	0.059493	1	11	13	13	10	11	42	35	40	43	29
ENSMUSG00000038014	chr13	Fam120a	48879219	48881095	5105	-0.76671	6.902366	1.42E-06	1.13E-05	0.029468	-1	1923	1423	3632	2567	2902	1092	1747	1589	2257	1484
ENSMUSG00000025612	chr16	Bach1	87698945	87699056	6179	-0.75369	4.585904	1.44E-06	1.14E-05	0.026402	-1	394	312	830	404	557	230	344	351	415	293
ENSMUSG00000025241	chr9	Fyco1	1.24E+08	1.24E+08	8653	-0.92075	8.061059	1.44E-06	1.14E-05	0.042802	-1	3342	2744	9375	6533	7722	2483	4365	2943	4428	2898
ENSMUSG00000028931	chr4	Kcnab2	1.52E+08	1.52E+08	5578	1.398337	1.039716	1.48E-06	1.17E-05	0.063813	1	9	10	27	22	19	44	38	56	57	55
ENSMUSG00000021466	chr13	Ptch1	63508328	63512075	8745	-0.85805	3.567466	1.48E-06	1.17E-05	0.032179	-1	180	146	380	230	326	88	190	154	185	155
ENSMUSG00000029552	chr6	Tes	17065149	17065313	3199	1.321777	1.181635	1.5E-06	1.19E-05	0.054632	1	20	13	19	22	23	58	81	46	61	34

ENSMUSG00000080850	chr4	Gm12439	48675156	48675520	365	0.86936	4.905628	1.5E-06	1.19E-05	0.036353	1	375	249	462	258	344	714	857	522	916	524
ENSMUSG00000044268	chr10	Gm4895	22153280	22154416	1137	-1.62148	0.195568	1.51E-06	1.19E-05	0.062915	-1	19	21	35	19	35	12	15	6	10	4
ENSMUSG00000030538	chr7	Cib1	80227156	80227386	2052	1.148117	2.600266	1.52E-06	1.2E-05	0.053609	1	76	51	56	41	62	117	172	172	176	111
ENSMUSG00000032942	chr7	Ucp3	1E+08	1E+08	3135	-1.12969	6.396927	1.52E-06	1.2E-05	0.063762	-1	1868	1701	1391	1680	2207	849	1531	1041	773	652
ENSMUSG00000040118	chr5	Cacna2d1	15934691	15935108	7514	-0.81036	8.706135	1.53E-06	1.2E-05	0.033482	-1	6583	5780	15639	6856	9615	4053	6357	5022	6803	5521
ENSMUSG00000022194	chr14	Pabpn1	54892500	54892738	3035	0.732479	4.928426	1.53E-06	1.21E-05	0.025374	1	379	274	477	313	375	603	825	691	789	547
ENSMUSG00000026610	chr1	Esrrg	1.88E+08	1.88E+08	6208	-2.32002	3.265043	1.54E-06	1.21E-05	0.244117	-1	106	63	154	523	468	25	76	22	137	50
ENSMUSG00000037321	chr17	Tap1	34187553	34188405	5476	1.189447	2.673848	1.54E-06	1.21E-05	0.060375	1	66	41	82	37	83	160	190	189	117	121
ENSMUSG00000089797	chr8	Gm16118	1.15E+08	1.15E+08	680	-1.61686	0.073295	1.55E-06	1.21E-05	0.059313	-1	21	19	21	25	29	7	7	9	14	6
ENSMUSG00000000600	chr5	Krit1	3803165	3803483	6151	-0.72102	3.936824	1.55E-06	1.22E-05	0.022806	-1	275	199	434	274	365	158	284	170	258	192
ENSMUSG00000034855	chr5	Cxcl10	92346638	92347385	1520	1.986539	0.809118	1.56E-06	1.22E-05	0.141842	1	8	4	5	14	21	34	96	35	28	45
ENSMUSG00000084145	chr11	Gm12263	59474284	59475765	1482	-1.69156	0.026673	1.56E-06	1.22E-05	0.06335	-1	14	11	41	26	25	8	9	7	7	8
ENSMUSG00000085882	chr11	2610507I01Rik	59199836	59200302	1360	-1.43745	1.365624	1.57E-06	1.23E-05	0.076816	-1	29	49	78	56	85	18	32	38	23	12
ENSMUSG00000098652	chr16	Gm27671	14128566	14128631	66	-2.00343	-0.22205	1.58E-06	1.23E-05	0.093382	-1	16	14	43	13	15	5	6	2	6	8
ENSMUSG00000020130	chr10	Tbc1d15	1.15E+08	1.15E+08	3773	-0.72714	4.797541	1.59E-06	1.24E-05	0.025055	-1	437	400	876	491	633	253	488	346	450	385
ENSMUSG00000039000	chr5	Ube3c	29569242	29569580	5033	-0.71767	5.927016	1.6E-06	1.25E-05	0.02553	-1	982	746	1994	1116	1442	649	989	760	1061	761
ENSMUSG00000066735	chr5	Vkorc1l1	1.3E+08	1.3E+08	2972	-0.76123	4.276956	1.63E-06	1.27E-05	0.026642	-1	358	250	641	285	474	208	329	256	286	231
ENSMUSG00000036611	chr9	Eepd1	25481547	25481896	2935	-0.78147	7.140459	1.63E-06	1.27E-05	0.031059	-1	2327	2405	4348	2260	3079	1497	2609	1505	2311	1667
ENSMUSG00000060550	chr17	H2-Q7	35439155	35439284	4265	1.40575	2.463431	1.63E-06	1.27E-05	0.084313	1	49	45	46	34	56	132	134	226	107	96
ENSMUSG00000024927	chr19	Rela	5637483	5637841	2716	0.678279	4.540866	1.64E-06	1.28E-05	0.021218	1	242	180	396	270	370	430	582	519	661	420
ENSMUSG00000032812	chr7	Arap1	1.01E+08	1.01E+08	7564	0.807236	4.540004	1.64E-06	1.28E-05	0.031037	1	198	162	343	314	360	494	504	560	608	481
ENSMUSG00000042719	chr5	Naa25	1.21E+08	1.21E+08	8298	-0.68876	5.262422	1.65E-06	1.29E-05	0.022947	-1	610	498	1274	686	847	413	640	526	670	449
ENSMUSG00000073139	chrX	BC023829	70459753	70461292	2513	-0.68213	5.100248	1.68E-06	1.3E-05	0.022335	-1	575	460	1048	590	788	386	636	407	574	417
ENSMUSG00000038886	chr7	Man2a2	80349098	80351851	6553	-0.76954	7.943048	1.68E-06	1.31E-05	0.030359	-1	3932	2903	8878	4458	5895	2420	3955	3205	4263	2926
ENSMUSG00000028757	chr4	Ddost	1.38E+08	1.38E+08	2120	0.688504	5.700344	1.69E-06	1.31E-05	0.023332	1	598	468	871	569	692	982	1364	1241	1373	896
ENSMUSG00000078878	chr2	Gm14305	1.77E+08	1.77E+08	2500	-1.08272	1.695151	1.71E-06	1.33E-05	0.040088	-1	55	42	91	69	93	25	61	32	38	31
ENSMUSG00000046480	chr9	Scn4b	45138437	45139102	4940	-0.88408	9.147319	1.71E-06	1.33E-05	0.040198	-1	8080	6115	16673	14724	15639	5059	10042	5872	9218	6820
ENSMUSG00000079165	chr5	Sap25	1.38E+08	1.38E+08	1569	1.214014	1.838675	1.72E-06	1.34E-05	0.054703	1	36	23	47	29	32	96	92	91	71	78
ENSMUSG00000047419	chr13	Cmya5	93040713	93041560	11850	-0.90426	11.11475	1.73E-06	1.34E-05	0.042131	-1	32499	26165	95033	42764	50433	19347	34988	24122	41095	24507
ENSMUSG00000036810	chr8	Cnep1r1	88118769	88118869	3563	-0.70136	5.104561	1.73E-06	1.34E-05	0.02384	-1	584	522	1008	586	746	313	589	490	607	419
ENSMUSG00000024976	chr19	Shoc2	53944306	53944402	4203	-0.71686	4.565173	1.76E-06	1.36E-05	0.024086	-1	354	294	779	470	538	231	373	315	419	303
ENSMUSG00000027007	chr2	Ssfa2	79635352	79635744	5599	-0.76397	4.006668	1.76E-06	1.36E-05	0.026489	-1	277	178	479	357	366	152	300	200	245	197
ENSMUSG00000051910	chr7	Sox6	1.15E+08	1.15E+08	8852	-0.83824	6.725502	1.78E-06	1.38E-05	0.035828	-1	1623	1202	4219	1917	2577	973	1810	1184	1814	1257
ENSMUSG00000069874	chr11	Irgm2	58199618	58199779	3621	1.659805	5.526996	1.78E-06	1.38E-05	0.135459	1	237	216	582	301	523	582	3838	740	1214	604
ENSMUSG00000030750	chr7	Nsmce1	1.25E+08	1.25E+08	1329	0.807816	3.885277	1.78E-06	1.38E-05	0.029089	1	145	152	202	179	161	278	468	329	388	255
ENSMUSG00000036617	chr2	Etl4	19909780	19910279	16067	-0.84785	6.267967	1.81E-06	1.4E-05	0.036499	-1	1066	934	2810	1563	1976	777	1389	715	1353	882
ENSMUSG00000019731	chr8	Slc35e1	72480641	72483993	4470	-0.80555	6.109383	1.83E-06	1.41E-05	0.032857	-1	1045	720	2206	1551	1830	706	1120	808	1292	733
ENSMUSG00000056629	chr19	Fkbp2	6977741	6977934	663	1.067238	3.230412	1.83E-06	1.41E-05	0.050356	1	94	82	84	110	93	190	226	293	225	192
ENSMUSG00000061232	chr17	H2-K1	33996017	33996476	2608	1.186985	7.154017	1.84E-06	1.42E-05	0.071603	1	1481	1348	1589	945	1361	3378	3239	5451	3236	2332
ENSMUSG00000038943	chr7	Prc1	80294450	80294591	8225	2.070433	0.261259	1.86E-06	1.43E-05	0.150946	1	1	2	9	4	19	36	20	37	31	29
ENSMUSG00000026781	chr2	Acbd5	23068168	23068286	4154	-0.71976	4.787351	1.87E-06	1.44E-05	0.024863	-1	456	381	763	514	677	243	426	369	479	392
ENSMUSG00000001829	chr7	Clpb	1.02E+08	1.02E+08	7855	-0.81365	5.912416	1.89E-06	1.45E-05	0.033502	-1	847	724	1563	1585	1564	541	979	807	1001	702
ENSMUSG00000055228	chr13	Zfp935	62454323	62455193	1062	-1.76494	0.308353	1.89E-06	1.45E-05	0.086584	-1	18	16	52	22	40	15	13	5	6	7
ENSMUSG00000029361	chr5	Nos1	1.18E+08	1.18E+08	11151	-1.2587	6.311413	1.89E-06	1.45E-05	0.080197	-1	1092	589	2939	2389	2613	432	912	840	1150	975
ENSMUSG00000003541	chr17	Ier3	35821684	35821928	1131	1.296786	3.088678	1.92E-06	1.48E-05	0.07729	1	49	55	74	106	102	143	408	153	333	111
ENSMUSG00000018126	chr15	Baiap2l2	79258195	79258652	2728	1.240539	1.356886	1.96E-06	1.51E-05	0.050791	1	22	15	36	23	21	50	63	43	102	57
ENSMUSG00000000244	chr7	Tspan32	1.43E+08	1.43E+08	2848	1.758749	0.417396	1.98E-06	1.52E-05	0.097154	1	7	7	16	4	11	31	32	56	26	22
ENSMUSG00000026077	chr1	Npas2	39193731	39194009	4791	1.974307	-0.09369	2E-06	1.53E-05	0.101268	1	3	1	5	10	7	15	31	21	43	11
ENSMUSG00000025138	chr11	Sirt7	1.21E+08	1.21E+08	5148	0.998623	2.980475	2.01E-06	1.54E-05	0.042744	1	81	71	108	70	81	179	173	221	236	128
ENSMUSG00000027496	chr2	Aurka	1.72E+08	1.72E+08	2531	-1.02665	3.383699	2.01E-06	1.54E-05	0.048317	-1	225	171	359	137	237	139	156	93	132	97
ENSMUSG00000032560	chr9	Dnajc13	1.04E+08	1.04E+08	11938	-0.76032	5.096447	2.01E-06	1.54E-05	0.02845	-1	540	392	1214	607	856	390	564	428	492	430
ENSMUSG00000023959	chr17	Clic5	44188572	44188961	5870	-0.81827	7.422453	2.03E-06	1.55E-05	0.034756	-1	2897	1929	6171	3118	4301	1665	3298	1860	2991	1797
ENSMUSG00000055239	chr6	Kcmf1	72841114	72843130	3251	-0.74628	7.793255	2.03E-06	1.55E-05	0.029007	-1	4140	3396	6555	3820	4495	2455	3366	2748	4365	2374
ENSMUSG00000037815	chr18	Ctnna1	35118888	35118981	3698	0.683835	6.289165	2.04E-06	1.56E-05	0.023834	1	782	700	1314	937	1122	1434	2014	1812	2117	1430
ENSMUSG00000046417	chr11	Lrrc75a	62604884	62606246	2089	0.974495	2.295398	2.04E-06	1.56E-05	0.037036	1	37	29	89	50	63	75	158	105	145	105
ENSMUSG00000030126	chr6	Tmcc1	1.16E+08	1.16E+08	7250	-0.76038	6.026484	2.05E-06	1.57E-05	0.029457	-1	1138	926	2214	1079	1379	795	959	815	1169	686
ENSMUSG00000021306	chr13	Gpr137b	13357623	13359423	2978	1.562436	1.721175	2.06E-06	1.57E-05	0.101237	1	19	14	31	32	34	56	85	163	79	46
ENSMUSG00000060131	chr2	Atp8b4	1.26E+08	1.26E+08	6660	2.13165	-0.17945	2.06E-06	1.57E-05	0.109598	1	0	6	3	7	6	21	22	28	16	23
ENSMUSG00000026675	chr1	Hsd17b7	1.7E+08	1.7E+08	5104	-1.01927	2.897796	2.07E-06	1.57E-05	0.045139	-1	135	98	286	106	201	78	88	80	137	65
ENSMUSG00000030096	chr6	Slc6a6	91684067	91684308	6169	-0.80273	6.574365	2.07E-06	1.58E-05	0.033216	-1	1175	1219	3231	2053	2470	955	1541	1095	1719	1108
ENSMUSG00000078853	chr11	Igtp	58199556	58199779	2022	1.316959	4.625331	2.07E-06	1.58E-05	0.08636	1	158	188	314	194	284	492	1563	367	648	316
ENSMUSG00000074634	chr13	Gm7120	1.19E+08	1.19E+08	3429	-1.77992	0.673644	2.08E-06	1.58E-05	0.109466	-1	31	24	50	31	55	13	18	22	5	3
ENSMUSG00000018501	chr11	Ncor1	62316426	62318030	12811	-0.80863	6.406797	2.08E-06	1.58E-05	0.033635	-1	1259	892	3092	1751	2150	790	1406	1092	1398	1002
ENSMUSG00000026430	chr1	Rassf5	1.31E+08	1.31E+08	3839	1.434936	0.759625	2.08E-06	1.58E-05	0.059884	1	14	9	21	12	12	35	43	55	53	23
ENSMUSG00000016262	chr1	Sertad4	1.93E+08	1.93E+08	3850	1.159906	2.181539	2.1E-06	1.6E-05	0.055155	1	34	25	62	49	53	73	82	126	146	123

ENSMUSG00000078684	chr3	5830417I10Rik	88775216	88775274	6190	-0.80111	3.323308	2.1E-06	1.6E-05	0.027333	-1	142	134	315	198	253	92	149	131	174	120
ENSMUSG00000029163	chr5	Emilin1	30913402	30914044	4938	0.95612	3.522257	2.11E-06	1.6E-05	0.042536	1	84	63	151	134	209	217	287	304	291	257
ENSMUSG00000056091	chr6	St3gal5	72097592	72097782	2618	-1.5575	5.658066	2.14E-06	1.62E-05	0.121916	-1	666	428	971	2159	1976	435	418	293	863	362
ENSMUSG00000045636	chr8	Mtus1	40990914	40993633	10078	-0.71245	7.145633	2.16E-06	1.63E-05	0.026419	-1	2346	1739	4436	2632	3395	1441	2335	1818	2643	1682
ENSMUSG00000021549	chr13	Rasa1	85214780	85216187	7296	-0.84994	3.927797	2.16E-06	1.64E-05	0.033948	-1	215	249	539	249	354	137	267	200	188	195
ENSMUSG00000004044	chr11	Ptrf	1.01E+08	1.01E+08	3587	0.765953	7.577003	2.17E-06	1.64E-05	0.030638	1	2156	1868	2619	1955	2572	3597	4658	4443	5142	3983
ENSMUSG00000035226	chr2	Rims4	1.64E+08	1.64E+08	4962	-1.90864	0.57338	2.19E-06	1.66E-05	0.12638	-1	18	17	33	44	70	5	10	15	7	15
ENSMUSG00000022371	chr15	Col14a1	55307750	55307984	7013	1.330834	4.614906	2.2E-06	1.66E-05	0.089121	1	92	124	384	242	344	282	674	899	557	740
ENSMUSG00000093674	chr10	Rpl41	1.29E+08	1.29E+08	1168	0.847991	7.549798	2.2E-06	1.66E-05	0.03754	1	2250	1927	2371	1794	2039	3851	5274	4230	5344	3366
ENSMUSG00000032313	chr9	AI118078	55326913	55327000	4714	-1.97027	1.715688	2.21E-06	1.67E-05	0.169999	-1	65	66	108	54	123	6	23	60	14	15
ENSMUSG00000042066	chr1	Tmcc2	1.32E+08	1.32E+08	5692	-0.70472	6.179998	2.24E-06	1.69E-05	0.025506	-1	1266	969	2077	1343	1665	778	1040	946	1329	942
ENSMUSG00000045165	chr7	AI467606	1.27E+08	1.27E+08	1918	1.25511	1.144483	2.25E-06	1.69E-05	0.049657	1	19	14	25	15	26	42	61	72	54	38
ENSMUSG00000096696	chr17	Zfp960	17064113	17064206	2667	-1.28537	1.150736	2.25E-06	1.69E-05	0.056031	-1	47	24	70	55	51	15	41	15	24	20
ENSMUSG00000058056	chr8	Palld	61513246	61513524	8479	-0.99522	4.907758	2.27E-06	1.71E-05	0.04997	-1	446	299	1246	594	843	223	506	307	382	418
ENSMUSG00000042500	chr4	Ago4	1.26E+08	1.26E+08	6947	-0.73342	4.422989	2.28E-06	1.72E-05	0.025604	-1	321	247	662	454	531	228	314	314	361	250
ENSMUSG00000022201	chr15	Zfr	12117831	12117947	5911	-0.67788	5.578392	2.3E-06	1.73E-05	0.023203	-1	759	617	1486	940	1028	470	846	611	858	608
ENSMUSG00000089862	chr6	Gm16039	8259288	8259493	10430	-0.75033	3.943806	2.31E-06	1.74E-05	0.025969	-1	283	250	459	231	325	166	241	196	255	186
ENSMUSG00000033855	chr17	Ston1	88597684	88597741	4521	-1.66966	0.650626	2.32E-06	1.75E-05	0.098687	-1	24	16	63	43	42	4	28	16	11	7
ENSMUSG00000032754	chr5	Slc8b1	1.21E+08	1.21E+08	3463	0.798445	3.819248	2.33E-06	1.75E-05	0.029441	1	141	93	202	185	210	297	320	315	367	301
ENSMUSG00000026126	chr1	Ptpn18	34459762	34461056	6492	1.220789	1.519793	2.33E-06	1.75E-05	0.05235	1	22	23	40	24	23	63	73	92	69	49
ENSMUSG00000027177	chr2	Hipk3	1.04E+08	1.04E+08	7987	-0.80203	8.349029	2.33E-06	1.75E-05	0.033968	-1	5622	4358	11812	5568	7084	2810	4980	3929	6230	4099
ENSMUSG00000040528	chr11	Milr1	1.07E+08	1.07E+08	2474	1.945473	0.150261	2.34E-06	1.75E-05	0.109684	1	8	5	4	3	12	36	33	32	18	20
ENSMUSG00000033618	chr16	Map3k13	21891969	21892440	6709	-1.88821	-0.1928	2.35E-06	1.76E-05	0.08662	-1	14	16	37	13	21	5	12	1	5	7
ENSMUSG00000039745	chr7	Htatip2	49759106	49759311	1465	0.808781	4.003444	2.36E-06	1.77E-05	0.03053	1	185	155	217	133	228	308	383	379	450	321
ENSMUSG00000013076	chr9	Amotl1	14541966	14547898	9798	-0.85029	8.82699	2.37E-06	1.77E-05	0.038234	-1	7450	5769	17149	7094	11775	5111	6381	4564	8440	5248
ENSMUSG00000024515	chr18	Smad4	73639009	73640469	3712	-0.74354	5.263501	2.37E-06	1.77E-05	0.027875	-1	562	493	1325	719	906	326	650	526	670	483
ENSMUSG00000026837	chr2	Col5a1	27886425	27886924	8490	0.914429	5.89827	2.39E-06	1.79E-05	0.043364	1	529	382	1131	541	885	1043	1191	1348	1692	1701
ENSMUSG00000047213	chr3	Ythdf3	16183212	16183520	5363	-0.82598	5.276371	2.41E-06	1.8E-05	0.034719	-1	527	535	1328	772	955	285	549	538	683	518
ENSMUSG00000050347	chr7	Gm9844	24862278	24862412	135	2.105945	-0.18817	2.41E-06	1.8E-05	0.109214	1	8	5	7	1	1	17	15	27	29	22
ENSMUSG00000033752	chr3	Mnd1	84087933	84088174	875	1.687238	0.351733	2.42E-06	1.8E-05	0.074037	1	11	10	6	6	9	35	44	28	31	21
ENSMUSG00000020309	chr11	Chac2	30976707	30977746	1315	-0.90137	3.237731	2.43E-06	1.81E-05	0.036751	-1	166	124	243	189	270	64	141	145	164	93
ENSMUSG00000030263	chr6	Lrmp	1.45E+08	1.45E+08	4070	1.617467	1.151068	2.43E-06	1.81E-05	0.099786	1	24	8	20	7	24	74	58	58	58	34
ENSMUSG00000026548	chr1	Slamf9	1.72E+08	1.72E+08	1313	1.31609	0.921768	2.44E-06	1.82E-05	0.05434	1	13	12	30	10	18	49	48	48	46	36
ENSMUSG00000030180	chr6	Kdm5a	1.2E+08	1.2E+08	14185	-0.78513	4.359363	2.44E-06	1.82E-05	0.029924	-1	302	238	718	373	547	177	370	272	345	232
ENSMUSG00000031253	chrX	Srpx2	1.34E+08	1.34E+08	2922	1.01409	2.78351	2.44E-06	1.82E-05	0.044743	1	53	54	102	61	95	143	142	141	186	195
ENSMUSG00000024063	chr17	Lbh	72918305	72918578	3207	0.818836	3.672453	2.49E-06	1.85E-05	0.030308	1	121	130	201	120	159	199	303	317	392	267
ENSMUSG00000028690	chr4	Mmachc	1.17E+08	1.17E+08	2224	-0.74745	4.920084	2.49E-06	1.85E-05	0.027871	-1	467	376	748	748	734	306	542	347	485	394
ENSMUSG00000092569	chr18	Gm20544	75365332	75365862	690	-1.34454	0.861134	2.49E-06	1.85E-05	0.055733	-1	28	39	45	38	47	19	23	16	14	16
ENSMUSG00000021009	chr12	Ptpn21	98676741	98678678	5738	-0.76499	5.354346	2.51E-06	1.86E-05	0.02975	-1	662	457	1467	768	966	422	565	520	753	511
ENSMUSG00000028383	chr4	Hsdl2	59581563	59581775	2795	-1.18379	5.6283	2.51E-06	1.86E-05	0.07249	-1	599	614	1022	1901	1405	330	880	509	651	465
ENSMUSG00000031519	chr8	Asb5	54550331	54550640	1579	-0.83589	7.224481	2.51E-06	1.86E-05	0.036894	-1	2750	2257	5040	2376	3262	1453	2733	1318	2633	1851
ENSMUSG00000098050	chr8	Gm5345	40853828	40854040	1014	-1.42925	0.253	2.54E-06	1.89E-05	0.050057	-1	17	17	35	26	36	6	17	9	16	7
ENSMUSG00000032374	chr9	Plod2	92542223	92542568	5392	1.364503	1.996571	2.56E-06	1.9E-05	0.081035	1	20	19	69	29	46	65	120	151	72	93
ENSMUSG00000026786	chr2	Apbb1ip	22774094	22774521	7414	1.12549	2.026761	2.58E-06	1.91E-05	0.051827	1	26	19	58	44	59	75	99	115	96	102
ENSMUSG00000004665	chr10	Cnn2	79988584	79988740	2460	0.839325	3.255553	2.58E-06	1.91E-05	0.030692	1	84	71	123	117	152	172	270	174	302	198
ENSMUSG00000049106	chr12	Dcaf5	80335847	80340276	5707	-0.70652	5.839694	2.65E-06	1.96E-05	0.025812	-1	1045	708	1902	993	1210	612	937	751	1048	660
ENSMUSG00000038080	chr13	Kdm1b	47043499	47043670	4829	-0.82959	3.385771	2.7E-06	2E-05	0.031009	-1	181	143	322	212	225	91	172	101	180	145
ENSMUSG00000011382	chr7	Dhdh	45472956	45475375	3678	-0.78707	5.767857	2.74E-06	2.02E-05	0.032235	-1	1024	888	1781	730	1174	621	875	741	811	594
ENSMUSG00000098148	chr8	Gm20204	1.17E+08	1.17E+08	5220	0.925596	2.732399	2.76E-06	2.04E-05	0.035651	1	55	58	105	71	74	137	187	171	194	96
ENSMUSG00000029413	chr5	Naaa	92257659	92258943	3721	0.797633	3.830771	2.78E-06	2.05E-05	0.02999	1	142	106	222	160	209	295	307	386	345	275
ENSMUSG00000053870	chr3	Fpgt	1.55E+08	1.55E+08	6282	-0.87544	2.546787	2.82E-06	2.08E-05	0.030504	-1	88	85	170	120	145	53	105	63	87	67
ENSMUSG00000025888	chr9	Casp1	5298517	5298723	1497	1.468547	1.396009	2.83E-06	2.08E-05	0.08157	1	23	24	23	12	21	65	95	79	60	36
ENSMUSG00000092534	chr7	Pagr1b	1.27E+08	1.27E+08	693	0.718041	3.865977	2.86E-06	2.11E-05	0.023788	1	136	118	238	177	222	294	342	299	395	300
ENSMUSG00000024308	chr17	Tapbp	33915899	33915964	3296	0.697137	5.563711	2.89E-06	2.13E-05	0.025072	1	514	392	777	524	717	847	1130	1250	1197	880
ENSMUSG00000017830	chr11	Dhx58	1.01E+08	1.01E+08	3272	1.667469	1.08531	2.91E-06	2.14E-05	0.107648	1	16	5	16	22	18	68	79	49	30	44
ENSMUSG00000022765	chr16	Snap29	17406003	17406359	3429	-0.78057	4.701395	2.96E-06	2.18E-05	0.030712	-1	507	391	835	402	528	334	436	284	444	255
ENSMUSG00000037613	chr7	Tnfrsf23	1.44E+08	1.44E+08	3353	0.9018	3.800278	2.96E-06	2.18E-05	0.038877	1	142	135	225	115	153	285	413	353	433	182
ENSMUSG00000026737	chr2	Pip4k2a	18842255	18844460	3477	0.889966	2.95986	2.99E-06	2.2E-05	0.034787	1	67	56	136	76	107	175	190	199	177	152
ENSMUSG00000025790	chr7	Slco3a1	74275419	74276088	8474	-1.06684	5.382942	3.02E-06	2.22E-05	0.059721	-1	518	409	1200	1237	1368	387	582	395	836	330
ENSMUSG00000010660	chr9	Plcd1	1.19E+08	1.19E+08	2651	0.853757	3.551316	3.02E-06	2.22E-05	0.033822	1	108	80	147	167	164	193	311	232	352	281
ENSMUSG00000024776	chr19	Stambpl1	34192229	34192631	5557	1.362711	0.903138	3.03E-06	2.23E-05	0.060429	1	15	11	33	9	12	35	59	53	45	37
ENSMUSG00000092329	chr8	Gm20388	1.2E+08	1.2E+08	3953	-0.70793	6.264122	3.06E-06	2.24E-05	0.026516	-1	1216	964	2204	1635	1793	821	1124	986	1394	1007
ENSMUSG00000021366	chr13	Hivep1	42052021	42052090	8753	-1.02696	3.917425	3.08E-06	2.25E-05	0.052384	-1	188	133	559	380	467	122	205	180	211	185
ENSMUSG00000033589	chr14	Reep4	70545251	70545738	1668	1.1028	1.545533	3.08E-06	2.26E-05	0.040927	1	27	19	32	30	34	59	62	69	86	68
ENSMUSG00000089715	chr15	Cbx6	79823896	79828978	6290	0.730956	4.750143	3.13E-06	2.29E-05	0.027082	1	223	193	527	328	410	451	661	656	749	542

ENSMUSG00000027646	chr2	Src	1.57E+08	1.57E+08	4371	0.98724	2.673612	3.13E-06	2.29E-05	0.042691	1	55	45	112	45	90	109	144	183	184	136
ENSMUSG00000008976	chr16	Gabpa	84834925	84835023	5687	-0.792	4.489631	3.14E-06	2.3E-05	0.031435	-1	285	280	734	502	566	190	384	295	348	293
ENSMUSG00000069769	chr11	Msi2	88339382	88344660	10405	-0.78813	6.931286	3.15E-06	2.3E-05	0.033371	-1	1777	1344	3678	2797	3282	1148	2098	1353	2162	1530
ENSMUSG00000098302	chr5	Gm28039	1.07E+08	1.07E+08	254	-1.40314	0.474663	3.16E-06	2.31E-05	0.057074	-1	25	26	40	23	38	6	20	7	19	14
ENSMUSG00000055200	chr7	Sertad3	27473768	27473871	1324	1.068313	2.278279	3.17E-06	2.31E-05	0.046901	1	44	35	45	60	57	109	127	97	173	82
ENSMUSG00000001281	chr15	Itgb7	1.02E+08	1.02E+08	2743	1.241016	1.441916	3.17E-06	2.31E-05	0.055825	1	18	22	35	21	28	71	61	79	60	53
ENSMUSG00000071203	chr13	Naip5	1E+08	1E+08	5204	1.790721	0.093835	3.17E-06	2.31E-05	0.09032	1	6	7	13	3	5	26	23	36	20	25
ENSMUSG00000091337	chr2	Eid1	1.26E+08	1.26E+08	1691	0.857781	4.766449	3.17E-06	2.31E-05	0.03744	1	245	274	313	340	337	381	670	713	848	602
ENSMUSG00000025348	chr10	Itga7	1.29E+08	1.29E+08	4013	0.70549	6.763441	3.18E-06	2.32E-05	0.026667	1	1130	809	1698	1468	1606	1838	3266	2151	2914	2236
ENSMUSG00000025372	chr11	Baiap2	1.2E+08	1.2E+08	4992	1.279971	1.833914	3.2E-06	2.33E-05	0.066114	1	36	28	47	24	24	64	68	111	107	88
ENSMUSG00000013707	chr3	Tnfaip8l2	95139521	95140596	1122	1.484672	1.247985	3.21E-06	2.34E-05	0.084476	1	17	14	24	18	22	75	55	80	56	29
ENSMUSG00000027180	chr2	Fbxo3	1.04E+08	1.04E+08	7237	-0.73495	6.638522	3.21E-06	2.34E-05	0.028948	-1	1425	1279	2769	2242	2497	999	1814	1115	1721	1265
ENSMUSG00000027536	chr3	Chmp4c	10366907	10367221	10087	-2.02404	0.342313	3.21E-06	2.34E-05	0.145053	-1	19	17	17	54	44	4	11	13	5	9
ENSMUSG00000021893	chr14	Capn7	31336638	31336983	4733	-0.65003	5.82083	3.22E-06	2.34E-05	0.02212	-1	978	817	1562	1036	1174	663	1031	732	950	662
ENSMUSG00000062054	chr12	Iah1	21316392	21316512	924	1.370672	2.681905	3.28E-06	2.38E-05	0.087335	1	64	59	49	36	60	120	195	247	116	137
ENSMUSG00000024909	chr19	Efemp2	5473973	5474323	2648	0.777912	3.377446	3.3E-06	2.39E-05	0.026891	1	91	87	170	118	150	169	256	245	275	236
ENSMUSG00000031165	chrX	Was	8081453	8081989	2381	1.48208	0.829064	3.3E-06	2.39E-05	0.075361	1	13	10	25	7	16	45	50	58	44	23
ENSMUSG00000055912	chr6	Tmem150a	72355447	72355544	1546	-0.68826	4.46856	3.3E-06	2.39E-05	0.023376	-1	410	344	596	363	470	249	380	275	412	244
ENSMUSG00000032562	chr9	Gnai2	1.08E+08	1.08E+08	3779	0.688534	6.314221	3.31E-06	2.4E-05	0.025295	1	786	645	1443	929	1194	1443	1873	1810	2269	1556
ENSMUSG00000011008	chr3	Mcoln2	1.46E+08	1.46E+08	3288	2.830612	0.362515	3.32E-06	2.41E-05	0.297416	1	2	6	9	0	5	21	119	22	18	13
ENSMUSG00000032491	chr9	Nradd	1.11E+08	1.11E+08	1162	1.537431	0.70438	3.33E-06	2.41E-05	0.078772	1	18	5	16	8	15	34	40	58	37	32
ENSMUSG00000078317	chrX	F8a	73228291	73230795	2505	0.870334	3.130263	3.33E-06	2.41E-05	0.033608	1	110	67	130	75	108	144	218	188	282	193
ENSMUSG00000007039	chr17	Ddah2	35059035	35059272	1593	0.786423	3.591462	3.36E-06	2.43E-05	0.028464	1	110	106	160	136	192	237	269	276	342	245
ENSMUSG00000040706	chr4	Agmat	1.42E+08	1.42E+08	1407	1.874862	-0.22063	3.38E-06	2.44E-05	0.080045	1	6	3	7	4	5	25	18	25	25	11
ENSMUSG00000022265	chr15	Ank	27466677	27467099	3608	-0.89326	7.393904	3.4E-06	2.46E-05	0.043267	-1	2499	1687	4759	4605	4610	1580	2746	1645	2856	2059
ENSMUSG00000043467	chr1	Zbtb37	1.61E+08	1.61E+08	18814	-0.96615	3.101151	3.47E-06	2.51E-05	0.043173	-1	140	104	340	131	235	91	134	72	130	100
ENSMUSG00000036606	chr15	Plxnb2	89155549	89156385	7119	0.794043	4.503316	3.51E-06	2.53E-05	0.032223	1	209	144	420	263	339	397	473	622	642	462
ENSMUSG00000044328	chr11	Trp53i13	77508099	77508377	2157	0.982117	2.469362	3.5E-06	2.53E-05	0.040485	1	50	39	62	68	72	104	117	148	169	114
ENSMUSG00000020340	chr11	Cyfip2	46193850	46196467	7103	2.522958	2.124236	3.51E-06	2.53E-05	0.292993	1	12	6	21	40	22	32	254	287	51	48
ENSMUSG00000060002	chr10	Chpt1	88452745	88453097	8324	-1.03077	6.87331	3.54E-06	2.55E-05	0.057452	-1	1550	1368	2825	3582	3589	841	1423	1818	1767	1223
ENSMUSG00000027784	chr3	Ppm1l	69316861	69317965	10496	-0.71897	7.666461	3.56E-06	2.56E-05	0.028257	-1	3200	2491	6848	3629	4926	2147	3505	2466	3733	2358
ENSMUSG00000058099	chr15	Nfam1	82997721	82999795	3222	1.382779	1.970169	3.63E-06	2.61E-05	0.085228	1	24	27	71	19	34	102	91	141	96	60
ENSMUSG00000020048	chr10	Hsp90b1	86690209	86691128	4032	0.757711	7.3313	3.64E-06	2.61E-05	0.031328	1	1736	1494	2273	1775	2250	3339	4236	4114	3784	2841
ENSMUSG00000026153	chr1	Fam135a	24011093	24012497	7773	-0.8541	3.921966	3.64E-06	2.61E-05	0.036189	-1	205	204	536	299	377	116	237	156	275	211
ENSMUSG00000027997	chr3	Casp6	1.3E+08	1.3E+08	1676	1.202061	1.401802	3.63E-06	2.61E-05	0.051627	1	17	15	24	35	31	39	78	59	80	66
ENSMUSG00000021319	chr13	Sfrp4	19623175	19623877	1756	1.579716	2.990043	3.65E-06	2.62E-05	0.123223	1	41	56	127	47	52	82	218	356	137	254
ENSMUSG00000031278	chrX	Acsl4	1.42E+08	1.42E+08	5405	-0.75219	4.820041	3.68E-06	2.64E-05	0.029167	-1	469	387	944	448	677	246	453	332	516	391
ENSMUSG00000009214	chr2	Tmem8c	27061636	27062337	1511	3.46588	2.907391	3.68E-06	2.64E-05	0.528001	1	3	0	3	72	19	241	136	180	452	215
ENSMUSG00000031696	chr8	Vps35	85260397	85261309	3180	-0.69429	6.056137	3.8E-06	2.72E-05	0.025901	-1	1043	874	2016	1332	1482	685	1290	806	1087	826
ENSMUSG00000021288	chr12	Klc1	1.12E+08	1.12E+08	4070	0.69151	5.969256	3.81E-06	2.73E-05	0.025555	1	694	582	925	692	934	1196	1550	1314	1751	1233
ENSMUSG00000053113	chr11	Socs3	1.18E+08	1.18E+08	2891	2.921674	4.81591	3.83E-06	2.74E-05	0.404853	1	17	59	91	42	359	469	3288	386	537	312
ENSMUSG00000037475	chrX	Thoc2	41794991	41797779	12666	-0.9033	3.835879	3.83E-06	2.74E-05	0.04059	-1	181	209	502	254	400	101	207	203	202	192
ENSMUSG00000015027	chr8	Galns	1.23E+08	1.23E+08	2585	1.234623	1.589888	3.86E-06	2.76E-05	0.060312	1	17	17	39	30	38	59	79	106	61	59
ENSMUSG00000016477	chr13	E2f3	29906575	29910165	4794	-0.76691	4.073684	3.86E-06	2.76E-05	0.029167	-1	314	206	546	284	393	148	300	177	319	212
ENSMUSG00000003037	chr8	Rab8a	72161200	72161482	4678	0.738851	3.850814	3.87E-06	2.76E-05	0.025802	1	167	130	224	162	173	304	363	322	357	272
ENSMUSG00000057948	chr11	Unc13d	1.16E+08	1.16E+08	4679	1.99937	-0.34741	3.89E-06	2.78E-05	0.095531	1	7	0	7	5	2	20	24	18	26	9
ENSMUSG00000079108	chr12	Srp54b	55155104	55155580	5603	-0.80563	3.665295	3.9E-06	2.78E-05	0.030963	-1	222	213	324	221	301	125	216	160	154	177
ENSMUSG00000038387	chr7	Rras	45017978	45018168	1103	0.73901	4.463243	3.91E-06	2.79E-05	0.027401	1	265	177	303	284	280	431	532	514	662	373
ENSMUSG00000059495	chr9	Arhgef12	42963842	42969192	10483	-0.86567	5.872044	3.94E-06	2.81E-05	0.040488	-1	751	604	2056	1362	1641	514	816	734	1007	737
ENSMUSG00000021719	chr13	Rgs7bp	1.05E+08	1.05E+08	5828	-1.91053	-0.07755	3.96E-06	2.82E-05	0.096056	-1	16	17	34	17	26	10	7	4	0	10
ENSMUSG00000028245	chr4	Nsmaf	6396207	6396817	8368	-0.64521	5.332058	3.98E-06	2.83E-05	0.021761	-1	610	524	1163	788	940	449	771	550	648	470
ENSMUSG00000029475	chr5	Kdm2b	1.23E+08	1.23E+08	11818	-0.82881	3.278369	3.98E-06	2.83E-05	0.031575	-1	167	134	314	159	239	86	134	109	175	132
ENSMUSG00000061755	chr5	Bod1l	41787542	41788949	10389	-0.69806	4.636723	4.01E-06	2.85E-05	0.024678	-1	364	334	796	411	641	271	429	339	377	312
ENSMUSG00000028041	chr3	Adam15	89338542	89338866	6145	0.760093	4.822026	4.06E-06	2.89E-05	0.03001	1	251	252	385	327	471	512	617	734	765	579
ENSMUSG00000059897	chr8	Zfp930	69226343	69226469	1323	-1.47628	0.934242	4.1E-06	2.91E-05	0.086283	-1	43	31	39	45	55	6	39	14	21	12
ENSMUSG00000051067	chr10	Lingo3	80832807	80836141	3433	-1.00112	3.797434	4.19E-06	2.98E-05	0.050388	-1	230	123	469	293	446	186	162	140	181	152
ENSMUSG00000029723	chr5	Tsc22d4	1.38E+08	1.38E+08	7509	0.718469	5.707848	4.26E-06	3.02E-05	0.027772	1	530	449	825	667	708	1074	1060	1162	1589	996
ENSMUSG00000064351	chrMT	mt-Co1	5328	6872	1545	-1.09318	14.40786	4.26E-06	3.02E-05	0.066106	-1	239409	236367	554488	640859	804497	191734	384342	198947	334051	192557
ENSMUSG00000024212	chr17	Mllt1	56892612	56894590	3608	-0.69416	5.088417	4.26E-06	3.02E-05	0.025253	-1	507	414	968	763	795	346	507	507	608	410
ENSMUSG00000031376	chrX	Atp2b3	73503086	73503334	4820	-1.19739	3.324407	4.29E-06	3.04E-05	0.072067	-1	140	99	386	263	287	63	169	93	84	140
ENSMUSG00000083649	chr7	Rasl2-9	5124938	5125950	1013	-1.96286	0.018567	4.33E-06	3.06E-05	0.128674	-1	21	15	11	34	35	7	12	3	10	3
ENSMUSG00000089704	chr8	Galnt2	1.24E+08	1.24E+08	4282	-0.69811	6.245379	4.34E-06	3.07E-05	0.026605	-1	1198	949	2168	1612	1763	814	1114	981	1383	994
ENSMUSG00000045954	chr1	Sdpr	51289126	51289868	3055	-0.76423	5.221966	4.4E-06	3.11E-05	0.031253	-1	602	585	776	796	968	329	592	591	582	441
ENSMUSG00000020664	chr12	Dld	31331564	31332242	2241	-0.83195	7.764307	4.46E-06	3.15E-05	0.038603	-1	3083	2871	5066	5771	5760	1893	4117	2340	3696	2563
ENSMUSG00000007659	chr2	Bcl2l1	1.53E+08	1.53E+08	4586	0.816999	3.886073	4.47E-06	3.16E-05	0.033195	1	154	94	175	187	249	294	363	301	433	312

ENSMUSG00000037851	chr13	Iars	49682100	49682203	5272	-0.70464	6.270353	4.47E-06	3.16E-05	0.027233	-1	1249	902	2423	1494	1868	762	1434	948	1400	909
ENSMUSG00000097295	chr10	Hmgb1-ps8	22262742	22263367	626	-1.61123	0.42574	4.47E-06	3.16E-05	0.088559	-1	25	19	66	16	32	4	18	8	16	11
ENSMUSG00000027330	chr2	Cdc25b	1.31E+08	1.31E+08	3728	1.192226	1.820355	4.49E-06	3.17E-05	0.058698	1	28	30	46	26	36	83	80	116	75	68
ENSMUSG00000029759	chr6	Pon3	5220852	5221722	3385	-0.75832	4.4809	4.49E-06	3.17E-05	0.029522	-1	367	284	706	420	531	230	345	382	285	256
ENSMUSG00000100862	chr1	Gm10925	24613974	24614651	678	-1.11212	3.905346	4.49E-06	3.17E-05	0.064431	-1	176	156	368	398	608	124	267	137	229	128
ENSMUSG00000032350	chr9	Gclc	77754535	77754959	3423	-0.75435	3.181742	4.52E-06	3.19E-05	0.025066	-1	168	127	248	176	191	102	133	130	150	96
ENSMUSG00000052299	chr16	Ltn1	87376651	87379007	7737	-0.7109	5.038527	4.52E-06	3.19E-05	0.02659	-1	464	451	1154	576	745	363	506	454	528	414
ENSMUSG00000047423	chr19	AI837181	5425157	5425308	1529	0.700279	5.227277	4.55E-06	3.2E-05	0.026035	1	413	311	643	463	472	765	824	758	1155	709
ENSMUSG00000026979	chr2	Psd4	24367580	24367802	11786	1.559502	0.416831	4.58E-06	3.22E-05	0.073983	1	14	5	10	4	16	29	33	41	34	26
ENSMUSG00000020038	chr10	Cry1	85131702	85132307	3014	-0.74785	3.603701	4.59E-06	3.23E-05	0.026527	-1	210	182	371	209	258	106	184	175	216	149
ENSMUSG00000036620	chr11	Mgat4b	50210890	50211030	2719	0.810658	6.028304	4.66E-06	3.28E-05	0.036111	1	726	508	1061	734	797	1375	1366	1236	2435	1209
ENSMUSG00000026634	chr1	Angel2	1.91E+08	1.91E+08	5559	-0.63754	4.951929	4.69E-06	3.29E-05	0.021181	-1	488	476	838	580	645	336	544	433	565	352
ENSMUSG00000027199	chr2	Gatm	1.23E+08	1.23E+08	3001	0.918427	3.212956	4.69E-06	3.29E-05	0.040697	1	74	50	147	135	116	210	226	177	284	190
ENSMUSG00000022844	chr16	Pdia5	35397313	35397538	1808	1.128289	1.744386	4.71E-06	3.3E-05	0.049257	1	32	26	50	30	24	80	109	75	87	53
ENSMUSG00000090231	chr17	Cfb	34856374	34856582	2825	1.253458	4.261166	4.72E-06	3.31E-05	0.083179	1	211	183	270	94	119	534	566	549	512	267
ENSMUSG00000039219	chr13	Arid4b	14063232	14063489	13702	-0.77249	3.672717	4.79E-06	3.35E-05	0.02877	-1	180	172	426	234	315	120	176	168	231	163
ENSMUSG00000051504	chr7	Siglech	55768178	55768370	3383	-1.68623	0.226254	4.81E-06	3.37E-05	0.088282	-1	24	27	41	16	24	12	9	13	9	3
ENSMUSG00000041235	chr4	Chd7	8690406	8690775	13786	-0.81479	4.555214	4.82E-06	3.37E-05	0.034873	-1	371	241	860	445	613	213	343	374	372	256
ENSMUSG00000021871	chr14	Pnp	50944302	50944593	3085	1.095329	3.70466	4.91E-06	3.44E-05	0.062137	1	127	87	188	90	182	323	338	437	209	248
ENSMUSG00000081788	chr7	Gm5898	63542479	63544549	2071	-1.07224	2.062461	4.92E-06	3.44E-05	0.048966	-1	69	50	135	87	118	28	66	34	55	59
ENSMUSG00000056952	chr6	Tatdn2	1.14E+08	1.14E+08	3548	-0.74472	4.677567	4.94E-06	3.45E-05	0.029211	-1	356	318	662	626	652	274	469	308	463	259
ENSMUSG00000028989	chr4	Angptl7	1.48E+08	1.48E+08	2157	-2.50572	4.383606	4.95E-06	3.46E-05	0.313859	-1	53	162	768	749	1404	183	97	108	48	88
ENSMUSG00000081752	chrX	Gm14680	62775585	62776685	1101	-1.01827	3.274779	4.96E-06	3.47E-05	0.051959	-1	192	217	274	121	205	100	141	87	148	106
ENSMUSG00000033307	chr10	Mif	75859353	75859543	554	0.741161	5.275449	4.97E-06	3.47E-05	0.029599	1	429	293	519	521	557	723	862	811	1293	745
ENSMUSG00000019577	chr6	Pdk4	5483351	5485592	3511	-1.15527	7.975732	4.99E-06	3.48E-05	0.074459	-1	3615	4653	4543	6996	7481	1656	5823	2546	3106	1828
ENSMUSG00000027589	chr2	Pcmtd2	1.82E+08	1.82E+08	4183	-0.81768	5.617472	5E-06	3.48E-05	0.036738	-1	724	801	1511	932	1121	339	719	672	807	724
ENSMUSG00000005871	chr18	Apc	34220924	34221276	15753	-0.69878	5.178227	5.01E-06	3.49E-05	0.026126	-1	502	467	1174	701	873	353	551	523	662	445
ENSMUSG00000033964	chr1	Zbtb41	1.39E+08	1.39E+08	8362	-0.75647	3.79289	5.01E-06	3.49E-05	0.027968	-1	201	163	463	266	354	125	221	196	242	162
ENSMUSG00000031799	chr8	Tpm4	72134975	72135049	2203	0.745543	5.255284	5.05E-06	3.52E-05	0.030093	1	311	297	551	515	649	699	1124	882	865	776
ENSMUSG00000033880	chr11	Lgals3bp	1.18E+08	1.18E+08	2847	0.965092	4.961254	5.07E-06	3.52E-05	0.050655	1	361	218	498	246	388	621	713	1066	593	655
ENSMUSG00000069184	chr13	Zfp72	74371426	74372827	1629	-1.68236	0.176236	5.09E-06	3.54E-05	0.089003	-1	16	25	38	29	19	7	13	2	11	12
ENSMUSG00000040904	chr11	Gm21988	70235206	70235468	1692	0.714976	6.265518	5.09E-06	3.54E-05	0.028292	1	906	705	1099	932	967	1401	1885	1669	2398	1425
ENSMUSG00000028414	chr4	Fktn	53713998	53714195	6491	-0.87083	3.763561	5.23E-06	3.63E-05	0.038063	-1	256	160	495	217	329	159	149	189	196	162
ENSMUSG00000027004	chr2	Frzb	80411970	80413472	3237	-2.33118	1.806291	5.24E-06	3.64E-05	0.258844	-1	20	28	68	162	200	9	39	8	22	27
ENSMUSG00000039844	chr2	Rapgef1	29619720	29620063	7385	-0.76702	7.536248	5.24E-06	3.64E-05	0.033286	-1	2866	2122	5605	4287	4476	1896	2815	2164	3837	2053
ENSMUSG00000021254	chr12	Gpatch2l	86241890	86241944	3953	-0.77941	3.876386	5.25E-06	3.64E-05	0.03045	-1	223	154	462	300	405	128	248	187	241	188
ENSMUSG00000069539	chr10	Scyl2	89638721	89641116	10099	-0.7402	3.950103	5.25E-06	3.64E-05	0.027205	-1	231	165	510	316	388	170	261	210	243	172
ENSMUSG00000029108	chr5	Pcdh7	57718021	57722278	10478	1.036317	2.602283	5.25E-06	3.64E-05	0.050107	1	42	45	104	52	79	92	144	140	160	185
ENSMUSG00000004319	chr8	Clcn3	60910389	60913175	17071	-0.74355	5.965588	5.31E-06	3.67E-05	0.030683	-1	953	711	1861	1286	1688	557	1119	737	1146	785
ENSMUSG00000098364	chr4	Gm27646	1.38E+08	1.38E+08	110	-0.81117	4.808914	5.32E-06	3.68E-05	0.035439	-1	508	523	853	450	501	274	489	320	392	380
ENSMUSG00000056941	chr2	Commd7	1.54E+08	1.54E+08	5493	0.771755	3.854026	5.35E-06	3.7E-05	0.029266	1	181	120	183	159	197	252	390	370	407	244
ENSMUSG00000006442	chr4	Srm	1.49E+08	1.49E+08	1599	0.806076	3.140472	5.37E-06	3.71E-05	0.029718	1	106	59	130	106	109	149	237	224	231	171
ENSMUSG00000013701	chr14	Timm23	32180162	32180670	1786	-0.74588	6.809477	5.37E-06	3.71E-05	0.03137	-1	1939	1802	2516	2470	2360	1190	2118	1186	2009	1283
ENSMUSG00000079470	chr1	Utp14b	78658038	78658103	7679	-1.42766	1.488048	5.44E-06	3.76E-05	0.089335	-1	50	38	138	30	81	15	30	21	48	23
ENSMUSG00000104139	chr1	Unspecified	34160330	34160496	7920	-2.49829	2.900788	5.49E-06	3.79E-05	0.308734	-1	48	28	651	205	245	17	33	14	75	63
ENSMUSG00000015852	chr3	Fcrls	87250758	87251396	2334	1.060726	3.171951	5.51E-06	3.8E-05	0.056508	1	96	65	157	58	95	238	241	239	165	182
ENSMUSG00000025743	chr4	Sdc3	1.31E+08	1.31E+08	5989	0.854553	4.893109	5.53E-06	3.81E-05	0.039923	1	238	166	448	411	488	594	697	765	699	664
ENSMUSG00000098579	chr12	Mir6937	28679325	28679389	65	-1.52044	0.351571	5.54E-06	3.82E-05	0.073768	-1	25	24	50	18	26	10	18	14	10	4
ENSMUSG00000068606	chr18	Gm4841	60268301	60271039	2838	1.828848	4.807037	5.6E-06	3.86E-05	0.178698	1	189	238	265	39	218	736	1201	333	1536	374
ENSMUSG00000038775	chr9	Vill	1.19E+08	1.19E+08	4409	1.887854	0.156047	5.61E-06	3.86E-05	0.112852	1	9	3	7	9	5	15	29	52	25	20
ENSMUSG00000014956	chr5	Ppp1cb	32458974	32459407	7004	-0.77771	8.422043	5.65E-06	3.89E-05	0.034611	-1	5143	4778	9497	7686	8189	2698	5887	3858	6401	4696
ENSMUSG00000002668	chr17	Dennd1c	57066056	57066641	2520	1.493299	0.355124	5.65E-06	3.89E-05	0.064705	1	8	8	18	6	9	36	38	31	30	19
ENSMUSG00000036040	chr2	Adamtsl2	27079379	27079573	7993	1.700506	0.749666	5.66E-06	3.89E-05	0.120284	1	6	2	13	16	24	58	42	42	44	26
ENSMUSG00000040813	chr9	Tex264	1.07E+08	1.07E+08	2874	0.634492	4.957634	5.68E-06	3.9E-05	0.021227	1	331	268	501	402	458	525	749	688	901	592
ENSMUSG00000029538	chr5	Srsf9	1.15E+08	1.15E+08	1360	0.887608	3.138501	5.68E-06	3.9E-05	0.036737	1	105	85	105	80	102	175	291	179	219	169
ENSMUSG00000021987	chr14	Mtmr6	60265205	60265361	3836	-0.65088	5.945933	5.72E-06	3.93E-05	0.023498	-1	1021	809	1834	1079	1432	673	1090	786	1095	769
ENSMUSG00000003814	chr8	Calr	84841850	84842844	2880	0.695007	7.575075	5.77E-06	3.96E-05	0.027574	1	2025	1605	2989	2358	2782	3385	4639	4888	5043	3531
ENSMUSG00000032253	chr9	Phip	82866159	82871861	33312	-0.87544	4.070656	5.77E-06	3.96E-05	0.040308	-1	242	223	701	285	380	127	246	206	279	228
ENSMUSG00000034021	chr5	Pds5b	1.51E+08	1.51E+08	9397	-0.7685	5.274468	5.77E-06	3.96E-05	0.032496	-1	668	645	1334	573	744	370	684	453	626	501
ENSMUSG00000028518	chr4	Prkaa2	1.05E+08	1.05E+08	7969	-0.79134	7.992842	5.81E-06	3.98E-05	0.035854	-1	4140	3148	9527	4372	5947	2156	4342	2877	4810	3208
ENSMUSG00000020814	chr11	Mxra7	1.17E+08	1.17E+08	2391	0.960204	3.474664	5.88E-06	4.03E-05	0.047157	1	61	85	149	128	190	200	260	308	281	260
ENSMUSG00000039377	chr1	Hlx	1.85E+08	1.85E+08	2278	0.985506	2.780637	5.89E-06	4.03E-05	0.045384	1	59	66	79	54	102	146	145	172	223	128
ENSMUSG00000042742	chr6	B630005N14Rik	13625677	13629100	4139	-0.88458	3.098188	5.91E-06	4.04E-05	0.037798	-1	146	125	284	155	192	53	125	120	151	104
ENSMUSG00000028991	chr4	Mtor	1.48E+08	1.48E+08	10109	-0.83747	5.028954	5.91E-06	4.04E-05	0.038502	-1	488	292	1122	789	842	332	524	354	589	364
ENSMUSG00000079020	chr15	Slc45a4	73577424	73582130	8471	-0.77988	4.932503	5.91E-06	4.04E-05	0.033048	-1	497	422	971	556	721	416	393	305	610	322

ENSMUSG00000026785	chr2	Pkn3	30077684	30077799	4255	0.983063	2.302371	5.92E-06	4.04E-05	0.040952	1	51	35	57	45	71	79	119	128	171	92
ENSMUSG00000038650	chr7	Rnh1	1.41E+08	1.41E+08	1911	0.685265	5.97675	5.93E-06	4.04E-05	0.026177	1	757	542	989	702	882	1268	1649	1300	1794	1091
ENSMUSG00000022351	chr15	Sqle	59315077	59316129	5546	1.344552	0.818621	5.93E-06	4.05E-05	0.062758	1	7	8	24	17	20	31	69	47	46	25
ENSMUSG00000034205	chr14	Loxl2	69609068	69609294	5405	0.910727	4.053101	5.95E-06	4.06E-05	0.044321	1	161	101	307	131	259	269	369	399	428	469
ENSMUSG00000041763	chr1	Tpp2	43933647	43933873	10078	-0.67431	5.383812	5.96E-06	4.06E-05	0.024949	-1	677	521	1273	786	968	409	865	492	727	501
ENSMUSG00000023015	chr15	Racgap1	99620496	99621464	7079	1.343085	1.412012	5.98E-06	4.07E-05	0.072353	1	27	22	33	16	15	71	60	57	67	68
ENSMUSG00000028986	chr5	Klhl7	24100590	24100874	3419	-0.80496	5.151817	5.99E-06	4.08E-05	0.035762	-1	475	498	1231	712	837	253	609	424	631	487
ENSMUSG00000022620	chr15	Arsa	89472476	89473557	3680	0.883065	3.20029	6.06E-06	4.12E-05	0.037793	1	70	76	146	100	128	134	230	260	219	223
ENSMUSG00000051329	chr2	Nup160	90677215	90677470	8761	-0.90177	2.581427	6.06E-06	4.12E-05	0.035906	-1	84	78	208	114	156	56	104	68	78	71
ENSMUSG00000021950	chr14	Anxa8	34085981	34086076	1880	1.198646	1.720193	6.15E-06	4.18E-05	0.063068	1	23	17	54	26	40	83	94	103	67	50
ENSMUSG00000035697	chr10	Hmha1	80016653	80016918	4478	1.139752	2.71755	6.22E-06	4.23E-05	0.063937	1	68	47	95	42	74	193	122	182	165	121
ENSMUSG00000071454	chr12	Dtnb	3572381	3572647	9603	-1.19685	1.321938	6.26E-06	4.25E-05	0.052676	-1	52	35	78	38	71	30	21	22	32	26
ENSMUSG00000038084	chr16	Opa1	29579334	29579571	7875	-0.7495	6.680484	6.28E-06	4.26E-05	0.03207	-1	1465	1161	2996	2361	2691	983	1933	1169	1838	1203
ENSMUSG00000099552	chr1	9830004L10Rik	80184719	80184852	2333	-1.57088	2.182867	6.31E-06	4.28E-05	0.12291	-1	146	95	129	66	83	48	44	29	77	13
ENSMUSG00000030036	chr6	Mogs	83115496	83115926	2892	0.735728	3.52064	6.33E-06	4.29E-05	0.025741	1	135	87	161	146	154	208	288	258	312	228
ENSMUSG00000037580	chr14	Gch1	47153895	47155924	2775	1.464588	1.628525	6.34E-06	4.3E-05	0.095777	1	21	11	20	41	32	39	153	71	85	62
ENSMUSG00000066568	chr7	Lsm14a	34344646	34345958	3104	-0.66933	6.295632	6.39E-06	4.33E-05	0.025401	-1	1342	1104	2159	1452	1753	751	1349	1002	1495	1016
ENSMUSG00000022769	chr16	Sdf2l1	17130138	17130788	1108	1.187165	2.556384	6.41E-06	4.34E-05	0.069238	1	71	25	70	36	85	156	141	157	135	122
ENSMUSG00000031099	chrX	Smarca1	47809368	47810120	6118	-1.00364	2.690408	6.42E-06	4.35E-05	0.04821	-1	145	107	194	95	141	46	106	99	78	62
ENSMUSG00000020561	chr12	Twistnb	33429624	33429908	2324	-0.8074	3.446732	6.49E-06	4.38E-05	0.032297	-1	216	170	289	186	241	124	200	96	177	128
ENSMUSG00000100685	chr1	Gm28610	1.52E+08	1.52E+08	406	-1.98587	0.70765	6.48E-06	4.38E-05	0.169435	-1	14	8	61	52	76	3	15	10	18	11
ENSMUSG00000096727	chr17	Psmb9	34181988	34182351	3659	1.248775	2.175743	6.5E-06	4.39E-05	0.072091	1	38	38	45	30	55	117	120	149	77	85
ENSMUSG00000020075	chr10	Ddx21	62580248	62582607	4742	-0.64503	5.531003	6.58E-06	4.44E-05	0.023061	-1	779	683	1373	748	996	531	867	622	746	543
ENSMUSG00000018377	chr11	Vezf1	88068279	88068433	4601	-0.69803	6.508208	6.82E-06	4.6E-05	0.027938	-1	1543	1270	3043	1554	1844	885	1634	1179	1645	1092
ENSMUSG00000038521	chr6	C1s1	1.25E+08	1.25E+08	3129	0.76658	6.402105	6.84E-06	4.61E-05	0.033682	1	830	804	1657	709	1115	1560	2240	2132	1960	1746
ENSMUSG00000052276	chr16	Ostn	27307489	27307701	1423	-1.78126	2.820279	6.84E-06	4.61E-05	0.166531	-1	313	137	162	119	83	45	99	66	76	16
ENSMUSG00000002083	chr7	Bbc3	16309616	16309861	2008	1.448778	1.122418	6.87E-06	4.63E-05	0.083265	1	25	11	16	18	16	51	34	61	74	49
ENSMUSG00000045045	chr19	Lrfn4	4611785	4612638	3366	1.399211	1.477357	6.88E-06	4.63E-05	0.087539	1	14	10	25	35	35	40	86	107	66	53
ENSMUSG00000021759	chr13	Ppap2a	1.13E+08	1.13E+08	1635	0.673974	5.796011	6.9E-06	4.64E-05	0.025507	1	618	485	796	725	791	924	1550	1035	1742	1075
ENSMUSG00000062661	chr2	Ncs1	31245823	31246242	4653	0.739404	3.507145	6.92E-06	4.66E-05	0.026735	1	113	75	199	129	180	186	302	240	363	213
ENSMUSG00000003161	chr5	Sri	8046078	8046215	3734	0.692278	3.786189	6.93E-06	4.66E-05	0.023514	1	133	123	215	170	203	231	353	338	343	275
ENSMUSG00000038188	chr11	Scarf1	75513540	75513690	2887	0.958233	2.665419	6.95E-06	4.67E-05	0.044087	1	53	32	98	68	100	111	155	192	174	117
ENSMUSG00000037499	chr1	Nenf	1.91E+08	1.91E+08	742	0.747604	5.85688	7E-06	4.7E-05	0.031582	1	689	597	702	642	732	1120	1569	1171	1706	1091
ENSMUSG00000040829	chr11	Zmynd15	70459433	70460080	4409	1.750389	-0.19703	7.01E-06	4.71E-05	0.068891	1	7	4	6	5	5	15	20	29	20	20
ENSMUSG00000079657	chr17	Rab26	24527241	24527961	2852	-1.6366	-0.26297	7.03E-06	4.72E-05	0.06753	-1	16	8	21	19	27	3	10	5	11	4
ENSMUSG00000037652	chr3	Phc3	30899371	30907490	17485	-0.85603	4.058449	7.05E-06	4.72E-05	0.039068	-1	190	217	653	296	461	155	267	206	246	207
ENSMUSG00000041319	chr17	Thoc6	23668614	23668886	2026	0.797953	3.17797	7.04E-06	4.72E-05	0.029561	1	97	78	107	116	118	154	239	187	277	185
ENSMUSG00000038463	chr1	Olfml2b	1.71E+08	1.71E+08	3095	0.861379	3.879643	7.05E-06	4.73E-05	0.039452	1	139	94	320	128	192	276	322	381	365	347
ENSMUSG00000038812	chr19	Trmt112	6909698	6909855	1233	0.757036	4.410238	7.06E-06	4.73E-05	0.030402	1	279	200	291	205	263	412	520	446	641	409
ENSMUSG00000023921	chr17	Mut	40934685	40934779	3675	-0.71659	6.175432	7.08E-06	4.74E-05	0.029407	-1	1100	954	2076	1495	1736	656	1522	867	1152	894
ENSMUSG00000028212	chr4	Ccne2	11191351	11191544	3495	-1.0579	2.244375	7.1E-06	4.75E-05	0.051683	-1	93	68	174	85	96	29	53	50	88	59
ENSMUSG00000090124	chr1	Ugt1a7c	88095062	88095303	4219	1.477873	1.61687	7.09E-06	4.75E-05	0.099312	1	37	13	32	17	25	61	64	132	73	57
ENSMUSG00000042369	chr2	Rbm45	76369984	76370428	1898	0.752843	3.186442	7.1E-06	4.75E-05	0.025782	1	95	85	141	94	122	166	269	215	231	154
ENSMUSG00000061462	chr11	Obscn	58994256	58994509	28892	-1.03563	10.53386	7.2E-06	4.81E-05	0.062405	-1	18497	12903	58580	37347	45040	12014	18968	14463	26248	18096
ENSMUSG00000030301	chr6	Ccdc91	1.47E+08	1.47E+08	2827	-0.73286	6.915722	7.24E-06	4.83E-05	0.031174	-1	2310	2059	3225	1936	2429	1367	2181	1345	2075	1398
ENSMUSG00000090389	chr14	Gm7236	43121772	43122101	330	-1.758	-0.08645	7.25E-06	4.84E-05	0.087708	-1	14	17	35	17	24	2	14	9	2	8
ENSMUSG00000100916	chr7	LHB	45420820	45420967	642	1.699225	-0.06158	7.25E-06	4.84E-05	0.069166	1	5	7	7	2	10	17	23	25	36	16
ENSMUSG00000029605	chr5	Oas1b	1.21E+08	1.21E+08	1992	1.94179	-0.09825	7.28E-06	4.86E-05	0.102318	1	6	6	6	5	3	24	33	27	11	20
ENSMUSG00000027188	chr2	Pamr1	1.03E+08	1.03E+08	6046	0.933962	3.370648	7.3E-06	4.87E-05	0.04521	1	65	79	185	109	145	156	301	254	222	282
ENSMUSG00000020150	chr10	Gamt	80258151	80258457	1444	1.132552	4.839171	7.36E-06	4.9E-05	0.072111	1	392	215	451	142	221	697	621	694	968	561
ENSMUSG00000026082	chr1	Rev1	38052786	38053198	6168	-0.68826	4.631312	7.36E-06	4.9E-05	0.025523	-1	344	309	813	532	531	254	436	336	428	292
ENSMUSG00000029461	chr7	Fam168a	1.01E+08	1.01E+08	6632	-0.66839	5.599359	7.35E-06	4.9E-05	0.025138	-1	751	582	1620	869	1135	496	869	636	812	628
ENSMUSG00000027327	chr2	1700037H04Rik	1.31E+08	1.31E+08	2286	1.323796	2.878316	7.38E-06	4.91E-05	0.089786	1	83	59	44	52	76	148	159	294	204	126
ENSMUSG00000059355	chr8	Wdr83os	85080740	85081063	1031	0.644063	5.462784	7.44E-06	4.94E-05	0.023082	1	505	407	693	545	596	822	1110	884	1329	788
ENSMUSG00000091649	chr14	Phf11b	59320964	59321283	1184	1.954107	0.270638	7.46E-06	4.96E-05	0.136478	1	5	7	6	9	8	36	32	24	13	45
ENSMUSG00000032033	chr9	Barx2	31846044	31847055	1968	-2.73588	1.171934	7.55E-06	5.01E-05	0.353704	-1	12	12	26	168	89	5	22	7	14	6
ENSMUSG00000021838	chr14	Samd4	46882854	46883168	8529	-0.77648	5.571163	7.55E-06	5.01E-05	0.03434	-1	744	511	1721	985	1085	440	685	560	978	582
ENSMUSG00000020647	chr12	Ncoa1	4247363	4249750	7328	-0.75136	4.946848	7.62E-06	5.05E-05	0.031331	-1	447	382	1170	491	774	377	507	375	501	337
ENSMUSG00000031858	chr8	Mau2	70016123	70019660	5390	-0.85025	4.298169	7.74E-06	5.13E-05	0.039436	-1	323	188	766	348	526	218	315	187	328	235
ENSMUSG00000039911	chr4	Spsb1	1.5E+08	1.5E+08	4396	0.875706	3.017973	7.77E-06	5.15E-05	0.037079	1	57	73	130	108	86	126	219	187	225	188
ENSMUSG00000052730	chr6	Gm5111	48589445	48589694	1140	1.821371	-0.23707	7.81E-06	5.17E-05	0.075699	1	5	3	4	8	5	21	29	22	21	10
ENSMUSG00000051851	chrX	Cxx1c	53608032	53608432	401	1.068398	1.44659	7.85E-06	5.2E-05	0.042089	1	25	15	35	28	33	56	57	64	75	65
ENSMUSG00000033972	chr17	Zfp944	22337989	22340107	2784	-0.83174	2.670122	7.88E-06	5.21E-05	0.031581	-1	105	111	179	115	135	59	116	72	97	73
ENSMUSG00000024247	chr17	Pkdcc	83215292	83216104	2712	-0.76806	6.500703	7.95E-06	5.26E-05	0.034378	-1	1872	922	2442	1812	2298	1004	1411	1053	1815	927
ENSMUSG00000033257	chr1	Ttll4	74661745	74661889	11527	-0.77752	4.351451	7.95E-06	5.26E-05	0.032721	-1	343	252	785	304	476	231	321	290	290	230

ENSMUSG00000024413	chr18	Npc1	12189693	12191002	10725	-0.91314	5.53022	7.97E-06	5.27E-05	0.047832	-1	888	460	1837	803	1124	656	564	458	744	459
ENSMUSG00000090264	chr18	Eif4ebp3	36664060	36664302	744	0.877405	2.772561	7.98E-06	5.27E-05	0.035029	1	74	59	82	77	82	136	164	167	211	116
ENSMUSG00000031264	chrX	Btk	1.35E+08	1.35E+08	3149	1.479736	0.839671	7.99E-06	5.28E-05	0.085889	1	16	9	26	5	16	52	44	52	42	29
ENSMUSG00000001542	chr13	Ell2	75707484	75707797	3647	-0.68487	4.042263	8.04E-06	5.31E-05	0.024078	-1	286	203	513	299	361	188	243	247	266	199
ENSMUSG00000028708	chr4	Mknk1	1.16E+08	1.16E+08	4502	-0.6574	4.718176	8.09E-06	5.34E-05	0.023479	-1	423	297	752	519	662	277	482	379	452	292
ENSMUSG00000017418	chr2	Arl5b	15049395	15049685	10428	-0.82848	3.890789	8.1E-06	5.34E-05	0.036366	-1	207	151	565	295	389	138	273	177	232	165
ENSMUSG00000037731	chr4	Themis2	1.33E+08	1.33E+08	3079	1.248934	1.879307	8.11E-06	5.34E-05	0.072017	1	45	12	42	34	37	103	102	93	97	56
ENSMUSG00000034647	chr17	Ankrd12	65967501	65970337	11508	-0.76523	3.615634	8.21E-06	5.41E-05	0.029593	-1	172	193	402	187	309	124	188	171	196	146
ENSMUSG00000031503	chr8	Col4a2	11312805	11313114	6619	0.788945	6.7122	8.37E-06	5.51E-05	0.036601	1	864	654	1704	1320	1869	1822	2391	2345	3307	2272
ENSMUSG00000039182	chr13	AW209491	14630245	14630284	2023	-0.74598	3.708522	8.37E-06	5.51E-05	0.02843	-1	213	161	335	278	340	158	250	136	190	155
ENSMUSG00000039217	chr9	Il18	50575273	50575348	714	1.687698	0.512794	8.45E-06	5.56E-05	0.110346	1	13	6	18	1	12	37	48	38	44	15
ENSMUSG00000050323	chr4	Ndufaf6	11051045	11051225	1235	-0.71302	4.026355	8.49E-06	5.58E-05	0.026911	-1	309	239	351	306	397	178	286	179	314	182
ENSMUSG00000089075	chr3	Gm23820	1.03E+08	1.03E+08	300	-1.59723	-0.07842	8.5E-06	5.58E-05	0.062162	-1	21	19	26	17	19	7	6	6	9	10
ENSMUSG00000029634	chr5	Rnf6	1.46E+08	1.46E+08	4022	-0.66426	5.340044	8.54E-06	5.6E-05	0.024981	-1	633	592	1212	669	949	383	746	544	648	557
ENSMUSG00000029765	chr6	Plxna4	32144268	32150584	12877	-1.6548	1.890005	8.56E-06	5.62E-05	0.136396	-1	39	24	109	146	146	27	39	43	23	24
ENSMUSG00000055546	chr11	Timd4	46810800	46810869	2173	-1.61971	0.546292	8.62E-06	5.65E-05	0.099124	-1	23	28	72	16	33	12	18	15	11	5
ENSMUSG00000082536	chr2	Gm13456	40555752	40557116	1365	0.903929	2.819718	8.63E-06	5.66E-05	0.039233	1	51	62	107	92	77	140	160	190	181	144
ENSMUSG00000035397	chr10	Klf16	80567124	80569222	2674	1.060074	1.895745	8.65E-06	5.67E-05	0.046804	1	38	33	52	23	40	68	107	74	136	66
ENSMUSG00000042529	chr11	Kcnj12	61022564	61022850	2750	-0.71646	5.423823	8.65E-06	5.67E-05	0.029282	-1	679	450	1342	810	1183	466	738	524	643	585
ENSMUSG00000044250	chr15	Pced1b	97247107	97247164	2198	1.383648	0.484312	8.66E-06	5.67E-05	0.055997	1	10	10	12	9	15	34	39	25	50	21
ENSMUSG00000043263	chr1	Pyhin1	1.74E+08	1.74E+08	3547	1.539039	0.597863	8.67E-06	5.67E-05	0.084989	1	11	10	17	9	10	46	37	42	23	34
ENSMUSG00000028278	chr4	Rragd	32983037	32983607	5173	-0.74858	8.148545	8.69E-06	5.68E-05	0.033383	-1	5253	4024	9341	4391	6163	2848	5274	3044	4452	3869
ENSMUSG00000040797	chr6	Iqsec3	1.21E+08	1.21E+08	13603	1.268377	0.908557	8.76E-06	5.73E-05	0.055646	1	14	8	17	18	26	41	47	31	65	42
ENSMUSG00000052305	chr7	Hbb-bs	1.04E+08	1.04E+08	863	0.797169	5.986288	8.77E-06	5.73E-05	0.036975	1	633	598	881	866	668	1313	1983	1086	1991	1081
ENSMUSG00000092511	chr17	Gm20547	34856412	34856582	3902	1.130806	4.696395	8.81E-06	5.75E-05	0.072715	1	298	261	366	152	179	658	719	779	664	382
ENSMUSG00000098416	chr15	Mir7117	27571494	27571558	65	-2.10214	0.041995	8.81E-06	5.75E-05	0.165306	-1	15	5	18	48	38	5	10	4	7	6
ENSMUSG00000079550	chr1	Mpp4	59120935	59121444	7063	1.017234	2.249636	8.94E-06	5.83E-05	0.045603	1	42	51	55	40	52	98	136	82	156	97
ENSMUSG00000090942	chr18	F830016B08Rik	60293380	60293486	3297	-1.85872	4.265466	9.01E-06	5.87E-05	0.192302	-1	233	215	1441	195	669	121	335	53	219	75
ENSMUSG00000015957	chr7	Wnt11	98835112	98835348	3633	0.922437	2.914077	9.03E-06	5.88E-05	0.042476	1	50	50	108	106	105	143	234	122	234	163
ENSMUSG00000022141	chr15	Nipbl	8291225	8291590	8815	-0.76058	4.875074	9.03E-06	5.88E-05	0.032584	-1	418	335	1153	523	699	324	460	396	460	343
ENSMUSG00000038143	chr8	Stox2	47180048	47186572	10839	-0.92351	3.101793	9.16E-06	5.97E-05	0.043339	-1	108	95	326	171	246	72	118	115	127	104
ENSMUSG00000027652	chr2	Ralgapb	1.58E+08	1.58E+08	12992	-0.72439	5.418865	9.26E-06	6.02E-05	0.030201	-1	676	426	1497	844	1048	430	756	545	705	531
ENSMUSG00000021357	chr13	Exoc2	30813919	30815391	4427	-0.65357	4.35128	9.28E-06	6.03E-05	0.022828	-1	349	283	576	352	461	206	324	327	332	255
ENSMUSG00000000058	chr6	Cav2	17281185	17281510	3335	-0.85753	4.262236	9.33E-06	6.06E-05	0.040996	-1	326	288	505	385	484	145	261	369	241	219
ENSMUSG00000038831	chr2	Ralgps1	33133417	33137709	7657	-1.02186	1.807395	9.33E-06	6.06E-05	0.042928	-1	46	50	128	65	91	40	53	36	44	32
ENSMUSG00000013160	chr8	Atp6v0d1	1.06E+08	1.06E+08	1793	0.637855	5.438025	9.34E-06	6.07E-05	0.023173	1	485	387	717	544	590	803	1041	1045	1128	776
ENSMUSG00000046598	chr16	Bdh1	31422280	31422512	3800	-4.7192	3.863058	9.42E-06	6.12E-05	0.950496	-1	12	16	60	1373	847	2	13	4	75	14
ENSMUSG00000018293	chr11	Pfn1	70651850	70652221	2405	0.703426	7.314137	9.43E-06	6.12E-05	0.029528	1	2018	1350	2283	1780	2215	3026	4104	3468	4736	2780
ENSMUSG00000059890	chr9	Ube4a	44923131	44925975	8635	-0.75029	5.524968	9.46E-06	6.14E-05	0.032631	-1	631	646	1808	809	944	531	710	576	735	568
ENSMUSG00000073489	chr1	Ifi204	1.74E+08	1.74E+08	3561	1.041043	3.325151	9.52E-06	6.17E-05	0.058128	1	90	84	172	68	114	243	345	269	161	180
ENSMUSG00000033940	chr6	Brk1	1.14E+08	1.14E+08	1092	0.654991	5.790034	9.54E-06	6.18E-05	0.024854	1	657	475	819	690	792	1108	1387	1174	1557	949
ENSMUSG00000028249	chr4	Sdcbp	6365650	6365759	6904	0.66729	5.698637	9.7E-06	6.28E-05	0.02579	1	580	477	819	618	716	835	1289	1389	1329	970
ENSMUSG00000041845	chr19	Rhod	4425459	4426256	1714	1.699509	0.318431	9.69E-06	6.28E-05	0.100455	1	7	8	9	3	15	30	26	42	44	14
ENSMUSG00000036473	chr17	Tbc1d24	24175431	24181395	8053	-0.89388	2.940437	9.75E-06	6.31E-05	0.039976	-1	124	75	272	156	204	61	137	88	123	85
ENSMUSG00000037868	chr10	Egr2	67535475	67535530	3398	1.523238	0.895882	9.75E-06	6.31E-05	0.095183	1	10	8	15	16	23	22	83	63	35	35
ENSMUSG00000029007	chr4	Agtrap	1.48E+08	1.48E+08	4236	0.676642	4.495048	9.76E-06	6.31E-05	0.025114	1	237	159	369	306	340	369	606	477	727	388
ENSMUSG00000025195	chr19	Dnmbp	43847967	43848278	4882	-0.85941	3.647153	9.81E-06	6.34E-05	0.039244	-1	178	127	503	238	325	122	197	140	197	155
ENSMUSG00000018593	chr11	Sparc	55394500	55395613	3367	0.693046	8.562916	9.89E-06	6.39E-05	0.029055	1	3921	3249	6933	4054	5481	7436	8785	7740	9707	8458
ENSMUSG00000089810	chr9	Gm16536	45856769	45858357	1589	0.759232	3.259466	9.9E-06	6.39E-05	0.028395	1	70	82	180	118	127	170	253	210	273	185
ENSMUSG00000021470	chr13	Ercc6l2	63815240	63815517	7681	-0.69621	4.80367	9.92E-06	6.4E-05	0.027243	-1	463	341	956	475	632	282	514	334	441	382
ENSMUSG00000022463	chr15	Srebf2	82147266	82147490	4989	0.67863	4.125253	9.94E-06	6.41E-05	0.024748	1	171	119	311	226	273	315	410	406	473	340
ENSMUSG00000030589	chr7	Rasgrp4	29134854	29135095	6359	1.366239	0.951322	1E-05	6.45E-05	0.072113	1	14	12	28	14	14	40	52	71	36	35
ENSMUSG00000037306	chr4	Man1c1	1.35E+08	1.35E+08	5722	0.783407	3.181437	1E-05	6.46E-05	0.030869	1	78	55	168	101	147	173	237	210	227	183
ENSMUSG00000032238	chr9	Rora	68653786	68653972	13071	-0.82781	6.592434	1E-05	6.46E-05	0.040921	-1	1686	1387	3977	1311	1973	956	1479	1223	1770	1008
ENSMUSG00000016319	chrX	Slc25a5	36795651	36795841	1646	0.744473	5.34026	1.01E-05	6.52E-05	0.032137	1	408	319	521	596	571	776	1022	1085	1058	672
ENSMUSG00000069729	chr17	Arid1b	4994332	4994399	12600	-0.66771	5.143194	1.02E-05	6.58E-05	0.025445	-1	534	428	1119	626	896	359	573	445	640	485
ENSMUSG00000007888	chr8	Crlf1	70493158	70493400	1644	1.084183	1.591091	1.02E-05	6.59E-05	0.047063	1	20	21	34	42	31	50	81	59	98	72
ENSMUSG00000024236	chr18	Svil	4920540	4920874	10640	-0.8068	7.818171	1.03E-05	6.6E-05	0.039309	-1	3097	2351	8484	4720	5826	2038	3632	2620	4090	2823
ENSMUSG00000020671	chr12	Rab10	3247430	3249870	3511	-0.71656	8.309627	1.03E-05	6.62E-05	0.03115	-1	5729	4811	10033	4913	6607	3148	5491	3756	6228	3721
ENSMUSG00000070469	chr7	Adamtsl3	82335694	82335910	7732	-1.21443	2.049692	1.04E-05	6.65E-05	0.071271	-1	46	53	148	96	133	29	65	36	35	56
ENSMUSG00000026443	chr1	Lrrn2	1.33E+08	1.33E+08	3595	1.634239	-0.02618	1.04E-05	6.68E-05	0.079934	1	5	2	9	4	14	11	27	22	37	23
ENSMUSG00000006585	chr8	Cdt1	1.23E+08	1.23E+08	2189	1.541497	0.090304	1.04E-05	6.69E-05	0.070535	1	7	3	9	6	14	22	19	24	32	29
ENSMUSG00000089788	chr1	Gm16586	1.78E+08	1.78E+08	2640	0.930216	3.189939	1.04E-05	6.7E-05	0.045098	1	97	77	146	54	129	168	225	264	225	186
ENSMUSG00000026103	chr1	Gls	52163448	52166314	15057	-0.69166	5.95065	1.05E-05	6.71E-05	0.028284	-1	986	698	1961	1164	1554	612	1069	867	1180	665
ENSMUSG00000097145	chr5	9230114K14Rik	52190681	52190937	2118	-1.74413	0.071412	1.05E-05	6.76E-05	0.097784	-1	12	21	40	18	30	6	4	4	11	14

ENSMUSG00000034485	chr9	Uaca	60794548	60794692	4428	-0.7778	7.556824	1.06E-05	6.78E-05	0.036617	-1	2501	2394	4934	4871	4761	1920	2928	2043	3582	2336
ENSMUSG00000025784	chr9	Clec3b	1.23E+08	1.23E+08	990	0.795271	6.210746	1.06E-05	6.8E-05	0.03771	1	791	723	1153	687	964	1399	1647	2208	1725	1454
ENSMUSG00000056602	chr5	Fry	1.5E+08	1.5E+08	10729	-0.7343	5.459527	1.07E-05	6.82E-05	0.031592	-1	642	466	1540	900	1081	389	785	600	743	539
ENSMUSG00000062031	chr7	Athl1	1.41E+08	1.41E+08	3346	0.902667	2.780722	1.08E-05	6.93E-05	0.040556	1	57	50	127	63	92	129	158	191	154	157
ENSMUSG00000068196	chr16	Col8a1	57624258	57628817	5108	1.109356	3.13762	1.09E-05	6.94E-05	0.067482	1	39	45	120	109	148	125	252	189	262	257
ENSMUSG00000063953	chr10	Amd2	35708691	35711891	3201	-2.29095	3.206125	1.1E-05	7.03E-05	0.284292	-1	335	163	444	90	209	85	124	15	63	6
ENSMUSG00000071708	chrX	Sms	1.57E+08	1.57E+08	6010	-0.93846	7.285222	1.1E-05	7.04E-05	0.053283	-1	3212	3540	4228	1917	2978	1582	2382	1690	2488	1694
ENSMUSG00000020386	chr11	Sar1b	51763687	51763791	1255	-0.83968	8.572101	1.11E-05	7.05E-05	0.042985	-1	6838	7933	10765	5901	6849	3372	6047	4447	6421	4884
ENSMUSG00000031618	chr8	Nr3c2	76899442	76899567	6474	-0.91502	3.410839	1.12E-05	7.13E-05	0.045115	-1	144	124	329	268	280	81	208	100	150	140
ENSMUSG00000042515	chrX	Mum1l1	1.39E+08	1.39E+08	4859	-1.07601	1.68804	1.12E-05	7.17E-05	0.050207	-1	47	60	103	56	79	22	47	49	33	33
ENSMUSG00000021508	chr13	Cxcl14	56288647	56289807	1823	0.819671	6.219479	1.13E-05	7.18E-05	0.040475	1	597	482	1329	822	1292	1710	2541	1397	1826	1243
ENSMUSG00000031561	chr8	Tenm3	48227682	48229201	11132	-1.00709	3.281883	1.14E-05	7.25E-05	0.055323	-1	130	109	436	165	270	77	192	95	134	100
ENSMUSG00000012017	chr16	Scarf2	17797282	17797527	3302	0.932365	2.910716	1.14E-05	7.28E-05	0.045319	1	65	43	120	75	119	135	142	176	232	191
ENSMUSG00000075590	chr15	Nrbp2	76085595	76087144	2495	1.014884	2.94965	1.15E-05	7.31E-05	0.052703	1	87	71	96	73	66	120	220	258	198	136
ENSMUSG00000053768	chr6	Chchd3	32790976	32791137	2905	-0.80084	7.803119	1.15E-05	7.31E-05	0.039189	-1	3395	2970	4917	6018	5491	2219	4435	2260	3830	2474
ENSMUSG00000003752	chr7	Itpkc	27207172	27208444	3644	0.840131	2.554623	1.15E-05	7.33E-05	0.032359	1	57	39	96	73	71	100	192	134	155	102
ENSMUSG00000046532	chrX	Ar	98149721	98151334	9096	-0.80986	5.367047	1.17E-05	7.42E-05	0.038898	-1	903	578	1243	529	1014	524	686	553	623	353
ENSMUSG00000025930	chr1	Msc	14753346	14754325	2546	1.461058	1.019306	1.17E-05	7.44E-05	0.093847	1	23	6	25	8	21	56	41	63	50	38
ENSMUSG00000021583	chr13	Erap1	74639872	74639893	4014	-0.6808	4.124377	1.18E-05	7.51E-05	0.025129	-1	265	271	554	276	382	188	276	257	281	215
ENSMUSG00000022639	chr16	5330426P16Rik	50719294	50720546	4679	1.014003	2.03558	1.19E-05	7.52E-05	0.048018	1	27	26	74	38	54	67	114	118	89	94
ENSMUSG00000022193	chr14	Psmb5	54614120	54614481	871	0.760808	7.127039	1.19E-05	7.56E-05	0.035267	1	1544	1439	1764	1614	1739	2706	3642	2720	4783	2422
ENSMUSG00000073705	chr4	Apitd1	1.49E+08	1.49E+08	1909	1.762944	-0.11395	1.19E-05	7.57E-05	0.081215	1	9	5	2	5	7	20	23	29	26	14
ENSMUSG00000038127	chr16	Ccdc50	27388869	27389137	8639	-0.85473	6.45625	1.2E-05	7.59E-05	0.044332	-1	1636	1678	3073	1141	1558	1011	1340	1033	1354	962
ENSMUSG00000044367	chr11	Slc16a13	70216789	70217921	2601	1.808788	0.024664	1.21E-05	7.64E-05	0.119055	1	6	0	5	9	12	28	23	14	39	22
ENSMUSG00000040061	chr2	Plcb2	1.19E+08	1.19E+08	6597	1.77475	-0.49443	1.21E-05	7.64E-05	0.057762	1	4	3	5	4	5	15	17	18	16	16
ENSMUSG00000023094	chr2	Msrb2	19371440	19371543	1377	-0.93546	4.267844	1.22E-05	7.71E-05	0.050799	-1	261	251	375	590	549	173	380	213	261	198
ENSMUSG00000067736	chr1	Gm10222	24612407	24612700	294	-1.64234	1.613709	1.23E-05	7.76E-05	0.135329	-1	18	28	107	87	147	16	33	24	31	27
ENSMUSG00000031078	chr7	Cttn	1.44E+08	1.44E+08	4192	0.627918	4.955454	1.23E-05	7.79E-05	0.022454	1	293	306	467	394	490	540	822	647	823	606
ENSMUSG00000069895	chr8	Atxn1l	1.1E+08	1.1E+08	7526	-0.7436	4.272765	1.23E-05	7.79E-05	0.031068	-1	259	223	617	364	561	171	311	260	332	252
ENSMUSG00000024889	chr19	Rce1	4622551	4623242	1446	0.914385	2.305472	1.24E-05	7.8E-05	0.037922	1	61	31	63	50	63	86	129	102	144	114
ENSMUSG00000022228	chr13	Zscan26	21442175	21445829	4371	-0.6627	3.978536	1.24E-05	7.81E-05	0.023489	-1	260	223	425	281	370	144	265	242	256	207
ENSMUSG00000061601	chr5	Pclo	14514918	14515460	19182	1.490042	0.395453	1.24E-05	7.84E-05	0.081712	1	10	4	24	4	10	22	46	22	36	35
ENSMUSG00000027490	chr2	E2f1	1.55E+08	1.55E+08	3154	1.29655	0.833695	1.26E-05	7.91E-05	0.060187	1	18	11	21	9	18	48	42	45	43	33
ENSMUSG00000036499	chr10	Eea1	95940663	95940972	7836	-0.75389	5.066063	1.26E-05	7.93E-05	0.033454	-1	489	438	1187	609	782	296	432	448	641	464
ENSMUSG00000001228	chr17	Uhrf1	56303321	56303561	4259	1.899702	0.295659	1.26E-05	7.96E-05	0.144681	1	6	2	8	13	9	42	27	31	14	37
ENSMUSG00000028339	chr4	Col15a1	47208161	47208362	6349	0.934879	5.662639	1.29E-05	8.1E-05	0.053015	1	376	268	781	577	923	759	1238	1371	1179	1423
ENSMUSG00000078945	chr13	Naip2	1E+08	1E+08	4846	1.353449	0.449404	1.29E-05	8.13E-05	0.056994	1	15	3	12	12	14	30	35	31	39	27
ENSMUSG00000029657	chr5	Hsph1	1.5E+08	1.5E+08	7042	-0.72014	6.46033	1.3E-05	8.16E-05	0.031644	-1	1770	1049	2092	1662	2282	1077	1216	1281	1368	1056
ENSMUSG00000028873	chr4	Cdca8	1.25E+08	1.25E+08	5177	1.785798	-0.22036	1.31E-05	8.23E-05	0.103085	1	6	1	9	5	6	20	20	25	11	25
ENSMUSG00000031441	chr8	Atp11a	12757014	12757352	11150	-0.85612	5.220158	1.31E-05	8.24E-05	0.043901	-1	513	318	1374	829	1079	339	601	488	635	391
ENSMUSG00000103508	chr9	Map4	1.1E+08	1.1E+08	3378	-0.80569	7.782837	1.32E-05	8.27E-05	0.040178	-1	3159	2413	7828	4552	5735	2054	3577	2125	3906	3112
ENSMUSG00000103653	chr1	WI1-1003N17.1	1.92E+08	1.92E+08	631	0.947973	3.596494	1.33E-05	8.33E-05	0.049519	1	134	126	182	115	81	201	319	281	418	240
ENSMUSG00000060032	chr6	H2afj	1.37E+08	1.37E+08	1827	0.935421	3.024461	1.33E-05	8.35E-05	0.044866	1	87	89	101	64	88	161	197	214	250	139
ENSMUSG00000060180	chr11	Myh13	67321658	67321806	6180	-2.75252	3.300784	1.34E-05	8.39E-05	0.405714	-1	53	7	801	423	300	14	75	32	67	50
ENSMUSG00000066456	chr9	Hmgn3	83109948	83110429	1869	1.101943	1.923387	1.34E-05	8.39E-05	0.054349	1	37	38	35	32	39	79	84	106	98	82
ENSMUSG00000062585	chr4	Cnr2	1.36E+08	1.36E+08	3982	1.728716	0.048878	1.34E-05	8.42E-05	0.098022	1	5	3	10	11	5	26	31	34	14	20
ENSMUSG00000020366	chr11	Mapk9	49846751	49846975	6784	-0.67577	5.928046	1.35E-05	8.44E-05	0.027646	-1	1036	924	1970	959	1212	693	1024	779	1027	763
ENSMUSG00000041355	chr3	Ssr2	88575876	88575980	1864	0.694477	5.375474	1.36E-05	8.49E-05	0.028603	1	529	402	657	452	462	760	1097	995	1111	724
ENSMUSG00000039153	chr17	Runx2	44495987	44497243	8837	1.339122	0.850758	1.37E-05	8.55E-05	0.070795	1	6	10	22	17	23	31	47	34	47	58
ENSMUSG00000033943	chr2	Mga	1.2E+08	1.2E+08	15340	-0.73066	4.729872	1.37E-05	8.55E-05	0.03105	-1	352	308	992	499	645	291	449	336	415	329
ENSMUSG00000096252	chr13	Tes3-ps	49493615	49494819	1205	-1.53265	0.485628	1.37E-05	8.59E-05	0.090853	-1	21	30	55	26	26	9	22	3	14	14
ENSMUSG00000046668	chr18	Cxxc5	35829818	35829986	2271	0.691397	4.811497	1.38E-05	8.61E-05	0.027706	1	259	281	482	324	379	397	898	570	722	612
ENSMUSG00000026491	chr1	Ahctf1	1.8E+08	1.8E+08	15116	-0.68368	5.365764	1.38E-05	8.61E-05	0.027869	-1	575	542	1432	726	963	425	747	620	620	487
ENSMUSG00000093156	chr14	Mir3076	30572149	30572208	60	1.803483	2.099244	1.38E-05	8.61E-05	0.172362	1	35	30	32	17	29	110	70	253	83	52
ENSMUSG00000032245	chr9	Cln6	62838785	62838954	2434	0.654511	4.452819	1.41E-05	8.81E-05	0.02415	1	219	181	336	295	339	361	525	438	681	446
ENSMUSG00000042842	chr13	Serpinb6b	32965209	32965543	2200	0.964855	2.328136	1.41E-05	8.81E-05	0.045071	1	40	34	70	63	62	81	157	80	144	133
ENSMUSG00000025362	chr10	Rps26	1.29E+08	1.29E+08	447	0.735494	6.871637	1.42E-05	8.85E-05	0.033449	1	1424	1243	1632	1207	1350	2322	3318	2462	3217	2093
ENSMUSG00000032932	chr16	Hspa13	75755190	75758448	5894	-0.70057	3.511945	1.42E-05	8.85E-05	0.0252	-1	171	160	364	195	264	122	190	157	172	146
ENSMUSG00000075330	chr16	A930003A15Rik	19876570	19877110	746	1.657093	1.753026	1.42E-05	8.85E-05	0.135834	1	44	26	11	13	20	70	123	62	112	86
ENSMUSG00000025277	chr14	Abhd6	8002902	8002963	2157	-0.82705	2.586329	1.44E-05	8.94E-05	0.032282	-1	120	74	165	124	130	63	107	79	88	56
ENSMUSG00000020593	chr12	Lpin1	16535669	16538572	5725	-0.81454	7.875507	1.44E-05	8.94E-05	0.041443	-1	4292	2121	8450	4763	5676	2742	3794	2687	4382	2165
ENSMUSG00000038970	chr5	Lmtk2	1.44E+08	1.44E+08	8114	-0.71496	5.057657	1.44E-05	8.97E-05	0.030337	-1	531	322	1088	673	858	349	513	424	612	414
ENSMUSG00000038633	chr1	Degs1	1.82E+08	1.82E+08	2591	0.650538	4.676863	1.45E-05	9E-05	0.024292	1	275	229	414	288	396	449	659	660	622	448
ENSMUSG00000038859	chr5	Baiap2l1	1.44E+08	1.44E+08	3366	1.763649	0.537118	1.45E-05	9E-05	0.140262	1	3	0	12	21	14	34	37	33	47	34
ENSMUSG00000029001	chr4	Fbxo44	1.48E+08	1.48E+08	3024	-1.17895	2.430933	1.47E-05	9.11E-05	0.074577	-1	79	44	146	177	165	44	73	42	96	48

ENSMUSG00000027287	chr2	Snap23	1.21E+08	1.21E+08	4293	-0.71541	5.197712	1.47E-05	9.13E-05	0.030677	-1	524	555	1150	624	888	376	758	450	478	483
ENSMUSG00000035004	chr7	Igsf6	1.21E+08	1.21E+08	2133	1.589079	1.003715	1.47E-05	9.13E-05	0.116366	1	15	9	28	5	21	63	46	71	38	31
ENSMUSG00000074807	chr2	Gm10762	1.29E+08	1.29E+08	1133	-0.71424	4.298235	1.47E-05	9.13E-05	0.029379	-1	403	298	482	329	425	170	313	253	402	242
ENSMUSG00000023272	chr15	Creld2	88819646	88819834	1364	0.927714	3.284374	1.48E-05	9.17E-05	0.046899	1	95	87	132	92	123	263	243	256	193	165
ENSMUSG00000021945	chr14	Zmym2	56887795	56887857	6876	-0.69317	5.157471	1.48E-05	9.17E-05	0.028775	-1	612	523	1199	560	715	378	706	398	642	409
ENSMUSG00000024068	chr17	Spast	74338987	74339445	4696	-0.64097	5.659687	1.49E-05	9.22E-05	0.024911	-1	821	810	1505	817	1020	529	917	658	929	616
ENSMUSG00000055296	chr4	Tmem245	56866923	56880292	17090	-0.73392	5.250496	1.49E-05	9.22E-05	0.032416	-1	495	419	1289	724	1092	386	692	515	594	442
ENSMUSG00000055493	chr10	Epm2a	11343404	11343768	3287	-0.63495	6.85907	1.49E-05	9.23E-05	0.025076	-1	1853	1640	3130	2282	2523	1261	2202	1391	2008	1520
ENSMUSG00000035620	chr10	Ric8b	84917616	84917825	3068	-0.81209	5.176343	1.5E-05	9.26E-05	0.039979	-1	483	398	950	958	1010	309	604	386	685	455
ENSMUSG00000022415	chr15	Syngr1	80091334	80091492	4808	-0.71348	5.136726	1.52E-05	9.4E-05	0.030652	-1	658	592	756	689	721	439	610	457	615	329
ENSMUSG00000001082	chr5	Mfsd10	34633642	34634014	2752	1.111231	2.095094	1.52E-05	9.4E-05	0.061848	1	21	32	55	33	75	99	114	122	108	70
ENSMUSG00000021456	chr13	Fbp2	62836884	62837280	1325	0.915436	5.47369	1.54E-05	9.51E-05	0.051336	1	540	312	664	487	459	670	1798	1159	1362	533
ENSMUSG00000029919	chr6	Hpgds	65117293	65120088	3586	1.428761	1.197305	1.55E-05	9.54E-05	0.096216	1	20	13	38	4	22	43	63	79	56	45
ENSMUSG00000027331	chr2	Knstrn	1.19E+08	1.19E+08	5158	2.045138	-0.47686	1.55E-05	9.57E-05	0.105268	1	1	6	3	5	3	19	15	19	12	20
ENSMUSG00000020722	chr11	Cacng1	1.08E+08	1.08E+08	1249	1.022728	8.540912	1.56E-05	9.6E-05	0.065532	1	4281	4064	5507	2295	2900	7829	10002	7335	13952	7075
ENSMUSG00000072214	chr16	Sept5	18621811	18622796	2127	1.041518	2.474122	1.56E-05	9.6E-05	0.056265	1	30	38	74	80	67	112	112	123	166	144
ENSMUSG00000022263	chr15	Trio	27730652	27733030	11494	-0.94127	4.698251	1.56E-05	9.62E-05	0.053432	-1	329	220	970	598	816	228	460	272	349	322
ENSMUSG00000067288	chr17	Rps28	33819027	33819218	1464	0.734449	6.537119	1.57E-05	9.66E-05	0.033536	1	1153	944	1237	1044	1052	1873	2547	1991	2570	1632
ENSMUSG00000003352	chr15	Cacnb3	98632220	98632520	3120	1.08639	0.942469	1.57E-05	9.69E-05	0.038779	1	15	12	25	19	22	40	50	45	45	41
ENSMUSG00000052920	chr19	Prkg1	30567551	30569336	7799	-2.70623	2.822178	1.58E-05	9.74E-05	0.397904	-1	20	26	160	434	394	11	87	16	39	28
ENSMUSG00000020463	chr11	Smek2	29172890	29173447	5694	-0.6538	4.225025	1.59E-05	9.77E-05	0.02405	-1	274	273	584	326	410	189	333	295	307	209
ENSMUSG00000036086	chr1	Zranb3	1.28E+08	1.28E+08	9079	-0.71424	3.247631	1.59E-05	9.8E-05	0.025739	-1	172	129	280	151	222	111	158	125	144	112
ENSMUSG00000022842	chr16	Ece2	20611593	20611820	6547	0.843655	2.289553	1.6E-05	9.8E-05	0.031127	1	49	39	60	55	70	88	140	111	135	88
ENSMUSG00000031778	chr8	Cx3cl1	94772009	94772334	3708	1.743211	1.733755	1.6E-05	9.81E-05	0.163194	1	4	10	20	42	45	46	129	121	77	78
ENSMUSG00000026880	chr2	Stom	35313986	35316055	2787	0.768873	6.240475	1.6E-05	9.81E-05	0.036727	1	776	613	943	1203	883	1237	2215	1626	2372	1402
ENSMUSG00000035278	chr10	Plekhj1	80796100	80796522	1259	0.704501	4.078263	1.6E-05	9.84E-05	0.027475	1	190	184	262	184	186	293	445	377	488	308
ENSMUSG00000029004	chr5	Kmt2e	23434441	23434783	7607	-0.85542	4.662494	1.61E-05	9.85E-05	0.043942	-1	334	295	965	506	660	193	316	325	450	362
ENSMUSG00000026207	chr1	Speg	75375297	75375833	12741	-0.83762	8.009715	1.62E-05	9.9E-05	0.044349	-1	3684	2513	9185	5731	6986	2314	3563	2830	4763	3529
ENSMUSG00000029053	chr4	Prkcz	1.55E+08	1.55E+08	6318	-1.04801	1.409605	1.62E-05	9.91E-05	0.044023	-1	37	35	94	64	55	27	32	33	36	24
ENSMUSG00000029177	chr5	Cenpa	30666777	30667113	2503	1.23185	0.814359	1.62E-05	9.94E-05	0.053187	1	12	12	15	15	24	43	50	31	44	39
ENSMUSG00000095990	chr17	Zfp97	17121415	17121537	2684	-1.34218	1.35026	1.62E-05	9.94E-05	0.086141	-1	39	40	83	64	62	19	57	17	14	22
ENSMUSG00000030330	chr6	Ing4	1.25E+08	1.25E+08	6675	0.648326	4.917743	1.63E-05	1E-04	0.024797	1	376	251	480	370	406	597	706	695	802	539
ENSMUSG00000035885	chr19	Cox8a	7215158	7215484	545	0.852441	5.248258	1.64E-05	0.0001	0.044482	1	470	272	422	470	502	746	839	1183	1042	614
ENSMUSG00000023021	chr15	Cers5	99734881	99736436	3542	0.91423	3.289929	1.64E-05	0.0001	0.045608	1	108	93	133	85	110	203	188	285	294	170
ENSMUSG00000032369	chr9	Plscr1	92249750	92250360	2462	1.353568	1.079533	1.65E-05	0.000101	0.080162	1	11	12	22	23	22	54	89	51	43	25
ENSMUSG00000046185	chr7	Zfp84	29768552	29768695	4113	-0.87957	2.684703	1.65E-05	0.000101	0.039171	-1	99	93	162	132	181	54	111	57	101	89
ENSMUSG00000001123	chr11	Lgals9	78962974	78963541	2137	0.824164	3.717793	1.65E-05	0.000101	0.038189	1	151	101	196	141	168	266	417	343	228	251
ENSMUSG00000020431	chr11	Adcy1	7063489	7064235	12522	-1.43628	0.853188	1.66E-05	0.000101	0.084976	-1	24	13	81	40	56	18	20	16	18	11
ENSMUSG00000028796	chr4	Phc2	1.29E+08	1.29E+08	7064	0.610141	4.645618	1.67E-05	0.000102	0.02138	1	272	216	398	333	372	453	623	527	709	449
ENSMUSG00000032112	chr9	Trappc4	44403761	44404098	1166	0.730902	4.407819	1.67E-05	0.000102	0.030824	1	252	229	289	216	256	421	551	471	616	355
ENSMUSG00000076275	chr7	Mir675	1.43E+08	1.43E+08	84	1.378048	6.135722	1.68E-05	0.000102	0.117099	1	341	346	480	1163	787	786	3530	1428	1898	1957
ENSMUSG00000024241	chr17	Sos1	80393752	80398672	8919	-0.68998	4.524335	1.68E-05	0.000102	0.027775	-1	318	277	773	443	557	239	337	293	445	298
ENSMUSG00000101609	chr7	Kcnq1ot1	1.43E+08	1.43E+08	84395	1.323693	1.078629	1.68E-05	0.000102	0.078149	1	15	10	27	10	32	55	48	55	40	53
ENSMUSG00000026630	chr1	Batf3	1.91E+08	1.91E+08	1597	1.884114	-0.24802	1.68E-05	0.000102	0.10667	1	11	0	5	4	4	21	27	14	25	16
ENSMUSG00000059741	chr9	Myl3	1.11E+08	1.11E+08	1306	-6.38912	5.1186	1.68E-05	0.000102	1.554595	-1	2	4	5	4185	1322	3	54	3	23	3
ENSMUSG00000066440	chr12	Zfyve26	79232347	79234169	9368	-0.69699	4.197841	1.69E-05	0.000103	0.02771	-1	291	191	624	339	453	193	300	225	337	229
ENSMUSG00000062210	chr18	Tnfaip8	49979427	49979626	10328	1.076672	2.496157	1.7E-05	0.000104	0.060011	1	60	48	68	46	58	126	184	174	101	91
ENSMUSG00000032436	chr9	Cmtm7	1.15E+08	1.15E+08	1136	0.944045	3.337943	1.73E-05	0.000105	0.04961	1	148	82	133	75	98	217	247	221	320	193
ENSMUSG00000058064	chr18	Gm10036	15832794	15833330	537	0.83633	3.4842	1.74E-05	0.000106	0.038271	1	123	125	168	85	125	229	327	243	300	199
ENSMUSG00000021763	chr13	BC067074	1.13E+08	1.13E+08	8410	1.553833	1.809632	1.75E-05	0.000106	0.12755	1	12	16	25	49	36	43	89	73	102	146
ENSMUSG00000040084	chr2	Bub1b	1.19E+08	1.19E+08	4275	1.522582	-0.10263	1.75E-05	0.000106	0.061391	1	5	4	14	4	7	15	20	25	27	22
ENSMUSG00000042680	chr18	Garem	21127201	21130022	4923	-1.13832	1.998239	1.75E-05	0.000106	0.065319	-1	45	46	157	80	129	27	64	32	54	48
ENSMUSG00000003545	chr7	Fosb	19302721	19305302	3751	2.382673	0.273494	1.77E-05	0.000107	0.25094	1	3	6	9	0	10	23	57	5	30	50
ENSMUSG00000054477	chr18	Kcnn2	45268860	45269416	7321	-1.5853	1.390196	1.77E-05	0.000107	0.127936	-1	34	13	69	90	114	19	29	17	29	21
ENSMUSG00000020154	chr10	Ptprb	1.16E+08	1.16E+08	11912	-0.75681	5.315459	1.77E-05	0.000107	0.035279	-1	499	417	1350	884	1077	366	658	541	677	485
ENSMUSG00000075702	chr11	Selm	3514684	3515073	1481	0.798531	3.637781	1.78E-05	0.000107	0.035203	1	145	136	175	111	138	240	300	301	336	243
ENSMUSG00000003420	chr7	Fcgrt	45092993	45093355	1738	0.744572	6.082807	1.79E-05	0.000108	0.03479	1	727	608	1114	737	888	1249	1369	1935	1644	1405
ENSMUSG00000019943	chr10	Atp2b1	98915152	98915371	7130	-0.68127	6.034909	1.8E-05	0.000109	0.02905	-1	979	819	2090	1224	1591	614	1125	792	1220	901
ENSMUSG00000032698	chr2	Lmo2	1.04E+08	1.04E+08	2166	0.836357	2.849065	1.8E-05	0.000109	0.035519	1	82	58	114	78	76	129	182	190	164	155
ENSMUSG00000025240	chr9	Sacm1l	1.24E+08	1.24E+08	3433	-0.59528	4.735277	1.81E-05	0.000109	0.020657	-1	401	381	727	478	611	298	443	380	474	342
ENSMUSG00000055737	chr15	Ghr	3317760	3320722	9053	-0.69178	7.251292	1.83E-05	0.000111	0.030556	-1	2528	2059	4734	2824	3282	1575	2126	2441	2404	2006
ENSMUSG00000043991	chr18	Pura	36281097	36281549	14943	-0.7433	5.292653	1.85E-05	0.000111	0.034147	-1	595	526	1471	626	887	325	596	537	707	532
ENSMUSG00000050052	chr8	Tdrp	13952009	13954135	4694	-0.85347	3.709337	1.85E-05	0.000112	0.042226	-1	306	218	323	223	243	125	194	220	180	127
ENSMUSG00000025232	chr9	Hexa	59539667	59539976	1865	0.705367	6.267689	1.85E-05	0.000112	0.031351	1	901	748	1274	835	903	1628	1772	1818	2032	1376
ENSMUSG00000023048	chr15	Prr13	1.02E+08	1.02E+08	1562	0.687981	5.058601	1.85E-05	0.000112	0.028601	1	386	353	501	340	430	703	820	740	865	588

ENSMUSG00000037940	chr8	Inpp4b	81342556	81342797	10176	-1.91351	1.131812	1.86E-05	0.000112	0.189727	-1	22	12	71	94	81	7	30	6	29	12
ENSMUSG00000030986	chr7	Dhx32	1.34E+08	1.34E+08	4173	-0.70743	5.013347	1.87E-05	0.000113	0.030715	-1	509	439	945	686	680	264	680	364	624	378
ENSMUSG00000038305	chr1	Spats2l	57774162	57774563	8041	0.957496	1.459757	1.87E-05	0.000113	0.035415	1	18	18	43	32	35	47	76	63	72	59
ENSMUSG00000019997	chr10	Ctgf	24595442	24595788	2861	1.429113	4.774695	1.87E-05	0.000113	0.125802	1	82	161	226	294	452	351	915	498	662	1159
ENSMUSG00000021779	chr14	Thrb	17660960	17661024	6555	-0.7085	4.06101	1.88E-05	0.000113	0.029006	-1	211	216	476	391	401	158	306	216	312	183
ENSMUSG00000019823	chr10	Mical1	41476314	41476540	6047	0.900725	2.537887	1.9E-05	0.000114	0.041712	1	55	36	97	48	92	99	133	150	152	136
ENSMUSG00000025862	chrX	Stag2	42149317	42149685	8273	-0.74207	6.010799	1.91E-05	0.000115	0.034794	-1	976	1096	2255	980	1289	641	949	868	1186	787
ENSMUSG00000006273	chr8	Atp6v1b2	69088646	69088928	5305	0.62841	6.439546	1.92E-05	0.000115	0.025014	1	999	712	1407	1026	1381	1564	2275	1937	2446	1467
ENSMUSG00000021767	chr14	Kat6b	21481434	21481553	16826	-0.84212	3.782747	1.93E-05	0.000116	0.041054	-1	196	138	496	274	387	113	238	206	182	161
ENSMUSG00000052917	chr16	Senp7	56075409	56075578	5287	-0.84232	2.770703	1.94E-05	0.000116	0.037096	-1	99	98	237	139	140	55	109	103	113	67
ENSMUSG00000034041	chr8	Lyl1	84701457	84701987	1800	1.036673	1.686298	1.94E-05	0.000117	0.048688	1	32	17	60	29	29	72	75	77	101	54
ENSMUSG00000060791	chr7	Gmfg	28437447	28437574	2817	1.118289	1.304462	1.98E-05	0.000119	0.054204	1	25	12	36	17	31	64	63	55	74	36
ENSMUSG00000063019	chr2	Manbal	1.57E+08	1.57E+08	1107	0.716203	3.906336	2E-05	0.00012	0.028975	1	189	131	224	163	190	278	377	383	428	231
ENSMUSG00000033781	chr13	Asb13	3634032	3634175	3347	-0.60772	4.220178	2E-05	0.00012	0.020926	-1	306	241	531	329	426	210	359	221	335	233
ENSMUSG00000024622	chr18	Hmgxb3	61131279	61132595	5101	-0.63415	4.394222	2E-05	0.00012	0.023383	-1	326	238	581	456	493	226	379	279	374	256
ENSMUSG00000027206	chr2	Cops2	1.26E+08	1.26E+08	3549	-0.66139	6.443252	2E-05	0.00012	0.027928	-1	1496	1437	2416	1487	1681	917	1527	1079	1558	1126
ENSMUSG00000025860	chrX	Xiap	42059679	42059851	9262	-0.62075	4.728979	2.01E-05	0.00012	0.022881	-1	392	326	777	487	667	271	479	378	447	342
ENSMUSG00000024597	chr18	Slc12a2	57878678	57879544	6520	-0.72345	6.56542	2.01E-05	0.00012	0.03358	-1	1668	1511	2763	1523	2047	900	1852	978	1935	1058
ENSMUSG00000041120	chr4	Nbl1	1.39E+08	1.39E+08	2033	0.926652	5.192586	2.02E-05	0.000121	0.05413	1	199	234	548	505	611	557	938	989	882	955
ENSMUSG00000037490	chr10	Slc2a12	22645011	22645313	4237	-0.85483	3.256942	2.03E-05	0.000121	0.041187	-1	132	115	286	230	246	67	194	106	151	114
ENSMUSG00000058748	chr8	Zfp958	4625840	4625966	1401	-0.9459	1.869434	2.03E-05	0.000121	0.040765	-1	61	59	116	56	91	28	67	44	47	39
ENSMUSG00000039004	chr13	Bmp6	38345716	38346587	2410	-1.04137	2.702425	2.05E-05	0.000122	0.060218	-1	91	81	148	172	214	44	105	102	71	64
ENSMUSG00000025006	chr19	Sorbs1	40295049	40295116	3075	-1.29043	4.553083	2.05E-05	0.000122	0.103607	-1	246	178	586	900	883	133	347	242	265	266
ENSMUSG00000020629	chr12	Adi1	28675231	28675372	1886	-0.76964	6.359187	2.07E-05	0.000123	0.037991	-1	1659	1486	2425	1160	1470	957	1316	1032	1344	902
ENSMUSG00000072640	chr11	Lyrm9	78826584	78826636	8146	-0.62382	3.961364	2.07E-05	0.000123	0.021636	-1	242	190	460	303	351	170	290	198	282	187
ENSMUSG00000029415	chr5	Sdad1	92284010	92286870	5020	-0.63184	4.286174	2.08E-05	0.000124	0.023152	-1	280	283	603	334	439	211	365	236	366	234
ENSMUSG00000092748	chr12	Gm22175	1.13E+08	1.13E+08	78	-1.93434	-0.15383	2.08E-05	0.000124	0.147182	-1	26	19	25	5	27	2	4	8	13	4
ENSMUSG00000015575	chr17	Atp6v0e	26676396	26676578	3261	0.7278	4.253192	2.08E-05	0.000124	0.031082	1	223	179	257	221	248	365	526	511	474	286
ENSMUSG00000032883	chr1	Acsl3	78657825	78658103	4357	-1.04065	5.035587	2.09E-05	0.000124	0.068153	-1	549	559	1571	389	638	344	324	300	592	385
ENSMUSG00000007480	chr18	Mc5r	68337603	68337725	1162	-1.38427	0.493886	2.1E-05	0.000125	0.072661	-1	20	18	60	33	27	4	18	12	18	15
ENSMUSG00000017747	chr11	Ghdc	1.01E+08	1.01E+08	2692	0.753665	3.363182	2.1E-05	0.000125	0.030551	1	112	95	152	115	130	207	243	261	292	161
ENSMUSG00000000605	chr7	Clcn4-2	7282316	7284274	4578	-0.65016	5.949238	2.11E-05	0.000125	0.026789	-1	901	808	1757	1204	1527	725	1206	723	954	797
ENSMUSG00000025876	chr13	Unc5a	54949411	54949731	4168	-0.74266	4.468606	2.11E-05	0.000125	0.033376	-1	382	234	667	434	576	178	337	269	416	323
ENSMUSG00000048668	chr6	Rhno1	1.28E+08	1.28E+08	2486	0.826892	2.309205	2.12E-05	0.000126	0.031268	1	42	42	73	59	65	85	139	103	126	111
ENSMUSG00000057236	chr4	Rbbp4	1.29E+08	1.29E+08	8744	0.623759	6.25969	2.12E-05	0.000126	0.02476	1	833	758	1278	915	1042	1409	2122	1463	2058	1465
ENSMUSG00000038736	chr15	Nudcd1	44375227	44376686	3447	-0.72632	3.051519	2.13E-05	0.000126	0.027105	-1	146	105	234	152	198	76	147	101	134	111
ENSMUSG00000086316	chrX	2210013O21Rik	1.54E+08	1.54E+08	1880	0.766184	3.731593	2.14E-05	0.000127	0.033151	1	157	143	207	112	151	254	401	271	362	237
ENSMUSG00000026849	chr2	Tor1a	30960627	30961197	1995	0.904616	2.386472	2.14E-05	0.000127	0.040473	1	55	43	73	48	66	114	150	130	103	102
ENSMUSG00000066057	chr17	Gm1976	94759944	94761577	1912	-1.11308	0.754808	2.17E-05	0.000128	0.039032	-1	27	22	52	37	40	16	22	19	22	13
ENSMUSG00000057766	chr18	Ankrd29	12252362	12254701	3295	-1.5268	0.216912	2.18E-05	0.000129	0.085201	-1	19	20	48	14	30	5	21	5	11	9
ENSMUSG00000038545	chr17	Cul7	46650337	46650715	7410	0.8488	2.867793	2.18E-05	0.000129	0.038772	1	59	44	106	96	116	132	164	185	197	158
ENSMUSG00000040511	chr7	Pvr	19903578	19905192	5408	0.745007	3.459168	2.19E-05	0.00013	0.030921	1	114	83	223	121	128	226	269	262	310	177
ENSMUSG00000056900	chr3	Usp13	32817546	32817872	7599	-0.68741	8.373927	2.19E-05	0.00013	0.030978	-1	5624	3888	10725	6060	7701	3705	5382	3709	6837	3912
ENSMUSG00000019579	chr17	D17Wsu104e	56175744	56177003	2222	0.651469	4.387277	2.2E-05	0.00013	0.024891	1	231	199	311	248	304	436	574	428	479	388
ENSMUSG00000031360	chrX	Ctps2	1.63E+08	1.63E+08	4720	0.797256	2.702998	2.2E-05	0.00013	0.031608	1	70	53	99	74	79	134	162	162	155	120
ENSMUSG00000056116	chr17	H2-T22	36037128	36039223	3414	0.693239	4.86204	2.2E-05	0.00013	0.029361	1	339	300	456	299	361	562	698	738	701	538
ENSMUSG00000101111	chr1	Gm28437	24613189	24613971	783	-1.008	4.129475	2.2E-05	0.00013	0.062762	-1	202	223	374	541	556	206	316	146	260	144
ENSMUSG00000076432	chr12	Ywhaq	21390071	21391415	3061	0.673679	4.012583	2.21E-05	0.00013	0.025955	1	189	139	238	181	244	291	443	408	365	287
ENSMUSG00000096472	chr9	Cdkn2d	21288463	21289332	1271	0.654043	4.057163	2.21E-05	0.00013	0.024306	1	170	152	256	226	226	321	444	309	505	284
ENSMUSG00000072596	chr14	Ear2	44102654	44102719	719	1.871909	0.635101	2.22E-05	0.000131	0.154656	1	15	11	11	5	5	64	44	41	29	20
ENSMUSG00000024251	chr17	Thada	84190056	84192331	7884	-0.82385	2.807733	2.22E-05	0.000131	0.035549	-1	98	95	244	133	164	60	134	77	108	84
ENSMUSG00000024270	chr18	Slc39a6	24579881	24581077	4073	0.916746	2.079208	2.22E-05	0.000131	0.039425	1	42	28	51	38	71	77	134	98	108	76
ENSMUSG00000027961	chr3	Lrrc39	1.17E+08	1.17E+08	5230	-0.7281	6.055041	2.22E-05	0.000131	0.034078	-1	1019	787	1693	1612	1655	661	1414	733	1063	787
ENSMUSG00000025584	chr7	Pde8a	81213596	81214088	4045	-0.93472	3.368239	2.26E-05	0.000133	0.051359	-1	124	136	246	291	300	71	166	151	164	103
ENSMUSG00000027375	chr2	Mal	1.28E+08	1.28E+08	2778	-1.29733	1.222866	2.27E-05	0.000134	0.080218	-1	30	31	70	72	58	11	47	19	21	23
ENSMUSG00000076270	chr14	Mir719	60228806	60228915	110	-1.19377	0.82653	2.29E-05	0.000134	0.053034	-1	28	24	58	28	55	18	29	15	16	15
ENSMUSG00000073000	chr12	Gm10451	76444560	76444665	1598	1.978785	-0.5245	2.29E-05	0.000134	0.130061	1	2	0	7	3	7	7	27	16	10	23
ENSMUSG00000078915	chr13	Hsp25-ps1	45078498	45078911	594	0.921054	2.707693	2.31E-05	0.000136	0.04642	1	57	36	98	88	84	109	132	188	207	129
ENSMUSG00000097799	chr2	Gm26899	1.21E+08	1.21E+08	3328	-4.36176	1.313476	2.31E-05	0.000136	0.876062	-1	1	1	245	136	35	0	0	3	13	4
ENSMUSG00000021188	chr12	Trip11	1.02E+08	1.02E+08	10150	-0.75725	4.666809	2.32E-05	0.000136	0.035479	-1	382	256	900	507	646	240	512	302	363	322
ENSMUSG00000034333	chr15	Zbed4	88751660	88751802	5764	-0.71384	3.215108	2.35E-05	0.000138	0.026818	-1	173	111	277	162	214	110	138	113	170	107
ENSMUSG00000031681	chr8	Smad1	79338395	79339792	5814	0.687304	3.521122	2.35E-05	0.000138	0.025772	1	120	95	200	134	159	204	383	235	292	186
ENSMUSG00000049672	chr17	Zbtb14	69383050	69383269	4231	-0.76044	3.379126	2.37E-05	0.000139	0.03208	-1	142	138	296	226	263	95	152	163	152	135
ENSMUSG00000056753	chr8	C330011M18Rik	84065236	84066803	1849	-1.85008	-0.22267	2.37E-05	0.000139	0.113024	-1	27	11	25	13	20	7	3	2	6	11
ENSMUSG00000046873	chrX	Mbtps2	1.58E+08	1.58E+08	10105	-0.69298	4.028547	2.37E-05	0.000139	0.027987	-1	235	208	564	270	400	171	250	206	283	224

ENSMUSG00000043671	chr7	Dpy19l3	35685165	35690942	11173	0.91745	2.368462	2.38E-05	0.000139	0.041577	1	42	51	89	48	51	77	175	104	156	102
ENSMUSG00000030031	chr6	Kbtbd8	95117240	95117348	5021	-1.29663	1.280043	2.38E-05	0.000139	0.082813	-1	31	38	99	54	54	12	49	30	23	13
ENSMUSG00000005686	chr7	Ampd3	1.11E+08	1.11E+08	5605	0.913063	4.011597	2.39E-05	0.00014	0.051271	1	108	105	239	219	245	229	700	292	505	271
ENSMUSG00000030402	chr7	Ppm1n	19276807	19277209	1631	-2.52902	-0.40356	2.4E-05	0.00014	0.287855	-1	28	22	28	2	9	2	6	2	9	0
ENSMUSG00000014426	chr17	Map3k4	12227621	12228120	5305	-0.65974	5.172085	2.41E-05	0.000141	0.027269	-1	483	421	1078	780	899	382	576	454	672	478
ENSMUSG00000060477	chr6	Irak2	1.14E+08	1.14E+08	4194	0.952209	3.446311	2.41E-05	0.000141	0.053736	1	133	64	136	89	173	207	288	266	426	142
ENSMUSG00000017776	chr11	Crk	75679259	75679664	4730	-0.62415	5.808847	2.41E-05	0.000141	0.024929	-1	756	747	1671	1120	1303	612	1032	807	1027	604
ENSMUSG00000032423	chr9	Syncrip	88449731	88454295	9575	-0.68339	5.990447	2.46E-05	0.000143	0.030247	-1	1110	952	1981	1027	1297	562	1039	967	1131	800
ENSMUSG00000047139	chr10	Cd24a	43579169	43579322	1813	-0.87017	8.194305	2.46E-05	0.000144	0.050033	-1	5647	2801	8097	6771	7954	2994	6307	2333	4682	3114
ENSMUSG00000026822	chr2	Lcn2	32384633	32384884	2623	2.049348	1.070148	2.47E-05	0.000144	0.214493	1	12	11	11	12	12	42	42	30	177	15
ENSMUSG00000050410	chr17	Tcf19	35512734	35513184	1782	1.435672	0.416114	2.48E-05	0.000144	0.08231	1	4	6	19	12	13	28	37	42	20	31
ENSMUSG00000038280	chr10	Ostm1	42583822	42583866	7211	-0.69537	5.079903	2.49E-05	0.000145	0.030458	-1	465	393	857	831	877	361	628	422	514	438
ENSMUSG00000035437	chr2	Rabgap1	37443279	37443456	7607	-0.61362	5.374459	2.51E-05	0.000146	0.023768	-1	687	509	1263	805	850	473	829	524	677	513
ENSMUSG00000067071	chr1	Hes6	91411483	91412802	1808	0.888339	3.253955	2.53E-05	0.000147	0.044944	1	105	67	103	131	117	205	190	217	321	178
ENSMUSG00000027806	chr3	Tsc22d2	58415689	58417613	8829	-0.65887	4.631971	2.53E-05	0.000147	0.026636	-1	382	344	819	428	522	224	458	345	403	337
ENSMUSG00000022443	chr15	Myh9	77760587	77762016	12928	0.706289	6.048135	2.54E-05	0.000147	0.032543	1	608	446	1177	813	1137	1043	1574	1698	1864	1322
ENSMUSG00000024883	chr19	Rin1	5050808	5050941	4176	1.427957	0.24965	2.54E-05	0.000147	0.075271	1	9	1	11	10	16	24	30	22	46	21
ENSMUSG00000003206	chr17	Ebi3	55952623	55952928	1170	1.890259	-0.34426	2.56E-05	0.000148	0.102204	1	6	5	5	2	4	24	12	21	26	11
ENSMUSG00000039275	chr11	Foxk2	1.21E+08	1.21E+08	5258	-0.60656	5.473946	2.56E-05	0.000149	0.023358	-1	682	574	1382	817	960	528	802	554	863	506
ENSMUSG00000010142	chr11	Tnfrsf13b	61126755	61126815	2836	1.366971	0.261398	2.58E-05	0.000149	0.057567	1	14	5	13	6	10	27	29	28	37	20
ENSMUSG00000033054	chr9	Npat	53537047	53537188	6248	-0.94148	2.429574	2.58E-05	0.000149	0.046241	-1	86	59	201	126	109	49	81	65	64	70
ENSMUSG00000100347	chr1	Gm7895	94468715	94469887	1173	-1.03339	1.157917	2.6E-05	0.00015	0.042209	-1	33	32	58	53	57	19	32	18	40	21
ENSMUSG00000048351	chr4	Coa7	1.08E+08	1.08E+08	3851	-0.6569	4.500043	2.6E-05	0.000151	0.026319	-1	331	281	621	460	575	257	459	236	393	276
ENSMUSG00000040540	chr10	Gm9770	1.3E+08	1.3E+08	810	-1.48606	0.649346	2.63E-05	0.000153	0.095608	-1	13	17	63	38	53	9	13	10	26	13
ENSMUSG00000039982	chr19	Dtx4	12466341	12469709	5765	0.808031	3.10299	2.64E-05	0.000153	0.036372	1	74	78	177	78	99	147	239	232	200	165
ENSMUSG00000070047	chr8	Fat1	44935447	44935621	15586	0.947744	3.233987	2.65E-05	0.000154	0.05377	1	68	49	174	106	138	143	197	299	244	221
ENSMUSG00000018412	chr11	Kansl1	1.04E+08	1.04E+08	6874	-0.71162	4.549164	2.67E-05	0.000154	0.031386	-1	318	277	796	497	534	211	412	365	343	293
ENSMUSG00000038543	chr3	BC028528	95883954	95884237	1402	0.999166	1.186348	2.67E-05	0.000154	0.037357	1	15	14	32	25	31	44	69	48	55	46
ENSMUSG00000024210	chr17	Ip6k3	27143969	27145322	2307	0.860729	5.512859	2.68E-05	0.000155	0.048314	1	300	281	605	754	719	842	1598	868	1236	901
ENSMUSG00000040761	chr4	Spen	1.41E+08	1.41E+08	14089	-0.95996	4.325598	2.69E-05	0.000155	0.058346	-1	288	146	816	426	616	150	306	240	323	236
ENSMUSG00000071302	chr8	2610044O15Rik8	1.29E+08	1.29E+08	3858	-0.63534	4.296621	2.69E-05	0.000156	0.024177	-1	307	273	475	413	450	216	378	223	321	270
ENSMUSG00000090935	chr12	Synj2bp	81497941	81502166	5866	-0.61241	5.883869	2.7E-05	0.000156	0.024354	-1	931	788	1557	1130	1397	619	1241	748	1023	706
ENSMUSG00000026074	chr1	Map4k4	39900913	39901286	9579	0.627727	4.624637	2.7E-05	0.000156	0.02406	1	290	221	427	263	359	452	582	614	627	436
ENSMUSG00000025911	chr1	Adhfe1	9547948	9548151	3780	-0.6976	5.525033	2.72E-05	0.000157	0.031475	-1	684	642	1609	789	997	471	795	785	663	497
ENSMUSG00000015714	chr3	Cers2	95314791	95314902	3676	0.641027	4.552775	2.76E-05	0.000159	0.025073	1	290	199	369	278	329	435	588	591	553	417
ENSMUSG00000029659	chr5	Medag	1.49E+08	1.49E+08	3956	0.757529	4.048572	2.78E-05	0.00016	0.034976	1	162	153	318	145	220	340	512	405	320	295
ENSMUSG00000097589	chr14	Dleu2	61602839	61603806	11334	0.900309	2.358747	2.78E-05	0.00016	0.040351	1	60	43	62	46	66	90	119	139	149	97
ENSMUSG00000089945	chr4	Palm2Akap2	57568179	57568415	8456	-1.08172	5.21535	2.83E-05	0.000163	0.076401	-1	414	309	888	1141	1492	293	535	404	552	411
ENSMUSG00000020476	chr11	Dbnl	5788488	5788642	2346	0.715166	4.081691	2.85E-05	0.000164	0.030683	1	175	162	200	212	257	348	395	361	417	359
ENSMUSG00000033287	chr15	Kctd17	78428564	78428867	2134	0.780315	3.155926	2.85E-05	0.000164	0.033508	1	98	77	105	105	128	162	202	230	226	184
ENSMUSG00000039967	chr4	Zfp292	34803113	34812043	9986	-0.74737	3.382408	2.85E-05	0.000164	0.031837	-1	142	135	348	187	269	89	195	138	165	128
ENSMUSG00000026536	chr1	Mnda	1.74E+08	1.74E+08	1785	1.157414	1.984002	2.86E-05	0.000164	0.073265	1	25	20	60	34	59	97	147	111	72	54
ENSMUSG00000062753	chr17	AI413582	27563575	27564016	1398	1.124046	1.409835	2.86E-05	0.000164	0.055929	1	29	19	38	24	17	69	67	55	77	46
ENSMUSG00000026821	chr2	Ralgds	28513125	28513560	6159	0.677598	4.192546	2.87E-05	0.000165	0.027566	1	210	181	334	169	232	299	526	454	452	324
ENSMUSG00000044296	chr11	Zfp879	50832031	50833971	2414	-1.10224	1.171101	2.9E-05	0.000167	0.052359	-1	34	30	67	47	64	16	34	13	42	23
ENSMUSG00000038607	chr4	Gng10	59035088	59035318	1314	0.882289	2.538288	2.91E-05	0.000167	0.040097	1	53	58	78	61	67	98	128	158	156	127
ENSMUSG00000004642	chr5	Slbp	33634952	33635175	4472	0.787855	2.572149	2.93E-05	0.000168	0.031603	1	58	38	102	75	77	113	161	124	181	101
ENSMUSG00000032492	chr9	Pth1r	1.11E+08	1.11E+08	2484	1.658306	1.201908	2.93E-05	0.000168	0.14684	1	10	13	30	9	25	50	47	122	38	35
ENSMUSG00000020546	chr11	Stxbp4	90476492	90480714	11834	-0.71799	4.701999	2.95E-05	0.000169	0.032543	-1	426	332	961	383	602	317	426	380	362	294
ENSMUSG00000021036	chr12	Sptlc2	87305058	87310020	8115	0.730827	3.399058	2.98E-05	0.00017	0.029833	1	98	109	153	109	158	194	302	260	268	170
ENSMUSG00000022075	chr14	Rhobtb2	69784990	69787735	5216	-0.64314	5.252138	2.98E-05	0.000171	0.026671	-1	681	617	1106	600	717	412	615	521	706	474
ENSMUSG00000034330	chr8	Plcg2	1.17E+08	1.17E+08	4296	1.178587	1.365973	2.99E-05	0.000171	0.066126	1	18	19	48	22	16	53	62	82	59	50
ENSMUSG00000062380	chr8	Tubb3	1.23E+08	1.23E+08	1868	1.466618	0.254975	3.02E-05	0.000172	0.072709	1	10	5	8	12	10	35	26	30	32	18
ENSMUSG00000024442	chr18	0610009O20Rik	38250249	38250399	2404	-0.66671	6.689409	3.02E-05	0.000173	0.029773	-1	1543	1198	2626	2427	2567	1163	1978	1241	1839	1167
ENSMUSG00000031803	chr8	B3gnt3	71691719	71693155	2103	1.00096	2.034396	3.02E-05	0.000173	0.052335	1	30	24	62	43	59	75	152	113	93	57
ENSMUSG00000038729	chr4	Akap2	57717657	57717758	8163	-1.0797	5.212426	3.02E-05	0.000173	0.076668	-1	413	308	883	1139	1490	293	533	403	551	412
ENSMUSG00000100291	chr6	2310069B03Rik	82877864	82879476	1902	-1.58044	-0.21586	3.02E-05	0.000173	0.086598	-1	15	10	22	23	23	3	16	4	11	2
ENSMUSG00000035933	chr12	Cog5	31654869	31654983	2997	-0.89644	2.412741	3.03E-05	0.000173	0.042103	-1	60	76	159	116	151	53	75	69	71	64
ENSMUSG00000043140	chr16	Tmem186	8633884	8636392	2736	-0.59456	4.422987	3.04E-05	0.000173	0.021466	-1	364	285	585	391	463	231	436	274	382	256
ENSMUSG00000097317	chr2	Gm17281	91250743	91254087	3589	-0.87681	4.635695	3.04E-05	0.000173	0.049971	-1	439	530	590	478	446	264	398	277	527	179
ENSMUSG00000027002	chr2	Nckap1	80500512	80501411	4964	-0.58735	5.699511	3.05E-05	0.000174	0.022455	-1	762	727	1563	923	1134	593	910	787	901	615
ENSMUSG00000019877	chr10	Serinc1	57515774	57517292	5150	-0.71026	7.357318	3.07E-05	0.000175	0.034108	-1	2373	2431	5027	3077	3763	1299	2799	2195	2793	2393
ENSMUSG00000059970	chr12	Hspa2	76404176	76404289	2520	1.150242	2.965	3.07E-05	0.000175	0.080548	1	41	33	89	119	112	148	248	111	325	161
ENSMUSG00000038194	chr7	Lhb	45418353	45418525	2501	1.226613	0.840763	3.08E-05	0.000176	0.057228	1	12	16	15	11	25	26	53	36	58	42
ENSMUSG00000030494	chr7	Rhpn2	35334170	35334411	6304	1.164615	2.354577	3.11E-05	0.000177	0.075388	1	40	59	76	26	41	77	170	161	136	93

ENSMUSG00000059263	chr7	Usp47	1.12E+08	1.12E+08	5540	-0.62946	8.43077	3.13E-05	0.000178	0.027019	-1	5399	4266	10436	6584	7915	3694	6603	4204	6403	4235
ENSMUSG00000029392	chr5	Rilpl1	1.24E+08	1.24E+08	2247	-0.65302	7.551965	3.15E-05	0.000179	0.028937	-1	3148	2173	5104	4064	4279	2404	3320	2230	3337	2104
ENSMUSG00000051502	chr5	Ufsp1	1.37E+08	1.37E+08	1037	0.654103	4.559608	3.15E-05	0.000179	0.026797	1	256	201	428	228	380	415	539	438	721	511
ENSMUSG00000038203	chr6	Hoxa13	52257694	52259148	2472	-2.24947	-0.2433	3.16E-05	0.00018	0.215337	-1	40	15	28	7	8	3	4	9	6	2
ENSMUSG00000048497	chr11	Mmgt2	62648664	62648816	4898	1.129631	2.217666	3.16E-05	0.00018	0.069189	1	49	47	69	22	37	84	114	141	134	92
ENSMUSG00000020325	chr10	Fstl3	79777272	79777397	2445	1.135961	1.216985	3.17E-05	0.00018	0.053603	1	24	19	16	23	25	34	69	53	66	55
ENSMUSG00000074746	chr19	Pdzd8	59296084	59301708	7076	-0.7226	3.903378	3.17E-05	0.00018	0.031472	-1	189	185	408	350	394	159	251	189	214	208
ENSMUSG00000040167	chr7	Ikzf5	1.31E+08	1.31E+08	4885	-0.7356	3.698691	3.18E-05	0.00018	0.032418	-1	210	166	396	286	261	100	199	180	260	161
ENSMUSG00000041426	chr1	Hibch	52844929	52848693	6059	-0.65444	5.251377	3.19E-05	0.000181	0.027901	-1	650	515	877	874	800	426	747	564	617	378
ENSMUSG00000036845	chr7	Lin37	30555441	30555608	1388	0.769815	2.547828	3.21E-05	0.000182	0.028877	1	61	52	85	65	76	111	153	130	166	101
ENSMUSG00000011832	chr8	Evi5l	4166567	4166763	8524	-0.60888	4.397465	3.23E-05	0.000183	0.022594	-1	333	270	509	440	501	262	335	294	381	247
ENSMUSG00000039395	chr1	Mreg	72159442	72161019	2284	-0.81122	5.170237	3.23E-05	0.000183	0.043475	-1	552	386	878	1020	902	298	682	379	721	385
ENSMUSG00000020423	chr1	Btg2	1.34E+08	1.34E+08	2743	1.977582	4.988855	3.23E-05	0.000183	0.247704	1	132	191	202	177	310	310	3526	360	642	341
ENSMUSG00000069495	chr2	Epc2	49451486	49451958	4697	-0.68001	3.904034	3.23E-05	0.000183	0.027865	-1	210	236	476	260	317	146	309	199	238	170
ENSMUSG00000038384	chr5	Setd1b	1.23E+08	1.23E+08	10874	-1.03714	2.98112	3.25E-05	0.000184	0.064724	-1	103	76	266	185	260	47	112	80	113	117
ENSMUSG00000054894	chr12	Atp5s	69724962	69725014	1485	-0.67108	3.71688	3.25E-05	0.000184	0.026438	-1	204	207	333	252	292	155	252	134	235	155
ENSMUSG00000016206	chr17	H2-M3	37270220	37270334	1438	0.957248	1.942225	3.28E-05	0.000185	0.04369	1	37	36	55	37	36	81	112	101	89	63
ENSMUSG00000018537	chr11	Pcgf2	97688823	97690358	3526	1.130144	1.440468	3.31E-05	0.000187	0.060344	1	18	19	32	29	33	63	42	73	83	57
ENSMUSG00000036503	chr3	Rnf13	57736066	57736200	2676	-0.61323	5.436824	3.34E-05	0.000189	0.02463	-1	668	665	1266	765	873	430	706	621	811	577
ENSMUSG00000031631	chr8	Cfap97	46151771	46151913	5157	-0.71232	3.919283	3.37E-05	0.00019	0.03109	-1	203	230	449	299	345	127	252	169	293	216
ENSMUSG00000036450	chr19	Hif1an	44562850	44563054	6606	-0.65592	8.171387	3.42E-05	0.000193	0.029587	-1	4819	4111	9375	4591	6061	3278	4374	3684	5522	3658
ENSMUSG00000028291	chr4	Akirin2	34550937	34551273	1711	0.60554	4.677571	3.43E-05	0.000193	0.022883	1	308	229	438	310	341	387	678	537	716	516
ENSMUSG00000034243	chr16	Golgb1	36875140	36875263	12639	-0.657	5.22869	3.45E-05	0.000194	0.028176	-1	578	470	1271	629	869	416	542	595	604	477
ENSMUSG00000030319	chr6	Cand2	1.16E+08	1.16E+08	4810	-0.78068	6.680047	3.45E-05	0.000194	0.041471	-1	1713	919	3476	2214	2616	953	1556	1102	1954	1395
ENSMUSG00000073423	chr17	Zfp414	33629090	33629216	1966	0.847981	2.180453	3.45E-05	0.000194	0.033668	1	48	40	65	50	48	76	114	101	127	99
ENSMUSG00000036087	chr5	Slain2	72914304	72915013	8446	-0.6785	6.840909	3.46E-05	0.000194	0.031377	-1	1770	1489	3561	2241	2563	1046	1820	1333	2404	1577
ENSMUSG00000046413	chr8	Irx3os	91800415	91800538	3687	-2.50222	0.970563	3.46E-05	0.000195	0.344313	-1	48	11	60	65	81	19	7	1	24	0
ENSMUSG00000020697	chr11	Lig3	82781108	82781276	7284	-0.6509	4.782711	3.5E-05	0.000197	0.027141	-1	387	326	887	539	657	299	489	306	504	370
ENSMUSG00000002900	chr12	Lamb1	31265234	31265344	9917	0.669433	5.104959	3.51E-05	0.000197	0.029472	1	335	240	600	401	621	538	926	793	814	769
ENSMUSG00000021775	chr14	Nr1d2	18204054	18206881	5001	-0.64838	6.894267	3.53E-05	0.000198	0.028722	-1	1679	1602	3466	2409	2765	1079	2158	1595	2075	1650
ENSMUSG00000028906	chr4	Epb4.1	1.32E+08	1.32E+08	8809	-0.64145	6.625046	3.56E-05	0.0002	0.028001	-1	1578	1097	3253	1858	2253	1068	1642	1353	1849	1190
ENSMUSG00000028127	chr3	Abcd3	1.22E+08	1.22E+08	3399	-0.73305	5.869682	3.57E-05	0.0002	0.036247	-1	760	671	1416	1573	1558	645	1035	726	971	664
ENSMUSG00000034252	chr9	Senp6	80066903	80067572	7016	-0.60277	5.361453	3.61E-05	0.000202	0.023875	-1	648	630	1224	689	823	485	776	573	661	493
ENSMUSG00000085438	chr2	1700020I14Rik	1.2E+08	1.2E+08	8306	-0.71014	9.643698	3.61E-05	0.000202	0.035002	-1	10889	8633	24767	17582	21398	8229	14251	9273	14659	9824
ENSMUSG00000048852	chr11	Gm12185	48904656	48908479	5587	1.308688	1.994673	3.62E-05	0.000203	0.09828	1	14	26	67	45	31	51	189	116	107	57
ENSMUSG00000036918	chr17	Ttc7	87282886	87283410	6315	0.683792	4.58465	3.63E-05	0.000203	0.02997	1	259	192	376	297	360	505	479	476	798	426
ENSMUSG00000038664	chr9	Herc1	66350450	66350621	27464	-0.73295	6.290783	3.63E-05	0.000203	0.036573	-1	1067	840	2790	1557	2031	684	1436	1047	1286	991
ENSMUSG00000051650	chr11	B3gnt2	22834747	22837195	3350	0.83432	3.12863	3.63E-05	0.000203	0.040473	1	86	75	114	88	134	135	353	155	227	166
ENSMUSG00000054555	chr7	Adam12	1.34E+08	1.34E+08	8273	1.861668	0.533625	3.64E-05	0.000204	0.178239	1	9	1	18	11	9	21	23	69	23	46
ENSMUSG00000001288	chr15	Rarg	1.02E+08	1.02E+08	4109	0.638012	3.932918	3.65E-05	0.000204	0.024603	1	167	120	294	157	238	288	372	339	364	308
ENSMUSG00000008730	chr3	Hipk1	1.04E+08	1.04E+08	8591	-0.67366	5.412085	3.65E-05	0.000204	0.030119	-1	538	477	1412	897	1072	456	701	589	703	547
ENSMUSG00000034620	chr10	Tmem5	1.22E+08	1.22E+08	5614	-0.7149	4.614339	3.65E-05	0.000204	0.033268	-1	460	436	654	396	453	292	495	285	411	233
ENSMUSG00000090187	chr13	AK157302	21495306	21495695	390	-1.08048	1.933729	3.65E-05	0.000204	0.062856	-1	57	40	99	103	118	45	64	27	56	29
ENSMUSG00000024095	chr17	Hnrnpll	80029487	80030540	11677	-0.67041	4.038921	3.66E-05	0.000204	0.027678	-1	244	242	516	302	339	140	282	253	274	214
ENSMUSG00000004317	chrX	Clcn5	7153810	7159819	11452	0.942612	2.10807	3.67E-05	0.000205	0.047091	1	33	26	85	43	52	92	94	116	102	90
ENSMUSG00000032280	chr9	Tle3	61372366	61373461	11653	0.872633	3.857182	3.68E-05	0.000205	0.048721	1	94	88	219	206	236	250	317	390	346	364
ENSMUSG00000026944	chr2	Abca2	25428703	25428835	8346	-0.79534	4.692434	3.69E-05	0.000206	0.041469	-1	343	239	804	634	738	250	346	357	445	323
ENSMUSG00000032515	chr9	Csrnp1	1.2E+08	1.2E+08	2870	1.414474	2.025385	3.72E-05	0.000208	0.115939	1	14	30	42	42	44	86	229	61	128	44
ENSMUSG00000027381	chr2	Bcl2l11	1.28E+08	1.28E+08	8029	0.942918	3.393545	3.74E-05	0.000208	0.055388	1	92	70	155	95	173	115	413	184	312	263
ENSMUSG00000037872	chr1	Ackr1	1.73E+08	1.73E+08	1405	1.019473	2.180671	3.76E-05	0.000209	0.057052	1	30	37	83	35	55	82	172	121	117	58
ENSMUSG00000028494	chr4	Plin2	86648386	86648579	3512	0.787853	5.486519	3.77E-05	0.00021	0.041743	1	509	419	599	484	581	789	1084	1496	966	780
ENSMUSG00000031897	chr8	Psmb10	1.06E+08	1.06E+08	1270	0.761276	3.841036	3.77E-05	0.00021	0.035284	1	172	137	160	156	201	291	349	359	400	230
ENSMUSG00000056394	chr7	Lig1	13277283	13277529	4268	1.175437	1.336088	3.81E-05	0.000212	0.066925	1	19	18	35	17	31	55	57	55	48	79
ENSMUSG00000006589	chr8	Aprt	1.23E+08	1.23E+08	866	0.60882	4.321938	3.82E-05	0.000213	0.022635	1	224	197	300	254	279	353	494	415	595	352
ENSMUSG00000011305	chr17	Plin5	56111601	56112541	2087	-2.33215	3.657817	3.85E-05	0.000214	0.338662	-1	104	70	186	891	458	26	228	39	86	39
ENSMUSG00000037411	chr5	Serpine1	1.37E+08	1.37E+08	3024	1.515302	3.199566	3.85E-05	0.000214	0.146375	1	50	54	93	97	81	87	727	136	242	141
ENSMUSG00000042622	chr15	Maff	79347541	79347754	2119	1.255061	1.347355	3.86E-05	0.000214	0.082129	1	11	7	34	35	32	61	92	53	68	39
ENSMUSG00000097705	chr10	Gm26740	22187013	22187143	1724	-0.81555	3.589024	3.87E-05	0.000215	0.040946	-1	230	187	400	157	270	125	186	120	174	180
ENSMUSG00000027022	chr2	Xirp2	67446002	67446154	11979	-0.71436	10.9103	3.89E-05	0.000216	0.03576	-1	24736	20916	61403	42929	51247	20436	32422	24317	31169	25104
ENSMUSG00000039840	chr18	Epg5	77938467	77938559	9672	-0.73581	5.180787	3.93E-05	0.000218	0.036183	-1	544	355	1404	632	936	383	548	483	623	448
ENSMUSG00000036155	chr1	Mgat5	1.27E+08	1.27E+08	10291	1.182001	1.699989	3.94E-05	0.000218	0.077221	1	21	13	43	40	41	64	78	118	60	67
ENSMUSG00000005973	chr2	Rcn1	1.05E+08	1.05E+08	3196	0.689001	3.797118	3.95E-05	0.000219	0.028496	1	135	152	237	144	176	280	356	285	326	289
ENSMUSG00000042747	chr3	Krtcap2	89245966	89246515	1522	0.633512	4.76236	3.95E-05	0.000219	0.025672	1	305	286	383	331	366	439	692	593	806	501
ENSMUSG00000004939	chr10	Nmrk2	81198170	81199446	1840	1.44139	8.081801	3.96E-05	0.000219	0.14078	1	3408	562	1555	2131	4109	8908	8652	5796	6583	5356
ENSMUSG00000020455	chr11	Trim11	58978093	58978644	3580	0.720145	3.310167	3.96E-05	0.000219	0.029873	1	124	76	168	98	134	160	284	252	252	174

ENSMUSG00000100599	chr15	1700120C14Rik	99251788	99252001	1731	0.67705	4.444111	3.97E-05	0.000219	0.029114	1	276	208	370	220	256	388	629	385	684	388
ENSMUSG00000060224	chr19	Pyroxd2	42725858	42726989	3119	1.51715	0.252294	3.99E-05	0.000221	0.089133	1	9	7	11	7	10	15	28	45	22	32
ENSMUSG00000047343	chr1	Mettl21c	44009408	44010033	4300	-1.6862	5.505632	4E-05	0.000221	0.188885	-1	1699	680	1245	671	1143	483	575	261	670	51
ENSMUSG00000025237	chr9	Parp6	59617284	59617408	2714	-0.59041	5.049652	4.05E-05	0.000224	0.022777	-1	608	419	820	668	679	419	563	446	570	408
ENSMUSG00000027247	chr2	Arhgap1	91649860	91650252	4275	0.73057	3.428106	4.06E-05	0.000224	0.031739	1	99	86	167	127	173	182	246	305	288	190
ENSMUSG00000004100	chr9	Ppan	20888175	20888317	2504	0.801776	2.954127	4.07E-05	0.000225	0.035763	1	95	75	98	76	93	137	224	194	204	131
ENSMUSG00000048279	chr14	Sacs	61138457	61138771	20414	-1.19567	4.187731	4.08E-05	0.000225	0.095459	-1	173	144	535	629	666	113	337	173	224	186
ENSMUSG00000103392	chr3	RP23-436F15.5	10321712	10321720	536	-0.94528	1.878765	4.09E-05	0.000226	0.044228	-1	79	61	106	51	82	35	53	41	48	46
ENSMUSG00000025188	chr19	Hps1	42755105	42755796	5855	1.267003	1.087524	4.1E-05	0.000226	0.073027	1	22	21	24	8	17	48	52	52	50	51
ENSMUSG00000029167	chr5	Ppargc1a	51454249	51458283	6641	-0.87458	4.776135	4.11E-05	0.000226	0.051288	-1	330	270	768	700	904	311	391	247	473	339
ENSMUSG00000031785	chr8	Gpr56	94977109	94977417	3864	0.792822	4.175297	4.15E-05	0.000228	0.040951	1	137	125	237	275	297	384	452	484	448	294
ENSMUSG00000071252	chr13	2210408I21Rik	77135540	77135630	4558	-1.09842	0.841052	4.15E-05	0.000228	0.046317	-1	28	32	57	28	43	19	25	14	26	15
ENSMUSG00000062604	chr5	Srpk2	23503356	23507720	6436	-0.60999	5.021908	4.17E-05	0.00023	0.024488	-1	488	419	1025	539	775	338	556	412	636	428
ENSMUSG00000028641	chr4	Lepre1	1.19E+08	1.19E+08	3846	0.6116	4.103221	4.17E-05	0.00023	0.022923	1	193	142	302	209	252	311	384	340	531	325
ENSMUSG00000086247	chr5	Gm15787	1.1E+08	1.1E+08	2992	-1.02146	1.458381	4.27E-05	0.000235	0.050132	-1	41	37	88	64	62	21	55	19	42	27
ENSMUSG00000024197	chr17	Plin3	56278962	56280073	2159	-0.88871	4.551598	4.28E-05	0.000235	0.052951	-1	323	252	544	719	643	264	282	348	407	197
ENSMUSG00000041957	chr16	Pkp2	16213318	16213595	5360	1.105568	2.161023	4.28E-05	0.000235	0.068141	1	54	39	42	21	60	100	104	113	126	92
ENSMUSG00000048503	chr9	Tmem136	43108653	43111858	3500	-1.01348	1.829044	4.28E-05	0.000235	0.052783	-1	69	39	80	73	116	28	47	35	50	49
ENSMUSG00000024073	chr17	Birc6	74528295	74528801	28830	-0.82451	5.188036	4.29E-05	0.000235	0.046273	-1	434	387	1468	756	950	286	537	497	620	478
ENSMUSG00000026495	chr1	Efcab2	1.78E+08	1.78E+08	4151	-0.58886	4.399627	4.3E-05	0.000236	0.021828	-1	371	288	579	386	417	259	373	271	394	247
ENSMUSG00000029713	chr5	Gnb2	1.38E+08	1.38E+08	3402	0.60824	6.339013	4.3E-05	0.000236	0.025549	1	848	686	1310	1154	1180	1458	2015	1733	2262	1480
ENSMUSG00000033152	chr6	Podxl2	88842558	88842976	3948	-0.5807	5.731108	4.31E-05	0.000236	0.022878	-1	848	766	1315	1067	1105	674	915	676	980	649
ENSMUSG00000003581	chr11	Rnf215	4135202	4135563	2232	0.796569	2.502672	4.31E-05	0.000237	0.033308	1	53	47	77	65	84	110	135	143	141	108
ENSMUSG00000018068	chr11	Ints2	86210681	86212801	10609	-0.94504	1.884097	4.32E-05	0.000237	0.044619	-1	53	52	113	63	110	26	52	45	52	50
ENSMUSG00000040713	chr1	Creg1	1.66E+08	1.66E+08	2362	-0.62767	5.873831	4.34E-05	0.000238	0.026964	-1	778	852	1697	1139	1353	681	1043	862	843	755
ENSMUSG00000008393	chr16	Carhsp1	8658587	8661103	2849	0.801638	4.266947	4.34E-05	0.000238	0.042024	1	207	188	335	189	197	383	447	606	439	316
ENSMUSG00000047810	chr19	Ccdc88b	6844623	6845119	4959	1.212663	0.711103	4.37E-05	0.000239	0.061718	1	9	7	25	9	26	35	45	36	37	38
ENSMUSG00000024621	chr18	Csf1r	61105572	61105684	4885	0.800071	5.29799	4.37E-05	0.000239	0.043978	1	365	269	895	368	523	926	788	1048	999	692
ENSMUSG00000000489	chr15	Pdgfb	79995900	79997257	2918	0.692901	4.61634	4.42E-05	0.000241	0.031549	1	304	199	365	240	397	394	568	464	846	515
ENSMUSG00000034059	chr2	Ypel4	84734058	84734293	2614	1.525473	-0.34168	4.42E-05	0.000242	0.065023	1	5	2	12	4	5	15	23	14	18	20
ENSMUSG00000074862	chr10	BC025920	81606270	81606390	3306	-0.8798	2.498191	4.42E-05	0.000242	0.044494	-1	87	79	149	130	140	41	126	67	84	51
ENSMUSG00000019370	chr7	Calm3	16915379	16916976	2423	-0.76634	8.632558	4.44E-05	0.000242	0.041576	-1	7800	7321	11872	5076	7690	4690	6017	4806	6780	4552
ENSMUSG00000004952	chr5	Rasa4	1.36E+08	1.36E+08	6191	0.604062	5.352147	4.46E-05	0.000243	0.024532	1	533	341	763	439	547	698	1073	815	1116	808
ENSMUSG00000049037	chr6	Clec4a1	1.23E+08	1.23E+08	1558	1.076824	1.87611	4.46E-05	0.000243	0.062828	1	36	27	61	22	40	107	95	83	92	55
ENSMUSG00000010609	chr1	Psen2	1.8E+08	1.8E+08	4332	0.72396	3.659749	4.47E-05	0.000244	0.032014	1	134	101	180	164	180	238	282	339	373	194
ENSMUSG00000026004	chr1	Kansl1l	66719248	66721006	6664	-0.74299	4.776096	4.49E-05	0.000245	0.037203	-1	459	405	978	431	547	206	509	314	526	360
ENSMUSG00000025656	chrX	Arhgef9	95048935	95052154	8714	-0.73424	3.885343	4.51E-05	0.000246	0.034368	-1	208	157	409	365	379	123	270	192	270	174
ENSMUSG00000041415	chr12	Dicer1	1.05E+08	1.05E+08	9851	-0.67708	5.828859	4.51E-05	0.000246	0.031606	-1	932	728	2080	843	1263	634	851	716	1057	739
ENSMUSG00000018752	chr11	Tnfsf12Tnfsf13	69682577	69683344	2235	0.663862	3.733749	4.52E-05	0.000246	0.026798	1	115	114	233	165	208	226	338	351	333	230
ENSMUSG00000024981	chr19	Acsl5	55253369	55254166	3150	0.779416	3.550261	4.55E-05	0.000248	0.037326	1	114	115	158	110	185	213	358	320	243	202
ENSMUSG00000009555	chr2	Cdk9	32705784	32708289	4611	0.659255	4.694952	4.56E-05	0.000248	0.028612	1	313	234	496	283	289	495	600	630	677	465
ENSMUSG00000023908	chr17	Pkmyt1	23726336	23726641	2039	1.3916	0.345851	4.58E-05	0.000249	0.073372	1	15	7	11	6	11	29	33	40	29	19
ENSMUSG00000047557	chr3	Lxn	67457998	67458327	1508	1.135817	1.074033	4.58E-05	0.000249	0.056573	1	16	10	22	26	26	52	51	54	60	30
ENSMUSG00000062825	chr11	Actg1	1.2E+08	1.2E+08	2658	0.657037	6.732045	4.59E-05	0.00025	0.03033	1	1393	732	1713	1277	1581	2158	2825	2189	2849	1857
ENSMUSG00000044030	chr7	Irf2bp1	19004065	19006761	2697	0.567793	4.623251	4.67E-05	0.000254	0.02052	1	282	238	403	304	358	428	597	527	674	455
ENSMUSG00000023961	chr17	Enpp4	44096308	44099677	4560	-0.61899	6.159802	4.68E-05	0.000254	0.026657	-1	1059	889	2011	1401	1763	706	1255	926	1322	988
ENSMUSG00000092035	chr6	Peg10	4747306	4747578	6667	1.210524	1.494866	4.69E-05	0.000254	0.077733	1	25	19	54	19	16	45	104	48	70	78
ENSMUSG00000031309	chrX	Rps6ka3	1.59E+08	1.59E+08	8322	-0.68963	5.906523	4.72E-05	0.000256	0.033118	-1	1026	826	2115	862	1305	533	1112	778	1050	782
ENSMUSG00000070476	chr2	Fam217b	1.78E+08	1.78E+08	4559	0.883928	1.926493	4.74E-05	0.000257	0.038624	1	36	24	60	41	50	61	138	79	92	72
ENSMUSG00000029802	chr6	Abcg2	58584523	58584535	4987	0.618069	4.794274	4.75E-05	0.000257	0.025148	1	261	270	483	332	422	417	865	501	799	538
ENSMUSG00000042323	chr14	Pbrm1	31019138	31019293	8846	-0.65918	5.135845	4.78E-05	0.000259	0.029465	-1	519	399	1207	641	842	316	595	506	622	470
ENSMUSG00000028944	chr5	Prkag2	24862744	24863887	6480	0.739184	4.631291	4.79E-05	0.00026	0.036554	1	301	209	432	252	297	511	655	577	812	305
ENSMUSG00000053510	chr4	Nrd1	1.09E+08	1.09E+08	7140	-0.59094	7.893642	4.79E-05	0.00026	0.024917	-1	3535	3372	6573	4646	5093	2713	4314	3064	4346	3034
ENSMUSG00000022601	chr16	Zbtb11	55973883	55974371	7440	-0.76632	3.42686	4.81E-05	0.00026	0.035705	-1	171	139	389	190	228	125	137	150	149	147
ENSMUSG00000040565	chr19	Btaf1	36926079	36926401	7204	-0.79685	3.355872	4.81E-05	0.000261	0.039267	-1	175	156	376	140	217	103	173	158	143	103
ENSMUSG00000026384	chr1	Ptpn4	1.2E+08	1.2E+08	11321	-0.7528	4.134363	4.83E-05	0.000261	0.037058	-1	262	175	711	327	398	164	288	238	305	207
ENSMUSG00000062098	chr2	Btbd3	1.38E+08	1.38E+08	5776	-0.70584	3.952229	4.9E-05	0.000265	0.031877	-1	213	222	436	269	428	132	283	198	230	231
ENSMUSG00000021816	chr14	Ppp3cb	20499364	20501662	6018	-0.63785	8.101904	4.94E-05	0.000267	0.029173	-1	4537	4142	8573	4446	5544	2826	4990	3365	5125	3585
ENSMUSG00000022947	chr16	Cbr3	93683215	93683613	1170	1.089305	1.284589	4.97E-05	0.000269	0.054318	1	20	22	31	18	27	39	54	78	60	53
ENSMUSG00000024122	chr17	Pdpk1	24073680	24079142	10935	-0.66787	5.188399	4.98E-05	0.000269	0.030529	-1	539	403	1267	667	885	324	675	485	654	472
ENSMUSG00000067818	chr2	Myl9	1.57E+08	1.57E+08	1162	0.677139	5.14384	4.99E-05	0.00027	0.031215	1	366	357	563	374	513	477	808	859	1174	700
ENSMUSG00000046753	chr14	Ccdc66	27482412	27482602	2940	-0.88897	2.835102	5.05E-05	0.000272	0.048173	-1	75	102	206	191	177	64	137	79	112	69
ENSMUSG00000078139	chr13	AK157302	21495223	21497146	1924	-1.024	2.057645	5.07E-05	0.000273	0.059386	-1	59	44	112	109	127	48	70	33	68	30
ENSMUSG00000042834	chr18	Nrep	33437019	33438839	2513	-0.94417	7.407998	5.07E-05	0.000273	0.063478	-1	2298	1306	4770	4331	6303	1890	2307	2057	2319	1917
ENSMUSG00000073590	chr18	3222401L13Rik	37655451	37661742	6292	-1.41158	0.834055	5.09E-05	0.000274	0.096644	-1	31	21	99	28	30	12	22	13	16	20

ENSMUSG00000046245	chr5	Pilra	1.38E+08	1.38E+08	3077	1.695864	-0.36262	5.11E-05	0.000275	0.076653	1	7	3	3	5	6	8	28	20	19	17
ENSMUSG00000015846	chr2	Rxra	27676440	27676515	5462	-0.62779	7.461468	5.12E-05	0.000275	0.028237	-1	2851	2089	5731	3175	3937	1957	2917	2284	3383	2209
ENSMUSG00000016024	chr2	Lbp	1.58E+08	1.58E+08	4831	0.776801	3.676647	5.11E-05	0.000275	0.038676	1	135	86	232	141	175	240	420	352	245	205
ENSMUSG00000020256	chr10	Aldh1l2	83487450	83490634	7503	-1.23042	2.435216	5.12E-05	0.000275	0.093317	-1	62	36	246	139	168	53	80	50	49	54
ENSMUSG00000048387	chr12	Osr1	9574442	9574742	2010	0.921806	2.046807	5.12E-05	0.000275	0.043652	1	39	43	63	29	47	76	114	97	131	66
ENSMUSG00000016921	chr2	Srsf6	1.63E+08	1.63E+08	4810	0.581677	5.692126	5.14E-05	0.000277	0.023328	1	589	507	893	606	726	855	1368	1235	1224	969
ENSMUSG00000061838	chr6	Suclg2	95474134	95475164	2279	-0.67553	6.072086	5.15E-05	0.000277	0.032204	-1	914	954	1561	1591	1645	699	1370	823	1095	810
ENSMUSG00000023143	chr16	Nagpa	5195289	5196058	2370	0.698714	3.063956	5.16E-05	0.000277	0.027651	1	93	62	125	105	123	140	215	206	213	158
ENSMUSG00000005882	chr2	Uqcc1	1.56E+08	1.56E+08	6044	-0.75151	7.136475	5.17E-05	0.000278	0.04044	-1	2117	1617	3009	3776	3791	1482	2659	1616	2552	1465
ENSMUSG00000040407	chr5	Akap9	3928054	3928342	15848	-0.70768	5.80609	5.17E-05	0.000278	0.035153	-1	715	624	1987	1118	1429	552	915	636	1062	753
ENSMUSG00000078671	chr7	Chd2	73426691	73430000	9656	-0.61973	5.443987	5.18E-05	0.000278	0.026496	-1	631	561	1277	869	992	433	880	531	695	620
ENSMUSG00000026187	chr1	Xrcc5	72307421	72307567	2555	-0.64811	5.365089	5.2E-05	0.000279	0.029011	-1	763	674	1165	579	845	505	642	550	698	519
ENSMUSG00000029752	chr6	Asns	7675169	7675524	2735	1.605085	2.063391	5.2E-05	0.000279	0.156457	1	41	37	28	22	22	78	88	227	75	74
ENSMUSG00000043940	chr5	Wdfy3	1.02E+08	1.02E+08	15351	-0.8685	4.858443	5.25E-05	0.000281	0.05226	-1	371	262	1286	550	793	240	457	390	499	314
ENSMUSG00000031147	chrX	Magix	7673164	7675191	2910	-0.94177	4.370553	5.25E-05	0.000281	0.06074	-1	269	184	492	690	604	202	319	288	276	205
ENSMUSG00000032412	chr9	Atp1b3	96332655	96333694	2389	0.559663	5.26269	5.26E-05	0.000282	0.021167	1	437	355	685	479	545	663	981	856	1050	645
ENSMUSG00000027164	chr2	Traf6	1.02E+08	1.02E+08	7883	-0.59994	4.305645	5.28E-05	0.000282	0.0231	-1	298	280	604	341	420	225	301	282	390	239
ENSMUSG00000042286	chr14	Stab1	31139013	31139203	10288	0.847751	4.863282	5.28E-05	0.000282	0.050085	1	260	184	593	291	417	650	475	721	708	727
ENSMUSG00000043004	chr14	Gng2	19872559	19875935	4390	0.869243	2.865668	5.34E-05	0.000286	0.044715	1	51	81	121	74	79	132	223	198	168	126
ENSMUSG00000036599	chr5	Chst12	1.41E+08	1.41E+08	2362	0.854114	3.105993	5.36E-05	0.000286	0.04481	1	89	80	134	69	114	162	170	254	200	190
ENSMUSG00000027514	chr2	Zbp1	1.73E+08	1.73E+08	3529	1.916361	0.755318	5.37E-05	0.000287	0.204046	1	12	8	23	2	9	51	68	45	11	43
ENSMUSG00000024501	chr18	Dpysl3	43320979	43324420	6265	0.93631	4.123699	5.37E-05	0.000287	0.060179	1	94	103	294	201	315	245	476	452	390	493
ENSMUSG00000063663	chrX	Brwd3	1.09E+08	1.09E+08	12692	-0.92928	1.595684	5.38E-05	0.000287	0.039911	-1	42	48	108	53	65	29	39	36	46	34
ENSMUSG00000022177	chr14	Haus4	54541785	54542257	1587	0.870616	2.305637	5.39E-05	0.000288	0.042361	1	43	26	77	68	66	102	107	109	146	101
ENSMUSG00000026842	chr2	Abl1	31688376	31689942	11596	-0.634	5.380047	5.4E-05	0.000288	0.0278	-1	658	487	1445	724	914	418	662	607	730	566
ENSMUSG00000064354	chrMT	mt-Co2	7013	7696	684	-1.29314	4.644954	5.4E-05	0.000288	0.116364	-1	219	220	563	824	1169	164	386	218	446	168
ENSMUSG00000033590	chr9	Myo5c	75232014	75232175	6733	-0.73484	3.247207	5.46E-05	0.000291	0.032356	-1	154	123	339	143	220	117	164	118	146	101
ENSMUSG00000030397	chr7	Mark4	19426075	19426411	2259	-0.68594	3.511273	5.47E-05	0.000292	0.028614	-1	165	130	314	249	292	125	186	132	193	157
ENSMUSG00000097867	chr16	1110054M08Rik	24391612	24393107	1603	0.655852	3.780033	5.49E-05	0.000292	0.026315	1	159	141	212	151	177	213	361	272	394	292
ENSMUSG00000025764	chr3	Jade1	41555731	41555819	8492	-0.73232	4.401762	5.5E-05	0.000293	0.036269	-1	338	276	687	400	469	140	334	330	373	288
ENSMUSG00000041852	chr15	Tcf20	82808629	82809787	7347	-0.66988	3.824094	5.51E-05	0.000293	0.028259	-1	177	200	483	262	313	168	237	196	225	166
ENSMUSG00000007036	chr17	Abhd16a	35089263	35089456	3220	-0.60241	6.411903	5.51E-05	0.000293	0.025859	-1	1521	1131	2245	1603	1786	1001	1348	1046	1693	1113
ENSMUSG00000043801	chr17	Oaz1-ps	17345456	17345935	681	0.690366	5.752084	5.53E-05	0.000294	0.033505	1	739	528	762	530	672	1052	1404	1044	1678	940
ENSMUSG00000055320	chr7	Tead1	1.13E+08	1.13E+08	11237	-0.81742	7.368754	5.53E-05	0.000294	0.048236	-1	2065	1719	5890	3647	4642	1393	2743	1666	3342	2055
ENSMUSG00000041912	chr3	Tdrkh	94413296	94413362	3806	-0.95433	2.843342	5.54E-05	0.000294	0.056379	-1	149	127	250	107	120	88	98	60	94	94
ENSMUSG00000001247	chr7	Lsr	30957775	30957901	2167	1.451871	-0.14934	5.55E-05	0.000295	0.067276	1	6	3	13	3	9	17	25	24	28	11
ENSMUSG00000025353	chr10	Ormdl2	1.29E+08	1.29E+08	2055	0.924648	1.9213	5.57E-05	0.000296	0.04472	1	31	25	54	42	54	65	94	117	103	60
ENSMUSG00000025804	chr9	Ccr1	1.24E+08	1.24E+08	2831	1.451893	0.630312	5.61E-05	0.000298	0.099325	1	16	8	17	3	17	31	73	30	34	25
ENSMUSG00000064145	chr9	Arih2	1.09E+08	1.09E+08	7672	-0.65369	6.340143	5.63E-05	0.000299	0.030601	-1	1481	1271	2433	1233	1563	933	1443	1003	1552	895
ENSMUSG00000061132	chr19	Blnk	40928927	40929292	5991	1.10597	1.88643	5.64E-05	0.000299	0.067805	1	25	35	41	46	31	84	74	118	96	65
ENSMUSG00000097164	chr10	Cep83os	94673493	94677129	4135	-0.95452	1.341637	5.64E-05	0.000299	0.040681	-1	41	40	68	51	60	21	50	26	28	28
ENSMUSG00000029223	chr5	Uchl1	66676098	66676322	1616	1.488636	1.723402	5.66E-05	0.0003	0.134562	1	16	9	15	49	45	58	72	111	131	58
ENSMUSG00000037211	chr3	Spry1	37639947	37640064	2906	0.593778	4.704114	5.68E-05	0.000301	0.02345	1	264	230	427	358	395	399	723	490	791	498
ENSMUSG00000079323	chr9	Gm20661	1.08E+08	1.08E+08	2160	1.393575	0.271715	5.68E-05	0.000301	0.068232	1	10	8	8	9	12	26	32	40	27	17
ENSMUSG00000031342	chrX	Gpm6b	1.66E+08	1.66E+08	5600	0.918946	2.882693	5.69E-05	0.000301	0.053215	1	53	41	126	89	110	105	220	215	147	175
ENSMUSG00000033400	chr3	Agl	1.17E+08	1.17E+08	12803	-0.6764	9.878225	5.76E-05	0.000305	0.033535	-1	16368	11233	32862	15125	21104	10485	16766	11076	18713	10339
ENSMUSG00000056492	chr17	Gpr116	43389466	43389707	8535	-0.74785	5.614372	5.76E-05	0.000305	0.039726	-1	600	506	1472	1125	1461	480	944	696	805	475
ENSMUSG00000047242	chrX	Taf9b	1.06E+08	1.06E+08	3158	-0.88693	3.507548	5.77E-05	0.000305	0.052069	-1	257	219	311	154	209	131	226	130	151	95
ENSMUSG00000027459	chr2	Fam110a	1.52E+08	1.52E+08	2207	1.220268	1.758151	5.85E-05	0.000309	0.088119	1	19	18	39	26	60	46	58	101	112	95
ENSMUSG00000026933	chr2	Camsap1	25926838	25930028	8368	-0.61676	5.142895	5.86E-05	0.00031	0.026282	-1	548	447	1182	628	734	362	562	468	693	477
ENSMUSG00000031931	chr9	Ankrd49	14780209	14781611	1753	-0.77729	2.465573	5.87E-05	0.00031	0.032495	-1	72	75	162	121	133	59	97	69	84	59
ENSMUSG00000044770	chr10	Scml4	42860370	42860853	7725	1.495769	-0.058	5.91E-05	0.000312	0.084023	1	6	1	9	5	15	16	26	19	23	28
ENSMUSG00000003418	chr2	St8sia6	13651021	13657290	7664	-1.70996	0.128059	5.92E-05	0.000312	0.13564	-1	5	13	32	35	42	4	10	6	16	7
ENSMUSG00000020817	chr11	Rabep1	70844778	70845008	6868	-0.57965	5.757471	5.92E-05	0.000312	0.023683	-1	901	710	1658	906	1137	667	989	782	934	605
ENSMUSG00000024194	chr17	Cuta	26937973	26938176	649	0.674282	5.925711	5.93E-05	0.000313	0.032326	1	763	634	862	683	717	1166	1520	1289	1845	1037
ENSMUSG00000035493	chr13	Tgfbi	56609603	56609780	2678	0.693826	5.504007	6.01E-05	0.000317	0.03422	1	356	434	923	474	670	964	987	1048	1057	946
ENSMUSG00000029772	chr6	Ahcyl2	29768011	29768317	11896	-0.63752	4.245377	6.01E-05	0.000317	0.026788	-1	294	227	468	434	446	190	317	310	314	225
ENSMUSG00000027953	chr3	Slc50a1	89268246	89268598	1466	0.659622	3.355438	6.02E-05	0.000317	0.025603	1	121	88	155	116	150	178	269	230	297	168
ENSMUSG00000058093	chr13	AA987161	67589443	67593915	4861	-0.94626	1.618164	6.05E-05	0.000318	0.044673	-1	54	55	99	53	55	23	48	42	41	33
ENSMUSG00000041859	chr1	Mcm3	20802968	20803654	3752	0.816654	2.277043	6.08E-05	0.00032	0.036538	1	38	38	83	48	74	82	116	100	133	117
ENSMUSG00000020919	chr11	Stat5b	1.01E+08	1.01E+08	5539	-0.69413	7.725311	6.09E-05	0.00032	0.035313	-1	3678	3022	7712	3134	4080	2249	3951	2420	3843	2531
ENSMUSG00000049091	chr7	Sephs2	1.27E+08	1.27E+08	1359	-0.55665	4.618406	6.15E-05	0.000323	0.020597	-1	406	322	670	438	536	253	453	372	463	293
ENSMUSG00000060012	chr14	Kif13b	64652531	64652656	5603	-1.07867	2.144459	6.15E-05	0.000323	0.068423	-1	58	43	187	86	130	31	67	54	43	57
ENSMUSG00000071350	chr14	Setdb2	59402009	59402416	4047	-0.92322	1.753738	6.16E-05	0.000323	0.044703	-1	59	55	108	56	71	31	64	43	50	23
ENSMUSG00000062203	chr16	Gspt1	11219292	11220879	4297	-0.60014	5.792537	6.19E-05	0.000325	0.025646	-1	874	747	1743	903	1230	600	1167	732	904	671

ENSMUSG00000013662	chr19	Atad1	32672563	32674364	2813	-0.69141	6.158429	6.21E-05	0.000326	0.034554	-1	984	900	1782	1657	1883	689	1443	807	1127	981
ENSMUSG00000019970	chr10	Sgk1	21882184	21882707	4903	-0.86846	7.048215	6.26E-05	0.000328	0.055134	-1	2605	2731	2848	2073	2954	1085	2854	1197	1890	1723
ENSMUSG00000002326	chr14	Gmpr2	55672235	55672384	1543	0.966444	1.629209	6.36E-05	0.000333	0.045058	1	25	24	33	40	38	56	80	88	85	50
ENSMUSG00000103316	chr11	Coil	88973949	88974202	1722	-0.95265	1.402463	6.37E-05	0.000334	0.041676	-1	42	47	81	44	58	28	47	26	31	27
ENSMUSG00000026088	chr1	Mitd1	37874801	37875125	2770	1.121337	1.040819	6.38E-05	0.000334	0.054495	1	16	17	19	22	22	30	75	56	46	37
ENSMUSG00000004233	chr3	Wars2	99141068	99141188	5946	-0.73749	2.608363	6.45E-05	0.000338	0.030182	-1	106	83	179	99	147	54	111	84	100	68
ENSMUSG00000040481	chr11	Bptf	1.07E+08	1.07E+08	13907	-0.70187	4.708093	6.45E-05	0.000338	0.034154	-1	356	262	960	517	651	260	439	377	426	320
ENSMUSG00000049551	chr5	Fzd9	1.35E+08	1.35E+08	2293	-0.87223	3.885236	6.47E-05	0.000339	0.052242	-1	204	179	470	375	346	137	206	116	363	156
ENSMUSG00000045690	chr12	Wdr89	75630596	75633508	3192	0.630676	4.133078	6.48E-05	0.000339	0.025607	1	205	187	254	214	217	301	454	354	508	330
ENSMUSG00000034714	chr11	Ttyh2	1.15E+08	1.15E+08	3739	0.678394	4.217621	6.49E-05	0.000339	0.030937	1	241	144	357	165	256	294	513	480	499	314
ENSMUSG00000103081	chr18	Pcdhgb8	37761801	37764299	4615	0.613422	5.488105	6.55E-05	0.000343	0.026788	1	454	401	925	473	664	706	1055	1087	1134	946
ENSMUSG00000102440	chr18	PCDHGA9	37736936	37739543	5586	0.612721	5.489037	6.56E-05	0.000343	0.02673	1	453	401	926	476	664	705	1057	1088	1135	946
ENSMUSG00000005103	chr5	Wdr1	38526814	38527912	2948	0.6621	5.850486	6.59E-05	0.000344	0.031671	1	596	391	812	852	982	998	1714	1108	1642	1074
ENSMUSG00000063160	chr7	Numbl	27258433	27258513	8673	0.857875	2.514656	6.62E-05	0.000346	0.044023	1	49	39	110	49	84	108	118	151	144	127
ENSMUSG00000042104	chr14	Uggt2	1.19E+08	1.19E+08	12796	-0.78501	2.708477	6.63E-05	0.000346	0.03629	-1	91	88	187	139	164	56	126	67	101	88
ENSMUSG00000022555	chr15	Dgat1	76502015	76502388	3054	1.062758	4.240465	6.65E-05	0.000347	0.079365	1	233	143	210	184	180	368	341	818	422	313
ENSMUSG00000102543	chr18	PCDHGC5	37819513	37822134	7627	0.612891	5.492076	6.69E-05	0.000349	0.026809	1	458	402	928	474	663	706	1059	1089	1136	951
ENSMUSG00000031749	chr8	St3gal2	1.11E+08	1.11E+08	5041	-0.65975	5.884326	6.69E-05	0.000349	0.031455	-1	793	666	2030	1279	1295	632	949	842	980	773
ENSMUSG00000000751	chr11	Rpa1	75298166	75301403	5578	0.569796	6.493368	6.7E-05	0.000349	0.023643	1	953	840	1680	1162	1244	1485	2486	1912	2415	1623
ENSMUSG00000052928	chr18	Ctif	75431224	75435409	6173	0.650198	3.895439	6.71E-05	0.00035	0.027887	1	147	97	300	179	236	244	352	335	453	277
ENSMUSG00000062101	chr17	Zfp119b	55938381	55939993	2166	-0.91964	1.632619	6.81E-05	0.000355	0.042993	-1	55	52	82	69	56	28	59	37	43	26
ENSMUSG00000016239	chrX	Lonrf3	36328353	36329399	3812	-1.38606	0.369739	6.83E-05	0.000356	0.081373	-1	14	17	58	28	28	13	7	14	16	9
ENSMUSG00000025610	chr16	Map3k7cl	87553330	87553595	1652	0.960212	4.283354	6.86E-05	0.000357	0.065056	1	72	186	245	274	282	329	640	472	474	430
ENSMUSG00000005698	chr8	Ctcf	1.06E+08	1.06E+08	4860	-0.58302	5.091476	6.92E-05	0.00036	0.023836	-1	508	497	1003	586	735	327	644	507	600	440
ENSMUSG00000024983	chr19	Vti1a	55316351	55316544	3405	-0.5962	4.330563	6.96E-05	0.000362	0.023695	-1	294	242	603	399	454	209	408	269	331	257
ENSMUSG00000030610	chr7	Det1	78822962	78823260	2877	-0.60281	3.791857	7E-05	0.000364	0.022839	-1	219	164	374	291	308	158	227	207	244	165
ENSMUSG00000060802	chr2	B2m	1.22E+08	1.22E+08	860	0.989713	7.345925	7.03E-05	0.000365	0.072323	1	1916	1673	1944	1242	1623	3285	4265	6069	3030	2742
ENSMUSG00000038708	chr9	Golga4	1.19E+08	1.19E+08	7535	-0.62276	9.06358	7.05E-05	0.000366	0.029108	-1	8307	6483	15924	10703	12094	5570	9138	6805	11331	6367
ENSMUSG00000025932	chr1	Eya1	14168954	14170996	7808	-0.67739	4.598708	7.06E-05	0.000366	0.03197	-1	463	317	856	322	501	257	436	319	406	293
ENSMUSG00000033530	chr12	Ttc7b	1E+08	1E+08	3441	-0.62789	6.444064	7.06E-05	0.000366	0.029027	-1	1266	1223	2364	1825	1902	969	1567	945	1826	1053
ENSMUSG00000049717	chr8	Lig4	9970020	9973807	4255	-0.72907	2.905062	7.07E-05	0.000367	0.031742	-1	122	130	216	122	152	82	126	99	133	74
ENSMUSG00000102428	chr18	PCDHGA12	37765580	37768540	6664	0.610707	5.496821	7.09E-05	0.000367	0.026812	1	456	403	933	478	669	710	1063	1096	1139	947
ENSMUSG00000027639	chr2	Samhd1	1.57E+08	1.57E+08	9150	0.588721	5.034125	7.14E-05	0.00037	0.024266	1	383	304	619	356	453	640	847	740	754	579
ENSMUSG00000042589	chr5	Cux2	1.22E+08	1.22E+08	8015	-2.40753	0.449669	7.15E-05	0.00037	0.324278	-1	9	3	25	68	75	3	7	12	4	9
ENSMUSG00000029534	chr6	St7	17692933	17693158	9109	-0.67836	3.164955	7.16E-05	0.000371	0.027912	-1	134	120	221	194	217	93	178	99	155	108
ENSMUSG00000078695	chr11	Cisd3	97685826	97685864	833	0.59728	5.458171	7.19E-05	0.000372	0.025433	1	455	419	639	625	647	765	1104	898	1350	760
ENSMUSG00000020205	chr10	Phlda1	1.12E+08	1.12E+08	2205	0.8103	2.6791	7.2E-05	0.000372	0.039136	1	47	59	109	60	98	98	215	114	194	126
ENSMUSG00000033488	chr1	BC026585	1.57E+08	1.57E+08	2534	1.297571	1.084386	7.23E-05	0.000374	0.089707	1	27	11	24	13	17	54	39	72	49	38
ENSMUSG00000023036	chr18	Pcdhgc4	37815079	37817983	5596	0.611027	5.489454	7.24E-05	0.000374	0.026903	1	454	404	928	473	663	704	1056	1088	1135	947
ENSMUSG00000029373	chr5	Pf4	90772435	90772678	586	0.925141	3.667059	7.26E-05	0.000375	0.05851	1	166	100	205	89	137	345	243	280	300	282
ENSMUSG00000035279	chr7	Ssc5d	4925844	4925979	4284	0.902151	4.413561	7.25E-05	0.000375	0.058449	1	124	122	358	251	398	343	434	557	569	577
ENSMUSG00000027333	chr2	Smox	1.31E+08	1.31E+08	3894	-1.25759	8.187443	7.28E-05	0.000376	0.116193	-1	8993	4656	7699	3721	7315	4510	2609	2303	4868	1235
ENSMUSG00000048728	chr11	Zfp454	50872720	50874287	2423	-0.93278	1.49326	7.3E-05	0.000377	0.040817	-1	43	32	96	59	66	30	49	31	33	28
ENSMUSG00000093315	chr19	Mir5114	44303171	44303231	61	-1.34777	0.297307	7.31E-05	0.000377	0.071964	-1	14	13	44	24	41	8	12	15	9	13
ENSMUSG00000035798	chr10	Zdhhc17	1.11E+08	1.11E+08	4948	-0.62158	4.327733	7.35E-05	0.000379	0.026034	-1	317	233	667	342	462	237	365	234	334	272
ENSMUSG00000087153	chr8	Gm6483	19682268	19682655	6290	-1.61061	-0.12922	7.35E-05	0.000379	0.10119	-1	16	10	37	9	31	6	13	8	3	6
ENSMUSG00000029178	chr5	Klf3	64803523	64803791	2479	-0.87917	2.099951	7.39E-05	0.000381	0.041914	-1	65	53	150	67	119	47	67	53	52	49
ENSMUSG00000028977	chr4	Casz1	1.49E+08	1.49E+08	12224	-0.60851	5.053958	7.41E-05	0.000382	0.026227	-1	467	395	1013	635	818	324	598	416	653	444
ENSMUSG00000022206	chr15	Npr3	11839896	11845288	6927	-1.65681	2.782559	7.41E-05	0.000382	0.186758	-1	192	217	163	79	122	22	48	59	44	117
ENSMUSG00000028820	chr4	Sfpq	1.27E+08	1.27E+08	4743	0.576635	5.578997	7.42E-05	0.000382	0.023853	1	540	478	744	564	734	923	1171	1056	1244	811
ENSMUSG00000021877	chr14	Arf4	26638074	26638486	2813	0.637347	5.211078	7.43E-05	0.000383	0.028984	1	430	370	603	413	489	660	877	1004	859	671
ENSMUSG00000047911	chr14	Npm2	70647302	70647549	997	1.879461	-0.23212	7.5E-05	0.000386	0.142637	1	7	3	6	4	4	15	52	17	15	8
ENSMUSG00000041798	chr11	Gck	5900820	5901087	3033	-1.75603	1.624994	7.51E-05	0.000386	0.198695	-1	85	18	112	103	64	31	14	14	60	8
ENSMUSG00000021451	chr13	Sema4d	51701246	51703531	6449	-0.57059	5.710827	7.51E-05	0.000386	0.023577	-1	862	638	1610	847	1214	604	1000	715	962	610
ENSMUSG00000038000	chr8	Acd	1.06E+08	1.06E+08	1425	0.75095	2.768638	7.53E-05	0.000387	0.032604	1	85	59	92	68	93	138	170	146	186	124
ENSMUSG00000028184	chr3	Lphn2	1.49E+08	1.49E+08	8403	-0.83727	3.132017	7.56E-05	0.000388	0.045649	-1	95	108	305	178	253	67	138	127	137	105
ENSMUSG00000099908	chr16	Gm28539	18836584	18836619	2982	-0.63238	4.416799	7.57E-05	0.000389	0.027597	-1	330	344	651	348	424	268	389	266	403	216
ENSMUSG00000019817	chr10	Plagl1	13060504	13060859	7819	1.398168	1.695398	7.62E-05	0.000391	0.120252	1	18	28	44	17	31	25	80	106	79	117
ENSMUSG00000034744	chr6	Nagk	83794982	83795282	3293	0.801002	2.968829	7.63E-05	0.000391	0.039251	1	65	90	126	79	87	168	216	183	189	133
ENSMUSG00000056342	chr11	Usp34	23306895	23307016	18453	-0.66753	5.938989	7.63E-05	0.000391	0.032821	-1	868	701	2304	1050	1457	656	1116	819	1093	697
ENSMUSG00000040325	chr9	Vprbp	1.07E+08	1.07E+08	7786	-0.66854	4.247944	7.7E-05	0.000395	0.030647	-1	257	211	677	341	478	190	355	245	322	238
ENSMUSG00000003184	chr7	Irf3	44997648	44997908	3187	0.646023	4.270428	7.73E-05	0.000396	0.028382	1	237	169	286	248	251	387	416	443	462	393
ENSMUSG00000040296	chr4	Ddx58	40203773	40204065	7050	0.938308	2.395418	7.74E-05	0.000396	0.052743	1	41	40	58	75	67	95	161	152	101	103
ENSMUSG00000060798	chr3	Intu	40531286	40531963	7429	-0.98941	1.498247	7.75E-05	0.000397	0.050487	-1	42	31	77	80	67	21	46	31	36	34
ENSMUSG00000061360	chr15	Phf5a	81865319	81865892	937	0.605335	5.295028	7.74E-05	0.000397	0.026123	1	438	433	568	482	523	705	1139	778	1039	692

ENSMUSG00000024404	chr18	Riok3	12128850	12128973	3661	-0.64568	7.415217	7.76E-05	0.000397	0.031403	-1	2957	2911	4691	2692	3350	2075	2757	2161	3246	1982
ENSMUSG00000000439	chr6	Mkrn2	1.16E+08	1.16E+08	2240	-0.58379	5.788301	7.79E-05	0.000398	0.02497	-1	936	751	1498	1009	1171	587	1097	630	1118	688
ENSMUSG00000007833	chr7	Aldh16a1	45140684	45142102	5501	0.6486	3.375367	7.78E-05	0.000398	0.025755	1	107	85	155	144	153	184	267	239	257	195
ENSMUSG00000035711	chr13	Dok3	55523235	55524111	1546	1.295514	0.663405	7.79E-05	0.000398	0.073669	1	6	18	18	10	15	37	32	36	44	37
ENSMUSG00000029482	chr5	Aacs	1.25E+08	1.25E+08	3668	1.647941	3.417315	7.82E-05	0.000399	0.189288	1	109	59	109	50	77	203	136	720	243	116
ENSMUSG00000004446	chr6	Bid	1.21E+08	1.21E+08	3550	1.284047	0.698294	7.85E-05	0.000401	0.076908	1	12	13	25	12	8	31	51	51	28	31
ENSMUSG00000070565	chr1	Rasal2	1.57E+08	1.57E+08	13740	-0.8569	2.826759	7.9E-05	0.000403	0.046076	-1	78	79	250	163	192	70	118	76	110	84
ENSMUSG00000029313	chr5	Aff1	1.04E+08	1.04E+08	9458	-0.66198	5.471409	7.91E-05	0.000403	0.031949	-1	658	476	1658	746	1073	514	706	637	747	528
ENSMUSG00000062949	chrX	Atp11c	60223290	60225793	7312	-0.92333	2.0485	7.9E-05	0.000403	0.048594	-1	56	65	129	68	118	26	55	60	66	50
ENSMUSG00000020432	chr11	Tcn2	3917192	3917709	2178	0.638291	4.829361	7.91E-05	0.000403	0.029043	1	258	233	513	355	464	457	661	780	680	553
ENSMUSG00000048612	chr19	Myof	37899036	37899767	7109	0.815353	3.680013	7.92E-05	0.000404	0.045997	1	87	83	266	149	193	211	278	385	322	268
ENSMUSG00000001313	chr11	Rnd2	1.01E+08	1.01E+08	1990	0.973758	1.654058	7.99E-05	0.000407	0.048008	1	30	25	27	35	44	53	71	70	107	66
ENSMUSG00000021496	chr13	Pcbd2	55727368	55727474	546	0.901963	2.417245	8E-05	0.000407	0.047516	1	51	50	63	71	50	80	179	137	148	88
ENSMUSG00000006010	chr1	BC003331	1.5E+08	1.5E+08	4100	-0.63401	4.795266	8.01E-05	0.000408	0.028622	-1	488	464	734	452	543	295	555	331	433	381
ENSMUSG00000033102	chr13	Cdc14b	64192545	64196675	6083	-0.76506	2.878847	8.03E-05	0.000409	0.035548	-1	110	92	247	130	182	64	128	91	105	105
ENSMUSG00000025437	chr3	Usp33	1.52E+08	1.52E+08	5950	-0.61746	4.198366	8.07E-05	0.000411	0.025785	-1	275	213	524	372	441	171	341	269	288	256
ENSMUSG00000032038	chr9	St3gal4	35046579	35047519	2029	0.881278	2.705761	8.08E-05	0.000411	0.049211	1	74	39	118	53	88	118	208	186	127	117
ENSMUSG00000078348	chr10	Sf3b5	13005343	13009183	3841	0.618576	4.507855	8.12E-05	0.000413	0.026327	1	306	215	343	243	310	400	540	468	657	443
ENSMUSG00000030830	chr7	Itgal	1.27E+08	1.27E+08	6380	1.208695	0.50187	8.14E-05	0.000414	0.058494	1	11	8	18	12	14	29	47	41	25	22
ENSMUSG00000022708	chr16	Zbtb20	42875881	42875924	30730	-0.95453	6.253928	8.17E-05	0.000415	0.068184	-1	802	734	3682	1479	2189	597	1029	982	1205	949
ENSMUSG00000034617	chr13	Mtrr	68560780	68562432	3692	-0.61053	4.280503	8.2E-05	0.000417	0.025322	-1	285	223	558	391	476	221	333	220	355	275
ENSMUSG00000034560	chr10	A230046K03Rik	83543941	83544102	5854	-0.77335	3.651321	8.3E-05	0.000421	0.040514	-1	198	148	457	200	322	95	206	206	181	158
ENSMUSG00000027751	chr3	Supt20	54693105	54693208	1968	-0.9241	2.049024	8.32E-05	0.000422	0.048987	-1	63	61	150	72	92	38	76	48	39	53
ENSMUSG00000046470	chr2	Sox18	1.82E+08	1.82E+08	1620	0.893759	3.321253	8.33E-05	0.000422	0.054445	1	94	54	154	154	108	190	190	254	375	170
ENSMUSG00000019832	chr10	Rab32	10545011	10546451	2108	0.879588	1.7163	8.45E-05	0.000428	0.039454	1	26	22	52	38	44	76	77	64	95	60
ENSMUSG00000021898	chr14	Asb14	26894557	26894672	2549	-0.63387	6.613322	8.49E-05	0.00043	0.030335	-1	1824	1422	2951	1637	1784	1232	1892	1183	1654	1098
ENSMUSG00000015843	chr1	Rxrg	1.68E+08	1.68E+08	2297	-0.71516	5.721028	8.52E-05	0.000431	0.038176	-1	1014	933	1466	759	1024	733	874	581	967	505
ENSMUSG00000103677	chr18	Pcdhga4	37685210	37687817	4727	0.603414	5.500832	8.54E-05	0.000432	0.026778	1	459	406	942	482	667	713	1063	1092	1140	950
ENSMUSG00000022748	chr16	Cmss1	57302199	57302282	930	-0.59813	4.709778	8.55E-05	0.000433	0.025342	-1	441	360	559	525	627	329	450	354	505	274
ENSMUSG00000040359	chr4	Ufl1	25248600	25249969	5706	-0.55699	4.787191	8.59E-05	0.000435	0.021768	-1	427	372	802	455	631	315	551	383	468	337
ENSMUSG00000047843	chr5	Bri3	1.44E+08	1.44E+08	1648	0.628422	4.263376	8.62E-05	0.000436	0.026894	1	217	176	254	285	254	348	539	384	523	339
ENSMUSG00000005410	chr8	Mcm5	75109528	75109621	3422	1.142213	1.003747	8.64E-05	0.000437	0.062857	1	18	16	25	14	21	51	41	44	41	52
ENSMUSG00000022514	chr16	Il1rap	26581704	26581886	11360	-1.06546	1.171865	8.64E-05	0.000437	0.055676	-1	34	27	81	50	50	19	37	16	24	31
ENSMUSG00000026764	chr2	Kif5c	49619298	49619787	7142	0.951576	2.70324	8.65E-05	0.000437	0.059295	1	41	58	129	34	102	140	173	144	175	132
ENSMUSG00000103037	chr18	Pcdhgb1	37680233	37682839	5776	0.602939	5.498372	8.75E-05	0.000442	0.026819	1	458	403	942	483	667	711	1059	1093	1139	947
ENSMUSG00000028282	chr4	Casp8ap2	32615451	32615492	6826	-0.84437	2.444033	8.8E-05	0.000444	0.042195	-1	87	67	154	95	164	50	89	73	61	74
ENSMUSG00000079737	chr16	3110001I22Rik	13671929	13672078	1722	-0.91795	1.787845	8.8E-05	0.000444	0.046124	-1	53	54	108	61	83	35	72	31	38	38
ENSMUSG00000019362	chr8	D8Ertd738e	84246237	84246693	659	0.647445	6.505566	8.94E-05	0.000451	0.031684	1	1076	967	1196	1114	1171	1713	2579	1739	2576	1607
ENSMUSG00000037098	chr17	Rab11fip3	25989036	25990885	6789	-0.66891	6.452915	8.97E-05	0.000452	0.033937	-1	1244	885	2795	1860	2257	876	1506	1064	1621	1173
ENSMUSG00000064360	chrMT	mt-Nd3	9459	9806	348	-1.67832	1.568359	8.98E-05	0.000453	0.183892	-1	24	17	76	114	140	11	33	19	50	17
ENSMUSG00000024677	chr19	Ms4a6b	11516512	11516545	4485	1.204843	1.494097	9E-05	0.000453	0.084932	1	23	18	49	21	23	83	71	88	50	41
ENSMUSG00000037221	chr5	Mospd3	1.38E+08	1.38E+08	1651	0.775391	2.98869	9.08E-05	0.000457	0.038605	1	91	48	124	90	118	114	182	213	238	159
ENSMUSG00000030536	chr7	Iqgap1	80711583	80713945	7359	0.642159	5.039375	9.08E-05	0.000457	0.030371	1	286	226	655	417	562	518	826	790	818	692
ENSMUSG00000103897	chr18	PCDHGB6	37725706	37728316	4730	0.602066	5.490961	9.1E-05	0.000458	0.026867	1	456	402	936	476	669	703	1056	1086	1135	944
ENSMUSG00000097328	chr11	Tnfsf12	69686250	69687091	1515	0.623205	3.952975	9.12E-05	0.000459	0.0263	1	153	126	273	194	244	258	345	409	412	276
ENSMUSG00000091736	chrX	Yy2	1.58E+08	1.58E+08	2867	-1.04896	1.28466	9.13E-05	0.000459	0.056137	-1	39	34	78	42	67	13	31	21	38	37
ENSMUSG00000041444	chr9	Arhgap32	32116136	32116251	17179	-0.96635	2.088459	9.17E-05	0.000461	0.055568	-1	56	46	136	86	138	27	59	61	59	52
ENSMUSG00000004460	chr16	Dnajb11	22857845	22858109	3236	0.55762	5.610206	9.17E-05	0.000461	0.022878	1	554	476	737	617	767	879	1218	1069	1255	879
ENSMUSG00000021500	chr13	Ddx46	55635027	55635195	5747	-0.56101	5.305497	9.19E-05	0.000462	0.023021	-1	551	551	1150	715	890	404	750	542	757	504
ENSMUSG00000022453	chr15	Naga	82329532	82330207	1913	0.666969	3.439529	9.19E-05	0.000462	0.028616	1	114	86	182	141	150	215	273	274	265	171
ENSMUSG00000049421	chr7	Zfp260	30094777	30094882	5790	-0.59642	5.208775	9.22E-05	0.000463	0.02609	-1	564	573	1083	602	785	447	768	435	622	441
ENSMUSG00000030788	chr7	Rnf141	1.11E+08	1.11E+08	5861	-0.60612	4.789665	9.29E-05	0.000466	0.026499	-1	482	400	782	470	557	242	496	424	477	378
ENSMUSG00000032271	chr9	Nnmt	48591877	48592182	1576	1.709158	3.14946	9.3E-05	0.000467	0.203618	1	113	78	31	30	38	184	280	432	194	125
ENSMUSG00000040451	chr19	Sgms1	32122727	32124524	10299	-0.5977	5.443108	9.31E-05	0.000467	0.026544	-1	673	639	1293	709	955	391	845	635	847	512
ENSMUSG00000023984	chr17	Gm20517	47611589	47611692	6495	-0.84553	2.942901	9.34E-05	0.000468	0.046273	-1	114	76	222	177	224	87	122	73	100	109
ENSMUSG00000002733	chr2	Plekha3	76675281	76675634	3126	-0.66166	3.399754	9.37E-05	0.000469	0.028204	-1	157	159	327	181	224	103	210	124	179	135
ENSMUSG00000004043	chr11	Stat5a	1.01E+08	1.01E+08	7133	0.644177	3.952861	9.38E-05	0.00047	0.028516	1	167	101	244	212	258	250	446	362	363	298
ENSMUSG00000013736	chr6	Trnt1	1.07E+08	1.07E+08	3869	-0.60459	3.802636	9.4E-05	0.00047	0.024269	-1	207	215	348	279	293	141	261	201	226	182
ENSMUSG00000030850	chr7	Ate1	1.3E+08	1.3E+08	4875	-0.55252	5.550656	9.41E-05	0.000471	0.022546	-1	746	621	1395	767	1039	571	921	617	802	578
ENSMUSG00000039087	chr13	Rreb1	37778400	37778557	13991	-0.73937	4.511994	9.41E-05	0.000471	0.03969	-1	352	227	812	404	618	192	323	285	437	330
ENSMUSG00000026502	chr1	Desi2	1.78E+08	1.78E+08	9156	-0.58102	5.58274	9.43E-05	0.000471	0.025092	-1	813	535	1434	876	1083	483	922	625	858	656
ENSMUSG00000008318	chr7	Relt	1.01E+08	1.01E+08	3279	-0.70637	4.019032	9.46E-05	0.000473	0.03507	-1	356	209	386	270	381	217	238	167	324	177
ENSMUSG00000001128	chrX	Cfp	20925454	20925759	1736	0.949637	3.533702	9.5E-05	0.000475	0.063546	1	144	101	192	72	117	319	253	310	263	194
ENSMUSG00000049999	chr2	Ppp1r3d	1.78E+08	1.78E+08	3267	1.187368	1.844443	9.51E-05	0.000475	0.08591	1	23	38	53	20	34	48	176	76	99	58
ENSMUSG00000002731	chr2	Prkra	76629898	76630568	2028	0.853174	2.360697	9.55E-05	0.000477	0.042344	1	55	45	67	60	56	123	122	106	153	82

ENSMUSG00000021250	chr12	Fos	85473890	85474180	2352	2.450087	4.547451	9.55E-05	0.000477	0.413491	1	39	125	84	104	211	159	3039	133	279	431
ENSMUSG00000008496	chr7	Pou2f2	25087344	25093002	8231	1.290594	0.31356	9.59E-05	0.000479	0.067217	1	9	11	17	5	10	30	39	31	25	19
ENSMUSG00000020173	chr11	Cobl	12236608	12238059	8142	0.566278	5.878214	9.6E-05	0.000479	0.023965	1	676	617	980	701	798	1008	1533	1226	1607	1069
ENSMUSG00000027227	chr2	Sord	1.22E+08	1.22E+08	2352	-0.59144	6.085057	9.61E-05	0.000479	0.026509	-1	1068	932	1504	1438	1596	764	1233	1017	1154	804
ENSMUSG00000033377	chr3	Palmd	1.17E+08	1.17E+08	3812	-0.79444	4.460969	9.61E-05	0.000479	0.046376	-1	361	234	399	614	636	215	343	262	419	248
ENSMUSG00000033033	chr19	Calhm2	47105353	47107208	4361	0.930339	1.63896	9.63E-05	0.00048	0.045079	1	27	21	41	31	47	49	64	87	96	62
ENSMUSG00000040483	chr11	Xaf1	72301629	72301709	4689	0.965453	1.830156	9.78E-05	0.000487	0.053404	1	36	21	57	33	43	71	132	84	61	66
ENSMUSG00000041203	chr8	2310036O22Rik	85026833	85027234	891	0.65349	5.251714	9.84E-05	0.00049	0.031576	1	478	402	513	452	459	754	969	747	1153	645
ENSMUSG00000051853	chr15	Arf3	98737621	98740494	3837	0.607171	4.683138	9.86E-05	0.000491	0.026606	1	264	210	430	296	460	396	594	634	701	501
ENSMUSG00000104346	chr18	PCDHGB6	37674307	37676907	4720	0.602352	5.495685	9.86E-05	0.000491	0.027181	1	454	405	940	476	674	704	1059	1093	1136	948
ENSMUSG00000020794	chr11	Ube2g1	72607283	72607635	4579	-0.62957	6.752037	9.94E-05	0.000494	0.030594	-1	1943	1620	3211	1737	2062	1040	1964	1300	2100	1450
ENSMUSG00000103567	chr18	Pcdhga5	37694380	37696924	4664	0.599486	5.50064	9.95E-05	0.000494	0.026942	1	458	410	937	478	676	706	1068	1092	1134	953
ENSMUSG00000056367	chr5	Actr3b	25759997	25760128	1741	-2.44507	4.184545	9.96E-05	0.000495	0.413217	-1	512	302	679	454	537	214	19	23	236	9
ENSMUSG00000029575	chr5	Mmab	1.14E+08	1.14E+08	3530	-0.53493	5.650161	9.97E-05	0.000495	0.021323	-1	880	614	1315	872	1151	584	937	686	913	647
ENSMUSG00000035413	chr11	Tmem98	80810175	80810459	1633	1.111976	0.712224	9.99E-05	0.000496	0.054432	1	16	7	21	12	22	31	36	48	44	29
ENSMUSG00000028680	chr4	Plk3	1.17E+08	1.17E+08	2531	1.543848	-0.28271	0.0001	0.000498	0.076088	1	4	5	4	5	10	10	31	19	26	11
ENSMUSG00000004069	chr16	Dnaja3	4639989	4640148	3912	-0.6116	6.884702	0.0001	0.000498	0.028927	-1	1883	1428	2833	2693	2736	1327	2308	1405	2195	1430
ENSMUSG00000044229	chr9	Nxpe4	48362041	48362175	3173	-1.08926	1.828185	0.000101	0.000499	0.074453	-1	43	43	104	79	123	17	69	43	56	25
ENSMUSG00000031299	chrX	Pdha1	1.6E+08	1.6E+08	3734	-0.73637	9.236337	0.000102	0.000504	0.042466	-1	8398	6782	13755	16012	16690	5888	11237	6773	11433	6936
ENSMUSG00000019951	chr10	Uhrf1bp1l	89744991	89745288	6446	-0.69256	3.809734	0.000102	0.000505	0.033011	-1	204	141	402	324	359	166	189	197	257	162
ENSMUSG00000079442	chr2	St6galnac4	32587095	32587227	6482	0.750609	4.107141	0.000102	0.000505	0.04057	1	158	108	208	288	270	262	520	364	531	324
ENSMUSG00000103332	chr18	Pcdhga2	37668953	37671525	4689	0.598302	5.496941	0.000102	0.000505	0.026921	1	460	404	943	478	671	705	1064	1089	1136	946
ENSMUSG00000000823	chr2	Znf512b	1.82E+08	1.82E+08	6810	-0.59721	4.238848	0.000102	0.000506	0.024868	-1	284	210	580	383	420	206	354	226	367	234
ENSMUSG00000039753	chr5	Fbxl5	43744616	43745375	9788	-0.56409	5.421794	0.000102	0.000506	0.023724	-1	727	587	1302	719	829	450	746	612	823	554
ENSMUSG00000048280	chr13	Zfp738	67667437	67671611	5217	-0.90563	1.460089	0.000102	0.000506	0.041352	-1	50	40	91	40	63	25	49	29	46	23
ENSMUSG00000055633	chr7	Zfp580	5051532	5051714	1101	0.942493	1.521705	0.000102	0.000506	0.043433	1	24	24	38	28	37	38	72	74	99	52
ENSMUSG00000064341	chrMT	mt-Nd1	2751	3707	957	-0.81676	13.39235	0.000102	0.000506	0.05225	-1	131338	113576	251430	284847	357199	106877	199281	118052	188095	114172
ENSMUSG00000026496	chr1	Parp1	1.81E+08	1.81E+08	5293	-0.58017	6.052924	0.000102	0.000506	0.025614	-1	1055	792	2015	1227	1477	777	1134	848	1204	903
ENSMUSG00000059975	chr7	Zfp74	29930815	29932240	5628	-0.73445	2.381187	0.000102	0.000506	0.030235	-1	87	65	150	95	127	48	82	65	98	62
ENSMUSG00000021962	chr14	Dcp1a	30479565	30479816	5616	-0.80435	2.858116	0.000103	0.000507	0.041669	-1	106	75	276	135	179	67	123	92	101	94
ENSMUSG00000045404	chr12	Kcnk13	99964499	99964801	3112	1.506821	-0.08823	0.000103	0.000509	0.104066	1	4	2	16	3	11	27	22	14	21	24
ENSMUSG00000021706	chr13	Zfyve16	92487108	92488623	7082	-0.71429	2.981531	0.000104	0.000513	0.0318	-1	125	94	272	142	174	77	134	119	118	94
ENSMUSG00000052062	chr1	Pard3b	61638824	61639362	13153	-0.90409	2.472741	0.000104	0.000513	0.051474	-1	71	49	185	141	154	53	81	64	86	64
ENSMUSG00000022742	chr16	Cpox	58670208	58670950	3186	-0.66161	4.491723	0.000104	0.000514	0.031733	-1	382	212	742	419	552	206	378	313	406	299
ENSMUSG00000017631	chr11	Abr	76416734	76419193	9730	0.774884	3.881566	0.000104	0.000515	0.043315	1	83	103	238	231	239	256	447	312	391	293
ENSMUSG00000000126	chr11	Wnt9a	59306928	59307067	3329	-0.60835	4.027241	0.000105	0.000519	0.02539	-1	281	177	450	313	389	215	260	218	309	175
ENSMUSG00000029551	chr5	Psmg3	1.4E+08	1.4E+08	2893	0.674181	3.214307	0.000106	0.00052	0.028437	1	112	88	129	110	120	187	236	196	232	171
ENSMUSG00000035898	chr5	Uba6	86110720	86112788	6726	-1.07983	2.004675	0.000106	0.000522	0.073713	-1	60	46	173	72	101	22	65	48	37	57
ENSMUSG00000026335	chr1	Pam	97795114	97795392	11892	0.697306	5.561194	0.000106	0.000524	0.037235	1	316	364	793	662	848	767	1190	1133	1194	1023
ENSMUSG00000022540	chr16	Rogdi	5008730	5009252	1421	0.866729	2.817598	0.000107	0.000526	0.049812	1	60	45	82	104	105	144	143	149	254	129
ENSMUSG00000017718	chr11	Afmid	1.18E+08	1.18E+08	3539	0.711392	2.529984	0.000108	0.000532	0.028623	1	62	51	89	62	81	110	157	109	155	111
ENSMUSG00000025366	chr10	Esyt1	1.29E+08	1.29E+08	3687	0.582604	5.445569	0.000108	0.000532	0.025531	1	484	421	816	452	654	711	1036	1100	1159	767
ENSMUSG00000071456	chr12	1110002L01Rik	3403878	3406711	4131	-0.67712	2.97544	0.000108	0.000533	0.028315	-1	147	102	231	122	179	93	139	101	125	90
ENSMUSG00000078619	chr11	Smarcd2	1.06E+08	1.06E+08	3589	0.628483	4.166223	0.000109	0.000533	0.02778	1	189	174	307	221	235	350	381	466	442	315
ENSMUSG00000059866	chr5	Tnip2	34496087	34496950	2879	0.942947	2.391296	0.000109	0.000536	0.05682	1	40	53	102	33	58	106	192	104	141	82
ENSMUSG00000020594	chr12	Pum2	8674134	8674170	7260	-0.60063	6.564582	0.00011	0.000541	0.028083	-1	1529	1297	3089	1582	1881	1094	1523	1299	1883	1123
ENSMUSG00000028670	chr4	Lypla2	1.36E+08	1.36E+08	2054	0.608844	5.255317	0.00011	0.000541	0.027756	1	510	335	531	443	579	651	881	824	1126	733
ENSMUSG00000030760	chr7	Acer3	98213658	98216890	4319	0.863974	1.852068	0.000111	0.000543	0.040424	1	23	29	61	44	45	68	113	71	83	76
ENSMUSG00000099411	chr16	2310015D24Rik	13514131	13516487	3035	0.660396	4.555366	0.000111	0.000543	0.031961	1	304	194	415	224	333	460	787	396	639	380
ENSMUSG00000027487	chr2	Cdk5rap1	1.54E+08	1.54E+08	3434	-0.79081	3.592707	0.000111	0.000544	0.044007	-1	256	199	255	260	211	168	180	130	163	147
ENSMUSG00000036826	chr7	Igflr1	30565427	30565466	1270	1.036505	1.296668	0.000111	0.000544	0.059092	1	28	12	46	17	23	52	61	65	53	51
ENSMUSG00000102742	chr18	PCDHGB6	37755731	37758367	4756	0.593899	5.495746	0.000111	0.000544	0.026811	1	461	401	940	480	678	704	1056	1086	1140	944
ENSMUSG00000001506	chr11	Col1a1	94936224	94936444	6563	1.052422	7.968399	0.000112	0.000546	0.086623	1	1115	1321	4543	2457	4713	3815	5409	5785	6950	8320
ENSMUSG00000024538	chr18	Ppic	53406341	53407065	1286	0.544023	4.637616	0.000112	0.000546	0.0211	1	283	234	457	300	358	431	616	468	668	504
ENSMUSG00000050299	chr16	Gm9843	76403209	76403712	504	0.71018	3.896671	0.000111	0.000546	0.035162	1	192	155	197	173	155	306	416	282	415	261
ENSMUSG00000103144	chr18	Pcdhga1	37661793	37665039	5366	0.592808	5.500188	0.000111	0.000546	0.026719	1	461	408	941	483	674	705	1064	1089	1139	947
ENSMUSG00000062822	chr13	4833420G17Rik	1.19E+08	1.19E+08	2574	0.618386	3.576616	0.000112	0.000546	0.025032	1	125	114	191	144	175	232	330	263	266	210
ENSMUSG00000031985	chr8	Gnpat	1.25E+08	1.25E+08	3587	-0.65495	7.388063	0.000112	0.000546	0.0338	-1	2458	1900	4113	4085	4199	1783	2759	2051	3323	2106
ENSMUSG00000020176	chr11	Grb10	11930508	11933609	9089	0.732355	5.450316	0.000112	0.000547	0.041226	1	435	397	991	410	473	650	1202	1149	942	1004
ENSMUSG00000022124	chr14	Fbxl3	1.03E+08	1.03E+08	5103	-0.56556	5.777365	0.000113	0.00055	0.024475	-1	847	751	1617	973	1158	547	1098	723	961	757
ENSMUSG00000009394	chr6	Syn2	1.15E+08	1.15E+08	5646	1.321288	0.532607	0.000113	0.000551	0.077873	1	17	6	11	17	8	21	44	25	48	36
ENSMUSG00000031885	chr8	Cbfb	1.05E+08	1.05E+08	3480	-0.77794	6.977766	0.000113	0.000551	0.04758	-1	2130	2440	4138	1665	2397	1098	1899	1721	1873	1854
ENSMUSG00000027809	chr3	Etfdh	79603788	79604165	7505	-1.04116	6.993184	0.000113	0.000553	0.084738	-1	1565	1350	2398	4803	3790	991	2556	1112	1993	1233
ENSMUSG00000050029	chrX	Rap2c	51003912	51006750	3545	-0.64222	4.841209	0.000113	0.000553	0.030831	-1	475	433	909	474	545	255	449	373	562	419
ENSMUSG00000001946	chr9	Esam	37528078	37528290	2867	0.644747	4.581908	0.000114	0.000556	0.030449	1	201	232	343	352	362	448	672	567	631	358

ENSMUSG00000090015	chr5	Gm15446	1.1E+08	1.1E+08	3780	-0.91463	2.332233	0.000115	0.000558	0.053311	-1	118	90	122	86	90	56	70	62	55	65
ENSMUSG00000005447	chr7	Pafah1b3	25295049	25295376	2107	1.39726	0.216976	0.000115	0.000559	0.077284	1	7	12	14	8	4	26	24	32	28	25
ENSMUSG00000009291	chr10	Pttg1ip	77581720	77581927	3426	0.625695	5.228921	0.000115	0.000559	0.029638	1	378	373	659	400	570	721	870	1002	823	671
ENSMUSG00000016541	chr15	Atxn10	85336381	85336580	2425	0.550509	5.334955	0.000115	0.00056	0.02273	1	446	359	650	567	609	703	984	909	993	766
ENSMUSG00000031751	chr8	Amfr	93971588	93973314	3953	-0.56137	7.60448	0.000115	0.000561	0.024955	-1	3242	2594	5442	3559	4021	2198	3383	2642	3746	2505
ENSMUSG00000042686	chr1	Jph1	16964560	16964577	4998	-0.6698	8.447783	0.000115	0.000561	0.035695	-1	6466	5369	10921	4728	7350	3702	6085	3918	6995	4320
ENSMUSG00000073802	chr4	Cdkn2b	89306289	89307314	1393	0.933092	1.360061	0.000116	0.000564	0.041148	1	31	19	34	23	27	48	61	52	85	48
ENSMUSG00000028737	chr4	Aldh4a1	1.4E+08	1.4E+08	4907	-0.61836	7.146296	0.000117	0.000568	0.030219	-1	2086	1499	4227	3023	3451	1463	2487	1914	2633	1817
ENSMUSG00000022667	chr16	Cd200r1	44765736	44766072	2034	1.406789	-0.00373	0.000117	0.000569	0.069956	1	6	6	9	10	7	12	22	29	25	27
ENSMUSG00000040010	chr8	Slc7a5	1.22E+08	1.22E+08	3708	0.908337	1.944322	0.000117	0.000569	0.048599	1	21	28	62	47	55	64	92	72	132	87
ENSMUSG00000030872	chr7	Gga2	1.22E+08	1.22E+08	9769	0.555978	4.950089	0.000117	0.00057	0.022902	1	351	257	574	381	474	504	749	619	778	686
ENSMUSG00000022199	chr14	Slc22a17	54906727	54907359	2294	1.001008	1.368309	0.000118	0.000572	0.05043	1	27	23	34	21	25	40	58	76	67	56
ENSMUSG00000015087	chr2	Rabl6	25583018	25583988	6379	-0.59848	6.930241	0.000118	0.000574	0.028282	-1	1792	1641	2849	2684	2885	1469	1968	1556	2416	1500
ENSMUSG00000022197	chr15	Pdzd2	12359711	12362239	21645	-0.82744	4.544896	0.000118	0.000574	0.051846	-1	284	235	707	542	744	182	387	394	292	279
ENSMUSG00000004891	chr3	Nes	87971078	87971988	6416	0.800933	5.983999	0.000118	0.000574	0.05034	1	406	393	971	926	1155	1134	1483	1201	2070	1461
ENSMUSG00000040321	chr2	Zfp770	1.14E+08	1.14E+08	6793	-0.65111	4.453945	0.000119	0.000575	0.031258	-1	316	279	597	471	521	200	429	230	378	334
ENSMUSG00000030282	chr6	Cmas	1.43E+08	1.43E+08	2783	0.64401	5.161936	0.000119	0.000577	0.031344	1	433	367	485	425	478	757	858	651	1100	616
ENSMUSG00000031980	chr8	Agt	1.25E+08	1.25E+08	1891	0.88947	3.867558	0.000119	0.000577	0.059299	1	156	46	273	191	191	327	359	286	446	291
ENSMUSG00000039542	chr9	Ncam1	49502136	49505563	7995	1.051466	3.068988	0.000119	0.000578	0.080449	1	31	43	144	115	124	140	195	154	286	241
ENSMUSG00000061603	chr12	Akap6	52699383	52699442	10263	-0.65459	6.051029	0.00012	0.000579	0.033441	-1	856	788	2287	1287	1599	759	1055	769	1201	918
ENSMUSG00000103585	chr18	Pcdhgb4	37720369	37722917	5812	0.591955	5.497739	0.00012	0.000579	0.026894	1	461	405	941	480	678	703	1057	1087	1140	947
ENSMUSG00000031684	chr8	Slc10a7	78509335	78509674	3630	-0.77453	2.385263	0.00012	0.00058	0.03543	-1	72	75	180	94	114	59	73	71	80	61
ENSMUSG00000021488	chr13	Nsd1	55209782	55209875	12784	-0.57919	5.842257	0.00012	0.000581	0.025929	-1	846	637	1792	1084	1370	659	1032	786	1098	670
ENSMUSG00000019726	chr13	Lyst	13590409	13590496	11806	-1.2483	1.830824	0.000121	0.000582	0.10273	-1	29	38	149	81	123	17	52	36	36	46
ENSMUSG00000048047	chrX	Zbtb33	38189793	38190082	5122	-0.83937	2.756828	0.000121	0.000582	0.046409	-1	93	89	235	127	169	50	85	105	98	96
ENSMUSG00000049687	chr15	Fam109b	82338942	82339085	3311	1.32026	0.130864	0.000121	0.000582	0.060007	1	3	10	10	12	9	23	27	23	31	22
ENSMUSG00000024787	chr19	Snx15	6119399	6119954	2184	0.651579	3.415258	0.000121	0.000585	0.028093	1	132	83	174	130	143	199	241	255	296	184
ENSMUSG00000003526	chr16	Prodh	18060357	18060757	3461	-0.98765	2.932508	0.000121	0.000586	0.067902	-1	121	99	276	161	177	111	55	110	115	58
ENSMUSG00000022442	chr15	Ttll1	83483772	83484313	2918	0.795062	2.614624	0.000121	0.000586	0.039392	1	50	54	70	77	100	110	144	155	171	114
ENSMUSG00000033207	chr19	Mamdc2	23302609	23303686	3338	1.381018	2.109191	0.000121	0.000586	0.13232	1	25	28	70	35	33	37	161	203	68	86
ENSMUSG00000050312	chr16	Nsun3	62732444	62735418	4816	-0.78366	3.049359	0.000123	0.000593	0.041026	-1	124	80	246	190	223	78	112	100	139	119
ENSMUSG00000019966	chr10	Kitl	1E+08	1E+08	5765	-0.75808	4.373041	0.000123	0.000593	0.04328	-1	237	254	581	459	629	147	350	277	384	271
ENSMUSG00000102222	chr18	Pcdhga10	37746993	37749605	4732	0.593284	5.497118	0.000123	0.000593	0.027133	1	454	403	952	481	677	706	1056	1087	1139	945
ENSMUSG00000074813	chr2	Gm14005	1.28E+08	1.28E+08	2045	1.166456	0.732239	0.000124	0.000596	0.064748	1	11	8	15	23	19	40	52	26	40	35
ENSMUSG00000020169	chr10	Best3	1.17E+08	1.17E+08	2719	-1.13422	2.708983	0.000125	0.000602	0.091102	-1	76	53	279	131	234	34	82	82	81	88
ENSMUSG00000026709	chr1	Dars2	1.61E+08	1.61E+08	5195	-0.66374	3.629176	0.000125	0.000602	0.030431	-1	167	147	295	292	330	143	222	159	208	142
ENSMUSG00000003200	chr17	Sh3gl1	56016753	56017736	2072	0.621242	3.542112	0.000126	0.000604	0.02568	1	135	105	221	124	152	225	269	255	305	215
ENSMUSG00000039298	chr4	Cdk5rap2	70216856	70223114	13012	-0.68272	3.06966	0.000126	0.000604	0.030096	-1	114	95	258	169	216	86	146	119	143	94
ENSMUSG00000054942	chr3	Fam73a	1.52E+08	1.52E+08	5355	-0.58398	3.569064	0.000126	0.000604	0.022286	-1	174	164	337	225	252	133	213	163	208	149
ENSMUSG00000035242	chr10	Oaz1	80826656	80826905	2558	0.67597	8.335193	0.000126	0.000605	0.036703	1	4044	3488	4893	3134	3963	6425	8078	6286	10280	5508
ENSMUSG00000035606	chr9	Ky	1.03E+08	1.03E+08	5879	-0.75664	8.435047	0.000126	0.000607	0.045994	-1	5259	3818	13548	6266	8089	3091	6265	3282	7391	4199
ENSMUSG00000045094	chr18	Arhgef37	61493794	61495049	3234	-1.18284	1.023143	0.000127	0.000609	0.07609	-1	41	22	85	39	37	13	36	20	15	24
ENSMUSG00000053093	chr14	Myh7	54970688	54970810	8586	-4.17444	3.21384	0.000127	0.000609	1.037465	-1	4	6	19	1269	65	7	33	7	24	21
ENSMUSG00000057411	chr17	Fam173a	25790508	25790778	800	0.60176	4.980546	0.000128	0.000612	0.027162	1	398	310	403	394	460	564	781	676	844	598
ENSMUSG00000103749	chr18	Pcdhgb5	37731009	37733559	6733	0.589456	5.500053	0.000129	0.000616	0.026921	1	460	404	950	486	675	705	1060	1092	1136	945
ENSMUSG00000041258	chr18	Zfp236	82593593	82597754	10471	-0.71859	3.54368	0.000129	0.000616	0.03636	-1	157	116	390	237	316	105	208	169	195	133
ENSMUSG00000046410	chr7	Kcnk6	29221928	29225259	4089	0.976075	1.461586	0.000129	0.000616	0.050839	1	16	26	42	21	39	42	78	79	67	53
ENSMUSG00000000753	chr11	Serpinf1	75409769	75410393	2359	0.667044	6.764324	0.000129	0.000617	0.035528	1	821	1038	2029	1213	1817	2114	2547	2653	2421	2237
ENSMUSG00000040502	chr10	March9	1.27E+08	1.27E+08	3037	1.177085	0.86018	0.000129	0.000618	0.066547	1	16	16	18	19	12	30	36	36	67	45
ENSMUSG00000002257	chr17	Def6	28207778	28207938	2524	0.962259	1.229615	0.000129	0.000619	0.045589	1	24	13	35	18	33	44	54	44	83	45
ENSMUSG00000041815	chr15	Poldip3	83125978	83128055	5679	0.552492	4.12431	0.000129	0.000619	0.021169	1	191	171	329	195	253	309	455	365	479	288
ENSMUSG00000026308	chr1	Klhl30	91351016	91351135	3089	0.65669	6.641052	0.00013	0.000619	0.034432	1	1011	607	1649	1492	1637	1847	2573	1920	2705	2089
ENSMUSG00000037029	chr7	Zfp146	30161274	30163228	2071	-0.57983	4.284822	0.000129	0.000619	0.024101	-1	279	293	538	355	420	245	362	290	277	240
ENSMUSG00000052957	chr13	Gas1	60174405	60177365	2961	0.704442	4.702345	0.00013	0.000619	0.037943	1	210	241	484	267	421	445	554	645	568	657
ENSMUSG00000037762	chr10	Slc16a9	70245100	70245378	3869	-0.93224	2.817478	0.00013	0.00062	0.060536	-1	165	117	216	74	163	76	96	99	118	52
ENSMUSG00000004451	chr1	Ralb	1.19E+08	1.19E+08	4930	0.645681	3.509744	0.00013	0.000622	0.027827	1	119	98	158	166	162	181	348	240	311	196
ENSMUSG00000006576	chr1	Slc4a3	75546266	75546382	8599	0.73162	2.648208	0.00013	0.000622	0.033224	1	58	48	99	78	93	106	160	106	193	140
ENSMUSG00000015095	chr2	Fbxw5	25500750	25500886	3052	-0.56027	6.339398	0.00013	0.000622	0.024815	-1	1287	1021	2039	1677	1798	949	1399	1101	1585	990
ENSMUSG00000031229	chrX	Atrx	1.06E+08	1.06E+08	15190	-0.65833	5.153501	0.000131	0.000626	0.033425	-1	501	447	1239	596	864	318	565	474	607	555
ENSMUSG00000023224	chr2	Serping1	84765387	84765827	2325	0.662452	6.89806	0.000132	0.000628	0.035185	1	1047	1144	2596	1118	1747	2466	2803	2804	3119	2052
ENSMUSG00000028689	chr4	Ccdc163	1.17E+08	1.17E+08	2519	0.949473	1.105693	0.000132	0.000629	0.039114	1	25	16	31	17	22	40	59	47	52	45
ENSMUSG00000036718	chr5	Micall2	1.4E+08	1.4E+08	4147	1.316064	0.229453	0.000132	0.000629	0.077208	1	6	2	13	17	11	18	29	25	32	32
ENSMUSG00000030516	chr7	Tjp1	65296165	65297667	7360	-0.7364	4.365564	0.000132	0.00063	0.040996	-1	253	216	612	474	598	160	345	309	353	259
ENSMUSG00000029190	chr5	D5Ertd579e	36584788	36584836	8215	-0.60318	6.94185	0.000132	0.000631	0.029163	-1	1758	1458	3446	2607	2955	1264	2501	1522	2129	1624
ENSMUSG00000042349	chr1	Ikbke	1.31E+08	1.31E+08	9018	1.264537	0.718109	0.000133	0.000633	0.084866	1	18	5	30	10	11	37	41	50	35	30

ENSMUSG00000044340	chr1	Phlpp1	1.06E+08	1.06E+08	6752	-0.75301	3.488479	0.000133	0.000635	0.03996	-1	149	108	361	237	325	112	167	166	166	143
ENSMUSG00000031274	chrX	Col4a5	1.41E+08	1.41E+08	6718	-1.05386	2.81483	0.000134	0.000636	0.078649	-1	112	81	353	87	179	78	59	87	103	76
ENSMUSG00000057895	chr9	Zfp105	1.23E+08	1.23E+08	2130	1.483658	-0.05847	0.000134	0.000639	0.086128	1	7	5	9	9	5	21	34	20	12	24
ENSMUSG00000000708	chr17	Kat2b	53566861	53566915	4867	-0.56939	6.466055	0.000135	0.00064	0.025824	-1	1394	1316	2601	1489	1770	987	1668	1170	1536	1179
ENSMUSG00000039899	chr5	Fgl2	21372642	21373308	3788	0.834731	4.262169	0.000136	0.000646	0.053605	1	130	146	390	150	345	328	793	397	477	301
ENSMUSG00000078870	chr2	Gm14410	1.77E+08	1.77E+08	2398	-1.38461	0.488017	0.000136	0.000647	0.098081	-1	12	16	50	30	51	9	26	10	9	12
ENSMUSG00000036093	chr2	Arl5a	52397951	52402432	5409	-0.54835	5.31713	0.000137	0.000648	0.02306	-1	608	500	1185	679	928	441	754	611	640	516
ENSMUSG00000021275	chr12	Tecpr2	1.11E+08	1.11E+08	7830	-0.74535	2.434462	0.000137	0.000649	0.03338	-1	71	76	179	106	117	58	83	72	91	60
ENSMUSG00000089847	chr7	Timm10b	1.06E+08	1.06E+08	4087	0.571567	4.394021	0.000137	0.000649	0.023599	1	258	194	328	276	286	406	533	442	545	356
ENSMUSG00000097184	chr16	4632428C04Rik	30008667	30008730	2430	-1.50368	1.699678	0.000137	0.000649	0.154461	-1	46	28	44	151	107	27	42	16	32	33
ENSMUSG00000046768	chr12	Rhoj	75308322	75309001	6484	0.603328	4.079478	0.000137	0.000651	0.026184	1	191	149	300	183	260	336	407	416	370	298
ENSMUSG00000023571	chr4	Fam132a	1.56E+08	1.56E+08	1366	0.682901	3.785507	0.000137	0.000651	0.032947	1	166	151	213	131	167	257	318	343	378	238
ENSMUSG00000041225	chr18	Arhgap12	6024427	6026730	8016	-0.53878	4.61249	0.000139	0.000657	0.021283	-1	400	285	682	448	556	303	477	350	414	283
ENSMUSG00000006395	chr4	Hyi	1.18E+08	1.18E+08	2209	0.823325	3.070707	0.000139	0.000659	0.045909	1	100	96	101	83	81	159	218	217	204	161
ENSMUSG00000003559	chr19	As3mt	46707443	46707536	1751	-0.93413	4.857128	0.000139	0.00066	0.06849	-1	320	348	618	960	845	316	439	253	367	414
ENSMUSG00000035529	chr10	Prdm4	85891970	85893439	3917	-0.58676	4.681233	0.00014	0.000661	0.025836	-1	443	302	781	423	586	329	484	295	480	297
ENSMUSG00000030016	chr6	Zfml	83914353	83914479	6470	-0.57649	5.058763	0.00014	0.000664	0.025424	-1	464	440	1010	635	730	378	677	479	485	427
ENSMUSG00000018500	chr11	Adora2b	62248984	62249436	1845	1.492526	-0.11422	0.000141	0.000667	0.092261	1	1	5	7	7	14	19	31	23	15	19
ENSMUSG00000063714	chr2	Sp3os	72979424	72979595	892	1.33367	0.369304	0.000141	0.000667	0.080123	1	7	10	8	16	11	39	32	27	31	21
ENSMUSG00000032875	chr7	Arhgef17	1.01E+08	1.01E+08	10250	-0.61223	6.538897	0.000141	0.000667	0.030112	-1	1568	1048	2970	1590	2175	1031	1440	1144	1849	1280
ENSMUSG00000027469	chr2	Tpx2	1.53E+08	1.53E+08	4677	-1.12265	2.881182	0.000141	0.000667	0.091383	-1	158	180	224	91	125	95	77	62	70	99
ENSMUSG00000040113	chr1	Mettl11b	1.64E+08	1.64E+08	1848	-0.87791	4.156417	0.000141	0.000667	0.059948	-1	408	302	449	312	334	121	415	171	364	142
ENSMUSG00000103793	chr18	Pcdhga6	37707039	37709652	4733	0.588019	5.503961	0.000141	0.000668	0.027125	1	458	417	950	480	675	707	1067	1092	1134	949
ENSMUSG00000098900	chr7	Gm18190	7265498	7266077	832	-1.07162	0.607019	0.000142	0.000669	0.049464	-1	19	19	42	32	47	11	24	17	22	11
ENSMUSG00000042302	chr11	Ehbp1	22005828	22006871	5825	-0.58081	3.76149	0.000143	0.000674	0.023041	-1	218	172	404	242	288	154	234	201	210	184
ENSMUSG00000013878	chr8	Rnf170	26119368	26119600	5032	-0.56644	4.776248	0.000144	0.000679	0.024285	-1	423	430	749	409	628	311	528	365	477	347
ENSMUSG00000021413	chr13	Prpf4b	34875494	34875694	4465	-0.60343	4.393845	0.000144	0.000679	0.02707	-1	287	306	688	339	466	214	393	319	343	261
ENSMUSG00000024854	chr19	Pold4	4231899	4232188	910	0.66957	3.795287	0.000144	0.000681	0.031683	1	151	164	195	154	167	280	347	282	358	266
ENSMUSG00000045665	chr15	Mfsd5	1.02E+08	1.02E+08	1742	0.537463	4.616354	0.000145	0.000682	0.021138	1	289	241	393	307	363	395	607	539	657	454
ENSMUSG00000103472	chr18	Pcdhga7	37714764	37717374	5217	0.586431	5.501808	0.000145	0.000682	0.027061	1	461	412	950	481	675	708	1058	1088	1135	949
ENSMUSG00000040699	chr11	Limd2	1.06E+08	1.06E+08	3707	1.016358	2.173567	0.000145	0.000684	0.066437	1	52	49	59	33	32	104	114	121	122	71
ENSMUSG00000033900	chr3	Map9	82358044	82358171	6671	-1.07381	1.095468	0.000146	0.000685	0.06152	-1	43	44	65	28	41	24	26	28	23	18
ENSMUSG00000021959	chr14	Lats2	57642077	57642160	7303	-0.58594	4.345999	0.000146	0.000686	0.025173	-1	296	261	623	363	464	222	295	281	383	295
ENSMUSG00000037234	chr8	Hook3	26021421	26032030	13132	-0.74034	6.394849	0.000146	0.000688	0.044306	-1	1039	886	3205	1551	2355	777	1447	938	1555	1119
ENSMUSG00000038319	chr5	Kcnh2	24319589	24320149	4845	1.098325	1.703497	0.000147	0.00069	0.077402	1	25	12	35	41	50	47	81	55	140	75
ENSMUSG00000003199	chr17	Mpnd	56005711	56005814	2305	-0.60384	5.612861	0.000147	0.000691	0.028854	-1	844	645	1093	1020	1121	646	680	615	993	600
ENSMUSG00000076128	chr14	Mir686	54616677	54616785	109	0.645023	5.858013	0.000147	0.000691	0.03309	1	709	609	749	705	753	1143	1544	1085	1798	951
ENSMUSG00000031864	chr8	Ints10	68793929	68794148	6706	-0.59544	4.132951	0.000147	0.000692	0.025673	-1	243	204	475	362	449	194	336	223	280	242
ENSMUSG00000031358	chrX	Msl3	1.69E+08	1.69E+08	2877	-0.66227	5.05419	0.000148	0.000693	0.034279	-1	477	322	874	749	959	359	614	382	574	436
ENSMUSG00000039997	chr1	Ifi203	1.74E+08	1.74E+08	6706	0.853472	3.200245	0.000148	0.000695	0.052911	1	66	67	157	125	116	181	335	250	159	143
ENSMUSG00000021392	chr13	Nol8	49653350	49653397	4242	-0.6139	3.504146	0.000149	0.000699	0.025678	-1	199	164	337	184	220	131	202	148	183	149
ENSMUSG00000021226	chr12	Acot2	83987861	83988481	2196	-1.08708	2.818451	0.00015	0.000704	0.086899	-1	96	91	111	267	187	57	101	98	108	51
ENSMUSG00000027422	chr2	Rrbp1	1.44E+08	1.44E+08	8786	0.543984	5.714808	0.000151	0.000706	0.023427	1	567	458	948	656	851	923	1256	1176	1207	1066
ENSMUSG00000014609	chr11	Chrne	70614883	70615128	1690	0.578134	4.049864	0.000151	0.000709	0.024073	1	177	148	341	188	227	319	396	307	480	301
ENSMUSG00000032308	chr9	Ulk3	57589452	57589686	2826	0.869964	2.124301	0.000151	0.00071	0.046436	1	43	30	65	47	58	76	139	99	149	51
ENSMUSG00000015133	chr7	Lrrk1	66226912	66226941	9487	0.695099	3.323547	0.000152	0.00071	0.034307	1	85	66	171	129	175	159	258	233	239	224
ENSMUSG00000097842	chr7	9330104G04Rik	16871354	16872913	2235	1.275991	0.476099	0.000152	0.000713	0.076917	1	11	7	19	7	16	18	49	19	58	25
ENSMUSG00000052139	chr5	Bre	31697684	31698077	4781	0.534745	4.767968	0.000152	0.000713	0.021403	1	334	246	472	342	392	467	685	571	769	464
ENSMUSG00000030688	chr7	Stard10	1.01E+08	1.01E+08	2383	0.684968	5.303104	0.000153	0.000716	0.037226	1	377	309	463	660	601	629	1111	858	1000	851
ENSMUSG00000024371	chr17	C2	34862604	34863031	3872	0.912663	3.147026	0.000153	0.000718	0.060055	1	97	94	128	80	75	159	197	309	216	150
ENSMUSG00000033478	chr19	Fam160b1	57361009	57361370	5630	-0.75028	3.643196	0.000154	0.000718	0.040953	-1	165	127	415	263	343	122	157	202	208	152
ENSMUSG00000023977	chr17	Ubr2	46928292	46930500	7747	-0.6821	6.472429	0.000154	0.000721	0.037858	-1	1250	824	2988	1916	2292	1002	1355	1090	1677	1123
ENSMUSG00000028838	chr4	Extl1	1.34E+08	1.34E+08	4333	-0.69911	5.798241	0.000155	0.000724	0.03945	-1	794	538	1501	1420	1457	580	892	668	1210	601
ENSMUSG00000039270	chr4	Megf9	70427065	70433531	8226	-0.90145	2.288046	0.000155	0.000725	0.053454	-1	74	73	161	78	129	29	61	77	71	67
ENSMUSG00000029272	chr5	Sult1e1	87575968	87576321	1260	-2.76898	-0.25291	0.000156	0.000727	0.40729	-1	28	22	36	5	14	12	0	0	4	0
ENSMUSG00000003528	chr16	Slc25a1	17925211	17925927	2176	1.727436	3.763702	0.000156	0.000727	0.227892	1	154	91	109	47	73	280	121	901	280	220
ENSMUSG00000019373	chr11	Cops3	59817795	59818108	3454	-0.60804	6.257063	0.000156	0.000727	0.030037	-1	1211	1315	1851	1420	1501	838	1582	960	1299	930
ENSMUSG00000021994	chr14	Wnt5a	28504750	28506114	7822	-1.14729	2.520763	0.000156	0.000729	0.093763	-1	116	81	222	77	152	52	44	96	40	74
ENSMUSG00000028766	chr4	Alpl	1.38E+08	1.38E+08	4033	-1.43	3.009641	0.000157	0.000731	0.155547	-1	79	54	155	315	371	55	146	44	98	64
ENSMUSG00000074909	chr19	Ranbp6	29808108	29812974	4867	-0.60489	3.869078	0.000158	0.000737	0.026363	-1	201	205	419	287	320	137	279	184	251	212
ENSMUSG00000026484	chr1	Rnf2	1.51E+08	1.51E+08	4127	-0.60654	3.675472	0.000159	0.000739	0.025889	-1	200	196	380	221	244	137	201	174	240	170
ENSMUSG00000040282	chr2	BC052040	1.16E+08	1.16E+08	4349	-0.97048	2.418146	0.000159	0.00074	0.065173	-1	116	76	204	76	100	39	59	95	78	53
ENSMUSG00000029730	chr5	Mcm7	1.38E+08	1.38E+08	4426	0.678292	3.362553	0.00016	0.000745	0.03192	1	126	82	184	122	118	206	287	242	259	152
ENSMUSG00000079426	chr6	Arpc4	1.13E+08	1.13E+08	2323	0.600306	5.49431	0.00016	0.000746	0.028556	1	610	464	711	484	549	816	1159	948	1245	803
ENSMUSG00000104063	chr18	Pcdhgb7	37751600	37754193	4713	0.580583	5.502999	0.000161	0.000749	0.026898	1	462	411	950	487	679	705	1060	1089	1133	948

ENSMUSG00000015002	chr15	Efr3a	65787034	65787246	11091	-0.53319	5.392932	0.000162	0.000752	0.022347	-1	655	528	1281	694	937	465	797	603	742	548
ENSMUSG00000028165	chr3	Cisd2	1.35E+08	1.35E+08	4360	-0.5705	5.176275	0.000162	0.000755	0.0257	-1	557	478	888	766	796	334	699	498	742	442
ENSMUSG00000021666	chr13	Gfm2	97137937	97138026	10685	-0.60332	6.260577	0.000164	0.00076	0.029709	-1	1167	843	1942	1755	1868	834	1501	970	1417	921
ENSMUSG00000037563	chr7	Rps16	28350652	28350851	807	0.586461	6.726536	0.000164	0.000761	0.028175	1	1264	1141	1644	1276	1345	1907	2645	2297	2876	1904
ENSMUSG00000071540	chr14	3425401B19Rik	32659119	32664178	5547	-1.07837	8.023358	0.000164	0.000761	0.095432	-1	3088	2108	8463	8525	7818	1422	3931	1974	4921	3510
ENSMUSG00000043424	chr18	Eif3j2	43475418	43477796	2379	-0.88163	2.539306	0.000164	0.000763	0.053748	-1	87	108	168	111	121	63	126	43	72	68
ENSMUSG00000028396	chr4	2310002L09Rik	73939371	73939598	2158	-0.75531	6.598596	0.000165	0.000764	0.046946	-1	1270	992	2718	2511	2645	974	1831	970	1394	1429
ENSMUSG00000022020	chr14	Naa16	79334204	79336485	6145	-0.78841	3.687232	0.000165	0.000766	0.04701	-1	254	242	406	146	248	133	228	168	174	155
ENSMUSG00000026421	chr1	Csrp1	1.36E+08	1.36E+08	1956	0.575953	5.057446	0.000166	0.000769	0.025765	1	370	356	459	415	505	525	852	714	899	657
ENSMUSG00000026437	chr1	Cdk18	1.32E+08	1.32E+08	4764	-0.90781	2.920922	0.000166	0.000771	0.059655	-1	113	85	200	202	201	66	108	148	85	66
ENSMUSG00000042073	chr9	Abhd14b	1.06E+08	1.06E+08	1820	0.81247	2.815047	0.000166	0.000771	0.045235	1	81	66	102	64	86	122	131	201	203	140
ENSMUSG00000039096	chr11	Rsad1	94539798	94542647	4391	-0.65552	3.175034	0.000168	0.000776	0.029151	-1	152	102	256	165	226	91	133	131	187	100
ENSMUSG00000059436	chr12	Max	76937269	76938755	2005	0.55425	4.471139	0.000168	0.000776	0.022854	1	251	227	355	278	315	418	529	492	556	391
ENSMUSG00000061244	chr14	Exoc5	49012146	49014349	9932	-0.58019	4.414598	0.000168	0.000776	0.025461	-1	318	333	629	321	471	230	402	283	359	290
ENSMUSG00000026028	chr1	Trak2	58900449	58904182	7088	-0.81321	6.724353	0.000169	0.000782	0.054685	-1	1432	913	2931	2923	3096	964	1747	1043	2134	1274
ENSMUSG00000001739	chr5	Cldn15	1.37E+08	1.37E+08	2124	1.247344	1.537722	0.000169	0.000782	0.09802	1	26	28	17	25	30	96	61	56	92	45
ENSMUSG00000015335	chr2	Zdhhc12	30090944	30091566	1785	0.904303	1.748433	0.000169	0.000782	0.047342	1	37	28	42	26	47	63	71	77	118	58
ENSMUSG00000071637	chr16	Cebpd	15887286	15888077	1180	1.532292	3.732443	0.000169	0.000783	0.182653	1	68	133	113	78	127	222	1112	252	195	136
ENSMUSG00000044712	chr12	Slc38a6	73286779	73287032	7783	0.878912	1.604718	0.00017	0.000788	0.042538	1	32	23	55	27	30	51	85	80	67	61
ENSMUSG00000052681	chr10	Rap1b	1.18E+08	1.18E+08	2024	0.550298	4.986674	0.000171	0.000789	0.023453	1	320	340	544	391	462	518	812	759	820	539
ENSMUSG00000025145	chr11	Lrrc45	1.21E+08	1.21E+08	3293	0.809504	2.309539	0.000171	0.000789	0.042503	1	43	39	104	43	62	106	123	122	111	93
ENSMUSG00000025245	chr9	Lztfl1	1.24E+08	1.24E+08	9249	-0.60133	3.828282	0.000171	0.000791	0.026319	-1	224	200	401	225	340	163	299	155	262	164
ENSMUSG00000044258	chr13	Ctla2a	60934155	60935028	1373	0.818126	2.651825	0.000172	0.000792	0.044199	1	63	54	63	86	85	103	204	159	159	102
ENSMUSG00000056268	chr1	Dennd1b	1.39E+08	1.39E+08	8314	-0.59523	4.27963	0.000172	0.000792	0.026651	-1	295	245	674	309	417	210	337	301	349	222
ENSMUSG00000055148	chr8	Klf2	72319033	72319149	1847	0.93945	4.122302	0.000172	0.000792	0.069234	1	160	198	192	140	230	247	857	322	358	360
ENSMUSG00000026618	chr1	Iars2	1.85E+08	1.85E+08	8885	-0.54893	6.239694	0.000172	0.000793	0.024662	-1	1137	953	2044	1521	1673	861	1465	1007	1446	902
ENSMUSG00000061778	chrX	Mospd2	1.65E+08	1.65E+08	7914	-0.74691	2.592931	0.000172	0.000793	0.036009	-1	97	93	187	90	141	58	92	81	86	86
ENSMUSG00000013483	chr11	Card14	1.19E+08	1.19E+08	4605	1.94469	1.702749	0.000173	0.000796	0.272886	1	21	9	37	13	26	83	246	18	120	16
ENSMUSG00000006800	chr2	Sulf2	1.66E+08	1.66E+08	5818	0.789191	4.063305	0.000174	0.000802	0.048602	1	188	129	256	172	240	314	289	513	343	397
ENSMUSG00000092412	chr17	Gm20507	33630759	33631463	2860	1.054865	1.416006	0.000174	0.000802	0.064186	1	34	20	38	21	18	45	65	83	77	44
ENSMUSG00000010914	chr2	Pdhx	1.03E+08	1.03E+08	3930	-0.65728	6.363266	0.000175	0.000805	0.035742	-1	1178	938	1882	2066	2145	861	1560	964	1566	987
ENSMUSG00000036529	chr15	Sbf1	89288236	89288725	6826	-0.60182	5.731491	0.000175	0.000805	0.02941	-1	851	552	1595	1120	1188	586	760	746	1051	712
ENSMUSG00000015312	chr10	Gadd45b	80930091	80930359	1266	0.968832	5.001941	0.000176	0.000807	0.076297	1	315	202	395	414	413	520	1547	315	879	744
ENSMUSG00000019907	chr10	Ppp1r12a	1.08E+08	1.08E+08	3403	-0.65497	3.166941	0.000176	0.000807	0.028851	-1	129	125	288	160	193	109	173	118	125	106
ENSMUSG00000027263	chr2	Tubgcp4	1.21E+08	1.21E+08	8395	-0.56578	3.760649	0.000175	0.000807	0.022432	-1	198	177	400	250	294	168	239	203	230	154
ENSMUSG00000034673	chr17	Pbx2	34591266	34591492	3640	0.562557	4.398658	0.000175	0.000807	0.023711	1	248	194	385	260	281	337	493	460	649	370
ENSMUSG00000059070	chr7	Rpl18	45715457	45715842	4042	0.628978	7.163562	0.000176	0.000807	0.032937	1	1820	1504	1967	1699	1803	2737	3712	2962	4153	2433
ENSMUSG00000023791	chr16	Pigx	32084418	32084626	2394	0.783557	3.076798	0.000176	0.000808	0.042683	1	100	86	113	88	92	167	255	131	283	142
ENSMUSG00000022957	chr16	Itsn1	91729281	91729599	22539	-0.59436	6.246399	0.000176	0.000808	0.029056	-1	1101	865	2234	1631	1720	806	1268	1037	1316	1096
ENSMUSG00000050914	chr8	Ankrd37	45996902	45997125	1403	1.083605	1.659124	0.000177	0.000812	0.073804	1	40	17	33	31	33	33	97	104	84	63
ENSMUSG00000029804	chr6	Herc3	58831465	58831642	7027	-0.83032	5.489202	0.000178	0.000815	0.056615	-1	630	415	1294	1174	1295	338	843	385	819	637
ENSMUSG00000026219	chr1	Trip12	84721189	84724814	16601	-0.57914	7.090503	0.000178	0.000815	0.027974	-1	1989	1595	4433	2561	3037	1479	2431	1878	2518	1760
ENSMUSG00000090150	chr9	Acad11	1.04E+08	1.04E+08	9351	-0.6767	6.062869	0.000179	0.000819	0.037801	-1	901	746	1677	1704	1724	626	1203	909	1037	941
ENSMUSG00000020894	chr11	Vamp2	69088490	69088627	3809	0.537506	5.843842	0.000179	0.00082	0.023406	1	592	581	938	734	915	943	1437	1148	1597	1112
ENSMUSG00000092787	chrX	Mir5116	56587852	56587914	63	-1.04859	1.233159	0.00018	0.000824	0.061022	-1	34	25	73	54	66	24	31	23	19	34
ENSMUSG00000057396	chr13	Zfp759	67128228	67128314	3482	-0.81996	1.589763	0.00018	0.000826	0.036102	-1	47	44	88	58	66	26	60	30	48	32
ENSMUSG00000028517	chr4	Ppap2b	1.05E+08	1.05E+08	3159	-0.60173	6.301285	0.000181	0.000828	0.029962	-1	1297	1025	2626	1178	1754	954	1370	1154	1452	834
ENSMUSG00000057789	chr17	Bak1	27019810	27021035	2407	0.625523	4.386329	0.000182	0.00083	0.029917	1	222	244	374	200	264	383	512	414	631	378
ENSMUSG00000003437	chr7	Paf1	28392951	28393254	3438	0.522132	4.929228	0.000182	0.000834	0.021121	1	325	289	497	399	501	507	747	637	848	550
ENSMUSG00000036565	chr5	Ttyh3	1.41E+08	1.41E+08	4650	0.74599	3.276696	0.000182	0.000834	0.041559	1	81	59	215	94	158	168	245	257	230	190
ENSMUSG00000029478	chr5	Ncor2	1.25E+08	1.25E+08	10479	-0.79911	6.238318	0.000183	0.000837	0.053105	-1	961	617	2457	1871	2271	696	1184	909	1211	1041
ENSMUSG00000040170	chr1	Fmo2	1.63E+08	1.63E+08	5609	-0.87042	3.831695	0.000183	0.000838	0.059419	-1	150	152	504	380	362	115	245	245	203	120
ENSMUSG00000053198	chr7	Prx	27499324	27499365	5579	-0.96111	2.758339	0.000183	0.000838	0.06843	-1	79	67	189	203	196	43	127	66	106	82
ENSMUSG00000036932	chrX	Aifm1	48474944	48475188	4006	-0.68188	5.2715	0.000184	0.000839	0.037933	-1	566	448	840	1001	996	430	853	438	611	422
ENSMUSG00000081344	chr2	Gm14303	1.73E+08	1.73E+08	171	0.650775	5.139973	0.000184	0.00084	0.033907	1	451	379	464	416	416	701	974	727	1010	544
ENSMUSG00000075595	chr11	Zfp652	95712673	95712733	15444	-0.5853	8.332186	0.000184	0.000841	0.028991	-1	5442	3847	9734	5801	7057	3526	5087	4099	6728	4316
ENSMUSG00000041684	chr1	Bivm	44118957	44119195	4206	-0.70885	2.511665	0.000185	0.000842	0.031945	-1	90	86	146	105	135	60	100	57	104	72
ENSMUSG00000049686	chr5	Orai1	1.23E+08	1.23E+08	2289	0.60637	6.127554	0.000186	0.000849	0.030431	1	806	581	1153	888	1053	1173	1560	1354	2458	1267
ENSMUSG00000036959	chrX	Bcorl1	48341358	48341483	8516	0.665331	3.466105	0.000187	0.00085	0.032637	1	114	78	243	101	172	188	262	236	326	218
ENSMUSG00000038145	chr9	Snrk	1.22E+08	1.22E+08	5763	-0.64662	5.098861	0.000187	0.000851	0.0338	-1	458	381	942	755	927	291	580	555	594	440
ENSMUSG00000103088	chr18	Pcdhgb6	37742094	37744658	4684	0.576538	5.512368	0.000188	0.000855	0.027085	1	467	421	948	484	689	709	1062	1094	1138	957
ENSMUSG00000073940	chr7	Hbb-bt	1.04E+08	1.04E+08	703	0.741518	2.885572	0.00019	0.000866	0.037485	1	86	54	97	105	92	134	182	130	232	156
ENSMUSG00000041827	chr5	Oasl1	1.15E+08	1.15E+08	2608	1.469546	0.240913	0.000191	0.000867	0.108956	1	6	7	8	7	17	24	45	32	12	27
ENSMUSG00000051469	chr18	Zfp191	24009702	24014685	6271	-0.53968	5.200451	0.000191	0.000868	0.023261	-1	600	463	1062	611	833	411	734	475	616	513
ENSMUSG00000041607	chr18	Mbp	82475146	82475394	8403	-0.74592	4.086645	0.000191	0.000868	0.04396	-1	223	232	409	453	395	140	378	171	266	226

ENSMUSG00000037364	chr5	Srrt	1.37E+08	1.37E+08	3024	0.540802	4.924625	0.000192	0.000871	0.02296	1	342	292	523	392	434	585	731	694	731	515
ENSMUSG00000022828	chr16	Gtf2e1	37509790	37511819	6285	-0.58722	3.857699	0.000193	0.000875	0.025351	-1	234	224	427	235	280	174	231	209	276	166
ENSMUSG00000027404	chr2	Snrpb	1.3E+08	1.3E+08	1976	0.568283	7.110877	0.000193	0.000875	0.027206	1	1634	1316	2305	1752	1905	2509	3320	2951	4123	2282
ENSMUSG00000047866	chr8	Lonp2	86624043	86624416	5346	-0.56811	6.221284	0.000193	0.000875	0.026876	-1	1274	1118	2089	1252	1438	780	1424	1020	1304	1007
ENSMUSG00000036112	chr10	Metap2	93858489	93861602	7588	-0.66879	7.512474	0.000193	0.000875	0.037919	-1	3069	3401	4837	2792	3627	2197	3293	1899	3567	2101
ENSMUSG00000036879	chr8	Phkb	85840959	85841103	7417	-0.65169	8.800004	0.000193	0.000876	0.036198	-1	8484	6599	14652	6247	8384	4990	8841	5356	7699	5231
ENSMUSG00000045107	chr14	Saysd1	20075646	20077644	2294	0.713514	3.169957	0.000193	0.000877	0.035225	1	97	104	104	92	128	156	250	189	241	175
ENSMUSG00000037926	chr11	Ssh2	77216287	77216515	18519	-0.73882	5.73607	0.000194	0.000881	0.045379	-1	661	463	1882	1235	1459	556	788	662	1030	638
ENSMUSG00000018554	chr11	Ybx2	69935796	69936248	1885	-1.36837	2.157822	0.000194	0.000882	0.140033	-1	47	38	64	194	171	31	53	43	63	36
ENSMUSG00000028037	chr3	Ifi44	1.52E+08	1.52E+08	6116	1.655111	-0.1059	0.000196	0.000889	0.133235	1	6	3	6	6	10	19	44	20	7	21
ENSMUSG00000057722	chr4	Lepr	1.02E+08	1.02E+08	7049	-1.46687	1.915464	0.000196	0.000889	0.158299	-1	27	52	105	93	178	14	48	37	21	55
ENSMUSG00000027329	chr2	Spef1	1.31E+08	1.31E+08	2747	1.082104	1.576032	0.000196	0.00089	0.074626	1	23	20	31	42	30	55	64	99	55	72
ENSMUSG00000024238	chr18	Zeb1	5591860	5591967	10112	-0.54991	5.259415	0.000197	0.00089	0.024355	-1	510	508	1205	670	872	425	699	577	654	492
ENSMUSG00000027245	chr2	Hypk	1.21E+08	1.21E+08	5278	0.615127	5.530519	0.000197	0.000893	0.030907	1	536	547	622	512	620	858	1254	922	1304	798
ENSMUSG00000035273	chr5	Hpse	1.01E+08	1.01E+08	3516	1.01475	1.785655	0.000197	0.000893	0.068084	1	36	23	75	16	33	74	97	86	90	58
ENSMUSG00000041949	chr8	Tango6	1.07E+08	1.07E+08	4409	-0.78703	3.059161	0.000198	0.000893	0.045323	-1	133	75	242	180	242	61	131	110	145	112
ENSMUSG00000033671	chr1	Cep350	1.56E+08	1.56E+08	16487	-0.72029	5.308894	0.000198	0.000894	0.042779	-1	523	378	1663	767	920	389	624	560	694	481
ENSMUSG00000041797	chr11	Abca9	1.1E+08	1.1E+08	8048	-0.91924	4.249026	0.000198	0.000895	0.068131	-1	198	201	808	365	580	174	216	278	218	278
ENSMUSG00000061393	chr9	Acvr2b	1.19E+08	1.19E+08	1753	-1.41239	1.332444	0.000199	0.000898	0.138804	-1	22	25	112	69	74	8	32	11	40	32
ENSMUSG00000045268	chr4	Zfp691	1.19E+08	1.19E+08	2399	-0.66193	3.87496	0.0002	0.000902	0.033473	-1	199	174	319	360	402	167	262	197	262	155
ENSMUSG00000032338	chr9	Hcn4	58823512	58824296	3798	-1.56188	0.049387	0.000201	0.000908	0.12609	-1	9	8	59	18	27	6	11	6	15	5
ENSMUSG00000025782	chr2	Taf3	9914552	9916466	6389	-0.63296	3.310186	0.000202	0.000912	0.027996	-1	176	128	279	189	198	104	151	166	174	111
ENSMUSG00000004267	chr6	Eno2	1.25E+08	1.25E+08	4705	1.288313	0.507802	0.000202	0.000914	0.090177	1	10	4	22	17	9	19	30	48	33	36
ENSMUSG00000062866	chr10	Phactr2	13207717	13214273	11688	-0.53286	4.702169	0.000203	0.000915	0.022124	-1	365	328	748	454	639	297	460	378	492	325
ENSMUSG00000041836	chr7	Ptpre	1.36E+08	1.36E+08	5411	0.948411	1.509425	0.000203	0.000917	0.056414	1	21	15	55	23	42	56	60	80	65	61
ENSMUSG00000004207	chr10	Psap	60277627	60277782	2744	0.579665	10.44581	0.000205	0.000922	0.028988	1	16044	12129	23620	18332	20232	27333	29854	31094	37398	25670
ENSMUSG00000033009	chr8	Ogfod1	94037198	94037442	5846	-0.55743	4.842189	0.000206	0.000927	0.024689	-1	385	342	868	567	665	302	512	389	540	390
ENSMUSG00000029502	chr5	Golga3	1.1E+08	1.1E+08	12671	-0.54556	5.745371	0.000206	0.000928	0.024588	-1	718	680	1603	1010	1251	596	907	738	1044	720
ENSMUSG00000019432	chr17	Ddx39b	35241746	35241852	3783	0.528799	6.49555	0.000206	0.000928	0.023525	1	998	806	1685	1197	1317	1476	2339	1770	2490	1727
ENSMUSG00000013419	chr9	Zfp651	1.22E+08	1.22E+08	6353	-0.57731	7.242643	0.000206	0.000929	0.028432	-1	2351	1786	3959	3208	3526	1657	2628	1863	3121	1975
ENSMUSG00000035310	chr5	Lin54	1E+08	1E+08	5820	-0.79162	2.239759	0.000207	0.000934	0.040352	-1	87	63	166	70	98	41	69	64	78	59
ENSMUSG00000004040	chr11	Stat3	1.01E+08	1.01E+08	9527	0.625669	6.175157	0.000208	0.000934	0.033049	1	677	594	1662	758	1067	1235	2282	1532	2011	1106
ENSMUSG00000022235	chr15	Cmbl	31568791	31568939	1228	-0.82054	6.074239	0.000209	0.00094	0.056987	-1	1483	1412	1774	860	1117	844	977	940	1052	617
ENSMUSG00000022504	chr16	Ciita	10488178	10488424	5254	1.208743	0.429962	0.00021	0.000942	0.067622	1	14	10	15	5	15	36	34	31	32	21
ENSMUSG00000059479	chr7	B3gnt8	25627624	25627722	1475	1.183452	0.5401	0.00021	0.000945	0.068887	1	17	4	13	17	14	31	36	25	39	36
ENSMUSG00000038274	chr19	Fau	6057888	6058001	815	0.6629	6.7746	0.000212	0.000952	0.037386	1	1340	1245	1416	1183	1382	2323	2651	2330	3026	1869
ENSMUSG00000067081	chr1	Asb18	89950220	89952863	3952	-0.80884	4.752755	0.000212	0.000952	0.054112	-1	367	221	736	728	821	228	554	296	439	312
ENSMUSG00000033294	chr5	Noc4l	1.11E+08	1.11E+08	2505	0.534197	4.429897	0.000213	0.000955	0.021989	1	212	187	401	285	350	368	587	402	626	367
ENSMUSG00000020836	chr11	Coro6	77462411	77462754	3011	-0.87349	7.100447	0.000213	0.000955	0.065168	-1	1745	1149	3486	4319	4116	1227	2452	1344	2363	1640
ENSMUSG00000027601	chr3	Mtfr1	19187327	19187358	4372	-0.80002	4.829047	0.000213	0.000957	0.053018	-1	331	311	696	793	845	226	457	313	484	425
ENSMUSG00000052087	chr13	Rgs14	55369732	55369936	2490	1.435431	-0.2213	0.000214	0.000961	0.083395	1	10	2	12	5	3	17	17	24	22	17
ENSMUSG00000026017	chr1	Carf	60098247	60098307	14557	-0.85363	1.720346	0.000214	0.000961	0.042115	-1	59	36	91	71	80	26	58	38	42	45
ENSMUSG00000040712	chr11	Camta2	70669463	70670262	5207	-0.6122	5.574247	0.000215	0.000962	0.031224	-1	772	494	1409	911	1200	492	647	723	982	609
ENSMUSG00000055003	chr6	Lrtm2	1.19E+08	1.19E+08	4102	-1.99474	3.178398	0.000215	0.000964	0.310357	-1	59	31	409	333	449	60	20	26	118	93
ENSMUSG00000029196	chr5	Tada2b	36473670	36476962	3791	-0.59245	4.173813	0.000215	0.000965	0.027002	-1	273	198	600	354	376	200	282	255	363	219
ENSMUSG00000022272	chr15	Myo10	25622525	25623030	10122	0.623207	6.080716	0.000216	0.000966	0.03292	1	727	506	1260	763	1145	1402	1529	1144	1875	1459
ENSMUSG00000032047	chr9	Acat1	53580522	53582665	3758	-0.75659	7.690032	0.000216	0.000966	0.049263	-1	2872	2626	4149	6126	5021	2076	4419	2295	3404	2180
ENSMUSG00000039789	chr16	Zfp597	3858321	3858581	6660	-0.76019	3.025962	0.000216	0.000967	0.042212	-1	119	123	246	154	185	52	132	134	124	109
ENSMUSG00000021483	chr13	Cdk20	64432553	64432670	1826	0.843965	2.028516	0.000216	0.000968	0.044464	1	41	31	63	49	44	60	143	85	86	93
ENSMUSG00000061689	chr2	Dlgap4	1.57E+08	1.57E+08	8451	0.600058	6.243333	0.000217	0.000971	0.030477	1	904	751	1360	793	1026	1348	1704	1389	2391	1529
ENSMUSG00000021745	chr14	Ptprg	11553532	11554332	10917	-0.7851	3.839477	0.000217	0.000971	0.049058	-1	186	149	440	318	420	96	311	194	204	173
ENSMUSG00000022125	chr14	Cln5	1.03E+08	1.03E+08	2396	-0.53132	4.158976	0.000218	0.000972	0.021139	-1	250	243	467	353	395	211	319	271	304	225
ENSMUSG00000029992	chr6	Gfpt1	87042846	87043005	7419	-0.54738	5.400904	0.000218	0.000973	0.024633	-1	624	508	1332	744	953	444	803	596	719	588
ENSMUSG00000073557	chr1	Ppp1r12b	1.35E+08	1.35E+08	14983	-0.76995	8.022401	0.000218	0.000974	0.051117	-1	3570	2089	8377	6353	7519	2435	4291	2970	5074	3116
ENSMUSG00000029064	chr4	Gnb1	1.55E+08	1.55E+08	4268	0.540768	5.878545	0.000218	0.000974	0.024499	1	606	498	1034	792	980	1012	1426	1386	1474	1054
ENSMUSG00000020315	chr11	Sptbn1	30099395	30100714	17492	-0.62434	6.959723	0.000219	0.000978	0.03344	-1	1570	1501	3455	2634	3358	1270	2087	1993	1950	1637
ENSMUSG00000008855	chr11	Hdac5	1.02E+08	1.02E+08	8780	-0.60687	5.811834	0.00022	0.00098	0.03102	-1	782	716	1490	1262	1282	549	976	633	1100	847
ENSMUSG00000028149	chr3	Rap1gds1	1.39E+08	1.39E+08	3663	-0.58067	6.297597	0.000221	0.000984	0.028681	-1	1481	1071	2322	1219	1557	936	1492	1067	1480	856
ENSMUSG00000040950	chr11	Mgl2	70130329	70130442	2094	0.937117	3.885081	0.000221	0.000984	0.070914	1	199	132	221	91	152	351	389	476	267	235
ENSMUSG00000020462	chr11	Cfap36	29221532	29221985	2744	0.812091	3.456356	0.000222	0.00099	0.050028	1	132	135	142	79	120	223	312	210	289	226
ENSMUSG00000034675	chr13	Dbn1	55473429	55474293	4514	0.846074	2.684753	0.000224	0.000998	0.052468	1	57	37	113	82	84	97	119	189	174	152
ENSMUSG00000079283	chr1	2310009B15Rik	1.39E+08	1.39E+08	1750	0.759351	2.797104	0.000225	0.001002	0.039499	1	84	69	87	68	91	137	189	124	227	116
ENSMUSG00000032116	chr9	Stt3a	36729344	36732962	8948	0.524539	4.98524	0.000225	0.001003	0.022079	1	351	331	592	348	468	557	859	663	757	571
ENSMUSG00000035476	chrX	Tab3	85574022	85574165	6639	-0.66924	2.964729	0.000227	0.001012	0.030958	-1	140	106	249	114	168	82	147	102	126	92
ENSMUSG00000035914	chr9	Cd276	58524300	58526361	3297	0.800499	3.139437	0.000228	0.001015	0.048492	1	59	66	146	130	119	171	202	136	328	181

ENSMUSG00000038482	chr8	Tfdp1	13339674	13339739	1700	-0.56576	5.108714	0.000228	0.001015	0.026399	-1	544	476	1037	552	760	366	773	430	629	397
ENSMUSG00000022571	chr15	Pycrl	75916463	75917079	1353	0.70415	3.048805	0.000229	0.001019	0.035162	1	93	64	120	122	97	144	235	210	188	146
ENSMUSG00000003355	chr15	Fkbp11	98724373	98724602	731	1.5976	-0.09678	0.00023	0.001021	0.12303	1	10	2	4	7	9	22	23	24	11	28
ENSMUSG00000102748	chr18	Pcdhgb2	37689828	37692369	4882	0.565768	5.516548	0.00023	0.001023	0.026835	1	467	411	967	500	695	712	1064	1092	1138	954
ENSMUSG00000006941	chr9	Eif1b	1.2E+08	1.2E+08	917	0.528041	4.916407	0.000231	0.001028	0.022317	1	329	306	471	406	456	554	801	589	794	522
ENSMUSG00000042298	chr11	Ttc19	62281473	62281693	4675	-0.57409	5.391349	0.000231	0.001028	0.027488	-1	647	462	1027	926	1039	494	733	492	840	545
ENSMUSG00000038764	chr4	Ptpn3	57190841	57194362	7238	-2.2481	5.931124	0.000232	0.001028	0.400219	-1	303	242	894	4112	2859	115	714	113	815	353
ENSMUSG00000024177	chr17	Nme4	26091734	26092152	1418	0.883188	1.654379	0.000232	0.001029	0.044813	1	38	26	47	26	33	56	68	85	87	60
ENSMUSG00000049327	chr5	Setd8	1.24E+08	1.24E+08	4034	-0.61683	6.896923	0.000232	0.00103	0.032891	-1	2183	1375	3597	2122	2591	1432	1828	2032	2164	1160
ENSMUSG00000041362	chr19	4930506M07Rik	58973358	58975208	4081	0.900217	1.608072	0.000233	0.001033	0.049106	1	22	26	44	25	49	60	71	88	79	48
ENSMUSG00000036986	chr9	Pml	58218076	58220569	5571	0.688285	2.650399	0.000233	0.001034	0.031519	1	62	45	115	83	81	95	179	146	153	125
ENSMUSG00000038884	chr9	A230050P20Rik	20868642	20868936	3417	1.036669	1.345225	0.000234	0.001039	0.068657	1	15	20	44	17	35	50	59	69	45	66
ENSMUSG00000026393	chr1	Nek7	1.38E+08	1.38E+08	7376	-0.57067	7.265208	0.000235	0.001043	0.028294	-1	2682	2121	4707	2375	3129	1790	2813	1955	2794	2024
ENSMUSG00000029126	chr5	Nsg1	38137193	38138872	2140	1.017764	1.245414	0.000236	0.001043	0.062433	1	17	16	35	25	28	32	64	66	43	66
ENSMUSG00000019944	chr10	Rhobtb1	69151434	69151488	6075	-0.79736	4.672316	0.000237	0.001049	0.053102	-1	390	335	875	479	604	173	332	485	315	370
ENSMUSG00000022519	chr16	Srl	4480216	4483284	5325	-0.6026	10.67383	0.000237	0.001049	0.031958	-1	25282	16959	49499	33531	38982	18708	27691	19507	31548	21862
ENSMUSG00000101678	chr5	Gm29609	31144739	31144752	3550	-0.58183	4.714648	0.000237	0.00105	0.02742	-1	441	305	795	471	577	301	554	327	376	363
ENSMUSG00000001156	chr6	Mxd1	86647044	86651079	4662	0.675759	2.722786	0.000239	0.001055	0.030879	1	70	49	129	79	82	114	196	144	150	126
ENSMUSG00000038773	chr18	Kdm3b	34777008	34777325	7112	-0.62702	4.744728	0.00024	0.001059	0.032213	-1	344	290	944	509	661	275	444	371	463	371
ENSMUSG00000022016	chr14	Akap11	78492246	78495946	9419	-0.63938	4.74321	0.00024	0.00106	0.033848	-1	443	402	952	378	503	251	494	354	522	324
ENSMUSG00000040354	chr10	Mars	1.27E+08	1.27E+08	3423	-0.5295	5.989836	0.00024	0.001061	0.023822	-1	993	765	1746	1249	1389	731	1179	877	1171	824
ENSMUSG00000035268	chr2	Pkig	1.64E+08	1.64E+08	3990	0.661537	6.110208	0.00024	0.001062	0.037485	1	809	776	906	851	802	1221	1839	1300	2316	1186
ENSMUSG00000096146	chr7	Kcnj11	46098725	46099897	1173	-0.66713	5.523272	0.000241	0.001063	0.037831	-1	795	438	1479	890	1118	402	776	540	809	733
ENSMUSG00000024901	chr19	Peli3	4930651	4932867	3786	-0.91798	1.095231	0.000242	0.00107	0.042807	-1	32	30	73	36	49	15	36	20	36	24
ENSMUSG00000026520	chr1	Pycr2	1.81E+08	1.81E+08	2958	0.60848	3.952043	0.000242	0.00107	0.028462	1	180	145	217	186	242	340	352	319	399	266
ENSMUSG00000017548	chr11	Suz12	79993106	79993599	4945	-0.54759	4.203679	0.000243	0.001071	0.02327	-1	272	255	532	319	403	191	352	222	350	262
ENSMUSG00000098701	chr10	Mir6914	1.28E+08	1.28E+08	69	-1.90938	0.084254	0.000243	0.001071	0.212336	-1	9	2	52	32	37	7	5	8	4	10
ENSMUSG00000074873	chr19	AI606181	41593363	41596158	2796	0.871177	1.548813	0.000244	0.001078	0.045205	1	28	13	49	29	45	43	77	59	94	62
ENSMUSG00000091345	chr9	Col6a5	1.06E+08	1.06E+08	9405	1.328122	0.468342	0.000245	0.001078	0.101179	1	9	6	28	9	8	35	25	45	39	18
ENSMUSG00000006638	chr5	Abhd1	30950066	30950248	1758	1.283927	-0.10168	0.000246	0.001083	0.063573	1	5	4	11	10	8	22	31	19	21	12
ENSMUSG00000005779	chr3	Psmb4	94884093	94884440	1384	0.632909	7.152397	0.000246	0.001083	0.034927	1	1612	1667	1996	1644	1764	2569	3736	2895	4438	2368
ENSMUSG00000018411	chr11	Mapt	1.04E+08	1.04E+08	7531	-0.6046	6.14996	0.000248	0.00109	0.031539	-1	1243	940	2360	1075	1439	825	1167	850	1469	884
ENSMUSG00000024991	chr19	Eif3a	60761116	60762304	5176	-0.55914	7.091988	0.000248	0.00109	0.027298	-1	2192	2003	3937	2059	3038	1522	2302	1960	2451	1856
ENSMUSG00000069008	chr3	Gm5537	58102609	58104269	1661	1.441535	0.409939	0.000248	0.001092	0.112556	1	15	10	17	5	4	40	41	31	30	17
ENSMUSG00000040219	chr9	Ttc12	49436963	49438456	4545	0.821881	1.587987	0.000248	0.001092	0.037273	1	23	24	37	36	48	47	83	69	84	56
ENSMUSG00000007613	chr4	Tgfbr1	47353222	47353396	6534	-0.64711	4.880774	0.000249	0.001096	0.034935	-1	469	443	1033	417	595	317	430	503	471	359
ENSMUSG00000092345	chr4	Gm20503	59003210	59003557	1294	0.738084	2.659001	0.00025	0.001098	0.037068	1	68	62	92	70	77	108	133	163	160	135
ENSMUSG00000022758	chr16	P2rx6	17561885	17562183	3995	0.562864	4.535048	0.00025	0.0011	0.025323	1	301	224	413	246	310	402	592	440	577	494
ENSMUSG00000024193	chr17	Phf1	26933127	26933534	2429	0.519018	4.174214	0.000252	0.001108	0.02044	1	206	176	328	226	253	320	425	376	472	334
ENSMUSG00000074916	chr2	Chst14	1.19E+08	1.19E+08	2090	0.818912	2.089756	0.000253	0.00111	0.044401	1	35	26	59	46	80	84	106	101	99	87
ENSMUSG00000069833	chr19	Ahnak	8989284	8989429	18543	0.593391	8.309624	0.000254	0.001116	0.031161	1	3057	2487	7127	4029	4426	5154	7658	6404	9263	6553
ENSMUSG00000045934	chr3	Mtmr11	96162004	96162258	3780	0.858973	1.899111	0.000255	0.001117	0.048515	1	23	28	61	42	57	67	80	83	92	96
ENSMUSG00000091549	chr17	Gm6548	78850792	78851956	1165	0.910103	1.365025	0.000256	0.001125	0.047632	1	30	14	39	19	37	52	75	63	64	39
ENSMUSG00000006611	chr13	Hfe	23702034	23704426	3572	0.592676	5.23137	0.000258	0.001129	0.029523	1	452	343	578	495	515	649	1074	967	931	534
ENSMUSG00000041328	chr7	Pcf11	92643712	92644777	6412	-0.63185	3.558796	0.00026	0.001139	0.030073	-1	158	159	385	221	253	119	229	181	171	143
ENSMUSG00000032014	chr9	Oaf	43221278	43222839	2388	0.752868	3.41923	0.00026	0.00114	0.043855	1	109	109	164	92	157	178	218	224	273	297
ENSMUSG00000096433	chr17	Gm4944	22197265	22201809	4880	-0.867	2.499667	0.00026	0.00114	0.054798	-1	94	118	187	73	104	63	77	59	95	66
ENSMUSG00000048440	chr17	Cyp4f16	32536558	32536655	3017	1.142409	0.934739	0.000261	0.001143	0.06925	1	19	21	13	19	13	39	46	46	54	38
ENSMUSG00000025135	chr11	Anapc11	1.21E+08	1.21E+08	5057	0.540916	4.78116	0.000262	0.001146	0.023669	1	343	290	445	322	370	478	718	546	712	518
ENSMUSG00000027995	chr3	Tlr2	83836272	83838789	3014	0.81526	1.563359	0.000262	0.001147	0.036834	1	25	23	58	24	39	47	83	60	84	59
ENSMUSG00000022309	chr15	Angpt1	42424727	42427130	4256	-0.81928	3.554978	0.000263	0.001151	0.054138	-1	130	145	322	332	297	83	206	172	157	158
ENSMUSG00000055128	chr14	Cgrrf1	46832134	46832379	3291	-0.55159	5.329706	0.000263	0.001152	0.025779	-1	722	640	945	660	812	526	730	539	727	463
ENSMUSG00000033055	chr15	Ankrd54	79053094	79054084	4270	0.708953	2.41868	0.000264	0.001156	0.032903	1	56	38	88	71	69	104	122	124	142	97
ENSMUSG00000040681	chr16	Hmgn1	96120618	96122417	3221	0.574306	4.887782	0.000265	0.001158	0.027201	1	310	342	476	332	421	518	718	717	768	503
ENSMUSG00000097431	chr14	Gm26782	50870364	50870556	2650	-0.77328	1.847939	0.000265	0.001158	0.035607	-1	57	45	122	61	81	35	62	40	57	44
ENSMUSG00000029720	chr5	Gm20605	1.38E+08	1.38E+08	4464	0.522624	4.747272	0.000265	0.001158	0.022324	1	285	219	530	367	402	486	633	581	688	486
ENSMUSG00000028126	chr3	Pip5k1a	95058530	95060085	4383	-0.5466	4.985295	0.000266	0.00116	0.02489	-1	543	363	953	589	638	342	580	401	670	394
ENSMUSG00000021373	chr13	Cap2	46501848	46502211	3322	-0.57922	7.916703	0.000267	0.001166	0.029824	-1	3806	3135	7483	4365	5030	2676	4611	2666	4418	3482
ENSMUSG00000080316	chr17	Spaca6	17830719	17830858	6897	0.948003	1.425991	0.000267	0.001166	0.053748	1	34	14	31	22	40	57	67	70	71	42
ENSMUSG00000031986	chr8	Sprtn	1.25E+08	1.25E+08	2116	-0.88374	1.789111	0.000268	0.001167	0.050403	-1	61	35	110	59	98	24	62	36	49	47
ENSMUSG00000027223	chr2	Mapk8ip1	92383676	92384421	4644	0.82712	2.852263	0.000268	0.001168	0.051706	1	47	71	130	84	84	86	200	172	186	188
ENSMUSG00000069135	chr17	Fgfr1op	8165501	8165698	4008	-0.54228	4.139783	0.00027	0.001175	0.022966	-1	288	207	442	304	462	191	332	236	338	224
ENSMUSG00000019851	chr10	Perp	18845071	18845406	1901	-1.03869	0.726458	0.00027	0.001176	0.059084	-1	27	30	41	31	39	12	24	13	36	11
ENSMUSG00000023075	chr4	Akirin1	1.24E+08	1.24E+08	3450	-0.59438	5.17613	0.00027	0.001177	0.03012	-1	689	521	1088	500	723	377	702	511	701	389
ENSMUSG00000028273	chr3	Pdlim5	1.42E+08	1.42E+08	6448	-0.68767	8.607362	0.00027	0.001177	0.042187	-1	7242	5155	10443	7448	8643	3691	8482	3238	7823	4962

ENSMUSG00000070583	chr4	Fv1	1.48E+08	1.48E+08	1380	-1.06225	1.708101	0.00027	0.001177	0.078324	-1	50	40	108	70	88	22	58	20	32	55
ENSMUSG00000043953	chr9	Ccrl2	1.11E+08	1.11E+08	2110	-0.75353	2.949862	0.000273	0.001186	0.043432	-1	148	118	169	164	159	61	163	76	127	104
ENSMUSG00000072770	chr6	Acrbp	1.25E+08	1.25E+08	3277	1.249951	0.844969	0.000274	0.001192	0.098145	1	19	9	32	11	10	33	42	69	38	30
ENSMUSG00000036550	chr8	Cnot1	95719451	95720485	8390	-0.58803	5.876278	0.000274	0.001193	0.029996	-1	812	629	2026	1092	1392	657	1051	835	1005	752
ENSMUSG00000039242	chr13	B3galnt2	13954674	13954919	3681	-0.59135	6.620969	0.000274	0.001193	0.030833	-1	1886	1190	3048	1452	2155	1088	1988	1274	1618	1268
ENSMUSG00000038668	chr4	Lpar1	58435255	58437634	4289	0.619024	3.649241	0.000275	0.001195	0.029671	1	103	113	240	142	210	223	354	295	265	234
ENSMUSG00000032411	chr9	Tfdp2	96196275	96196560	14029	-0.64824	5.286998	0.000275	0.001196	0.036139	-1	624	396	1498	679	842	451	636	515	810	402
ENSMUSG00000048118	chr12	Arid4a	71015990	71016161	5615	-0.71508	3.259249	0.000276	0.001199	0.03954	-1	158	153	260	135	249	77	183	138	129	133
ENSMUSG00000001227	chr17	Sema6b	56123085	56124917	3977	0.902658	2.051486	0.000276	0.001199	0.056859	1	38	24	57	40	71	91	135	110	89	54
ENSMUSG00000028057	chr3	Rit1	88716838	88716957	3229	0.524712	4.669753	0.000276	0.001199	0.022218	1	310	244	426	324	361	455	649	492	726	431
ENSMUSG00000030824	chr7	Nucb1	45492874	45493949	5796	0.559851	5.932764	0.000277	0.001199	0.027268	1	656	504	1074	838	947	1071	1283	1451	1630	1161
ENSMUSG00000031385	chrX	Plxnb3	73757090	73757150	6493	-1.72178	0.156235	0.000277	0.001199	0.171989	-1	16	6	24	41	42	15	12	3	8	4
ENSMUSG00000070939	chr1	Tgfbrap1	43047200	43049835	10972	-0.58735	4.270176	0.000276	0.001199	0.02768	-1	287	190	565	406	473	235	313	282	353	223
ENSMUSG00000022186	chr15	Oxct1	4026383	4026849	3701	-0.85037	8.862536	0.000277	0.001202	0.06444	-1	5701	4002	11287	13933	15132	4366	7920	5096	7027	6106
ENSMUSG00000070031	chr1	Sp140	85600378	85600599	3328	1.296891	1.307247	0.000277	0.001202	0.115537	1	27	22	27	6	25	70	65	76	45	41
ENSMUSG00000044452	chr7	Zfp507	35772343	35776327	7121	-0.62706	3.975261	0.000277	0.001202	0.031408	-1	220	173	521	306	371	172	312	162	294	201
ENSMUSG00000014776	chr8	Nol3	1.05E+08	1.05E+08	2869	0.597663	6.220106	0.000278	0.001203	0.031278	1	846	686	1083	1051	1050	1348	1788	1333	2478	1342
ENSMUSG00000072653	chr6	Zfp783	47943171	47943377	6848	-0.94952	1.989189	0.000278	0.001203	0.063568	-1	74	71	144	44	84	31	54	54	48	53
ENSMUSG00000010663	chr19	Fads1	10182888	10183264	3456	0.75325	3.713251	0.000278	0.001204	0.046493	1	129	86	232	146	209	264	238	405	286	257
ENSMUSG00000020335	chr11	Zfp354b	50921823	50923840	2888	-0.88472	1.39735	0.000278	0.001204	0.04526	-1	45	41	69	52	58	18	41	28	35	41
ENSMUSG00000085342	chr11	Gm12254	58508791	58509261	471	0.67519	3.547099	0.000279	0.001205	0.034778	1	151	120	196	126	111	203	313	257	334	203
ENSMUSG00000023953	chr17	Polh	46172004	46173096	2569	-0.62545	3.578366	0.000279	0.001206	0.030027	-1	218	140	385	191	254	121	229	145	195	168
ENSMUSG00000048450	chr5	Msx1	37820485	37821700	3097	0.969079	1.834031	0.00028	0.001209	0.063548	1	30	38	58	18	43	53	81	77	122	85
ENSMUSG00000006281	chr14	Tep1	50824062	50824290	8168	0.551095	4.204883	0.00028	0.001211	0.024254	1	195	164	398	198	271	324	408	397	502	354
ENSMUSG00000018761	chr11	Mpdu1	69656697	69657328	2420	0.804327	3.310556	0.000281	0.001213	0.050798	1	127	84	151	109	95	222	211	294	215	170
ENSMUSG00000028484	chr4	Psip1	83455680	83457079	5082	-0.5696	4.195858	0.000281	0.001213	0.02591	-1	243	258	520	333	432	181	350	291	279	246
ENSMUSG00000072772	chr6	Grcc10	1.25E+08	1.25E+08	1988	0.685666	6.010097	0.000281	0.001213	0.041141	1	855	704	721	732	775	1249	1816	1382	1780	1072
ENSMUSG00000051166	chr12	Eml5	98786604	98790386	10136	-0.93424	1.993135	0.000283	0.00122	0.060023	-1	59	46	166	72	88	58	58	34	54	37
ENSMUSG00000060639	chr13	Hist1h4i	22040636	22041362	727	-0.75058	4.67095	0.000285	0.00123	0.048298	-1	607	437	582	333	527	339	332	280	481	289
ENSMUSG00000030168	chr6	Adipor2	1.19E+08	1.19E+08	5979	-0.57446	7.187026	0.000286	0.001235	0.029461	-1	2418	1792	3961	2835	3219	1542	2520	2606	2370	1687
ENSMUSG00000032123	chr9	Dpagt1	44326845	44327205	1905	0.532242	4.130981	0.000287	0.001236	0.02225	1	176	154	324	228	281	305	382	384	488	320
ENSMUSG00000034354	chr11	Mtmr3	4480868	4482939	7588	-0.5619	6.279726	0.000287	0.001237	0.027803	-1	1211	886	2478	1430	1693	875	1455	953	1477	1029
ENSMUSG00000020170	chr10	Frs2	1.17E+08	1.17E+08	5682	-0.6562	3.604061	0.000288	0.00124	0.03338	-1	166	143	385	229	309	105	197	175	196	184
ENSMUSG00000042694	chr19	Obfc1	47501033	47501717	4045	0.718316	2.466696	0.000289	0.001242	0.034506	1	50	47	78	73	81	99	184	106	132	99
ENSMUSG00000053128	chr9	Rnf26	44066327	44067231	4546	0.804583	2.198234	0.00029	0.001247	0.044585	1	45	26	68	58	69	90	87	106	137	94
ENSMUSG00000038206	chr8	Fbxo8	56551090	56551376	3740	-0.56799	4.124351	0.00029	0.001248	0.02593	-1	299	280	431	310	326	179	299	229	330	248
ENSMUSG00000047379	chr19	B3gnt1	5038826	5040032	2035	0.518384	4.986513	0.00029	0.001249	0.022349	1	378	299	505	412	488	553	749	594	899	612
ENSMUSG00000085218	chr2	BB218582	1.07E+08	1.07E+08	1311	-0.89689	2.713485	0.00029	0.001249	0.063901	-1	142	112	118	128	156	51	160	58	99	62
ENSMUSG00000074582	chr2	Arfgef2	1.67E+08	1.67E+08	8770	-0.69129	5.046734	0.000291	0.001252	0.041261	-1	434	279	980	795	953	340	560	448	577	398
ENSMUSG00000061286	chr7	Exosc5	25659153	25659383	1030	0.598183	4.275502	0.000292	0.001253	0.028754	1	243	210	275	232	240	377	472	366	541	359
ENSMUSG00000018750	chr11	Zbtb4	69765912	69766085	8117	-0.51833	5.483517	0.000293	0.001259	0.023045	-1	657	565	1237	877	969	529	914	610	717	599
ENSMUSG00000040560	chr18	Wdr7	63708695	63708919	7109	-0.56799	5.249326	0.000293	0.001259	0.027638	-1	587	399	1292	666	868	428	737	509	683	468
ENSMUSG00000061877	chr7	BC048679	81494275	81494378	640	-3.78733	2.012778	0.000293	0.001259	0.97985	-1	2	8	27	386	180	0	33	1	19	3
ENSMUSG00000036291	chr14	Ap5m1	49066495	49066864	3165	-0.68235	3.10543	0.000294	0.00126	0.034733	-1	130	109	264	175	185	78	190	93	130	116
ENSMUSG00000030469	chr7	Zfp719	43579610	43579766	4706	-0.73673	2.149622	0.000294	0.001262	0.034227	-1	74	54	129	82	106	43	77	65	56	56
ENSMUSG00000067336	chr1	Bmpr2	59763400	59764728	17983	-0.60336	6.508481	0.000294	0.001262	0.032381	-1	1331	1052	3152	1627	2053	901	1480	1197	1914	1200
ENSMUSG00000086863	chr6	Gm15543	1.45E+08	1.45E+08	361	-2.37349	1.995502	0.000294	0.001262	0.441563	-1	18	21	42	252	207	13	63	4	34	11
ENSMUSG00000037876	chr10	Jmjd1c	67096125	67096718	14397	-0.60528	4.505341	0.000295	0.001263	0.030602	-1	294	298	680	404	589	232	525	299	344	269
ENSMUSG00000087380	chr6	2210408F21Rik	31220351	31220519	1476	-0.59971	5.071028	0.000295	0.001266	0.031001	-1	662	548	781	550	636	424	647	398	639	360
ENSMUSG00000021733	chr14	Slc4a7	14703025	14703280	7389	-0.71041	2.87162	0.000296	0.001268	0.036743	-1	116	84	256	128	165	61	122	109	116	96
ENSMUSG00000079278	chr5	Tmem233	1.16E+08	1.16E+08	2477	-0.68805	8.108564	0.000296	0.001269	0.042713	-1	5758	4780	8055	3535	4906	3423	4871	3226	4743	3143
ENSMUSG00000066036	chr4	Ubr4	1.39E+08	1.39E+08	17997	-0.71565	7.19639	0.000296	0.001269	0.045965	-1	1881	1552	5802	2779	3624	1464	2007	1822	3160	1808
ENSMUSG00000020612	chr11	Prkar1a	1.1E+08	1.1E+08	4321	0.580683	7.392654	0.000297	0.001269	0.030313	1	1839	1445	3036	2050	2613	2329	4635	3232	4452	3893
ENSMUSG00000006215	chr4	Zbtb17	1.41E+08	1.41E+08	3877	-0.58734	4.772788	0.000298	0.001275	0.029111	-1	368	324	678	667	634	313	435	368	533	350
ENSMUSG00000026321	chr1	Tnfrsf11a	1.06E+08	1.06E+08	5985	0.958023	0.98192	0.000301	0.001288	0.045385	1	17	20	31	12	21	35	55	40	60	35
ENSMUSG00000031143	chrX	Ccdc22	7593809	7594167	3427	0.551283	4.068967	0.000301	0.001288	0.024126	1	197	132	297	229	244	332	374	347	446	300
ENSMUSG00000030674	chr7	Qprt	1.27E+08	1.27E+08	2645	1.087206	0.674341	0.000302	0.001291	0.064161	1	16	9	25	8	19	25	35	49	37	35
ENSMUSG00000059248	chr11	Sept9	1.17E+08	1.17E+08	7565	0.551774	4.475774	0.000302	0.001291	0.02507	1	267	184	430	270	314	453	498	438	635	375
ENSMUSG00000017677	chr11	Wsb1	79239372	79240462	3987	0.727913	2.936435	0.000303	0.001295	0.039524	1	81	78	123	59	115	145	219	161	159	166
ENSMUSG00000005949	chr11	Ctns	73183596	73185051	3391	0.625659	2.827068	0.000305	0.001303	0.026573	1	64	62	123	89	109	123	179	155	195	125
ENSMUSG00000079428	chrX	Tceal7	1.36E+08	1.36E+08	1217	0.911772	4.28577	0.000306	0.001306	0.071476	1	131	220	299	206	212	239	760	283	469	595
ENSMUSG00000046034	chr15	Otulin	27605919	27606461	1491	0.57989	4.004008	0.000306	0.001307	0.026337	1	189	159	225	223	213	280	440	308	468	269
ENSMUSG00000082292	chr11	Gm12250	58187739	58189012	1274	1.972241	-0.48806	0.000307	0.001311	0.204051	1	3	0	0	6	10	14	29	22	6	14
ENSMUSG00000054484	chr2	Tmem62	1.21E+08	1.21E+08	3348	0.738906	2.223109	0.000308	0.001313	0.036587	1	35	40	91	46	69	82	128	103	108	97
ENSMUSG00000058690	chr14	Ccser2	36874936	36879762	8715	-0.54258	6.617655	0.000309	0.001317	0.02635	-1	1460	1182	3054	1866	2074	1081	1912	1380	1860	1175

ENSMUSG00000058291	chr5	Zfp68	1.39E+08	1.39E+08	3834	-0.53645	4.598431	0.00031	0.00132	0.023967	-1	397	338	641	455	474	264	535	354	386	285
ENSMUSG00000098465	chr8	Mir1668	83723878	83723984	107	0.806118	1.66909	0.00031	0.001321	0.038416	1	31	22	38	39	49	61	79	67	76	69
ENSMUSG00000032702	chr19	Kank1	25236975	25237317	6166	-0.53181	4.601367	0.000311	0.001323	0.023377	-1	355	331	738	388	542	280	499	343	392	306
ENSMUSG00000019087	chrX	Atp6ap1	74297097	74297321	3026	0.549462	7.504183	0.000312	0.001327	0.027321	1	2167	1889	3129	2024	2567	3381	4670	3681	4816	3196
ENSMUSG00000037358	chrX	4930578C19Rik	18414881	18416093	3499	-1.11785	1.044925	0.000312	0.00133	0.07953	-1	22	21	63	66	51	13	38	24	23	17
ENSMUSG00000082454	chr11	Gm12183	48751867	48753714	1848	-0.82636	2.117636	0.000313	0.00133	0.047227	-1	69	75	129	70	96	35	82	56	47	60
ENSMUSG00000084347	chr11	Akt2-ps	16514533	16515981	1449	-0.67895	2.406146	0.000313	0.001333	0.030214	-1	97	73	152	89	109	52	95	69	89	64
ENSMUSG00000098387	chr2	Pet117	1.44E+08	1.44E+08	693	-0.97144	1.668944	0.000314	0.001336	0.0653	-1	44	32	91	79	93	29	43	21	68	33
ENSMUSG00000035247	chr12	Hectd1	51743722	51744658	9048	-0.6204	7.277936	0.000315	0.001338	0.034871	-1	2047	1678	5368	3107	3690	1686	2851	1848	2922	2002
ENSMUSG00000031333	chrX	Abcb7	1.04E+08	1.04E+08	5905	-0.60213	5.916159	0.000315	0.001339	0.0322	-1	801	658	1714	1359	1511	612	1055	780	1087	869
ENSMUSG00000031266	chrX	Gla	1.35E+08	1.35E+08	3265	0.750941	2.375796	0.000316	0.00134	0.039041	1	43	48	88	54	74	86	146	144	112	92
ENSMUSG00000037253	chr18	Mex3c	73573044	73573776	3738	-0.64248	3.555307	0.000316	0.001344	0.032487	-1	186	165	382	202	232	97	198	178	195	169
ENSMUSG00000018143	chr5	Mafk	1.4E+08	1.4E+08	3901	0.681574	4.176541	0.000317	0.001345	0.039282	1	145	118	277	292	304	271	557	319	511	395
ENSMUSG00000018381	chr11	Abi3	95830074	95832876	4153	0.892517	1.629434	0.000319	0.001352	0.053459	1	14	22	55	34	48	61	71	60	87	71
ENSMUSG00000011752	chr19	Pgam1	41911871	41912186	1831	0.763	2.86649	0.000319	0.001353	0.044793	1	70	48	113	87	118	127	179	230	174	112
ENSMUSG00000057541	chr5	Pus7	23740648	23741976	5171	-0.57262	3.754704	0.000319	0.001355	0.025771	-1	215	183	414	202	305	140	266	182	263	153
ENSMUSG00000074749	chr2	Kiz	1.47E+08	1.47E+08	2278	-0.53947	4.768784	0.000322	0.001364	0.024673	-1	415	388	602	571	598	331	558	351	484	322
ENSMUSG00000052151	chr10	Ppap2c	79526430	79527248	1645	1.266603	0.551055	0.000322	0.001366	0.094628	1	15	6	26	5	13	37	38	38	45	15
ENSMUSG00000002732	chr2	Fkbp7	76663044	76663352	1485	0.705027	2.851498	0.000323	0.001368	0.03625	1	78	60	110	100	84	143	171	162	155	158
ENSMUSG00000087440	chr3	4930577N17Rik	51276759	51278383	1625	-1.11389	0.537114	0.000323	0.001368	0.064862	-1	31	19	27	39	31	13	16	10	21	18
ENSMUSG00000021264	chr12	Yy1	1.09E+08	1.09E+08	2902	-0.52914	4.354047	0.000324	0.001374	0.02294	-1	316	280	598	351	420	199	384	287	400	275
ENSMUSG00000053436	chr17	Mapk14	28691342	28691855	4361	-0.56064	7.175094	0.000325	0.001376	0.028572	-1	2454	1545	4232	2752	3255	1648	2830	1812	2799	1745
ENSMUSG00000039934	chr5	Gsap	21186267	21186459	3745	1.138719	0.557496	0.000325	0.001377	0.076186	1	8	6	27	6	24	26	47	30	32	34
ENSMUSG00000026853	chr2	Crat	30400471	30402793	5388	-0.67017	8.90231	0.000326	0.001381	0.041198	-1	6901	5060	11700	12879	11590	4848	8985	5846	9762	5162
ENSMUSG00000076612	chr12	Ighg2c	1.13E+08	1.13E+08	1326	-2.01811	1.368705	0.000327	0.001384	0.322581	-1	82	91	84	20	27	15	12	16	53	2
ENSMUSG00000021957	chr14	Tkt	30548359	30548614	6533	1.251085	4.880446	0.000328	0.001386	0.137913	1	332	249	352	184	234	609	404	1596	533	473
ENSMUSG00000071054	chr17	Safb	56584825	56585350	7268	0.525552	5.418289	0.000328	0.001387	0.024019	1	524	416	746	494	631	781	941	961	1170	736
ENSMUSG00000091264	chr13	Smim13	41249860	41250314	4464	-0.52855	6.242518	0.000329	0.001388	0.025032	-1	1210	916	1938	1539	1669	867	1440	973	1450	990
ENSMUSG00000030835	chr7	Nomo1	46033698	46033972	5936	-0.57409	6.530996	0.000333	0.001405	0.029813	-1	1250	1175	2808	1863	2042	937	1432	1311	1828	1311
ENSMUSG00000063388	chr18	BC023105	60441753	60442361	1227	-1.07161	5.818255	0.000334	0.001411	0.103236	-1	1283	879	2512	373	1347	596	1094	495	885	357
ENSMUSG00000092416	chr7	Zfp141	42473386	42476683	4665	-0.77063	2.286423	0.000334	0.001411	0.041576	-1	76	89	158	72	93	52	80	56	77	59
ENSMUSG00000038267	chr13	Slc22a23	34179158	34183311	6386	-0.99769	3.601986	0.000335	0.001414	0.085286	-1	144	76	314	409	412	112	196	132	179	123
ENSMUSG00000063406	chr5	Tmed5	1.08E+08	1.08E+08	7688	-0.72462	4.713847	0.000338	0.001425	0.046064	-1	334	394	752	562	619	193	305	433	468	397
ENSMUSG00000015291	chrX	Gdi1	74304998	74305441	4296	0.520623	5.795296	0.000342	0.001443	0.024016	1	653	591	1008	626	771	971	1485	1058	1389	1075
ENSMUSG00000037638	chr12	Zbtb42	1.13E+08	1.13E+08	3490	0.989705	1.238583	0.000342	0.001444	0.058134	1	18	22	39	23	18	36	84	52	76	31
ENSMUSG00000021022	chr12	Ppp2r3c	55280814	55281805	2395	-0.57943	4.146922	0.000343	0.001444	0.027758	-1	356	253	492	266	329	221	317	256	296	203
ENSMUSG00000082922	chr7	Gm6939	1.27E+08	1.27E+08	864	0.996783	0.629865	0.000344	0.001447	0.042667	1	15	12	20	14	15	23	36	37	48	30
ENSMUSG00000072082	chr17	Ccnf	24223232	24224346	3099	1.323932	0.241366	0.000345	0.001454	0.096286	1	13	4	15	7	10	24	41	30	13	28
ENSMUSG00000021025	chr12	Nfkbia	55489411	55489969	1577	0.59946	4.435998	0.000346	0.001458	0.030302	1	238	216	352	246	321	362	786	379	490	393
ENSMUSG00000033222	chr3	Ttf2	1.01E+08	1.01E+08	6564	-0.70229	2.772506	0.000346	0.001458	0.03622	-1	119	102	227	109	124	80	104	76	126	84
ENSMUSG00000040390	chr7	Map3k10	27656375	27656986	4142	-0.53416	5.533723	0.000347	0.00146	0.025237	-1	745	578	1114	891	1111	552	686	613	955	647
ENSMUSG00000056579	chr11	Tug1	3639785	3645523	8325	-0.51634	5.057004	0.000347	0.00146	0.023064	-1	508	468	921	565	718	400	704	487	566	369
ENSMUSG00000025423	chr18	Pias2	77065208	77065419	5433	-0.51258	5.569505	0.000348	0.001462	0.023244	-1	717	634	1441	802	986	525	914	634	954	598
ENSMUSG00000067780	chr1	Pi15	17601901	17602042	6923	1.025606	1.237746	0.000349	0.001466	0.065412	1	14	24	37	16	28	37	43	67	69	55
ENSMUSG00000026623	chr1	Lpgat1	1.92E+08	1.92E+08	7610	-0.70225	4.835729	0.00035	0.00147	0.043558	-1	368	280	776	717	800	238	444	471	479	361
ENSMUSG00000072704	chr6	2700089E24Rik	1.33E+08	1.33E+08	2738	-0.55803	7.471049	0.000353	0.001482	0.028742	-1	3121	2830	4550	2836	3488	2069	3114	2409	3401	2217
ENSMUSG00000060429	chr15	Sntb1	55638843	55639427	2869	-1.10994	0.527015	0.000353	0.001483	0.061993	-1	26	16	49	22	39	10	26	20	12	10
ENSMUSG00000026238	chr1	Ptma	86526726	86526950	1462	0.629222	5.754905	0.000353	0.001483	0.035675	1	495	543	700	651	997	839	1190	1351	1453	1127
ENSMUSG00000037936	chr5	Scarb1	1.25E+08	1.25E+08	6291	0.69124	4.676789	0.000353	0.001484	0.042075	1	319	173	452	260	396	417	747	781	607	349
ENSMUSG00000024242	chr17	Map4k3	80580512	80581935	4231	-0.59551	3.985898	0.000354	0.001484	0.029185	-1	210	200	469	313	375	136	299	220	272	232
ENSMUSG00000023809	chr17	Rps6ka2	7170115	7170443	5404	-0.75982	7.28468	0.000354	0.001484	0.053176	-1	2064	1305	4724	4266	4171	1478	2742	1649	2903	1984
ENSMUSG00000020707	chr11	Rnf135	80183851	80184255	2140	0.862443	1.684814	0.000355	0.00149	0.046128	1	35	34	44	28	32	55	91	65	74	77
ENSMUSG00000024941	chr19	Scyl1	5758427	5758696	2637	-0.51957	6.608639	0.000356	0.001493	0.024633	-1	1637	1284	2382	1898	2050	1242	1653	1310	1862	1264
ENSMUSG00000040033	chr10	Stat2	1.28E+08	1.28E+08	4397	0.769523	2.931305	0.000357	0.001497	0.046407	1	65	64	120	79	125	149	234	214	132	128
ENSMUSG00000041638	chr5	Gcn1l1	1.16E+08	1.16E+08	15903	-0.63974	5.160466	0.000357	0.001498	0.036374	-1	488	335	1167	742	949	368	549	446	724	483
ENSMUSG00000031984	chr8	2810004N23Rik	1.25E+08	1.25E+08	1382	-0.53754	4.532023	0.000358	0.001499	0.024445	-1	356	318	536	459	527	302	477	268	403	281
ENSMUSG00000047473	chr7	Zfp30	29783998	29784901	6078	-0.75611	2.180309	0.000358	0.001499	0.039032	-1	63	58	105	110	116	44	65	64	75	54
ENSMUSG00000040760	chr14	Appl1	26918988	26923871	8719	-0.50047	4.934891	0.000359	0.001502	0.021431	-1	465	389	909	500	682	366	589	421	557	392
ENSMUSG00000062300	chr7	Pvrl2	19716644	19717787	3440	0.903718	1.695447	0.000359	0.001503	0.052045	1	29	30	44	39	30	54	73	81	120	48
ENSMUSG00000062373	chr15	Tmem65	58782269	58785010	3747	-1.29017	7.147884	0.000359	0.001503	0.150521	-1	1228	1070	2545	6502	5331	814	2166	1076	2147	1541
ENSMUSG00000000134	chrX	Tfe3	7762560	7762630	9261	0.585121	3.765455	0.000361	0.001508	0.027765	1	122	102	266	204	196	229	318	300	394	245
ENSMUSG00000036334	chr3	Igsf10	59316735	59320374	10150	0.88452	2.757792	0.000361	0.00151	0.064678	1	49	32	137	60	122	107	206	178	130	160
ENSMUSG00000092397	chr2	C130080G10Rik	1.14E+08	1.14E+08	2586	1.451337	-0.08775	0.000362	0.001512	0.106493	1	8	6	10	3	8	28	12	19	35	14
ENSMUSG00000035692	chr4	Isg15	1.56E+08	1.56E+08	756	1.345293	1.379588	0.000362	0.001514	0.131544	1	25	19	19	24	21	57	123	58	23	61
ENSMUSG00000045624	chr2	Esf1	1.4E+08	1.4E+08	4471	-0.60799	4.236263	0.000363	0.001515	0.031411	-1	309	318	508	271	411	240	400	252	267	205

ENSMUSG00000022561	chr15	Gpaa1	76331231	76331463	2846	0.509536	5.153394	0.000364	0.00152	0.022571	1	390	327	610	523	510	579	847	739	1007	658
ENSMUSG00000046330	chr1	Rpl37a	72711260	72711323	584	0.659693	7.246418	0.000365	0.001522	0.040213	1	1938	1720	1965	1776	1668	3096	4150	3113	4078	2578
ENSMUSG00000069972	chr7	Rps13-ps2	88530446	88530898	453	0.820992	2.389002	0.000365	0.001522	0.048088	1	60	53	72	57	48	100	186	113	119	84
ENSMUSG00000036819	chr11	Jmjd4	59450045	59450512	7115	-0.71501	3.431535	0.00037	0.001543	0.041719	-1	142	101	337	260	276	113	199	117	170	145
ENSMUSG00000041828	chr11	Abca8a	1.1E+08	1.1E+08	6272	-0.67716	5.919949	0.00037	0.001544	0.041861	-1	724	707	2182	1094	1621	562	955	859	921	931
ENSMUSG00000033020	chr15	Polr2f	79141351	79141434	543	0.595317	4.436189	0.000375	0.001562	0.03015	1	246	211	286	317	292	436	562	372	574	417
ENSMUSG00000005672	chr5	Kit	75574916	75575118	5831	1.048441	1.309321	0.000376	0.001565	0.072711	1	26	19	40	15	24	30	58	77	57	65
ENSMUSG00000033228	chr15	Scaf11	96411698	96414916	7724	-0.52114	5.310476	0.000377	0.001571	0.024053	-1	573	488	1235	663	919	428	768	603	702	500
ENSMUSG00000031198	chrX	Fundc2	75382399	75382451	2785	-0.52272	7.514349	0.00038	0.001582	0.025488	-1	2817	2495	4865	3384	3935	2069	3682	2387	3409	2342
ENSMUSG00000024644	chr18	Cndp2	84667470	84668100	2119	0.525017	4.968678	0.00038	0.001582	0.023937	1	362	326	558	367	439	590	723	719	793	523
ENSMUSG00000038515	chr8	Grtp1	13176869	13177142	1310	-1.06903	1.598984	0.000381	0.001586	0.083363	-1	38	31	55	96	104	25	35	33	46	34
ENSMUSG00000021408	chr13	Ripk1	34002363	34002706	6138	0.766923	2.667228	0.000382	0.001589	0.044983	1	56	52	102	62	105	116	221	164	134	89
ENSMUSG00000019139	chr8	Isyna1	70594481	70594543	1836	0.943363	2.101587	0.000384	0.001595	0.065651	1	38	43	52	49	42	91	62	115	129	93
ENSMUSG00000032966	chr2	Fkbp1a	1.52E+08	1.52E+08	3857	0.548559	7.085774	0.000384	0.001595	0.027949	1	1715	1337	2245	1649	1838	2438	3340	2863	3977	2234
ENSMUSG00000042133	chr2	Ppig	69722545	69722957	8122	-0.52759	4.831106	0.000384	0.001595	0.024259	-1	425	422	778	426	677	329	548	399	560	320
ENSMUSG00000041453	chr5	Rpl21	1.47E+08	1.47E+08	3400	0.610489	7.809783	0.000384	0.001598	0.034859	1	2764	2546	3065	2630	2797	4429	6375	4502	5764	3791
ENSMUSG00000070424	chr7	Art5	1.02E+08	1.02E+08	1806	0.738487	5.399189	0.000385	0.001599	0.049645	1	299	430	522	658	588	656	1326	643	1239	1014
ENSMUSG00000040242	chr6	Fgfr1op2	1.47E+08	1.47E+08	4619	-0.50125	5.820141	0.000386	0.001602	0.022759	-1	882	764	1465	990	1267	621	1169	731	1066	745
ENSMUSG00000039682	chr5	Lap3	45493374	45493561	3072	-0.50069	5.410347	0.000388	0.00161	0.022346	-1	671	534	1004	823	997	512	812	532	827	559
ENSMUSG00000031077	chr7	Fadd	1.45E+08	1.45E+08	3903	0.70276	2.571375	0.000388	0.001611	0.035806	1	61	40	84	84	90	98	188	118	169	98
ENSMUSG00000050505	chr14	Pcdh20	88464743	88469730	5492	-1.5129	-0.09568	0.000391	0.001623	0.125415	-1	17	15	39	15	16	4	3	18	10	4
ENSMUSG00000060510	chr9	Zfp266	20495068	20500477	6283	-0.60851	3.703992	0.000393	0.001632	0.030147	-1	216	177	384	210	291	144	246	145	194	205
ENSMUSG00000024276	chr18	Zfp397	23954688	23954861	5487	-0.60128	3.990395	0.000394	0.001632	0.030413	-1	240	249	494	244	326	169	311	175	267	233
ENSMUSG00000004285	chr6	Atp6v1f	29467718	29467974	1063	0.618498	5.876121	0.000396	0.001639	0.035005	1	807	627	830	654	683	1124	1614	1220	1651	934
ENSMUSG00000030214	chr6	Plbd1	1.37E+08	1.37E+08	2633	-1.20372	4.124121	0.000396	0.00164	0.129814	-1	200	134	294	801	545	203	206	222	207	111
ENSMUSG00000047388	chr8	Atmin	1.17E+08	1.17E+08	4877	-0.51344	5.320059	0.000396	0.00164	0.023499	-1	652	465	1219	735	794	474	693	573	795	490
ENSMUSG00000025261	chrX	Huwe1	1.52E+08	1.52E+08	23507	-0.70494	7.305555	0.000397	0.001644	0.04659	-1	2072	1417	6094	3214	4101	1528	2660	1914	2997	2035
ENSMUSG00000060771	chr1	Tsga10	37754776	37755521	10662	-0.67455	2.49331	0.000399	0.001651	0.032048	-1	106	85	139	93	122	58	107	68	91	69
ENSMUSG00000079144	chr1	A130010J15Rik	1.93E+08	1.93E+08	4403	-0.64971	2.706278	0.000399	0.001652	0.030928	-1	97	96	185	114	148	70	122	68	128	77
ENSMUSG00000029621	chr5	Arpc1a	1.45E+08	1.45E+08	2567	0.531327	4.8887	0.0004	0.001655	0.024715	1	319	255	448	451	470	501	760	663	741	529
ENSMUSG00000020137	chr10	Thap2	1.15E+08	1.15E+08	3408	-0.79734	1.970594	0.000401	0.001657	0.044455	-1	46	59	122	86	85	37	80	49	55	38
ENSMUSG00000060090	chrX	Rp2h	20364481	20364828	5141	-0.78971	2.279019	0.000401	0.001657	0.044924	-1	53	76	173	84	115	47	80	61	70	61
ENSMUSG00000006476	chr2	Nsmf	25054355	25054671	4896	0.616672	3.189547	0.000403	0.001666	0.029857	1	94	65	185	122	120	157	215	218	220	180
ENSMUSG00000025626	chrX	Phf6	52912266	52912436	6946	-0.77195	2.248079	0.000404	0.001667	0.042158	-1	74	60	131	94	122	35	84	73	59	64
ENSMUSG00000042476	chr5	Abcb4	8893721	8893907	4074	-0.63181	7.071457	0.000404	0.001668	0.037479	-1	1980	1279	3756	3305	3261	1359	2609	1642	2483	1706
ENSMUSG00000027130	chr2	Slc12a6	1.12E+08	1.12E+08	10165	-0.60038	4.914684	0.000405	0.00167	0.032105	-1	447	338	1130	499	651	321	485	458	514	405
ENSMUSG00000029469	chr5	Ift81	1.23E+08	1.23E+08	3453	0.863413	1.63205	0.000405	0.001673	0.046337	1	32	26	31	35	43	51	98	57	72	73
ENSMUSG00000041420	chr7	Meis3	16175090	16175184	3173	1.186935	0.923289	0.000408	0.001682	0.093868	1	12	12	18	10	36	44	62	54	44	21
ENSMUSG00000040006	chr10	Ginm1	7767947	7768585	2996	-0.52611	5.805531	0.000409	0.001686	0.025394	-1	805	877	1331	1124	1119	661	1108	798	996	661
ENSMUSG00000070427	chr7	Il18bp	1.02E+08	1.02E+08	1400	1.035274	1.170345	0.000409	0.001687	0.06632	1	17	16	15	31	31	54	65	50	57	34
ENSMUSG00000034349	chr3	Smc4	69004738	69005090	5210	0.685356	3.02512	0.00041	0.001691	0.036207	1	88	84	152	76	95	179	212	167	186	149
ENSMUSG00000042745	chr2	Id1	1.53E+08	1.53E+08	1160	0.801733	3.255332	0.00041	0.001691	0.052767	1	71	123	95	107	135	163	319	185	256	186
ENSMUSG00000023972	chr17	Ptk7	46564451	46565495	4255	0.983104	0.653082	0.000412	0.001696	0.047307	1	11	13	25	12	18	26	35	31	44	39
ENSMUSG00000034853	chr4	Acot11	1.07E+08	1.07E+08	6056	-1.34988	3.114765	0.000413	0.001701	0.160341	-1	62	51	224	347	366	46	137	63	108	96
ENSMUSG00000021557	chr13	Agtpbp1	59449537	59449746	12833	-0.49951	5.882955	0.000414	0.001704	0.022835	-1	934	735	1609	1134	1218	757	1116	791	1092	730
ENSMUSG00000026170	chr1	Cyp27a1	74713574	74713891	2173	-0.72824	6.038447	0.000414	0.001706	0.049469	-1	1200	977	2179	961	1382	1006	814	735	1373	575
ENSMUSG00000027852	chr3	Nras	1.03E+08	1.03E+08	4514	0.565336	5.462775	0.000417	0.001716	0.029016	1	580	457	746	419	626	745	1094	876	1357	780
ENSMUSG00000063236	chr15	1110038F14Rik	76948539	76948544	1010	0.543165	3.900003	0.000418	0.001719	0.023839	1	187	138	237	179	225	288	364	275	418	262
ENSMUSG00000030882	chr7	Dnhd1	1.06E+08	1.06E+08	15578	0.516315	4.248694	0.000418	0.00172	0.022089	1	234	177	311	254	269	355	490	384	473	329
ENSMUSG00000060568	chr1	Fam78b	1.67E+08	1.67E+08	6325	-0.89319	1.547484	0.000419	0.001724	0.054437	-1	58	30	91	48	77	18	60	37	46	25
ENSMUSG00000046785	chr9	Epm2aip1	1.11E+08	1.11E+08	7169	-0.57367	5.483025	0.000421	0.001731	0.030107	-1	683	484	1507	805	1001	430	878	599	758	646
ENSMUSG00000027439	chr2	Gzf1	1.49E+08	1.49E+08	4472	-0.56046	4.706224	0.000424	0.00174	0.027625	-1	363	321	715	542	605	372	512	337	386	306
ENSMUSG00000033813	chr1	Tcea1	4857814	4857976	3017	-0.57971	4.241968	0.000424	0.001741	0.029117	-1	312	313	485	304	387	183	386	246	294	280
ENSMUSG00000066880	chr8	Zfp617	71908635	71908738	3024	-0.57323	3.617765	0.000424	0.001742	0.026728	-1	207	156	312	227	281	137	278	141	210	145
ENSMUSG00000093803	chr9	Ppp2r3d	1.24E+08	1.24E+08	1861	0.706291	2.664275	0.000427	0.001752	0.036603	1	72	63	103	59	81	133	144	139	146	130
ENSMUSG00000006262	chr5	Mob1b	88720855	88721121	10927	-0.62095	4.982251	0.000427	0.001753	0.035155	-1	471	388	993	556	768	231	607	410	696	402
ENSMUSG00000052102	chr18	Gnpda1	38327558	38328973	2392	0.561121	3.693645	0.000428	0.001756	0.025116	1	144	130	207	162	185	257	318	273	296	238
ENSMUSG00000101493	chr4	2810405F17Rik	1.37E+08	1.37E+08	1117	1.292592	-0.31212	0.000428	0.001756	0.059855	1	5	4	12	6	5	12	16	18	27	16
ENSMUSG00000025255	chr3	Zfhx4	5218526	5218927	15737	-1.23156	3.619147	0.000428	0.001757	0.135421	-1	86	96	611	273	468	98	121	119	110	191
ENSMUSG00000020993	chr12	Trappc6b	59043093	59043676	1254	-0.55303	5.020159	0.000429	0.001759	0.027668	-1	603	521	748	515	654	375	653	398	613	393
ENSMUSG00000032349	chr9	Elovl5	77917364	77917526	3522	0.628817	3.571151	0.000431	0.001765	0.032903	1	106	96	211	153	193	195	325	321	240	219
ENSMUSG00000020128	chr11	Vps54	21239281	21239371	7515	-0.52985	4.628954	0.000433	0.001775	0.024584	-1	415	338	748	372	510	251	444	378	456	330
ENSMUSG00000002028	chr9	Kmt2a	44803355	44808177	16670	-0.76605	4.509305	0.000434	0.001779	0.053205	-1	256	238	980	417	587	212	325	251	412	337
ENSMUSG00000043639	chr19	Rbm20	53677306	53677592	6790	-0.56765	5.599944	0.000436	0.001785	0.029824	-1	751	577	1508	903	1049	408	961	640	990	655
ENSMUSG00000027509	chr2	Rae1	1.73E+08	1.73E+08	2554	0.529366	3.88643	0.000436	0.001785	0.022704	1	191	125	264	182	209	264	367	302	410	249

ENSMUSG00000033434	chr5	Gtpbp6	1.1E+08	1.1E+08	2825	0.602603	3.15327	0.000437	0.001787	0.027321	1	99	87	128	101	142	177	215	182	230	158
ENSMUSG00000024908	chr19	Ppp6r3	3454933	3457051	4952	-0.54698	6.356153	0.000439	0.001797	0.028098	-1	1235	891	2605	1519	1870	883	1505	1151	1569	1041
ENSMUSG00000039611	chr4	Tmem246	49584506	49587241	3325	0.660148	4.894545	0.000444	0.001815	0.039845	1	374	178	357	460	477	522	868	595	828	540
ENSMUSG00000027230	chr2	Creb3l1	91982328	91983007	2603	0.804425	2.610671	0.00045	0.00184	0.052486	1	49	46	128	50	92	133	108	128	172	140
ENSMUSG00000101939	chr1	Gm28438	24612775	24613119	345	-1.02727	2.5878	0.00045	0.00184	0.090151	-1	74	56	120	195	208	46	75	71	127	47
ENSMUSG00000035299	chrX	Mid1	1.7E+08	1.7E+08	6720	-1.02896	1.391626	0.000452	0.001847	0.073704	-1	37	22	104	43	84	25	46	23	27	30
ENSMUSG00000040374	chr3	Pex2	5560188	5561764	2270	-0.49634	4.798725	0.000454	0.001855	0.021798	-1	434	388	725	495	585	317	588	360	500	364
ENSMUSG00000020393	chr11	Kremen1	5191552	5195121	7722	-0.62695	5.853886	0.000456	0.001859	0.037051	-1	883	630	1511	1436	1280	609	1100	673	1317	581
ENSMUSG00000031538	chr8	Plat	22757744	22757828	2531	0.673194	2.915799	0.000455	0.001859	0.035767	1	78	60	161	68	107	144	193	185	166	139
ENSMUSG00000042496	chr9	Prdm10	31280538	31280662	6075	-0.84239	1.090641	0.000456	0.001859	0.039565	-1	34	31	60	40	47	21	43	24	31	16
ENSMUSG00000026466	chr1	Tor1aip1	1.56E+08	1.56E+08	5406	-0.55226	6.941791	0.000457	0.001863	0.029096	-1	1854	1492	4013	2177	2614	1206	2396	1717	2250	1662
ENSMUSG00000022100	chr14	Xpo7	70654246	70666094	15121	-0.51321	5.736877	0.000459	0.001871	0.024441	-1	786	654	1708	924	1127	603	1047	741	1009	661
ENSMUSG00000063415	chr6	Cyp26b1	84571414	84574659	4849	-1.84386	2.928045	0.00046	0.001873	0.296845	-1	133	30	310	40	547	51	86	38	29	83
ENSMUSG00000026069	chr1	Il1rl1	40429570	40429630	6894	1.126233	0.897801	0.000461	0.00188	0.082092	1	24	11	30	9	14	34	75	43	38	30
ENSMUSG00000028706	chr4	Nsun4	1.16E+08	1.16E+08	5993	-0.64527	4.681105	0.000465	0.001893	0.038001	-1	396	247	611	618	695	269	499	267	482	335
ENSMUSG00000045817	chr17	Zfp36l2	84183931	84187156	3530	0.594824	4.191645	0.000465	0.001894	0.031007	1	205	173	345	177	277	325	447	482	365	350
ENSMUSG00000006850	chr18	Tmco6	36735068	36735256	1817	0.652529	3.229173	0.000465	0.001895	0.033341	1	101	104	130	115	116	174	220	178	298	169
ENSMUSG00000001666	chr10	Ddt	75771230	75771506	773	0.614106	4.426086	0.00047	0.001911	0.033651	1	235	171	255	339	347	412	519	483	556	383
ENSMUSG00000050965	chr11	Prkca	1.08E+08	1.08E+08	8992	-0.61152	6.094271	0.00047	0.001911	0.035457	-1	996	714	2409	1169	1709	735	1429	802	1203	848
ENSMUSG00000020840	chr11	Blmh	76924809	76924877	5891	0.495207	5.379393	0.000471	0.001917	0.022375	1	488	426	711	477	667	770	1015	814	1106	735
ENSMUSG00000035890	chr10	Rnf126	79758515	79759236	1639	-0.50954	5.01509	0.000472	0.001918	0.023385	-1	478	422	889	626	675	422	497	487	638	386
ENSMUSG00000028229	chr4	Rmdn1	19575162	19575327	1963	-0.80624	4.115366	0.000475	0.001932	0.059481	-1	228	181	342	542	491	151	358	177	273	212
ENSMUSG00000020290	chr11	Xpo1	23256041	23256162	7181	-0.5103	4.853474	0.000478	0.001941	0.023428	-1	479	428	749	475	592	313	595	422	477	383
ENSMUSG00000050071	chrX	Bex1	1.36E+08	1.36E+08	1186	0.670885	3.997044	0.000479	0.001947	0.039362	1	174	193	282	146	172	294	463	255	434	340
ENSMUSG00000045210	chr1	Vcpip1	9718622	9725350	9749	-0.59932	4.009625	0.00048	0.001948	0.031254	-1	216	218	501	274	389	138	251	268	315	205
ENSMUSG00000070780	chr5	Rbm47	66016549	66019436	6859	1.71337	0.595286	0.00048	0.001948	0.203568	1	16	14	12	2	5	33	27	71	26	31
ENSMUSG00000035093	chr2	Secisbp2l	1.26E+08	1.26E+08	8222	-0.55526	4.237776	0.000481	0.001951	0.026839	-1	254	265	574	330	415	178	321	312	324	260
ENSMUSG00000032372	chr9	Plscr2	92275602	92276018	3180	1.4075	0.600379	0.000481	0.001952	0.131236	1	8	11	14	11	16	10	81	44	27	28
ENSMUSG00000039841	chr6	Zfp800	28239931	28241657	4827	-0.95466	1.111057	0.000482	0.001955	0.057325	-1	30	26	84	30	59	14	33	28	35	20
ENSMUSG00000019467	chr10	Arhgef25	1.27E+08	1.27E+08	2387	0.528134	3.872818	0.000483	0.001959	0.023049	1	170	130	261	185	218	269	321	329	392	252
ENSMUSG00000032097	chr9	Ddx6	44604892	44604984	6065	-0.51259	6.798586	0.000485	0.001965	0.02519	-1	1821	1452	3283	1770	2403	1287	1916	1658	2026	1503
ENSMUSG00000017493	chr11	Igfbp4	99041244	99041845	4416	0.737011	6.242051	0.000487	0.001973	0.052034	1	794	808	1304	668	959	1460	1677	2528	1524	1272
ENSMUSG00000034906	chr2	Ncaph	1.27E+08	1.27E+08	4307	1.163114	0.395568	0.000488	0.001977	0.075586	1	9	10	19	6	16	35	30	36	23	23
ENSMUSG00000064215	chr12	Ifi27	1.03E+08	1.03E+08	1467	0.808225	5.281013	0.000489	0.001979	0.061587	1	450	455	494	355	417	786	775	1333	866	650
ENSMUSG00000020654	chr12	Adcy3	4133103	4133778	6246	0.922217	1.929874	0.000489	0.001981	0.065008	1	34	27	52	30	65	57	79	128	85	85
ENSMUSG00000019843	chr10	Fyn	39368855	39369065	4363	0.600722	3.521858	0.000491	0.001988	0.030592	1	107	78	227	150	190	184	261	271	296	236
ENSMUSG00000031453	chr8	Rasa3	13566950	13568766	5093	0.680513	4.112589	0.000492	0.00199	0.041612	1	186	160	311	176	237	332	422	549	334	268
ENSMUSG00000030421	chr7	Uri1	37960002	37961697	3431	-0.53961	4.801931	0.000493	0.001992	0.026481	-1	447	360	881	504	514	296	534	355	592	337
ENSMUSG00000048878	chr11	Hexim1	1.03E+08	1.03E+08	3495	0.521305	4.851148	0.000493	0.001994	0.024447	1	295	293	473	375	463	460	626	654	804	553
ENSMUSG00000000056	chr11	Narf	1.21E+08	1.21E+08	4806	-0.54317	6.98538	0.000494	0.001997	0.028498	-1	1856	1549	3671	2494	2804	1229	2498	1703	2281	1824
ENSMUSG00000032596	chr9	Uba7	1.08E+08	1.08E+08	6692	0.737453	2.460872	0.000494	0.001997	0.041499	1	48	44	100	74	63	118	139	136	111	101
ENSMUSG00000032293	chr9	Ireb2	54863755	54863896	5808	-0.50086	5.068287	0.000495	0.002001	0.022838	-1	467	416	955	604	795	366	669	451	630	448
ENSMUSG00000044968	chr5	Napepld	21662901	21665362	3956	-0.59412	3.873727	0.000496	0.002002	0.030696	-1	212	173	397	297	364	145	343	180	272	153
ENSMUSG00000043496	chr6	Tril	53815466	53820830	5365	0.815831	2.458186	0.000496	0.002004	0.0546	1	50	35	123	51	68	117	102	117	137	137
ENSMUSG00000025380	chr11	Fscn2	1.2E+08	1.2E+08	2110	-2.07051	0.730316	0.000497	0.002006	0.332156	-1	32	37	73	17	50	20	3	1	29	2
ENSMUSG00000026810	chr2	Dpm2	32570858	32570912	1971	0.678584	3.298408	0.000498	0.002007	0.037847	1	139	87	140	109	115	194	278	227	259	141
ENSMUSG00000040482	chr17	Dxo	34837019	34837216	1961	0.721666	2.853668	0.000498	0.002007	0.040878	1	77	63	92	115	76	126	174	166	214	131
ENSMUSG00000022098	chr14	Bmp1	70474557	70475249	3757	0.581985	4.49676	0.000498	0.002008	0.030821	1	238	168	437	276	369	458	454	545	509	442
ENSMUSG00000016940	chr11	Kctd2	1.15E+08	1.15E+08	3009	0.613666	4.31466	0.000499	0.002011	0.033461	1	223	180	238	310	282	334	515	490	552	314
ENSMUSG00000035064	chr7	Eef2k	1.21E+08	1.21E+08	7166	-0.56369	6.2511	0.000499	0.002011	0.030423	-1	1334	926	2523	1178	1559	960	1343	997	1501	861
ENSMUSG00000030401	chr7	Rtn2	19282662	19282865	2034	0.564929	10.08	0.000499	0.002012	0.031321	1	13938	11272	18740	11919	13495	19437	26234	22054	31134	19664
ENSMUSG00000087221	chr15	BC037032	4020114	4024492	7125	-1.41793	0.48567	0.0005	0.002012	0.133285	-1	13	10	46	41	50	8	18	4	15	19
ENSMUSG00000034738	chr2	Nostrin	69135800	69135916	1888	1.232477	0.280149	0.000503	0.002024	0.090519	1	4	4	24	12	11	33	33	21	23	27
ENSMUSG00000023118	chr7	Sympk	19024377	19024506	7777	-0.54467	6.756455	0.000503	0.002024	0.028642	-1	1444	1283	3006	2335	2508	1165	1950	1407	2075	1505
ENSMUSG00000030432	chr7	Rpl28	4792874	4792998	1138	0.560198	7.238429	0.000504	0.002028	0.030444	1	1913	1529	2277	1950	1951	2774	3573	3295	4239	2585
ENSMUSG00000048758	chr9	Rpl29	1.06E+08	1.06E+08	796	0.527059	6.9575	0.000504	0.002029	0.026844	1	1587	1181	1986	1621	1731	2245	3128	2530	3463	2110
ENSMUSG00000025591	chr8	Tma16	66474330	66476909	4752	-0.63143	2.935961	0.000508	0.00204	0.031037	-1	119	121	214	124	165	93	152	82	127	92
ENSMUSG00000064127	chrX	Med14	12675369	12677651	8763	-0.5538	4.829997	0.000507	0.00204	0.027963	-1	435	275	880	540	698	346	535	365	530	343
ENSMUSG00000059555	chr2	Tor4a	25192966	25195925	3301	0.876515	1.649803	0.000508	0.002044	0.054492	1	26	23	41	21	63	65	91	70	76	54
ENSMUSG00000052105	chr17	Mtcl1	66336982	66338154	9268	-0.95783	2.009795	0.000509	0.002046	0.072348	-1	34	46	140	104	114	37	75	34	57	44
ENSMUSG00000038914	chr2	Dido1	1.81E+08	1.81E+08	13307	-0.60599	4.091512	0.00051	0.002048	0.032414	-1	194	203	576	350	396	168	293	255	302	220
ENSMUSG00000001034	chr11	Mapk7	61488812	61489270	4394	0.700583	2.260175	0.000511	0.00205	0.033634	1	52	49	75	47	61	86	117	104	117	100
ENSMUSG00000054404	chr11	Slfn5	82951349	82951481	4427	-0.79158	3.821325	0.000511	0.00205	0.057089	-1	183	180	477	252	404	111	371	188	155	142
ENSMUSG00000001435	chr10	Col18a1	77052178	77053407	7021	0.683392	4.27296	0.000516	0.002071	0.043123	1	194	126	376	246	284	302	375	424	465	550
ENSMUSG00000027684	chr3	Mecom	29951296	29952850	12427	-0.81068	2.023031	0.000516	0.002071	0.048478	-1	46	43	118	99	115	37	68	51	66	44

ENSMUSG00000028878	chr4	Fam76a	1.33E+08	1.33E+08	3088	-0.49547	5.15421	0.000521	0.002088	0.022692	-1	595	515	930	612	689	411	655	460	719	476
ENSMUSG00000027706	chr3	Sec62	30792875	30793383	4343	-0.54139	5.775116	0.000521	0.002091	0.02798	-1	792	914	1413	885	1194	528	1064	817	976	735
ENSMUSG00000025812	chr8	Pard3	1.27E+08	1.27E+08	14506	-0.51855	4.888992	0.000522	0.002091	0.02449	-1	492	326	868	497	698	332	533	388	551	426
ENSMUSG00000033805	chr5	Ephx4	1.07E+08	1.07E+08	1646	1.312947	-0.31459	0.000522	0.002091	0.073611	1	4	3	11	4	10	16	17	23	24	9
ENSMUSG00000010608	chr12	Rbm25	83631236	83631356	17376	-0.53061	5.506028	0.000523	0.002094	0.026584	-1	669	755	1173	698	1007	498	829	642	781	648
ENSMUSG00000020253	chr9	Ppm1m	1.06E+08	1.06E+08	3485	0.964563	2.620757	0.000524	0.002096	0.079461	1	58	57	89	53	69	118	133	256	120	87
ENSMUSG00000027427	chr2	Polr3f	1.45E+08	1.45E+08	7710	-0.58013	3.353857	0.000524	0.002096	0.027396	-1	168	153	287	161	214	109	204	154	157	123
ENSMUSG00000046546	chr16	Fam43a	30599723	30602797	3075	0.604308	3.263116	0.000526	0.002104	0.029683	1	94	74	149	120	178	148	263	226	250	168
ENSMUSG00000025731	chr17	0610011F06Rik	25875464	25875726	1109	0.518708	4.851163	0.000528	0.002111	0.024365	1	393	274	457	339	420	496	796	548	732	538
ENSMUSG00000024818	chr19	Slc25a45	5877808	5878095	2650	0.970062	1.360847	0.000529	0.002115	0.066824	1	29	17	39	11	39	62	61	61	65	43
ENSMUSG00000047888	chr15	Tnrc6b	80711319	80711488	17327	-0.66311	5.501906	0.000529	0.002115	0.042103	-1	604	473	1770	784	1123	380	797	562	883	634
ENSMUSG00000028668	chr4	Tceb3	1.36E+08	1.36E+08	4708	-0.51893	6.082741	0.00053	0.002116	0.025822	-1	1094	859	1964	1178	1441	872	1288	822	1209	907
ENSMUSG00000030584	chr7	Dpf1	29303951	29304112	3529	-1.38991	0.339403	0.000529	0.002116	0.11914	-1	35	11	42	20	31	18	5	14	15	5
ENSMUSG00000031156	chrX	Slc35a2	7884041	7884433	3081	0.567939	3.487565	0.00053	0.002117	0.026165	1	136	94	164	145	179	191	267	217	319	220
ENSMUSG00000011257	chr4	Pabpc4	1.23E+08	1.23E+08	4027	-0.51609	7.953466	0.000531	0.00212	0.026227	-1	3997	3156	6192	4973	5289	3001	4299	3119	4912	3396
ENSMUSG00000042766	chr3	Trim46	89234177	89235292	3792	1.429776	-0.34077	0.000533	0.002128	0.079065	1	3	7	2	9	7	18	18	17	20	15
ENSMUSG00000063972	chr2	Nr6a1	38723370	38727915	7488	-0.83984	1.789358	0.000533	0.002128	0.050672	-1	73	49	102	53	72	35	66	53	37	30
ENSMUSG00000032418	chr9	Me1	86581371	86582907	3848	-0.76902	8.1373	0.000533	0.002128	0.058142	-1	5751	5749	8587	3140	4672	3385	3921	3957	4620	3033
ENSMUSG00000002844	chr16	Adprh	38445399	38446104	1583	0.491747	5.32599	0.000534	0.00213	0.022438	1	419	392	657	565	644	631	1069	768	1114	740
ENSMUSG00000024799	chr19	Tm7sf2	6062821	6063073	3484	0.63154	3.236389	0.000534	0.00213	0.03219	1	93	96	153	104	141	167	204	214	310	147
ENSMUSG00000005371	chr17	Fbxo11	87990859	87992175	4144	-0.51494	5.360658	0.000535	0.002133	0.024933	-1	642	597	1194	694	790	482	856	501	734	545
ENSMUSG00000037621	chr6	Atoh8	72206177	72207155	2355	0.867699	1.964155	0.000536	0.002137	0.05674	1	30	22	46	61	58	72	122	71	86	93
ENSMUSG00000047824	chr3	Pygo2	89430214	89430453	3631	0.554785	4.110724	0.00054	0.002152	0.026872	1	165	174	311	251	218	287	376	363	496	343
ENSMUSG00000089669	chr11	Tnfsf13	69682846	69683344	1637	0.73408	2.345527	0.00054	0.002152	0.040835	1	42	38	86	65	74	85	152	139	110	82
ENSMUSG00000075700	chr3	Selt	58576636	58576873	3436	-0.52556	7.36899	0.000542	0.002159	0.02718	-1	2614	2305	4689	2925	3316	1766	3290	2120	3075	2283
ENSMUSG00000031149	chrX	Praf2	7728439	7728762	1339	0.719097	2.394695	0.000544	0.002167	0.038011	1	63	46	66	48	87	83	155	106	141	104
ENSMUSG00000063558	chr1	Aox1	58029931	58030058	8690	-0.56448	4.250652	0.00055	0.002188	0.028508	-1	297	276	568	335	362	192	353	307	269	272
ENSMUSG00000025792	chr11	Slc25a10	1.2E+08	1.2E+08	3455	1.320975	3.671979	0.000552	0.002197	0.162341	1	152	71	125	102	119	234	155	769	217	202
ENSMUSG00000022676	chr16	Snai2	14705852	14706052	2031	0.869945	1.098729	0.000555	0.002206	0.044751	1	12	15	36	27	27	41	46	51	58	41
ENSMUSG00000049090	chr18	Zadh2	84088158	84088373	3321	-0.49604	5.77092	0.000555	0.002208	0.02357	-1	909	671	1403	1046	1151	646	1088	718	1132	626
ENSMUSG00000029661	chr6	Col1a2	4504814	4504865	12136	0.770758	8.657748	0.000556	0.002211	0.058879	1	2311	2787	8067	4460	7921	7167	8811	8589	10761	10485
ENSMUSG00000098923	chr1	Tmem185b	1.2E+08	1.2E+08	2824	0.712414	2.533022	0.000557	0.002215	0.039099	1	62	37	78	84	86	83	179	119	163	110
ENSMUSG00000000628	chr6	Hk2	82725025	82727454	5969	-0.66717	8.295174	0.000559	0.00222	0.044214	-1	4162	3288	8004	7673	8823	3154	6167	3192	6503	3765
ENSMUSG00000036459	chr7	Wtip	34109543	34110239	2233	0.723516	2.206928	0.000561	0.002229	0.037698	1	36	48	74	45	71	87	106	106	128	83
ENSMUSG00000092907	chrX	Mir5132	74023528	74023598	71	-1.6223	-0.33244	0.000563	0.002233	0.140597	-1	16	1	28	18	25	4	9	7	3	7
ENSMUSG00000039262	chr2	Prrc2b	32151082	32151291	11262	-0.61054	7.617976	0.000567	0.002249	0.037001	-1	2675	1959	7111	3672	4824	2131	3325	2557	3717	2579
ENSMUSG00000038485	chr11	Socs7	97362551	97363423	7265	-0.51583	6.496682	0.000569	0.002257	0.026043	-1	1459	1046	2776	1507	2018	1042	1645	1278	1790	1107
ENSMUSG00000064289	chr2	Tank	61578585	61578693	6096	-0.56693	3.443428	0.00057	0.002261	0.02651	-1	156	151	322	197	228	113	221	133	187	149
ENSMUSG00000029238	chr5	Clock	76212177	76216878	7478	-0.56935	4.238654	0.000571	0.002263	0.029148	-1	287	200	661	321	421	211	391	251	317	229
ENSMUSG00000039294	chr11	BC017643	1.21E+08	1.21E+08	4213	0.653037	3.060743	0.000571	0.002263	0.034699	1	98	79	145	80	113	157	239	211	190	123
ENSMUSG00000018932	chr11	Map2k3	60932033	60932271	3314	0.549419	7.588904	0.000572	0.002264	0.030014	1	2085	1494	3493	2694	3050	3452	4939	3264	6055	3456
ENSMUSG00000029174	chr5	Tbc1d1	64159451	64160505	7140	-1.15739	5.690606	0.000572	0.002264	0.13004	-1	454	429	1302	1986	1817	218	749	675	577	713
ENSMUSG00000029474	chr5	Rnf34	1.23E+08	1.23E+08	1954	-0.51801	4.469261	0.000574	0.002272	0.024411	-1	358	298	555	408	481	243	421	258	497	274
ENSMUSG00000018428	chr11	Akap1	88830792	88831829	4390	-0.92522	5.919504	0.000576	0.002282	0.083933	-1	801	389	1487	2069	1894	473	1036	645	1002	729
ENSMUSG00000008763	chr3	Man1a2	1.01E+08	1.01E+08	7969	-0.54009	4.034966	0.000577	0.002285	0.025433	-1	214	213	516	294	364	191	275	262	293	196
ENSMUSG00000019055	chr4	Plod1	1.48E+08	1.48E+08	6765	0.557117	5.355926	0.000578	0.002288	0.029857	1	384	307	727	601	708	753	856	943	1054	792
ENSMUSG00000002043	chr7	Trappc6a	19508670	19508832	1317	1.034704	1.482348	0.00058	0.002295	0.075391	1	37	25	18	25	29	48	63	82	74	58
ENSMUSG00000038872	chr8	Zfhx3	1.09E+08	1.09E+08	17569	-0.6718	3.603013	0.000581	0.002297	0.039662	-1	169	136	446	204	299	106	168	181	229	169
ENSMUSG00000002781	chr7	Tmem143	45896941	45897101	5636	-0.55376	5.815908	0.000584	0.002308	0.029865	-1	858	629	1318	1306	1338	549	1094	804	1126	680
ENSMUSG00000025223	chr19	Ldb1	46032593	46033341	3583	0.512581	4.541604	0.000584	0.002308	0.023771	1	262	203	388	320	373	384	537	514	707	374
ENSMUSG00000058258	chr13	Idi1	8885501	8885996	3505	-0.79166	1.37448	0.000584	0.002308	0.038801	-1	42	40	61	44	68	24	46	38	35	25
ENSMUSG00000083563	chr2	Gm13340	22588103	22589647	1545	-0.86819	3.010755	0.000585	0.002311	0.067799	-1	74	111	222	238	200	52	162	88	138	92
ENSMUSG00000042726	chr5	Trafd1	1.21E+08	1.21E+08	4486	0.485873	5.483366	0.000586	0.002312	0.022371	1	513	465	790	548	670	776	1042	983	1192	770
ENSMUSG00000085385	chr2	9430008C03Rik	1.58E+08	1.58E+08	7052	0.889133	1.481706	0.000586	0.002313	0.051893	1	35	26	39	22	26	64	78	62	68	43
ENSMUSG00000037062	chr3	Sh3glb1	1.45E+08	1.45E+08	3949	-0.56503	7.69548	0.000587	0.002318	0.031909	-1	2851	2498	5347	4784	4753	2293	3694	2572	4507	2494
ENSMUSG00000024019	chr17	Cmtr1	29660595	29660771	7890	-0.51446	5.545306	0.00059	0.002327	0.025361	-1	716	482	1434	915	1021	540	840	675	870	604
ENSMUSG00000052825	chr8	Gm9892	52196065	52197056	992	-0.69823	3.484566	0.00059	0.002327	0.043738	-1	189	212	338	172	183	123	234	119	165	140
ENSMUSG00000029468	chr5	P2rx7	1.23E+08	1.23E+08	5408	0.723155	1.886583	0.000592	0.002334	0.035204	1	38	28	64	37	53	72	86	82	85	77
ENSMUSG00000093930	chr13	Hmgcs1	1.2E+08	1.2E+08	3233	-0.55757	5.046047	0.000593	0.002337	0.029631	-1	479	465	843	621	776	267	555	520	668	463
ENSMUSG00000034320	chr18	Slc26a2	61192919	61199658	12370	-0.59105	3.351084	0.000594	0.002342	0.029205	-1	145	150	284	166	247	103	195	125	167	151
ENSMUSG00000029208	chr5	Guf1	69556924	69557165	9114	-0.53487	4.324984	0.000597	0.002351	0.026005	-1	314	270	430	417	461	219	428	248	337	273
ENSMUSG00000046828	chr1	Mettl21e	44204070	44206753	3961	-1.0443	1.780039	0.000598	0.002354	0.091017	-1	69	55	124	29	94	24	59	31	71	23
ENSMUSG00000100164	chr6	2610306M01Rik	86848399	86849440	1042	0.775001	2.41622	0.0006	0.002363	0.046357	1	72	41	54	65	70	104	162	101	151	89
ENSMUSG00000079018	chr15	Ly6c1	75044018	75044332	1677	0.623392	5.893229	0.000602	0.002368	0.038159	1	598	581	835	810	895	1339	1633	1451	1195	877
ENSMUSG00000027312	chr2	Atrn	1.31E+08	1.31E+08	13208	-0.59321	4.481294	0.000602	0.00237	0.032666	-1	297	232	754	456	515	214	360	340	401	312

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ENSMUSG00000001376	chr6	Ccdc132	3498382	3498555	9936	-0.50289	4.96432	0.000603	0.002372	0.02376	-1	565	414	855	516	603	335	612	404	598	433
ENSMUSG00000020029	chr10	Nudt4	95547007	95549490	3231	-0.55414	8.773009	0.000604	0.002376	0.030976	-1	6110	6418	13089	7276	9767	4404	8694	6042	7093	6367
ENSMUSG00000047907	chr2	Tshz2	1.7E+08	1.7E+08	7781	-0.65081	3.398757	0.000606	0.002383	0.036609	-1	115	135	315	205	295	96	183	150	193	131
ENSMUSG00000058486	chr6	Wdr91	34880426	34880968	2990	0.663491	2.558278	0.000608	0.002389	0.034377	1	62	44	116	59	87	96	133	148	159	110
ENSMUSG00000020785	chr11	Camkk1	73019008	73019127	3728	1.085912	0.151164	0.000608	0.00239	0.053859	1	6	7	13	12	13	14	27	22	32	28
ENSMUSG00000028096	chr3	Gpr89	96868281	96871594	5365	-0.49127	4.511721	0.000609	0.002393	0.021772	-1	350	278	675	423	456	266	389	328	453	300
ENSMUSG00000022754	chr16	Tmem45a	56805161	56806776	3056	0.915858	1.168208	0.00061	0.002396	0.054603	1	16	15	33	18	39	42	58	59	42	49
ENSMUSG00000021678	chr13	F2rl1	95511732	95514281	2754	1.308239	-0.02942	0.000612	0.002402	0.081055	1	9	7	9	6	8	12	21	23	22	32
ENSMUSG00000037001	chr11	Zfp39	58888153	58891546	3890	-0.81489	2.035438	0.000612	0.002402	0.050608	-1	66	45	118	74	120	34	75	35	61	62
ENSMUSG00000064225	chr9	Paqr9	95559657	95568023	8367	-1.80029	2.002393	0.000614	0.002409	0.288912	-1	29	23	90	177	196	17	17	78	24	18
ENSMUSG00000031813	chr8	Mvb12a	71542930	71543057	1060	0.543212	4.121385	0.000615	0.002412	0.026199	1	187	151	253	273	264	310	480	327	487	290
ENSMUSG00000049932	chr9	H2afx	44334694	44336077	1384	0.696111	2.72049	0.000616	0.002413	0.038156	1	77	63	90	65	98	138	153	160	176	100
ENSMUSG00000031438	chrX	Rnf128	1.4E+08	1.4E+08	3464	-0.56783	4.63246	0.000617	0.002419	0.030433	-1	378	348	635	520	498	208	474	439	422	303
ENSMUSG00000062093	chr14	Gm10110	89896223	89896981	2169	-0.54781	3.728379	0.000617	0.002419	0.025738	-1	214	193	325	244	278	182	233	153	218	184
ENSMUSG00000034158	chr16	Lrrc58	37868389	37868980	8604	-0.52587	4.993697	0.000617	0.002419	0.026123	-1	468	424	950	544	697	366	473	560	580	394
ENSMUSG00000024843	chr19	Chka	3851773	3852413	12024	0.993766	0.878284	0.000622	0.002436	0.064645	1	9	12	34	19	21	36	31	50	48	40
ENSMUSG00000028059	chr3	Arhgef2	88607454	88607580	9496	0.524718	4.395408	0.000623	0.00244	0.025319	1	193	167	412	283	368	349	591	383	592	374
ENSMUSG00000023022	chr15	Lima1	99778470	99781290	7167	0.561903	4.307162	0.000624	0.002444	0.029278	1	179	160	360	237	380	328	555	466	417	375
ENSMUSG00000037337	chr7	Map4k1	28982854	28983054	2699	1.130404	0.64079	0.000626	0.00245	0.079889	1	11	15	20	11	15	44	31	45	30	25
ENSMUSG00000020277	chr10	Pfkl	77986947	77988357	4395	0.694848	3.794237	0.000629	0.002459	0.044227	1	172	110	181	183	189	201	291	439	345	267
ENSMUSG00000031511	chr8	Arhgef7	11728105	11728416	13075	-0.62264	5.310294	0.000632	0.00247	0.037891	-1	486	398	1047	1045	1008	442	710	558	731	441
ENSMUSG00000020687	chr11	Cdc27	1.05E+08	1.05E+08	6248	-0.50568	4.653377	0.000633	0.002473	0.023712	-1	366	362	756	404	520	279	493	343	457	339
ENSMUSG00000029684	chr6	Wasl	24613805	24616346	4923	-0.51256	4.106617	0.000633	0.002474	0.023166	-1	263	239	442	299	390	198	279	298	284	225
ENSMUSG00000047216	chr1	Cdh19	1.11E+08	1.11E+08	4280	-1.31798	0.234324	0.000633	0.002474	0.108273	-1	14	17	43	19	35	3	20	8	7	18
ENSMUSG00000027281	chr2	Slx4ip	1.37E+08	1.37E+08	5905	-0.90492	1.941124	0.000634	0.002474	0.062818	-1	61	54	137	53	101	50	37	55	41	47
ENSMUSG00000031700	chr8	Gpt2	85492576	85492689	5643	-0.78911	7.949086	0.000634	0.002476	0.062841	-1	4931	4647	7477	3518	4199	3945	4122	2987	3646	1740
ENSMUSG00000103212	chr1	AC132393.1	1.2E+08	1.2E+08	1788	0.707753	2.497367	0.000635	0.002479	0.03883	1	62	36	76	80	85	83	175	113	160	106
ENSMUSG00000021224	chr12	Numb	83794034	83796154	3823	-0.54018	3.893732	0.000637	0.002486	0.025405	-1	204	185	460	263	339	167	273	211	232	215
ENSMUSG00000027650	chr2	Tti1	1.58E+08	1.58E+08	4129	-0.48353	4.656323	0.000638	0.002487	0.021501	-1	388	309	709	461	535	287	518	346	453	331
ENSMUSG00000049307	chr9	Fut4	14748459	14752122	3664	1.214453	0.277182	0.000638	0.002487	0.090352	1	7	3	13	18	12	12	45	33	28	23
ENSMUSG00000098457	chr15	Mir8097	36240046	36240164	119	0.966007	0.42992	0.000638	0.002487	0.041225	1	11	7	17	16	16	21	38	30	36	24
ENSMUSG00000098381	chr3	Mir7225	97690509	97690562	54	0.512008	8.264259	0.000639	0.002489	0.026622	1	3747	2729	5847	3897	4357	5189	8153	5520	8976	5597
ENSMUSG00000050212	chr4	Eva1b	1.26E+08	1.26E+08	1942	0.751047	2.240322	0.00064	0.002494	0.043929	1	44	37	71	51	76	85	90	115	113	114
ENSMUSG00000002365	chr17	Snx9	5841328	5841546	2411	-0.52048	4.652609	0.000643	0.002504	0.025297	-1	390	306	702	481	541	242	513	357	415	371
ENSMUSG00000028692	chr4	Akr1a1	1.17E+08	1.17E+08	2750	0.604535	7.966225	0.000645	0.002513	0.037074	1	3269	2860	3728	2588	3020	5070	6606	5138	6681	4107
ENSMUSG00000032328	chr9	Tmem30a	79768943	79771479	5646	-0.56103	6.723593	0.000647	0.002518	0.031677	-1	1594	1794	2836	1660	2201	1009	1759	1598	1971	1508
ENSMUSG00000039236	chr7	Isg20	78913424	78913494	1826	1.053446	0.801849	0.000648	0.002523	0.066335	1	17	15	23	11	18	40	55	45	41	19
ENSMUSG00000038417	chr10	Fig4	41188172	41188699	3263	-0.53723	3.498891	0.000648	0.002523	0.02421	-1	181	155	333	189	225	116	204	164	213	147
ENSMUSG00000032348	chr9	Gsta4	78191966	78192064	957	-0.69782	3.232637	0.000649	0.002523	0.043296	-1	126	133	199	252	211	99	137	144	186	90
ENSMUSG00000043702	chr14	Pde12	26659958	26665967	7725	-0.66916	2.936171	0.000649	0.002524	0.037294	-1	129	97	244	127	168	75	159	119	93	90
ENSMUSG00000020415	chr11	Pttg1	43420250	43420408	2000	0.812922	1.31348	0.00065	0.002527	0.040361	1	23	15	37	34	30	47	73	50	53	51
ENSMUSG00000032849	chr14	Abcc4	1.18E+08	1.18E+08	5729	-0.55881	3.919812	0.00065	0.002527	0.027683	-1	220	155	472	282	371	157	261	236	265	198
ENSMUSG00000020454	chr11	Eif4enif1	3202392	3202556	6370	-0.47953	5.119518	0.000653	0.002536	0.021787	-1	503	406	949	683	780	427	631	492	637	466
ENSMUSG00000019790	chr10	Stxbp5	9755547	9760954	12871	-0.57385	3.733636	0.000654	0.002538	0.028835	-1	196	157	457	212	301	146	239	212	221	157
ENSMUSG00000025358	chr10	Cdk2	1.29E+08	1.29E+08	2432	0.697907	2.211666	0.000657	0.002549	0.035788	1	53	36	68	60	59	92	99	104	123	87
ENSMUSG00000031458	chr8	Coprs	13884788	13885201	802	0.74002	2.700493	0.000657	0.002549	0.045375	1	51	54	80	106	91	116	177	109	211	125
ENSMUSG00000032911	chr9	Cspg4	56865104	56865277	8050	0.698915	3.578391	0.000657	0.002549	0.044965	1	116	74	206	136	218	152	269	235	415	284
ENSMUSG00000038374	chr3	Rbm8a	96629928	96630028	2604	0.575541	4.973989	0.000657	0.002549	0.031633	1	411	366	488	341	358	552	856	656	860	530
ENSMUSG00000046603	chr9	Tcaim	1.23E+08	1.23E+08	3126	-0.64415	5.083559	0.000657	0.002549	0.040765	-1	403	410	811	863	892	280	637	425	688	442
ENSMUSG00000074671	chr2	Tspyl3	1.53E+08	1.53E+08	3072	1.075103	0.474705	0.000659	0.002556	0.06539	1	6	12	19	13	16	27	29	42	27	29
ENSMUSG00000004455	chr5	Ppp1cc	1.22E+08	1.22E+08	3424	-0.51896	5.96712	0.000661	0.002564	0.026768	-1	1122	797	1550	1152	1312	790	1253	903	1163	645
ENSMUSG00000031400	chrX	G6pdx	74409483	74410297	3080	1.034139	3.349002	0.000664	0.002572	0.100915	1	113	88	154	76	95	205	188	473	186	147
ENSMUSG00000050174	chr3	Nudt6	37404910	37405494	1635	-0.61077	3.679012	0.000665	0.002576	0.034023	-1	224	159	275	277	299	120	274	160	267	129
ENSMUSG00000018796	chr8	Acsl1	46471041	46471230	9449	-0.95162	7.854273	0.000666	0.002579	0.091571	-1	2926	2006	4923	8576	6625	1825	3159	4317	3015	2114
ENSMUSG00000051518	chr15	Rps19bp1	80260614	80261130	830	0.784813	2.929905	0.000667	0.002583	0.052634	1	94	74	90	93	77	171	202	152	253	98
ENSMUSG00000005148	chr14	Klf5	99298691	99299222	1721	1.076931	1.706385	0.000669	0.002587	0.09767	1	17	14	47	46	44	44	97	51	77	116
ENSMUSG00000022205	chr15	Sub1	11981339	11984297	3930	-0.69452	5.928344	0.000672	0.0026	0.04853	-1	1188	1239	1683	744	1022	749	1043	773	1029	666
ENSMUSG00000026387	chr1	Sctr	1.2E+08	1.2E+08	2012	0.830286	2.964813	0.000672	0.0026	0.060392	1	108	75	96	87	61	153	171	133	256	182
ENSMUSG00000041794	chr9	Myrip	1.2E+08	1.2E+08	5440	-1.16373	0.343432	0.000674	0.002605	0.076806	-1	11	26	42	23	30	12	18	11	9	15
ENSMUSG00000038976	chr11	Ppp1r9b	94991035	94992918	5083	0.51644	5.061828	0.000677	0.002616	0.025761	1	341	289	586	450	571	599	689	785	881	602
ENSMUSG00000042918	chr7	Mamstr	45639977	45640030	4877	0.667483	5.09783	0.000678	0.002619	0.043763	1	438	387	577	229	459	611	980	826	838	587
ENSMUSG00000063382	chr9	Bcl9l	44499136	44499273	5304	-0.68506	4.393206	0.000678	0.002619	0.045251	-1	285	209	697	393	605	153	389	255	376	318
ENSMUSG00000024561	chr18	Mbd1	74268272	74268433	2689	-0.52602	3.680589	0.000679	0.002621	0.023517	-1	215	150	380	212	280	150	226	193	225	162
ENSMUSG00000024283	chr18	Wac	7868832	7869091	5962	-0.48845	4.839457	0.000681	0.00263	0.022527	-1	457	392	811	495	553	370	552	434	488	333
ENSMUSG00000036737	chr9	Oxsr1	1.19E+08	1.19E+08	5350	-0.48357	6.776197	0.000684	0.002641	0.023662	-1	1688	1435	2981	2065	2223	1318	2104	1528	2119	1363

ENSMUSG00000046798	chr5	Cldn12	5505015	5508454	4169	-0.51074	4.237628	0.000685	0.002644	0.02386	-1	274	254	558	338	384	189	389	296	343	222
ENSMUSG00000034472	chr8	Rasd2	75213944	75214078	3176	-1.27652	6.127333	0.000686	0.002647	0.162382	-1	1844	1656	3085	517	733	797	740	595	1340	332
ENSMUSG00000021377	chr13	Dek	47084775	47086079	3089	-0.49432	4.982696	0.000687	0.002648	0.023487	-1	491	473	892	518	610	357	635	435	628	377
ENSMUSG00000045691	chr14	Thtpa	55053884	55054019	5967	-0.50947	4.614109	0.000687	0.002648	0.024316	-1	378	285	567	523	574	312	473	303	436	323
ENSMUSG00000058355	chr8	Abce1	79683442	79685277	3813	-0.5056	5.956204	0.000687	0.00265	0.02546	-1	910	771	1758	1159	1384	796	1292	849	1021	751
ENSMUSG00000021930	chr14	Spryd7	61531993	61535241	4002	-0.6287	5.684051	0.000689	0.002655	0.039743	-1	1033	900	1404	715	867	534	981	589	1074	595
ENSMUSG00000029405	chr5	G3bp2	92052146	92055053	4677	-0.50646	6.442182	0.000692	0.002667	0.025889	-1	1318	1113	2512	1490	1951	870	1617	1327	1599	1207
ENSMUSG00000070392	chr3	Gm20634	96245554	96248509	2956	-0.85908	1.930826	0.000692	0.002667	0.058545	-1	76	66	107	53	82	53	45	50	67	26
ENSMUSG00000044949	chr11	Ubtd2	32455370	32455546	1012	-0.74913	1.569145	0.000694	0.00267	0.035875	-1	44	43	91	52	64	33	52	34	38	38
ENSMUSG00000060419	chr5	Rps16-ps2	1.29E+08	1.29E+08	441	0.599207	3.82244	0.000694	0.002672	0.031906	1	184	164	197	143	183	250	377	301	374	248
ENSMUSG00000006304	chr1	Arpc2	74236084	74236322	2033	0.526678	6.340213	0.000697	0.002679	0.027915	1	978	887	1324	980	1080	1539	2061	1617	2092	1418
ENSMUSG00000044339	chr5	Alkbh2	1.14E+08	1.14E+08	1115	1.435184	-0.11701	0.000696	0.002679	0.09993	1	11	6	4	7	5	24	28	11	30	14
ENSMUSG00000041297	chr13	Cdk13	17715962	17718911	7081	-0.61339	3.562749	0.000697	0.002682	0.03301	-1	144	141	394	231	277	133	178	180	190	160
ENSMUSG00000024878	chr19	Cbwd1	24919916	24920702	1944	-0.5315	4.007385	0.000698	0.002682	0.025603	-1	234	236	389	319	341	184	341	189	269	222
ENSMUSG00000026743	chr2	Mllt10	18055237	18055371	5907	-0.59775	3.675951	0.000698	0.002682	0.031882	-1	237	138	424	211	257	138	212	160	225	188
ENSMUSG00000020473	chr11	Aebp1	5861947	5862398	4058	0.732208	6.246586	0.0007	0.002687	0.054518	1	725	715	1953	543	839	1252	1704	1719	2182	1754
ENSMUSG00000085148	chr11	Mir22hg	75461539	75461755	1924	0.576841	4.353293	0.0007	0.002687	0.031099	1	198	219	323	279	281	294	680	362	496	426
ENSMUSG00000037070	chr8	Rbmxl1	78505271	78506863	1723	0.628098	2.635681	0.000701	0.002691	0.030292	1	70	53	93	76	93	122	182	122	150	102
ENSMUSG00000032528	chr9	Vipr1	1.22E+08	1.22E+08	5564	-1.09359	0.62941	0.000701	0.002693	0.076083	-1	11	26	45	35	45	12	23	12	27	12
ENSMUSG00000019975	chr10	Ikbip	91082940	91083296	4894	0.577283	3.31315	0.000705	0.002705	0.027874	1	103	107	167	114	140	190	237	222	228	186
ENSMUSG00000022462	chr15	Slc38a2	96687394	96690228	4626	-0.65879	6.091022	0.000705	0.002706	0.043987	-1	1266	783	2201	1081	1587	901	957	1216	1175	558
ENSMUSG00000028683	chr4	Eif2b3	1.17E+08	1.17E+08	6520	-0.52582	4.163219	0.000706	0.002707	0.025544	-1	316	285	427	299	341	219	339	265	330	194
ENSMUSG00000032826	chr3	Ank2	1.27E+08	1.27E+08	35218	-0.85107	5.385727	0.000706	0.002708	0.073034	-1	513	318	1042	1327	1297	348	904	451	639	455
ENSMUSG00000031928	chr9	Mre11a	14784654	14784757	5902	-0.58579	3.779369	0.000709	0.002718	0.031019	-1	239	149	446	237	288	150	280	151	232	193
ENSMUSG00000061046	chr17	Haghl	25779843	25780154	2643	0.584976	3.657925	0.000711	0.002724	0.030094	1	150	118	172	163	192	250	327	203	334	253
ENSMUSG00000032405	chr9	Pias1	62880077	62882261	3855	-0.60283	3.728102	0.000715	0.002739	0.032822	-1	155	170	463	256	284	141	225	193	213	182
ENSMUSG00000054364	chr12	Rhob	8497763	8499985	2223	0.630619	5.088733	0.000715	0.002739	0.039297	1	281	385	479	408	567	468	1011	823	717	753
ENSMUSG00000028468	chr4	Rgp1	43578715	43579003	6199	-0.51484	5.342224	0.000717	0.002744	0.026095	-1	585	449	1084	870	933	406	736	605	769	560
ENSMUSG00000026580	chr1	Selp	1.64E+08	1.64E+08	4413	1.530293	1.673571	0.000719	0.002752	0.20973	1	21	13	40	14	42	47	246	71	60	18
ENSMUSG00000068551	chr6	Zfp467	48427697	48427879	4255	-0.73729	4.512833	0.00072	0.002755	0.053636	-1	466	463	673	241	394	270	354	317	342	266
ENSMUSG00000104344	chr9	RP23-444I6.3	1.05E+08	1.05E+08	3245	-0.81897	1.606123	0.00072	0.002755	0.047532	-1	51	36	98	46	81	35	62	26	44	30
ENSMUSG00000005417	chr11	Mprip	59661305	59661418	13327	-0.51954	6.533659	0.00072	0.002755	0.02747	-1	1238	1100	2774	1873	2060	1024	1660	1317	1715	1274
ENSMUSG00000032525	chr9	Nktr	1.22E+08	1.22E+08	17457	-0.52114	5.446069	0.000723	0.002765	0.026832	-1	678	449	1387	796	979	507	832	635	708	588
ENSMUSG00000091811	chr7	Inafm1	16272014	16273692	1679	0.538783	4.066345	0.000726	0.002774	0.026075	1	191	188	275	203	219	264	439	400	438	274
ENSMUSG00000026281	chr1	Dtymk	93792576	93792943	2631	0.637793	3.416149	0.000729	0.002783	0.035533	1	151	102	147	102	150	211	313	210	263	180
ENSMUSG00000027854	chr3	Sike1	1.03E+08	1.03E+08	4627	0.501215	3.935103	0.000729	0.002783	0.021977	1	172	159	276	184	220	282	373	283	410	278
ENSMUSG00000045038	chr17	Prkce	86167785	86168940	7261	-0.64139	4.050772	0.000729	0.002783	0.039041	-1	294	265	580	209	292	190	248	250	283	202
ENSMUSG00000007216	chr6	Zfp775	48613180	48613259	4083	-0.59032	3.360889	0.000731	0.002788	0.030591	-1	167	129	236	211	246	98	162	142	232	122
ENSMUSG00000022512	chr16	Cldn1	26356642	26359200	3247	-1.32552	1.35109	0.00073	0.002788	0.149403	-1	21	28	81	82	82	11	55	14	18	32
ENSMUSG00000037855	chr10	Zfp365	67886103	67889091	5205	1.570752	0.850955	0.000731	0.002788	0.20825	1	3	3	7	24	32	21	50	56	77	30
ENSMUSG00000028048	chr3	Gba	89202928	89203086	1950	0.516882	4.195233	0.000732	0.002793	0.024348	1	197	200	359	216	234	310	454	418	443	330
ENSMUSG00000021375	chr13	Kif13a	46749087	46750626	6866	-0.53358	6.76792	0.000733	0.002797	0.029195	-1	1694	1115	3307	2065	2573	1291	1973	1402	2241	1329
ENSMUSG00000054717	chr8	Hmgb2	57511843	57512005	2692	0.833211	2.239322	0.000736	0.002805	0.058352	1	47	31	65	40	88	118	139	94	86	91
ENSMUSG00000038740	chr2	Mvb12b	33729953	33733531	8741	-0.51171	5.919011	0.000739	0.002816	0.026358	-1	914	664	1801	1142	1377	744	1000	822	1196	802
ENSMUSG00000090862	chr7	Rps13	1.16E+08	1.16E+08	582	0.581846	6.93452	0.000739	0.002816	0.034793	1	1555	1409	1725	1455	1459	2303	3290	2445	3345	2086
ENSMUSG00000028693	chr4	Nasp	1.17E+08	1.17E+08	7518	0.527171	3.627365	0.00074	0.002818	0.024099	1	131	119	229	151	183	233	275	274	299	227
ENSMUSG00000037946	chr13	Fgd3	49261554	49264035	6012	0.989437	0.959645	0.00074	0.00282	0.062865	1	12	13	18	33	21	32	46	43	57	43
ENSMUSG00000039232	chr10	Stx11	12939983	12941983	2396	1.414932	-0.10986	0.000742	0.002826	0.119417	1	5	4	2	7	17	18	25	27	14	21
ENSMUSG00000029169	chr5	Dhx15	52150209	52150778	3009	-0.51057	5.287759	0.000745	0.002834	0.02581	-1	604	532	1122	637	851	380	838	552	651	554
ENSMUSG00000036570	chr7	Fxyd1	31051681	31051815	709	0.519236	8.113372	0.000745	0.002834	0.028032	1	3266	2786	4313	3800	3917	4890	7425	4910	7805	5052
ENSMUSG00000035158	chr6	Mitf	97807058	97807287	6215	-0.59948	3.735936	0.000746	0.002838	0.032892	-1	184	134	385	281	346	120	228	191	272	167
ENSMUSG00000032705	chr12	Exd2	80463095	80463280	3323	-0.4796	5.084798	0.000747	0.00284	0.022345	-1	554	418	912	592	743	397	732	483	551	441
ENSMUSG00000074922	chr19	Fam122a	24476502	24477356	855	-0.58287	3.186895	0.000748	0.002843	0.028916	-1	170	114	224	140	229	98	148	137	181	102
ENSMUSG00000023009	chr15	Nckap5l	99422035	99422908	5002	0.800782	1.690869	0.000749	0.002845	0.048168	1	31	16	50	34	56	46	75	71	93	76
ENSMUSG00000032609	chr9	Klhdc8b	1.08E+08	1.08E+08	8419	0.872895	2.659472	0.000749	0.002845	0.066328	1	81	71	87	58	40	134	139	151	181	120
ENSMUSG00000077450	chr17	Rab11b	33742484	33747813	6109	0.496988	6.375459	0.00075	0.002849	0.025173	1	1003	733	1481	1161	1178	1349	2177	1653	2364	1439
ENSMUSG00000030717	chr7	Nupr1	1.27E+08	1.27E+08	2514	0.783595	3.400771	0.000752	0.002855	0.056878	1	143	103	154	101	100	250	219	301	238	170
ENSMUSG00000038085	chr2	Cnbd2	1.56E+08	1.56E+08	3879	1.009726	1.134263	0.000752	0.002855	0.071448	1	32	11	29	18	20	55	46	53	63	33
ENSMUSG00000057440	chr18	Mpp7	7347962	7351144	4975	-0.81545	1.189734	0.000753	0.002858	0.03963	-1	28	33	66	44	57	24	41	29	29	22
ENSMUSG00000024807	chr19	Syvn1	6046576	6047128	4772	0.505793	4.822817	0.000759	0.00288	0.024859	1	338	225	571	331	454	434	640	644	762	548
ENSMUSG00000030699	chr7	Tbx6	1.27E+08	1.27E+08	1804	1.571851	-0.34847	0.000764	0.002897	0.128321	1	1	11	10	1	3	15	21	14	26	15
ENSMUSG00000064193	chr2	Gm4735	80837141	80838442	1302	1.175728	0.323229	0.000766	0.002904	0.084008	1	11	7	16	8	14	24	14	30	49	25
ENSMUSG00000045275	chr16	Lca5l	96158407	96159867	6521	0.977741	0.816687	0.000767	0.002906	0.055889	1	21	12	23	15	17	28	43	28	66	36
ENSMUSG00000056130	chr18	Ticam2	46559155	46561072	3928	1.401427	-0.41175	0.000767	0.002907	0.094812	1	8	2	8	2	8	14	10	17	20	21
ENSMUSG00000040661	chr9	Rad54l2	1.07E+08	1.07E+08	11828	-0.58862	3.511623	0.000769	0.002914	0.030793	-1	146	130	355	215	290	107	206	170	201	150

ENSMUSG00000002718	chr2	Cse1l	1.67E+08	1.67E+08	5273	-0.5125	6.203932	0.00077	0.002915	0.026874	-1	1202	1027	2166	1132	1540	859	1491	949	1294	997
ENSMUSG00000051735	chr7	Rinl	28788969	28789005	2871	1.178115	0.554834	0.00077	0.002915	0.089281	1	10	13	12	14	16	34	26	53	33	21
ENSMUSG00000029465	chr5	Arpc3	1.22E+08	1.22E+08	2581	0.563978	5.565051	0.000773	0.002922	0.031973	1	622	515	629	590	611	928	1310	963	1162	790
ENSMUSG00000030890	chr7	Ilk	1.06E+08	1.06E+08	2744	0.477327	5.634372	0.000773	0.002922	0.022724	1	591	485	791	706	735	870	1253	993	1252	907
ENSMUSG00000036779	chr8	Papd5	88199213	88199313	4937	-0.55337	3.8801	0.000773	0.002922	0.028088	-1	258	171	395	255	345	127	259	224	263	219
ENSMUSG00000046186	chr9	Cd109	78615546	78615952	6900	1.080485	1.896777	0.000772	0.002922	0.104687	1	15	11	54	49	68	53	89	95	97	107
ENSMUSG00000040952	chr7	Rps19	24884371	24884667	4685	0.599529	6.944454	0.000773	0.002924	0.037245	1	1577	1383	1585	1493	1539	2434	3280	2746	3109	1983
ENSMUSG00000030061	chr6	Uba3	97183670	97184865	2589	-0.52017	5.108587	0.000775	0.002928	0.026881	-1	517	535	890	626	686	361	744	421	598	493
ENSMUSG00000030704	chr7	Rab6a	1.01E+08	1.01E+08	3728	-0.51663	6.304826	0.000775	0.002928	0.027418	-1	1398	1126	2206	1197	1591	935	1569	1021	1404	1053
ENSMUSG00000027868	chr3	Tbx15	99240381	99240446	3747	-0.52993	8.624609	0.000776	0.002933	0.02948	-1	5868	4430	11693	6862	10022	4791	6299	5677	7216	5423
ENSMUSG00000039100	chr15	March6	31455899	31459279	6236	-0.52114	7.581059	0.000778	0.002939	0.028369	-1	2896	2412	6108	3320	3940	2062	3441	2575	3895	2570
ENSMUSG00000040209	chr3	Zfp704	9427020	9438898	15255	-0.70581	3.398221	0.00078	0.002943	0.045917	-1	126	111	416	204	250	100	193	154	144	136
ENSMUSG00000026426	chr1	Arl8a	1.35E+08	1.35E+08	2299	0.508772	4.115947	0.000782	0.002951	0.023831	1	203	151	366	197	250	264	423	359	521	306
ENSMUSG00000084817	chr1	Gm5526	45857332	45857754	423	1.18368	0.601475	0.000784	0.002957	0.085855	1	15	17	17	9	8	33	44	45	34	20
ENSMUSG00000038456	chr6	Dennd2a	39462378	39463451	5429	0.720081	2.719321	0.000786	0.002966	0.045643	1	50	42	121	91	102	103	174	187	141	127
ENSMUSG00000035459	chr10	Stab2	86841198	86841658	8757	-1.14609	3.753624	0.000788	0.002973	0.130866	-1	307	251	470	219	229	215	126	80	299	50
ENSMUSG00000022744	chr16	Cldn25	58727910	58728084	2563	-0.49956	4.984045	0.00079	0.002978	0.024571	-1	534	439	938	487	613	346	664	454	563	395
ENSMUSG00000063316	chr11	Rpl27	1.01E+08	1.01E+08	1535	0.610973	6.870964	0.000794	0.002993	0.038826	1	1558	1325	1557	1270	1459	2368	3349	2366	3095	1818
ENSMUSG00000051748	chr11	Wfdc21	83746940	83747123	434	2.381352	0.173403	0.000795	0.002997	0.433474	1	9	7	7	0	1	23	12	83	26	6
ENSMUSG00000033446	chr14	Lpar6	73237895	73243294	5400	0.827008	1.821218	0.000796	0.002998	0.051134	1	45	27	44	45	33	53	85	97	89	73
ENSMUSG00000021147	chr13	Wdr37	8802968	8805946	8729	-0.51724	4.876307	0.000797	0.003003	0.026263	-1	394	391	832	553	660	291	559	389	526	452
ENSMUSG00000038086	chr9	Hspb2	50751072	50751733	840	0.557564	6.313926	0.000798	0.003004	0.032042	1	1034	829	1124	1010	1042	1563	2029	1550	2220	1315
ENSMUSG00000031604	chr8	Msmo1	64718139	64719181	6144	0.697311	2.45628	0.000798	0.003005	0.038548	1	50	55	88	62	74	74	146	139	172	87
ENSMUSG00000026380	chr1	Tfcp2l1	1.19E+08	1.19E+08	9438	-1.40427	3.959732	0.000799	0.003008	0.195997	-1	270	207	848	240	377	290	72	78	256	49
ENSMUSG00000026932	chr2	Nacc2	26055535	26060473	7815	-0.50173	5.095142	0.0008	0.003009	0.02484	-1	522	360	962	649	820	401	692	509	560	432
ENSMUSG00000044252	chr18	Osbpl1a	12755314	12756307	7392	-0.58681	5.397855	0.000801	0.003012	0.035028	-1	554	448	1087	980	1112	410	856	489	797	579
ENSMUSG00000066861	chr5	Oas1g	1.21E+08	1.21E+08	2340	1.706206	-0.56992	0.000805	0.003026	0.141055	1	8	2	1	3	6	11	22	19	6	18
ENSMUSG00000081111	chr8	Gm5913	97427712	97429110	1399	-0.79589	1.303183	0.000805	0.003026	0.039708	-1	39	29	86	45	50	20	40	30	42	28
ENSMUSG00000028413	chr4	B4galt1	40804602	40807317	4234	0.50401	5.686228	0.000808	0.003035	0.025896	1	553	396	1083	637	867	837	1442	1047	1491	797
ENSMUSG00000039985	chr6	Fam60a	1.49E+08	1.49E+08	3851	1.326971	-0.17667	0.000809	0.003039	0.082315	1	6	7	5	5	11	15	36	20	20	10
ENSMUSG00000040820	chr16	Hlcs	94129195	94131965	5060	-0.61174	3.899061	0.00081	0.003043	0.035229	-1	189	147	447	326	395	194	266	166	266	183
ENSMUSG00000038502	chr7	Ptov1	44863068	44863444	4212	0.51871	6.55284	0.000812	0.003047	0.027911	1	1199	918	1640	1144	1267	1580	2053	2050	2716	1717
ENSMUSG00000039478	chr8	Micu3	40307458	40308410	6153	-0.54876	4.230546	0.000812	0.003047	0.028909	-1	285	315	568	272	354	200	361	253	356	235
ENSMUSG00000050552	chr5	Lamtor4	1.38E+08	1.38E+08	1176	0.636185	5.538575	0.000812	0.003047	0.041256	1	629	527	544	549	534	921	1214	934	1387	740
ENSMUSG00000074001	chr9	Klhl40	1.22E+08	1.22E+08	2455	0.541032	7.159676	0.000812	0.003047	0.030665	1	1802	1306	2353	1739	2145	2600	4065	2183	3965	2801
ENSMUSG00000037622	chr4	Wdtc1	1.33E+08	1.33E+08	4800	-0.52779	7.103456	0.000817	0.003063	0.029199	-1	1975	1778	3950	2676	2937	1617	2045	1840	2939	1881
ENSMUSG00000025508	chr7	Rplp2	1.41E+08	1.41E+08	2072	0.596093	7.565975	0.000819	0.003069	0.037377	1	2445	2183	2509	2194	2338	3482	4699	3962	5555	3262
ENSMUSG00000021610	chr13	Clptm1l	73604002	73604399	2378	0.469618	5.233365	0.000819	0.00307	0.021856	1	454	320	647	528	599	639	951	783	1003	631
ENSMUSG00000024539	chr18	Ptpn2	67665511	67665874	3125	0.535253	3.825137	0.000821	0.003075	0.02575	1	154	142	233	182	210	251	455	253	355	228
ENSMUSG00000052331	chr1	Ankrd44	54645340	54648335	14175	-0.76741	2.926781	0.000821	0.003075	0.052876	-1	164	93	267	88	171	104	106	103	106	81
ENSMUSG00000020864	chr11	Ankrd40	94328001	94328387	4255	-0.51222	8.075261	0.000822	0.003077	0.027744	-1	4135	3005	6936	5591	6348	3092	5097	3481	5368	3523
ENSMUSG00000001173	chrX	Ocrl	47912387	47912691	9486	-0.58368	4.304561	0.000823	0.003079	0.033152	-1	398	236	640	268	401	208	402	293	319	233
ENSMUSG00000020467	chr11	Efemp1	28853204	28853324	2037	-0.76818	3.870357	0.000823	0.003079	0.057761	-1	268	244	500	205	270	168	176	272	151	185
ENSMUSG00000059883	chr15	Irak4	94543643	94543826	5021	0.978001	1.548559	0.000823	0.003079	0.079234	1	13	15	54	36	41	67	79	88	55	45
ENSMUSG00000025134	chr11	Alyref	1.21E+08	1.21E+08	3839	0.543157	3.848351	0.000823	0.003079	0.026855	1	180	131	233	186	201	302	353	259	398	235
ENSMUSG00000029499	chr5	Pxmp2	1.1E+08	1.1E+08	1200	0.54394	5.254019	0.000826	0.003087	0.029845	1	369	331	568	611	618	559	1162	722	1005	744
ENSMUSG00000020427	chr11	Igfbp3	7206086	7207506	3130	0.878169	4.36047	0.000828	0.003096	0.07794	1	180	237	366	144	223	363	499	805	352	350
ENSMUSG00000063889	chr18	Crem	3266048	3267732	5895	0.572796	3.245495	0.000829	0.003097	0.027598	1	91	98	141	133	138	154	275	189	252	165
ENSMUSG00000026037	chr1	Orc2	58462771	58464290	3857	-0.50878	3.842321	0.00083	0.0031	0.023296	-1	245	174	340	289	302	178	275	210	230	182
ENSMUSG00000031320	chrX	Rps4x	1.02E+08	1.02E+08	1631	0.579013	8.305937	0.000831	0.003105	0.035517	1	3967	3670	5032	3456	3741	6107	8725	6495	8557	5006
ENSMUSG00000038102	chr8	Trappc11	47490115	47490918	6482	-0.48669	4.829211	0.000832	0.003106	0.023168	-1	445	385	832	421	629	312	548	420	524	373
ENSMUSG00000006169	chr11	Clint1	45852051	45852192	6946	-0.54404	5.11848	0.000833	0.00311	0.029775	-1	531	429	1138	550	773	318	584	540	637	512
ENSMUSG00000042628	chr12	Zfyve1	83546941	83548115	3869	-0.52447	4.646483	0.000834	0.003111	0.026808	-1	409	301	801	389	541	311	410	308	506	341
ENSMUSG00000019864	chr10	Rtn4ip1	43901807	43902536	3135	-0.77441	4.887987	0.000836	0.00312	0.061526	-1	358	282	606	905	914	275	570	312	510	362
ENSMUSG00000029221	chr5	Slc30a9	67306955	67307197	9861	-0.49865	6.451522	0.000837	0.003121	0.025922	-1	1414	1115	2147	1715	1891	1002	1893	1110	1577	1136
ENSMUSG00000032536	chr9	Trak1	1.21E+08	1.21E+08	4883	-0.81775	7.205198	0.000837	0.003121	0.070361	-1	1900	1030	3781	4412	4746	1379	2329	1680	2662	1823
ENSMUSG00000026356	chr1	Dars	1.28E+08	1.28E+08	4358	-0.52953	6.047444	0.00084	0.003129	0.02914	-1	1044	998	1697	1197	1326	693	1509	816	1201	831
ENSMUSG00000026577	chr1	Blzf1	1.64E+08	1.64E+08	5336	-0.48913	4.223536	0.00084	0.003129	0.022366	-1	280	258	528	328	374	224	388	228	338	249
ENSMUSG00000028108	chr3	Ecm1	95734147	95734470	2521	0.637817	5.369377	0.00084	0.003129	0.042053	1	407	291	855	486	660	781	640	989	1268	843
ENSMUSG00000040263	chr8	Klhdc4	1.22E+08	1.22E+08	3708	0.594706	3.22342	0.000842	0.003135	0.030076	1	110	101	151	105	116	175	234	217	239	148
ENSMUSG00000040715	chr4	Rsc1a1	1.42E+08	1.42E+08	1749	-0.69491	4.59534	0.000842	0.003135	0.048903	-1	362	350	927	332	520	280	548	197	415	278
ENSMUSG00000047284	chr11	Neurl4	69901072	69901148	5889	-0.50621	5.169034	0.000844	0.003143	0.02565	-1	507	379	953	743	905	438	634	497	696	460
ENSMUSG00000008140	chr7	Emc10	44489937	44490970	2917	0.50701	5.859324	0.000845	0.003144	0.026435	1	593	544	899	831	992	1018	1302	1225	1660	1025
ENSMUSG00000030304	chr6	Ergic2	1.48E+08	1.48E+08	6727	-0.48712	5.687075	0.000845	0.003144	0.024313	-1	840	785	1327	854	1004	618	1074	660	964	648
ENSMUSG00000001424	chr6	Snd1	28475139	28475207	9757	0.493033	5.933308	0.000847	0.003151	0.024968	1	733	605	1072	769	891	1020	1462	1213	1858	1039

ENSMUSG00000035781	chr10	R3hdm4	79910053	79911139	1897	0.527938	7.437498	0.000848	0.003153	0.029464	1	2186	1776	2905	1920	2537	2971	4137	3417	5367	3007
ENSMUSG00000030256	chr6	Bhlhe41	1.46E+08	1.46E+08	6262	-0.53208	5.682337	0.000849	0.003155	0.029144	-1	937	629	1424	809	1153	603	831	590	1175	679
ENSMUSG00000036672	chr8	Cenpt	1.06E+08	1.06E+08	1767	0.865307	1.17643	0.000855	0.003178	0.047084	1	23	17	24	31	25	47	56	44	71	35
ENSMUSG00000047617	chr2	BC029214	25455141	25455648	2066	0.606292	3.026216	0.000855	0.003178	0.030989	1	97	74	130	99	110	169	217	148	232	124
ENSMUSG00000025766	chr3	D3Ertd751e	41742611	41742689	5813	-0.73366	2.350363	0.000857	0.003181	0.045724	-1	76	83	119	116	104	44	99	85	75	46
ENSMUSG00000037318	chr1	Traf3ip3	1.93E+08	1.93E+08	5756	1.029115	0.384068	0.000857	0.003181	0.054212	1	12	10	18	14	8	28	30	22	42	23
ENSMUSG00000037730	chr3	Mynn	30602065	30602695	6764	-0.57792	3.426005	0.000857	0.003181	0.030301	-1	162	154	334	184	210	98	223	139	185	148
ENSMUSG00000044098	chr3	Rsbn1	1.04E+08	1.04E+08	6861	-0.69246	3.039628	0.000857	0.003181	0.043198	-1	115	112	269	158	175	62	107	131	146	122
ENSMUSG00000021996	chr14	Esd	74732297	74732388	3366	0.569631	5.917863	0.000858	0.003183	0.033576	1	714	707	896	735	744	1234	1615	1164	1638	961
ENSMUSG00000028044	chr3	Cks1b	89415472	89415963	1126	0.957691	1.624923	0.00086	0.003188	0.072314	1	32	32	51	22	23	63	82	89	53	63
ENSMUSG00000045962	chr6	Wnk1	1.2E+08	1.2E+08	15780	-0.57035	8.184499	0.000863	0.003201	0.034684	-1	4531	3218	10567	4577	6488	3619	4656	3796	5578	3755
ENSMUSG00000019054	chr5	Fis1	1.37E+08	1.37E+08	1714	0.565882	6.896407	0.000866	0.00321	0.03378	1	1582	1251	1648	1500	1514	2292	3028	2254	3471	2018
ENSMUSG00000058013	chr5	Sept11	93093457	93093597	5008	0.566108	6.236929	0.000867	0.003212	0.033593	1	719	787	1634	739	1110	1143	2087	1340	2123	1615
ENSMUSG00000037196	chr17	Pacrg	10403012	10403478	1572	0.997843	0.915694	0.000868	0.003214	0.070945	1	10	8	30	27	22	27	53	28	67	43
ENSMUSG00000023046	chr15	Igfbp6	1.02E+08	1.02E+08	1112	0.708902	5.674419	0.000869	0.003218	0.052687	1	364	384	923	639	925	898	990	1525	1003	1190
ENSMUSG00000027377	chr2	Mall	1.28E+08	1.28E+08	2006	0.806844	1.774863	0.000875	0.00324	0.048093	1	23	34	43	41	51	60	72	89	102	60
ENSMUSG00000032625	chr6	Thsd7a	12311610	12317451	13737	-0.98272	1.662613	0.000879	0.003252	0.081523	-1	45	41	162	36	66	29	46	30	54	31
ENSMUSG00000092360	chr10	Gm20441	75771451	75771506	756	0.582586	4.267128	0.00088	0.003258	0.033136	1	212	155	232	304	320	363	461	430	509	330
ENSMUSG00000024206	chr17	Rfx2	56775897	56777074	3353	0.96044	1.945425	0.000881	0.003258	0.081251	1	22	17	46	66	57	68	81	77	112	106
ENSMUSG00000097415	chr7	AU020206	75769762	75770237	656	0.897749	0.983943	0.000881	0.003258	0.05425	1	10	13	34	21	29	27	43	50	63	39
ENSMUSG00000022019	chr14	Tdrd3	87416639	87416848	5643	-0.46312	4.303863	0.000887	0.003279	0.020014	-1	319	256	527	344	405	236	345	293	363	274
ENSMUSG00000028826	chr4	Tmem57	1.35E+08	1.35E+08	6744	-0.49023	4.917997	0.00089	0.003289	0.024007	-1	454	467	815	519	579	344	504	481	595	379
ENSMUSG00000024691	chr19	Fam111a	12545740	12545855	4125	0.8364	2.039021	0.000892	0.003296	0.059564	1	26	31	79	37	66	80	126	105	67	83
ENSMUSG00000049739	chr7	Zfp646	1.28E+08	1.28E+08	6727	-0.65941	3.41828	0.000894	0.003301	0.040273	-1	121	120	314	236	293	117	183	167	143	136
ENSMUSG00000025817	chr2	Nudt5	5845019	5845385	6484	0.748702	1.991775	0.000895	0.003307	0.042576	1	36	37	55	49	53	72	102	112	84	68
ENSMUSG00000033658	chr8	Ddx19b	1.11E+08	1.11E+08	6742	-0.53198	4.692778	0.000897	0.003313	0.028162	-1	426	250	737	448	680	287	483	350	522	313
ENSMUSG00000025234	chr9	Arih1	59388258	59393378	7707	-0.5	6.981068	0.000898	0.003316	0.026578	-1	2128	1613	3788	2096	2493	1480	2460	1645	2424	1652
ENSMUSG00000020486	chr11	Sept4	87568903	87568958	3563	0.590751	3.084153	0.000899	0.003318	0.029914	1	88	68	133	100	155	129	245	191	235	134
ENSMUSG00000011179	chr12	Odc1	17544873	17545168	2547	-0.86564	7.277119	0.0009	0.00332	0.079765	-1	3716	3088	3929	1621	3202	2056	2632	1194	3124	1243
ENSMUSG00000033308	chr3	Dpyd	1.19E+08	1.19E+08	8040	-0.84513	1.52709	0.0009	0.00332	0.052537	-1	42	35	75	75	64	22	35	50	44	31
ENSMUSG00000041408	chr14	Wapal	34673928	34674360	6623	-0.45813	5.37616	0.000901	0.003322	0.02129	-1	631	550	1152	718	863	477	809	558	806	572
ENSMUSG00000032511	chr9	Scn5a	1.19E+08	1.19E+08	8764	1.344578	-0.26297	0.000902	0.003326	0.104426	1	1	6	14	6	6	21	21	25	15	10
ENSMUSG00000042810	chr6	Krba1	48395586	48395887	9314	-0.52542	4.992135	0.000905	0.003335	0.027801	-1	510	387	1029	483	702	382	560	417	515	488
ENSMUSG00000059920	chr16	4930453N24Rik	64751751	64752176	5948	-0.52994	6.043305	0.000905	0.003335	0.029537	-1	1188	990	1624	1074	1331	828	1159	794	1428	780
ENSMUSG00000040721	chr14	Zfhx2	55060262	55063571	18166	-0.71551	2.893284	0.000907	0.003339	0.045286	-1	110	67	260	141	194	78	98	102	118	106
ENSMUSG00000021843	chr14	Ktn1	47648448	47648577	9582	-0.50018	7.653264	0.000915	0.003368	0.026857	-1	2837	2621	5408	3841	4584	2131	3896	2690	3709	2941
ENSMUSG00000041729	chr9	Coro2b	62419492	62421413	5919	0.816843	2.789319	0.000927	0.003413	0.063038	1	61	50	138	67	93	153	107	221	181	111
ENSMUSG00000031367	chrX	Ap1s2	1.64E+08	1.64E+08	4965	0.492096	5.520472	0.000928	0.003415	0.025075	1	459	429	960	611	663	853	1038	860	1168	932
ENSMUSG00000031103	chrX	Elf4	48411046	48415446	6148	0.699956	2.350802	0.000943	0.003468	0.042229	1	44	31	108	51	85	96	113	109	150	95
ENSMUSG00000032024	chr9	Clmp	40685962	40686359	4591	0.662193	2.961791	0.000943	0.003468	0.039304	1	63	83	144	71	123	138	172	203	198	142
ENSMUSG00000087249	chr11	Gm16062	59810080	59810261	771	0.666092	3.106453	0.000943	0.003468	0.039645	1	117	80	116	114	87	169	250	186	204	143
ENSMUSG00000028532	chr4	Cachd1	1.01E+08	1.01E+08	6020	-0.78018	2.64127	0.000945	0.003474	0.055048	-1	111	106	216	66	136	70	83	99	96	63
ENSMUSG00000070509	chr7	Rgma	73375520	73375888	3782	0.498022	5.369649	0.000945	0.003474	0.025644	1	425	346	796	538	712	564	1132	807	1095	866
ENSMUSG00000079334	chr9	Nat6	1.08E+08	1.08E+08	3154	0.529946	4.230198	0.000946	0.003475	0.027205	1	231	159	324	264	252	326	394	437	558	305
ENSMUSG00000072940	chr6	Gm10443	86334031	86334240	210	1.101768	0.857403	0.000947	0.003478	0.085968	1	23	13	22	19	7	48	46	33	53	29
ENSMUSG00000030137	chr6	Tuba8	1.21E+08	1.21E+08	2225	-0.48381	7.841893	0.000958	0.003517	0.025357	-1	3828	3223	6069	3679	4820	2753	4470	3310	3910	3085
ENSMUSG00000009112	chr6	Bcl2l13	1.21E+08	1.21E+08	6933	-0.56717	6.413859	0.000959	0.003522	0.034418	-1	1217	829	2310	2007	2080	873	1700	1127	1599	1082
ENSMUSG00000021589	chr13	Rhobtb3	75869537	75872461	5684	-0.54688	4.393522	0.00096	0.003523	0.029778	-1	367	269	717	310	390	233	382	274	421	264
ENSMUSG00000025586	chr7	Cpeb1	81347026	81348439	4192	-0.72643	5.236388	0.000965	0.00354	0.055642	-1	817	524	1333	424	752	593	493	452	630	377
ENSMUSG00000022044	chr14	Stmn4	66344296	66344411	1916	-1.1402	0.483928	0.000966	0.003544	0.089218	-1	32	23	41	19	29	20	13	15	22	4
ENSMUSG00000057123	chr3	Gja5	97032416	97032485	3166	0.72475	2.04113	0.000966	0.003544	0.040519	1	36	39	67	46	55	78	101	97	129	54
ENSMUSG00000066315	chr4	Gm12918	10848420	10849055	636	0.731814	2.616522	0.000967	0.003544	0.046613	1	50	79	104	53	73	109	155	140	187	100
ENSMUSG00000003660	chr2	Snrnp200	1.27E+08	1.27E+08	7819	-0.51745	6.134104	0.000969	0.003551	0.028441	-1	1095	793	2158	1274	1536	729	1380	938	1238	1031
ENSMUSG00000029650	chr5	Slc46a3	1.48E+08	1.48E+08	2458	-0.59547	3.137743	0.00097	0.003553	0.03108	-1	133	102	201	201	213	114	139	121	139	115
ENSMUSG00000024592	chr18	C330018D20Rik	56955833	56957921	3233	-0.61982	3.365382	0.00097	0.003554	0.036414	-1	138	177	248	221	200	92	213	133	171	138
ENSMUSG00000043251	chr8	Exoc3l	1.05E+08	1.05E+08	2497	0.947589	1.17735	0.000971	0.003554	0.065875	1	24	10	20	29	34	41	60	33	75	50
ENSMUSG00000044345	chr19	Marveld1	42147400	42149559	4304	0.524348	4.162468	0.000971	0.003556	0.02653	1	184	174	281	245	289	303	361	424	491	330
ENSMUSG00000024646	chr18	Cyb5a	84851338	84851607	2143	0.674548	5.217763	0.000978	0.003578	0.047738	1	458	440	581	368	379	695	901	1089	758	663
ENSMUSG00000055305	chr7	Zfp93	24270420	24270681	2666	-0.63298	2.718399	0.000979	0.003583	0.034055	-1	113	98	149	121	149	80	127	70	96	91
ENSMUSG00000083669	chr7	Gm10169	29965218	29965565	348	1.008721	0.621453	0.00098	0.003586	0.061421	1	12	12	20	10	22	26	28	48	40	29
ENSMUSG00000053297	chr6	AI854703	48626764	48627113	4156	-0.78825	1.446747	0.000982	0.00359	0.045715	-1	52	37	72	50	58	19	41	27	60	33
ENSMUSG00000046229	chr2	Scand1	1.56E+08	1.56E+08	759	0.66012	4.135898	0.000987	0.003608	0.04344	1	241	208	250	157	192	348	378	406	479	325
ENSMUSG00000043924	chr4	Ncmap	1.35E+08	1.35E+08	2227	-0.97706	1.182097	0.000989	0.003615	0.076171	-1	28	38	60	52	55	10	48	16	35	29
ENSMUSG00000003226	chr10	Ranbp2	58446852	58447051	9477	-0.53239	6.293286	0.000993	0.003626	0.030376	-1	1139	1072	2677	1212	1591	893	1560	1109	1319	1013
ENSMUSG00000030555	chr7	Ttc23	67647410	67647845	6343	-0.59812	3.128741	0.000994	0.003632	0.032044	-1	149	115	276	124	194	87	169	107	146	125

ENSMUSG00000021643	chr13	Serf1	1E+08	1E+08	1315	0.953745	2.051358	0.000997	0.00364	0.079622	1	58	44	55	24	31	94	97	104	95	85
ENSMUSG00000027597	chr2	Ahcy	1.55E+08	1.55E+08	2805	-0.5238	4.72476	0.000998	0.003642	0.027879	-1	480	384	724	398	517	377	443	336	515	305
ENSMUSG00000024231	chr18	Cul2	3382988	3383172	4138	-0.46865	5.907619	0.001002	0.003656	0.023236	-1	931	833	1598	1043	1234	727	1242	799	1092	780
ENSMUSG00000027067	chr2	Ssrp1	85037234	85037328	3737	0.459299	5.22414	0.001002	0.003656	0.021584	1	448	360	648	454	624	658	922	702	944	713
ENSMUSG00000040026	chr7	Saa3	46711998	46712264	531	1.725955	-0.13127	0.001002	0.003656	0.205849	1	6	4	4	6	9	38	15	27	25	3
ENSMUSG00000034403	chrX	Pja1	99465734	99468314	3324	0.504635	4.130829	0.001003	0.003657	0.024326	1	220	182	328	185	241	315	447	362	402	330
ENSMUSG00000046152	chr8	Fut10	31187331	31187462	5007	-0.55245	3.665497	0.001004	0.003658	0.028503	-1	203	158	416	215	245	172	244	161	203	153
ENSMUSG00000045180	chrX	Shroom2	1.53E+08	1.53E+08	8375	-1.28593	0.055477	0.001005	0.003663	0.109539	-1	10	6	34	28	34	7	20	7	9	7
ENSMUSG00000028189	chr3	Ctbs	1.46E+08	1.46E+08	2892	-0.72557	2.573766	0.001006	0.003666	0.046752	-1	90	94	209	85	123	69	123	66	73	73
ENSMUSG00000031722	chr8	Hp	1.1E+08	1.1E+08	1343	1.733142	5.718323	0.001008	0.003672	0.309005	1	689	438	387	69	186	2206	729	2277	1190	531
ENSMUSG00000038718	chr2	Pbx3	34171457	34172973	6109	0.864285	1.339617	0.001009	0.003674	0.050934	1	34	22	32	19	28	57	64	47	72	43
ENSMUSG00000029725	chr5	Ppp1r35	1.38E+08	1.38E+08	1085	0.809575	2.22781	0.001014	0.003691	0.055981	1	51	56	70	31	53	99	98	108	125	93
ENSMUSG00000021702	chr13	Thbs4	92751590	92751812	3289	1.014972	7.514894	0.001014	0.003692	0.111364	1	780	892	2482	2338	3846	2305	6820	4092	3350	5746
ENSMUSG00000029685	chr6	Asb15	24528144	24528269	4497	-0.91834	6.615397	0.001015	0.003693	0.091171	-1	787	867	3034	2802	3513	822	1598	829	1571	1426
ENSMUSG00000035142	chr12	Nubpl	52097737	52097891	4954	-0.62142	3.002374	0.001016	0.003694	0.035035	-1	149	130	175	143	160	93	140	83	152	106
ENSMUSG00000038608	chr1	Dock10	80501073	80501826	18267	0.731382	2.161754	0.001016	0.003694	0.045259	1	46	29	92	40	65	61	124	122	110	83
ENSMUSG00000035212	chr4	Leprot	1.02E+08	1.02E+08	1898	0.509731	4.027903	0.001025	0.003728	0.024621	1	169	183	263	182	273	273	424	360	398	287
ENSMUSG00000049807	chr11	Arhgap23	97415533	97415667	6637	0.560389	3.418295	0.001027	0.003733	0.029116	1	119	86	237	108	158	203	247	214	279	203
ENSMUSG00000031352	chrX	Hccs	1.69E+08	1.69E+08	5151	-0.56573	4.675419	0.001028	0.003735	0.032958	-1	350	290	574	656	599	266	473	351	450	350
ENSMUSG00000084013	chr2	Gm14270	1.7E+08	1.7E+08	846	0.715217	1.672975	0.001028	0.003735	0.035746	1	31	28	53	32	44	64	69	63	97	55
ENSMUSG00000003070	chr10	Efna2	80179482	80179890	2131	1.191046	0.164566	0.001029	0.003737	0.089272	1	16	5	14	2	12	25	25	26	26	23
ENSMUSG00000060397	chr7	Zfp128	12881177	12881360	4087	-0.86044	1.21678	0.001036	0.003762	0.053262	-1	38	22	71	47	60	13	41	34	31	27
ENSMUSG00000024190	chr17	Dusp1	26505590	26506650	2697	0.937141	5.851082	0.001038	0.003768	0.094742	1	375	494	761	836	704	692	3204	723	1275	1357
ENSMUSG00000060913	chr3	Trim55	19644474	19644776	2659	-0.47532	6.343184	0.001039	0.003771	0.024334	-1	1303	1062	2247	1325	1767	911	1551	1136	1566	1099
ENSMUSG00000021785	chr14	Ngly1	16249280	16249497	5274	-0.47846	5.599121	0.00104	0.003771	0.024183	-1	785	719	1373	785	887	559	901	688	916	655
ENSMUSG00000051695	chr6	Pcbp1	86524492	86526321	1830	0.48637	6.840896	0.00104	0.003771	0.025708	1	1420	1023	2145	1468	1681	1764	2654	2501	3140	2202
ENSMUSG00000047767	chr7	Atg16l2	1.01E+08	1.01E+08	3881	0.820329	2.008949	0.00104	0.003772	0.060542	1	31	17	85	44	63	88	99	86	83	90
ENSMUSG00000038235	chr1	F11r	1.71E+08	1.71E+08	2663	0.606165	3.492559	0.001042	0.003777	0.03452	1	110	98	142	172	184	175	348	211	330	191
ENSMUSG00000021773	chr14	Comtd1	21845861	21847427	2464	0.780512	2.423599	0.001042	0.003778	0.052922	1	58	57	59	65	61	129	125	116	156	76
ENSMUSG00000026062	chr1	Slc9a2	40680574	40682165	6984	-0.60014	5.054956	0.001044	0.003782	0.037977	-1	480	303	920	752	882	324	622	371	647	480
ENSMUSG00000029299	chr5	Abcg3	1.05E+08	1.05E+08	3550	1.044923	0.312677	0.001045	0.003785	0.055442	1	10	11	13	11	13	22	39	32	21	23
ENSMUSG00000028974	chr4	Dffa	1.49E+08	1.49E+08	3540	-0.53277	5.966769	0.00105	0.003801	0.03052	-1	917	673	1560	1366	1556	725	1230	740	1175	845
ENSMUSG00000037977	chr9	6430571L13Rik	1.07E+08	1.07E+08	2912	-0.48564	5.753419	0.001054	0.003816	0.025106	-1	879	583	1482	990	1248	584	991	851	1102	635
ENSMUSG00000024959	chr19	Bad	6941861	6942440	2007	0.610322	3.522996	0.001055	0.00382	0.035012	1	152	116	159	133	148	214	238	232	369	205
ENSMUSG00000020614	chr11	Fam20a	1.1E+08	1.1E+08	3634	0.834726	1.162388	0.001058	0.003826	0.046974	1	18	15	35	17	40	36	52	57	57	45
ENSMUSG00000013921	chr7	Clip3	30291672	30291842	3991	0.91595	1.951631	0.001065	0.003853	0.076456	1	18	22	61	51	65	63	75	111	91	98
ENSMUSG00000030172	chr6	Erc1	1.2E+08	1.2E+08	11598	-0.60977	4.824696	0.001068	0.00386	0.038991	-1	424	247	984	525	727	271	453	372	559	406
ENSMUSG00000013584	chr9	Aldh1a2	71215789	71215963	2264	1.471385	0.87094	0.001069	0.003864	0.187351	1	8	11	15	18	19	42	54	27	109	7
ENSMUSG00000036299	chr18	BC031181	75005900	75006114	1047	0.551089	4.751728	0.001069	0.003864	0.031069	1	332	332	408	282	346	491	674	547	719	485
ENSMUSG00000021693	chr13	Kif2a	1.07E+08	1.07E+08	7046	-0.49497	3.778269	0.00107	0.003866	0.022908	-1	224	194	375	227	270	164	245	218	253	159
ENSMUSG00000002147	chr10	Stat6	1.28E+08	1.28E+08	4402	0.45272	4.966648	0.001071	0.003867	0.020936	1	375	286	644	370	476	521	775	598	817	590
ENSMUSG00000084329	chr11	Gm6733	72833461	72835380	1920	-1.0289	0.784918	0.001071	0.003867	0.075011	-1	17	23	75	30	39	10	28	23	20	17
ENSMUSG00000047181	chr11	Samd14	95009879	95010576	3379	1.020749	0.727086	0.001074	0.003877	0.076974	1	5	8	28	16	28	31	31	39	50	35
ENSMUSG00000020142	chr11	Slc1a4	20302180	20304500	3926	1.342425	-0.01601	0.001078	0.003889	0.108107	1	4	6	10	14	5	14	18	38	22	20
ENSMUSG00000029068	chr4	Ccnl2	1.56E+08	1.56E+08	5278	0.52588	4.839464	0.001078	0.00389	0.028467	1	348	319	510	305	380	510	771	669	613	500
ENSMUSG00000052459	chr16	Atp6v1a	44085402	44087516	6044	0.498788	4.858604	0.001079	0.003892	0.025608	1	343	287	566	315	432	504	685	717	685	489
ENSMUSG00000074207	chr3	Adh1	1.38E+08	1.38E+08	2233	0.703381	4.775013	0.001082	0.003902	0.052393	1	243	269	309	424	386	553	620	832	696	366
ENSMUSG00000003190	chr7	Bcl2l12	44991222	44991454	1976	0.575521	2.817473	0.001085	0.00391	0.027452	1	78	66	119	81	105	122	194	142	158	140
ENSMUSG00000006818	chr17	Sod2	13007839	13008068	3824	-0.65584	7.809997	0.001085	0.003912	0.047595	-1	2909	2217	5057	6148	6276	2260	4273	2644	4355	2715
ENSMUSG00000032540	chr9	Abhd5	1.22E+08	1.22E+08	3618	-0.52415	5.417246	0.001087	0.003916	0.029229	-1	567	518	1081	962	986	467	757	762	716	505
ENSMUSG00000031521	chr8	Aga	53511702	53511931	1289	0.583594	3.357665	0.001093	0.003935	0.031681	1	113	97	156	121	164	164	241	230	222	239
ENSMUSG00000036698	chr15	Ago2	73095844	73107016	13705	-0.64255	6.180812	0.001093	0.003935	0.045124	-1	1059	653	2815	1241	1841	666	1151	1070	1439	913
ENSMUSG00000095930	chr13	Nim1k	1.2E+08	1.2E+08	8466	-0.80151	1.38869	0.001093	0.003935	0.046511	-1	39	53	66	41	56	24	41	35	36	32
ENSMUSG00000090093	chr2	Gm14399	1.75E+08	1.75E+08	2561	-1.0939	0.283079	0.001095	0.00394	0.075655	-1	17	17	24	18	48	9	19	12	12	13
ENSMUSG00000027015	chr2	Cybrd1	71117923	71118312	5339	-1.5059	-0.14138	0.001099	0.003953	0.149251	-1	5	13	30	25	26	4	11	6	2	14
ENSMUSG00000031596	chr8	Slc7a2	40862396	40862557	9135	-0.61851	5.971739	0.001099	0.003955	0.041704	-1	716	670	2272	1248	1572	567	1082	906	1233	803
ENSMUSG00000073413	chr17	Ly6g6d	35071443	35071759	1172	-1.62905	-0.19632	0.001104	0.003969	0.182714	-1	31	16	22	14	9	14	5	2	9	4
ENSMUSG00000028902	chr4	Sf3a3	1.25E+08	1.25E+08	2785	0.512468	3.941969	0.001106	0.003975	0.024966	1	182	157	243	202	217	268	445	258	383	294
ENSMUSG00000047976	chr6	Kcna1	1.27E+08	1.27E+08	8970	-0.99048	1.16375	0.001109	0.003987	0.077723	-1	37	29	68	30	72	11	48	27	21	26
ENSMUSG00000018076	chr5	Med13l	1.19E+08	1.19E+08	9293	-0.64158	4.483949	0.00111	0.003988	0.043049	-1	304	222	831	383	583	184	347	344	395	328
ENSMUSG00000031782	chr8	Coq9	94838321	94838497	3055	-0.68514	8.29538	0.001111	0.003991	0.052209	-1	4666	2926	6729	8754	8665	3265	6571	3365	5821	3544
ENSMUSG00000028973	chr5	Abcb8	24393663	24393702	4739	-0.57496	5.412793	0.001115	0.004004	0.035568	-1	583	409	1105	1052	1067	452	714	548	886	559
ENSMUSG00000004872	chr1	Pax3	78101267	78102835	6187	-1.58456	-0.09329	0.001116	0.004006	0.180768	-1	4	9	43	18	34	3	4	11	6	12
ENSMUSG00000000386	chr16	Mx1	97447035	97448372	3646	1.172075	-0.20531	0.001117	0.004008	0.060741	1	4	5	9	8	11	20	19	17	18	19
ENSMUSG00000039530	chr8	Tusc3	39005867	39006200	1511	0.632581	2.508735	0.001119	0.004014	0.032598	1	59	55	94	68	75	78	149	132	147	116

ENSMUSG00000022752	chr16	Tomm70a	57121714	57122194	3778	-0.47095	6.03352	0.001124	0.004032	0.024037	-1	1027	868	1668	1196	1398	810	1269	829	1270	874
ENSMUSG00000033629	chr9	Ptplad1	64986985	64988529	2731	0.53017	3.737933	0.001125	0.004035	0.026532	1	156	143	237	155	174	245	328	315	315	219
ENSMUSG00000046865	chr7	Fbl	28169748	28169818	1159	0.533874	4.128343	0.001132	0.004058	0.028262	1	183	166	252	256	278	328	424	411	464	255
ENSMUSG00000022948	chr16	Setd4	93583457	93583684	4702	1.147252	0.327566	0.001136	0.004071	0.077522	1	13	14	12	3	13	26	36	22	32	26
ENSMUSG00000020721	chr11	Helz	1.08E+08	1.08E+08	15044	-0.53942	4.23315	0.001138	0.004077	0.029224	-1	226	227	620	328	461	212	312	302	329	240
ENSMUSG00000044629	chr11	Cnrip1	17051586	17051824	4003	0.762549	1.490899	0.001142	0.00409	0.040728	1	31	19	33	34	43	44	69	61	71	63
ENSMUSG00000006134	chr16	Crkl	17451987	17452788	3863	-0.53381	4.476572	0.001147	0.004108	0.029104	-1	330	217	687	453	505	278	433	299	343	300
ENSMUSG00000028128	chr3	F3	1.22E+08	1.22E+08	1876	0.785861	2.989519	0.001147	0.004108	0.060786	1	68	57	112	102	129	96	154	159	251	240
ENSMUSG00000047022	chr12	Mipol1	57230427	57230611	9342	-0.90673	1.733146	0.00115	0.004116	0.070917	-1	44	38	103	98	63	22	66	43	35	41
ENSMUSG00000018401	chr11	Mtmr4	87592162	87592250	6240	-0.5474	3.866585	0.001151	0.004118	0.029519	-1	178	195	433	293	319	136	242	215	283	209
ENSMUSG00000024660	chr19	Incenp	9872297	9872873	3217	0.801297	1.563224	0.001155	0.004131	0.050643	1	23	19	44	45	37	66	67	63	62	64
ENSMUSG00000051113	chr7	Fam71e1	44496588	44496730	849	1.019883	0.181762	0.001156	0.004134	0.050824	1	7	6	15	15	11	18	27	22	38	20
ENSMUSG00000073599	chr18	Ecscr	35713086	35713434	1680	0.678371	2.818199	0.001158	0.00414	0.042258	1	68	54	104	96	110	114	270	128	185	105
ENSMUSG00000002980	chr7	Bcam	19756131	19756619	3199	0.635695	5.544337	0.001159	0.004145	0.04414	1	437	383	651	701	773	841	1016	742	1872	815
ENSMUSG00000042712	chrX	Wbp5	1.36E+08	1.36E+08	1037	0.532147	4.374661	0.001161	0.004148	0.028618	1	214	238	306	253	326	301	556	418	512	449
ENSMUSG00000022682	chr16	Rrn3	13780699	13780839	3597	-0.46307	5.398011	0.001164	0.004159	0.022782	-1	699	477	1212	722	908	474	768	658	782	568
ENSMUSG00000027304	chr2	Rtf1	1.2E+08	1.2E+08	5731	-0.44584	5.487631	0.001167	0.00417	0.021151	-1	628	566	1208	814	1020	527	855	655	870	588
ENSMUSG00000035713	chr7	Usp35	97309380	97310496	5285	1.035238	1.25046	0.001169	0.004176	0.086707	1	34	16	35	14	19	37	50	81	54	51
ENSMUSG00000021536	chr13	Adcy2	68620043	68620872	4211	-0.53091	5.541448	0.001174	0.004191	0.030621	-1	690	492	1196	1076	1058	475	925	562	956	626
ENSMUSG00000032009	chr9	Sesn3	14276301	14276629	2162	-1.27059	1.178728	0.001184	0.004226	0.143847	-1	21	14	96	41	96	15	33	12	23	31
ENSMUSG00000045664	chr19	Cdc42ep2	5917556	5918993	1491	0.744513	4.4247	0.001184	0.004226	0.059818	1	163	99	302	414	344	350	595	455	621	444
ENSMUSG00000048807	chr11	Slc35e4	3907021	3907984	3063	0.482289	5.206451	0.001185	0.004228	0.02463	1	486	357	658	432	533	654	871	655	1045	705
ENSMUSG00000077220	chr1	Gm23436	1.61E+08	1.61E+08	66	1.390237	-0.42502	0.001188	0.004237	0.097574	1	4	5	15	2	2	9	26	17	16	15
ENSMUSG00000028970	chr5	Abcb1b	8798147	8798289	4344	-0.66027	3.090668	0.00119	0.004242	0.041967	-1	101	109	273	166	211	76	188	88	139	117
ENSMUSG00000051306	chr5	Usp42	1.44E+08	1.44E+08	6238	-0.68155	2.633605	0.001193	0.004251	0.041916	-1	91	60	228	110	148	59	110	87	96	79
ENSMUSG00000092187	chr7	Gm20457	64337550	64337933	682	-0.7646	1.358676	0.001196	0.004261	0.040819	-1	42	39	74	35	63	29	49	28	36	26
ENSMUSG00000030259	chr6	Rassf8	1.46E+08	1.46E+08	5559	-0.53929	3.931307	0.001198	0.004268	0.028865	-1	191	171	408	326	391	155	289	230	263	202
ENSMUSG00000052031	chr17	Tagap1	6954965	6957024	2358	-0.54259	4.167138	0.001198	0.004268	0.029951	-1	287	195	398	408	432	192	318	220	332	273
ENSMUSG00000086605	chr2	Gm14290	1.67E+08	1.67E+08	1894	-0.65369	3.12205	0.001199	0.00427	0.040611	-1	165	98	287	113	213	96	124	138	164	92
ENSMUSG00000042650	chr11	Alkbh5	60536381	60536637	5987	-0.49383	7.452206	0.001201	0.004276	0.027395	-1	2709	2175	5255	2882	3886	1920	3111	2415	3459	2481
ENSMUSG00000042275	chr13	Pelo	1.15E+08	1.15E+08	1600	0.546596	3.623091	0.001202	0.004277	0.028146	1	136	143	213	144	152	220	323	249	347	196
ENSMUSG00000032898	chr5	Fbxo21	1.18E+08	1.18E+08	3909	-0.57067	3.89754	0.001203	0.004281	0.032915	-1	297	221	333	250	299	169	207	265	266	177
ENSMUSG00000071074	chr17	Yipf3	46248080	46248328	2693	0.482992	5.086144	0.001204	0.004281	0.024691	1	417	290	590	483	502	498	769	758	940	658
ENSMUSG00000020114	chr10	Cand1	1.19E+08	1.19E+08	8357	0.490728	4.140989	0.001205	0.004283	0.023838	1	218	159	323	241	234	332	412	383	411	317
ENSMUSG00000019768	chr10	Esr1	4611593	4612155	13661	-0.52464	4.723659	0.001205	0.004285	0.029041	-1	392	375	829	440	511	246	559	391	432	370
ENSMUSG00000027447	chr2	Cst3	1.49E+08	1.49E+08	1266	0.558839	9.030439	0.001206	0.004287	0.035377	1	7102	5017	7843	6026	7514	11308	11315	10038	14233	9413
ENSMUSG00000044211	chr6	Gm7887	48524372	48525105	734	-1.07139	0.303118	0.001213	0.004308	0.065725	-1	22	16	32	30	24	12	19	7	10	18
ENSMUSG00000024816	chr19	Frmd8	5849702	5852742	5082	0.652941	2.694058	0.001214	0.004312	0.038062	1	53	71	126	70	80	116	146	160	176	110
ENSMUSG00000027207	chr2	Galk2	1.26E+08	1.26E+08	6088	0.758281	2.383399	0.001215	0.004316	0.050883	1	71	50	73	42	63	109	123	136	111	96
ENSMUSG00000029082	chr5	Bst1	43818886	43819093	2419	1.40469	-0.05355	0.001217	0.00432	0.130449	1	8	7	13	0	9	23	42	17	17	13
ENSMUSG00000042744	chr5	Gm15800	1.21E+08	1.21E+08	16416	-0.65093	4.257961	0.001221	0.004332	0.04463	-1	282	161	708	325	523	177	292	265	358	269
ENSMUSG00000043903	chr8	Gm22	1.22E+08	1.22E+08	3082	1.206288	-0.18395	0.00123	0.004365	0.089737	1	3	3	11	5	16	14	15	17	27	23
ENSMUSG00000021111	chr12	Papola	1.06E+08	1.06E+08	6595	-0.44336	5.632788	0.001235	0.004378	0.021247	-1	752	653	1269	906	1051	644	959	759	851	626
ENSMUSG00000028261	chr4	Ndufaf4	24898083	24898302	3902	-0.48732	4.923852	0.001234	0.004378	0.025095	-1	482	329	710	665	688	354	585	457	525	393
ENSMUSG00000047746	chr16	Fbxo40	36963460	36966285	5517	-0.49754	8.583043	0.001236	0.004381	0.028142	-1	5437	4439	11792	7477	8138	4646	6677	5694	7242	4895
ENSMUSG00000024483	chr18	Ankhd1	36559987	36560101	9845	-0.49112	4.974931	0.001238	0.004387	0.025497	-1	461	334	1018	539	722	387	569	464	588	387
ENSMUSG00000028807	chr4	Zbtb8a	1.29E+08	1.29E+08	2321	0.958769	0.498263	0.001239	0.004389	0.049268	1	11	12	19	16	12	19	42	36	31	28
ENSMUSG00000020057	chr10	Dram1	88322804	88324785	3045	1.055735	2.962002	0.001239	0.004391	0.114441	1	111	80	76	38	73	133	206	312	136	144
ENSMUSG00000035559	chr8	Mpv17l2	70758649	70759024	955	0.532158	3.66932	0.00124	0.004392	0.026702	1	168	129	220	142	163	213	322	260	368	212
ENSMUSG00000059273	chr7	Zc3h4	16401196	16401306	6049	-0.49438	4.862069	0.001241	0.004393	0.025723	-1	448	327	894	546	593	320	475	455	531	417
ENSMUSG00000079110	chr2	Capn3	1.2E+08	1.2E+08	5023	-0.49655	7.000399	0.001241	0.004393	0.027733	-1	1992	1496	3480	2482	2839	1563	2570	1477	2435	1750
ENSMUSG00000026615	chr1	Eprs	1.85E+08	1.85E+08	18102	-0.49848	7.921573	0.001242	0.004394	0.028192	-1	3454	3142	7153	4544	5044	2945	4546	2921	5162	3053
ENSMUSG00000027300	chr2	Ubox5	1.31E+08	1.31E+08	5585	-0.52595	3.745063	0.001242	0.004394	0.026627	-1	181	148	373	280	317	179	236	184	221	173
ENSMUSG00000048222	chr2	Mfap1b	1.21E+08	1.21E+08	3362	0.476035	3.969581	0.001242	0.004394	0.021821	1	164	161	271	195	259	281	391	284	423	280
ENSMUSG00000038843	chr19	Gcnt1	17326141	17330488	5571	1.021744	0.148104	0.001244	0.004398	0.051202	1	9	6	18	9	11	19	28	30	22	21
ENSMUSG00000087298	chr7	Gm9392	46820864	46821417	554	-0.90794	1.100607	0.001246	0.004405	0.066877	-1	37	41	56	28	52	14	46	17	39	19
ENSMUSG00000039646	chr16	Vasn	4639941	4640148	3007	0.586801	3.366031	0.001255	0.004434	0.033374	1	112	95	197	107	153	174	195	208	296	235
ENSMUSG00000005899	chr16	Smpd4	17619354	17619434	8926	-0.48231	3.787386	0.001257	0.00444	0.022338	-1	222	175	379	245	282	151	252	185	289	182
ENSMUSG00000015217	chrX	Hmgb3	71555918	71556008	2234	-0.68283	2.251094	0.001258	0.004444	0.039697	-1	69	69	107	109	107	61	87	46	77	57
ENSMUSG00000033417	chr19	Cacul1	60524696	60529087	5790	-0.46355	5.343019	0.001258	0.004444	0.023172	-1	642	504	1209	652	860	464	753	574	858	507
ENSMUSG00000032181	chr9	Scg3	75643264	75643944	2249	1.328417	0.345694	0.001259	0.004445	0.132896	1	13	8	6	9	15	15	33	47	16	36
ENSMUSG00000052727	chr13	Map1b	99421464	99425961	11852	0.759594	3.782649	0.001259	0.004445	0.061606	1	110	83	295	150	223	285	224	235	564	265
ENSMUSG00000044792	chr13	Isca1	59755409	59757003	4288	-0.54728	7.676404	0.001263	0.004455	0.034052	-1	3356	2268	4542	4721	4773	2372	3890	2517	4435	2296
ENSMUSG00000071796	chr8	6820431F20Rik	20262613	20262670	5006	-1.15262	0.323627	0.001264	0.00446	0.093682	-1	23	11	33	31	32	7	31	6	12	11
ENSMUSG00000031910	chr8	Has3	1.07E+08	1.07E+08	6380	-1.06873	1.286054	0.001278	0.004505	0.099044	-1	38	12	85	56	79	23	44	15	33	24

ENSMUSG00000021156	chr13	Zmynd11	9684836	9686984	7055	-0.46308	6.299686	0.001278	0.004507	0.023913	-1	1120	1036	2150	1476	1668	940	1517	1111	1497	1031
ENSMUSG00000035632	chr7	Cnot3	3645290	3645584	4340	0.498586	4.167893	0.001279	0.004509	0.025238	1	202	140	291	266	304	304	393	390	478	341
ENSMUSG00000056973	chr8	Ces1d	93166068	93166438	2369	-1.56972	5.947547	0.00128	0.004509	0.267683	-1	1544	1610	2406	672	990	254	240	1629	290	314
ENSMUSG00000015647	chr2	Lama5	1.8E+08	1.8E+08	11388	-0.59146	4.494293	0.001281	0.004514	0.037259	-1	302	217	770	392	618	236	378	267	474	303
ENSMUSG00000067786	chr2	Nnat	1.58E+08	1.58E+08	1829	-2.29657	4.049822	0.001282	0.004516	0.536778	-1	776	739	173	50	92	43	84	209	24	130
ENSMUSG00000035764	chr16	Fbxo45	32230112	32233268	4179	-0.45708	4.843358	0.001285	0.004522	0.022001	-1	503	365	779	461	583	341	581	414	547	348
ENSMUSG00000070305	chr9	Mpzl3	45055186	45055318	6987	-1.00132	1.791	0.001285	0.004522	0.092449	-1	90	53	113	29	79	44	37	30	44	45
ENSMUSG00000005615	chr16	Pcyt1a	32430921	32431031	5751	-0.50476	7.3543	0.001287	0.004526	0.028968	-1	2354	2029	4888	3125	3431	1893	2809	2140	3631	2060
ENSMUSG00000024640	chr19	Psat1	15904678	15906151	4254	1.141673	2.49034	0.001287	0.004526	0.132092	1	81	51	61	37	31	136	104	230	109	89
ENSMUSG00000045983	chr16	Eif4g1	20668313	20668424	7227	-0.47395	9.39963	0.001287	0.004526	0.0258	-1	10409	8768	18987	11839	14221	8077	12656	9306	13537	8633
ENSMUSG00000092541	chr9	Gm20537	88407432	88407482	1009	-0.53542	3.430546	0.001292	0.004542	0.027226	-1	194	141	301	184	205	133	223	144	165	135
ENSMUSG00000030089	chr6	Slc41a3	90604725	90605008	2812	-0.51718	6.467021	0.001294	0.004548	0.030078	-1	1458	883	2451	1514	2356	1056	1589	1181	1587	1239
ENSMUSG00000028417	chr4	Tal2	53779705	53779773	2971	1.001629	0.497418	0.001294	0.004549	0.067958	1	8	5	18	13	27	23	49	28	30	28
ENSMUSG00000020834	chr11	Dhrs13	78032280	78032498	1967	0.90645	0.917293	0.001301	0.004571	0.056698	1	15	13	21	29	20	33	39	34	61	43
ENSMUSG00000023505	chr6	Cdca3	1.25E+08	1.25E+08	2866	0.97766	0.548076	0.001303	0.004575	0.058336	1	17	8	12	13	22	29	33	34	32	32
ENSMUSG00000032340	chr9	Neo1	58874679	58877357	7387	-0.53363	5.685796	0.001303	0.004575	0.031538	-1	687	551	1688	1005	1180	532	855	767	885	789
ENSMUSG00000028884	chr4	Rpa2	1.33E+08	1.33E+08	2993	0.487751	4.808114	0.001306	0.004585	0.024968	1	368	284	450	356	386	473	727	537	822	457
ENSMUSG00000048249	chr17	Crebrf	26715650	26715774	8564	-0.52668	4.250872	0.001308	0.00459	0.028681	-1	296	209	616	332	412	178	362	312	324	256
ENSMUSG00000053559	chr15	Smagp	1.01E+08	1.01E+08	1142	0.939516	1.46426	0.001311	0.004601	0.070333	1	32	30	33	24	21	48	67	87	76	39
ENSMUSG00000023460	chr17	Rab12	66494512	66495803	3021	-0.57901	7.916098	0.001316	0.004615	0.038442	-1	4712	3710	6344	3708	4564	3170	4296	2408	5205	2851
ENSMUSG00000093661	chr6	Eif4e3	99625135	99627053	2515	-0.46451	5.255837	0.001324	0.004642	0.023418	-1	702	465	944	669	789	434	787	580	644	503
ENSMUSG00000030946	chr7	Lhpp	1.33E+08	1.33E+08	2085	-0.45127	4.228757	0.001325	0.004644	0.020406	-1	322	244	494	312	373	221	368	264	356	244
ENSMUSG00000056121	chr17	Fez2	78377885	78378745	2020	-0.51755	6.635338	0.001327	0.00465	0.030398	-1	1665	1593	2469	1664	1905	1339	1819	1142	1807	1354
ENSMUSG00000000787	chrX	Ddx3x	13280970	13281157	5277	-0.66264	7.253003	0.001328	0.004652	0.050217	-1	2519	1955	5177	2560	3300	1012	3193	2387	2057	2278
ENSMUSG00000033732	chr8	Sf3b3	1.11E+08	1.11E+08	4299	0.472148	4.851476	0.001328	0.004652	0.023864	1	298	255	655	352	437	496	684	630	727	515
ENSMUSG00000039994	chr10	Timeless	1.28E+08	1.28E+08	6115	0.838409	2.301148	0.001329	0.004653	0.06774	1	42	23	63	72	83	98	173	126	111	61
ENSMUSG00000021709	chr13	Erbb2ip	1.04E+08	1.04E+08	7939	-0.45224	5.355258	0.00133	0.004657	0.022246	-1	651	494	1166	739	818	447	809	595	809	536
ENSMUSG00000037664	chr7	Cdkn1c	1.43E+08	1.43E+08	1931	0.706309	4.423321	0.001332	0.004661	0.053973	1	231	277	306	207	234	450	398	621	525	372
ENSMUSG00000037426	chr5	Depdc5	32863701	32863743	11767	-0.50684	3.322468	0.001336	0.004677	0.02361	-1	153	125	264	180	228	111	174	142	205	124
ENSMUSG00000035173	chr19	Ccdc186	56787481	56791046	6899	-0.54141	4.675556	0.001342	0.004694	0.031537	-1	376	362	874	342	552	260	472	352	472	357
ENSMUSG00000027547	chr2	Sall4	1.69E+08	1.69E+08	5536	-0.87283	1.309477	0.001345	0.004703	0.060697	-1	45	27	73	55	52	19	24	36	56	21
ENSMUSG00000052298	chr11	Cdc42se2	54717456	54719724	3661	-0.48162	5.2673	0.001345	0.004703	0.025374	-1	658	545	1106	550	779	475	682	575	774	449
ENSMUSG00000079478	chr19	Sssca1	5728088	5728868	3083	0.49804	5.196897	0.001347	0.004708	0.026907	1	490	362	585	483	483	651	855	792	1041	592
ENSMUSG00000062519	chr6	Zfp398	47835661	47835920	6478	-1.01923	1.222694	0.001347	0.004709	0.09156	-1	30	20	87	55	61	9	43	18	37	31
ENSMUSG00000039771	chr5	Polr2j	1.36E+08	1.36E+08	1106	0.510796	4.54647	0.001348	0.004711	0.027255	1	300	246	358	304	305	437	666	400	583	421
ENSMUSG00000018736	chr11	Ndel1	68821434	68822665	3253	-0.46363	6.211135	0.001352	0.004722	0.024135	-1	1125	883	2068	1355	1622	948	1377	1010	1378	987
ENSMUSG00000036639	chr5	Nudt1	1.4E+08	1.4E+08	1390	0.715203	2.498635	0.001353	0.004726	0.046433	1	79	46	67	64	74	118	174	115	118	100
ENSMUSG00000022517	chr16	Mgrn1	4886100	4886473	3293	-0.64668	5.914039	0.001354	0.004727	0.047337	-1	819	537	1411	1704	1597	666	997	736	1142	778
ENSMUSG00000026893	chr2	Gca	62664285	62664459	3409	-0.81989	2.0259	0.001356	0.004732	0.060885	-1	42	53	95	102	124	33	77	41	61	54
ENSMUSG00000027187	chr2	Cat	1.03E+08	1.03E+08	2613	-0.84371	6.285346	0.00136	0.004745	0.08106	-1	1103	1022	1574	2315	2012	629	1193	1771	908	604
ENSMUSG00000074158	chr7	9830147E19Rik	42609526	42614223	4995	-1.17126	-0.11063	0.001363	0.004753	0.081714	-1	16	17	24	13	22	3	16	15	8	5
ENSMUSG00000024043	chr17	Arhgap28	67842713	67845817	5377	0.787612	1.413548	0.001364	0.004757	0.044094	1	32	28	33	21	33	51	63	56	74	49
ENSMUSG00000050966	chr4	Lin28a	1.34E+08	1.34E+08	3996	1.463164	1.264763	0.001368	0.004769	0.20149	1	41	13	27	3	9	51	63	56	107	34
ENSMUSG00000028398	chr4	Tmem261	75277354	75277769	741	0.502433	4.854699	0.001369	0.00477	0.026907	1	390	310	422	348	405	511	726	564	787	512
ENSMUSG00000032352	chr9	Lrrc1	77430823	77432280	8247	0.939764	0.558314	0.001369	0.00477	0.049945	1	13	11	17	15	18	16	40	36	38	33
ENSMUSG00000074794	chr13	Arrdc3	80883384	80883929	6259	-0.6352	5.311512	0.00137	0.004774	0.045233	-1	499	616	1078	753	979	324	808	528	489	684
ENSMUSG00000041084	chr3	Ostc	1.31E+08	1.31E+08	1058	0.473655	4.470837	0.001373	0.004781	0.023125	1	241	232	377	327	298	383	559	446	540	413
ENSMUSG00000041515	chr8	Irf8	1.21E+08	1.21E+08	7055	0.709413	2.602233	0.001375	0.004787	0.047959	1	75	45	114	56	79	146	135	149	148	87
ENSMUSG00000030104	chr6	Edem1	1.09E+08	1.09E+08	5858	0.682017	3.502572	0.001379	0.0048	0.047796	1	127	121	171	100	166	216	231	346	232	209
ENSMUSG00000024766	chr19	Lipo1	33517740	33517777	3431	-0.71818	2.5941	0.001379	0.0048	0.048817	-1	100	92	201	91	121	47	88	109	84	81
ENSMUSG00000027598	chr2	Itch	1.55E+08	1.55E+08	9709	-0.5278	4.539895	0.001387	0.004826	0.029698	-1	376	251	778	400	480	228	393	385	410	324
ENSMUSG00000049858	chr10	Suox	1.29E+08	1.29E+08	2349	-0.50237	5.750124	0.00139	0.004834	0.028366	-1	930	689	1353	1011	1102	660	918	599	1247	697
ENSMUSG00000042675	chr7	Ypel3	1.27E+08	1.27E+08	1848	0.551482	6.183674	0.001392	0.00484	0.034462	1	928	866	1161	772	879	1338	1813	1511	2057	1209
ENSMUSG00000056569	chr1	Mpz	1.71E+08	1.71E+08	2111	-0.82351	4.682313	0.001392	0.00484	0.076018	-1	258	290	686	703	789	197	609	198	371	360
ENSMUSG00000054091	chr3	1810037I17Rik	1.23E+08	1.23E+08	1131	0.603412	4.704139	0.001393	0.00484	0.039575	1	399	265	344	271	322	534	665	542	723	402
ENSMUSG00000073792	chr4	Alg6	99715664	99715706	8544	-0.72445	2.400598	0.001399	0.004862	0.049675	-1	99	95	153	79	89	45	115	61	90	56
ENSMUSG00000026193	chr1	Fn1	71585520	71586283	11685	0.752412	7.074781	0.001407	0.004885	0.065379	1	1050	735	3641	1349	2018	1995	3097	3621	3114	3406
ENSMUSG00000035161	chr14	Ints6	62676330	62678167	4993	-0.7281	2.281942	0.001407	0.004885	0.048046	-1	60	62	190	88	100	46	100	64	73	50
ENSMUSG00000022089	chr14	Bin3	70100145	70100196	1712	0.611951	2.690982	0.00141	0.004895	0.032699	1	68	71	98	64	99	113	153	132	191	114
ENSMUSG00000000301	chr11	Pemt	59970614	59970875	2104	0.921459	1.083633	0.001412	0.0049	0.064411	1	31	14	36	13	17	39	50	54	53	41
ENSMUSG00000050666	chr14	Vstm4	32856756	32856966	2741	0.89016	1.49689	0.001416	0.004915	0.065872	1	41	17	42	20	32	44	96	40	81	64
ENSMUSG00000008398	chr10	Elk3	93247414	93250108	4550	0.516475	3.937531	0.00142	0.004927	0.0273	1	135	129	265	238	256	233	366	326	431	291
ENSMUSG00000037860	chr1	Aim2	1.73E+08	1.73E+08	3501	1.129483	-0.06781	0.001422	0.004931	0.06773	1	7	6	9	5	15	18	23	28	22	13
ENSMUSG00000033760	chr19	Rbm4b	4756543	4756661	9886	0.733265	1.78158	0.001432	0.004967	0.041147	1	31	39	47	32	49	50	93	72	92	73
ENSMUSG00000033420	chr6	Antxr1	87133854	87137355	5263	0.682517	4.353944	0.001435	0.004975	0.051837	1	137	147	405	244	386	309	517	508	386	529

ENSMUSG00000066037	chr4	Hnrnpr	1.36E+08	1.36E+08	8733	-0.55095	4.507917	0.001436	0.004977	0.033	-1	314	389	538	400	506	210	350	314	453	360
ENSMUSG00000024507	chr18	Hsd17b4	50128201	50128409	3404	-0.52992	5.643704	0.001437	0.004977	0.0318	-1	730	604	1116	1156	1166	476	1085	805	856	584
ENSMUSG00000025871	chr13	4833439L19Rik	54551218	54552817	3187	-0.45989	8.114361	0.001439	0.004986	0.024667	-1	4406	3712	7334	4880	5684	3200	5582	3852	5349	3603
ENSMUSG00000020171	chr10	Yeats4	1.17E+08	1.17E+08	1407	0.544586	3.684386	0.001441	0.004987	0.029474	1	165	135	197	148	175	241	279	292	348	215
ENSMUSG00000021846	chr14	Peli2	48120869	48121233	5849	-0.58885	3.277039	0.001441	0.004987	0.034607	-1	146	162	271	148	203	79	175	149	184	125
ENSMUSG00000022594	chr15	Lynx1	74747852	74751427	4662	-0.87691	7.364968	0.001441	0.004987	0.08882	-1	2397	1071	3354	5973	4810	1656	2610	1612	2820	2011
ENSMUSG00000035311	chr10	Gnptab	88379132	88379296	5883	-0.52772	4.263432	0.001441	0.004987	0.029524	-1	306	275	628	279	365	215	369	319	327	213
ENSMUSG00000033475	chr17	Tomm6	47686646	47687008	1131	0.550394	5.645806	0.001442	0.00499	0.034059	1	663	594	742	550	604	917	1269	996	1488	808
ENSMUSG00000091952	chr8	Gm17709	1.22E+08	1.22E+08	1096	-1.18376	0.2857	0.00145	0.005015	0.109314	-1	26	27	34	17	19	9	28	4	15	9
ENSMUSG00000079444	chr17	Gm21981	47686739	47687008	2721	0.544642	5.666356	0.001456	0.005035	0.033413	1	669	601	760	562	618	933	1279	1007	1502	823
ENSMUSG00000031976	chr8	Urb2	1.24E+08	1.24E+08	6153	-0.64711	2.968744	0.001466	0.005066	0.040137	-1	130	76	286	128	176	88	117	108	126	108
ENSMUSG00000075706	chr10	Gpx4	80047166	80047375	1724	0.568324	8.229121	0.00147	0.005078	0.037784	1	3595	3387	3886	3990	3910	6045	7673	5267	8792	5131
ENSMUSG00000021192	chr12	Golga5	1.02E+08	1.02E+08	2897	-0.44115	4.924744	0.001478	0.005108	0.021022	-1	513	392	759	525	629	400	603	430	566	364
ENSMUSG00000046364	chr7	Rpl27a	1.1E+08	1.1E+08	2774	0.544521	6.915392	0.001482	0.00512	0.034377	1	1550	1399	1797	1453	1444	2287	3393	2388	2956	2087
ENSMUSG00000045679	chr12	Pqlc3	16988648	16989895	5408	0.81737	1.785183	0.001487	0.005136	0.0589	1	23	30	53	37	53	43	96	102	68	77
ENSMUSG00000025747	chr5	Tyms	30058202	30061133	6089	1.156307	0.316036	0.001489	0.005142	0.086502	1	8	14	9	11	12	31	37	34	22	16
ENSMUSG00000096606	chr7	Gm4980	99624082	99627103	3022	0.647832	6.730228	0.00149	0.005143	0.048752	1	1521	1054	2011	949	1038	1696	2828	1908	3819	1887
ENSMUSG00000070520	chr7	Ndnl2	64867052	64872997	5946	0.55072	3.240446	0.001499	0.005173	0.028315	1	122	94	147	111	128	170	259	174	268	153
ENSMUSG00000029142	chr5	Mrpl33	31596935	31597021	7473	0.593813	6.275344	0.001502	0.005183	0.040676	1	1059	896	1101	825	894	1485	2431	1468	1953	1256
ENSMUSG00000023175	chr10	Bsg	79704491	79704584	1814	0.471986	9.401546	0.001518	0.005235	0.026364	1	7539	6080	13208	9510	9864	11969	16933	13473	18365	11493
ENSMUSG00000026730	chr2	Pter	12924041	12924198	4682	-0.47371	4.202658	0.001518	0.005235	0.02357	-1	284	248	498	344	354	191	389	245	385	224
ENSMUSG00000026479	chr1	Lamc2	1.53E+08	1.53E+08	8039	1.031159	0.835867	0.001527	0.005263	0.088838	1	4	10	24	27	25	37	34	38	56	37
ENSMUSG00000022389	chr15	Tef	81802421	81802886	7865	-0.48003	8.551147	0.001528	0.005265	0.027223	-1	6128	4699	10980	6456	7545	4742	6143	5512	7578	4725
ENSMUSG00000032410	chr9	Xrn1	95954760	95954943	18585	-0.59748	3.964698	0.001539	0.005302	0.038113	-1	190	161	609	290	348	181	273	208	299	179
ENSMUSG00000047459	chr2	Dynlrb1	1.55E+08	1.55E+08	1009	0.549477	5.878058	0.001542	0.00531	0.034616	1	719	705	867	698	723	1193	1651	1083	1519	952
ENSMUSG00000027889	chr3	Ampd2	1.08E+08	1.08E+08	5069	0.617452	2.873463	0.001547	0.005327	0.036258	1	96	64	124	60	116	131	169	157	212	130
ENSMUSG00000025130	chr11	P4hb	1.21E+08	1.21E+08	2861	0.470798	7.886744	0.001555	0.005353	0.026152	1	3070	2376	4238	2899	3289	3999	6302	4653	6319	4077
ENSMUSG00000034088	chr1	Hdlbp	93405940	93408259	11320	-0.537	8.488222	0.001563	0.005376	0.034192	-1	4939	3614	10131	8083	8633	3838	6271	4891	7351	4748
ENSMUSG00000055805	chr11	Fmnl1	1.03E+08	1.03E+08	4868	0.657661	2.805328	0.001563	0.005376	0.042987	1	73	39	118	84	128	146	144	158	187	125
ENSMUSG00000091994	chr10	E130317F20Rik	79851381	79854511	3265	-0.77261	1.491437	0.001573	0.00541	0.046324	-1	48	40	83	38	71	27	54	32	32	38
ENSMUSG00000072568	chr15	Fam84b	60818994	60823991	5926	-0.75211	2.162191	0.001574	0.005413	0.052606	-1	70	40	140	96	113	30	74	74	77	48
ENSMUSG00000010721	chr5	Lmbr1	29229814	29233148	4940	-0.52219	4.04742	0.001577	0.005422	0.028486	-1	207	224	535	273	371	205	259	235	287	238
ENSMUSG00000022109	chr14	Med4	73510049	73510185	1304	0.493229	4.291604	0.001584	0.005445	0.025542	1	223	223	331	241	267	374	552	381	456	320
ENSMUSG00000072969	chrX	Armcx5	1.36E+08	1.36E+08	4247	-0.62362	2.254588	0.001587	0.005451	0.034156	-1	84	74	128	81	88	44	83	63	89	61
ENSMUSG00000023052	chr15	Npff	1.03E+08	1.03E+08	1002	1.228539	-0.11852	0.001587	0.005452	0.094101	1	8	4	14	4	9	15	13	31	30	13
ENSMUSG00000030452	chr7	Nipa2	55931287	55933547	5386	-0.45698	5.081255	0.001596	0.005477	0.023278	-1	555	481	948	514	670	387	666	460	656	459
ENSMUSG00000033436	chrX	Armcx2	1.35E+08	1.35E+08	4532	0.695136	2.459343	0.001596	0.005477	0.047122	1	35	36	105	72	96	97	136	116	128	125
ENSMUSG00000048442	chr11	Smim5	1.16E+08	1.16E+08	1649	1.365798	-0.38544	0.001595	0.005477	0.121109	1	4	0	7	11	7	11	24	7	27	17
ENSMUSG00000021928	chr14	Ebpl	61339763	61341404	2077	0.65918	2.894638	0.001598	0.005484	0.041665	1	91	89	110	63	92	130	170	166	202	147
ENSMUSG00000002104	chr2	Rapsn	91035620	91035988	1802	0.471174	5.058891	0.001602	0.005493	0.024674	1	418	298	546	450	528	551	823	560	948	667
ENSMUSG00000029095	chr5	Ablim2	35757880	35758060	7047	0.467936	5.648586	0.001601	0.005493	0.025094	1	611	374	1003	687	785	818	1396	885	1328	940
ENSMUSG00000067365	chr5	Tmem128	38260185	38260492	1942	0.588042	2.963679	0.001605	0.005502	0.03252	1	96	73	117	107	94	149	206	161	171	149
ENSMUSG00000031796	chr8	Cfap20	95420252	95420669	1292	0.624526	2.418032	0.001606	0.005507	0.033375	1	57	52	76	65	78	91	143	94	133	117
ENSMUSG00000003680	chr19	Taf6l	8772522	8772834	5884	0.584971	3.287247	0.001608	0.005511	0.033937	1	123	80	138	145	128	200	241	215	238	157
ENSMUSG00000053040	chr9	Aph1c	66814994	66819461	5205	0.838415	1.656944	0.001609	0.005513	0.061983	1	30	31	55	21	39	61	66	94	61	65
ENSMUSG00000033014	chr3	Trim33	1.03E+08	1.03E+08	8868	-0.54788	3.640391	0.001611	0.005518	0.030804	-1	174	159	421	205	265	113	240	194	221	163
ENSMUSG00000028049	chr3	Scamp3	89177473	89177657	2270	0.467031	5.458672	0.001612	0.00552	0.024739	1	572	376	729	562	736	698	1002	895	1291	801
ENSMUSG00000017774	chr11	Myo1c	75650504	75650764	6585	0.504855	5.977975	0.001614	0.005524	0.029629	1	739	461	1096	958	995	971	1502	1450	1730	1136
ENSMUSG00000064128	chr14	Cenpj	56526761	56527111	4363	-0.74496	1.69627	0.001615	0.005527	0.045046	-1	53	50	113	44	63	37	53	45	44	35
ENSMUSG00000044550	chrX	Tceal3	1.37E+08	1.37E+08	3546	1.252154	-0.02028	0.001615	0.005527	0.096141	1	5	5	3	16	11	16	31	18	22	24
ENSMUSG00000037525	chr15	Bcdin3d	99470084	99471079	1271	0.752777	2.496737	0.001617	0.005532	0.054568	1	61	45	51	92	73	117	161	102	159	97
ENSMUSG00000060579	chr14	Fhit	9550092	9550398	1491	1.068597	0.219295	0.001619	0.005539	0.059823	1	12	7	10	14	10	19	33	19	42	18
ENSMUSG00000003731	chr4	Kpna6	1.3E+08	1.3E+08	6729	-0.46359	6.72041	0.001624	0.005554	0.025246	-1	1595	1178	3028	1943	2365	1267	2092	1434	2018	1367
ENSMUSG00000094638	chr1	Gm21972	86133637	86133784	776	0.610362	6.001588	0.00163	0.005571	0.04347	1	809	786	920	629	781	1365	1554	1240	1965	970
ENSMUSG00000058966	chr7	Fam57b	1.27E+08	1.27E+08	2804	1.045345	5.529032	0.00164	0.005605	0.127649	1	166	153	583	778	891	586	1547	872	1903	996
ENSMUSG00000001751	chr11	Naglu	1.01E+08	1.01E+08	2658	0.666905	3.050571	0.001641	0.005606	0.046142	1	93	48	123	125	125	134	175	237	205	157
ENSMUSG00000026791	chr2	Slc2a8	32972990	32973732	3209	0.478055	3.821603	0.001647	0.005623	0.023006	1	154	130	255	202	208	213	336	322	384	247
ENSMUSG00000044442	chr16	N6amt1	87354185	87354386	6135	-0.56146	3.289353	0.001647	0.005623	0.031445	-1	149	154	232	186	200	108	187	124	142	151
ENSMUSG00000053475	chr2	Tnfaip6	52038009	52038269	1710	0.967427	0.749782	0.001647	0.005624	0.063125	1	15	16	17	16	19	28	68	36	34	25
ENSMUSG00000034659	chr19	Tmem109	10870660	10872149	3798	0.473187	8.885489	0.001649	0.005628	0.026862	1	5780	4644	9550	5314	6880	8095	12338	9003	12203	8813
ENSMUSG00000002274	chr17	Metrn	25794571	25795291	1434	-0.49349	4.887778	0.00165	0.00563	0.027267	-1	584	357	642	501	683	367	465	435	590	384
ENSMUSG00000025175	chr11	Fn3k	1.21E+08	1.21E+08	4399	0.490057	4.390698	0.001657	0.005653	0.025905	1	232	197	375	292	306	355	478	345	636	424
ENSMUSG00000049553	chr6	Polr1a	71909053	71909239	6105	-0.56397	5.234256	0.001664	0.005676	0.036628	-1	476	348	1119	886	936	381	694	516	751	473
ENSMUSG00000039936	chr4	Pik3cd	1.5E+08	1.5E+08	6259	-0.6104	4.117176	0.001666	0.005681	0.041035	-1	243	139	498	393	484	167	296	256	310	229
ENSMUSG00000050222	chr14	Il17d	57524829	57524921	1221	0.867241	0.863648	0.001667	0.005681	0.054112	1	15	13	35	13	23	31	34	47	46	40

ENSMUSG00000000838	chrX	Fmr1	68678541	68678867	8966	-0.76102	2.74669	0.001669	0.005688	0.059164	-1	102	114	215	100	147	55	76	106	87	115
ENSMUSG00000041961	chr11	Znrf3	5276324	5279761	7893	-0.76379	1.753197	0.001674	0.005702	0.051904	-1	55	47	118	52	68	20	57	42	67	41
ENSMUSG00000076387	chr5	Mir671	24592114	24592211	98	0.91555	1.078272	0.001678	0.005714	0.064553	1	20	23	34	12	21	38	43	60	63	33
ENSMUSG00000036948	chr5	BC037034	1.38E+08	1.38E+08	3860	0.661205	2.344339	0.001682	0.005728	0.039443	1	63	41	82	45	80	101	111	121	133	85
ENSMUSG00000060923	chr11	Acyp2	30505991	30506439	863	-0.53237	6.413074	0.001683	0.005728	0.033593	-1	1488	1422	2065	1402	1568	993	1956	1051	1433	1032
ENSMUSG00000091964	chr5	BC037034	1.38E+08	1.38E+08	3581	0.661205	2.344339	0.001683	0.005728	0.039446	1	63	41	82	45	80	101	111	121	133	85
ENSMUSG00000018509	chr11	Cenpv	62524946	62525287	1811	0.551857	3.6376	0.001686	0.005736	0.031018	1	151	125	184	170	161	184	383	288	278	219
ENSMUSG00000026574	chr1	Dpt	1.65E+08	1.65E+08	1724	0.728765	6.853778	0.00169	0.00575	0.063223	1	1472	1304	2174	770	1177	2147	2712	3361	2347	2347
ENSMUSG00000072694	chr5	1500011B03Rik	1.15E+08	1.15E+08	1746	0.955971	0.608005	0.001692	0.005753	0.061785	1	14	15	19	9	19	38	32	28	47	23
ENSMUSG00000059475	chr9	Zfp426	20468549	20471248	4888	-0.51663	3.11373	0.001694	0.005761	0.025081	-1	160	111	225	145	173	100	164	122	151	110
ENSMUSG00000026504	chr1	Sdccag8	1.77E+08	1.77E+08	4129	-0.7296	3.599467	0.001696	0.005763	0.058789	-1	246	238	367	131	206	168	160	144	207	139
ENSMUSG00000017291	chr11	Taok1	77529162	77538328	12421	-0.48862	5.715248	0.001698	0.005769	0.02769	-1	688	576	1698	936	1256	589	1007	750	982	698
ENSMUSG00000013698	chr1	Pea15a	1.72E+08	1.72E+08	3861	0.495295	5.377972	0.00171	0.00581	0.028225	1	447	372	632	661	652	781	956	964	1025	684
ENSMUSG00000041075	chr1	Fzd7	59482424	59486955	4532	-0.59486	5.692441	0.001716	0.005827	0.0417	-1	991	659	1520	703	1218	367	960	702	1010	795
ENSMUSG00000020689	chr11	Itgb3	1.05E+08	1.05E+08	5901	0.822814	1.404767	0.00172	0.005841	0.056335	1	21	21	46	27	34	48	56	86	66	37
ENSMUSG00000034460	chr12	Six4	73099609	73104238	10855	-0.56825	4.275928	0.001721	0.005841	0.035875	-1	247	208	514	454	482	178	367	235	352	302
ENSMUSG00000027466	chr2	Rbck1	1.52E+08	1.52E+08	4601	0.457304	5.264038	0.001724	0.005849	0.02376	1	411	358	615	596	619	652	910	802	1009	685
ENSMUSG00000022894	chr16	Adamts5	85858170	85863177	8091	0.567369	4.613482	0.001729	0.005866	0.036294	1	275	259	501	224	334	385	660	505	853	335
ENSMUSG00000039105	chr4	Atp6v1g1	63544772	63544999	1135	0.60021	7.696948	0.001736	0.005889	0.043333	1	2680	2652	3255	1918	2256	3586	5402	4301	5656	3990
ENSMUSG00000056608	chr8	Chd9	90828835	90828914	11565	-0.58342	3.99108	0.001746	0.00592	0.037148	-1	220	151	590	274	384	156	284	243	271	210
ENSMUSG00000032501	chr15	Trib1	59648350	59649522	5699	0.632358	4.359438	0.001748	0.005928	0.0454	1	165	166	294	299	382	253	740	364	632	368
ENSMUSG00000032220	chr9	Myo1e	70207350	70207703	4944	0.526854	3.584462	0.001749	0.005928	0.028496	1	138	94	212	137	217	159	311	263	340	227
ENSMUSG00000036376	chr13	Abt1	23421539	23422335	1278	0.54012	3.413908	0.001751	0.005934	0.02904	1	126	96	161	144	161	192	257	195	341	170
ENSMUSG00000041132	chr5	N4bp2l1	1.51E+08	1.51E+08	1906	0.994654	1.668548	0.001753	0.005936	0.095019	1	38	28	31	29	33	69	60	124	65	45
ENSMUSG00000087119	chr3	Atg4a-ps	1.04E+08	1.04E+08	1185	-0.92325	0.65255	0.001752	0.005936	0.05898	-1	20	31	55	22	29	14	24	19	20	16
ENSMUSG00000025724	chr7	Sec11a	80904889	80905051	4614	0.476178	4.450758	0.001755	0.005943	0.024579	1	238	249	411	269	290	416	557	409	536	389
ENSMUSG00000055639	chr14	Dach1	97786853	97789619	7317	-1.00704	1.310416	0.001756	0.005943	0.095164	-1	33	26	58	68	76	7	43	26	42	31
ENSMUSG00000027324	chr2	Rpusd2	1.19E+08	1.19E+08	2706	-0.72328	1.331181	0.001764	0.00597	0.037258	-1	35	37	65	49	58	29	33	27	49	29
ENSMUSG00000028653	chr4	Trit1	1.23E+08	1.23E+08	2087	0.598359	3.310451	0.001766	0.005974	0.036494	1	138	75	131	142	133	180	255	185	304	166
ENSMUSG00000043535	chr2	Setx	29124181	29124269	11380	-0.5106	5.401506	0.001766	0.005974	0.030218	-1	581	399	1303	861	1027	486	749	605	774	576
ENSMUSG00000020262	chr10	Adarb1	77290726	77294961	11272	-0.70107	3.3248	0.001769	0.005982	0.052684	-1	112	112	336	211	266	146	144	141	183	76
ENSMUSG00000020275	chr11	Rel	23741514	23743040	2799	-1.33689	0.243427	0.00177	0.005983	0.144967	-1	13	10	58	14	39	9	26	7	7	7
ENSMUSG00000039615	chr17	Stub1	25830636	25831010	1672	0.492956	6.600664	0.001771	0.005986	0.028955	1	1243	976	1384	1325	1429	1795	2488	1844	2616	1661
ENSMUSG00000007815	chr9	Rhoa	1.08E+08	1.08E+08	7494	0.464213	6.983934	0.001774	0.005996	0.02581	1	1520	1369	2207	1521	1874	2212	3114	2670	3239	2189
ENSMUSG00000096056	chrX	Gm21986	1.01E+08	1.01E+08	5560	0.730686	2.076488	0.001779	0.00601	0.049824	1	58	22	84	44	45	72	108	92	130	70
ENSMUSG00000036442	chr8	Thap11	1.06E+08	1.06E+08	1848	0.454078	4.623267	0.001782	0.006019	0.022538	1	318	231	428	334	350	386	607	454	675	485
ENSMUSG00000035828	chr15	Pim3	88862186	88862752	2419	0.544572	4.786238	0.001786	0.006026	0.033685	1	291	284	352	380	463	508	915	502	641	449
ENSMUSG00000041841	chr15	Rpl37	5116613	5116684	867	0.553536	6.576807	0.001785	0.006026	0.036634	1	1308	1076	1362	1119	1137	1902	2541	1877	2485	1577
ENSMUSG00000071226	chr6	Cecr2	1.21E+08	1.21E+08	13306	-0.57899	3.614914	0.001785	0.006026	0.035751	-1	179	136	376	220	303	149	269	113	224	151
ENSMUSG00000005124	chr15	Wisp1	66891320	66891634	5518	1.081568	0.388622	0.001791	0.006042	0.084465	1	2	11	18	13	18	19	48	26	26	29
ENSMUSG00000022774	chr16	Ncbp2	31948513	31948727	2305	0.52386	4.116594	0.001791	0.006042	0.029551	1	191	190	241	232	262	323	445	403	359	309
ENSMUSG00000017686	chr11	Rhot1	80209019	80209323	7077	-0.43667	5.450504	0.001794	0.00605	0.022007	-1	687	580	1186	789	830	536	900	593	836	561
ENSMUSG00000010110	chr19	Stx5a	8741413	8741575	5808	0.451214	4.220785	0.001795	0.00605	0.021705	1	226	162	361	249	276	330	460	404	414	337
ENSMUSG00000044456	chr12	Rin3	1.02E+08	1.02E+08	6835	0.754521	2.591707	0.001802	0.006073	0.059446	1	37	41	89	93	102	129	117	163	149	107
ENSMUSG00000004151	chr12	Etv1	38779380	38779479	5889	-1.0194	0.870339	0.001805	0.006081	0.083067	-1	19	21	76	35	45	12	21	25	17	27
ENSMUSG00000014550	chr6	Zfyve20	92186712	92190458	5757	-0.4448	4.512599	0.001808	0.006092	0.021514	-1	335	260	650	423	495	263	460	328	420	305
ENSMUSG00000039001	chr2	Rps21	1.8E+08	1.8E+08	810	0.572143	6.729986	0.001815	0.006115	0.039365	1	1446	1279	1551	1043	1292	2010	3014	2203	2657	1758
ENSMUSG00000043017	chr7	Ptgir	16906490	16906910	3334	0.776489	1.858465	0.001822	0.006133	0.056584	1	25	23	57	49	59	60	90	100	67	81
ENSMUSG00000074264	chr3	Amy1	1.14E+08	1.14E+08	3446	-0.52608	5.828132	0.001822	0.006133	0.032932	-1	1021	800	1075	1145	1236	650	924	993	1103	609
ENSMUSG00000033352	chr11	Map2k4	65688243	65690804	4664	-0.45942	6.64379	0.001824	0.006137	0.025331	-1	1677	1235	2854	1622	2089	1156	1859	1384	2065	1315
ENSMUSG00000035936	chr13	Aldh5a1	24907579	24911766	5647	-0.61677	3.445852	0.001826	0.006143	0.04061	-1	143	110	241	263	319	113	204	151	190	130
ENSMUSG00000035953	chr14	Tmem55b	50926070	50928037	4489	0.49996	4.012071	0.001826	0.006143	0.026694	1	212	150	303	197	206	322	390	350	380	261
ENSMUSG00000035954	chr12	Dock4	40446053	40446394	8063	-0.67854	3.315346	0.001827	0.006145	0.049381	-1	135	85	353	184	281	93	154	172	159	116
ENSMUSG00000071035	chr17	Gm5499	87078271	87079155	885	-1.13823	0.018215	0.001838	0.006181	0.0781	-1	14	9	26	25	29	8	12	6	9	16
ENSMUSG00000028214	chr4	Gem	11704457	11704566	2104	0.806572	1.630866	0.001839	0.006183	0.055629	1	24	29	43	31	47	33	112	76	82	52
ENSMUSG00000020282	chr11	Rhbdf1	32209585	32210223	5433	0.469636	4.32683	0.001842	0.006188	0.024206	1	202	165	369	292	345	309	455	407	567	390
ENSMUSG00000024369	chr17	Nelfe	34850391	34850674	2076	0.596828	3.228135	0.001849	0.006212	0.035795	1	132	95	119	111	118	177	226	201	241	168
ENSMUSG00000022565	chr15	Plec	76170974	76178385	18113	-0.71414	9.074462	0.00185	0.006213	0.062256	-1	6527	4705	15666	14509	15094	5101	8667	5151	12282	7005
ENSMUSG00000026563	chr1	Tada1	1.66E+08	1.66E+08	4110	0.583304	2.652929	0.00185	0.006213	0.031222	1	82	50	106	71	90	102	150	150	156	117
ENSMUSG00000033910	chr3	Gucy1a3	82092427	82094899	6968	-0.68008	3.076957	0.001852	0.006215	0.048941	-1	91	102	248	159	261	67	179	109	129	112
ENSMUSG00000036430	chr17	Tbcc	46890621	46892463	1843	0.600774	2.671082	0.001854	0.006221	0.033477	1	59	61	82	88	107	111	176	133	160	111
ENSMUSG00000044477	chr17	Zfand3	30005087	30005308	2616	-0.47275	6.88972	0.001855	0.006223	0.027033	-1	1857	1349	3114	2392	2562	1250	2203	1635	2442	1660
ENSMUSG00000030689	chr7	Ino80e	1.27E+08	1.27E+08	4648	0.542968	3.358847	0.001862	0.006246	0.029509	1	123	105	145	140	139	187	239	198	260	207
ENSMUSG00000101086	chr14	Gm28651	32685648	32685781	644	-1.09755	0.82039	0.001865	0.006253	0.109135	-1	22	16	31	58	58	11	37	14	24	14
ENSMUSG00000014778	chr8	Fhod1	1.05E+08	1.05E+08	4666	0.501004	5.946317	0.001865	0.006254	0.029956	1	757	475	1167	789	994	854	1673	1091	1910	1206

ENSMUSG00000022359	chr15	Wdyhv1	58141436	58141581	1322	0.848334	2.032453	0.001869	0.006264	0.072959	1	17	27	53	71	64	80	125	82	95	83
ENSMUSG00000059552	chr11	Trp53	69580359	69580515	4045	0.561684	3.91013	0.001875	0.006284	0.034118	1	215	162	252	143	179	248	372	356	371	276
ENSMUSG00000095438	chr18	Gm21747	10781723	10781939	395	-0.70172	2.566467	0.001878	0.006293	0.050807	-1	100	89	147	111	133	64	141	46	115	54
ENSMUSG00000064370	chrMT	mt-Cytb	14145	15288	1144	-0.75865	13.63716	0.001882	0.006303	0.070494	-1	127522	126756	275191	356624	448873	127251	250104	137255	235600	136918
ENSMUSG00000031613	chr8	Hpgd	56294552	56294712	1719	-0.73919	1.301385	0.001884	0.006308	0.04123	-1	44	41	59	35	58	31	36	28	42	25
ENSMUSG00000025762	chr3	Larp1b	40950631	40950684	7216	-0.45015	5.855856	0.001887	0.006315	0.02404	-1	936	795	1606	947	1136	684	1239	841	1020	731
ENSMUSG00000037106	chr15	Fer1l6	58510048	58510126	8053	-1.22716	2.031129	0.001886	0.006315	0.16229	-1	39	25	102	174	128	25	49	42	31	65
ENSMUSG00000033184	chr18	Tmed7	46560235	46561072	8839	-0.51836	4.946644	0.001889	0.006319	0.031123	-1	444	392	936	523	700	270	492	487	570	496
ENSMUSG00000097243	chr14	Gm26908	70205324	70205453	1637	-0.941	0.940274	0.001889	0.006319	0.074987	-1	40	31	66	27	30	18	33	10	34	21
ENSMUSG00000051950	chr5	B3glct	1.5E+08	1.5E+08	4798	0.71763	2.063516	0.001892	0.006328	0.049434	1	41	20	83	40	74	60	103	95	123	84
ENSMUSG00000057322	chr11	Rpl38	1.15E+08	1.15E+08	542	0.571569	6.021028	0.001895	0.006334	0.039134	1	842	795	876	764	737	1215	1789	1356	1648	1100
ENSMUSG00000055866	chr1	Per2	91415982	91418020	5856	-0.66744	3.919567	0.001896	0.006337	0.050041	-1	184	162	525	324	364	170	165	242	220	236
ENSMUSG00000039410	chr4	Prdm16	1.54E+08	1.54E+08	9321	-0.88292	1.853737	0.001898	0.006342	0.077399	-1	36	40	86	74	145	25	61	43	57	43
ENSMUSG00000027162	chr2	Lin7c	1.1E+08	1.1E+08	4521	-0.50047	4.484859	0.001899	0.006344	0.028234	-1	317	309	588	408	504	202	355	383	423	331
ENSMUSG00000040123	chr14	Zmym5	56790585	56794500	5541	-0.48273	4.40694	0.001904	0.006361	0.026048	-1	354	289	602	323	437	207	449	315	363	296
ENSMUSG00000024939	chr19	Fam89b	5728087	5728878	1209	0.508681	4.531313	0.001907	0.006368	0.02896	1	301	248	373	286	292	433	535	523	634	348
ENSMUSG00000047003	chr15	Zfp41	75616679	75616820	4068	-0.78852	1.667078	0.001907	0.006368	0.053713	-1	38	47	105	63	68	45	31	42	49	35
ENSMUSG00000018861	chr11	Fdxr	1.15E+08	1.15E+08	2806	0.731841	2.276038	0.001911	0.006379	0.052198	1	35	40	53	78	78	74	130	103	120	111
ENSMUSG00000022807	chr16	Osbpl11	33185071	33186000	4520	-0.49451	4.038602	0.001914	0.006385	0.026442	-1	219	197	415	321	418	170	286	277	297	216
ENSMUSG00000021978	chr14	Extl3	65052060	65054822	5977	-0.4843	6.203201	0.001916	0.006393	0.028182	-1	1198	784	2196	1274	1679	870	1174	1141	1408	1008
ENSMUSG00000067424	chr17	Zfp563	33089310	33089479	2198	-0.89312	0.595134	0.001918	0.006396	0.054132	-1	14	24	37	34	40	12	22	17	25	15
ENSMUSG00000022144	chr15	Gdnf	7811011	7811114	3509	1.207012	0.400074	0.001919	0.006397	0.127493	1	1	5	31	15	10	28	44	30	29	21
ENSMUSG00000073435	chr17	Nme3	24896500	24896559	876	0.617774	2.567374	0.001924	0.006412	0.035833	1	71	57	99	70	69	123	140	133	133	105
ENSMUSG00000026113	chr1	Inpp4a	37299865	37300118	10387	-0.45592	4.441083	0.001931	0.006435	0.023014	-1	294	301	634	360	464	245	408	297	444	292
ENSMUSG00000079111	chr5	Kdelr2	1.43E+08	1.43E+08	1846	0.478013	4.541265	0.001936	0.006451	0.025442	1	275	269	402	253	343	393	587	506	524	443
ENSMUSG00000039197	chr14	Adk	21052574	21052700	1781	-0.81366	5.626719	0.001938	0.006455	0.080136	-1	500	463	1118	1645	1486	379	1056	494	768	654
ENSMUSG00000053038	chr8	Gm6180	42246911	42247411	501	0.935903	0.388459	0.001946	0.006479	0.054584	1	9	9	20	16	12	25	26	32	27	30
ENSMUSG00000040690	chr4	Col16a1	1.3E+08	1.3E+08	6750	0.78785	3.670931	0.001951	0.006496	0.071667	1	58	104	204	174	228	172	287	315	293	369
ENSMUSG00000026313	chr1	Hdac4	91928779	91933386	15375	-0.53959	5.488957	0.001956	0.006511	0.034799	-1	709	652	1448	650	900	430	676	830	819	589
ENSMUSG00000055865	chr3	Fam19a3	1.05E+08	1.05E+08	4484	-0.53809	3.234378	0.001959	0.006517	0.029133	-1	138	105	272	164	236	102	190	118	155	134
ENSMUSG00000040447	chr11	Spns2	72451638	72453115	4083	-0.83697	5.841964	0.001963	0.00653	0.085216	-1	1665	848	1438	786	1003	804	917	582	1226	315
ENSMUSG00000014355	chr2	Anapc1	1.29E+08	1.29E+08	16714	-0.48719	5.324399	0.001973	0.006562	0.027963	-1	560	437	1319	705	898	446	836	592	665	529
ENSMUSG00000027342	chr2	Pcna	1.32E+08	1.32E+08	2400	0.453908	4.221982	0.001976	0.006571	0.022073	1	240	183	307	243	278	294	484	338	494	362
ENSMUSG00000024013	chr17	Fgd2	29360914	29361157	4134	0.943495	1.105196	0.00198	0.006582	0.078112	1	23	12	43	15	22	46	41	70	43	38
ENSMUSG00000040785	chr16	Ttc3	94370618	94370861	15134	-0.47979	6.010674	0.001981	0.006584	0.027683	-1	892	738	2005	1200	1414	857	1104	902	1167	865
ENSMUSG00000021282	chr12	Eif5	1.12E+08	1.12E+08	4061	-0.47628	7.422706	0.001982	0.006585	0.027966	-1	2799	2371	4776	2878	3361	1988	3768	2458	2863	2177
ENSMUSG00000008153	chr6	Clstn3	1.24E+08	1.24E+08	4968	1.733956	1.243458	0.001984	0.006589	0.314846	1	18	16	17	14	15	19	35	190	20	40
ENSMUSG00000096054	chr10	Syne1	5020203	5022247	11801	-0.4879	5.431887	0.001985	0.006591	0.028283	-1	824	508	1303	647	842	533	810	548	879	543
ENSMUSG00000036644	chr11	Tbc1d9b	50131396	50131556	6429	-0.48821	5.266544	0.001986	0.006594	0.028035	-1	513	402	1043	856	900	452	684	606	669	511
ENSMUSG00000023938	chr17	Aars2	45506841	45507081	3348	-0.52646	4.384152	0.001989	0.0066	0.031589	-1	341	204	505	462	499	198	374	286	412	305
ENSMUSG00000038949	chr1	Cnst	1.8E+08	1.8E+08	8859	-0.43716	5.52539	0.001991	0.006606	0.022561	-1	748	536	1248	829	968	512	895	628	921	653
ENSMUSG00000021552	chr13	Gkap1	58233351	58233658	1518	-0.47714	4.136494	0.001992	0.006608	0.025195	-1	286	281	383	299	363	221	364	236	315	212
ENSMUSG00000090799	chr14	Klhl33	50891389	50891941	1602	-0.5883	5.745268	0.001995	0.006615	0.04194	-1	685	660	1303	1122	1519	541	1260	712	662	762
ENSMUSG00000020132	chr10	Rab21	1.15E+08	1.15E+08	1823	-0.47603	5.251121	0.001999	0.00663	0.026723	-1	501	447	964	777	947	388	716	533	789	523
ENSMUSG00000020044	chr10	Timp3	86300372	86300974	8144	-0.59327	7.089894	0.002001	0.006633	0.04338	-1	1771	1813	4631	2023	3518	1504	2209	2631	1920	1578
ENSMUSG00000085779	chr10	Atcayos	81194609	81194722	4375	-0.72034	6.229667	0.002001	0.006633	0.063681	-1	1288	1538	1892	1266	1273	905	1129	767	1966	581
ENSMUSG00000005893	chr6	Nr2c2	92091390	92091742	9152	-0.52064	4.8694	0.002002	0.006635	0.031587	-1	408	294	1050	536	622	334	540	402	544	384
ENSMUSG00000055991	chr5	Zkscan5	1.45E+08	1.45E+08	4114	-0.50702	3.459701	0.002009	0.006655	0.026835	-1	160	147	271	229	228	110	220	141	211	153
ENSMUSG00000040018	chr19	Cox15	43733254	43736852	4909	-0.50483	5.017632	0.002012	0.006664	0.029968	-1	460	332	828	705	805	314	624	442	650	451
ENSMUSG00000027195	chr2	Hsd17b12	94032689	94033661	2407	0.852087	3.443027	0.002016	0.006674	0.082859	1	137	112	109	96	137	201	241	432	206	161
ENSMUSG00000067158	chr1	Col4a4	82448423	82453394	10612	-1.56912	1.794247	0.00202	0.006685	0.267156	-1	74	63	152	36	96	65	4	17	40	18
ENSMUSG00000064043	chr17	Trerf1	47140875	47140965	9070	0.765549	1.286182	0.002021	0.006688	0.047382	1	18	19	46	18	41	47	60	55	53	49
ENSMUSG00000073889	chr4	Il11ra1	41699989	41700116	4471	0.464053	5.833737	0.002022	0.006688	0.02586	1	639	538	871	810	986	994	1260	1250	1495	1016
ENSMUSG00000073418	chr17	C4b	34728380	34728627	5695	1.082654	5.654075	0.002029	0.00671	0.142103	1	551	484	939	211	405	1435	801	2057	1201	523
ENSMUSG00000018821	chr19	Avpi1	42123273	42123848	1236	0.609791	3.868366	0.00203	0.006712	0.041415	1	179	145	166	194	213	283	371	236	507	229
ENSMUSG00000027406	chr2	Idh3b	1.3E+08	1.3E+08	3422	-0.61131	8.593163	0.002031	0.006713	0.046534	-1	5475	4434	7768	10217	9825	4075	8999	4446	6757	4380
ENSMUSG00000043683	chr17	Fem1a	56256793	56263608	6816	-0.47458	8.892553	0.002031	0.006713	0.028114	-1	7544	5135	12599	9652	10465	5524	8994	6338	9331	6496
ENSMUSG00000022195	chr15	6030458C11Rik	12808177	12810844	3974	-0.42369	5.278456	0.002039	0.006739	0.020973	-1	610	515	1028	623	833	451	724	570	747	547
ENSMUSG00000030428	chr7	Ttyh1	4119408	4119424	6345	-1.18774	-0.25163	0.002052	0.006777	0.095836	-1	20	7	25	12	20	7	14	6	14	1
ENSMUSG00000028382	chr4	Ptbp3	59471868	59477015	7480	0.501349	3.841135	0.002056	0.006789	0.027495	1	138	124	283	175	251	211	319	353	375	267
ENSMUSG00000024516	chr18	Sec11c	65800549	65800711	3084	0.531604	4.365988	0.002056	0.00679	0.031948	1	276	230	314	242	252	414	508	446	517	322
ENSMUSG00000020364	chr11	Zfp354a	51059257	51059402	4318	-0.55076	2.763529	0.002065	0.006814	0.028761	-1	111	95	193	119	127	77	132	92	108	89
ENSMUSG00000058173	chr9	Smco4	15505487	15505641	988	0.652766	3.351973	0.002065	0.006814	0.047436	1	83	69	138	144	211	135	302	252	262	192
ENSMUSG00000024844	chr19	Banf1	5364641	5365158	820	0.494913	6.49363	0.002067	0.006818	0.030005	1	1188	948	1332	1196	1207	1563	2401	1605	2466	1663
ENSMUSG00000033808	chr2	Tmem87a	1.2E+08	1.2E+08	7528	-0.61743	5.691985	0.002067	0.006818	0.04665	-1	889	952	1599	581	991	608	926	533	1087	628

ENSMUSG00000048039	chr3	Isg20l2	87930314	87930611	2893	0.524065	3.255307	0.002069	0.006822	0.027827	1	120	71	150	136	148	169	233	186	255	175
ENSMUSG00000059474	chr11	Mbtd1	93885852	93886062	13896	-0.62191	2.927163	0.00207	0.006823	0.039793	-1	109	112	265	101	168	84	127	123	132	78
ENSMUSG00000021814	chr14	Anxa7	20455261	20456601	2965	0.505643	6.902495	0.002072	0.006828	0.031577	1	1397	1305	2044	1467	1650	2267	3234	1884	3609	1996
ENSMUSG00000070737	chr4	Gm12942	1.27E+08	1.27E+08	1910	0.714997	2.112588	0.002075	0.006836	0.046583	1	46	53	68	37	47	90	115	91	110	70
ENSMUSG00000021400	chr13	Wrnip1	32802038	32803044	2633	0.52448	3.01317	0.002078	0.006845	0.026876	1	85	71	138	113	121	148	198	163	184	158
ENSMUSG00000040658	chr17	Dnph1	46496789	46496972	1106	-0.62617	2.541026	0.002079	0.006848	0.038523	-1	118	86	165	80	110	66	100	69	103	75
ENSMUSG00000029104	chr5	Htt	34761740	34762109	18808	-0.5759	3.873205	0.002084	0.006861	0.036931	-1	184	137	480	289	388	168	239	233	232	191
ENSMUSG00000079003	chr8	Samd1	83997672	83998565	2071	0.550326	3.664651	0.002084	0.006861	0.032909	1	172	110	257	130	159	215	270	312	335	227
ENSMUSG00000021094	chr12	Dhrs7	72650356	72650617	1301	0.548167	4.103173	0.002088	0.006872	0.034093	1	172	141	254	297	251	256	415	428	400	347
ENSMUSG00000033249	chr8	Hsf4	1.05E+08	1.05E+08	1753	0.535213	3.658325	0.002098	0.006902	0.030786	1	153	128	247	144	150	239	257	264	368	220
ENSMUSG00000067150	chr17	Xpo5	46202855	46203025	3709	-0.60063	3.388383	0.002099	0.006904	0.039009	-1	132	118	316	196	284	96	200	160	144	154
ENSMUSG00000097177	chr9	9330159M07Rik	88840236	88840726	6831	-0.63135	2.248154	0.002106	0.006926	0.037193	-1	63	72	132	89	104	51	90	46	94	58
ENSMUSG00000022679	chr16	Mpv17l	13903161	13903280	3760	1.028363	0.034547	0.002114	0.00695	0.060694	1	9	7	16	7	9	15	19	30	26	20
ENSMUSG00000021550	chr13	2210016F16Rik	58380046	58382009	2822	0.589158	4.020406	0.002116	0.006956	0.03896	1	212	204	201	163	211	312	416	324	434	283
ENSMUSG00000037325	chr3	Bbs7	36573142	36573622	3957	-0.52097	3.135651	0.002118	0.00696	0.027134	-1	146	121	229	145	188	96	176	108	144	131
ENSMUSG00000078486	chr4	Perm1	1.56E+08	1.56E+08	3901	-1.25461	7.421438	0.002118	0.00696	0.192009	-1	1481	789	3058	8344	6553	929	2944	1488	2757	1552
ENSMUSG00000038302	chr10	Lace1	42312585	42313616	2705	-0.61302	3.907372	0.002125	0.006979	0.043375	-1	210	147	321	391	407	138	301	185	298	182
ENSMUSG00000031805	chr8	Jak3	71676296	71676583	5352	0.609986	2.627923	0.002126	0.006981	0.036284	1	62	54	98	72	103	114	154	164	146	90
ENSMUSG00000028664	chr4	Ephb2	1.37E+08	1.37E+08	12608	1.146973	0.358197	0.002128	0.006987	0.108892	1	7	2	15	16	20	23	27	46	23	24
ENSMUSG00000042626	chr3	Shc1	89418443	89418709	5645	0.440327	4.762837	0.002131	0.006993	0.022159	1	343	269	506	314	420	450	670	597	695	446
ENSMUSG00000058070	chr12	Eml1	1.08E+08	1.08E+08	7436	-0.47591	6.747376	0.002138	0.007014	0.028077	-1	1903	1207	3235	1664	2313	1435	1990	1489	1911	1379
ENSMUSG00000091449	chr18	Gm10269	20682592	20682963	372	0.706103	1.798576	0.002138	0.007014	0.041626	1	39	36	46	42	38	65	88	62	109	59
ENSMUSG00000056209	chr19	Npm3	45747734	45748051	1187	0.538754	3.493781	0.002142	0.007026	0.030322	1	159	117	166	124	150	187	315	229	283	200
ENSMUSG00000030655	chr7	Smg1	1.18E+08	1.18E+08	21225	-0.57703	5.331715	0.002162	0.007088	0.040418	-1	543	362	1597	720	927	486	694	576	675	512
ENSMUSG00000049349	chr3	Gm5105	1.38E+08	1.38E+08	1665	-0.83263	0.624418	0.002164	0.007093	0.041866	-1	26	19	42	31	32	16	27	21	19	12
ENSMUSG00000068134	chr2	Zfp120	1.5E+08	1.5E+08	4376	-0.51056	3.564076	0.002164	0.007093	0.027612	-1	177	180	309	196	250	154	243	143	183	161
ENSMUSG00000025702	chr6	March8	1.16E+08	1.16E+08	6536	-0.42048	5.398497	0.002167	0.007099	0.021037	-1	658	524	1048	753	934	497	843	571	822	588
ENSMUSG00000060743	chr1	H3f3a	1.81E+08	1.81E+08	3504	-0.48202	6.467863	0.002169	0.007106	0.028843	-1	1319	1313	2317	1667	1672	874	1771	1244	1598	1326
ENSMUSG00000074151	chr8	Nlrc5	94472763	94473054	7646	1.057158	0.913859	0.002174	0.007118	0.101034	1	14	12	24	18	25	54	54	58	29	18
ENSMUSG00000025271	chrX	Pfkfb1	1.51E+08	1.51E+08	4017	-0.63264	5.778683	0.002175	0.007119	0.049518	-1	777	517	1128	1590	1425	640	1117	643	1016	586
ENSMUSG00000027763	chr3	Mbnl1	60472830	60472884	18717	-0.53168	8.277442	0.002175	0.007119	0.035685	-1	5199	4777	9922	4465	5440	3143	6055	4102	6205	4100
ENSMUSG00000028911	chr4	Srsf4	1.32E+08	1.32E+08	3561	0.440803	4.726462	0.002175	0.007119	0.0224	1	344	221	489	344	420	448	622	574	664	465
ENSMUSG00000062743	chr17	Zfp677	21383748	21384020	2917	-0.90902	0.430466	0.002182	0.007139	0.053118	-1	22	24	32	25	27	8	15	19	19	18
ENSMUSG00000028256	chr3	Odf2l	1.45E+08	1.45E+08	2584	-0.67882	2.578054	0.002186	0.007149	0.047856	-1	108	102	151	74	144	61	123	65	82	84
ENSMUSG00000079487	chrX	Med12	1.01E+08	1.01E+08	7704	-0.60526	4.007426	0.002187	0.00715	0.042292	-1	236	141	629	267	385	156	312	233	264	206
ENSMUSG00000026399	chr1	Cd55	1.3E+08	1.3E+08	4853	0.624249	6.514061	0.002195	0.007177	0.048599	1	1410	892	1392	849	1093	1479	3464	1776	2156	1498
ENSMUSG00000039449	chr2	Prpf18	4622058	4624526	5310	-0.42252	5.503488	0.002196	0.007178	0.021402	-1	697	606	1201	769	940	576	891	596	869	624
ENSMUSG00000025894	chr9	Aasdhppt	4294793	4296839	2870	-0.45094	4.110537	0.002198	0.007181	0.022356	-1	233	229	436	350	363	195	308	254	341	237
ENSMUSG00000073433	chr17	Arhgdig	26196226	26196331	3252	1.081474	-0.02244	0.002203	0.007196	0.07013	1	4	8	8	13	11	16	18	22	26	24
ENSMUSG00000062908	chr3	Acadm	1.54E+08	1.54E+08	2932	-0.79572	8.016471	0.002206	0.007204	0.079613	-1	3101	2467	4711	9155	7295	2442	5386	2698	4644	2662
ENSMUSG00000043192	chr8	Gm1840	5639584	5640996	1413	0.529214	3.695731	0.002208	0.00721	0.030924	1	130	114	279	161	182	197	275	284	430	219
ENSMUSG00000097565	chr13	Gm26965	67491152	67492150	1520	-0.74915	1.162638	0.00221	0.007215	0.041753	-1	42	28	63	46	38	22	40	25	30	29
ENSMUSG00000003380	chr7	Rabac1	24969750	24970009	875	0.495833	6.840084	0.002215	0.007229	0.030713	1	1360	1250	1607	1508	1755	2043	2669	2301	3413	1903
ENSMUSG00000032041	chr9	Tirap	35184551	35187930	4929	-0.55421	4.114701	0.002217	0.007234	0.035574	-1	314	195	540	234	420	172	371	288	290	179
ENSMUSG00000002227	chr3	Mov10	1.05E+08	1.05E+08	4223	1.021115	0.984242	0.002224	0.007254	0.094302	1	27	11	28	12	21	37	37	64	33	49
ENSMUSG00000055723	chr7	Rras2	1.14E+08	1.14E+08	2272	0.439861	4.093019	0.002227	0.007262	0.020774	1	198	184	310	216	246	290	442	335	427	296
ENSMUSG00000018822	chr19	Sfrp5	42197971	42199031	1900	-0.95017	2.575151	0.002228	0.007263	0.102847	-1	55	68	122	191	198	34	126	50	105	66
ENSMUSG00000097451	chr12	Rian	1.1E+08	1.1E+08	17475	0.630325	3.284554	0.002231	0.007272	0.044045	1	110	93	210	78	128	146	239	218	213	241
ENSMUSG00000065336	chr15	Snora34	98519716	98519853	138	1.221145	-0.49862	0.002232	0.007275	0.0689	1	7	4	8	6	3	14	16	17	12	15
ENSMUSG00000022400	chr15	Rbx1	81466316	81466450	1655	0.45342	6.336826	0.002233	0.007275	0.02543	1	982	827	1365	1054	1221	1358	2214	1450	2205	1404
ENSMUSG00000027134	chr2	Lpcat4	1.12E+08	1.12E+08	2823	0.839567	0.814103	0.002236	0.007284	0.051796	1	16	6	26	25	23	27	47	40	47	32
ENSMUSG00000056214	chr18	Pard6g	80046895	80047142	3143	0.868202	1.016071	0.002237	0.007285	0.061635	1	23	11	30	13	33	34	42	59	57	32
ENSMUSG00000091086	chr10	Gm5428	1.11E+08	1.11E+08	888	0.587364	3.855881	0.002238	0.007287	0.038562	1	184	180	170	167	181	256	379	281	373	286
ENSMUSG00000036990	chr8	Otud4	79639618	79640064	8096	-0.49398	5.957579	0.002245	0.007306	0.030216	-1	906	778	1934	1013	1391	565	1199	893	1284	862
ENSMUSG00000020079	chr10	Supv3l1	62429209	62429834	2969	-0.63362	3.83116	0.002258	0.007347	0.046828	-1	169	145	352	404	346	138	274	159	276	185
ENSMUSG00000040128	chr4	Pnrc1	33245423	33246507	2095	0.521346	6.012221	0.00226	0.00735	0.033656	1	804	733	1217	712	738	951	1730	1248	1738	1337
ENSMUSG00000029401	chr5	Rilpl2	1.24E+08	1.24E+08	1391	0.616816	2.499484	0.002268	0.007375	0.036621	1	72	45	91	65	79	97	160	143	127	87
ENSMUSG00000039419	chr6	Cntnap2	45060061	45060386	7183	-1.00449	3.269927	0.002268	0.007375	0.119595	-1	250	214	328	91	113	66	163	115	90	145
ENSMUSG00000040964	chr4	Arhgef10l	1.41E+08	1.41E+08	5693	-0.51717	6.033998	0.002273	0.007387	0.033277	-1	1075	650	1666	1392	1553	748	1207	736	1318	956
ENSMUSG00000026872	chr2	Zeb2	44983634	44989153	19658	-0.56619	4.161813	0.002275	0.007395	0.037366	-1	225	228	587	296	443	148	314	302	281	270
ENSMUSG00000022452	chr15	Smdt1	82338959	82339085	1077	0.48673	6.373366	0.002278	0.0074	0.029521	1	1126	837	1246	1062	1173	1514	2021	1619	2325	1395
ENSMUSG00000055065	chr15	Ddx17	79527707	79530517	4761	0.470905	6.168986	0.002278	0.0074	0.027576	1	883	700	1472	736	1121	1184	1882	1510	1656	1389
ENSMUSG00000033256	chr2	Shf	1.22E+08	1.22E+08	2305	0.875642	0.783222	0.002284	0.007418	0.051401	1	21	13	19	21	15	27	40	38	44	39
ENSMUSG00000055900	chr4	Tmem69	1.17E+08	1.17E+08	2069	-0.4498	4.253496	0.002289	0.007432	0.022966	-1	277	278	467	321	426	207	398	251	380	254
ENSMUSG00000034973	chr9	Dopey1	86467154	86467296	20476	-0.53401	3.609195	0.002294	0.007447	0.031068	-1	161	130	406	215	294	160	234	165	209	140

ENSMUSG00000097769	chr18	Snhg4	35553371	35553469	4666	0.737836	2.053758	0.002298	0.007458	0.04965	1	40	48	43	51	53	70	112	72	138	75
ENSMUSG00000037095	chr17	Lrg1	56119680	56120944	1351	0.803223	4.101699	0.002319	0.007525	0.078214	1	185	111	186	304	197	364	405	595	410	191
ENSMUSG00000032086	chr9	Bace1	45838580	45839288	6348	-0.53482	5.39848	0.002322	0.007532	0.035335	-1	717	609	1386	532	847	535	824	488	875	472
ENSMUSG00000037857	chr11	Nufip2	77686155	77686507	5792	-0.45855	4.567095	0.002323	0.007532	0.024541	-1	329	338	682	399	484	232	449	351	461	345
ENSMUSG00000036446	chr10	Lum	97565501	97565885	2075	0.568929	5.978549	0.002337	0.007578	0.040644	1	513	587	1123	901	1021	806	1428	1582	1520	1499
ENSMUSG00000052146	chr17	Rps10	27630422	27630506	1937	0.552137	6.836141	0.00234	0.007585	0.038558	1	1588	1336	1510	1245	1472	2242	2824	2311	3000	1999
ENSMUSG00000035024	chr9	Ncapd3	27030175	27030499	5499	-0.63003	2.920026	0.002342	0.007587	0.042155	-1	102	98	258	147	148	64	133	135	110	96
ENSMUSG00000079418	chrX	Atg4a	1.41E+08	1.41E+08	2661	-0.48095	4.987693	0.002342	0.007587	0.027979	-1	549	485	782	524	595	426	639	350	614	405
ENSMUSG00000036368	chr17	Rmdn2	79614900	79614987	1802	-0.59596	2.893502	0.002348	0.007606	0.03703	-1	131	93	181	149	158	70	135	88	114	126
ENSMUSG00000026972	chr2	Arrdc1	24925352	24925676	2510	0.642655	2.775499	0.002349	0.007606	0.043039	1	89	71	108	60	89	157	155	129	182	118
ENSMUSG00000027774	chr3	Gfm1	67430096	67430322	4419	-0.51481	6.883285	0.002367	0.007659	0.033694	-1	1734	1235	2731	2753	2905	1347	2399	1469	2362	1460
ENSMUSG00000035686	chr7	Thrsp	97412938	97413515	1277	1.261737	5.09443	0.002366	0.007659	0.196422	1	415	302	300	224	278	721	362	2111	531	447
ENSMUSG00000061544	chr17	Zfp229	21730795	21731051	5139	-0.71422	1.897644	0.002367	0.007659	0.048827	-1	54	46	132	55	90	37	62	44	82	32
ENSMUSG00000039568	chr16	Ubald1	4874778	4875869	5538	0.461481	5.608491	0.002369	0.007662	0.026308	1	633	379	984	663	694	789	1105	941	1351	976
ENSMUSG00000031835	chr8	Mbtps1	1.2E+08	1.2E+08	4370	-0.45894	5.129372	0.002386	0.007717	0.025333	-1	479	413	1001	641	811	426	606	578	559	497
ENSMUSG00000078485	chr4	Plekhn1	1.56E+08	1.56E+08	2210	1.042677	0.124136	0.002387	0.007717	0.074566	1	7	5	10	14	15	16	20	35	26	21
ENSMUSG00000032803	chr9	Cdv3	1.03E+08	1.03E+08	7403	-0.45612	7.655413	0.002388	0.00772	0.026646	-1	3065	2705	4823	4113	4043	2559	3828	2611	4087	2589
ENSMUSG00000031070	chr7	Mrgprf	1.45E+08	1.45E+08	2214	0.730723	1.789182	0.002393	0.007732	0.050758	1	23	26	61	48	48	73	69	89	90	55
ENSMUSG00000037254	chr2	Itih2	10094593	10094901	3315	0.995104	0.536644	0.002393	0.007732	0.078793	1	5	11	24	13	20	28	40	44	35	15
ENSMUSG00000025875	chr13	Tspan17	54789377	54789681	1657	0.705752	3.832521	0.002397	0.007744	0.05872	1	225	156	207	100	143	279	323	309	455	240
ENSMUSG00000034613	chr10	Ppm1h	1.23E+08	1.23E+08	10226	0.735381	1.207378	0.0024	0.00775	0.041618	1	17	14	37	28	39	43	52	53	60	41
ENSMUSG00000078495	chr4	Gm13157	1.48E+08	1.48E+08	2912	-0.75049	1.321553	0.002402	0.007756	0.047263	-1	51	39	66	39	46	31	41	32	43	18
ENSMUSG00000044496	chr4	2510039O18Rik	1.48E+08	1.48E+08	2731	0.436604	4.549719	0.002404	0.007758	0.022041	1	271	205	384	341	401	398	567	441	628	425
ENSMUSG00000035407	chr4	Kank4	98754898	98756585	4795	-1.03134	0.276007	0.002408	0.007769	0.066673	-1	16	11	38	23	36	11	12	18	10	14
ENSMUSG00000096474	chr1	Gm5561	1.8E+08	1.8E+08	480	1.087608	0.499055	0.002408	0.007769	0.092566	1	19	8	17	11	10	26	54	26	47	12
ENSMUSG00000056050	chr1	Mia3	1.83E+08	1.83E+08	4431	-0.45945	6.608229	0.00241	0.007775	0.02673	-1	1523	1150	2717	1719	2176	1249	1573	1320	2126	1271
ENSMUSG00000030486	chr7	Zfp108	24257644	24257658	1929	-0.96665	0.564747	0.002426	0.007824	0.069502	-1	21	12	48	33	38	16	23	7	21	18
ENSMUSG00000079057	chr8	Cyp4v3	45269671	45270093	6246	0.920174	2.162178	0.00243	0.007836	0.09075	1	54	50	52	32	44	70	113	172	111	56
ENSMUSG00000029672	chr6	Fam3c	22306520	22308538	3713	0.50132	3.567106	0.002442	0.007871	0.027169	1	117	114	216	153	190	156	301	274	298	236
ENSMUSG00000030697	chr7	Ppp4c	1.27E+08	1.27E+08	1293	0.509246	4.512275	0.002446	0.007881	0.030448	1	286	258	307	291	323	425	550	428	680	371
ENSMUSG00000063884	chr6	Ptcd3	71880648	71881231	2585	-0.56639	5.610571	0.002451	0.007895	0.040398	-1	695	518	1035	1270	1216	507	1125	611	795	621
ENSMUSG00000015668	chrX	Pdzd11	1.01E+08	1.01E+08	2127	0.545789	3.4512	0.002458	0.007914	0.032265	1	140	111	152	121	173	190	312	226	224	216
ENSMUSG00000029166	chr5	Mapre3	30814641	30814898	3407	0.52715	6.442539	0.002457	0.007914	0.035345	1	1216	886	1739	854	1010	1579	2079	1668	2471	1600
ENSMUSG00000020358	chr11	Hnrnpab	51600100	51601478	2782	0.484491	6.899308	0.002464	0.007929	0.029961	1	1596	1327	1970	1357	1594	2095	3236	2345	3143	2001
ENSMUSG00000046139	chr19	Patl1	11912399	11912577	4221	-0.4982	4.663147	0.002463	0.007929	0.029699	-1	344	242	748	509	637	281	457	355	494	342
ENSMUSG00000076236	chr13	Mir682	75645046	75645141	96	0.617057	3.414847	0.002468	0.007941	0.042202	1	145	112	141	130	120	231	320	187	256	173
ENSMUSG00000044562	chr7	Rasip1	45627488	45627590	3202	0.533797	3.498641	0.002471	0.007949	0.031807	1	123	77	196	166	188	195	274	259	330	164
ENSMUSG00000020121	chr10	Srgap1	1.22E+08	1.22E+08	9132	1.076814	0.47388	0.002474	0.007954	0.09284	1	11	9	24	14	8	23	29	51	39	15
ENSMUSG00000030138	chr6	Bms1	1.18E+08	1.18E+08	4286	-0.42364	5.177494	0.002474	0.007954	0.021703	-1	582	484	938	560	794	454	717	510	642	502
ENSMUSG00000018171	chr11	Vmp1	86583865	86585451	3862	-0.45965	5.739566	0.002484	0.007985	0.026443	-1	939	699	1491	881	999	697	1140	647	989	674
ENSMUSG00000024758	chr19	Rtn3	7425901	7427875	5030	0.433392	5.728495	0.002495	0.008018	0.023356	1	625	509	1039	711	767	896	1297	1231	1281	858
ENSMUSG00000042426	chr13	Dhx29	1.13E+08	1.13E+08	4405	-0.46444	4.399767	0.002499	0.008029	0.025215	-1	288	257	606	450	398	248	376	312	423	268
ENSMUSG00000098802	chr7	Mir7046	24970010	24970075	66	0.750217	1.327426	0.002513	0.008072	0.045043	1	17	22	36	39	29	45	60	49	77	44
ENSMUSG00000084939	chr4	Gm830	95464724	95467895	3502	1.839232	3.002241	0.002515	0.008076	0.396351	1	56	107	70	2	8	213	226	265	258	155
ENSMUSG00000061207	chr17	Stk19	34823993	34824324	3155	0.616155	2.925158	0.002521	0.008094	0.03988	1	103	73	97	83	109	164	208	153	186	114
ENSMUSG00000036078	chr4	Sigmar1	41738493	41739580	3136	0.586376	3.188694	0.002525	0.008105	0.038011	1	90	65	161	135	139	128	251	252	195	164
ENSMUSG00000029560	chr5	Snx8	1.4E+08	1.4E+08	2615	0.498824	4.024953	0.002533	0.008129	0.028585	1	186	147	230	226	285	327	362	340	434	259
ENSMUSG00000093445	chr5	Lrch4	1.38E+08	1.38E+08	3925	0.431665	4.548628	0.002535	0.008132	0.021956	1	248	196	480	338	370	393	544	490	614	409
ENSMUSG00000026409	chr1	Pfkfb2	1.31E+08	1.31E+08	7254	-0.71646	3.079987	0.002536	0.008135	0.058812	-1	82	90	217	199	282	80	159	95	127	120
ENSMUSG00000005687	chr3	Bcas2	1.03E+08	1.03E+08	4390	0.45365	5.366997	0.002537	0.008136	0.025235	1	486	478	649	522	610	718	1043	758	1143	717
ENSMUSG00000037419	chr9	Endod1	14353990	14357887	4470	0.610246	2.367262	0.002544	0.008155	0.037025	1	37	43	88	72	87	88	142	110	120	97
ENSMUSG00000037110	chr2	Ralgapa2	1.46E+08	1.46E+08	18352	-0.61094	3.809665	0.00255	0.008172	0.044016	-1	197	142	408	296	361	130	205	290	216	163
ENSMUSG00000096974	chr4	Gm26881	43046034	43046277	592	0.789847	1.362446	0.00255	0.008172	0.053736	1	36	15	27	27	38	44	58	59	81	43
ENSMUSG00000025742	chrX	Prps2	1.67E+08	1.67E+08	3873	0.668943	1.50962	0.002552	0.008177	0.035083	1	25	27	50	35	33	47	65	60	75	58
ENSMUSG00000041390	chr6	Mdfic	15720661	15720963	7427	0.485463	3.728309	0.002558	0.008191	0.025939	1	146	122	217	201	194	187	337	267	342	275
ENSMUSG00000052926	chr8	Rnaseh2a	84956610	84957864	3509	0.471114	3.804754	0.002558	0.008192	0.024205	1	164	151	224	161	228	251	371	262	369	228
ENSMUSG00000058388	chr3	Phtf1	1.04E+08	1.04E+08	7294	0.596246	2.701654	0.002564	0.008209	0.036642	1	70	53	103	93	91	128	126	157	162	119
ENSMUSG00000043719	chr9	Col6a6	1.06E+08	1.06E+08	9166	0.70124	3.954818	0.00257	0.008226	0.06059	1	153	121	401	102	219	346	316	267	538	273
ENSMUSG00000041540	chr6	Sox5	1.44E+08	1.44E+08	14376	-1.12832	-0.07789	0.002572	0.008227	0.093014	-1	10	16	36	12	22	5	12	15	14	3
ENSMUSG00000046006	chr13	Gapt	1.1E+08	1.1E+08	2055	1.120624	-0.21219	0.002571	0.008227	0.06562	1	8	8	10	5	6	17	25	16	15	19
ENSMUSG00000015882	chr5	Lcorl	45697181	45701997	10945	-0.89498	1.49324	0.002576	0.008237	0.080776	-1	33	45	102	41	73	11	55	38	37	36
ENSMUSG00000032456	chr9	Nmnat3	98287435	98287576	5004	-0.51853	4.152304	0.002576	0.008237	0.031844	-1	277	173	425	422	408	197	379	222	333	221
ENSMUSG00000033278	chr17	Ptprm	66666848	66667681	5569	-0.64625	4.22197	0.002577	0.008238	0.050984	-1	177	173	610	451	522	195	302	237	340	254
ENSMUSG00000032289	chr9	Thsd4	59966931	59972538	13986	-0.97639	0.436243	0.002582	0.008251	0.072496	-1	13	17	48	30	30	8	19	22	21	8
ENSMUSG00000036199	chr8	Ndufa13	69894188	69894410	1243	0.523036	8.562923	0.002583	0.008253	0.035733	1	4670	3803	4878	5695	5255	6822	10287	6579	10750	6734

ENSMUSG00000042682	chr14	Selk	29968308	29968536	1240	0.513756	6.14411	0.002596	0.008291	0.033633	1	881	867	1073	815	899	1231	1839	1405	2026	1171
ENSMUSG00000048416	chr3	Mlf1	67374097	67374262	1719	-0.54171	7.597849	0.002603	0.008313	0.038287	-1	3329	2217	5175	3824	4212	1981	4978	2239	3746	2030
ENSMUSG00000039989	chr11	Cbx4	1.19E+08	1.19E+08	5210	0.799526	1.878222	0.002604	0.008315	0.063607	1	39	31	50	41	46	53	64	126	103	64
ENSMUSG00000027829	chr3	Ccnl1	65946151	65946948	5997	0.518074	3.596571	0.002607	0.008319	0.029571	1	154	119	203	141	171	191	372	276	248	209
ENSMUSG00000032565	chr9	Nudt16	1.05E+08	1.05E+08	2573	0.531719	3.386197	0.002607	0.008319	0.030556	1	130	114	177	99	155	202	256	192	275	189
ENSMUSG00000050240	chr16	Hic2	17233572	17233730	6354	-0.77265	1.036963	0.002607	0.008319	0.043644	-1	35	18	59	42	49	19	35	29	27	22
ENSMUSG00000061983	chr10	Rps12	23785211	23785273	476	0.542784	7.469571	0.00261	0.008326	0.038323	1	2455	2074	2527	1871	2264	3402	4745	3559	4605	2950
ENSMUSG00000025040	chrX	Fundc1	17556564	17558011	2353	-0.44034	4.625602	0.002612	0.00833	0.023076	-1	346	339	669	449	501	259	435	405	464	352
ENSMUSG00000089917	chr2	Uckl1	1.82E+08	1.82E+08	4629	-0.45087	4.358078	0.002614	0.008335	0.023717	-1	318	232	568	377	444	281	425	267	380	237
ENSMUSG00000090330	chr7	9130221H12Rik	25228687	25228773	1577	0.575182	2.48972	0.002617	0.008343	0.032748	1	61	44	110	59	89	87	142	119	132	120
ENSMUSG00000029638	chr6	Glcci1	8509600	8510319	7756	-0.79064	1.837924	0.002621	0.008354	0.062709	-1	63	44	143	47	72	36	37	56	66	37
ENSMUSG00000040312	chr17	Cchcr1	35517100	35517229	5508	0.998061	0.63162	0.002625	0.008362	0.090961	1	17	3	28	7	25	34	41	30	46	23
ENSMUSG00000040562	chr3	Gstm2	1.08E+08	1.08E+08	1679	0.609634	6.512698	0.002626	0.008365	0.048043	1	1030	1174	1667	813	998	1376	2525	2231	1914	1982
ENSMUSG00000026112	chr1	Coa5	37417084	37420627	5220	-0.44964	7.345536	0.002628	0.008367	0.026298	-1	2488	1815	4144	3248	3686	2010	2958	2421	3076	2137
ENSMUSG00000079197	chr14	Psme2	55587441	55587565	1764	0.553092	4.785835	0.002628	0.008367	0.037517	1	369	331	379	301	345	528	737	642	670	412
ENSMUSG00000029417	chr5	Cxcl9	92321331	92323906	2905	1.09979	1.13386	0.002634	0.008383	0.116296	1	22	21	14	23	21	62	75	56	27	33
ENSMUSG00000049734	chr9	Trex1	1.09E+08	1.09E+08	1314	0.511745	4.272189	0.002643	0.008409	0.030882	1	243	206	340	236	234	369	575	311	543	296
ENSMUSG00000074925	chr19	Ptar1	23687400	23687545	2064	-1.12083	0.371429	0.002645	0.008415	0.103682	-1	10	9	58	32	31	12	12	12	17	14
ENSMUSG00000031715	chr8	Smarca5	80698507	80701128	7777	-0.44078	5.281347	0.002654	0.008441	0.024206	-1	574	576	942	701	791	435	833	513	698	560
ENSMUSG00000009487	chr7	Otog	46240987	46241119	10043	-1.23267	0.26442	0.00266	0.008459	0.129738	-1	25	10	31	16	46	15	5	6	23	10
ENSMUSG00000040740	chr4	Slc25a34	1.42E+08	1.42E+08	2670	-2.54498	3.434251	0.002668	0.008482	0.737455	-1	7	40	56	916	476	10	182	21	47	53
ENSMUSG00000103627	chr6	IFFO1	1.25E+08	1.25E+08	1680	0.560021	3.007225	0.002671	0.008489	0.032697	1	84	76	117	103	134	119	229	132	224	169
ENSMUSG00000042625	chr17	Safb2	56560965	56561206	8165	0.452607	4.377856	0.002673	0.008493	0.024206	1	254	186	384	240	358	341	492	492	474	375
ENSMUSG00000044700	chr4	Tmem201	1.5E+08	1.5E+08	8944	-0.53011	5.767372	0.002674	0.008493	0.035972	-1	767	500	1379	1316	1364	572	960	732	1086	758
ENSMUSG00000060733	chr10	Ipmk	71347763	71348090	7093	-0.46477	4.41807	0.002675	0.008495	0.025672	-1	290	240	555	476	464	239	423	303	396	289
ENSMUSG00000022150	chr15	Dab2	6299788	6299899	7342	0.526878	4.682544	0.00268	0.008511	0.034578	1	268	213	611	242	424	457	782	539	519	463
ENSMUSG00000006005	chr1	Tpr	1.5E+08	1.5E+08	10496	-0.44144	6.510954	0.002683	0.008516	0.025159	-1	1215	1190	2535	1591	2103	1118	1837	1281	1756	1147
ENSMUSG00000008822	chr12	Acyp1	85272398	85272827	1380	-0.66204	4.021655	0.002684	0.008517	0.054306	-1	327	360	350	204	269	177	294	211	279	193
ENSMUSG00000027599	chr3	Armc1	19131402	19134223	3673	-0.45964	4.508101	0.002691	0.008538	0.025327	-1	302	272	577	463	538	240	491	308	415	315
ENSMUSG00000026761	chr2	Orc4	48902824	48905599	7458	-0.48726	3.86433	0.002696	0.008552	0.027367	-1	272	210	391	216	267	174	297	196	247	193
ENSMUSG00000020974	chr12	Pole2	69201779	69201882	1695	1.175985	-0.1394	0.002699	0.008561	0.088266	1	8	5	15	7	4	10	26	25	15	23
ENSMUSG00000024792	chr19	Zfpl1	6080762	6081214	1798	0.545531	3.267238	0.002704	0.008572	0.032193	1	120	95	168	112	124	181	199	190	304	160
ENSMUSG00000042729	chr19	Wdr74	8735839	8735905	1203	0.507478	3.664002	0.00271	0.008591	0.028354	1	146	149	195	156	172	228	311	261	353	201
ENSMUSG00000026361	chr1	Cdc73	1.44E+08	1.44E+08	17538	-0.46414	5.078389	0.002714	0.008601	0.026743	-1	529	451	1063	470	710	381	588	481	668	483
ENSMUSG00000029330	chr5	Cds1	1.02E+08	1.02E+08	3939	-1.48362	1.095256	0.002717	0.008609	0.242377	-1	26	12	25	88	96	11	17	41	18	10
ENSMUSG00000009207	chr2	Lnp	74520291	74522297	9154	-0.61388	5.0058	0.00272	0.008613	0.04787	-1	444	417	1087	571	711	225	423	544	599	524
ENSMUSG00000048832	chr19	Vps37c	10688815	10688979	2415	0.432614	5.437585	0.00272	0.008613	0.023338	1	558	441	800	507	653	676	1038	889	1243	741
ENSMUSG00000074129	chr7	Rpl13a	45125558	45126032	3034	0.544049	8.080959	0.002719	0.008613	0.038965	1	3457	3438	3729	2954	3403	4998	7241	5339	7228	4695
ENSMUSG00000006095	chr7	Tbcb	30224131	30224347	1442	0.559442	4.622895	0.002737	0.008665	0.038418	1	326	305	341	261	300	463	546	523	745	401
ENSMUSG00000079084	chr9	Ccdc82	13246982	13247021	1847	-1.00019	0.633065	0.002748	0.008698	0.083481	-1	17	14	68	27	39	9	29	13	20	18
ENSMUSG00000037239	chr7	Spred3	29158829	29162194	5997	-0.93321	0.986649	0.002753	0.008709	0.076864	-1	41	22	75	28	39	28	22	15	38	15
ENSMUSG00000014498	chr10	Ankrd52	1.28E+08	1.28E+08	8401	-0.69057	5.771588	0.002755	0.008712	0.061893	-1	602	454	1839	1382	1489	445	996	638	888	875
ENSMUSG00000022191	chr15	Drosha	12824815	12824942	5934	-0.4952	5.571377	0.002754	0.008712	0.031322	-1	540	579	1364	1031	1088	488	839	664	984	668
ENSMUSG00000030203	chr6	Dusp16	1.35E+08	1.35E+08	7650	-0.48542	4.543518	0.002756	0.008712	0.028654	-1	308	265	648	474	547	215	428	382	420	338
ENSMUSG00000038264	chr9	Sema7a	57940113	57940328	3296	0.565579	3.720091	0.002756	0.008712	0.03791	1	114	97	205	194	256	263	367	290	264	229
ENSMUSG00000027555	chr3	Car13	14641727	14641845	2299	0.963583	0.833925	0.002758	0.008717	0.080897	1	13	13	19	12	34	29	69	46	35	24
ENSMUSG00000036275	chr11	9530068E07Rik	52396428	52396603	3296	0.453631	6.285498	0.00276	0.00872	0.026546	1	959	874	1367	885	1155	1303	1918	1555	2101	1395
ENSMUSG00000020986	chr12	Sec23a	58958383	58960086	4840	-0.45934	6.749626	0.002762	0.008722	0.027558	-1	1632	1473	3205	1704	2186	1175	2242	1499	1867	1560
ENSMUSG00000023020	chr15	Cox14	99725618	99725848	723	0.508237	6.537887	0.002762	0.008722	0.033615	1	1320	934	1295	1172	1287	1736	2501	1669	2643	1515
ENSMUSG00000000934	chr15	Top1mt	75657035	75657214	1903	-0.47853	3.760643	0.002764	0.008727	0.025969	-1	245	181	325	231	275	200	252	179	246	151
ENSMUSG00000055675	chr8	Kbtbd11	15011025	15011314	7137	0.92596	1.548297	0.002766	0.008729	0.08826	1	34	25	50	16	31	61	63	105	62	39
ENSMUSG00000047591	chr15	Mafa	75746843	75747922	1080	0.525706	3.968076	0.002773	0.008751	0.032883	1	189	150	335	146	221	254	425	330	311	342
ENSMUSG00000075415	chr2	Fnbp1	31026206	31033188	10030	0.507435	4.111356	0.002781	0.008772	0.031209	1	158	123	329	251	318	314	419	412	383	301
ENSMUSG00000048550	chr2	Thnsl1	21205724	21205845	4043	-0.60794	3.039969	0.002786	0.008786	0.041776	-1	142	134	211	121	178	85	147	78	144	136
ENSMUSG00000026173	chr1	Plcd4	74542888	74543028	7045	-0.6687	7.15414	0.002791	0.0088	0.058933	-1	2892	2443	4510	1548	2631	2226	2144	1725	2569	1317
ENSMUSG00000025855	chr5	Prkar1b	1.39E+08	1.39E+08	3810	0.853712	1.005418	0.002793	0.008805	0.059986	1	14	18	25	20	31	28	64	57	36	37
ENSMUSG00000022387	chr15	Brd1	88687300	88688480	8138	-0.41574	4.942091	0.002794	0.008807	0.021052	-1	452	379	851	547	643	356	555	495	576	425
ENSMUSG00000024471	chr18	Myot	44334074	44334156	2209	-0.61562	9.727553	0.002802	0.008828	0.050384	-1	11152	9428	19805	22926	20484	7564	18503	8803	16673	11456
ENSMUSG00000017344	chr11	Vtn	78499091	78499622	2030	0.491476	4.507913	0.002809	0.008851	0.029424	1	238	215	378	294	400	389	538	398	791	351
ENSMUSG00000032323	chr9	Cyp11a1	58006411	58006555	4804	1.311963	-0.46064	0.002815	0.008865	0.091957	1	6	7	5	5	4	17	23	18	9	11
ENSMUSG00000059511	chr13	Gm20563	62006666	62006941	276	0.92733	1.082612	0.002816	0.008866	0.073556	1	25	24	25	20	12	30	58	37	66	50
ENSMUSG00000003549	chr7	Ercc1	19344778	19345196	3111	0.454335	4.077465	0.002819	0.008873	0.023619	1	198	183	281	202	267	302	375	326	479	292
ENSMUSG00000025967	chr1	Eef1b2	63176825	63177291	2532	0.532448	7.567492	0.002819	0.008873	0.037485	1	2460	2262	2640	2248	2402	3535	5623	3579	4649	3241
ENSMUSG00000040734	chr7	Ppp1r13l	19359749	19359798	3604	0.731716	1.749635	0.002827	0.008895	0.051258	1	26	26	50	45	51	60	55	79	106	67
ENSMUSG00000036995	chr4	Asap3	1.36E+08	1.36E+08	4225	0.615239	2.407856	0.002835	0.008919	0.038326	1	50	44	91	60	90	102	143	129	132	70

ENSMUSG00000095098	chr19	Ccdc85b	5456789	5457397	609	0.570886	4.847527	0.00284	0.008933	0.041167	1	441	256	424	308	396	558	536	592	957	490
ENSMUSG00000049134	chr19	Nrap	56320035	56320302	5507	-0.63268	9.931815	0.002842	0.008937	0.053353	-1	10968	10422	27180	27249	22768	8759	18428	10866	20826	12964
ENSMUSG00000028125	chr3	Abca4	1.22E+08	1.22E+08	11829	-1.30481	0.580716	0.002846	0.008946	0.174924	-1	35	36	59	15	14	19	18	18	16	3
ENSMUSG00000037395	chr1	Rcor3	1.92E+08	1.92E+08	13622	-0.47683	4.272267	0.002848	0.008951	0.027367	-1	325	203	523	352	439	175	361	283	414	265
ENSMUSG00000031592	chr8	Pcm1	41239759	41239963	8380	-0.47825	5.991094	0.002852	0.008961	0.029703	-1	985	909	2050	913	1217	742	1153	968	1190	824
ENSMUSG00000001098	chr5	Kctd10	1.14E+08	1.14E+08	4046	0.479036	4.39934	0.002871	0.009018	0.027765	1	203	198	329	316	371	314	516	505	562	355
ENSMUSG00000037348	chr4	Paqr7	1.34E+08	1.34E+08	4259	0.610799	2.66762	0.002871	0.009018	0.039498	1	78	46	103	78	95	88	127	144	198	134
ENSMUSG00000006782	chr11	Cnp	1.01E+08	1.01E+08	3639	0.461145	3.783042	0.002879	0.009041	0.024333	1	136	120	280	182	228	255	356	234	369	239
ENSMUSG00000017692	chr11	Rhbdl3	80300912	80301271	4734	-0.65769	3.588256	0.002882	0.009047	0.052577	-1	278	185	331	131	241	165	178	148	243	116
ENSMUSG00000061576	chr5	Dpp6	26817203	26818118	10030	-0.9304	0.705199	0.002883	0.009047	0.06783	-1	20	19	54	30	44	21	11	16	26	20
ENSMUSG00000027010	chr2	Slc25a12	71271063	71275353	7342	-0.58618	8.705691	0.00289	0.009067	0.045924	-1	5508	3653	10767	10491	11447	4165	8209	5383	7712	5522
ENSMUSG00000020184	chr10	Mdm2	1.18E+08	1.18E+08	5070	-0.42066	5.616063	0.002901	0.0091	0.022564	-1	779	552	1412	831	1053	578	971	750	931	632
ENSMUSG00000098098	chr18	Gm20748	61639542	61639732	699	0.748882	1.281195	0.002907	0.009115	0.045484	1	24	20	34	30	30	43	70	42	83	32
ENSMUSG00000020064	chr10	Herc4	63243797	63244163	4019	-0.50519	4.623015	0.002911	0.009124	0.031905	-1	461	388	696	343	415	303	476	317	419	342
ENSMUSG00000038248	chr10	Sobp	43002500	43004414	5529	-0.4861	5.068417	0.00291	0.009124	0.029992	-1	570	449	1003	500	670	412	607	359	725	471
ENSMUSG00000044617	chr10	Zbtb39	1.28E+08	1.28E+08	5946	-0.6131	2.775251	0.002912	0.009125	0.040612	-1	86	83	235	108	174	68	98	104	130	89
ENSMUSG00000029594	chr5	Rbm19	1.2E+08	1.2E+08	2963	-0.57551	2.99548	0.002913	0.009127	0.036014	-1	117	80	211	179	190	103	144	88	132	110
ENSMUSG00000086604	chr7	Gm15510	5050730	5050918	548	-0.73884	1.472933	0.002917	0.009136	0.049887	-1	44	50	78	42	55	35	52	22	42	33
ENSMUSG00000038025	chr13	Phf2	48801750	48803687	5260	-0.52301	5.714608	0.00292	0.009143	0.035554	-1	793	488	1771	956	1225	524	805	823	1063	738
ENSMUSG00000061613	chr17	U2af1	31647082	31647355	974	0.463325	4.726572	0.002921	0.009146	0.026233	1	296	310	418	334	397	478	715	482	729	418
ENSMUSG00000037679	chr12	Inf2	1.13E+08	1.13E+08	4600	0.564909	3.422509	0.002932	0.009177	0.037214	1	86	92	188	151	185	140	241	273	295	213
ENSMUSG00000026492	chr1	Tfb2m	1.8E+08	1.8E+08	2804	-0.45578	5.182624	0.002934	0.00918	0.026466	-1	621	465	884	684	719	401	855	451	660	479
ENSMUSG00000060019	chr8	Gm10073	1.07E+08	1.07E+08	496	0.689455	2.563057	0.002934	0.00918	0.05125	1	81	58	93	69	47	126	161	125	142	96
ENSMUSG00000005732	chr16	Ranbp1	18239784	18240193	1666	0.57598	3.811888	0.002939	0.009192	0.039133	1	162	188	202	144	171	265	377	300	380	211
ENSMUSG00000028792	chr4	Ak2	1.29E+08	1.29E+08	2140	0.623475	5.193833	0.002942	0.009202	0.050196	1	514	413	478	386	425	657	724	1082	948	595
ENSMUSG00000042444	chr9	Fam63b	70599014	70605289	8081	-0.64499	4.829153	0.002951	0.009226	0.053632	-1	341	223	851	717	802	244	563	382	473	388
ENSMUSG00000034525	chr13	Ice1	70588689	70589812	7675	-0.49098	4.803447	0.002955	0.009234	0.030227	-1	376	289	885	514	671	280	581	413	474	390
ENSMUSG00000042271	chrX	Nxt2	1.42E+08	1.42E+08	3176	-0.75121	1.424151	0.002955	0.009234	0.050914	-1	33	42	73	57	58	19	39	49	41	29
ENSMUSG00000020982	chr12	Nemf	69311544	69312080	3721	-0.45734	4.409305	0.002957	0.009238	0.025442	-1	293	307	554	389	439	255	486	291	337	275
ENSMUSG00000047485	chrX	Klhl34	1.58E+08	1.58E+08	1935	-2.44179	2.362651	0.002958	0.009239	0.691369	-1	15	4	29	421	232	6	54	7	66	24
ENSMUSG00000100551	chr1	Gm19503	1.52E+08	1.52E+08	241	-0.85615	0.573245	0.002963	0.009254	0.052272	-1	25	25	33	34	25	16	27	17	20	11
ENSMUSG00000028066	chr3	Pmf1	88394143	88394570	1351	0.472074	3.775481	0.002979	0.009301	0.025094	1	166	137	200	196	204	222	366	268	328	261
ENSMUSG00000045100	chr6	Slc25a26	94500314	94500457	1915	-0.41252	4.637313	0.002982	0.009307	0.020599	-1	405	311	580	440	552	330	463	359	487	313
ENSMUSG00000047787	chr19	Flrt1	7092014	7097229	5859	-1.01251	0.388707	0.002986	0.009317	0.08176	-1	19	12	55	15	36	14	16	9	23	11
ENSMUSG00000072594	chr14	Gm16439	44596665	44597228	564	-0.87586	0.720384	0.002995	0.009345	0.062482	-1	31	26	36	37	29	14	31	25	14	16
ENSMUSG00000037992	chr11	Rara	98927818	98927910	4365	0.66964	3.674129	0.002996	0.009346	0.055844	1	117	59	180	186	272	180	371	261	398	240
ENSMUSG00000027185	chr2	Nat10	1.04E+08	1.04E+08	7199	-0.40948	4.281007	0.003002	0.009362	0.019594	-1	294	255	516	335	395	249	381	290	363	244
ENSMUSG00000035983	chr12	Gm7008	40222758	40223553	1524	-0.95545	-0.0202	0.003004	0.009365	0.056374	-1	12	15	28	19	21	7	17	8	18	6
ENSMUSG00000090086	chr5	AI480526	1.23E+08	1.23E+08	4725	0.670031	2.48581	0.003006	0.009371	0.050046	1	69	39	120	42	81	98	113	130	142	124
ENSMUSG00000015869	chr11	Prpsap1	1.16E+08	1.16E+08	3407	0.609927	3.399923	0.003008	0.009374	0.043261	1	142	117	155	101	133	194	198	259	310	184
ENSMUSG00000020273	chr11	Papolg	23862646	23864056	5491	-0.74364	2.059208	0.003009	0.009375	0.057649	-1	55	51	134	84	99	30	67	49	54	76
ENSMUSG00000034875	chr7	Nudt19	35547185	35548123	2680	-0.44111	5.597873	0.003015	0.009391	0.025282	-1	855	668	1036	874	991	566	1036	680	966	569
ENSMUSG00000020018	chr10	Snrpf	93583029	93583530	861	0.523448	4.377534	0.003018	0.009397	0.033625	1	294	220	287	253	271	430	560	400	495	336
ENSMUSG00000036752	chr2	Tubb4b	25222160	25223368	2088	0.497395	7.8176	0.00302	0.009401	0.033243	1	2808	2749	3964	2291	2942	3910	5904	4478	5554	4296
ENSMUSG00000032743	chr7	D430042O09Rik	1.26E+08	1.26E+08	7191	-0.56762	2.640799	0.003023	0.00941	0.03337	-1	83	78	185	118	141	56	127	85	105	85
ENSMUSG00000040694	chr17	Apobec2	48419231	48419633	1218	0.519747	8.601841	0.003026	0.009417	0.036479	1	4671	2990	6193	5795	6214	5630	11834	6519	9574	8716
ENSMUSG00000062980	chr6	Cped1	21985916	21987059	8279	-0.48092	4.911325	0.003043	0.009468	0.029272	-1	413	418	874	490	675	328	589	489	419	452
ENSMUSG00000027560	chr2	Dok5	1.71E+08	1.71E+08	1768	-1.32198	0.675519	0.003045	0.009471	0.184309	-1	21	6	27	60	63	9	19	7	26	18
ENSMUSG00000064342	chrMT	mt-Ti	3706	3774	69	-0.57408	6.400988	0.003057	0.009506	0.044053	-1	1238	981	1851	2224	1857	953	1586	1123	1968	760
ENSMUSG00000023191	chr6	Leprel2	1.25E+08	1.25E+08	3930	0.639777	3.0479	0.003066	0.009533	0.048807	1	56	57	167	108	148	133	194	203	172	192
ENSMUSG00000039529	chr18	Atp8b1	64528979	64531564	6440	0.84127	2.029613	0.00307	0.009543	0.079778	1	23	34	77	35	67	51	173	100	72	77
ENSMUSG00000027668	chr3	Mfn1	32529465	32529695	6114	-0.66438	7.454984	0.003077	0.009562	0.05946	-1	2127	1597	4001	5248	4805	1707	3358	1958	3524	2150
ENSMUSG00000090112	chr10	Shprh	11149427	11149586	14066	-0.54623	3.390878	0.003084	0.009581	0.03432	-1	143	132	372	148	241	114	188	159	178	136
ENSMUSG00000058603	chr1	Rpl28-ps1	1.28E+08	1.28E+08	414	0.634381	2.495956	0.003085	0.009583	0.041566	1	80	48	87	58	72	112	153	105	169	81
ENSMUSG00000033871	chr18	Ppargc1b	61298136	61298783	3990	-1.08516	2.236781	0.003091	0.009599	0.141669	-1	45	31	103	152	198	23	71	44	61	72
ENSMUSG00000021273	chr14	Fdft1	63145153	63146968	2860	-0.53792	6.250699	0.003092	0.0096	0.038669	-1	1095	991	1571	1917	1625	856	1679	1015	1509	765
ENSMUSG00000025314	chr2	Ptprj	90429754	90430046	8352	0.614241	2.747621	0.003095	0.009607	0.043275	1	48	52	157	76	106	125	180	136	142	140
ENSMUSG00000071793	chr8	2610005L07Rik	20385782	20388402	4163	-1.01876	-0.02617	0.003099	0.009615	0.064123	-1	13	10	27	19	28	9	15	4	13	12
ENSMUSG00000098274	chr16	Rpl24	55966275	55966438	1030	0.518511	7.727083	0.003099	0.009615	0.036292	1	2877	2456	3116	2532	2548	3935	5734	4176	5794	3363
ENSMUSG00000020674	chr12	Pxdn	29938036	29938324	9517	0.504075	4.492445	0.003101	0.009618	0.031761	1	297	204	383	277	326	342	516	626	481	416
ENSMUSG00000041354	chr17	Rgl2	33929543	33930044	4625	0.424351	4.78922	0.003109	0.009642	0.02241	1	288	263	521	394	448	447	631	622	673	504
ENSMUSG00000017299	chr2	Dnttip1	1.65E+08	1.65E+08	2122	0.470548	3.999911	0.003111	0.009644	0.025789	1	205	180	267	181	223	280	386	324	445	260
ENSMUSG00000083716	chr2	Gm13436	36807826	36808392	567	0.642734	2.526214	0.003111	0.009644	0.042817	1	77	61	82	64	61	85	140	128	178	104
ENSMUSG00000068457	chrY	Uty	1096861	1098573	9791	-2.70561	2.652195	0.003114	0.009649	0.837246	-1	106	138	304	147	199	54	1	1	98	0
ENSMUSG00000019066	chr9	Rab3d	21907491	21910671	4196	0.726832	3.276467	0.003119	0.009662	0.064472	1	106	98	178	91	106	177	162	342	211	171

ENSMUSG00000037375	chr1	Hhat	1.92E+08	1.92E+08	9150	1.003495	0.001234	0.003123	0.009672	0.065726	1	12	3	9	10	13	21	21	18	24	22
ENSMUSG00000032215	chr9	Rsl24d1	73113426	73113480	1716	0.466426	4.992216	0.003127	0.009682	0.027539	1	388	354	499	367	506	617	855	546	868	502
ENSMUSG00000041483	chr1	Zfp281	1.37E+08	1.37E+08	4937	-0.54378	3.298199	0.003127	0.009682	0.034172	-1	117	140	277	184	230	83	191	142	176	142
ENSMUSG00000030424	chr7	Zfp939	39449518	39449653	2480	-0.82323	0.707903	0.003128	0.009683	0.05099	-1	27	18	51	31	34	18	35	14	20	15
ENSMUSG00000022636	chr16	Alcam	52248996	52251646	7121	1.112708	1.118592	0.003147	0.009735	0.132067	1	19	10	39	22	17	36	58	101	35	23
ENSMUSG00000068036	chr17	Mllt4	13760539	13760778	10223	-0.4836	5.213446	0.003147	0.009735	0.030324	-1	529	397	1023	718	914	331	763	549	667	551
ENSMUSG00000026676	chr2	Ccdc3	5137776	5138307	2670	-0.81943	3.437628	0.003151	0.009747	0.084277	-1	97	97	294	250	432	100	146	160	131	159
ENSMUSG00000094114	chr13	Gm21967	1.2E+08	1.2E+08	1648	-0.95545	2.920187	0.003154	0.009753	0.113952	-1	117	109	161	186	221	69	114	180	46	49
ENSMUSG00000059775	chr8	Rps26-ps1	1.07E+08	1.07E+08	410	0.573409	2.779316	0.003155	0.009755	0.034143	1	76	72	90	93	97	125	204	134	164	114
ENSMUSG00000059708	chrX	Akap17b	36608314	36612664	6003	-0.76453	1.987046	0.003159	0.009764	0.061507	-1	64	30	129	73	115	43	52	37	70	58
ENSMUSG00000020829	chr11	Slc46a1	78465697	78466005	3080	1.054848	0.604608	0.003162	0.00977	0.1009	1	16	7	16	9	26	37	20	45	44	23
ENSMUSG00000059159	chr6	Gm8129	52346730	52346942	213	0.926437	1.447709	0.003165	0.009778	0.086082	1	27	35	38	16	24	73	87	52	60	38
ENSMUSG00000062190	chr6	Lancl2	57702601	57703263	2958	-0.52621	3.271774	0.003168	0.009786	0.031685	-1	126	126	248	195	227	92	215	122	165	134
ENSMUSG00000033149	chr16	Phldb2	45746243	45747931	7577	-0.56661	3.253066	0.003171	0.009791	0.037049	-1	115	131	285	173	226	92	156	137	145	160
ENSMUSG00000047649	chr7	Cd3eap	19356849	19358016	1657	-0.52022	3.280471	0.00318	0.009819	0.030676	-1	176	149	200	173	196	120	159	125	178	138
ENSMUSG00000029550	chr5	Sppl3	1.15E+08	1.15E+08	4240	0.427972	4.802253	0.00319	0.009846	0.02278	1	351	282	494	370	401	490	623	576	758	469
ENSMUSG00000026925	chr2	Inpp5e	26396249	26397971	4301	-0.54392	3.556677	0.003192	0.009851	0.035023	-1	165	114	313	275	278	115	206	158	224	172
ENSMUSG00000066621	chr5	Tecpr1	1.44E+08	1.44E+08	9665	-0.43248	4.975064	0.003197	0.009863	0.023566	-1	478	336	875	584	704	399	514	478	588	449
ENSMUSG00000001507	chr11	Itga3	95044474	95045763	5710	0.612267	2.583514	0.0032	0.009871	0.040427	1	46	53	117	77	89	89	197	135	158	85
ENSMUSG00000054509	chr14	Parp4	56575619	56575730	6534	-0.49508	3.658669	0.003206	0.009888	0.028466	-1	161	140	394	235	296	133	241	179	230	176
ENSMUSG00000071573	chr19	Rnls	33137747	33138274	1627	-0.62552	2.275455	0.003208	0.00989	0.040443	-1	66	68	135	91	110	44	92	50	79	78
ENSMUSG00000040669	chr6	Phc1	1.22E+08	1.22E+08	5297	-0.51809	4.427362	0.003219	0.009922	0.034035	-1	385	334	671	301	346	274	374	268	414	284
ENSMUSG00000015568	chr8	Lpl	68880491	68880840	6810	-1.0856	9.059372	0.003223	0.009932	0.15807	-1	5826	4909	7535	24075	16129	4288	5582	11213	5627	4075
ENSMUSG00000036968	chr5	Cnpy4	1.38E+08	1.38E+08	2399	0.63979	2.129618	0.003226	0.00994	0.041249	1	36	47	84	45	58	87	93	104	114	72
ENSMUSG00000025786	chr9	Zdhhc3	1.23E+08	1.23E+08	11846	-0.4325	6.493942	0.00323	0.00995	0.025093	-1	1330	1144	2607	1631	1770	1081	1699	1226	1866	1206
ENSMUSG00000036114	chr4	Rpp25l	41712033	41712814	856	0.495621	4.934699	0.003234	0.009958	0.031444	1	413	352	501	334	388	608	707	635	798	496
ENSMUSG00000005575	chr7	Ube2m	13035120	13035754	2287	0.455533	6.627348	0.003236	0.009963	0.0279	1	1225	943	1627	1473	1381	1684	2451	1892	2923	1617
ENSMUSG00000022974	chr16	Paxbp1	91014037	91015178	5508	0.496535	3.287587	0.003246	0.009991	0.027557	1	118	90	196	121	124	170	264	206	210	179
ENSMUSG00000000693	chr6	Loxl3	83034173	83034289	4196	0.771643	2.102421	0.003253	0.01001	0.067218	1	29	34	74	53	64	104	93	103	64	98
ENSMUSG00000027363	chr2	Usp8	1.27E+08	1.27E+08	4193	-0.42632	4.441689	0.003257	0.010021	0.022016	-1	300	263	588	392	497	300	380	318	393	289
ENSMUSG00000045098	chr19	Suv420h1	3767421	3767730	14116	-0.46455	4.207825	0.003258	0.010021	0.026157	-1	220	220	556	350	429	223	358	277	307	249
ENSMUSG00000006699	chr4	Cdc42	1.37E+08	1.37E+08	2966	0.443864	7.881137	0.003261	0.010026	0.026897	1	2829	2634	4096	3073	3231	4051	6214	4554	6074	4092
ENSMUSG00000063273	chr3	Naa15	51415148	51416376	15427	-0.4421	6.031275	0.003266	0.010042	0.026029	-1	1090	891	1823	1013	1293	899	1204	953	1192	811
ENSMUSG00000033793	chr1	Atp6v1h	5070018	5070144	9746	0.434361	4.280625	0.00327	0.01005	0.022491	1	216	221	342	250	284	333	503	396	509	304
ENSMUSG00000098371	chr16	Gm28037	55966343	55966438	611	0.513675	7.728777	0.00327	0.01005	0.036023	1	2881	2457	3138	2540	2564	3934	5730	4174	5795	3364
ENSMUSG00000019979	chr10	Apaf1	90989311	90991596	9028	0.627961	2.081751	0.003284	0.010088	0.040373	1	41	30	82	46	68	81	90	106	94	79
ENSMUSG00000002778	chr7	Kdelr1	45872772	45873101	1873	0.442365	5.91023	0.00329	0.010104	0.025941	1	660	676	1139	786	818	975	1365	1284	1577	1120
ENSMUSG00000005699	chr8	Pard6a	1.06E+08	1.06E+08	1430	0.574709	2.712872	0.003291	0.010104	0.034941	1	79	62	103	87	81	109	137	124	200	134
ENSMUSG00000022671	chr16	Mzt2	15848441	15848729	1236	0.596982	3.471541	0.003291	0.010104	0.042226	1	142	113	160	117	159	165	380	163	355	186
ENSMUSG00000062075	chr10	Lmnb2	80901203	80902900	4286	0.740621	2.232844	0.003294	0.01011	0.062359	1	39	36	77	51	79	100	66	121	111	108
ENSMUSG00000015733	chr6	Capza2	17636234	17636317	5890	-0.53454	8.440031	0.0033	0.010126	0.039283	-1	6565	5838	9687	4477	6098	4168	6556	4403	6946	4190
ENSMUSG00000006456	chr19	Rbm14	4800569	4801805	3910	0.531229	3.098951	0.003301	0.010128	0.031923	1	71	75	155	118	148	128	204	212	216	155
ENSMUSG00000097233	chr19	Gm17552	4169566	4171741	3877	1.245121	-0.30578	0.003304	0.010134	0.11338	1	4	3	9	11	6	9	22	17	11	28
ENSMUSG00000037236	chr18	Matr3	35562146	35562259	9869	-0.45614	6.004897	0.003305	0.010136	0.027867	-1	933	1038	1639	1064	1262	730	1194	899	1193	944
ENSMUSG00000045039	chr7	Megf8	25317164	25317693	10159	-0.45504	5.675168	0.003319	0.010176	0.027409	-1	689	599	1480	949	1174	528	839	763	1026	790
ENSMUSG00000004947	chr5	Dtx2	1.36E+08	1.36E+08	7032	0.534832	3.25392	0.003337	0.010224	0.033004	1	113	82	192	110	131	168	191	240	217	187
ENSMUSG00000027864	chr3	Ptgfrn	1.01E+08	1.01E+08	5902	0.692098	4.581876	0.003337	0.010224	0.063899	1	166	119	474	367	429	366	494	646	533	598
ENSMUSG00000063229	chr7	Ldha	46841475	46841652	2982	0.47739	11.72653	0.003336	0.010224	0.031565	1	48541	29896	61542	40589	47400	56610	89519	65611	101989	53247
ENSMUSG00000034586	chr11	Hid1	1.15E+08	1.15E+08	4595	0.824347	0.720796	0.003344	0.01024	0.051123	1	18	10	25	18	18	20	35	41	49	34
ENSMUSG00000045917	chr4	6330416G13Rik	63558781	63558957	3974	-0.41612	4.3466	0.003343	0.01024	0.020896	-1	309	240	509	365	468	248	384	334	356	266
ENSMUSG00000049119	chr4	Fam110b	5644090	5644410	8164	0.604038	2.005451	0.003354	0.010269	0.034399	1	42	35	74	47	53	74	113	62	108	75
ENSMUSG00000020460	chr11	Rps27a	29545846	29546029	1972	0.594329	7.541495	0.003362	0.010289	0.048443	1	2485	2426	2510	1801	2127	3602	5505	3623	4927	3007
ENSMUSG00000022574	chr15	Naprt	75890964	75891060	1890	0.575729	2.710272	0.003362	0.010289	0.035291	1	76	56	86	102	90	110	177	127	189	108
ENSMUSG00000031974	chr8	Abcb10	1.24E+08	1.24E+08	4306	-0.46033	4.930052	0.003364	0.010291	0.027312	-1	424	303	783	637	770	369	603	421	583	386
ENSMUSG00000060244	chr1	Alyref2	1.72E+08	1.72E+08	1273	0.808298	0.932736	0.003365	0.010294	0.052378	1	20	11	17	24	32	33	47	38	48	41
ENSMUSG00000040701	chr14	Ap1g2	55098578	55099161	4177	0.622737	2.257599	0.003368	0.0103	0.039857	1	68	34	81	54	59	73	119	119	122	85
ENSMUSG00000059714	chr17	Flot1	35823230	35823501	2893	0.510099	6.2897	0.003377	0.010325	0.035174	1	1021	905	1242	891	995	1484	2061	1405	2354	1195
ENSMUSG00000102752	chr1	Gm7694	1.7E+08	1.7E+08	3827	-1.35807	0.329613	0.003382	0.010339	0.186791	-1	28	39	32	5	26	14	11	18	9	7
ENSMUSG00000031787	chr8	Katnb1	95081201	95081304	3425	-0.52175	3.117164	0.003396	0.010379	0.030327	-1	119	92	243	180	203	106	142	109	180	111
ENSMUSG00000033166	chr14	Dis3	99076634	99077465	3722	-0.53798	3.251912	0.003408	0.010413	0.033827	-1	140	115	283	187	194	81	204	126	159	143
ENSMUSG00000028195	chr3	Cyr61	1.46E+08	1.46E+08	2028	0.885485	5.048471	0.003413	0.010424	0.105603	1	188	275	315	479	604	403	1322	399	759	1077
ENSMUSG00000051639	chr17	Gm5812	6121208	6122164	957	0.957475	0.427835	0.003421	0.010447	0.061826	1	13	13	10	12	17	24	43	21	43	19
ENSMUSG00000038372	chr13	Gmds	31819579	31819978	3323	0.882907	0.891664	0.003426	0.010459	0.066194	1	24	15	20	18	19	33	30	52	48	39
ENSMUSG00000041733	chr5	Coq5	1.15E+08	1.15E+08	2037	-0.61135	6.284487	0.00343	0.010469	0.051116	-1	947	765	1724	2144	2177	759	1526	913	1558	999
ENSMUSG00000052337	chr6	Immt	71831331	71831515	4964	-0.51775	8.269181	0.003434	0.010478	0.037147	-1	4253	3638	6571	7567	7367	3541	6769	3849	5822	3669

ENSMUSG00000028403	chr4	Zdhhc21	82798738	82806461	12972	-0.45242	4.288541	0.003435	0.01048	0.025268	-1	269	266	582	290	446	235	387	254	345	285
ENSMUSG00000012443	chr19	Kif11	37376403	37376667	4819	1.235519	0.276306	0.003438	0.010488	0.155884	1	1	2	14	23	14	31	27	22	37	21
ENSMUSG00000021598	chr13	Med10	69809882	69810052	862	0.6548	2.799937	0.003446	0.010509	0.048749	1	114	55	96	73	81	133	219	132	180	109
ENSMUSG00000047090	chr10	Tmem198b	1.29E+08	1.29E+08	3363	0.564885	2.500278	0.003451	0.010523	0.033615	1	55	50	114	66	81	94	129	128	127	120
ENSMUSG00000059401	chrX	Mamld1	71050256	71050349	4796	0.727899	1.505477	0.003452	0.010524	0.0524	1	27	19	71	25	29	43	81	66	75	48
ENSMUSG00000031902	chr8	Nfatc3	1.06E+08	1.06E+08	6014	-0.47754	5.262486	0.003461	0.010548	0.030102	-1	544	439	1352	612	806	421	686	591	673	557
ENSMUSG00000022485	chr15	Hoxc5	1.03E+08	1.03E+08	3089	-0.42957	4.245747	0.003464	0.010556	0.022367	-1	301	241	458	329	426	255	304	270	355	275
ENSMUSG00000063696	chr8	Gm8730	1.03E+08	1.03E+08	1075	0.598372	2.692018	0.003474	0.010583	0.037939	1	72	77	92	81	73	108	192	126	157	119
ENSMUSG00000022961	chr16	Son	91647506	91647984	14354	-0.47649	7.121712	0.003486	0.010614	0.031296	-1	2048	1654	4787	2095	3011	1584	2504	2072	2726	1835
ENSMUSG00000071176	chr8	Arhgef10	14911663	14911763	9210	-0.62769	2.86841	0.003486	0.010614	0.045187	-1	86	73	242	159	177	76	139	108	98	96
ENSMUSG00000001036	chr11	Epn2	61517249	61519707	5228	-0.42049	5.057789	0.003495	0.010636	0.022903	-1	515	436	928	558	664	363	582	536	635	487
ENSMUSG00000086329	chr2	Gm14233	1.31E+08	1.31E+08	439	0.798496	1.941224	0.003494	0.010636	0.067903	1	53	40	61	28	31	52	104	105	115	62
ENSMUSG00000042677	chr4	Zc3h12a	1.25E+08	1.25E+08	2882	0.790621	1.910073	0.003499	0.010643	0.069076	1	24	25	55	56	58	54	156	72	71	75
ENSMUSG00000047721	chr7	Bola2	1.27E+08	1.27E+08	1658	0.592388	3.711686	0.003499	0.010643	0.042902	1	176	154	141	158	165	245	352	265	373	204
ENSMUSG00000087523	chr11	Gm12319	70654741	70654896	357	-0.47689	4.89859	0.0035	0.010643	0.029894	-1	594	410	775	422	575	380	591	431	587	314
ENSMUSG00000026525	chr1	Opn3	1.76E+08	1.76E+08	1913	1.51556	0.483	0.003502	0.010646	0.241021	1	14	15	14	3	4	15	29	74	19	32
ENSMUSG00000028760	chr4	Eif4g3	1.38E+08	1.38E+08	11063	-0.50055	7.491357	0.003502	0.010646	0.034716	-1	2523	2356	6119	2849	3721	1927	3151	2230	3987	2522
ENSMUSG00000087993	chr10	Mir1982	80828797	80828870	74	1.015681	1.205728	0.003516	0.010686	0.106807	1	25	28	28	12	19	74	49	42	65	32
ENSMUSG00000041688	chrX	Amot	1.45E+08	1.45E+08	8402	-0.50805	6.553392	0.003531	0.010729	0.035471	-1	1323	947	3179	1596	2298	946	1845	1283	1666	1402
ENSMUSG00000087259	chr11	2610035D17Rik	1.13E+08	1.13E+08	2121	0.613238	3.024119	0.003535	0.010738	0.044534	1	76	62	141	113	127	86	226	190	198	193
ENSMUSG00000093076	chr17	Mir3082	25831365	25831428	64	0.434204	4.218305	0.003536	0.010738	0.022828	1	227	191	299	244	296	348	487	327	482	307
ENSMUSG00000049323	chr11	Smcr8	60777524	60781067	8078	-0.49804	4.868631	0.003539	0.010745	0.032469	-1	393	294	1051	518	641	340	563	399	516	400
ENSMUSG00000004383	chr8	Large	72814599	72816021	7883	-0.49058	4.647443	0.00354	0.010745	0.031262	-1	332	262	654	588	570	286	473	306	531	330
ENSMUSG00000037761	chr2	Actr5	1.59E+08	1.59E+08	4186	0.708584	1.405648	0.003541	0.010748	0.04654	1	30	11	40	36	40	46	75	49	72	47
ENSMUSG00000041642	chr1	Kif21b	1.36E+08	1.36E+08	12184	0.944564	0.657107	0.003543	0.01075	0.082318	1	11	9	34	6	24	30	30	33	40	39
ENSMUSG00000025950	chr1	Idh1	65158616	65159555	2771	0.589475	4.998275	0.003545	0.010751	0.046603	1	346	263	459	489	485	513	813	1041	619	489
ENSMUSG00000096842	chr13	Gm10736	1.12E+08	1.12E+08	78	0.525482	4.741748	0.003544	0.010751	0.035843	1	365	326	352	297	347	515	665	525	696	467
ENSMUSG00000039501	chr2	Znfx1	1.67E+08	1.67E+08	8189	-0.48264	4.628443	0.003546	0.010752	0.02996	-1	339	232	744	487	612	293	445	406	439	302
ENSMUSG00000021645	chr13	Smn1	1E+08	1E+08	2592	0.548276	3.129423	0.003548	0.010753	0.03431	1	81	92	165	122	105	177	242	153	241	131
ENSMUSG00000090115	chr17	Usp49	47630690	47630915	8581	-0.61026	2.505708	0.003547	0.010753	0.039703	-1	81	58	145	121	151	78	89	83	86	64
ENSMUSG00000037075	chr15	Rnf139	58889229	58889494	4348	-0.44642	5.736912	0.003555	0.010772	0.026923	-1	971	736	1317	907	977	703	1104	643	1042	671
ENSMUSG00000038170	chr3	Pde4dip	97689824	97690853	16508	-0.50952	11.64294	0.003556	0.010772	0.036419	-1	42745	33238	109866	61928	69897	33231	63360	41335	61062	45454
ENSMUSG00000031736	chr8	Crnde	92326038	92326266	2012	-1.24692	0.362958	0.003557	0.010774	0.151058	-1	19	19	23	38	35	7	6	8	13	28
ENSMUSG00000099913	chr1	Gm28551	53325507	53326457	3142	-0.43646	6.683776	0.003562	0.010786	0.026236	-1	1552	1467	2469	1905	2089	1247	2152	1268	2076	1354
ENSMUSG00000000131	chr7	Xpo6	1.26E+08	1.26E+08	9692	0.476537	4.129399	0.003567	0.010798	0.028746	1	219	129	402	197	262	316	480	370	379	302
ENSMUSG00000034379	chr16	Wdr5b	36041190	36042973	1784	-0.70203	1.464317	0.003575	0.010821	0.046118	-1	48	36	59	61	60	27	54	23	45	38
ENSMUSG00000041720	chr16	Pi4ka	17280351	17280620	11257	-0.46315	4.499974	0.003577	0.010823	0.027224	-1	288	250	645	466	519	264	376	383	409	298
ENSMUSG00000038122	chr10	Tbc1d32	56014298	56017704	7235	-0.64774	1.50629	0.003578	0.010824	0.035896	-1	48	32	75	48	71	24	49	36	50	38
ENSMUSG00000020284	chr10	1810043G02Rik	77978524	77978781	6627	0.643878	2.553906	0.003583	0.010836	0.045584	1	66	64	85	80	57	105	145	154	138	96
ENSMUSG00000063457	chr10	Rps15	80292453	80292483	630	0.512192	7.892925	0.003584	0.010838	0.036568	1	3264	2729	3357	2787	3081	4708	6081	4791	6158	3808
ENSMUSG00000026418	chr1	Tnni1	1.36E+08	1.36E+08	3600	2.322371	4.10256	0.003597	0.010876	0.666775	1	8	3	8	339	96	388	484	279	687	719
ENSMUSG00000021131	chr12	Erh	80634022	80634527	1350	0.47098	4.510814	0.003605	0.010897	0.02802	1	294	270	348	269	310	420	614	435	558	386
ENSMUSG00000047603	chr7	Zfp235	24134174	24134487	2466	-0.74102	1.217092	0.003607	0.0109	0.049651	-1	32	27	68	50	52	23	54	20	34	24
ENSMUSG00000028036	chr3	Ptgfr	1.52E+08	1.52E+08	4362	-0.84111	1.107576	0.003609	0.010903	0.066312	-1	28	30	78	43	39	20	39	30	16	28
ENSMUSG00000029204	chr5	Rhoh	65863569	65863881	4960	1.261938	-0.18305	0.003613	0.010913	0.113441	1	5	8	9	10	3	18	33	18	9	19
ENSMUSG00000047044	chr19	D030056L22Rik	18713193	18713659	1677	0.598887	2.433339	0.003634	0.010973	0.036882	1	69	56	83	57	68	100	129	129	126	93
ENSMUSG00000021669	chr13	Col4a3bp	96542618	96542644	5390	-0.43382	5.678136	0.003652	0.011025	0.025442	-1	823	637	1549	801	1026	550	951	772	1120	649
ENSMUSG00000039756	chr3	Dnttip2	1.22E+08	1.22E+08	2401	-0.48963	4.702375	0.003652	0.011025	0.031592	-1	433	433	668	398	477	349	577	341	401	313
ENSMUSG00000044921	chr10	Rassf9	1.03E+08	1.03E+08	2118	-0.92095	0.898835	0.003654	0.011026	0.081694	-1	21	23	40	36	70	14	32	17	20	28
ENSMUSG00000061894	chr4	Zscan20	1.29E+08	1.29E+08	8375	-0.73607	1.561668	0.003654	0.011026	0.052428	-1	35	30	97	72	63	27	55	39	38	37
ENSMUSG00000078867	chr2	Gm14418	1.77E+08	1.77E+08	2441	-1.28321	-0.30869	0.003664	0.011051	0.124396	-1	13	13	17	21	16	14	12	6	4	1
ENSMUSG00000020311	chr11	Erlec1	30930774	30931848	3260	-0.40116	5.111069	0.003667	0.011059	0.021062	-1	506	462	803	644	749	440	690	494	669	443
ENSMUSG00000059237	chr9	Ppp1r2-ps4	66805306	66805938	633	-0.94252	0.333677	0.003682	0.0111	0.069058	-1	14	21	30	20	39	6	22	13	15	17
ENSMUSG00000007122	chr1	Casq1	1.72E+08	1.72E+08	1951	0.477323	12.21399	0.003685	0.011109	0.03224	1	59446	46844	93701	50139	72178	90197	96389	96662	136757	83401
ENSMUSG00000047182	chr5	Irs3	1.38E+08	1.38E+08	2337	1.532375	1.10371	0.003699	0.011147	0.273797	1	23	19	10	10	16	43	21	134	25	39
ENSMUSG00000027951	chr3	Adar	89715022	89715150	6786	0.594448	2.551936	0.003707	0.011168	0.039399	1	50	44	96	84	101	113	148	144	130	93
ENSMUSG00000032030	chr9	Cul5	53614582	53618010	8165	-0.43112	6.562607	0.00371	0.011176	0.025726	-1	1485	1262	2714	1443	1967	1137	1900	1284	1782	1306
ENSMUSG00000031530	chr8	Dusp4	34807297	34808173	2740	0.783475	1.269354	0.003717	0.01119	0.058589	1	25	15	46	26	26	34	49	50	59	69
ENSMUSG00000031590	chr8	Frg1	41397457	41397644	1085	0.551372	4.492971	0.003717	0.01119	0.039606	1	290	281	319	237	282	450	677	361	602	367
ENSMUSG00000038696	chr2	Mapkap1	34406771	34406848	4059	-0.41879	5.367262	0.003717	0.01119	0.023449	-1	654	506	921	852	858	482	834	582	765	582
ENSMUSG00000009293	chr10	Ube2g2	77622275	77622416	2431	0.486385	6.856145	0.003737	0.011245	0.032966	1	1582	1188	1867	1342	1667	2069	3128	1929	3637	1820
ENSMUSG00000036564	chr8	Ndrg4	95676980	95677092	4887	0.757257	1.297295	0.003739	0.011251	0.056461	1	17	15	42	27	43	36	45	61	67	57
ENSMUSG00000010376	chr14	Nedd8	55662265	55662400	604	0.532693	6.197444	0.003744	0.011262	0.039181	1	949	918	961	860	922	1372	2070	1380	1938	1222
ENSMUSG00000056216	chr7	Cebpg	35046422	35050932	4935	-0.41591	5.548561	0.003746	0.011265	0.023296	-1	655	566	1135	923	1077	552	849	754	964	575
ENSMUSG00000037266	chr4	Rsrp1	1.35E+08	1.35E+08	3349	0.615803	7.053054	0.003747	0.011267	0.05311	1	1712	1659	2281	987	1571	2545	3495	3119	2638	2664

ENSMUSG00000063694	chr6	Cycs	50562563	50565385	3404	-0.63293	7.89307	0.003756	0.01129	0.056431	-1	3633	2459	4420	6694	6100	2687	5302	2261	4435	2768
ENSMUSG00000071711	chr15	Mpst	78406712	78406744	1509	-0.43647	5.673902	0.00376	0.0113	0.025921	-1	849	797	1192	837	973	650	841	776	934	732
ENSMUSG00000000028	chr16	Cdc45	18780447	18780573	2252	0.630008	1.851626	0.003763	0.011307	0.03835	1	39	27	60	47	49	80	89	62	96	59
ENSMUSG00000047804	chr11	Akap10	61871307	61873021	6451	-0.53095	3.060969	0.00377	0.011326	0.032135	-1	135	81	224	157	209	101	167	128	135	90
ENSMUSG00000040822	chr14	1700123O20Rik	54686171	54687120	1889	0.496464	2.902053	0.003773	0.011332	0.026316	1	87	68	132	92	115	132	190	139	213	120
ENSMUSG00000090386	chr16	Mir99ahg	77236317	77236335	14045	0.893799	0.805552	0.003776	0.01134	0.07764	1	18	4	26	19	27	19	43	48	47	37
ENSMUSG00000032840	chr5	2410131K14Rik	1.18E+08	1.18E+08	5649	-0.46561	3.94736	0.003783	0.011356	0.026666	-1	211	171	371	314	393	184	247	233	315	202
ENSMUSG00000040430	chr11	Pitpnc1	1.07E+08	1.07E+08	6612	-0.78967	6.339608	0.003788	0.011365	0.087044	-1	863	538	2405	2475	2479	754	1573	765	1171	1193
ENSMUSG00000065037	chr9	Rn7sk	78175303	78175633	331	1.114176	0.252288	0.003787	0.011365	0.103512	1	8	11	17	10	8	25	24	10	37	36
ENSMUSG00000030616	chr7	Sytl2	90348699	90348892	6888	1.015636	3.087422	0.003789	0.011368	0.133998	1	96	118	137	24	49	159	232	210	203	209
ENSMUSG00000029213	chr5	Commd8	72157000	72159893	3464	-0.452	4.451924	0.003792	0.011372	0.026434	-1	346	356	539	342	422	304	415	289	424	258
ENSMUSG00000038612	chr3	Mcl1	95658721	95659487	3485	0.436943	7.410419	0.003793	0.011373	0.02684	1	1791	1650	3075	2576	2593	2732	4833	3318	4334	2887
ENSMUSG00000020802	chr11	Ube2o	1.17E+08	1.17E+08	5288	-0.45661	4.840289	0.003794	0.011373	0.027501	-1	394	298	733	646	649	320	525	412	582	384
ENSMUSG00000026404	chr1	Ddx59	1.36E+08	1.36E+08	2953	-0.47089	3.462529	0.003798	0.011385	0.025841	-1	171	155	301	189	212	153	205	134	201	144
ENSMUSG00000092232	chr14	Gm20521	54883441	54883506	1245	0.422563	4.876977	0.003806	0.011404	0.023255	1	403	274	502	377	450	526	726	599	704	504
ENSMUSG00000037361	chr12	Sf3b6	4817608	4817819	1115	0.52935	4.195272	0.003814	0.011428	0.03577	1	223	222	271	230	215	361	563	308	448	299
ENSMUSG00000040596	chr1	Pogk	1.66E+08	1.66E+08	9586	-0.48227	3.771254	0.003823	0.01145	0.028373	-1	206	155	447	214	297	154	245	234	242	164
ENSMUSG00000037353	chr15	Letmd1	1E+08	1E+08	2579	0.536475	3.161318	0.003824	0.011452	0.033827	1	89	90	157	94	155	140	190	237	213	168
ENSMUSG00000013622	chr5	Atraid	31048312	31048432	2092	0.451686	5.569891	0.003835	0.011481	0.027625	1	666	511	780	583	617	827	1196	940	1303	776
ENSMUSG00000023087	chr3	Ccrn4l	51224447	51225287	10658	0.636624	4.433842	0.003839	0.011492	0.055105	1	170	123	361	380	367	495	543	536	479	308
ENSMUSG00000055368	chr8	Slc6a2	92960079	92960181	6176	-1.05946	-0.00508	0.003843	0.0115	0.076159	-1	15	9	32	20	24	5	11	17	7	12
ENSMUSG00000043207	chr4	Zmpste24	1.21E+08	1.21E+08	7145	-0.42753	4.878094	0.003845	0.011504	0.024053	-1	451	395	871	441	599	324	582	459	543	397
ENSMUSG00000027583	chr2	Zbtb46	1.81E+08	1.81E+08	8508	-0.56112	2.452854	0.003851	0.011518	0.032732	-1	76	66	173	92	125	61	95	67	109	69
ENSMUSG00000026407	chr1	Cacna1s	1.36E+08	1.36E+08	6550	-0.53228	9.845425	0.003855	0.011527	0.040367	-1	10830	9759	28005	20805	21853	9938	14263	12638	17793	14049
ENSMUSG00000028923	chr4	Necap2	1.41E+08	1.41E+08	3095	0.438227	4.321932	0.003861	0.011543	0.024291	1	271	164	337	255	340	323	485	419	565	321
ENSMUSG00000002332	chr14	Dhrs1	55739020	55739420	2760	0.446984	5.275036	0.003873	0.011574	0.026782	1	486	414	632	519	540	706	940	666	1156	640
ENSMUSG00000040054	chr10	Baz2a	1.28E+08	1.28E+08	8372	-0.44978	4.489348	0.003872	0.011574	0.026012	-1	315	246	730	389	482	247	410	341	420	319
ENSMUSG00000043067	chr9	Dpy19l1	24411776	24414423	6350	0.575999	2.963705	0.003876	0.01158	0.039244	1	60	77	143	97	127	139	180	191	154	162
ENSMUSG00000004655	chr6	Aqp1	55336432	55336874	2627	-0.55863	7.820323	0.003904	0.011661	0.044338	-1	2585	2266	5884	5072	6757	2528	4604	3558	3414	2697
ENSMUSG00000009073	chr11	Nf2	4765845	4768273	6825	-0.44613	6.474767	0.003906	0.011665	0.027843	-1	1239	959	2264	1896	2080	1047	1680	1334	1757	1125
ENSMUSG00000021510	chr13	A530054K11Rik	67617001	67621849	5217	-0.64892	1.616437	0.003916	0.011694	0.039246	-1	51	39	88	52	66	24	62	42	43	42
ENSMUSG00000006288	chr14	Ttc5	50765415	50766022	1841	0.551241	2.609238	0.003929	0.011728	0.031666	1	80	58	84	74	89	99	169	120	156	110
ENSMUSG00000068747	chr3	Sort1	1.08E+08	1.08E+08	7560	-0.62094	6.912715	0.003941	0.011761	0.054599	-1	2279	1559	4904	1314	2197	1535	1729	1723	2241	1408
ENSMUSG00000085156	chr11	Gm11974	6525591	6525817	1359	1.03846	0.335914	0.003955	0.0118	0.088401	1	18	7	15	12	7	34	36	27	27	15
ENSMUSG00000041471	chr14	Fam35a	34237041	34237586	3446	-0.57019	2.962628	0.003969	0.011841	0.037997	-1	97	108	254	140	162	75	162	100	117	116
ENSMUSG00000028634	chr4	Hivep3	1.2E+08	1.2E+08	17427	0.63616	2.074911	0.003981	0.011874	0.041723	1	32	38	61	59	69	73	122	82	126	60
ENSMUSG00000052934	chr8	Fbxo31	1.22E+08	1.22E+08	5482	-0.45764	7.315507	0.003983	0.011876	0.029793	-1	2182	2010	4476	3092	3374	1617	3347	2067	3249	2229
ENSMUSG00000022420	chr15	Dnal4	79761453	79762049	2340	0.555631	3.053676	0.003997	0.011913	0.036394	1	110	57	116	130	118	134	215	159	232	157
ENSMUSG00000089682	chr14	Bcl2l2	54883377	54883506	4462	-0.4515	5.355311	0.003997	0.011913	0.027897	-1	582	448	973	899	957	480	848	509	838	531
ENSMUSG00000048271	chr5	Rbm33	28317121	28317410	10592	-0.43688	5.043219	0.004001	0.011922	0.025525	-1	474	353	1032	617	677	402	664	456	586	458
ENSMUSG00000046345	chr16	Smco1	32271468	32271658	1408	-0.44622	5.848081	0.004014	0.011957	0.027715	-1	894	628	1441	1168	1300	576	1264	834	1157	725
ENSMUSG00000019838	chr10	Slc16a10	40033535	40037404	5394	-0.50623	5.473339	0.004028	0.011999	0.035609	-1	757	634	1457	562	863	512	752	570	1031	540
ENSMUSG00000046201	chr17	Scaf8	3114972	3115418	4869	-0.4018	4.47757	0.00403	0.012001	0.020555	-1	337	262	591	387	494	252	428	327	451	307
ENSMUSG00000032042	chr9	Srpr	35200175	35200213	3364	-0.44119	8.37086	0.004034	0.012009	0.027946	-1	5351	4781	9180	5011	6539	3879	6808	4516	6131	4566
ENSMUSG00000019210	chr6	Atp6v1e1	1.21E+08	1.21E+08	1203	0.466534	6.928862	0.004043	0.012034	0.030839	1	1454	1447	1870	1630	1606	2148	3223	2283	3249	2101
ENSMUSG00000046743	chr3	Fat4	38886940	38892134	17165	-0.73745	2.639711	0.004045	0.012036	0.06628	-1	56	61	241	108	198	67	94	80	98	79
ENSMUSG00000102504	chr4	RP23-411B7.7	42714926	42719893	4968	-1.03551	1.003353	0.004056	0.012068	0.113394	-1	18	23	72	39	65	31	32	24	13	11
ENSMUSG00000022999	chr15	Lmbr1l	98903921	98904508	4217	0.582024	2.420233	0.004066	0.012095	0.035709	1	72	51	92	56	64	95	158	106	130	88
ENSMUSG00000029640	chr5	Usp12	1.47E+08	1.47E+08	4639	-0.44424	4.16415	0.004078	0.012128	0.025182	-1	256	196	430	386	413	207	376	247	353	220
ENSMUSG00000005823	chr17	Gpr108	57234914	57235366	2095	0.399358	5.104182	0.004088	0.012155	0.021274	1	387	332	624	496	554	529	816	719	909	612
ENSMUSG00000010538	chr3	Tsacc	88282757	88282984	1112	0.922603	1.07962	0.004095	0.012172	0.080436	1	28	25	21	14	17	30	72	35	64	42
ENSMUSG00000022280	chr15	Rnf19a	36239934	36242065	4276	-0.45965	4.099254	0.004098	0.012172	0.027185	-1	218	249	438	317	380	158	352	277	309	234
ENSMUSG00000047037	chr7	Nipa1	55977567	55979903	3183	-0.57849	2.299763	0.004097	0.012172	0.035326	-1	65	72	138	79	119	47	81	80	92	57
ENSMUSG00000065987	chr8	Cd209b	3917655	3918827	2115	-1.31563	1.390936	0.004097	0.012172	0.212009	-1	82	53	111	15	29	34	24	39	20	12
ENSMUSG00000024426	chr17	Atat1	35897595	35897915	4586	0.656256	2.120319	0.004105	0.012192	0.044776	1	62	43	57	41	55	84	97	94	122	74
ENSMUSG00000008206	chr8	Cers4	4493026	4493068	12268	0.563255	2.415519	0.004106	0.012192	0.03444	1	53	46	91	56	98	98	121	123	137	88
ENSMUSG00000001348	chr9	Acp5	22126731	22127262	1612	1.461469	3.500933	0.004116	0.012218	0.285804	1	179	104	71	37	36	195	223	720	180	143
ENSMUSG00000024925	chr19	Rnaseh2c	5601873	5602080	1455	0.525074	3.53418	0.004124	0.012238	0.033373	1	138	139	155	138	165	169	293	247	289	240
ENSMUSG00000001249	chr7	Hpn	31098725	31099073	4101	-0.55092	2.503682	0.004127	0.012244	0.032571	-1	78	70	157	119	118	70	113	80	88	64
ENSMUSG00000068115	chr2	Ninl	1.51E+08	1.51E+08	5952	0.9757	0.111174	0.004127	0.012244	0.061939	1	8	9	11	15	8	20	28	15	35	19
ENSMUSG00000032602	chr9	Slc25a20	1.09E+08	1.09E+08	4844	-0.68648	6.242037	0.004129	0.012247	0.067153	-1	895	776	1396	2540	1946	769	1496	909	1448	806
ENSMUSG00000028933	chr5	Xrcc2	25689812	25692828	5216	-0.56338	2.598937	0.004132	0.01225	0.03596	-1	72	94	175	105	135	68	130	77	99	71
ENSMUSG00000037204	chr15	Atg101	1.01E+08	1.01E+08	1230	0.478036	5.169867	0.004132	0.01225	0.03113	1	494	400	530	445	478	704	822	735	975	575
ENSMUSG00000028124	chr3	Gclm	1.22E+08	1.22E+08	5543	-0.53838	3.928263	0.004137	0.012262	0.038055	-1	272	228	453	199	301	192	231	245	331	140
ENSMUSG00000028885	chr4	Smpdl3b	1.33E+08	1.33E+08	2006	-0.75045	1.749644	0.004145	0.012282	0.058972	-1	47	34	79	81	95	47	42	32	50	47

ENSMUSG00000042642	chr3	Flad1	89401004	89402312	4087	-0.5054	5.357556	0.004148	0.012285	0.03551	-1	555	423	927	1056	960	455	719	550	784	596
ENSMUSG00000045176	chr11	2310047M10Rik	69059717	69061578	1862	0.456156	4.780463	0.004147	0.012285	0.027695	1	359	284	438	375	371	528	603	544	772	444
ENSMUSG00000009549	chr2	Srp14	1.18E+08	1.18E+08	1195	0.502221	6.477361	0.004151	0.012291	0.035753	1	1157	1111	1325	981	1148	1531	2416	1719	2544	1456
ENSMUSG00000026641	chr1	Usf1	1.71E+08	1.71E+08	2806	0.441555	4.359684	0.004162	0.01232	0.024944	1	236	219	295	282	343	315	502	425	550	371
ENSMUSG00000009470	chr13	Tnpo1	98839019	98844620	8579	-0.46712	5.265683	0.004169	0.012336	0.030025	-1	615	438	1286	578	804	405	639	642	719	545
ENSMUSG00000028426	chr4	Rad23b	55350043	55350427	5733	-0.46969	7.036421	0.004169	0.012336	0.031644	-1	2251	2065	3674	1937	2279	1494	2463	1811	2607	1780
ENSMUSG00000030660	chr7	Pik3c2a	1.16E+08	1.16E+08	8042	-0.60151	2.53438	0.004171	0.012339	0.041238	-1	69	71	189	108	136	52	121	89	96	63
ENSMUSG00000036820	chr17	Amdhd2	24155833	24156085	2728	0.504517	3.0316	0.004173	0.012344	0.029058	1	98	63	129	118	131	129	200	163	239	142
ENSMUSG00000028629	chr4	Exo5	1.21E+08	1.21E+08	2008	0.848291	0.580937	0.004176	0.01235	0.05469	1	13	10	27	15	15	20	27	33	50	32
ENSMUSG00000046491	chr11	C1qtnf2	43474276	43474387	1308	0.758013	2.04543	0.004187	0.012378	0.068252	1	24	36	73	37	77	58	115	117	74	92
ENSMUSG00000026960	chr2	Arl6ip6	53191726	53191880	2703	-0.61549	2.637183	0.0042	0.012415	0.045573	-1	116	101	178	80	121	48	121	84	112	85
ENSMUSG00000024513	chr18	Mbd2	70568189	70568967	3214	-0.42525	5.316091	0.004214	0.012454	0.024943	-1	632	602	1088	632	711	484	796	556	802	501
ENSMUSG00000020109	chr10	Dnajb12	59879556	59879810	3369	-0.42983	6.039438	0.004231	0.0125	0.026038	-1	996	814	1994	1111	1301	786	1223	911	1382	869
ENSMUSG00000006333	chr7	Rps9	3703993	3704064	2526	0.540865	8.265846	0.004234	0.012505	0.042361	1	4163	3734	3911	3509	3958	6205	7562	6085	8526	4989
ENSMUSG00000040843	chr1	Tiprl	1.65E+08	1.65E+08	5473	0.452558	4.595177	0.004234	0.012505	0.026962	1	320	276	420	269	324	440	660	479	552	410
ENSMUSG00000084786	chr9	Ubl5	20642878	20644893	3468	0.516797	6.257388	0.004257	0.012568	0.037967	1	967	956	1121	922	900	1446	2218	1464	1936	1220
ENSMUSG00000016494	chr1	Cd34	1.95E+08	1.95E+08	7290	0.440021	6.356805	0.004262	0.012581	0.027625	1	821	722	1688	1118	1388	1387	1921	1915	1884	1460
ENSMUSG00000042700	chr12	Sipa1l1	82170016	82170076	7697	-0.5435	3.640608	0.00427	0.012601	0.037859	-1	190	151	435	188	263	128	230	238	196	134
ENSMUSG00000018199	chr1	Trove2	1.44E+08	1.44E+08	9541	-0.55314	2.76917	0.004271	0.012602	0.034599	-1	89	82	208	113	173	80	99	91	136	92
ENSMUSG00000067369	chrX	Trmt2b	1.34E+08	1.34E+08	4648	-0.56194	4.297695	0.004274	0.012609	0.042828	-1	262	192	444	517	500	216	438	234	305	267
ENSMUSG00000054519	chr11	Zfp867	59461197	59464286	3412	-0.77951	1.874459	0.004276	0.01261	0.072503	-1	68	46	70	68	111	22	91	39	48	47
ENSMUSG00000018800	chr11	Abca5	1.1E+08	1.1E+08	11437	-0.45886	3.822853	0.004281	0.012623	0.026361	-1	221	177	396	244	293	183	212	195	327	172
ENSMUSG00000036591	chr2	Arhgap21	20847919	20850385	9271	-0.61256	3.953008	0.004285	0.012631	0.050174	-1	182	127	512	342	427	146	231	244	263	225
ENSMUSG00000035401	chr7	2210018M11Rik	98590615	98590884	4005	-0.56179	3.245573	0.004301	0.012675	0.038959	-1	113	98	247	220	250	111	139	145	167	127
ENSMUSG00000030032	chr6	Wdr54	83149361	83152897	6562	0.946465	0.569646	0.004302	0.012678	0.07255	1	18	14	12	7	22	26	36	24	45	33
ENSMUSG00000066979	chr7	Bub3	1.32E+08	1.32E+08	2055	0.415322	5.288362	0.00431	0.012696	0.023549	1	524	383	684	542	534	659	1033	738	1024	653
ENSMUSG00000032177	chr9	Pde4a	21165714	21166232	7655	-0.71882	5.757723	0.004313	0.012703	0.07389	-1	679	369	1319	1509	1795	527	892	532	994	811
ENSMUSG00000042790	chr9	Rnf214	45863425	45864998	5922	-0.53413	3.731775	0.004318	0.012716	0.036814	-1	145	146	470	265	295	148	267	179	243	161
ENSMUSG00000074800	chr13	Gm4149	75644864	75645162	362	0.539715	4.237004	0.004323	0.012728	0.038632	1	254	216	277	234	207	392	552	379	428	279
ENSMUSG00000022802	chr16	Lmln	33062521	33062734	6511	-0.72046	2.082214	0.004327	0.012736	0.05785	-1	59	43	151	82	98	57	53	35	77	60
ENSMUSG00000029648	chr5	Flt1	1.48E+08	1.48E+08	11583	-0.59385	5.272172	0.004334	0.012751	0.049876	-1	415	351	1009	939	1192	397	822	547	627	458
ENSMUSG00000034621	chr11	Gpatch8	1.02E+08	1.02E+08	8178	-0.43903	5.085195	0.004334	0.012751	0.026254	-1	449	377	1038	618	772	424	580	506	594	506
ENSMUSG00000029826	chr6	Zc3hav1	38305286	38307456	6518	0.478726	3.566342	0.004338	0.012761	0.028579	1	118	107	236	147	197	193	344	279	244	193
ENSMUSG00000026558	chr1	Uck2	1.67E+08	1.67E+08	5464	0.512256	4.202521	0.00434	0.012762	0.035032	1	177	146	272	294	337	328	549	295	549	286
ENSMUSG00000040563	chr9	Lppr2	21937033	21937158	2750	0.99244	0.276746	0.004344	0.012773	0.08531	1	11	4	17	9	19	13	20	28	38	33
ENSMUSG00000002608	chr7	Ccdc97	25711106	25713113	3939	0.431934	5.765518	0.004361	0.012813	0.026348	1	622	439	1002	772	955	815	1226	1041	1521	1118
ENSMUSG00000035596	chr7	Mboat7	3677790	3678849	7716	0.487279	3.598942	0.00436	0.012813	0.029644	1	133	103	220	182	173	188	251	306	312	219
ENSMUSG00000038312	chr2	Edem2	1.56E+08	1.56E+08	3463	0.671241	3.068232	0.004361	0.012813	0.056921	1	105	98	140	70	89	152	185	259	190	132
ENSMUSG00000028085	chr3	Gatb	85574119	85574319	4299	-0.43499	4.344201	0.004364	0.012819	0.025006	-1	319	282	411	419	415	249	388	274	420	257
ENSMUSG00000023088	chr16	Abcc1	14361558	14361643	12366	-0.44784	5.185713	0.00437	0.012832	0.027729	-1	530	376	1144	648	811	381	717	501	736	513
ENSMUSG00000074743	chr2	Thbd	1.48E+08	1.48E+08	3723	0.669801	4.790847	0.00437	0.012832	0.063179	1	268	251	514	289	419	397	1387	537	489	409
ENSMUSG00000076431	chr13	Sox4	28948919	28953713	4795	0.66826	2.228092	0.004383	0.012867	0.052158	1	44	34	90	40	85	52	121	97	145	105
ENSMUSG00000025060	chr19	Slk	47579678	47580343	8284	-0.41904	5.556754	0.004385	0.01287	0.02457	-1	721	537	1348	763	1081	505	968	703	993	581
ENSMUSG00000047766	chr9	Lrrc49	60568859	60570598	6310	0.621576	1.729413	0.004396	0.0129	0.0362	1	41	27	51	33	51	46	84	74	92	61
ENSMUSG00000031109	chrX	Enox2	49009707	49011634	4356	-1.24336	4.054106	0.004397	0.0129	0.216113	-1	441	596	400	101	133	215	223	149	236	83
ENSMUSG00000042377	chr11	Fam83g	61684091	61684168	6659	0.794639	1.86275	0.004401	0.012909	0.07447	1	48	21	83	22	40	79	89	73	119	50
ENSMUSG00000067847	chr2	Romo1	1.56E+08	1.56E+08	747	0.526419	6.114405	0.004423	0.012969	0.039654	1	972	815	912	807	866	1296	1785	1337	2014	1100
ENSMUSG00000029122	chr5	Evc	37289098	37289654	7701	-1.29707	4.001645	0.004428	0.012981	0.234211	-1	74	71	306	761	713	132	150	118	233	199
ENSMUSG00000020744	chr11	Slc25a19	1.16E+08	1.16E+08	4026	-0.45647	5.134692	0.004431	0.012988	0.028911	-1	593	398	736	702	842	471	586	606	630	398
ENSMUSG00000079105	chr15	C7	4988762	4989006	2709	-1.7322	4.10567	0.004443	0.013021	0.407989	-1	217	329	939	229	550	319	29	29	291	24
ENSMUSG00000001785	chr10	Pwp1	85871831	85872014	2730	-0.39822	4.543198	0.004445	0.013022	0.020892	-1	354	305	588	405	490	281	519	335	428	292
ENSMUSG00000069515	chr10	Lyz1	1.17E+08	1.17E+08	1264	0.943956	2.663742	0.004447	0.013026	0.118075	1	64	47	108	64	63	257	138	120	152	52
ENSMUSG00000000759	chr8	Tubgcp3	12614277	12615296	8568	-0.56013	3.064012	0.004448	0.013027	0.037818	-1	107	85	258	157	220	106	160	115	115	111
ENSMUSG00000022856	chr16	Tmem41a	21934327	21935045	1359	0.607926	2.113739	0.00446	0.013056	0.038826	1	55	32	69	40	75	72	105	97	125	69
ENSMUSG00000030074	chr6	Gxylt2	1.01E+08	1.01E+08	2678	1.187666	-0.36605	0.00446	0.013056	0.112477	1	7	2	14	1	9	6	27	19	16	16
ENSMUSG00000027452	chr2	Acss1	1.51E+08	1.51E+08	4128	-0.92108	4.79722	0.004464	0.013061	0.120974	-1	230	221	553	1128	873	198	557	272	404	359
ENSMUSG00000036875	chr10	Dna2	62947026	62947169	5878	0.948174	-0.12659	0.004464	0.013061	0.055966	1	10	3	12	8	11	19	20	18	21	17
ENSMUSG00000000811	chr6	Txnrd3	89643988	89644402	2836	-0.5635	2.900487	0.004473	0.013084	0.038592	-1	143	118	174	114	148	99	119	115	144	69
ENSMUSG00000042284	chr13	Itga1	1.15E+08	1.15E+08	5984	-0.80498	2.375451	0.004489	0.013128	0.081994	-1	45	43	214	100	163	49	96	68	86	45
ENSMUSG00000010290	chr1	AI597479	43098710	43098862	3458	-0.40293	4.595507	0.004494	0.013139	0.021599	-1	346	318	613	440	511	260	465	338	517	342
ENSMUSG00000012819	chr10	Cdh23	60302748	60303700	16939	-1.00833	1.318734	0.004497	0.013147	0.117876	-1	21	18	65	66	101	15	30	37	32	30
ENSMUSG00000066571	chr7	4931406P16Rik	34236707	34239237	6437	-0.48658	5.059362	0.004501	0.013155	0.03303	-1	487	298	1009	647	825	359	631	414	672	485
ENSMUSG00000029056	chr4	Pank4	1.55E+08	1.55E+08	3487	-0.48583	4.787963	0.004524	0.013216	0.032491	-1	388	249	740	622	675	327	497	372	500	402
ENSMUSG00000078963	chr18	Hsbp1l1	80229758	80230561	1251	1.001278	0.918331	0.004524	0.013216	0.108861	1	7	10	13	32	33	29	55	47	39	44
ENSMUSG00000021750	chr14	Fam107a	8296274	8298797	3870	-0.82028	0.706164	0.004525	0.013218	0.058548	-1	17	23	44	34	42	18	29	23	23	9

ENSMUSG00000028064	chr3	Sema4a	88435959	88437252	5406	0.783085	2.668333	0.004538	0.013251	0.08	1	76	44	141	44	77	146	126	205	109	110
ENSMUSG00000100807	chr9	Gm29521	1.02E+08	1.02E+08	3749	-1.32559	0.193938	0.004546	0.013271	0.184226	-1	27	12	22	19	41	13	6	1	27	8
ENSMUSG00000066113	chr4	Adamtsl1	86053915	86054120	10870	-0.75868	3.326141	0.004553	0.01329	0.077092	-1	152	96	449	136	250	132	145	175	93	109
ENSMUSG00000039648	chr2	Ccbl1	30185124	30185569	2923	-0.47431	4.159393	0.004572	0.013343	0.030072	-1	254	232	383	433	352	230	356	229	347	212
ENSMUSG00000044674	chr5	Fzd1	4753873	4758035	4163	0.756099	2.332675	0.004574	0.013345	0.071975	1	38	39	85	64	74	66	144	168	74	106
ENSMUSG00000009376	chr6	Met	17463800	17464248	7679	-0.44407	4.270377	0.004588	0.013382	0.025991	-1	251	233	573	359	417	199	398	287	328	286
ENSMUSG00000031877	chr8	Ces2g	1.05E+08	1.05E+08	2859	1.144566	1.28318	0.004597	0.013405	0.159759	1	22	22	36	9	27	36	48	120	31	47
ENSMUSG00000038803	chr5	Ost4	30905885	30906766	1272	0.495172	5.674447	0.004608	0.013434	0.034972	1	697	595	777	592	639	1022	1478	929	1281	774
ENSMUSG00000037020	chr7	Wdr62	30240138	30240484	5743	-0.88799	1.131181	0.004611	0.013441	0.082606	-1	48	16	77	40	45	24	23	35	39	13
ENSMUSG00000084799	chr1	Ino80dos	63113078	63113219	2880	-0.9486	0.486849	0.004631	0.013495	0.085083	-1	10	20	56	31	26	8	21	13	24	16
ENSMUSG00000034614	chr11	Pik3ip1	3330401	3331004	4272	-0.42427	5.53246	0.004634	0.013502	0.025496	-1	883	565	1217	759	851	573	901	640	833	665
ENSMUSG00000023951	chr17	Vegfa	46016993	46018879	4293	-0.69558	6.301549	0.004636	0.013502	0.070773	-1	952	642	1747	2305	2469	621	1722	1004	1308	990
ENSMUSG00000058905	chr5	Gm10051	1.33E+08	1.33E+08	414	0.992341	0.029293	0.004637	0.013502	0.071786	1	11	5	9	12	11	21	16	24	22	24
ENSMUSG00000095432	chr13	Zfp748	67538641	67542910	4970	-0.65096	1.538462	0.004635	0.013502	0.041504	-1	56	36	83	52	51	29	63	34	43	33
ENSMUSG00000014294	chr18	Ndufa2	36742332	36742658	572	0.497241	7.459446	0.00465	0.013537	0.036394	1	2226	1947	2286	2440	2461	3101	4833	3246	5190	2762
ENSMUSG00000033389	chr11	Arhgap44	65002039	65003450	5819	-0.68128	2.871249	0.004653	0.013541	0.060255	-1	71	88	162	198	210	62	130	85	142	97
ENSMUSG00000018707	chr12	Dync1h1	1.11E+08	1.11E+08	15658	-0.49693	7.334883	0.004655	0.013543	0.036377	-1	2037	1692	5338	3153	3736	1759	2574	2386	3486	2141
ENSMUSG00000036111	chr7	Lmo1	1.09E+08	1.09E+08	1071	0.701068	1.204289	0.004655	0.013543	0.045133	1	20	12	35	34	35	42	50	51	65	39
ENSMUSG00000022841	chr16	Ap2m1	20535478	20535601	4172	0.416583	6.498899	0.004659	0.013549	0.025188	1	950	902	1566	1341	1487	1494	2257	1716	2506	1556
ENSMUSG00000023034	chr15	Nr4a1	1.01E+08	1.01E+08	2474	0.622871	7.335745	0.004659	0.013549	0.057125	1	1632	2007	2623	1714	2022	2965	6010	1878	4671	2884
ENSMUSG00000019194	chr7	Scn1b	31116524	31117136	1801	0.433513	9.322872	0.004662	0.013553	0.027952	1	7547	5806	11185	9415	10090	10437	14375	13517	15986	12646
ENSMUSG00000025931	chr1	Paqr8	20890606	20890686	5488	0.88962	0.021121	0.004671	0.013576	0.048241	1	8	5	14	9	15	18	22	23	26	17
ENSMUSG00000021223	chr12	Papln	83763634	83763716	5635	-1.37011	0.028674	0.0047	0.013657	0.196389	-1	9	1	35	32	36	6	15	5	15	6
ENSMUSG00000055053	chr10	Nfic	81396186	81401071	6534	-0.50706	8.242407	0.004713	0.013693	0.038183	-1	4257	2913	9926	5808	7153	2885	5463	4049	6332	4469
ENSMUSG00000092686	chr10	Gm25745	86705316	86705448	133	-0.62132	1.971766	0.004718	0.013706	0.04101	-1	67	52	94	72	89	32	63	72	60	49
ENSMUSG00000078676	chr11	Casc3	98804905	98804986	4303	0.385766	4.837158	0.004725	0.013722	0.020149	1	328	271	568	397	446	475	670	572	731	505
ENSMUSG00000040697	chr4	Dnajc16	1.42E+08	1.42E+08	6510	-0.42472	4.619085	0.004738	0.013753	0.024352	-1	377	251	699	406	603	290	453	352	497	334
ENSMUSG00000095677	chr17	Dynlt1f	6648941	6649337	807	0.739934	1.607835	0.004738	0.013753	0.057541	1	45	24	46	30	29	62	90	72	74	38
ENSMUSG00000042558	chr4	Adprhl2	1.26E+08	1.26E+08	2475	0.523048	3.466829	0.004753	0.013793	0.03406	1	161	118	164	124	137	199	309	223	275	179
ENSMUSG00000046844	chr8	Vat1l	1.14E+08	1.14E+08	5462	-1.04965	0.066766	0.004754	0.013793	0.083662	-1	13	19	24	26	20	9	7	18	9	12
ENSMUSG00000022390	chr15	Zc3h7b	81744848	81745346	5958	-0.40922	5.454733	0.004758	0.013803	0.023674	-1	640	480	1219	863	916	499	813	653	897	606
ENSMUSG00000026921	chr2	Egfl7	26580014	26580109	3581	0.434823	5.036374	0.004766	0.013824	0.026259	1	402	306	512	510	491	545	913	621	917	499
ENSMUSG00000041329	chr11	Atp1b2	69599736	69601412	4085	0.671762	8.496283	0.00477	0.013831	0.067043	1	4770	3552	8479	2103	3883	5389	8287	8201	10391	8281
ENSMUSG00000036333	chr12	Kidins220	24974932	24975062	7402	-0.42602	5.386426	0.004774	0.013841	0.025627	-1	593	469	1273	666	997	498	815	626	715	604
ENSMUSG00000051506	chr14	Wdfy4	32959547	32960004	10512	0.820047	1.512756	0.004776	0.013842	0.079869	1	19	10	53	39	46	51	50	84	71	57
ENSMUSG00000053483	chr1	Usp21	1.71E+08	1.71E+08	4756	0.44	4.123018	0.004789	0.013877	0.025568	1	199	158	321	223	295	333	376	401	446	258
ENSMUSG00000031792	chr8	Usb1	95332292	95332465	2791	0.533359	2.2939	0.004792	0.013884	0.029675	1	58	38	84	59	79	81	133	90	128	89
ENSMUSG00000032119	chr9	Hinfp	44295673	44296580	2100	-0.6768	1.139507	0.004799	0.013899	0.038558	-1	35	31	66	34	45	26	41	30	29	22
ENSMUSG00000025921	chr1	Rdh10	16105774	16106306	4160	0.630252	2.247083	0.004802	0.013907	0.044079	1	58	40	54	61	75	71	153	104	103	87
ENSMUSG00000103766	chr3	RHBG	88243380	88243448	1524	0.966516	0.706026	0.004811	0.01393	0.084488	1	25	17	14	10	12	30	54	32	41	27
ENSMUSG00000029173	chr5	Sepsecs	52640087	52644107	5347	-0.52042	3.366141	0.004816	0.013937	0.034898	-1	183	132	278	148	241	91	245	143	172	133
ENSMUSG00000031148	chrX	Gpkow	7697131	7697395	3737	-0.424	3.96165	0.004816	0.013937	0.02309	-1	216	207	397	301	319	177	331	233	259	216
ENSMUSG00000033405	chr14	Nudt15	73519864	73521674	2592	-0.70815	1.389841	0.00483	0.013973	0.0474	-1	53	33	65	38	64	36	42	38	31	26
ENSMUSG00000035595	chr10	1600002K03Rik	80172944	80173174	678	0.777235	2.464461	0.004831	0.013975	0.075632	1	69	76	69	35	55	117	129	104	133	129
ENSMUSG00000037470	chr1	Uggt1	36140027	36144251	12853	-0.49358	6.262585	0.004842	0.014003	0.03572	-1	965	844	2673	1389	1720	981	1276	936	1492	1124
ENSMUSG00000059901	chr10	Adamts14	61197112	61198959	5197	0.892471	0.858083	0.004845	0.014008	0.081687	1	15	13	28	14	27	34	24	32	52	54
ENSMUSG00000024140	chr17	Epas1	86753907	86754308	5309	-0.63464	6.727489	0.004856	0.014037	0.059722	-1	1206	868	2564	2882	3293	997	2072	1502	1936	1230
ENSMUSG00000087107	chr11	Al662270	83223576	83223651	1489	1.110714	0.987528	0.004872	0.014081	0.146282	1	10	11	15	8	54	49	45	49	46	38
ENSMUSG00000025192	chr19	Entpd7	43689672	43689904	8963	0.919279	0.216081	0.004882	0.014106	0.060443	1	10	11	19	6	12	17	21	25	35	26
ENSMUSG00000099081	chr11	Gm27624	3644776	3644952	177	-0.89942	0.818365	0.004896	0.014144	0.078472	-1	30	25	54	28	40	15	39	25	9	18
ENSMUSG00000031066	chrX	Usp11	20703906	20704119	4732	0.763492	1.618819	0.004902	0.01416	0.068436	1	16	16	54	46	51	48	62	66	84	76
ENSMUSG00000058927	chr19	Gm10053	24875686	24876634	949	-0.67353	4.092163	0.004918	0.014202	0.064702	-1	222	203	323	477	457	139	387	139	339	233
ENSMUSG00000060538	chr7	Tmem219	1.27E+08	1.27E+08	2292	0.529555	3.47347	0.004923	0.014212	0.035247	1	149	131	159	122	141	202	259	206	319	202
ENSMUSG00000028015	chr3	Ctso	81932601	81932775	5123	-0.52841	3.527589	0.004928	0.014223	0.036913	-1	185	207	294	165	221	157	221	181	173	122
ENSMUSG00000024259	chr18	Slc25a46	31580168	31583769	4371	-0.40235	5.77959	0.004959	0.01431	0.023432	-1	834	681	1400	991	1180	641	1158	691	1133	762
ENSMUSG00000021660	chr13	Btf3	98309896	98310201	1739	0.498392	7.175194	0.004965	0.014324	0.037018	1	1860	1804	2167	1637	1831	2750	4003	2652	3734	2407
ENSMUSG00000032612	chr9	Usp4	1.08E+08	1.08E+08	8628	-0.40764	6.832337	0.004968	0.01433	0.024621	-1	1894	1421	2957	1892	2392	1548	1987	1626	2283	1505
ENSMUSG00000038195	chr11	Rilp	75510094	75510372	1583	0.548737	5.252248	0.004978	0.014352	0.04401	1	399	208	591	672	675	671	967	671	1039	784
ENSMUSG00000086859	chr11	2810008D09Rik	1.17E+08	1.17E+08	2166	0.768899	1.532444	0.004977	0.014352	0.062918	1	31	35	44	27	24	63	70	59	55	65
ENSMUSG00000032382	chr9	Snx1	66088133	66088569	4339	0.446027	3.873702	0.004981	0.01436	0.025358	1	154	172	234	176	246	223	390	300	360	269
ENSMUSG00000006423	chrX	C330007P06Rik	36823737	36824169	7424	-0.476	3.844185	0.004986	0.014368	0.029913	-1	208	225	326	244	324	173	283	223	194	209
ENSMUSG00000019872	chr10	Smpdl3a	57794335	57794409	2065	-0.46424	6.535305	0.004986	0.014368	0.031991	-1	1519	1451	2690	1406	1579	1057	1884	1340	1548	1318
ENSMUSG00000024217	chr17	Snrpc	27839974	27840169	6217	0.447355	5.056368	0.004991	0.014377	0.028104	1	436	390	512	391	475	602	890	595	871	561
ENSMUSG00000057375	chr4	Yipf1	1.07E+08	1.07E+08	6783	0.484279	3.124918	0.004996	0.014388	0.027405	1	105	92	149	113	113	143	201	174	218	177
ENSMUSG00000017188	chr11	Coa3	1.01E+08	1.01E+08	886	0.448942	5.879931	0.005003	0.014407	0.029338	1	792	616	861	796	847	1088	1610	1025	1476	1028

ENSMUSG00000020522	chr11	Mfap3	57518664	57518712	5801	-0.45627	3.531407	0.005009	0.014421	0.025861	-1	164	128	342	201	267	138	238	156	228	137
ENSMUSG00000058006	chr4	Mdn1	32657119	32657352	21836	-0.57622	3.154702	0.00501	0.014421	0.042531	-1	116	81	328	172	201	84	162	137	161	110
ENSMUSG00000068329	chr6	Htra2	83051266	83051634	2764	0.485486	4.217025	0.005015	0.01443	0.03231	1	212	137	262	310	323	318	451	376	551	296
ENSMUSG00000041653	chr15	Pnpla3	84167816	84168060	4640	1.059955	3.06773	0.005019	0.014439	0.157325	1	129	48	83	68	92	150	156	442	102	132
ENSMUSG00000075289	chr19	Carns1	4164324	4166564	3968	0.425706	5.371274	0.005028	0.014462	0.026092	1	567	329	875	471	657	633	1070	791	1068	795
ENSMUSG00000031697	chr8	Orc6	85299632	85299992	1653	0.72195	2.043215	0.00503	0.014464	0.059122	1	48	50	43	49	42	93	112	85	89	71
ENSMUSG00000034981	chr5	Parm1	91517615	91517957	5068	-0.54557	5.27585	0.005049	0.014517	0.043528	-1	753	528	1337	428	731	431	748	640	680	408
ENSMUSG00000023104	chr5	Rfc2	1.35E+08	1.35E+08	1518	0.440599	4.025361	0.00507	0.014572	0.025236	1	221	168	264	196	242	300	419	327	414	248
ENSMUSG00000023259	chr9	Slc26a6	1.09E+08	1.09E+08	5411	-0.54525	3.411308	0.005072	0.014578	0.038878	-1	189	96	329	175	257	128	203	110	224	131
ENSMUSG00000024431	chr18	Nr3c1	39410545	39414634	7425	-0.47872	6.365124	0.005082	0.014601	0.034074	-1	1217	1115	2579	1333	1652	761	1463	1296	1426	1349
ENSMUSG00000028949	chr5	Smarcd3	24590818	24593118	4545	-0.51122	7.346029	0.005083	0.014601	0.039349	-1	3155	2723	4106	2365	2682	2114	2728	2066	3442	1990
ENSMUSG00000078772	chr4	Gm12353	19605451	19605536	554	-0.71406	2.49889	0.005084	0.014602	0.066511	-1	63	81	101	142	168	48	128	57	98	65
ENSMUSG00000020183	chr10	Cpm	1.18E+08	1.18E+08	5964	-0.87005	2.028684	0.005093	0.014625	0.096473	-1	27	42	127	86	158	43	67	34	66	48
ENSMUSG00000025464	chr7	Paox	1.4E+08	1.4E+08	1765	0.652366	2.079172	0.005109	0.014667	0.047645	1	46	44	72	52	40	71	97	118	96	73
ENSMUSG00000047832	chr12	Cdca4	1.13E+08	1.13E+08	2417	0.671017	1.871788	0.005113	0.014676	0.051865	1	35	17	59	63	50	58	91	79	97	73
ENSMUSG00000037709	chr6	Fam13a	58932090	58935711	6328	-0.55843	3.44894	0.005135	0.014734	0.041519	-1	167	142	220	229	278	84	183	183	183	170
ENSMUSG00000037816	chr13	Fbxw17	50417864	50417987	3818	0.648611	2.184407	0.005144	0.014756	0.048321	1	57	44	83	33	61	74	113	122	119	68
ENSMUSG00000034892	chr12	Rps29	69157722	69157821	693	0.527921	7.79408	0.005157	0.014793	0.042112	1	3041	2678	3018	2653	2597	4504	6077	4335	5667	3435
ENSMUSG00000032096	chr9	Arcn1	44741564	44744016	6084	-0.42685	6.635381	0.005181	0.014857	0.027229	-1	1593	1246	2936	1546	2044	1216	2067	1267	1843	1412
ENSMUSG00000029915	chr6	Clec5a	40574894	40578080	3840	1.084297	-0.31896	0.005207	0.014929	0.079066	1	5	4	6	8	12	10	23	19	12	20
ENSMUSG00000031659	chr8	Adcy7	88272403	88272613	6330	0.64628	2.860416	0.005239	0.015017	0.056393	1	53	40	137	105	134	133	181	196	139	136
ENSMUSG00000025350	chr10	Rdh5	1.29E+08	1.29E+08	2809	0.521348	6.177838	0.005245	0.01503	0.040495	1	973	878	953	872	897	1323	2225	1280	1860	1198
ENSMUSG00000021217	chr7	Tshz3	36698118	36698289	5456	0.682046	1.450098	0.005247	0.015033	0.047691	1	19	19	50	38	39	33	88	59	68	51
ENSMUSG00000030201	chr6	Lrp6	1.34E+08	1.34E+08	9822	-0.48538	5.819786	0.005266	0.015086	0.034894	-1	676	547	1794	1129	1431	651	934	833	1114	776
ENSMUSG00000033066	chr11	Gas7	67455437	67455774	11342	0.555297	3.748113	0.005269	0.01509	0.043378	1	139	88	320	148	217	223	264	361	296	279
ENSMUSG00000015013	chr8	Trappc2l	1.23E+08	1.23E+08	607	0.498974	4.792864	0.005273	0.015099	0.035354	1	374	340	391	332	333	503	785	488	706	491
ENSMUSG00000035585	chr7	Tsen34	3693375	3693889	2416	0.447343	4.865056	0.005277	0.015105	0.028381	1	338	272	433	492	420	499	684	574	812	506
ENSMUSG00000073434	chr17	Wdr90	25844771	25845225	8466	0.935497	0.308482	0.005278	0.015105	0.0714	1	8	9	15	11	19	12	34	37	24	27
ENSMUSG00000032216	chr9	Nedd4	72662346	72662613	10973	-0.43649	8.622955	0.005286	0.015126	0.029103	-1	6136	4920	12319	6144	7965	4310	7406	5913	7511	5685
ENSMUSG00000025597	chrX	Klhl4	1.14E+08	1.14E+08	3584	-1.17545	0.048856	0.005292	0.015138	0.13326	-1	7	18	24	19	38	4	6	13	11	17
ENSMUSG00000081434	chr2	Gm14165	1.52E+08	1.52E+08	952	0.866296	1.206546	0.005293	0.015138	0.083176	1	24	16	41	26	18	48	98	38	56	24
ENSMUSG00000068114	chr15	Ccdc134	82127922	82128049	2043	0.635777	3.728712	0.005299	0.015153	0.056428	1	215	132	206	103	151	270	268	352	307	236
ENSMUSG00000027244	chr2	Atg13	91674618	91676463	4368	-0.3945	5.318332	0.005335	0.015254	0.022371	-1	667	474	1077	695	772	546	708	573	789	528
ENSMUSG00000046441	chr8	Cmtr2	1.1E+08	1.1E+08	4115	-0.54443	2.30417	0.005342	0.01527	0.033076	-1	83	70	132	71	110	52	92	60	100	61
ENSMUSG00000005981	chr16	Trap1	4039971	4040224	2573	-0.42261	7.392459	0.005347	0.015279	0.027166	-1	2754	2483	4026	2848	3232	2191	3425	2379	3102	2108
ENSMUSG00000019820	chr10	Utrn	12382188	12384196	12382	-0.47425	4.711227	0.005348	0.015279	0.032067	-1	300	318	796	490	630	276	485	467	420	351
ENSMUSG00000014418	chr7	Hps5	46760466	46761450	6482	-0.4555	4.318833	0.005354	0.015293	0.028745	-1	334	272	573	291	401	228	410	326	280	283
ENSMUSG00000015889	chr10	Lta4h	93453396	93453668	2066	0.410513	4.539002	0.005356	0.015297	0.023096	1	298	250	454	269	325	379	594	485	538	418
ENSMUSG00000031012	chrX	Cask	13517080	13522347	9145	-0.49363	3.429118	0.005364	0.015317	0.031598	-1	177	154	325	141	223	116	181	151	204	160
ENSMUSG00000019960	chr10	Dusp6	99263231	99264091	2796	0.564507	4.002271	0.005374	0.015342	0.045398	1	149	108	250	215	341	204	476	335	348	379
ENSMUSG00000003573	chr8	Homer3	70282827	70283100	3440	0.640305	2.578726	0.005393	0.015392	0.050032	1	61	70	80	66	83	109	128	176	128	101
ENSMUSG00000033159	chr1	Cnppd1	75134554	75136932	5635	0.436302	4.760063	0.005404	0.015421	0.027031	1	315	277	528	345	388	462	505	570	761	520
ENSMUSG00000029061	chr4	Mmp23	1.56E+08	1.56E+08	2340	0.818128	1.279222	0.005409	0.015431	0.069489	1	22	31	30	24	23	38	55	73	48	51
ENSMUSG00000028062	chr3	Lamtor2	88549819	88550004	1218	0.465854	5.426603	0.005412	0.015435	0.031759	1	624	481	615	509	580	806	1098	841	1068	733
ENSMUSG00000023886	chr17	Smoc2	14279506	14279799	2832	0.435245	7.436267	0.005418	0.01545	0.028892	1	1857	1939	3415	1992	2699	2818	4298	3422	3992	3578
ENSMUSG00000027879	chr3	Sec22b	97901190	97901420	3709	0.39837	5.057015	0.005424	0.015465	0.022535	1	438	348	607	396	506	579	851	625	792	601
ENSMUSG00000002393	chr8	Nr2f6	71374123	71374421	2983	0.445513	4.317218	0.005457	0.015553	0.027322	1	271	189	335	266	279	307	421	377	560	422
ENSMUSG00000038535	chr9	Zfp280d	72274860	72275029	19017	-0.53493	3.588116	0.005457	0.015553	0.038603	-1	150	170	386	205	256	113	221	162	181	210
ENSMUSG00000025153	chr11	Fasn	1.21E+08	1.21E+08	9849	1.56374	6.282143	0.005471	0.015587	0.35625	1	894	298	1252	292	538	1275	277	6094	1075	1249
ENSMUSG00000074121	chr7	Ntf5	45413695	45413788	1962	0.576537	3.091423	0.005477	0.015602	0.043005	1	108	64	97	125	143	138	199	149	248	187
ENSMUSG00000032555	chr9	Topbp1	1.03E+08	1.03E+08	11122	-0.48049	3.273116	0.005491	0.015639	0.029346	-1	136	140	235	179	209	112	205	151	136	127
ENSMUSG00000027932	chr3	Slc27a3	90385239	90385533	2569	0.827165	1.264848	0.00551	0.015688	0.078003	1	22	18	44	22	29	63	49	73	42	32
ENSMUSG00000015247	chr4	Nipsnap3b	53011880	53012047	1687	0.768728	1.089141	0.005531	0.015744	0.054943	1	24	24	26	23	19	40	45	56	53	35
ENSMUSG00000045658	chr1	Pid1	84036296	84038507	8172	0.543616	3.055597	0.005533	0.015744	0.038456	1	68	75	151	104	150	162	175	213	187	139
ENSMUSG00000075391	chr2	Gm13443	35340409	35340963	555	-0.55443	2.283567	0.005533	0.015744	0.033934	-1	85	67	126	69	113	57	95	59	77	66
ENSMUSG00000052675	chr7	Zfp112	24112314	24112436	4095	-0.51841	2.63802	0.005535	0.015747	0.032002	-1	99	86	177	109	115	73	137	74	110	73
ENSMUSG00000049556	chr9	Lingo1	56618475	56621315	3925	1.051578	0.544302	0.005543	0.015766	0.115221	1	14	9	29	9	10	28	25	27	72	16
ENSMUSG00000036246	chr8	Gmip	69808679	69808820	5552	0.59027	2.229896	0.005551	0.015785	0.041597	1	52	33	98	54	64	96	113	115	104	70
ENSMUSG00000031312	chrX	Itgb1bp2	1.01E+08	1.01E+08	1799	0.44311	7.577396	0.005575	0.01585	0.030211	1	2181	1568	3265	2835	3339	3340	4795	3124	5402	3585
ENSMUSG00000045114	chr7	Prrt2	1.27E+08	1.27E+08	3272	0.500703	2.715141	0.005589	0.015887	0.029192	1	71	62	122	70	110	110	155	143	183	104
ENSMUSG00000033386	chr3	Frrs1	1.17E+08	1.17E+08	2396	0.777667	0.648097	0.00559	0.015887	0.049739	1	16	10	20	17	23	33	34	36	30	31
ENSMUSG00000029775	chr6	Klhdc10	30401868	30402150	8443	-0.42103	5.798698	0.005604	0.01592	0.02641	-1	773	570	1571	1052	1338	701	1028	754	1112	770
ENSMUSG00000074785	chr10	Plxnc1	94790866	94793290	7836	0.88408	1.370735	0.005604	0.01592	0.097586	1	21	15	61	14	37	67	45	61	48	59
ENSMUSG00000026442	chr1	Nfasc	1.33E+08	1.33E+08	14145	0.962628	0.283987	0.005613	0.015942	0.096652	1	6	2	24	13	18	21	30	38	28	15
ENSMUSG00000022204	chr14	Ngdn	55015454	55015588	1198	0.434575	3.973287	0.005622	0.015965	0.025161	1	190	165	277	185	248	309	425	276	393	241

ENSMUSG00000034602	chr10	Mon2	1.23E+08	1.23E+08	9303	-0.45242	5.325521	0.005628	0.015976	0.03019	-1	572	423	1368	621	924	449	722	634	726	564
ENSMUSG00000041571	chr7	Sepw1	15917208	15917539	736	0.537181	10.35591	0.005657	0.016057	0.044852	1	19972	15405	19395	12470	15414	23730	36224	26264	33968	22540
ENSMUSG00000006386	chr4	Tek	94739289	94739692	4712	-0.42749	4.161438	0.005667	0.016078	0.025057	-1	239	218	481	342	397	193	400	284	293	233
ENSMUSG00000085014	chr2	Gm13490	51656966	51658001	2409	-1.11465	0.797962	0.005667	0.016078	0.137489	-1	23	10	45	43	68	24	20	10	12	24
ENSMUSG00000029075	chr4	Tnfrsf4	1.56E+08	1.56E+08	1365	0.965823	0.487855	0.005669	0.01608	0.086211	1	13	17	24	4	11	24	40	22	37	32
ENSMUSG00000018830	chr16	Myh11	14194527	14195184	6632	-0.52823	4.876797	0.005671	0.016081	0.041489	-1	334	456	800	515	721	213	538	443	622	426
ENSMUSG00000021127	chr12	Zfp36l1	80107760	80110548	2984	0.517948	4.851434	0.005676	0.016093	0.03952	1	244	305	509	359	505	415	1087	612	606	452
ENSMUSG00000022146	chr15	Osmr	6813577	6815928	12113	0.798894	3.188489	0.005697	0.01615	0.0922	1	86	52	174	85	156	181	341	301	133	91
ENSMUSG00000002477	chr18	Snrpd1	10617796	10617926	837	0.558768	3.579194	0.005701	0.016156	0.042151	1	153	145	135	124	184	223	357	223	299	196
ENSMUSG00000030614	chr7	Tmem126b	90468194	90469161	3984	-0.41332	4.93683	0.005706	0.016167	0.024855	-1	505	425	636	561	648	407	662	414	576	361
ENSMUSG00000013275	chr1	Slc41a1	1.32E+08	1.32E+08	4912	-0.91218	5.657251	0.005707	0.016168	0.126632	-1	404	317	1102	1893	1846	451	1006	453	850	528
ENSMUSG00000033106	chr8	Slc7a6os	1.06E+08	1.06E+08	1525	0.511478	2.90306	0.005713	0.016179	0.031483	1	98	76	134	74	105	137	199	158	176	121
ENSMUSG00000026922	chr2	Agpat2	26593057	26593762	2130	1.213789	3.828934	0.005722	0.0162	0.217222	1	169	84	102	173	127	284	134	902	200	186
ENSMUSG00000027200	chr2	Sema6d	1.24E+08	1.24E+08	10559	-0.5379	4.143322	0.005722	0.0162	0.041457	-1	202	196	642	313	418	159	364	216	321	270
ENSMUSG00000050891	chr15	Tatdn1	58890153	58890697	1366	-0.51435	4.069597	0.005724	0.016201	0.037986	-1	350	267	368	266	284	208	367	184	302	212
ENSMUSG00000018893	chr15	Mb	77015489	77016072	1252	-1.95853	10.39193	0.005751	0.016273	0.548025	-1	3151	4333	10792	98188	60370	2398	22523	2811	17404	9777
ENSMUSG00000021811	chr14	Dnajc9	20384638	20385478	1631	0.451458	4.547287	0.005763	0.016298	0.028784	1	276	287	417	288	285	396	656	399	611	418
ENSMUSG00000030246	chr6	Ldhb	1.42E+08	1.42E+08	1570	-2.11854	6.50255	0.005762	0.016298	0.631506	-1	130	208	716	7049	4103	138	1323	179	889	780
ENSMUSG00000031490	chr8	Eif4ebp1	27260327	27260550	981	0.465453	5.322971	0.005762	0.016298	0.032117	1	559	429	687	487	487	749	1015	814	1143	555
ENSMUSG00000035439	chr8	Haus8	71248561	71251544	5278	0.692347	2.071811	0.005766	0.016303	0.056137	1	44	42	39	64	54	88	108	81	89	88
ENSMUSG00000078349	chr4	AW011738	1.56E+08	1.56E+08	1848	-0.79654	0.980542	0.00578	0.016334	0.06476	-1	26	15	49	55	51	19	28	25	36	18
ENSMUSG00000090553	chr1	Snrpe	1.34E+08	1.34E+08	1372	0.557598	4.275468	0.005779	0.016334	0.044509	1	248	251	260	213	226	398	593	309	501	311
ENSMUSG00000039515	chr2	Ppp2r4	30416039	30416332	5188	0.415404	6.337355	0.005789	0.016357	0.026283	1	890	806	1317	1195	1351	1326	1877	1648	2023	1546
ENSMUSG00000026385	chr1	Dbi	1.2E+08	1.2E+08	1422	0.616294	6.773832	0.005817	0.016433	0.058644	1	1536	1198	1173	1414	1265	2089	2562	3250	2518	1579
ENSMUSG00000020457	chr11	Drg1	3187360	3187410	3460	0.406619	5.554813	0.005827	0.016456	0.024525	1	584	486	791	674	679	832	1308	810	1193	786
ENSMUSG00000030849	chr7	Fgfr2	1.3E+08	1.3E+08	7240	-0.91486	-0.13968	0.005828	0.016456	0.051237	-1	14	12	27	12	21	7	12	12	13	7
ENSMUSG00000021044	chr12	Adck1	88360554	88360595	2330	-0.48637	4.585772	0.005837	0.016478	0.034581	-1	342	241	505	587	601	283	468	315	500	285
ENSMUSG00000001755	chr11	Coasy	1.01E+08	1.01E+08	2867	0.575478	3.460821	0.005845	0.016496	0.046352	1	118	81	178	157	179	192	213	342	276	159
ENSMUSG00000031907	chr8	Zfp90	1.06E+08	1.06E+08	2632	0.689258	1.359376	0.005847	0.016496	0.049358	1	24	20	46	34	28	44	60	63	46	58
ENSMUSG00000042446	chr4	Zmym4	1.27E+08	1.27E+08	8139	-0.43081	3.947124	0.005846	0.016496	0.025051	-1	200	195	453	253	356	175	295	200	312	223
ENSMUSG00000007050	chr17	Lsm2	34981862	34982085	3152	0.524649	3.211984	0.00588	0.016586	0.035736	1	130	90	175	109	95	137	233	214	237	170
ENSMUSG00000029265	chr5	Dr1	1.08E+08	1.08E+08	3478	-0.4659	4.198853	0.005893	0.016618	0.030662	-1	262	239	471	329	428	168	292	329	314	294
ENSMUSG00000093264	chr11	Gm23419	1.2E+08	1.2E+08	84	0.474593	4.631398	0.0059	0.016636	0.033025	1	363	162	401	325	428	468	658	443	640	423
ENSMUSG00000020100	chr10	Slc29a3	60712072	60716490	5834	0.621651	2.420669	0.005914	0.01667	0.050036	1	47	34	111	66	87	104	113	137	101	111
ENSMUSG00000028393	chr4	Alad	62509169	62509310	1871	-0.55334	5.330973	0.005924	0.016695	0.046585	-1	594	466	738	1090	933	431	615	773	671	476
ENSMUSG00000095597	chrX	Gm6472	1.53E+08	1.53E+08	651	0.638827	3.559919	0.005928	0.016703	0.056956	1	147	156	139	114	142	269	362	207	303	165
ENSMUSG00000042572	chr3	Ube2q1	89773609	89774038	3081	0.37987	4.566114	0.005932	0.01671	0.020113	1	265	231	419	346	395	386	580	461	583	431
ENSMUSG00000027983	chr3	Cyp2u1	1.31E+08	1.31E+08	2331	-0.74179	1.362818	0.005939	0.016726	0.059299	-1	34	24	70	61	67	17	47	31	36	39
ENSMUSG00000037656	chr8	Slc20a2	22476700	22476925	3649	-0.57262	5.92043	0.00594	0.016726	0.050515	-1	796	543	1506	1541	1628	661	1151	581	1283	847
ENSMUSG00000021916	chr14	Glt8d1	31001393	31001428	2521	0.465701	3.730535	0.005947	0.016743	0.029362	1	178	126	261	142	187	197	348	299	279	268
ENSMUSG00000024359	chr18	Hspa9	34937414	34938393	3932	-0.49619	9.045797	0.005951	0.016749	0.038711	-1	7065	6068	11289	13005	12771	5972	11792	6713	9960	6455
ENSMUSG00000063605	chr8	Ccdc102a	94902869	94903391	2504	0.662362	2.30853	0.005961	0.016776	0.053095	1	66	57	85	39	48	81	132	109	151	76
ENSMUSG00000029635	chr5	Cdk8	1.46E+08	1.46E+08	3881	-0.44745	3.378832	0.005979	0.016823	0.025272	-1	145	139	280	192	212	136	170	169	189	130
ENSMUSG00000064061	chr16	Dzip3	48924232	48926102	9081	-0.69032	1.362434	0.005997	0.01687	0.047956	-1	35	26	68	66	55	21	41	35	44	33
ENSMUSG00000021240	chr12	Abcd4	84602531	84603159	2527	0.448314	3.238369	0.005999	0.016871	0.025181	1	112	83	159	130	153	149	214	199	236	183
ENSMUSG00000024645	chr18	Timm21	84947294	84947745	1315	-0.52781	4.037776	0.006036	0.016971	0.040297	-1	221	182	342	420	399	169	376	231	248	214
ENSMUSG00000103565	chr15	Sgsm3	81002628	81002664	2283	-0.42956	3.84246	0.006044	0.01699	0.024992	-1	266	189	351	236	269	198	253	199	283	178
ENSMUSG00000035215	chr10	Lsm7	80852825	80853100	468	0.625848	2.752017	0.006047	0.016995	0.050054	1	96	68	80	70	92	133	221	118	179	94
ENSMUSG00000004360	chr10	9330159F19Rik	29211643	29211866	5644	-0.42643	4.823392	0.006052	0.017001	0.026772	-1	505	419	716	456	482	368	537	364	565	379
ENSMUSG00000008301	chr18	Phax	56562443	56562723	2223	0.465503	4.206076	0.006051	0.017001	0.030326	1	236	221	287	228	235	369	464	362	451	292
ENSMUSG00000093769	chr3	Hist2h3c1	96246685	96248504	1820	-0.7343	1.762835	0.006054	0.017003	0.065311	-1	68	59	93	47	61	50	41	46	65	24
ENSMUSG00000024725	chr19	Ostf1	18579328	18581328	4784	0.457663	4.988011	0.006056	0.017007	0.030825	1	446	374	488	334	445	528	794	664	874	514
ENSMUSG00000051934	chr15	Spats2	99126578	99126887	3065	0.49239	2.879532	0.006077	0.017063	0.029892	1	77	57	131	105	122	140	184	131	201	121
ENSMUSG00000005802	chr2	Slc30a4	1.23E+08	1.23E+08	5482	-0.41798	4.86244	0.006085	0.017079	0.025617	-1	463	372	890	437	566	384	592	398	577	343
ENSMUSG00000019791	chr10	Hint3	30608141	30608423	990	-0.43115	4.462268	0.006091	0.017094	0.026912	-1	329	360	540	388	385	295	448	313	407	257
ENSMUSG00000030861	chr7	Acadsb	1.31E+08	1.31E+08	4474	-0.43244	6.974279	0.006096	0.017097	0.029232	-1	1641	1926	3463	2174	2493	1340	2557	1911	2275	1784
ENSMUSG00000041926	chr1	Rnpep	1.35E+08	1.35E+08	6977	0.428805	4.445529	0.006095	0.017097	0.026358	1	261	205	409	286	336	377	417	524	559	377
ENSMUSG00000097487	chr11	Ptges3l	1.01E+08	1.01E+08	2108	0.461374	6.409933	0.006095	0.017097	0.032985	1	1312	793	1346	963	1258	1655	2105	1540	2170	1501
ENSMUSG00000044948	chr19	Cfap43	47737561	47737887	9955	0.83583	0.683638	0.006109	0.017129	0.069937	1	12	5	28	26	17	21	42	38	38	35
ENSMUSG00000034684	chr9	Sema3f	1.08E+08	1.08E+08	5197	0.538594	2.638024	0.006125	0.01717	0.036047	1	68	41	105	100	92	107	165	139	157	97
ENSMUSG00000027524	chr2	Edn3	1.75E+08	1.75E+08	4113	-0.91003	0.143203	0.006126	0.01717	0.070149	-1	26	17	21	14	26	10	20	9	19	7
ENSMUSG00000028560	chr4	Usp1	98923810	98924243	3733	-0.40683	3.909318	0.006145	0.017218	0.022367	-1	253	194	392	253	285	163	303	226	278	213
ENSMUSG00000063077	chr4	Kif1b	1.49E+08	1.49E+08	17608	-0.48165	8.834621	0.006146	0.017218	0.036743	-1	6147	4898	13653	8673	11163	4242	9167	5713	9687	6762
ENSMUSG00000021023	chr12	1110008L16Rik	55299577	55299666	4452	-0.44576	3.259141	0.006153	0.017235	0.025326	-1	154	128	231	155	216	120	190	131	195	107
ENSMUSG00000032872	chr9	Cyb5r4	87022014	87022253	6736	-0.3947	5.39984	0.006181	0.01731	0.023464	-1	673	552	959	786	873	569	875	551	861	510

ENSMUSG00000054199	chr3	Gon4l	88835231	88835296	7564	-0.44803	4.017818	0.006182	0.01731	0.027737	-1	252	187	481	253	365	206	276	292	251	209
ENSMUSG00000079215	chr5	Zfp664	1.25E+08	1.25E+08	5729	-0.41575	4.607014	0.006189	0.017324	0.024934	-1	332	264	595	504	585	303	479	391	451	291
ENSMUSG00000049580	chr7	Tsku	98350668	98353130	2859	0.67678	1.131091	0.00619	0.017325	0.042527	1	15	17	30	32	35	37	59	48	51	38
ENSMUSG00000069601	chr10	Ank3	69533772	69534284	33152	-0.46778	6.270399	0.006201	0.01735	0.034002	-1	988	782	2503	1456	1836	827	1413	1067	1506	1145
ENSMUSG00000032182	chr9	Yipf2	21588709	21589558	2150	0.479388	3.002722	0.006205	0.017358	0.027784	1	86	83	121	109	128	133	195	159	194	157
ENSMUSG00000005474	chr5	Myl10	1.37E+08	1.37E+08	822	-2.50312	0.926414	0.00621	0.017368	0.82558	-1	9	2	22	134	86	0	37	0	15	4
ENSMUSG00000001910	chr8	Nacc1	84670483	84673304	4300	-0.41189	4.938462	0.006215	0.017375	0.024888	-1	474	327	783	570	715	379	503	433	593	479
ENSMUSG00000031617	chr8	Tmem184c	77595982	77597180	2723	-0.56529	3.016646	0.006214	0.017375	0.043225	-1	158	128	236	103	141	93	175	113	122	92
ENSMUSG00000022427	chr15	Tomm22	79670861	79671008	1113	0.428945	5.685465	0.006225	0.017399	0.027914	1	638	606	768	683	738	852	1432	938	1388	851
ENSMUSG00000090247	chr10	Bloc1s1	1.29E+08	1.29E+08	1288	0.504503	6.208127	0.006263	0.017502	0.039557	1	997	899	1000	898	915	1325	2263	1319	1878	1230
ENSMUSG00000001665	chr10	Gstt3	75774115	75775010	2627	0.639603	2.147571	0.006283	0.017556	0.05156	1	37	33	91	50	69	70	101	137	109	63
ENSMUSG00000002012	chrX	Pnck	73655994	73656386	1971	0.550464	4.044992	0.006296	0.017586	0.043856	1	264	180	267	129	203	283	437	312	447	311
ENSMUSG00000007777	chr11	0610009B22Rik	51685386	51686092	998	-0.45538	4.343084	0.006297	0.017586	0.030424	-1	370	318	501	293	374	248	466	266	361	240
ENSMUSG00000042340	chr7	Ctf1	1.28E+08	1.28E+08	1345	0.474291	3.340517	0.006304	0.017603	0.028797	1	123	104	155	144	139	164	247	176	294	191
ENSMUSG00000022641	chr16	Bbx	50191844	50197646	14205	-0.51401	3.225942	0.006321	0.017639	0.035394	-1	152	117	283	120	229	93	193	131	149	136
ENSMUSG00000027435	chr2	Cd93	1.48E+08	1.48E+08	6677	0.494966	4.629526	0.006321	0.017639	0.036944	1	218	167	444	381	495	340	621	498	755	466
ENSMUSG00000030796	chr7	Tead2	45215753	45215832	4668	0.866888	0.770813	0.006321	0.017639	0.078636	1	9	9	19	31	23	30	37	38	37	42
ENSMUSG00000026239	chr1	Pde6d	86542994	86543583	2178	0.417188	4.577323	0.006333	0.017668	0.025366	1	306	184	388	335	441	374	570	483	609	453
ENSMUSG00000050954	chr13	Zfp169	48487647	48489318	8017	-0.87298	0.005409	0.006335	0.017669	0.056821	-1	13	17	27	20	17	5	17	12	16	9
ENSMUSG00000019763	chr10	Rmnd1	4401915	4403501	5894	-0.59153	4.550709	0.006351	0.01771	0.053209	-1	317	218	441	693	613	252	473	275	415	309
ENSMUSG00000020246	chr10	Hcfc2	82696160	82696207	5485	-0.39378	4.616105	0.006388	0.017809	0.022401	-1	402	279	675	407	514	279	487	327	507	353
ENSMUSG00000028292	chr4	Rars2	34614957	34615026	2771	-0.4325	4.104017	0.006399	0.017836	0.026901	-1	299	272	386	286	307	205	349	242	351	203
ENSMUSG00000022040	chr14	Ephx2	66084377	66084760	2035	-0.82503	5.119938	0.00641	0.017864	0.106145	-1	498	416	504	1174	924	279	498	817	361	314
ENSMUSG00000042215	chr1	Bag2	33745484	33747016	3059	-0.41604	4.241873	0.006411	0.017864	0.024641	-1	262	214	483	368	442	216	429	251	374	234
ENSMUSG00000022108	chr14	Itm2b	73362231	73363143	1773	0.424018	8.195351	0.006414	0.017868	0.028692	1	3445	3181	5309	3784	4322	4982	6642	6893	6614	5304
ENSMUSG00000028224	chr4	Nbn	15957925	15958110	2533	-0.39432	4.14238	0.006432	0.017915	0.021643	-1	303	230	456	274	351	200	344	266	342	246
ENSMUSG00000059412	chr9	Fxyd2	45403138	45403300	632	0.945449	0.714812	0.006451	0.017964	0.098517	1	14	15	29	6	21	32	22	49	39	36
ENSMUSG00000067194	chrX	Eif1ax	1.59E+08	1.59E+08	5266	-0.40524	6.776222	0.006459	0.017981	0.025922	-1	1701	1575	2932	1732	2147	1250	2102	1556	2149	1616
ENSMUSG00000097666	chr18	A330094K24Rik	77729681	77730478	1027	-0.85757	1.680251	0.006471	0.018011	0.09913	-1	80	71	69	39	48	36	70	24	49	29
ENSMUSG00000030495	chr7	Slc7a10	35186385	35186650	2463	1.679835	2.519274	0.006483	0.01804	0.409505	1	75	49	38	13	19	89	57	477	57	65
ENSMUSG00000035342	chr19	Lzts2	45015176	45015323	2921	0.478388	4.355181	0.006495	0.018067	0.033777	1	253	164	298	326	323	344	407	503	484	399
ENSMUSG00000040260	chr17	Daam2	49456022	49458747	6045	0.61819	2.408594	0.006494	0.018067	0.05058	1	51	35	95	45	116	81	128	109	139	117
ENSMUSG00000031641	chr8	Cbr4	61487734	61487990	3047	-0.48297	4.336894	0.006501	0.01808	0.034882	-1	322	287	399	435	413	241	480	216	401	234
ENSMUSG00000003429	chr7	Rps11	45122388	45122558	602	0.422995	7.37189	0.006508	0.018093	0.028468	1	2163	1696	2996	2251	2180	2996	4122	3310	4302	2668
ENSMUSG00000041164	chr11	Zmiz2	6389074	6389140	4655	-0.44476	5.776193	0.006508	0.018093	0.030729	-1	852	535	1472	1062	1308	638	841	862	1249	684
ENSMUSG00000016018	chr13	Skiv2l2	1.13E+08	1.13E+08	3309	-0.3965	5.544066	0.006511	0.018096	0.024098	-1	723	635	1270	771	896	564	1050	649	797	646
ENSMUSG00000025352	chr10	Gdf11	1.29E+08	1.29E+08	4062	-0.83938	4.808857	0.006514	0.0181	0.109514	-1	305	429	1091	325	907	419	206	198	533	413
ENSMUSG00000058997	chr14	Vwa8	78849178	78849443	6928	-0.48949	6.891366	0.006525	0.018128	0.03811	-1	1619	1137	3027	2940	2728	1374	2429	1501	2473	1425
ENSMUSG00000020475	chr11	Pgam2	5801640	5801839	840	0.44185	11.45144	0.006527	0.018131	0.031498	1	38783	24604	45661	38277	42959	49864	66495	53495	84517	43778
ENSMUSG00000030987	chr7	Stim1	1.02E+08	1.02E+08	3597	-0.52607	7.604592	0.006534	0.018146	0.044249	-1	2552	1734	5660	4350	5048	2063	3516	2220	3795	3078
ENSMUSG00000038495	chr3	Otud7b	96104527	96104819	8497	-0.40779	6.212332	0.006544	0.018168	0.026072	-1	1107	977	2177	1172	1498	837	1515	1046	1507	999
ENSMUSG00000035248	chr13	Zcchc6	59771879	59772859	5551	-0.38031	5.017975	0.006547	0.018174	0.021437	-1	465	389	892	589	664	376	629	486	618	471
ENSMUSG00000044583	chrX	Tlr7	1.67E+08	1.67E+08	4082	0.785359	1.361532	0.006565	0.018219	0.075583	1	23	17	54	22	34	67	56	68	40	43
ENSMUSG00000055044	chr19	Pdlim1	40221173	40222771	5260	0.927713	4.134152	0.006567	0.01822	0.13323	1	76	72	139	391	305	238	567	341	637	370
ENSMUSG00000078866	chr2	Gm14420	1.77E+08	1.77E+08	2172	-0.49752	3.647219	0.006574	0.018238	0.034619	-1	209	164	316	231	255	192	241	118	206	178
ENSMUSG00000086191	chr11	Zfp652os	95700106	95700515	537	0.834695	0.428852	0.006586	0.018267	0.057337	1	12	11	19	10	19	19	28	40	38	19
ENSMUSG00000044763	chr16	Trmt10c	56032609	56035291	3002	-0.42855	3.979703	0.006591	0.018276	0.025997	-1	216	234	366	295	333	173	350	242	254	213
ENSMUSG00000040021	chr10	Lats1	7681209	7681450	7300	-0.38347	4.356998	0.006594	0.018281	0.020853	-1	289	285	548	335	421	251	398	324	395	261
ENSMUSG00000099233	chr16	Gm27883	19883799	19883900	102	1.162916	0.354731	0.006605	0.018309	0.13154	1	19	14	6	7	7	27	42	15	35	28
ENSMUSG00000012519	chr8	Mlkl	1.11E+08	1.11E+08	2303	0.80268	0.722782	0.006627	0.018366	0.06397	1	12	11	32	15	22	21	56	35	28	38
ENSMUSG00000060992	chr15	Copz1	1.03E+08	1.03E+08	1669	0.403507	5.728694	0.006632	0.018375	0.025069	1	656	597	879	721	755	940	1268	1048	1412	861
ENSMUSG00000037533	chr11	Rapgef6	54522847	54523118	12911	-0.55646	3.045606	0.006643	0.018399	0.041602	-1	109	77	285	149	204	86	163	134	128	97
ENSMUSG00000050079	chr8	Rspry1	94601955	94602430	6425	-0.46486	3.083847	0.006644	0.018399	0.027607	-1	115	122	247	134	177	101	172	127	141	106
ENSMUSG00000023755	chr15	Rhebl1	98877778	98878297	1940	0.738997	1.276575	0.006647	0.018405	0.055039	1	34	19	28	26	29	43	72	36	80	37
ENSMUSG00000013155	chr8	Enkd1	1.06E+08	1.06E+08	1272	0.900181	0.05552	0.00666	0.018436	0.064665	1	7	5	20	8	13	24	23	23	27	12
ENSMUSG00000024613	chr18	Tcof1	60813755	60814188	5266	-0.41463	4.666421	0.006667	0.018452	0.025524	-1	377	286	710	490	516	285	474	343	592	326
ENSMUSG00000026965	chr2	Anapc2	25272478	25272677	3445	0.372459	5.38513	0.006676	0.018475	0.020989	1	497	432	773	572	652	655	976	875	1041	757
ENSMUSG00000032184	chr9	Lysmd2	75625732	75626037	1200	0.504203	3.13899	0.00668	0.01848	0.032979	1	125	94	147	93	110	157	213	193	205	158
ENSMUSG00000074766	chr2	Ism1	1.4E+08	1.4E+08	2965	1.185002	0.220163	0.006716	0.018575	0.163895	1	7	6	15	6	19	20	25	52	9	22
ENSMUSG00000032434	chr9	Cmtm6	1.15E+08	1.15E+08	3352	0.409981	3.922811	0.00673	0.018607	0.023288	1	161	133	267	220	273	225	373	330	395	260
ENSMUSG00000032557	chr9	Uba5	1.04E+08	1.04E+08	5243	0.452841	4.372711	0.00673	0.018607	0.030037	1	288	227	387	193	295	383	514	416	504	354
ENSMUSG00000041731	chr19	Pgm5	24683016	24684574	3611	0.777727	4.405322	0.006732	0.01861	0.094714	1	102	97	262	435	399	386	506	392	683	470
ENSMUSG00000029298	chr5	Gbp9	1.05E+08	1.05E+08	3693	-0.64038	1.885065	0.006747	0.018646	0.048562	-1	45	47	126	52	97	32	72	55	59	42
ENSMUSG00000025017	chr19	Pik3ap1	41274218	41274353	2615	0.916791	0.847442	0.006751	0.018654	0.098494	1	12	11	40	17	17	21	66	46	24	43
ENSMUSG00000027284	chr2	Cdan1	1.21E+08	1.21E+08	11421	-0.50349	3.181316	0.006754	0.018657	0.033447	-1	119	89	303	168	208	110	153	124	172	121

ENSMUSG00000069372	chr18	Ctxn3	57468486	57468836	1472	1.11278	6.35554	0.006763	0.018678	0.194952	1	1047	1169	994	203	367	1649	2036	1433	4109	1346
ENSMUSG00000040618	chr14	Pck2	55540266	55540513	3400	0.581215	2.287301	0.006768	0.018689	0.043008	1	46	33	84	66	85	70	103	121	118	106
ENSMUSG00000049881	chr1	2810025M15Rik	1.57E+08	1.57E+08	1410	0.602851	2.291763	0.006771	0.018693	0.043916	1	45	56	65	68	65	95	143	92	134	68
ENSMUSG00000007827	chr6	Ankrd26	1.19E+08	1.19E+08	7253	-0.71434	1.746893	0.006773	0.018695	0.061251	-1	29	52	107	64	83	28	59	49	42	47
ENSMUSG00000054693	chr9	Adam10	70678997	70679259	4913	-0.41007	4.358092	0.006778	0.018705	0.024369	-1	294	263	620	335	407	220	364	319	427	287
ENSMUSG00000045333	chr8	Zfp423	87661810	87662507	5608	-0.50675	3.07007	0.00678	0.018706	0.033432	-1	135	82	239	155	196	94	129	120	145	134
ENSMUSG00000029649	chr5	Pomp	1.48E+08	1.48E+08	734	0.528973	6.617472	0.006783	0.018712	0.044688	1	1341	1282	1409	1023	1109	1912	2534	1828	2753	1618
ENSMUSG00000026596	chr1	Abl2	1.57E+08	1.57E+08	10800	-0.50227	4.543325	0.006787	0.018719	0.038147	-1	241	239	728	502	591	270	378	331	485	304
ENSMUSG00000050912	chr9	Tmem123	7764041	7764312	3109	-0.44053	4.896312	0.006799	0.018748	0.029534	-1	476	405	902	437	579	307	465	491	605	440
ENSMUSG00000034245	chr6	Hdac11	91156665	91156847	3849	-0.45068	3.583429	0.006812	0.018778	0.027709	-1	167	125	318	255	267	138	249	157	228	158
ENSMUSG00000003500	chr6	Impdh1	29200434	29201219	3294	0.504833	4.202436	0.006819	0.018794	0.038592	1	190	112	338	286	331	347	367	320	562	360
ENSMUSG00000029249	chr5	Rest	77265491	77265788	7222	-0.43266	3.744955	0.006829	0.018818	0.026154	-1	232	174	377	195	268	139	265	185	280	183
ENSMUSG00000031644	chr8	Nek1	60993195	60993763	7886	-0.48724	2.697502	0.006847	0.018863	0.029276	-1	85	90	162	119	150	70	125	92	109	92
ENSMUSG00000026311	chr1	Asb1	91540544	91540864	6432	-0.55513	3.877768	0.006848	0.018864	0.045874	-1	203	122	382	356	386	123	310	203	262	204
ENSMUSG00000056366	chr10	Fabp3-ps1	86731754	86732409	656	-1.39414	4.897332	0.006894	0.018986	0.301583	-1	139	183	285	1984	884	178	540	174	436	243
ENSMUSG00000098140	chr5	Gm26938	1.4E+08	1.4E+08	744	0.541514	2.5351	0.006898	0.018992	0.036081	1	67	57	88	79	77	124	141	113	127	102
ENSMUSG00000020211	chr10	Sf3a2	80798198	80798805	2658	0.391403	4.566814	0.00692	0.019047	0.02266	1	290	188	498	339	363	390	558	449	643	420
ENSMUSG00000022674	chr16	Ube2v2	15552677	15556543	4275	-0.43661	3.641495	0.006921	0.019047	0.026452	-1	183	184	318	209	255	137	270	151	235	181
ENSMUSG00000021000	chr12	Ctage5	59129720	59129896	9323	-0.39209	5.954187	0.006934	0.01908	0.02425	-1	929	771	1579	1134	1308	724	1373	861	1168	836
ENSMUSG00000025485	chr7	Ric8	1.41E+08	1.41E+08	4742	0.379585	4.48347	0.006951	0.019118	0.020901	1	240	209	425	340	360	357	546	450	553	401
ENSMUSG00000041658	chrX	Rragb	1.53E+08	1.53E+08	2258	-0.74911	0.620086	0.00695	0.019118	0.047374	-1	26	24	37	30	27	17	29	13	20	19
ENSMUSG00000037313	chr5	Tacc3	33658128	33658727	3551	0.789089	1.481469	0.006959	0.019136	0.076669	1	30	28	53	14	34	72	65	43	62	60
ENSMUSG00000026867	chr2	Gapvd1	34676184	34678177	8287	-0.38347	5.169888	0.006967	0.019156	0.022384	-1	553	388	1012	630	777	418	720	531	718	492
ENSMUSG00000015776	chr2	Med22	26905262	26908301	3614	0.411031	4.323371	0.00697	0.01916	0.024772	1	236	157	388	315	301	328	468	450	496	337
ENSMUSG00000017679	chr2	Ttpal	1.64E+08	1.64E+08	5951	0.503565	2.768068	0.006989	0.019207	0.032013	1	70	68	124	84	102	109	193	155	133	126
ENSMUSG00000038217	chr11	Tlcd2	75461715	75461755	1936	0.549106	2.765414	0.006993	0.019215	0.0393	1	57	68	105	102	104	100	182	132	151	158
ENSMUSG00000006463	chr19	Zdhhc24	4878668	4878736	2916	0.654711	2.078425	0.007016	0.019273	0.05253	1	60	44	64	31	53	83	86	89	123	75
ENSMUSG00000036989	chr7	Trim3	1.06E+08	1.06E+08	4569	0.397965	4.07669	0.007017	0.019273	0.022162	1	202	172	323	212	260	289	384	319	491	272
ENSMUSG00000026185	chr1	Igfbp5	72857932	72862508	6006	-0.52651	9.456987	0.007029	0.019301	0.045378	-1	11951	8732	24988	8663	15108	8351	10219	12920	12661	8230
ENSMUSG00000026029	chr1	Casp8	58795374	58795738	2893	0.560306	2.248125	0.00704	0.019328	0.037012	1	51	51	72	51	74	94	127	101	116	67
ENSMUSG00000018567	chr11	Gabarap	69991143	69991802	1844	0.44164	7.354219	0.007045	0.019337	0.03163	1	1951	1965	2602	2219	2140	2825	4257	3151	4445	2700
ENSMUSG00000032640	chr7	Chsy1	66109515	66110227	4167	0.716675	2.03912	0.007052	0.019353	0.066662	1	23	44	62	53	61	54	101	133	97	69
ENSMUSG00000064080	chr6	Fbln2	91212455	91212900	5876	0.553611	6.043722	0.007061	0.019373	0.049539	1	500	401	1409	982	1257	925	1524	1477	1742	1488
ENSMUSG00000068245	chr14	Phf11d	59347407	59349051	4498	0.704155	1.526587	0.007065	0.019379	0.056456	1	27	29	43	30	39	52	106	65	47	44
ENSMUSG00000023411	chr14	Nfatc4	55824795	55825136	4019	0.612206	2.42765	0.007066	0.01938	0.050045	1	35	57	90	60	97	97	100	114	147	116
ENSMUSG00000031709	chr8	Tbc1d9	83165352	83166204	5887	0.771214	0.926364	0.007069	0.019384	0.059284	1	14	18	39	20	16	29	45	55	46	30
ENSMUSG00000032228	chr9	Tcf12	71842688	71846560	15529	-0.45519	4.437863	0.007072	0.019386	0.030982	-1	258	258	708	400	465	244	426	290	364	341
ENSMUSG00000027293	chr2	Ehd4	1.2E+08	1.2E+08	4007	0.412203	5.521678	0.007102	0.019466	0.02665	1	471	411	765	752	790	684	1212	1003	1146	785
ENSMUSG00000057858	chr19	Fam204a	60198586	60199487	2035	-0.42536	3.846484	0.00711	0.019485	0.025647	-1	202	212	380	249	281	169	294	173	272	215
ENSMUSG00000064262	chr6	Gimap8	48647234	48647285	3654	-0.66078	1.327335	0.007114	0.019489	0.044497	-1	29	34	67	61	49	22	44	35	41	30
ENSMUSG00000063450	chr12	Syne2	75818134	75818188	26726	-0.3917	4.497007	0.007119	0.019501	0.022542	-1	351	246	638	380	494	268	489	326	430	289
ENSMUSG00000003779	chr18	Kif20a	34624624	34624852	3796	0.877654	0.204254	0.007135	0.01954	0.067788	1	9	6	22	11	12	25	22	26	19	27
ENSMUSG00000052833	chr7	Sae1	16327053	16327929	1884	0.399233	5.069007	0.007147	0.019569	0.024263	1	436	372	589	423	474	623	843	655	803	550
ENSMUSG00000045975	chr16	C2cd2	97855210	97859576	6555	-0.44536	7.70529	0.007153	0.019581	0.032445	-1	3535	2651	6907	2908	3888	2643	4032	2969	3975	2638
ENSMUSG00000034667	chr10	Xpot	1.22E+08	1.22E+08	5992	-0.38194	4.925706	0.007156	0.019586	0.022043	-1	486	359	783	482	696	378	572	514	582	372
ENSMUSG00000016510	chr5	Mtif3	1.47E+08	1.47E+08	5127	-0.448	4.108571	0.007158	0.019587	0.029864	-1	269	245	332	338	388	232	366	215	349	185
ENSMUSG00000046516	chr16	Cox17	38346991	38347207	5773	0.505581	6.019304	0.00716	0.019589	0.040926	1	900	799	850	760	805	1215	1854	1208	1687	1042
ENSMUSG00000024750	chr19	Zfand5	21272278	21272742	6193	-0.48415	8.078818	0.007169	0.019607	0.038475	-1	4547	4528	7608	3867	4606	2999	5486	3082	5578	3802
ENSMUSG00000024220	chr17	Zfp523	28177207	28177415	3991	-0.40005	3.902887	0.007173	0.019616	0.022305	-1	235	178	405	263	301	173	270	256	297	184
ENSMUSG00000098706	chr18	Mir6979	37854605	37854660	56	-1.07051	-0.02594	0.007179	0.019629	0.098751	-1	20	9	16	24	27	13	8	8	7	14
ENSMUSG00000025144	chr11	Stra13	1.21E+08	1.21E+08	1077	0.440636	3.97438	0.007199	0.01968	0.027434	1	222	164	258	202	201	245	441	316	412	251
ENSMUSG00000021493	chr13	Pdlim7	55495795	55496020	4849	0.453196	8.325542	0.007205	0.019692	0.033755	1	4824	3122	6020	3445	4242	5704	7258	6849	8577	5481
ENSMUSG00000095440	chr15	Fignl2	1.01E+08	1.01E+08	4206	0.827898	0.616366	0.007219	0.019724	0.066198	1	19	12	26	10	15	22	34	48	33	27
ENSMUSG00000024780	chr19	Cdc37l1	28990494	28990669	2517	-0.42733	5.166579	0.007237	0.019771	0.028471	-1	480	380	869	791	858	414	734	475	680	516
ENSMUSG00000031314	chrX	Taf1	1.02E+08	1.02E+08	8428	-0.41471	3.834921	0.007243	0.019784	0.02389	-1	208	177	398	215	336	180	277	231	239	184
ENSMUSG00000044783	chr1	Hjurp	88262471	88266658	8331	0.424261	3.933613	0.007257	0.019817	0.026192	1	171	118	313	207	261	275	399	339	319	251
ENSMUSG00000031273	chrX	Col4a6	1.41E+08	1.41E+08	7973	-1.22642	0.317098	0.007272	0.019853	0.17577	-1	27	23	58	5	20	17	7	12	17	8
ENSMUSG00000057835	chr17	Zfp119a	55864892	55866650	2018	-0.67171	1.506556	0.007276	0.019859	0.050115	-1	41	34	94	43	68	30	58	28	35	42
ENSMUSG00000022114	chr14	Spry2	1.06E+08	1.06E+08	2085	0.452116	3.547027	0.007297	0.019914	0.02833	1	138	116	237	137	165	184	276	213	276	265
ENSMUSG00000032288	chr9	Imp3	56937475	56938398	924	0.40941	5.032562	0.007316	0.019961	0.025624	1	411	395	563	392	453	556	811	632	854	563
ENSMUSG00000027765	chr3	P2ry1	61002795	61004599	4291	-1.07232	3.437381	0.00732	0.019967	0.179188	-1	71	60	216	441	443	72	145	94	145	172
ENSMUSG00000028673	chr4	Fuca1	1.36E+08	1.36E+08	3276	0.42741	4.810776	0.007329	0.019989	0.027898	1	328	320	490	354	407	489	612	693	683	440
ENSMUSG00000001783	chr10	Rtcb	85938637	85939119	2615	0.399572	6.007466	0.00734	0.020015	0.025506	1	833	641	1050	880	1018	1153	1636	1244	1604	1060
ENSMUSG00000021908	chr12	Gm6768	1.19E+08	1.19E+08	3339	-0.97148	1.064895	0.007361	0.020067	0.121779	-1	41	11	92	39	42	11	50	22	20	22
ENSMUSG00000061981	chr11	Flot2	78037931	78038112	2740	0.404085	6.564416	0.007375	0.020101	0.02655	1	1116	778	1721	1401	1633	1583	2378	1707	2665	1616

ENSMUSG00000021012	chr12	Zc3h14	98746968	98747158	4184	-0.36845	5.600468	0.007386	0.020123	0.02136	-1	731	615	1242	891	950	640	944	668	977	657
ENSMUSG00000027887	chr3	Sypl2	1.08E+08	1.08E+08	4377	0.436297	9.106864	0.007386	0.020123	0.031587	1	6824	3912	11686	7122	9460	8344	13799	10742	15666	10105
ENSMUSG00000031706	chr8	Rfx1	84066836	84067048	4172	0.535901	2.722193	0.007423	0.02022	0.03909	1	74	44	133	69	120	114	144	114	192	137
ENSMUSG00000018845	chr11	Unc45b	82910550	82911253	4493	-0.40841	8.552295	0.007426	0.020221	0.027652	-1	6590	4217	9705	6300	8151	4847	6723	5061	7574	5338
ENSMUSG00000025453	chr13	Nnt	1.19E+08	1.19E+08	7037	-0.80026	6.49201	0.007427	0.020221	0.104767	-1	867	832	1647	3512	2465	664	1958	907	1505	1152
ENSMUSG00000036775	chr17	Decr2	26081211	26082261	2288	0.581456	2.382577	0.007432	0.020232	0.042768	1	47	60	82	60	77	109	145	117	108	76
ENSMUSG00000052997	chr7	Uba2	34140689	34141466	4092	-0.40424	5.410723	0.007436	0.02024	0.025873	-1	670	597	1223	646	796	481	940	579	783	599
ENSMUSG00000040205	chr7	Cuzd1	1.31E+08	1.31E+08	2256	-0.73115	1.258948	0.007466	0.020316	0.064155	-1	38	40	71	40	42	19	61	33	26	22
ENSMUSG00000051212	chr14	Gpr183	1.22E+08	1.22E+08	2942	0.807042	0.345855	0.007476	0.020341	0.054824	1	11	8	20	13	16	27	34	14	35	24
ENSMUSG00000028106	chr3	Rprd2	95759873	95766420	8419	-0.42427	4.375141	0.007515	0.02044	0.026991	-1	243	251	635	408	430	244	396	310	411	267
ENSMUSG00000041028	chr14	Ghitm	37120444	37122226	3081	-0.40031	8.926102	0.00753	0.020477	0.026704	-1	7443	6031	11302	9261	10753	5862	10632	6781	9111	6425
ENSMUSG00000000127	chr17	Fer	63896018	63896283	3473	-0.44806	3.216882	0.007533	0.020479	0.026481	-1	152	113	265	136	206	108	163	127	182	134
ENSMUSG00000043079	chr18	Synpo	60593973	60596488	9533	-0.49185	7.221689	0.007533	0.020479	0.039976	-1	1941	1500	3839	3529	3634	1767	2536	1705	3291	2139
ENSMUSG00000025980	chr1	Hspd1	55077835	55078440	2642	-0.43036	7.805924	0.00757	0.020573	0.030764	-1	3549	2925	4317	4630	5026	2826	4814	3329	3947	2673
ENSMUSG00000020133	chr10	2310011J03Rik	80318254	80319547	1649	0.469112	3.659865	0.007587	0.020616	0.0312	1	157	131	179	197	162	227	309	271	297	219
ENSMUSG00000043259	chr10	Fam13c	70440668	70440898	3520	-0.45696	3.071818	0.0076	0.020647	0.027131	-1	136	97	246	134	179	88	152	133	159	113
ENSMUSG00000014554	chr6	Dguok	83480217	83480436	2191	0.439732	3.729518	0.007609	0.020666	0.026905	1	164	157	205	167	186	232	328	276	322	224
ENSMUSG00000024474	chr18	Ik	36744656	36744788	1996	0.387019	6.038501	0.007611	0.020666	0.024138	1	739	719	1225	875	1016	1142	1632	1246	1668	1130
ENSMUSG00000082044	chr2	Gm14284	1.31E+08	1.31E+08	279	0.853609	0.227225	0.007612	0.020666	0.061599	1	8	6	18	16	13	18	24	22	26	32
ENSMUSG00000024286	chr18	Ccny	9314044	9316672	4017	-0.38681	6.492368	0.007624	0.020694	0.024451	-1	1447	1191	2420	1496	1711	1133	1694	1283	1792	1256
ENSMUSG00000016344	chr2	Ppdpf	1.81E+08	1.81E+08	1336	0.436499	4.949572	0.00766	0.020786	0.029669	1	448	301	432	437	439	553	822	538	798	542
ENSMUSG00000030386	chr7	Zfp606	12478293	12478706	7680	-0.5324	2.648375	0.007661	0.020786	0.037793	-1	79	101	151	128	126	65	140	75	110	79
ENSMUSG00000071415	chr11	Rpl23	97777527	97778164	1770	0.520977	7.946868	0.007675	0.02082	0.045192	1	3212	3266	3385	2744	2919	4768	7303	4909	5863	3875
ENSMUSG00000063894	chr13	Zkscan8	21513222	21520962	8901	-0.50721	2.836285	0.007679	0.020827	0.033571	-1	83	90	214	123	177	79	122	103	126	102
ENSMUSG00000058925	chr18	1700011I03Rik	57533780	57533968	1352	1.417902	-0.02356	0.00769	0.020854	0.225299	1	15	6	4	3	7	24	13	13	57	10
ENSMUSG00000027425	chr2	Csrp2bp	1.44E+08	1.44E+08	4699	-0.43118	4.414459	0.0077	0.020875	0.028247	-1	293	220	535	475	482	257	376	286	455	292
ENSMUSG00000002496	chr17	Tsc2	24595937	24596766	6018	-0.44846	6.310597	0.007703	0.020881	0.032987	-1	1054	789	2283	1720	1787	964	1327	1109	1707	1063
ENSMUSG00000025815	chr2	Dhtkd1	5896115	5898812	6333	-0.64957	1.038169	0.00771	0.020891	0.038611	-1	36	23	55	32	49	19	38	31	31	21
ENSMUSG00000038301	chr6	Snx10	51523901	51524034	4912	-0.66931	3.602467	0.00771	0.020891	0.069749	-1	295	205	381	116	179	122	186	174	255	128
ENSMUSG00000053617	chr19	Sh3pxd2a	47260174	47268936	10464	-0.463	6.333582	0.007717	0.020904	0.035201	-1	1267	833	2647	1214	1902	893	1305	1410	1422	1137
ENSMUSG00000024769	chr19	Cdc42bpg	6306456	6306875	6099	-0.42411	3.445631	0.00772	0.020909	0.024346	-1	167	141	295	177	229	149	179	155	222	138
ENSMUSG00000054150	chr12	Syne3	1.05E+08	1.05E+08	5532	-0.71059	1.28944	0.007723	0.020914	0.056643	-1	28	23	72	52	68	18	49	36	37	25
ENSMUSG00000020077	chr10	Srgn	62493833	62495106	2196	0.534384	3.467217	0.007729	0.020925	0.041496	1	128	104	145	139	197	152	383	263	250	162
ENSMUSG00000019718	chr12	L3hypdh	72073428	72074036	2679	1.088199	0.911875	0.007737	0.020942	0.149897	1	22	19	26	11	10	28	26	83	37	39
ENSMUSG00000028743	chr4	Akr7a5	1.39E+08	1.39E+08	1793	0.39569	4.913013	0.007748	0.020966	0.024231	1	335	303	552	454	445	489	643	662	830	502
ENSMUSG00000022180	chr14	Slc7a8	54722216	54724251	4033	0.471647	4.065941	0.007751	0.020971	0.034023	1	213	143	381	164	250	368	365	333	412	267
ENSMUSG00000017897	chr2	Eya2	1.66E+08	1.66E+08	2963	-0.91494	1.036017	0.007788	0.021065	0.102321	-1	12	27	51	54	67	27	28	17	24	25
ENSMUSG00000078622	chr11	Ccdc47	1.06E+08	1.06E+08	6414	-0.39448	6.872939	0.007789	0.021065	0.025772	-1	1774	1672	3045	1881	2380	1373	2536	1675	2130	1629
ENSMUSG00000047675	chr4	Rps8	1.17E+08	1.17E+08	1726	0.497625	7.847634	0.007791	0.021066	0.041372	1	3192	2889	3155	2531	2934	4544	6086	4490	5851	3706
ENSMUSG00000034055	chrX	Phka1	1.03E+08	1.03E+08	6259	-0.51767	10.00175	0.007832	0.021174	0.045114	-1	20536	13651	33960	11814	19033	13212	18954	13176	21096	11569
ENSMUSG00000037251	chr8	Pomk	25980604	25983644	3601	0.386927	4.114977	0.007838	0.021184	0.021748	1	210	167	325	226	280	319	428	316	386	322
ENSMUSG00000031075	chr7	Ano1	1.45E+08	1.45E+08	5206	-0.64663	1.946263	0.007852	0.021219	0.052956	-1	50	36	96	84	114	32	66	44	75	54
ENSMUSG00000025956	chr1	Mettl21a	64606473	64608137	3005	0.405882	3.580403	0.007865	0.02125	0.022292	1	138	123	220	151	191	175	318	239	298	215
ENSMUSG00000020908	chr11	Myh3	67078300	67078324	6057	2.267029	7.083077	0.007867	0.021252	0.767781	1	49	15	2058	574	1845	607	383	5813	8806	5140
ENSMUSG00000039737	chr5	Prkrip1	1.36E+08	1.36E+08	3967	0.440279	3.768336	0.007875	0.021267	0.027684	1	177	143	226	188	175	269	320	263	331	229
ENSMUSG00000063268	chr15	Parp10	76231174	76231378	4275	0.534101	2.907512	0.007879	0.021274	0.03991	1	73	63	127	101	128	102	196	215	170	120
ENSMUSG00000025487	chr7	Psmd13	1.41E+08	1.41E+08	3395	0.482883	6.720105	0.007884	0.021284	0.03867	1	1372	1345	1462	1214	1393	2042	2679	1925	2952	1689
ENSMUSG00000027099	chr2	Mtx2	74825803	74826043	3675	-0.60795	4.329446	0.007899	0.021319	0.059172	-1	240	213	330	605	564	222	376	243	376	250
ENSMUSG00000057219	chr11	Armc7	1.15E+08	1.15E+08	3069	0.855984	1.159403	0.00791	0.021344	0.089224	1	34	12	21	13	40	28	55	58	59	49
ENSMUSG00000053565	chr7	Eif3k	28971373	28971438	773	0.428588	6.214901	0.007914	0.021352	0.030111	1	935	895	1150	945	1029	1228	1793	1490	2017	1296
ENSMUSG00000022536	chr16	Glyr1	5013906	5015602	3348	-0.36519	5.669353	0.007918	0.021359	0.021371	-1	791	610	1271	948	1026	687	998	768	913	690
ENSMUSG00000032402	chr9	Smad3	63646767	63650385	5542	-0.56333	6.548811	0.007926	0.021374	0.052975	-1	2129	1348	2372	1280	1714	1301	2040	1252	1741	709
ENSMUSG00000042148	chr11	Cox10	63962627	63964528	3037	-0.63115	5.347769	0.007927	0.021374	0.065525	-1	492	306	886	1247	1172	408	720	496	807	527
ENSMUSG00000057880	chr16	Abat	8513429	8513574	7748	-0.95085	1.229563	0.007933	0.021387	0.122387	-1	20	15	62	86	64	20	41	19	43	20
ENSMUSG00000020605	chr12	Hs1bp3	8313433	8313497	2958	0.514659	3.445748	0.007947	0.021419	0.03886	1	102	111	176	147	179	140	245	299	244	225
ENSMUSG00000021051	chr12	Ppp2r5e	75450883	75453813	4808	-0.40143	5.166674	0.007979	0.0215	0.025562	-1	550	371	1073	650	745	410	764	507	655	513
ENSMUSG00000032279	chr9	Idh3a	54586511	54586543	2403	-0.49219	9.15122	0.007984	0.02151	0.040957	-1	7929	5356	13672	13895	13997	5813	11533	7338	11760	7631
ENSMUSG00000024736	chr19	Tmem132a	10857822	10859151	4069	0.951913	2.660975	0.00799	0.021518	0.139518	1	30	35	39	143	89	105	129	123	203	180
ENSMUSG00000082361	chr5	Btc	91357261	91359327	2876	-0.88131	0.033983	0.00799	0.021518	0.063518	-1	15	19	30	18	14	9	14	9	20	8
ENSMUSG00000022474	chr15	Pmm1	81951108	81951612	2776	0.475049	4.134327	0.00801	0.021563	0.034635	1	185	148	262	299	281	339	372	371	524	254
ENSMUSG00000068856	chr3	Sf3b4	96172332	96172607	2162	0.439064	3.217527	0.008009	0.021563	0.026429	1	117	68	189	127	139	154	231	192	233	160
ENSMUSG00000028776	chr4	Tinagl1	1.3E+08	1.3E+08	4358	0.42069	4.532033	0.008025	0.021597	0.027134	1	292	251	358	258	410	438	619	443	520	384
ENSMUSG00000052310	chr3	Slc39a1	90248172	90248259	2364	0.375704	5.89868	0.008034	0.021617	0.022972	1	706	569	1121	761	1064	914	1629	1128	1525	1030
ENSMUSG00000006191	chr13	Cdkal1	29191746	29193146	12799	-0.42791	4.125559	0.00805	0.021657	0.027792	-1	304	235	417	278	367	242	340	195	388	206
ENSMUSG00000033809	chr16	Alg3	20605451	20605717	1451	0.425218	3.845443	0.008079	0.02173	0.026704	1	162	118	280	201	237	263	293	261	426	252

ENSMUSG00000030805	chr7	Stx4a	1.28E+08	1.28E+08	2364	0.422934	5.876224	0.00809	0.021756	0.029216	1	785	682	864	721	873	1018	1455	1090	1525	1065
ENSMUSG00000054321	chr18	Taf4b	14783245	14783934	5149	-0.67399	1.465955	0.008109	0.021801	0.05137	-1	49	27	80	61	51	22	53	42	34	37
ENSMUSG00000025384	chr11	2310003H01Rik	1.2E+08	1.2E+08	5212	-0.49511	4.137294	0.008117	0.02182	0.037766	-1	276	146	404	402	461	226	295	248	296	252
ENSMUSG00000028134	chr3	Ptbp2	1.2E+08	1.2E+08	3364	-0.41482	3.868598	0.008121	0.021825	0.025083	-1	219	205	420	236	269	164	268	205	278	225
ENSMUSG00000037536	chr14	Fbxo34	47472561	47472717	3726	-0.42473	3.454807	0.008127	0.021836	0.024834	-1	163	118	298	205	242	129	213	178	195	138
ENSMUSG00000008435	chr7	Rdh13	4424770	4425638	6595	-0.48131	3.92352	0.008138	0.021862	0.035252	-1	195	147	355	351	403	160	271	227	313	194
ENSMUSG00000093904	chr8	Tomm20	1.27E+08	1.27E+08	4986	-0.43658	5.79471	0.00816	0.021918	0.031558	-1	958	865	1168	1016	994	700	1207	650	1124	696
ENSMUSG00000103183	chr4	RP23-118E21.11	1.56E+08	1.56E+08	4105	0.792735	1.087898	0.008165	0.021925	0.066128	1	16	30	28	16	25	34	62	33	55	49
ENSMUSG00000025968	chr1	Ndufs1	63143596	63143922	8086	-0.52978	8.744895	0.008186	0.021977	0.04769	-1	5719	4503	8923	10996	11214	4606	9996	4838	8322	5209
ENSMUSG00000062202	chr17	Btbd9	30215524	30220144	6857	-0.45224	3.800992	0.008189	0.021983	0.030009	-1	208	134	375	282	325	170	208	233	270	184
ENSMUSG00000032115	chr9	Hyou1	44379490	44379595	7230	0.391719	5.084914	0.008193	0.021988	0.024618	1	387	268	684	474	604	554	752	755	817	617
ENSMUSG00000037214	chr8	Thap1	26158212	26158521	1328	-0.75764	0.6243	0.008195	0.021989	0.054931	-1	31	14	35	29	38	15	29	22	23	10
ENSMUSG00000021646	chr13	Mccc2	99948533	99948956	2123	-0.39304	5.165145	0.008213	0.022034	0.024708	-1	488	412	879	770	769	406	739	553	670	488
ENSMUSG00000021906	chr14	Oxnad1	32085374	32085566	5769	-0.52621	4.61365	0.008232	0.022078	0.044767	-1	308	249	542	643	617	247	552	269	465	335
ENSMUSG00000022346	chr15	Myc	61985341	61985951	2767	0.94412	2.780977	0.008234	0.022079	0.136999	1	81	91	80	20	79	94	336	159	151	104
ENSMUSG00000033728	chr15	Lrrc14	76710623	76710927	5647	0.411307	3.882256	0.008239	0.02209	0.024751	1	176	127	239	206	269	246	318	290	396	275
ENSMUSG00000025420	chr18	Katnal2	76977148	76977525	4061	0.974432	2.915434	0.00825	0.022114	0.150976	1	31	54	160	76	107	230	62	110	305	163
ENSMUSG00000029103	chr5	Lrpap1	35091490	35093386	4127	0.365902	5.675827	0.008255	0.022122	0.021755	1	636	487	980	668	848	828	1201	1023	1185	991
ENSMUSG00000043881	chr14	Kbtbd7	79426511	79431039	4529	-0.55242	2.782086	0.008259	0.02213	0.043113	-1	86	85	189	140	164	51	115	95	155	97
ENSMUSG00000063275	chr2	Ptpla	13850282	13851259	2118	0.416008	5.880114	0.008266	0.022143	0.028462	1	829	640	1070	625	849	1002	1624	1130	1425	1002
ENSMUSG00000055214	chr1	Pld5	1.76E+08	1.76E+08	10094	-0.92357	2.486846	0.008269	0.022148	0.130662	-1	130	95	244	30	97	80	90	63	59	50
ENSMUSG00000055371	chr2	Stam2	52691664	52694937	6007	-0.41206	3.572166	0.008306	0.022242	0.023804	-1	201	137	324	205	233	138	229	188	235	145
ENSMUSG00000026754	chr2	Golga1	39016261	39018489	5392	-0.39716	3.956573	0.008324	0.022284	0.02319	-1	209	222	425	266	304	174	316	225	293	220
ENSMUSG00000002602	chr7	Axl	25757273	25759013	5033	0.497766	5.841002	0.008332	0.022302	0.041622	1	468	385	1335	797	1058	976	1238	1332	1294	1195
ENSMUSG00000076051	chr7	Mir707	44849699	44849771	73	-0.82008	0.299467	0.008342	0.022324	0.067055	-1	20	21	27	22	25	8	31	12	18	8
ENSMUSG00000020485	chr11	Supt4a	87737552	87737668	942	0.447817	4.504375	0.008345	0.022328	0.031079	1	291	273	329	292	306	425	644	394	546	382
ENSMUSG00000022897	chr16	Dyrk1a	94570010	94570534	8251	-0.40925	6.385792	0.008349	0.022333	0.028029	-1	1237	947	2510	1498	1706	998	1636	1083	1840	1106
ENSMUSG00000061410	chr8	Zcchc14	1.22E+08	1.22E+08	7780	-0.44754	4.441836	0.008368	0.02238	0.031324	-1	281	212	654	392	565	222	435	327	398	309
ENSMUSG00000026072	chr1	Il1r1	40225080	40225306	6363	0.497477	3.268245	0.008392	0.022441	0.036075	1	114	84	185	88	177	166	300	206	200	153
ENSMUSG00000026697	chr1	Myoc	1.63E+08	1.63E+08	2074	0.601984	6.555858	0.008396	0.022445	0.061472	1	654	745	2008	1138	1774	1695	1917	2440	1559	2366
ENSMUSG00000004565	chr8	Pnpla6	3515384	3515556	4496	0.451214	2.956027	0.008405	0.022467	0.027096	1	78	64	146	105	137	131	182	165	197	133
ENSMUSG00000020553	chr11	Pctp	89982665	89984756	2723	-0.54612	2.363323	0.008414	0.022475	0.03978	-1	100	71	133	70	109	66	95	73	98	47
ENSMUSG00000030741	chr7	Spns1	1.26E+08	1.26E+08	3707	0.378195	5.035628	0.008412	0.022475	0.022619	1	391	322	596	466	519	472	758	660	944	582
ENSMUSG00000039081	chr14	Zfp503	21983962	21986516	4213	0.742897	4.465217	0.008413	0.022475	0.091461	1	94	191	555	298	259	236	546	529	517	665
ENSMUSG00000042688	chr9	Mapk6	75369062	75369149	6675	-0.37984	5.071036	0.008419	0.022485	0.02288	-1	511	381	970	517	762	436	631	531	634	437
ENSMUSG00000002346	chr8	Slc25a42	70184340	70185225	5996	-0.44815	5.451608	0.008422	0.022488	0.033078	-1	549	447	1031	998	1135	465	846	653	824	619
ENSMUSG00000030045	chr6	Mrpl19	81957851	81962162	5450	-0.5091	4.168238	0.008427	0.022493	0.040871	-1	197	191	407	452	483	213	345	219	326	253
ENSMUSG00000070730	chr2	Rmdn3	1.19E+08	1.19E+08	3537	0.623401	2.634913	0.008427	0.022493	0.055313	1	76	56	88	68	95	135	137	185	124	82
ENSMUSG00000055670	chr11	Zzef1	72796226	72796650	16363	-0.42573	4.3165	0.008433	0.022505	0.027727	-1	268	207	629	350	454	230	330	311	382	293
ENSMUSG00000098906	chr11	Mir7652	55501226	55501281	56	-0.96744	0.204628	0.008451	0.022548	0.090871	-1	14	12	42	13	36	12	25	8	11	9
ENSMUSG00000041488	chr19	Stx3	11775119	11776588	4979	0.768617	1.374002	0.008457	0.02256	0.078222	1	26	7	50	35	35	41	67	78	62	37
ENSMUSG00000053012	chr6	Krcc1	71272019	71272059	1748	-0.42806	4.540311	0.008471	0.022592	0.029195	-1	377	368	476	385	493	233	404	404	476	307
ENSMUSG00000025571	chr11	Tnrc6c	1.18E+08	1.18E+08	12843	-0.44663	4.714152	0.008476	0.022601	0.031874	-1	319	291	822	466	638	264	472	356	556	399
ENSMUSG00000026832	chr2	Cytip	58129137	58134193	6744	0.91915	0.229226	0.008478	0.022601	0.078892	1	14	8	16	12	8	30	36	23	17	18
ENSMUSG00000057457	chrX	Phex	1.57E+08	1.57E+08	6291	-1.15189	-0.17052	0.008482	0.022609	0.143678	-1	15	16	35	5	18	2	11	5	20	8
ENSMUSG00000033460	chrX	Armcx1	1.35E+08	1.35E+08	3227	0.641379	1.068798	0.008498	0.022646	0.037689	1	19	19	33	30	23	34	54	43	49	40
ENSMUSG00000024778	chr19	Fas	34290659	34290744	1801	0.574266	2.213156	0.008502	0.022652	0.040176	1	52	58	71	47	58	80	133	94	111	78
ENSMUSG00000066441	chr12	Rdh11	79174337	79176250	3455	0.550082	2.019476	0.008516	0.022684	0.035752	1	47	38	75	45	53	73	83	74	113	82
ENSMUSG00000103125	chr18	RP23-407E2.6	36975941	36976278	429	-0.78926	1.410877	0.008528	0.022713	0.077541	-1	30	26	91	57	69	29	60	22	25	35
ENSMUSG00000102836	chr18	RP23-407E2.5	36969916	36970137	313	-0.78926	1.410877	0.008536	0.022728	0.077563	-1	30	26	91	57	69	29	60	22	25	35
ENSMUSG00000061878	chr11	Sphk1	1.17E+08	1.17E+08	4774	1.151208	-0.16888	0.008562	0.022793	0.143728	1	3	3	4	6	23	19	29	12	22	15
ENSMUSG00000096956	chr15	Snhg18	32240569	32241769	1482	0.594821	2.28144	0.00857	0.02281	0.045798	1	69	48	78	45	60	85	97	121	134	82
ENSMUSG00000019814	chr10	Ltv1	13178640	13178996	1766	-0.40612	4.627031	0.008625	0.022951	0.026203	-1	423	381	566	370	487	344	505	337	443	311
ENSMUSG00000020491	chr11	2810021J22Rik	58867216	58867309	3928	-0.72291	0.779207	0.008631	0.022963	0.049485	-1	25	28	46	31	32	24	30	14	24	19
ENSMUSG00000009614	chr2	Sardh	27188393	27189644	5432	0.64004	1.444894	0.008644	0.022984	0.045854	1	31	21	48	30	35	38	57	78	72	45
ENSMUSG00000022883	chr16	Robo1	72663149	72664194	7563	-0.9249	0.715576	0.008644	0.022984	0.094216	-1	23	14	56	29	48	11	14	20	18	31
ENSMUSG00000038500	chr17	Prr3	35972541	35973803	3783	0.661549	1.408756	0.008644	0.022984	0.047355	1	27	30	34	29	35	40	79	68	56	42
ENSMUSG00000029270	chr5	Fam69a	1.08E+08	1.08E+08	2892	-0.57802	4.925989	0.008648	0.02299	0.055779	-1	650	574	841	333	439	378	561	405	573	329
ENSMUSG00000014932	chr5	Yes1	32611171	32611375	4608	-0.54073	2.687511	0.008656	0.023008	0.040433	-1	84	88	179	111	155	50	121	91	109	105
ENSMUSG00000028270	chr3	Gbp2	1.43E+08	1.43E+08	2516	0.580689	3.406354	0.00868	0.023066	0.051938	1	108	97	149	133	189	183	360	286	168	154
ENSMUSG00000048720	chr19	Tbc1d12	38836579	38837446	4209	-0.64763	1.746873	0.008682	0.023066	0.049888	-1	62	40	95	45	84	41	56	44	37	50
ENSMUSG00000028458	chr4	Tesk1	43441939	43443638	4434	-0.41277	6.082755	0.008685	0.02307	0.028638	-1	1061	781	1804	1321	1350	818	1084	935	1543	961
ENSMUSG00000050043	chr2	Tmx2	84671316	84672532	2330	-0.44072	5.484678	0.008702	0.023111	0.03225	-1	639	464	942	971	1190	617	883	570	829	577
ENSMUSG00000044221	chr5	Grsf1	88659448	88660459	3036	-0.43567	6.964443	0.008707	0.023118	0.032472	-1	1673	1494	2813	2833	2834	1422	2716	1573	2533	1641
ENSMUSG00000062184	chrX	Hs6st2	51387212	51390361	7807	0.706614	2.654248	0.008733	0.023184	0.075853	1	33	72	142	58	83	109	167	101	132	179

ENSMUSG00000021622	chr13	Ckmt2	91853387	91853648	1486	-1.06118	10.06588	0.008742	0.023198	0.190603	-1	10203	5034	15537	46873	43302	8584	19899	7181	20242	10296
ENSMUSG00000030935	chr7	Acsm3	1.2E+08	1.2E+08	4936	1.363816	1.377589	0.00874	0.023198	0.272697	1	26	25	24	13	18	44	35	180	29	26
ENSMUSG00000040146	chr9	Rgl3	21971527	21972009	2550	0.809063	0.632717	0.008749	0.023213	0.070065	1	21	4	22	22	15	24	35	34	46	28
ENSMUSG00000032050	chr9	Rdx	52047150	52047235	4841	-0.47228	7.245641	0.008762	0.023243	0.038327	-1	2117	1904	4718	2500	3409	1268	2630	2253	3007	2554
ENSMUSG00000021635	chr13	Rad17	1.01E+08	1.01E+08	2846	-0.39212	3.968923	0.008786	0.023302	0.023011	-1	241	222	394	271	293	204	338	206	292	201
ENSMUSG00000045128	chr8	Rpl18a	70894722	70895507	1291	0.449213	8.196539	0.008827	0.023405	0.034881	1	3894	3542	4548	3664	3671	5281	8078	5558	7560	4735
ENSMUSG00000037243	chr11	Zfp692	58307069	58307256	1963	0.503297	2.529588	0.008829	0.023405	0.03342	1	74	50	106	58	92	111	133	124	137	97
ENSMUSG00000036748	chr19	Cuedc2	46329812	46330834	1941	0.403458	5.705151	0.008852	0.023458	0.027071	1	621	529	815	823	776	932	1199	978	1495	847
ENSMUSG00000074219	chr8	Gm10644	83932329	83934606	2798	-0.93849	0.633516	0.008852	0.023458	0.104126	-1	21	22	51	36	26	18	19	32	16	5
ENSMUSG00000060703	chr2	Cd302	60251993	60252491	1354	0.475706	3.713911	0.008878	0.023516	0.034114	1	149	161	264	115	185	217	381	271	312	214
ENSMUSG00000080776	chr11	Gm12174	46727818	46728630	813	0.606003	2.78783	0.008876	0.023516	0.05302	1	90	74	124	80	57	129	212	155	171	90
ENSMUSG00000047648	chr10	Fbxo30	11281330	11281500	5197	-0.45688	3.70197	0.008888	0.023538	0.031272	-1	155	136	367	259	331	139	245	205	236	177
ENSMUSG00000044876	chr7	Zfp444	6172226	6172399	3421	0.502448	2.50708	0.008896	0.023555	0.033113	1	71	48	95	63	96	104	124	118	133	111
ENSMUSG00000035370	chr10	Adat3	80602880	80602949	4586	0.370556	4.774051	0.008913	0.023595	0.021606	1	359	273	490	344	446	449	627	558	708	472
ENSMUSG00000103458	chr18	PCDHA4	36952741	36955150	2856	-0.50539	2.825908	0.008917	0.0236	0.035388	-1	87	82	208	131	174	79	154	91	110	98
ENSMUSG00000002249	chr17	Tead3	28331671	28332833	4398	0.526337	2.574368	0.008943	0.023665	0.039285	1	53	38	126	76	108	104	164	127	130	105
ENSMUSG00000038534	chr11	Osbpl7	97050628	97050953	5920	0.578068	2.140666	0.008946	0.023668	0.0424	1	44	41	87	52	56	54	109	79	149	88
ENSMUSG00000042737	chr3	Dpm3	89259358	89259591	919	0.592614	2.564944	0.008962	0.023706	0.047877	1	73	73	74	74	63	99	157	133	167	88
ENSMUSG00000049600	chr7	Zbtb45	13004936	13005328	2722	0.563693	2.126768	0.008976	0.023738	0.040042	1	48	34	62	63	69	65	87	96	127	88
ENSMUSG00000060843	chr10	Ctnna3	63430098	63430179	7227	-0.731	3.056809	0.008997	0.023789	0.08463	-1	96	63	260	256	189	83	207	76	149	72
ENSMUSG00000026341	chr1	Actr3	1.25E+08	1.25E+08	4631	0.370187	5.520522	0.00901	0.02382	0.022531	1	544	491	780	644	736	699	1214	957	1121	771
ENSMUSG00000016327	chrX	Atp1b4	38316184	38316329	4201	1.128072	1.842195	0.009013	0.023822	0.198981	1	7	15	40	44	78	26	151	72	71	118
ENSMUSG00000033068	chr2	Entpd6	1.51E+08	1.51E+08	4775	-0.42378	3.661055	0.009015	0.023822	0.026514	-1	224	156	326	207	252	148	220	232	227	154
ENSMUSG00000046691	chr8	Chtf8	1.07E+08	1.07E+08	3036	0.372509	4.653341	0.009021	0.023834	0.022018	1	279	230	518	353	409	438	563	538	611	425
ENSMUSG00000021252	chr12	0610007P14Rik	85815448	85816193	4235	0.652601	1.790694	0.009048	0.0239	0.054606	1	49	22	48	36	54	53	104	93	80	47
ENSMUSG00000019254	chr7	Ppp1r12c	4481520	4482158	4981	0.382137	4.470726	0.009085	0.023993	0.022722	1	256	234	391	290	370	375	477	496	547	377
ENSMUSG00000029705	chr5	Cux1	1.36E+08	1.36E+08	20024	-0.39639	6.437878	0.009088	0.023997	0.026887	-1	1308	948	2388	1574	1910	1024	1672	1149	1948	1153
ENSMUSG00000035258	chr16	Abi3bp	56477846	56477992	4735	-0.62383	4.625348	0.009101	0.024027	0.064925	-1	223	261	808	491	769	272	368	379	285	416
ENSMUSG00000005481	chr8	Ddx39	83715177	83715337	5155	0.408977	3.886151	0.009109	0.024043	0.024911	1	181	138	249	222	222	278	401	254	364	239
ENSMUSG00000023018	chr15	Smarcd1	99702287	99702498	3153	0.450124	3.387757	0.009117	0.024059	0.029409	1	144	93	212	129	130	187	242	197	293	177
ENSMUSG00000019866	chr10	Aim1	43950307	43951957	7416	0.608759	1.687004	0.009124	0.024068	0.048329	1	21	20	68	41	56	57	94	63	71	58
ENSMUSG00000024076	chr17	Vit	78508063	78508325	2720	-0.90159	1.563481	0.009124	0.024068	0.114156	-1	29	34	82	66	100	19	60	31	19	51
ENSMUSG00000072692	chr5	Rpl37rt	1.15E+08	1.15E+08	682	0.503424	4.7849	0.009136	0.024094	0.041723	1	388	319	397	296	370	578	880	451	631	420
ENSMUSG00000044350	chr14	Lacc1	77024200	77024974	3644	0.656923	1.30285	0.00914	0.0241	0.04959	1	25	21	37	27	37	54	63	52	39	49
ENSMUSG00000035521	chr17	Gnptg	25233331	25234722	2249	0.427752	3.7939	0.009144	0.024106	0.027235	1	188	143	257	153	200	222	405	293	300	231
ENSMUSG00000032593	chr9	Amigo3	1.08E+08	1.08E+08	2543	-1.20549	1.010797	0.009158	0.024134	0.20743	-1	14	10	29	84	85	21	27	12	26	19
ENSMUSG00000048920	chr7	Fkrp	16809270	16811976	2803	-0.37562	5.907814	0.009158	0.024134	0.02378	-1	951	649	1636	1069	1269	722	1191	882	1169	841
ENSMUSG00000033411	chr2	Ctdspl2	1.22E+08	1.22E+08	9251	-0.61275	1.886441	0.009161	0.024136	0.048265	-1	40	58	117	68	74	34	74	39	67	50
ENSMUSG00000032370	chr9	Lactb	66955393	66956200	2031	-0.44219	4.269699	0.009186	0.024193	0.031542	-1	350	299	476	289	342	249	358	261	442	203
ENSMUSG00000093133	chr11	Gm25994	1.07E+08	1.07E+08	101	-0.4846	3.438853	0.009186	0.024193	0.034931	-1	195	150	311	149	212	154	201	140	155	158
ENSMUSG00000027255	chr2	Arfgap2	91264974	91265404	4129	-0.47306	7.848514	0.009196	0.024196	0.039113	-1	4682	3516	6097	2964	4032	3084	4310	2920	4722	2759
ENSMUSG00000030731	chr7	Syt3	44384102	44384176	3118	-0.52688	2.019192	0.009195	0.024196	0.033446	-1	70	44	99	81	85	41	71	54	80	53
ENSMUSG00000041000	chr4	Trim62	1.29E+08	1.29E+08	5015	0.899384	0.137174	0.009191	0.024196	0.064521	1	8	13	15	10	8	19	22	18	38	20
ENSMUSG00000041130	chr17	Zfp598	24669752	24669973	3286	-0.39019	4.351371	0.009191	0.024196	0.023718	-1	314	254	584	334	403	251	343	355	417	248
ENSMUSG00000092781	chr10	Mir3057	81271597	81271687	91	-0.58932	2.815412	0.009193	0.024196	0.0512	-1	91	71	163	191	166	79	117	80	113	114
ENSMUSG00000004562	chr14	Arhgef40	51984719	51984991	10366	0.523945	3.643832	0.0092	0.024202	0.04349	1	108	104	214	200	204	191	220	327	302	273
ENSMUSG00000027291	chr2	Vps39	1.2E+08	1.2E+08	8605	-0.36937	4.835648	0.009229	0.024272	0.0219	-1	453	337	787	475	577	341	598	467	524	361
ENSMUSG00000015357	chr9	Clpx	65294260	65294565	3494	-0.4235	6.09514	0.009233	0.024278	0.030765	-1	960	852	1730	1401	1424	781	1702	880	1228	857
ENSMUSG00000039873	chr2	Neurl2	1.65E+08	1.65E+08	1014	0.409708	4.461384	0.009272	0.024375	0.026561	1	285	212	383	317	310	376	487	369	670	399
ENSMUSG00000039787	chr2	Cercam	29869164	29869345	3383	0.781124	1.902934	0.009275	0.024377	0.090919	1	21	21	64	47	71	44	77	76	92	122
ENSMUSG00000024824	chr19	Rad9a	4195198	4196082	2046	0.534401	2.328508	0.009296	0.024429	0.036102	1	54	56	75	56	78	84	103	101	144	97
ENSMUSG00000051098	chr13	Mblac2	81711417	81711982	3881	-0.73615	0.779839	0.009311	0.024463	0.051218	-1	27	24	42	32	38	15	20	28	20	26
ENSMUSG00000087635	chr2	Gm13414	34649514	34650240	727	-0.7637	0.400141	0.009316	0.024473	0.052572	-1	21	15	29	28	31	13	24	8	21	17
ENSMUSG00000026767	chr2	Fam188a	12347263	12348203	6294	-0.4809	2.815443	0.009324	0.024487	0.032452	-1	129	109	171	103	132	84	126	100	137	86
ENSMUSG00000034800	chr2	Zfp661	1.28E+08	1.28E+08	5165	-0.53939	2.109313	0.009334	0.024509	0.035939	-1	56	65	102	86	93	44	79	63	66	62
ENSMUSG00000031442	chr8	Mcf2l	12873806	12874061	12760	-0.54322	3.27719	0.009351	0.024548	0.044633	-1	118	109	241	214	256	155	125	141	167	112
ENSMUSG00000030662	chr14	Ipo5	1.21E+08	1.21E+08	4591	-0.39593	7.316409	0.009355	0.024556	0.027377	-1	2211	2020	4090	3165	3252	1910	3339	2096	3302	2123
ENSMUSG00000021069	chr12	Pygl	70190811	70191156	3828	0.929509	2.715042	0.009369	0.024588	0.138805	1	94	52	92	60	50	95	127	332	98	101
ENSMUSG00000025213	chr19	Kazald1	45075241	45075518	1681	-0.59783	2.620331	0.009387	0.024629	0.05243	-1	92	121	169	81	117	85	111	80	76	82
ENSMUSG00000079641	chrX	Rpl39	37082520	37082749	1434	0.502061	6.297047	0.009392	0.024636	0.043541	1	1168	964	1095	876	887	1453	2204	1541	1938	1317
ENSMUSG00000020850	chr11	Prpf8	75486816	75487191	7461	-0.4206	7.038731	0.009394	0.024639	0.03083	-1	1782	1359	4116	2390	2994	1459	2477	1903	2613	1905
ENSMUSG00000058443	chr9	Rpl10-ps3	50344240	50344981	742	0.908577	0.992094	0.009398	0.024643	0.104387	1	29	14	35	12	14	50	59	42	56	17
ENSMUSG00000028233	chr4	Tgs1	3574875	3575129	5314	-0.40664	3.492936	0.009401	0.024645	0.023589	-1	173	147	294	182	239	130	214	193	201	143
ENSMUSG00000052040	chr7	Klf13	63886347	63891797	7535	0.416889	5.1651	0.009406	0.024656	0.02918	1	385	336	873	437	509	620	881	859	850	534
ENSMUSG00000029681	chr5	Bcl7b	1.35E+08	1.35E+08	2404	0.371528	4.517751	0.009413	0.024669	0.021842	1	264	205	439	330	383	380	517	507	585	366

ENSMUSG00000028962	chr5	Slc4a2	24423837	24424151	6195	0.412008	4.008616	0.00942	0.02468	0.026097	1	180	165	299	226	235	266	317	380	400	291
ENSMUSG00000025020	chr19	Slit1	41600257	41601700	5921	0.80136	0.752986	0.009428	0.024697	0.075762	1	12	5	30	25	23	31	45	22	43	40
ENSMUSG00000031095	chrX	Cul4b	38533274	38533728	3873	-0.45556	3.391252	0.00944	0.024724	0.030574	-1	159	144	297	168	212	126	187	200	168	119
ENSMUSG00000026181	chr16	Ppm1f	16896469	16896624	4922	-0.3909	4.351897	0.009444	0.024727	0.024008	-1	296	222	474	392	504	231	374	314	416	285
ENSMUSG00000030199	chr6	Etv6	1.34E+08	1.34E+08	5983	0.433683	3.241049	0.009445	0.024727	0.026842	1	114	76	194	122	146	166	246	169	267	145
ENSMUSG00000024145	chr17	Pigf	86997256	86997567	988	0.752663	0.877541	0.009466	0.024778	0.066901	1	14	9	40	22	22	41	33	36	40	42
ENSMUSG00000031657	chr8	Heatr3	88137855	88138157	4497	-0.40307	5.589104	0.009477	0.024802	0.027614	-1	812	695	1336	720	848	634	1017	608	904	647
ENSMUSG00000011831	chr5	Evi5	1.08E+08	1.08E+08	8060	-0.46099	3.817896	0.009484	0.024815	0.033569	-1	244	209	398	202	256	141	305	251	228	166
ENSMUSG00000062376	chr19	2010012O05Rik	46689906	46690085	2176	-0.41741	3.462243	0.0095	0.024853	0.025305	-1	167	137	259	201	249	119	236	167	183	156
ENSMUSG00000006219	chr4	Fblim1	1.42E+08	1.42E+08	4457	0.777665	0.71907	0.00951	0.024874	0.063518	1	19	12	26	20	13	23	43	50	34	26
ENSMUSG00000029314	chr5	Agpat9	1.01E+08	1.01E+08	3502	1.066325	3.011687	0.009521	0.024897	0.186937	1	96	63	64	73	102	110	130	500	107	105
ENSMUSG00000035726	chr14	Supt16	52160419	52161822	4491	0.368581	4.153137	0.009541	0.024943	0.020943	1	199	160	363	243	300	311	411	353	418	320
ENSMUSG00000051550	chr7	Zfp579	4983483	4983540	4159	0.526789	3.189381	0.00957	0.025016	0.043086	1	71	68	164	140	168	161	181	170	234	212
ENSMUSG00000054072	chr18	Iigp1	60376029	60376130	3121	0.715974	3.114043	0.009597	0.02508	0.082066	1	86	91	132	57	154	173	397	158	167	101
ENSMUSG00000035891	chr15	Cerk	86139128	86141612	4812	0.538885	3.08302	0.009606	0.0251	0.044659	1	86	49	144	155	125	136	242	194	187	149
ENSMUSG00000021464	chr13	Ror2	53109312	53111668	4242	0.890003	-0.00857	0.009613	0.025111	0.076782	1	5	4	22	12	8	19	17	18	29	20
ENSMUSG00000014763	chr17	Fam120b	15396246	15396560	4518	-0.39383	4.209055	0.009625	0.025134	0.024227	-1	266	193	494	384	383	224	391	280	346	229
ENSMUSG00000029422	chr5	Rsrc2	1.24E+08	1.24E+08	8172	-0.43685	5.448764	0.009624	0.025134	0.03269	-1	638	786	1023	659	849	549	951	566	730	606
ENSMUSG00000030905	chr7	Crym	1.2E+08	1.2E+08	3391	-0.57959	2.307628	0.00965	0.025192	0.047883	-1	79	73	108	99	105	53	107	39	102	63
ENSMUSG00000062488	chr19	I830012O16Rik	34607970	34607998	2000	-0.58156	3.311825	0.009651	0.025192	0.053684	-1	163	202	262	133	166	126	182	149	117	136
ENSMUSG00000051000	chr3	Fam160a1	85660061	85661218	7521	-0.44318	5.929066	0.009658	0.025206	0.033936	-1	780	608	1958	1245	1312	685	1157	786	1262	877
ENSMUSG00000028005	chr3	Gucy1b3	82032004	82033281	3951	-0.65961	2.373505	0.009674	0.025241	0.065399	-1	50	61	149	99	163	38	118	62	104	52
ENSMUSG00000080935	chr5	Got2-ps1	1.38E+08	1.38E+08	1293	-0.83947	3.374145	0.009679	0.025251	0.117283	-1	92	64	221	362	370	82	190	105	171	136
ENSMUSG00000026319	chr1	2310035C23Rik	1.06E+08	1.06E+08	9500	-0.48026	2.859197	0.009681	0.025251	0.031477	-1	110	79	224	121	158	85	128	116	114	101
ENSMUSG00000034780	chr2	B3galt1	67565871	67566034	5753	-1.13494	2.435902	0.00971	0.025322	0.209137	-1	24	29	132	224	214	41	87	46	47	78
ENSMUSG00000033610	chr19	Pank1	34810894	34812387	3692	-0.86247	3.419129	0.009715	0.025331	0.124234	-1	99	76	211	389	364	81	203	83	170	161
ENSMUSG00000025613	chr16	Cct8	87483326	87484065	3088	0.405818	7.285965	0.009727	0.025351	0.028989	1	1932	1761	2504	2088	2324	2738	4265	2881	4047	2484
ENSMUSG00000044469	chr17	Tnfaip8l1	56162477	56162606	2379	1.012405	-0.03173	0.009725	0.025351	0.082388	1	9	11	8	9	7	20	24	26	26	9
ENSMUSG00000036553	chr5	Sh3tc1	35697180	35697568	5705	0.584855	2.074053	0.009748	0.025399	0.044995	1	56	36	70	38	64	64	93	113	94	81
ENSMUSG00000003062	chr13	Stard3nl	19357677	19358129	1283	0.550675	2.366174	0.009765	0.025441	0.040484	1	50	54	84	64	76	84	147	134	101	81
ENSMUSG00000078441	chr10	Scamp4	80602882	80602949	1863	0.364822	4.74922	0.009768	0.025442	0.021405	1	356	266	483	341	438	443	619	540	694	465
ENSMUSG00000090381	chr14	Gm6158	24070074	24070637	564	0.869354	-0.01712	0.009801	0.025524	0.064394	1	12	2	15	11	10	16	20	20	25	21
ENSMUSG00000038210	chr6	Hoxa11	52242106	52243592	2287	-1.83216	0.017403	0.009807	0.025533	0.480888	-1	43	31	30	3	2	11	8	3	16	1
ENSMUSG00000019971	chr10	Cep290	1E+08	1E+08	8006	-0.57439	1.827926	0.009814	0.025544	0.039165	-1	45	45	110	62	79	45	62	46	48	50
ENSMUSG00000041669	chr12	Prima1	1.03E+08	1.03E+08	1253	-0.94831	0.228162	0.009815	0.025544	0.098166	-1	9	12	48	24	26	5	15	20	13	13
ENSMUSG00000021281	chr12	Tnfaip2	1.11E+08	1.11E+08	4984	0.599634	6.516956	0.009823	0.025562	0.06349	1	698	650	1454	1173	2115	1466	3789	1358	2249	1554
ENSMUSG00000039715	chr2	Wdr34	30031546	30031972	2359	0.513043	2.499656	0.009829	0.025572	0.034147	1	71	61	95	65	71	84	158	102	157	102
ENSMUSG00000025140	chr11	Pycr1	1.21E+08	1.21E+08	3935	0.560887	2.699039	0.009834	0.025579	0.045251	1	85	70	131	46	83	121	174	123	162	115
ENSMUSG00000033350	chr9	Chst2	95399292	95406473	7328	0.812862	0.435862	0.009839	0.025586	0.063744	1	13	8	22	10	20	16	47	35	25	22
ENSMUSG00000089832	chr7	Shkbp1	27342133	27342544	4230	0.49702	2.257864	0.009871	0.025664	0.030481	1	51	44	86	58	75	85	121	102	125	69
ENSMUSG00000034940	chr11	Synrg	83964428	83964546	8744	-0.40867	5.875303	0.009884	0.025694	0.028858	-1	829	664	1983	963	1168	708	1062	854	1196	811
ENSMUSG00000069744	chr11	Psmb3	97703399	97703490	2300	0.425972	6.631323	0.009897	0.025722	0.031828	1	1275	1162	1583	1255	1366	1700	2484	1761	3005	1584
ENSMUSG00000021820	chr14	Camk2g	20734875	20736852	3703	-0.38892	7.549123	0.009922	0.025781	0.026862	-1	2696	2176	5196	3398	4035	2203	3780	2558	3568	2807
ENSMUSG00000056481	chr19	Cd248	5068078	5070637	2560	0.500857	4.363608	0.009923	0.025781	0.042388	1	220	161	506	210	330	316	373	569	538	379
ENSMUSG00000022702	chr16	Hira	18877037	18877214	6132	-0.43273	4.608681	0.009938	0.025814	0.031248	-1	367	384	703	363	438	343	460	324	532	255
ENSMUSG00000070394	chr11	Tmem256	69838514	69838573	1105	0.521309	5.551676	0.009943	0.025823	0.046999	1	669	609	612	527	511	915	1389	845	1166	760
ENSMUSG00000042419	chr17	Nfkbil1	35220175	35220976	1746	0.497358	2.704473	0.009961	0.025864	0.033701	1	74	66	102	91	90	122	128	129	182	119
ENSMUSG00000028223	chr4	Decr1	15917240	15919094	3879	-0.50628	6.885695	0.009983	0.025895	0.045536	-1	1576	1335	2139	3203	2900	1319	2534	1644	2199	1392
ENSMUSG00000031245	chrX	Hmgn5	1.09E+08	1.09E+08	1934	-0.51634	3.629875	0.00998	0.025895	0.042923	-1	176	176	248	201	366	98	247	205	206	179
ENSMUSG00000046567	chr10	4930430F08Rik	1.01E+08	1.01E+08	2419	-0.51679	2.238073	0.009978	0.025895	0.033525	-1	75	62	129	74	103	52	82	74	68	69
ENSMUSG00000070544	chr2	Top1	1.61E+08	1.61E+08	10426	-0.37367	5.260566	0.009978	0.025895	0.023558	-1	651	517	1009	569	743	459	680	615	755	542
ENSMUSG00000091661	chr9	Gm17021	1.24E+08	1.24E+08	462	-0.42809	3.880161	0.009982	0.025895	0.028361	-1	214	139	382	307	346	180	275	200	268	218
ENSMUSG00000036856	chr4	Wnt4	1.37E+08	1.37E+08	4194	-0.61752	5.181119	0.009986	0.025898	0.066668	-1	756	756	995	380	508	370	724	566	521	446
ENSMUSG00000029408	chr5	Abcb9	1.24E+08	1.24E+08	5817	-0.68692	3.010362	0.009998	0.025925	0.075895	-1	107	57	175	254	218	69	127	101	143	120
ENSMUSG00000026723	chr2	Trdmt1	13509014	13511690	3835	-0.58348	2.161386	0.010002	0.02593	0.046378	-1	55	59	113	101	99	35	76	55	85	72
ENSMUSG00000020451	chr11	Limk2	3344256	3345884	6099	-0.39179	3.925388	0.010009	0.025932	0.02318	-1	238	177	412	249	329	220	249	230	285	201
ENSMUSG00000038174	chr1	Fam126b	58522806	58530259	12041	-0.60146	2.907397	0.010005	0.025932	0.056536	-1	77	95	229	169	171	48	124	128	143	103
ENSMUSG00000090516	chr9	Rps11-ps1	59471759	59472233	475	0.921214	0.050321	0.010007	0.025932	0.071352	1	4	11	11	15	9	19	20	24	29	17
ENSMUSG00000007892	chr9	Rplp1	61913284	61913521	495	0.462589	8.797317	0.010022	0.025958	0.038348	1	6307	5260	6144	5440	5786	8239	12148	8405	11212	7365
ENSMUSG00000031807	chr8	Pgls	71592176	71592504	3770	0.469028	4.202616	0.010023	0.025958	0.035418	1	239	216	251	267	217	330	401	402	502	304
ENSMUSG00000054000	chr4	Tusc1	93334138	93335511	1374	0.816163	0.711079	0.010051	0.026025	0.067564	1	17	16	13	19	21	38	37	28	33	37
ENSMUSG00000063171	chr6	Rps4l	1.48E+08	1.48E+08	943	0.639676	1.923586	0.010054	0.026029	0.054888	1	46	36	50	48	47	78	73	105	75	68
ENSMUSG00000028228	chr4	Cpne3	19519254	19523294	7131	-0.44641	3.639042	0.010057	0.026032	0.030623	-1	176	149	405	180	281	127	249	207	227	158
ENSMUSG00000025504	chr7	Eps8l2	1.41E+08	1.41E+08	4370	0.721053	1.440603	0.010077	0.026078	0.066998	1	25	18	28	42	44	66	54	48	84	41
ENSMUSG00000045875	chr14	Adra1a	66635251	66635603	8144	-0.96253	0.86395	0.01008	0.026081	0.118853	-1	26	10	77	38	44	11	19	20	19	34

ENSMUSG00000040488	chr7	Ltbp4	27305136	27305550	6463	0.621076	6.858489	0.010096	0.026117	0.06878	1	875	676	2011	1821	2316	1292	2383	3065	3125	2933
ENSMUSG00000018900	chr11	Slc22a5	53864542	53865896	3071	-0.51349	3.472048	0.0101	0.026122	0.041496	-1	174	105	237	297	235	137	222	151	184	138
ENSMUSG00000020580	chr12	Rock2	16894978	16895330	8012	-0.45555	6.977841	0.010139	0.026218	0.036994	-1	2169	1939	3816	1541	2338	1643	2244	2038	2357	1452
ENSMUSG00000024121	chr17	Atp6v0c	24163866	24164608	3384	0.389531	5.982685	0.010141	0.026218	0.026413	1	784	586	1025	898	1107	1038	1468	1251	1789	1052
ENSMUSG00000039887	chr3	Alg14	1.21E+08	1.21E+08	910	0.473477	2.739038	0.010157	0.026255	0.030827	1	85	57	110	84	107	96	161	140	159	140
ENSMUSG00000026490	chr1	Cdc42bpa	1.8E+08	1.8E+08	21522	-0.42697	4.765489	0.010177	0.026301	0.030577	-1	377	274	845	448	674	304	479	393	627	345
ENSMUSG00000027285	chr2	Haus2	1.21E+08	1.21E+08	3218	-0.42924	3.616117	0.010249	0.026483	0.028474	-1	165	153	360	204	272	127	284	158	226	170
ENSMUSG00000024273	chr18	2700062C07Rik	24470861	24470980	1040	0.617407	1.539219	0.010254	0.026489	0.043729	1	32	33	52	25	34	49	68	70	65	54
ENSMUSG00000017756	chr13	Slc12a7	73763697	73763890	5131	0.429298	3.192237	0.010274	0.026537	0.027384	1	98	68	192	118	162	148	225	185	213	175
ENSMUSG00000002658	chr17	Gtf2f1	57003405	57003631	1717	0.383578	4.498957	0.010297	0.026591	0.023978	1	287	209	384	289	409	414	498	498	403	574	425
ENSMUSG00000029910	chr6	Mad2l1	66535390	66535599	2203	0.704845	0.690584	0.010313	0.026627	0.044821	1	22	12	22	13	22	27	45	31	40	27
ENSMUSG00000022248	chr15	Rad1	10486018	10486264	7400	0.537525	2.472539	0.010382	0.026799	0.040068	1	48	61	103	62	85	87	124	147	145	86
ENSMUSG00000031703	chr8	Itfg1	85717557	85718927	3355	-0.37503	5.933965	0.010395	0.026827	0.024661	-1	1019	849	1528	950	1197	711	1220	945	1178	844
ENSMUSG00000038260	chr7	Trpm4	45303155	45303692	4245	-0.38499	4.478221	0.010419	0.026886	0.024273	-1	347	250	532	438	478	263	430	280	491	318
ENSMUSG00000032314	chr9	Etfa	55454508	55454762	1835	-0.5825	7.249679	0.010423	0.026891	0.061123	-1	1817	1616	2909	4639	3801	1438	3483	1859	2817	1855
ENSMUSG00000035000	chr2	Dpp4	62330073	62332719	6319	-0.57765	2.653494	0.010457	0.026973	0.04986	-1	111	94	192	88	117	66	112	123	75	75
ENSMUSG00000037343	chr15	Taf2	55015129	55016601	5033	-0.43958	3.559211	0.010462	0.026979	0.029353	-1	160	120	299	239	294	158	216	169	235	135
ENSMUSG00000070871	chr1	Ccnyl1	64690455	64690676	3456	-0.41829	4.402293	0.010482	0.027025	0.029143	-1	332	325	624	284	387	250	413	293	443	270
ENSMUSG00000089718	chr9	2310075C17Rik	1.12E+08	1.12E+08	326	-1.06003	1.541347	0.010484	0.027025	0.179735	-1	17	28	42	126	96	20	54	22	52	25
ENSMUSG00000034341	chr11	Wbp2	1.16E+08	1.16E+08	3177	0.380181	6.683522	0.010491	0.027033	0.02579	1	1312	958	2068	1318	1607	1651	2239	1913	2881	1960
ENSMUSG00000059518	chr5	Znhit1	1.37E+08	1.37E+08	1860	0.44204	5.075627	0.010491	0.027033	0.033327	1	462	419	480	404	444	621	846	603	881	593
ENSMUSG00000014303	chr16	Glis2	4594713	4594935	4373	0.514984	2.991993	0.0105	0.027052	0.041607	1	77	50	152	108	151	130	163	182	185	172
ENSMUSG00000029536	chr5	Gatc	1.15E+08	1.15E+08	1794	-0.36092	5.109108	0.010507	0.027065	0.022086	-1	566	433	820	557	756	452	727	503	694	412
ENSMUSG00000041594	chr14	Tmtc4	1.23E+08	1.23E+08	7367	-0.72442	0.978166	0.010526	0.027104	0.059752	-1	27	17	64	50	35	16	38	24	29	23
ENSMUSG00000080824	chr6	Gm9001	75782358	75782756	399	-0.76439	0.381939	0.010526	0.027104	0.052719	-1	24	20	24	24	28	16	15	15	16	18
ENSMUSG00000036545	chr11	Adamts2	50602084	50602299	9336	0.431649	4.875927	0.010569	0.027204	0.032218	1	280	250	689	382	481	459	554	673	792	575
ENSMUSG00000097188	chr19	Snhg1	8723496	8725256	2947	0.616923	2.52613	0.01057	0.027204	0.055782	1	72	68	89	63	56	109	162	151	132	72
ENSMUSG00000049288	chr3	Lix1l	96601133	96601473	2509	0.461423	3.23784	0.010606	0.027294	0.032318	1	79	98	187	115	163	157	222	184	209	205
ENSMUSG00000029922	chr6	Mkrn1	39397804	39399434	4439	0.414336	4.172589	0.010627	0.027343	0.02742	1	214	221	298	220	261	336	436	390	432	273
ENSMUSG00000022899	chr16	Slc15a2	36750178	36751954	7360	-1.87475	1.078931	0.010647	0.027383	0.559425	-1	33	24	149	43	26	0	3	23	57	2
ENSMUSG00000034543	chr11	Morc2a	3649494	3650146	6013	-0.39822	4.360549	0.010646	0.027383	0.025897	-1	303	263	658	311	387	243	384	301	391	299
ENSMUSG00000043154	chr9	Ppp2r3a	1.01E+08	1.01E+08	12455	-0.4051	8.037383	0.010663	0.027419	0.029851	-1	3678	3033	7309	5040	5628	3037	5694	3173	5537	3614
ENSMUSG00000026966	chr2	Ssna1	25271039	25271581	1276	0.413726	4.315751	0.01068	0.027458	0.027808	1	285	208	319	245	287	384	540	360	474	313
ENSMUSG00000025794	chr9	Rpl14	1.21E+08	1.21E+08	935	0.452134	7.484312	0.010688	0.027473	0.037022	1	2419	2227	2736	2139	2208	3188	4697	3395	4859	2927
ENSMUSG00000020264	chr11	Slc36a2	55158470	55159615	3255	1.447457	2.09703	0.010695	0.027485	0.344789	1	55	28	33	34	19	78	39	324	31	53
ENSMUSG00000098374	chr17	Gm28043	29614876	29615078	6521	-0.36597	5.909627	0.010702	0.027498	0.023518	-1	882	676	1684	1108	1221	758	1166	906	1172	817
ENSMUSG00000023971	chr17	Rrp36	46667458	46668086	1195	0.451325	3.550104	0.010711	0.027515	0.03094	1	162	133	171	138	165	197	290	226	332	190
ENSMUSG00000008136	chr1	Fhl2	43123074	43123665	1897	1.103234	0.354523	0.010715	0.02752	0.168139	1	1	3	11	21	25	15	32	36	34	27
ENSMUSG00000028197	chr3	Col24a1	1.45E+08	1.45E+08	7621	0.728886	2.766899	0.010719	0.02752	0.089151	1	39	38	138	76	141	160	170	207	122	87
ENSMUSG00000033576	chr15	Apol6	77044729	77045171	4499	-0.8753	4.46488	0.010719	0.02752	0.135481	-1	232	179	248	926	713	167	347	326	381	225
ENSMUSG00000097404	chr19	Gm10814	6012620	6012684	1933	0.684053	0.6637	0.010729	0.027541	0.041923	1	16	12	27	17	19	32	39	32	40	22
ENSMUSG00000048310	chr8	Pskh1	1.06E+08	1.06E+08	3255	-0.37435	4.383927	0.01075	0.027588	0.022734	-1	341	218	503	397	456	252	396	313	423	283
ENSMUSG00000051444	chr3	Bbs12	37312554	37312585	2436	0.827178	0.076966	0.010757	0.0276	0.052605	1	11	8	14	9	12	13	27	26	21	22
ENSMUSG00000022978	chr16	Mis18a	90719312	90719978	2863	0.787307	0.408932	0.010776	0.02764	0.056649	1	10	11	25	14	12	30	27	29	36	17
ENSMUSG00000041881	chr17	Ndufa7	33824591	33824680	1701	0.401932	6.968417	0.010776	0.02764	0.029119	1	1635	1360	1937	1757	1812	2131	3185	2368	3464	2013
ENSMUSG00000030934	chr7	Oat	1.33E+08	1.33E+08	2155	-0.40125	7.854829	0.010779	0.027641	0.029335	-1	3467	2934	6571	3910	4716	2459	4960	3174	4066	3706
ENSMUSG00000020464	chr11	Pnpt1	29130744	29130918	3516	-0.42447	3.841141	0.01081	0.027716	0.02878	-1	198	176	392	270	302	177	355	182	227	184
ENSMUSG00000027455	chr2	Nsfl1c	1.51E+08	1.51E+08	3967	0.40146	6.208054	0.010814	0.02772	0.028682	1	905	895	1325	884	1032	1259	1782	1369	2027	1288
ENSMUSG00000060708	chr5	Bloc1s4	36747374	36748679	1306	0.506912	2.576497	0.010826	0.027745	0.035386	1	68	63	97	77	80	78	151	115	154	132
ENSMUSG00000040415	chr10	Dtx3	1.27E+08	1.27E+08	2572	0.3914	5.018494	0.010836	0.027766	0.026134	1	421	361	628	352	480	589	708	647	860	540
ENSMUSG00000030091	chr6	Nup210	91013068	91014496	8163	-0.48247	5.291933	0.010838	0.027767	0.041044	-1	566	324	1225	773	970	465	672	428	889	560
ENSMUSG00000073725	chr1	Lmbrd1	24678630	24678816	5960	-0.34919	5.573407	0.010844	0.027775	0.021164	-1	677	611	1184	837	1021	582	964	726	866	694
ENSMUSG00000028698	chr4	Pik3r3	1.16E+08	1.16E+08	5300	-0.52767	2.771342	0.010846	0.027775	0.042715	-1	96	74	195	134	159	59	135	75	166	85
ENSMUSG00000001467	chr5	Cyp51	4081145	4083303	4286	0.527056	2.737018	0.010873	0.027838	0.041451	1	69	48	94	105	119	121	179	139	130	131
ENSMUSG00000028369	chr4	Svep1	58042442	58043168	16117	0.471101	4.797777	0.010875	0.027838	0.038976	1	292	222	732	250	476	513	602	530	816	485
ENSMUSG00000032185	chr9	Carm1	21546894	21547230	4324	-0.40248	6.199851	0.010887	0.027866	0.028976	-1	1073	767	2138	1404	1562	911	1239	1072	1647	960
ENSMUSG00000046079	chr5	Lrrc8d	1.06E+08	1.06E+08	12573	0.534606	2.284233	0.01089	0.027868	0.039101	1	53	38	77	71	75	75	118	119	97	100
ENSMUSG00000031486	chr8	Gpr124	27085583	27086211	5775	0.547168	2.358655	0.010893	0.02787	0.043332	1	55	32	98	71	80	76	111	123	114	114
ENSMUSG00000005320	chr13	Fgfr4	55152640	55152927	3542	0.647392	1.568723	0.010897	0.027874	0.053587	1	31	29	52	35	31	56	66	87	58	46
ENSMUSG00000036138	chr9	Acaa1a	1.19E+08	1.19E+08	4414	0.36524	5.604849	0.010901	0.027879	0.023246	1	569	510	858	708	759	776	1094	1080	1248	810
ENSMUSG00000027665	chr3	Pik3ca	32397671	32397800	9088	-0.37235	5.694585	0.010959	0.028022	0.024405	-1	764	640	1535	775	1107	584	1088	798	962	727
ENSMUSG00000032409	chr9	Atr	95857597	95857783	23492	-0.44879	2.837772	0.010965	0.028032	0.028084	-1	118	83	179	122	161	99	134	104	132	78
ENSMUSG00000083325	chr2	Gm14121	1.5E+08	1.51E+08	1380	-1.05473	0.352168	0.01097	0.02804	0.148735	-1	10	17	28	38	36	3	31	7	14	17
ENSMUSG00000102426	chrX	RP23-330G24.3	1.52E+08	1.52E+08	1477	0.973013	0.074658	0.011004	0.028121	0.097832	1	10	6	14	6	15	6	26	29	24	28
ENSMUSG00000057378	chr2	Ryr3	1.13E+08	1.13E+08	17682	-1.0324	-0.066	0.01101	0.028129	0.11455	-1	18	10	40	6	22	11	14	4	15	7

ENSMUSG00000030316	chr6	Tamm41	1.15E+08	1.15E+08	5276	0.529006	2.569269	0.01102	0.02815	0.039321	1	54	70	86	89	77	108	159	110	137	112
ENSMUSG00000030317	chr6	Timp4	1.15E+08	1.15E+08	1416	-0.57686	4.137158	0.011026	0.028161	0.057418	-1	215	197	318	491	473	274	239	254	322	179
ENSMUSG00000030337	chr6	Vamp1	1.25E+08	1.25E+08	8746	-0.40963	4.854525	0.011041	0.028187	0.028831	-1	446	291	731	558	685	368	587	324	608	404
ENSMUSG00000097119	chr17	B230354K17Rik	45433852	45434227	4897	-0.42351	3.39649	0.011041	0.028187	0.027064	-1	154	126	269	170	262	143	227	140	183	127
ENSMUSG00000064264	chr7	Zfp428	24507006	24507436	1308	0.703743	1.084559	0.011059	0.028228	0.058227	1	16	16	22	33	35	31	49	42	51	52
ENSMUSG00000067038	chr19	Rps12-ps3	59322290	59322783	494	0.911731	0.013948	0.011086	0.028291	0.076179	1	7	7	12	7	17	26	29	12	25	14
ENSMUSG00000034108	chr19	Ccs	4825366	4825664	1057	0.454988	3.762	0.011091	0.028298	0.032636	1	159	162	169	190	205	200	359	271	346	256
ENSMUSG00000029726	chr5	Mepce	1.38E+08	1.38E+08	3292	0.373446	4.808386	0.011108	0.028333	0.023378	1	334	323	507	378	395	469	634	557	725	494
ENSMUSG00000060657	chr16	Marf1	14109166	14111771	7765	-0.35287	5.019939	0.011108	0.028333	0.021149	-1	440	407	887	582	658	414	646	506	618	427
ENSMUSG00000057530	chr4	Ece1	1.38E+08	1.38E+08	5300	-0.39409	5.973462	0.011122	0.028363	0.027788	-1	881	673	1643	1161	1541	746	1123	976	1381	789
ENSMUSG00000020604	chr11	Arsg	1.09E+08	1.09E+08	3906	0.66031	0.747871	0.011132	0.028382	0.041555	1	16	12	33	16	22	30	43	28	48	27
ENSMUSG00000058624	chr19	Gda	21391307	21395258	6135	0.612606	3.841381	0.011158	0.028444	0.064966	1	140	120	266	162	237	268	459	463	219	159
ENSMUSG00000021676	chr13	Iqgap2	95627177	95628120	5771	0.617335	1.739682	0.011172	0.028474	0.053545	1	39	15	64	34	60	63	69	76	80	64
ENSMUSG00000002059	chr11	Rab34	78188430	78188511	2385	0.772935	2.561866	0.011194	0.028524	0.09744	1	85	62	81	43	62	144	104	197	96	99
ENSMUSG00000029466	chr5	Anapc7	1.22E+08	1.22E+08	5119	0.390445	4.390916	0.011201	0.028535	0.025265	1	240	198	338	300	381	396	504	374	569	329
ENSMUSG00000102828	chr18	RP23-407E2.30	37823879	37824425	1530	-0.45428	3.360628	0.011229	0.028601	0.031591	-1	129	119	306	176	250	112	217	149	160	150
ENSMUSG00000028098	chr3	Rnf115	96727611	96727910	2265	-0.39009	5.966579	0.011244	0.028635	0.027375	-1	919	781	1598	1168	1301	791	1427	782	1296	747
ENSMUSG00000024258	chr18	Polr2d	31789159	31789244	956	0.45431	3.395029	0.011265	0.028683	0.031313	1	113	133	159	123	165	195	270	195	253	184
ENSMUSG00000025228	chr19	Actr1a	46376814	46378469	2742	0.380374	6.686801	0.011282	0.02872	0.026352	1	1274	887	1906	1524	1682	1664	2275	1957	2967	1843
ENSMUSG00000032503	chr9	Arpp21	1.12E+08	1.12E+08	17428	1.081394	2.87958	0.011297	0.028753	0.203093	1	20	16	46	165	138	123	219	173	235	156
ENSMUSG00000035151	chr8	Elmod2	83312632	83316461	11138	-0.46521	3.371529	0.01131	0.028782	0.03397	-1	154	148	324	133	219	113	197	153	168	156
ENSMUSG00000096370	chr19	Gm21992	4742913	4744867	5780	0.441639	3.358097	0.011334	0.028837	0.03039	1	108	79	166	155	194	165	283	214	231	179
ENSMUSG00000034623	chr14	Prss55	64075438	64075786	1403	-0.91132	0.309625	0.011343	0.028853	0.086551	-1	17	23	29	23	27	13	16	16	5	20
ENSMUSG00000097125	chr17	Gm26885	29461896	29462147	1688	-0.97939	0.991683	0.011348	0.028861	0.141767	-1	39	57	53	17	28	27	30	11	23	25
ENSMUSG00000024777	chr19	Ppp2r5b	6227765	6228531	2895	-0.37609	5.34368	0.011381	0.028927	0.024795	-1	624	422	992	825	882	522	716	574	831	585
ENSMUSG00000029563	chr6	Foxp2	14901349	14901761	13457	-0.65999	0.881916	0.011378	0.028927	0.04415	-1	25	21	54	38	37	18	37	19	26	24
ENSMUSG00000071660	chr19	Ttc9c	8809075	8811838	3984	-0.41865	3.89286	0.011379	0.028927	0.028475	-1	240	191	457	213	287	165	327	201	255	217
ENSMUSG00000030770	chr7	Parva	1.12E+08	1.12E+08	10157	0.41935	4.269164	0.011432	0.029051	0.029807	1	200	176	360	248	360	291	460	487	379	370
ENSMUSG00000090213	chr2	Tmem189	1.68E+08	1.68E+08	3265	0.382329	4.725978	0.011437	0.029058	0.025153	1	328	211	559	379	404	464	572	556	703	431
ENSMUSG00000097245	chr10	Gm5421	22343439	22345792	2354	-0.78115	1.817694	0.011468	0.029133	0.094805	-1	33	34	98	112	82	17	62	48	65	44
ENSMUSG00000061080	chr16	Lsamp	39984361	39984727	17213	0.721641	1.537932	0.011477	0.029151	0.075693	1	31	24	61	16	42	67	56	58	55	70
ENSMUSG00000027935	chr3	Rab13	90213695	90213822	1651	0.471516	3.672135	0.011485	0.029163	0.035395	1	159	157	165	165	176	238	285	242	353	221
ENSMUSG00000037443	chr4	Cep85	1.34E+08	1.34E+08	5269	-0.36119	5.481435	0.011524	0.029257	0.023081	-1	683	506	1134	824	953	559	920	579	964	597
ENSMUSG00000024357	chr18	Sil1	35266400	35266909	1695	0.396287	4.453877	0.011527	0.02926	0.026444	1	310	204	419	273	311	363	462	506	571	360
ENSMUSG00000042961	chr15	Egflam	7206120	7207802	6121	-0.38128	4.947472	0.011536	0.029276	0.025381	-1	528	424	657	537	622	434	651	396	612	372
ENSMUSG00000042807	chr1	Hecw2	53806876	53813333	12947	-0.67841	1.488925	0.011575	0.02937	0.060073	-1	31	27	90	56	76	37	51	41	30	29
ENSMUSG00000048371	chr8	Pdp2	1.05E+08	1.05E+08	3485	-0.76439	1.962783	0.011579	0.029376	0.090885	-1	56	27	83	99	132	30	90	41	48	52
ENSMUSG00000020003	chr10	Pex7	19859929	19860994	2351	-0.42474	4.647805	0.011602	0.029428	0.03168	-1	386	430	529	401	505	262	571	345	449	352
ENSMUSG00000030067	chr6	Foxp1	98925338	98930234	14266	0.465363	3.236376	0.011606	0.029432	0.034685	1	75	73	201	146	156	162	234	193	211	182
ENSMUSG00000027596	chr2	a	1.55E+08	1.55E+08	1169	-0.65528	1.102502	0.011609	0.029433	0.048271	-1	42	30	55	35	39	26	45	23	24	27
ENSMUSG00000042632	chr15	Pla2g6	79286228	79286895	4980	-0.37741	4.553757	0.011611	0.029433	0.023925	-1	372	275	619	409	484	290	356	401	469	335
ENSMUSG00000046994	chr1	Mars2	55237177	55248470	11294	-0.57248	3.118153	0.011622	0.029456	0.054122	-1	135	81	197	186	246	65	220	127	129	107
ENSMUSG00000063179	chr7	Pstk	1.31E+08	1.31E+08	2179	-0.4116	4.381116	0.011632	0.029474	0.029074	-1	356	272	391	435	419	269	435	268	414	260
ENSMUSG00000010067	chr9	Rassf1	1.08E+08	1.08E+08	5845	0.369723	4.065115	0.011646	0.029505	0.021572	1	194	179	288	228	275	272	450	298	439	274
ENSMUSG00000039883	chr5	Lrrc17	21543527	21543719	2186	0.557462	2.569916	0.011656	0.029525	0.047335	1	69	62	128	60	62	126	114	122	163	101
ENSMUSG00000020680	chr11	Taf15	83473086	83473206	2919	0.359951	4.940116	0.011672	0.029549	0.022253	1	401	305	535	408	502	561	758	589	691	529
ENSMUSG00000022215	chr14	Fitm1	55575617	55575947	969	0.393807	7.6433	0.011672	0.029549	0.028844	1	2446	1634	3459	3213	3262	3268	4875	3753	5461	3542
ENSMUSG00000030921	chr7	Trim30a	1.04E+08	1.04E+08	4419	0.60422	2.27639	0.011672	0.029549	0.054041	1	64	42	87	49	60	84	169	116	80	74
ENSMUSG00000036712	chr8	Cyld	88697028	88697099	8035	-0.35543	5.371317	0.011679	0.02956	0.022241	-1	613	545	1155	628	852	527	816	587	800	595
ENSMUSG00000040621	chrX	Gemin8	1.66E+08	1.66E+08	2487	0.842853	0.289185	0.011702	0.029614	0.066938	1	12	11	16	9	15	21	32	38	24	14
ENSMUSG00000037933	chr13	Bicd2	49341549	49341641	6351	-0.35646	5.244083	0.011758	0.029748	0.022408	-1	597	499	960	641	735	463	698	602	842	463
ENSMUSG00000046909	chr11	Tefm	80136678	80137279	1570	-0.43242	3.660591	0.01176	0.029748	0.030427	-1	165	150	294	261	307	124	280	170	241	179
ENSMUSG00000056917	chr19	Sipa1	5651185	5651562	3868	0.468388	3.208091	0.011762	0.029748	0.034705	1	80	86	167	140	151	150	184	215	213	193
ENSMUSG00000030083	chr6	Abtb1	88835915	88836452	1879	0.417487	5.025611	0.011806	0.029848	0.030667	1	458	348	591	353	467	489	700	692	1020	536
ENSMUSG00000031714	chr8	Gab1	80764434	80766487	4859	-0.40102	4.445116	0.011804	0.029848	0.027414	-1	293	248	595	432	466	236	380	286	499	328
ENSMUSG00000060261	chr5	Gtf2i	1.34E+08	1.34E+08	7120	-0.37659	6.835279	0.011825	0.029891	0.0262	-1	1650	1285	3266	2050	2414	1297	2112	1713	2320	1692
ENSMUSG00000041238	chr18	Rbbp8	11633276	11633524	3867	0.649149	1.16788	0.011865	0.029987	0.047735	1	23	23	42	17	29	45	68	40	46	38
ENSMUSG00000036782	chrX	Klhl13	23219271	23220852	4253	0.600015	2.240884	0.011873	0.030001	0.054106	1	43	42	89	53	73	63	117	108	83	128
ENSMUSG00000024666	chr19	Tmem138	10570478	10571268	1590	0.735586	0.748575	0.011943	0.030171	0.059716	1	19	12	28	15	21	40	39	42	30	24
ENSMUSG00000044730	chr4	9930104L06Rik	1.25E+08	1.25E+08	5592	-0.38713	3.426503	0.011951	0.030185	0.022367	-1	157	134	266	182	245	128	210	166	202	143
ENSMUSG00000020743	chr11	Mif4gd	1.16E+08	1.16E+08	2010	0.378396	4.799976	0.011962	0.030209	0.024832	1	360	246	445	399	493	495	679	589	636	459
ENSMUSG00000002105	chr2	Slc39a13	91061791	91062978	4869	0.365827	4.907433	0.011971	0.030225	0.023209	1	393	284	583	416	435	492	647	635	798	509
ENSMUSG00000079297	chrX	Gm2223	33505661	33507010	1350	-0.76256	1.758651	0.011984	0.030251	0.0877	-1	53	35	101	66	88	17	73	42	31	60
ENSMUSG00000003810	chr4	Mast2	1.16E+08	1.16E+08	7645	-0.45958	6.650155	0.012015	0.030324	0.03927	-1	1333	921	2983	2214	2305	1341	1465	1404	2185	1319
ENSMUSG00000024118	chr17	1600002H07Rik	24215054	24216005	2551	0.684792	1.348633	0.012052	0.030411	0.056414	1	32	28	39	21	27	41	92	50	54	40

ENSMUSG00000073910	chr4	Mob3b	34949074	34954047	6200	0.813331	0.367945	0.01207	0.030453	0.065439	1	15	12	21	8	12	21	24	38	30	22
ENSMUSG00000026622	chr1	Nek2	1.92E+08	1.92E+08	4516	1.163585	-0.45483	0.012073	0.030455	0.153855	1	5	5	10	4	7	24	8	17	6	18
ENSMUSG00000018334	chr11	Ksr1	79013440	79016263	6621	-0.42859	7.142866	0.012099	0.030513	0.034402	-1	2335	1970	4562	1755	2702	1786	2643	2076	2648	1883
ENSMUSG00000038569	chr5	Rad9b	1.22E+08	1.22E+08	2920	-1.0564	0.305023	0.012106	0.030524	0.145001	-1	9	15	31	52	17	8	10	19	18	12
ENSMUSG00000058135	chr3	Gstm1	1.08E+08	1.08E+08	1394	0.416762	7.676531	0.01211	0.030529	0.032642	1	2377	2378	4376	2263	2731	3163	4484	4586	5692	3555
ENSMUSG00000027884	chr3	Clcc1	1.09E+08	1.09E+08	4368	-0.35657	5.108633	0.012183	0.030707	0.022435	-1	509	465	909	605	642	444	736	478	630	485
ENSMUSG00000030545	chr7	Pex11a	79735957	79737910	2368	-0.49418	4.310277	0.012185	0.030707	0.043206	-1	274	215	365	526	480	248	390	331	337	203
ENSMUSG00000089774	chr16	Slc5a3	92058322	92058480	10913	0.659806	2.794285	0.012251	0.030868	0.071905	1	88	63	85	87	93	100	133	245	123	144
ENSMUSG00000036046	chr15	5031439G07Rik	84943936	84949278	9604	-0.44998	7.724825	0.012256	0.030873	0.038245	-1	4101	2347	6060	3479	3968	2909	3430	2921	5112	2186
ENSMUSG00000020441	chr11	2310033P09Rik	59208321	59208673	1285	0.606733	1.588642	0.012263	0.03088	0.047093	1	36	22	46	43	37	68	68	66	61	50
ENSMUSG00000024309	chr17	Pfdn6	33938821	33939111	1193	0.389717	4.986683	0.012263	0.03088	0.026609	1	434	353	475	413	477	550	802	575	859	516
ENSMUSG00000000740	chr8	Rpl13	1.23E+08	1.23E+08	2352	0.441013	7.903032	0.012268	0.030887	0.036712	1	3284	2995	3792	2804	2891	4324	6092	4732	6189	3950
ENSMUSG00000037415	chr8	Ranbp10	1.06E+08	1.06E+08	5308	-0.38872	5.147203	0.012275	0.030899	0.026901	-1	552	359	1078	597	756	504	687	465	708	447
ENSMUSG00000041889	chr1	Shisa4	1.35E+08	1.35E+08	2418	0.401247	7.668213	0.012283	0.030912	0.030353	1	2477	2176	3324	2919	3024	3354	4580	3413	5987	3938
ENSMUSG00000023994	chr17	Nfya	48386885	48389342	7315	0.449833	2.927021	0.012304	0.030959	0.029929	1	80	74	138	82	142	124	190	173	173	130
ENSMUSG00000042647	chr5	Acad12	1.22E+08	1.22E+08	5007	-0.45263	4.516924	0.012317	0.030985	0.036231	-1	320	211	533	509	604	221	448	314	450	349
ENSMUSG00000096952	chr8	Gm26572	1.21E+08	1.21E+08	3231	0.647139	0.915581	0.012329	0.03101	0.040594	1	21	17	28	23	21	31	54	30	52	32
ENSMUSG00000028042	chr3	Zbtb7b	89377644	89379994	5591	-0.37868	4.978065	0.012366	0.031099	0.02533	-1	538	377	851	514	614	371	503	552	593	465
ENSMUSG00000019810	chr10	Fuca2	13499540	13499587	6161	0.384883	3.865236	0.012377	0.03112	0.024004	1	188	121	247	211	248	260	355	281	371	234
ENSMUSG00000032085	chr9	Tagln	45929628	45930515	1586	0.518223	5.155528	0.012385	0.031133	0.048837	1	387	540	485	341	486	497	965	826	1018	590
ENSMUSG00000017561	chr11	Crlf3	80046493	80047737	4261	0.569086	2.40556	0.012391	0.031142	0.049991	1	36	39	77	92	97	85	141	113	140	91
ENSMUSG00000034422	chr16	Parp14	35832874	35834935	9306	0.483584	3.729004	0.012406	0.031174	0.040106	1	138	130	305	143	187	268	375	318	236	192
ENSMUSG00000029071	chr4	Dvl1	1.56E+08	1.56E+08	4996	-0.3703	7.179277	0.012412	0.031184	0.025814	-1	2368	1609	3613	2704	3022	1808	2862	2034	3018	1948
ENSMUSG00000021268	chr12	Meg3	1.1E+08	1.1E+08	18089	0.660456	3.237247	0.012436	0.031237	0.076935	1	117	71	243	55	122	183	180	238	179	227
ENSMUSG00000020831	chr11	0610010K14Rik	70235206	70235464	1896	0.431675	4.039634	0.012441	0.031245	0.031021	1	199	204	239	221	223	306	386	343	417	259
ENSMUSG00000020308	chr10	Tpgs1	79669410	79669783	1101	0.423382	3.867105	0.012456	0.031278	0.029434	1	208	158	237	159	218	255	306	310	390	250
ENSMUSG00000021597	chr13	Ankrd32	77043088	77044030	5881	-0.47607	3.147094	0.012463	0.031287	0.036644	-1	108	112	221	178	216	77	190	137	190	96
ENSMUSG00000021134	chr12	Srsf5	80945504	80945672	3988	0.425128	6.344472	0.012487	0.031343	0.033714	1	1104	911	1369	824	1296	1380	2528	1472	1940	1305
ENSMUSG00000039738	chr16	Slx4	3979105	3980172	7657	-0.51733	2.385613	0.012534	0.031455	0.037925	-1	95	55	155	81	111	69	94	78	73	68
ENSMUSG00000000776	chr14	Polr3d	70438748	70439578	2156	-0.36577	4.212205	0.012539	0.031459	0.022521	-1	317	230	402	317	402	214	406	287	335	246
ENSMUSG00000058729	chr1	Lin9	1.81E+08	1.81E+08	7244	-0.51089	2.475376	0.01254	0.031459	0.039305	-1	85	82	141	87	124	46	115	67	103	87
ENSMUSG00000014773	chr17	Dll1	15367354	15368035	4219	0.486911	2.279615	0.012572	0.031533	0.031492	1	56	47	78	53	84	77	110	99	134	87
ENSMUSG00000064317	chr10	Gm10146	78393309	78393756	448	0.749664	0.673896	0.012613	0.031628	0.0599	1	16	16	15	15	25	38	41	28	33	27
ENSMUSG00000047123	chr17	Ticam1	56269319	56272217	2992	0.570819	1.964759	0.012619	0.031639	0.045284	1	40	34	60	55	56	79	81	87	73	83
ENSMUSG00000020303	chr11	Stc2	31357307	31360528	5175	0.605505	1.930289	0.01263	0.031661	0.051493	1	44	36	64	36	56	50	106	87	68	93
ENSMUSG00000005505	chr2	Kbtbd4	90904740	90904812	3139	-0.3697	4.122631	0.012638	0.031675	0.022975	-1	285	236	420	314	310	202	379	256	319	239
ENSMUSG00000070923	chr4	Klhl9	88718292	88722465	4174	-0.37814	5.795852	0.012669	0.031746	0.026413	-1	788	720	1505	1012	1088	586	1142	746	1073	902
ENSMUSG00000037197	chr2	Rbm17	11585437	11585728	2405	0.369765	5.08082	0.01268	0.031768	0.024222	1	439	393	614	401	495	590	828	640	876	556
ENSMUSG00000061780	chr10	Cfd	79890853	79890980	923	1.644243	8.726837	0.01271	0.031835	0.485089	1	6266	4478	1433	754	978	8588	4112	33205	4776	4699
ENSMUSG00000022707	chr16	Gbe1	70313949	70314295	5352	-0.75944	5.644256	0.012728	0.031875	0.108516	-1	452	373	995	1823	1579	385	1026	480	952	654
ENSMUSG00000068798	chr3	Rap1a	1.06E+08	1.06E+08	2401	-0.35439	5.733639	0.012734	0.031884	0.023122	-1	757	719	1276	968	1092	572	1051	830	1103	759
ENSMUSG00000043602	chr11	Zfp3	70764209	70764549	2061	-0.39541	3.973637	0.012745	0.031906	0.026534	-1	270	213	329	265	338	186	362	195	296	212
ENSMUSG00000028082	chr3	Sh3d19	85971109	85971424	8888	0.548545	3.709239	0.012749	0.031909	0.053672	1	103	95	284	167	239	197	232	396	293	264
ENSMUSG00000035829	chr2	Ppp1r26	28446800	28446896	5619	-0.62669	1.522422	0.012776	0.031971	0.054189	-1	39	34	79	47	79	19	69	41	43	32
ENSMUSG00000028883	chr5	Sema3a	13396784	13397082	6470	-0.86296	1.891983	0.01279	0.032002	0.120966	-1	64	76	131	39	67	65	28	33	77	28
ENSMUSG00000057036	chr3	Gm7536	24333068	24333511	444	0.50552	4.959346	0.012823	0.032078	0.04664	1	457	383	417	337	375	681	877	527	785	461
ENSMUSG00000050530	chr2	Fam171a1	3114224	3114265	4442	0.435475	2.994338	0.012842	0.032117	0.02838	1	102	68	132	100	138	114	198	166	221	136
ENSMUSG00000051495	chr8	Irf2bp2	1.27E+08	1.27E+08	5080	0.491891	4.677471	0.012849	0.03213	0.043549	1	279	370	377	230	390	370	645	603	655	466
ENSMUSG00000028643	chr4	Ccdc23	1.19E+08	1.19E+08	1065	0.540307	3.481076	0.01286	0.032144	0.048811	1	129	153	151	127	134	220	258	235	345	148
ENSMUSG00000031774	chr8	Fam192a	94574943	94575857	1797	0.366935	4.823297	0.012859	0.032144	0.023587	1	386	309	527	320	429	470	714	551	695	484
ENSMUSG00000046806	chr6	3110062M04Rik	34871771	34874695	4269	0.528573	2.009073	0.012864	0.03215	0.037927	1	52	32	64	47	63	70	91	86	84	85
ENSMUSG00000010517	chr4	Faf1	1.1E+08	1.1E+08	5093	-0.36596	6.237229	0.012876	0.032174	0.025124	-1	1158	1046	1790	1349	1463	956	1551	1008	1519	1041
ENSMUSG00000033444	chr10	Specc1l	75212073	75212219	6075	-0.37259	5.99399	0.012883	0.032185	0.025823	-1	898	718	1870	1115	1359	798	1180	1008	1319	805
ENSMUSG00000022394	chr15	L3mbtl2	81663889	81664024	5945	-0.39744	3.663212	0.012898	0.032215	0.025452	-1	223	152	325	211	247	170	216	164	255	185
ENSMUSG00000003546	chr17	Klc4	46630631	46631073	2322	0.376952	4.217188	0.01291	0.032233	0.023968	1	208	173	314	311	289	304	433	362	509	313
ENSMUSG00000031393	chrX	Mecp2	74026592	74036494	10592	-0.42191	5.176673	0.012912	0.032233	0.032578	-1	481	354	1199	656	804	359	703	534	745	520
ENSMUSG00000039084	chr11	Chad	94565047	94565868	1680	-1.45763	3.362015	0.012912	0.032233	0.380684	-1	13	66	226	339	662	50	146	136	35	118
ENSMUSG00000070002	chr8	Ell	70539675	70539841	3085	0.398252	3.684713	0.012922	0.032251	0.025991	1	159	119	287	130	210	209	327	253	328	217
ENSMUSG00000029191	chr5	Rfc1	65261852	65263146	6000	-0.36686	4.665366	0.012938	0.032285	0.023562	-1	335	335	578	504	548	343	471	356	485	361
ENSMUSG00000031479	chr8	Vps36	22192809	22192966	3706	-0.35005	5.653877	0.012945	0.032297	0.02255	-1	812	630	1289	833	1008	652	1132	691	963	650
ENSMUSG00000000581	chr11	C1d	17257579	17257658	3995	-0.4163	5.057999	0.012951	0.032299	0.031872	-1	498	581	747	571	585	383	633	417	697	496
ENSMUSG00000026457	chr1	Adipor1	1.34E+08	1.34E+08	5025	-0.38656	8.362101	0.012949	0.032299	0.028757	-1	5592	4764	8426	4964	6137	4118	6236	4642	7132	4241
ENSMUSG00000020076	chr10	Ddx50	62616023	62616516	2527	-0.38102	5.531173	0.012977	0.032358	0.026892	-1	722	736	1219	687	810	551	921	701	906	618
ENSMUSG00000031487	chr8	Brf2	27123832	27124620	1383	0.451334	2.791412	0.013024	0.032469	0.02953	1	84	70	114	89	103	105	169	137	160	145
ENSMUSG00000078193	chr1	Gm2000	1.56E+08	1.56E+08	445	0.488458	3.554253	0.01303	0.032479	0.0397	1	153	134	183	136	156	236	333	182	348	161

ENSMUSG00000028274	chr4	Rngtt	33310311	33310524	7094	-0.4381	3.285723	0.013039	0.032489	0.030291	-1	146	97	237	215	214	123	173	156	173	124
ENSMUSG00000035762	chr13	Tmem161b	84222314	84222434	2572	-0.45033	3.257445	0.013042	0.032489	0.03293	-1	140	131	257	158	204	102	237	119	147	136
ENSMUSG00000052605	chr7	Isoc2b	4844959	4845365	1297	-0.52407	2.276627	0.013037	0.032489	0.040513	-1	74	70	94	96	112	68	73	71	96	48
ENSMUSG00000059878	chr6	Zfp422	1.17E+08	1.17E+08	3625	0.425795	3.49812	0.013047	0.032495	0.029106	1	136	127	234	114	160	192	284	199	319	189
ENSMUSG00000031959	chr8	Wdr59	1.11E+08	1.11E+08	5222	-0.38601	3.807531	0.013058	0.032512	0.024046	-1	201	163	405	212	324	188	256	216	257	184
ENSMUSG00000047714	chr16	Ppp1r2	31251537	31254733	4440	-0.35704	6.860183	0.013058	0.032512	0.024256	-1	1760	1583	2766	2025	2359	1404	2415	1649	2361	1588
ENSMUSG00000030281	chr6	Il17rc	1.13E+08	1.13E+08	2671	0.546367	2.397615	0.013085	0.032573	0.043957	1	71	55	77	61	66	86	112	130	157	77
ENSMUSG00000018449	chr11	Rpain	70970213	70970587	2842	0.521428	2.91626	0.013093	0.032586	0.041964	1	86	95	112	83	103	131	244	146	192	102
ENSMUSG00000044018	chr4	Mrpl50	49512596	49514577	2114	-0.36968	5.719726	0.013096	0.032588	0.025441	-1	891	648	1112	949	1158	701	1187	714	994	650
ENSMUSG00000032320	chr9	Rcn2	56041845	56042204	4745	0.375471	5.175601	0.013108	0.032611	0.025481	1	474	409	675	401	549	574	807	694	974	678
ENSMUSG00000000631	chr11	Myo18a	77763246	77763379	14864	-0.42218	7.292354	0.01312	0.032634	0.034197	-1	2397	1733	5026	2489	3354	1819	2532	2137	3767	2138
ENSMUSG00000023883	chr17	Phf10	14945009	14945184	4914	-0.37527	5.616818	0.013125	0.032637	0.026236	-1	736	746	1293	799	866	596	961	705	1094	605
ENSMUSG00000027808	chr3	Serp1	58521969	58523868	2440	0.435874	4.461397	0.013126	0.032637	0.033922	1	258	254	476	211	309	358	510	548	463	403
ENSMUSG00000026879	chr2	Gsn	35279663	35279718	2977	0.457039	10.96612	0.013133	0.032649	0.040507	1	23680	20882	41681	20350	30668	39491	36138	50327	45734	35152
ENSMUSG00000059447	chr5	Hadhb	30155248	30155339	6595	-0.56869	8.167167	0.013137	0.032653	0.062347	-1	3495	2733	5589	8861	7311	3018	6242	3344	5638	3453
ENSMUSG00000021982	chr14	Cdadc1	59560896	59560921	1901	-0.39517	4.782357	0.013141	0.032656	0.028274	-1	403	414	588	511	560	354	635	329	494	376
ENSMUSG00000029617	chr5	Ccz1	1.44E+08	1.44E+08	1762	-0.39602	5.370358	0.013155	0.032685	0.029199	-1	711	663	942	666	710	501	920	587	792	508
ENSMUSG00000015943	chr3	Bola1	96196588	96197279	1082	0.422819	3.999127	0.013161	0.032695	0.03042	1	236	165	265	176	235	323	402	289	361	274
ENSMUSG00000036721	chr13	Zscan12	21362827	21362872	2228	-0.52356	2.85823	0.01317	0.032704	0.044264	-1	133	122	160	117	131	93	144	76	109	112
ENSMUSG00000039210	chr1	Gpatch2	1.87E+08	1.87E+08	7684	-0.46739	3.210041	0.013169	0.032704	0.035548	-1	121	115	302	145	203	81	177	136	173	143
ENSMUSG00000036561	chr15	Ppp6r2	89253035	89253261	2887	-0.40261	5.612756	0.01319	0.032745	0.030269	-1	768	452	1261	1038	1070	558	1038	654	1052	623
ENSMUSG00000079508	chrX	Apoo	94367117	94367162	1255	-0.42671	6.314096	0.013191	0.032745	0.034709	-1	1339	1211	1893	1358	1431	1015	1960	915	1432	989
ENSMUSG00000006276	chr8	Eps15l1	72341001	72341524	3141	-0.40941	4.170422	0.013202	0.032764	0.028892	-1	227	176	476	392	426	226	340	249	364	238
ENSMUSG00000040620	chr11	Dhx33	70984091	70987427	10031	-0.41646	3.405387	0.013228	0.032823	0.028109	-1	146	149	304	163	220	116	229	173	178	134
ENSMUSG00000025648	chr9	Pfkfb4	1.09E+08	1.09E+08	3333	-0.52067	5.763582	0.013233	0.03283	0.051538	-1	1098	801	1576	679	986	795	1132	818	980	401
ENSMUSG00000020799	chr11	Tekt1	72344722	72344971	1622	-0.95506	1.192193	0.013256	0.032882	0.148539	-1	37	68	70	14	36	26	43	16	36	19
ENSMUSG00000041025	chr4	Iffo2	1.4E+08	1.4E+08	6216	0.559931	2.099997	0.013334	0.033068	0.046578	1	38	32	80	54	74	82	93	117	97	61
ENSMUSG00000031557	chr8	Plekha2	25039144	25043038	5397	0.347917	5.044485	0.013337	0.03307	0.021715	1	440	322	632	408	539	518	753	644	838	617
ENSMUSG00000018326	chr2	Ywhab	1.64E+08	1.64E+08	3382	0.485386	6.22993	0.013342	0.033077	0.044951	1	948	864	1229	826	1066	1241	1550	2283	1565	1240
ENSMUSG00000040782	chr1	Rfwd2	1.59E+08	1.59E+08	17516	-0.38651	6.56396	0.013365	0.033126	0.028569	-1	1628	1392	2351	1411	1775	1238	2015	1270	1747	1271
ENSMUSG00000017144	chr2	Rnd3	51130438	51132545	4432	0.526009	3.128937	0.013412	0.033235	0.046665	1	55	82	152	130	162	135	248	196	171	178
ENSMUSG00000052214	chr7	Opa3	19228334	19228584	4554	-0.37649	6.594403	0.013414	0.033235	0.027096	-1	1567	1040	2207	1969	2069	1206	1974	1351	1971	1267
ENSMUSG00000071652	chr19	Ints5	8888926	8888964	3889	0.340487	4.58409	0.013427	0.033262	0.020052	1	307	236	474	306	385	415	604	438	586	403
ENSMUSG00000034889	chr10	Cactin	81321103	81321446	2724	0.374679	3.785118	0.013443	0.033295	0.023078	1	159	118	254	195	246	204	326	267	358	263
ENSMUSG00000040549	chr2	Ckap5	91526762	91526850	9462	-0.38706	5.483015	0.013498	0.03342	0.027849	-1	612	469	1403	786	971	508	942	632	810	670
ENSMUSG00000059811	chr17	Atl2	79848392	79850278	3616	-0.4075	8.212854	0.013498	0.03342	0.032318	-1	4528	4841	7757	4342	5565	3930	5709	3812	5460	4376
ENSMUSG00000078937	chr15	Cpt1b	89416405	89416979	3372	-0.58625	8.080949	0.01352	0.033463	0.066762	-1	3453	2204	5839	8241	7074	2853	5816	2757	5404	3449
ENSMUSG00000086889	chr13	Phf2os1	48871112	48871203	498	1.054032	-0.0315	0.013521	0.033463	0.112264	1	12	11	9	5	6	28	21	21	26	9
ENSMUSG00000034570	chr11	Inpp5j	3494375	3495166	5092	-1.73675	0.026918	0.013553	0.033536	0.465864	-1	7	2	3	53	51	3	7	16	7	5
ENSMUSG00000072720	chr5	Myo18b	1.13E+08	1.13E+08	10698	-0.42798	8.361845	0.013563	0.033553	0.035711	-1	4226	3726	9801	6508	7150	3526	5353	4437	8056	4668
ENSMUSG00000031691	chr8	Tnpo2	85036915	85036977	4990	-0.36242	5.128341	0.013566	0.033555	0.024031	-1	583	403	1003	569	662	427	678	509	770	445
ENSMUSG00000040506	chr2	Ambra1	91730134	91730379	6122	-0.38581	4.349483	0.013627	0.033699	0.025876	-1	255	228	631	353	456	245	360	314	402	291
ENSMUSG00000029229	chr5	Chic2	75001026	75006763	6712	0.410928	3.192482	0.013633	0.03371	0.026022	1	118	88	191	107	125	155	224	172	247	150
ENSMUSG00000081944	chr11	Gm12276	62331421	62331721	301	0.812423	0.566975	0.013667	0.033787	0.077707	1	18	12	15	14	19	30	31	45	38	14
ENSMUSG00000035504	chr10	Reep6	80329953	80330345	2506	-0.89087	1.457839	0.01369	0.033837	0.129212	-1	44	49	74	45	65	22	24	76	32	14
ENSMUSG00000005161	chr8	Prdx2	84969587	84969762	3050	0.417892	7.075615	0.013695	0.033843	0.033826	1	1530	1297	1870	2261	2216	2424	3370	2439	3780	2197
ENSMUSG00000003458	chr1	Ncstn	1.72E+08	1.72E+08	3975	0.347506	5.40657	0.013733	0.033924	0.022406	1	489	359	866	644	700	638	1056	844	1094	738
ENSMUSG00000031239	chrX	Itm2a	1.07E+08	1.07E+08	1744	0.475331	7.103608	0.013731	0.033924	0.043922	1	1795	1345	3258	1258	1779	1662	4049	3122	3283	2717
ENSMUSG00000001768	chr2	Rin2	1.46E+08	1.46E+08	5399	0.408624	4.239569	0.013743	0.03394	0.029572	1	212	180	386	228	315	305	632	380	363	300
ENSMUSG00000071347	chr14	C1qtnf9	60768134	60768168	1903	-0.42477	4.302759	0.013744	0.03394	0.032452	-1	235	239	406	441	508	218	420	288	384	248
ENSMUSG00000026987	chr2	Baz2b	59899363	59900802	17604	-0.44271	3.641282	0.013752	0.033952	0.033511	-1	146	130	357	242	319	130	274	191	228	153
ENSMUSG00000018733	chr11	Pex12	83294642	83296440	3536	-0.40067	3.512536	0.013778	0.03401	0.026502	-1	176	164	312	163	230	137	242	180	208	134
ENSMUSG00000008958	chr3	Vps72	95111022	95111214	3639	-0.42334	5.167748	0.013804	0.034068	0.033689	-1	715	529	943	468	619	457	620	525	772	446
ENSMUSG00000029463	chr5	Fam216a	1.22E+08	1.22E+08	1388	0.540346	1.837555	0.013852	0.034181	0.041363	1	33	23	77	47	54	60	89	59	110	61
ENSMUSG00000037531	chr3	Mrpl47	32725397	32727717	4419	-0.4334	4.12141	0.013866	0.034209	0.033794	-1	229	218	347	413	391	188	399	239	346	206
ENSMUSG00000031669	chr8	Gins3	95633559	95633783	2412	0.835073	0.272425	0.013872	0.034217	0.068971	1	15	11	14	7	15	27	36	23	19	21
ENSMUSG00000022893	chr16	Adamts1	85793827	85796100	5302	-0.43384	5.104106	0.013877	0.034223	0.035344	-1	491	395	1117	634	643	409	858	539	577	342
ENSMUSG00000024235	chr18	Map3k8	4331327	4332436	4504	0.905542	0.624755	0.013937	0.034363	0.117541	1	6	10	29	14	23	20	79	29	30	17
ENSMUSG00000040841	chr7	Six5	19094594	19095418	3007	0.535718	1.933481	0.013941	0.034363	0.038471	1	42	37	72	52	40	62	84	85	93	74
ENSMUSG00000086841	chr11	2410006H16Rik	62602877	62603023	462	0.557207	3.153244	0.013939	0.034363	0.052003	1	132	101	116	88	114	189	240	186	239	107
ENSMUSG00000027692	chr3	Tnik	28263214	28263699	19282	-0.53632	4.878341	0.013945	0.034364	0.054398	-1	307	234	881	724	810	295	615	364	563	392
ENSMUSG00000033396	chr2	Spg11	1.22E+08	1.22E+08	8042	-0.48276	2.845915	0.013957	0.034389	0.036563	-1	111	72	208	132	162	70	127	128	112	103
ENSMUSG00000020695	chr11	Mrc2	1.05E+08	1.05E+08	6674	0.47074	4.179727	0.013969	0.034411	0.0409	1	148	140	370	227	384	255	387	401	433	420
ENSMUSG00000050900	chrX	Gm7327	61785381	61786032	652	-0.62876	1.02291	0.013975	0.034419	0.042556	-1	30	26	59	32	45	28	38	28	25	19
ENSMUSG00000020483	chr11	Dynll2	87979525	87981570	2736	-0.39519	8.682424	0.013987	0.034444	0.030767	-1	6810	6083	9119	6725	8332	5700	6439	6298	8699	5238

ENSMUSG00000042156	chr14	Dzip1	1.19E+08	1.19E+08	4744	0.621481	1.420922	0.013991	0.034446	0.049383	1	28	22	34	31	47	54	83	43	51	51
ENSMUSG00000032741	chr5	Tpcn1	1.21E+08	1.21E+08	4645	-0.40551	6.005615	0.014007	0.03448	0.031478	-1	860	628	1883	1310	1434	779	1099	939	1280	950
ENSMUSG00000102171	chr14	RP23-117H6.2	47737339	47739894	2556	0.750533	0.402063	0.014042	0.034559	0.052853	1	14	11	22	13	12	27	41	26	27	17
ENSMUSG00000038683	chr13	Pak1ip1	41001023	41001413	4049	0.377464	5.329101	0.014058	0.034593	0.026445	1	560	445	698	495	566	686	1033	684	1102	677
ENSMUSG00000066000	chr4	2610305D13Rik	1.48E+08	1.48E+08	4111	-0.70054	0.993615	0.014136	0.034778	0.064547	-1	23	32	41	41	51	11	32	23	35	32
ENSMUSG00000030630	chr7	Fah	84585159	84585344	2103	1.06898	2.060322	0.014146	0.034795	0.198551	1	58	41	35	43	18	84	69	214	60	57
ENSMUSG00000006462	chr2	A530013C23Rik	1.68E+08	1.68E+08	5964	0.654244	2.317993	0.014159	0.034814	0.066545	1	53	67	51	72	44	95	146	89	122	93
ENSMUSG00000022386	chr15	Trmu	85879312	85879458	3974	0.521877	2.951046	0.014157	0.034814	0.044582	1	81	61	107	144	107	124	210	172	220	108
ENSMUSG00000021900	chr14	Btd	31641028	31641135	2353	0.438301	3.232323	0.01417	0.034836	0.030885	1	122	103	159	104	140	155	207	227	219	162
ENSMUSG00000010097	chr19	Nxf1	8757073	8757259	5980	0.368582	6.434328	0.014184	0.034863	0.026221	1	1141	898	1460	1166	1347	1550	2105	1506	2272	1492
ENSMUSG00000028654	chr4	Mycl	1.23E+08	1.23E+08	4038	1.156139	-0.1098	0.014196	0.034888	0.171058	1	3	12	16	1	8	21	14	21	37	9
ENSMUSG00000026869	chr2	Psmd5	34852088	34852833	3750	0.351699	4.286339	0.01421	0.034914	0.021206	1	243	202	404	256	274	310	492	373	515	318
ENSMUSG00000020758	chr11	Itgb4	1.16E+08	1.16E+08	7015	-0.68307	2.478686	0.014213	0.034914	0.079737	-1	51	54	127	178	146	43	97	70	104	76
ENSMUSG00000024120	chr17	Lrpprc	84705247	84705472	8504	-0.4376	6.707035	0.014219	0.034923	0.037459	-1	1388	1091	2227	2447	2668	1235	2229	1280	2168	1346
ENSMUSG00000039068	chr3	Zzz3	1.52E+08	1.52E+08	8401	-0.37895	4.459831	0.014231	0.034947	0.02558	-1	289	247	640	362	527	248	455	369	397	288
ENSMUSG00000004931	chr10	Apba3	81268172	81268319	2106	-0.43951	5.731765	0.01426	0.034998	0.037207	-1	747	505	1166	1358	1214	589	936	788	1107	733
ENSMUSG00000026727	chr2	Rsu1	13076821	13077607	9299	0.337032	4.55117	0.01426	0.034998	0.020044	1	289	226	472	296	397	389	542	448	573	426
ENSMUSG00000039328	chr8	Rnf122	31111820	31112172	7080	0.422572	3.10404	0.014259	0.034998	0.027674	1	98	88	145	99	155	132	254	157	201	153
ENSMUSG00000048078	chr7	Tenm4	96171244	96171493	21030	1.362385	2.107627	0.014273	0.035024	0.331282	1	60	35	49	18	17	60	46	320	44	57
ENSMUSG00000010175	chr1	Prox1	1.9E+08	1.9E+08	8390	0.641676	0.732669	0.014282	0.035039	0.042586	1	15	10	31	18	25	32	42	33	35	29
ENSMUSG00000024587	chr18	Nars	64499665	64500649	2632	-0.35165	6.998558	0.014291	0.035048	0.024185	-1	1913	1709	3050	2205	2688	1695	2514	1843	2631	1660
ENSMUSG00000079260	chr9	Tmppe	1.14E+08	1.14E+08	6855	0.51394	1.859955	0.01429	0.035048	0.034855	1	44	28	72	36	57	57	92	80	84	65
ENSMUSG00000021277	chr12	Traf3	1.11E+08	1.11E+08	7350	-0.42804	4.528329	0.014297	0.035051	0.033553	-1	286	221	600	512	575	263	377	341	500	322
ENSMUSG00000093798	chr10	Gm8355	14745362	14746117	756	0.449566	3.464147	0.014297	0.035051	0.034084	1	123	117	170	150	176	207	228	281	257	167
ENSMUSG00000038670	chr7	Mybpc2	44501699	44501842	3624	-0.4889	12.49313	0.014327	0.035117	0.047521	-1	118082	84290	181651	67159	92608	69871	94353	82303	122731	72448
ENSMUSG00000024527	chr18	Afg3l2	67404767	67405514	3085	-0.47086	6.254382	0.014339	0.03514	0.043296	-1	997	721	1690	1948	1929	794	1469	987	1623	1069
ENSMUSG00000030204	chr6	Ddx47	1.35E+08	1.35E+08	4952	0.354597	4.80701	0.014343	0.035143	0.022582	1	352	304	459	386	447	481	684	530	722	456
ENSMUSG00000035208	chr11	Slfn8	83002158	83003889	4091	0.805711	0.939927	0.014355	0.035167	0.092125	1	17	17	37	13	23	32	68	48	20	39
ENSMUSG00000025484	chr7	Bet1l	1.41E+08	1.41E+08	1552	0.396916	3.467036	0.01438	0.03522	0.025302	1	143	106	192	143	176	191	320	200	258	177
ENSMUSG00000031201	chrX	Brcc3	75416628	75416841	7887	-0.37619	4.392469	0.014402	0.035266	0.025464	-1	301	322	510	371	383	295	438	282	396	261
ENSMUSG00000079469	chr9	Pigb	73007419	73008780	10434	-0.52798	2.222851	0.014404	0.035266	0.041349	-1	67	54	154	75	99	39	77	73	90	66
ENSMUSG00000001150	chr10	Mcm3ap	76468971	76469214	6382	-0.39274	4.287645	0.014418	0.035294	0.027328	-1	261	187	540	391	460	228	395	287	358	278
ENSMUSG00000020661	chr12	Dnmt3a	3806007	3806232	16642	-0.44981	5.813773	0.014432	0.035313	0.039207	-1	660	559	1587	1181	1457	518	1256	859	967	809
ENSMUSG00000022475	chr15	Hdac7	97792664	97793742	5530	0.387253	4.023917	0.014435	0.035313	0.026497	1	170	125	344	232	292	219	417	326	433	301
ENSMUSG00000024006	chr17	Stk38	28970885	28972676	8489	0.344991	5.126441	0.014434	0.035313	0.02205	1	414	347	697	449	590	610	852	748	771	569
ENSMUSG00000034259	chr15	Exosc4	76327397	76327663	1945	0.363234	4.250467	0.014436	0.035313	0.022833	1	232	201	321	257	314	312	401	391	505	335
ENSMUSG00000003808	chr8	Farsa	84856989	84857181	4538	0.369602	4.627998	0.014521	0.035513	0.024612	1	340	229	412	348	392	415	563	488	708	384
ENSMUSG00000027680	chr3	Fxr1	34020079	34020163	2323	-0.39213	8.434615	0.014531	0.035532	0.030617	-1	5312	5583	8495	5439	6389	4366	7234	4531	6722	4753
ENSMUSG00000001518	chr6	Itfg2	1.28E+08	1.28E+08	5069	-0.40422	3.786768	0.014536	0.035537	0.027921	-1	212	131	343	265	337	161	236	219	290	180
ENSMUSG00000031403	chrX	Dkc1	75095854	75096127	4121	-0.38887	4.728427	0.014571	0.035616	0.028135	-1	373	425	702	422	482	325	612	364	473	343
ENSMUSG00000035757	chr15	Selo	89089084	89089665	3744	-0.41518	4.110686	0.014597	0.035673	0.030916	-1	243	177	419	395	374	170	352	293	318	230
ENSMUSG00000025583	chr11	Rptor	1.2E+08	1.2E+08	13471	-0.44383	5.054114	0.014606	0.035688	0.037391	-1	466	272	880	746	828	365	645	442	629	503
ENSMUSG00000001285	chr15	Myg1	1.02E+08	1.02E+08	2823	0.396296	3.790006	0.014638	0.035761	0.026204	1	175	160	226	185	190	218	311	287	365	246
ENSMUSG00000028803	chr4	Nipal3	1.35E+08	1.35E+08	7588	-0.43022	3.894691	0.014685	0.035869	0.032392	-1	192	149	367	344	345	204	242	215	266	213
ENSMUSG00000051341	chr17	Zfp52	21555046	21555075	2175	-0.6063	2.032973	0.014688	0.03587	0.056785	-1	53	40	82	113	104	49	72	50	61	56
ENSMUSG00000037784	chr9	Dzip1l	99629496	99629669	7984	0.590012	1.122659	0.014694	0.035877	0.037999	1	27	18	30	21	36	38	59	41	54	35
ENSMUSG00000016356	chr2	Col20a1	1.81E+08	1.81E+08	4193	-0.5383	2.070259	0.014724	0.035944	0.044154	-1	60	58	138	60	85	40	90	54	88	42
ENSMUSG00000025494	chr7	Sigirr	1.41E+08	1.41E+08	1990	0.64667	0.818075	0.014734	0.035962	0.046962	1	13	11	30	24	27	24	40	33	54	34
ENSMUSG00000050732	chr6	Vamp8	72385223	72385653	2311	0.436083	4.892145	0.014759	0.036017	0.035719	1	402	307	374	413	475	600	814	518	766	430
ENSMUSG00000038005	chr8	2700029M09Rik	60890418	60890536	1701	0.505894	2.888223	0.014809	0.036131	0.041386	1	70	97	108	78	123	130	203	167	172	112
ENSMUSG00000004837	chr11	Grap	61653265	61653424	1793	0.557732	2.336234	0.014814	0.036138	0.049333	1	60	34	68	62	100	100	102	121	134	76
ENSMUSG00000033237	chr15	Arid2	96287518	96287786	10737	-0.42945	3.910337	0.014831	0.036172	0.032758	-1	235	162	487	231	317	145	262	281	291	195
ENSMUSG00000050930	chr8	Map10	1.26E+08	1.26E+08	3542	-0.66476	1.46157	0.014861	0.036238	0.064043	-1	36	29	94	46	68	37	57	21	54	22
ENSMUSG00000025479	chr7	Cyp2e1	1.41E+08	1.41E+08	1827	1.563849	6.343373	0.01487	0.036253	0.461022	1	1229	792	401	230	205	2101	505	6109	985	652
ENSMUSG00000097715	chr13	Gpr137b-ps	12619084	12621408	2997	0.824402	0.261972	0.014873	0.036253	0.0761	1	8	6	18	12	20	16	31	40	23	16
ENSMUSG00000022053	chr14	Ebf2	67233292	67233956	6928	-0.60573	2.797038	0.014889	0.036286	0.063857	-1	86	117	214	98	162	49	97	128	101	117
ENSMUSG00000034544	chr3	Rsrc1	66981390	66981542	12000	-0.39965	4.133753	0.014893	0.03629	0.028812	-1	250	272	490	261	334	177	362	297	303	248
ENSMUSG00000027642	chr2	Rpn2	1.57E+08	1.57E+08	4430	0.378514	6.530154	0.014917	0.036342	0.028186	1	1176	1038	1810	1073	1340	1584	2094	2047	2132	1621
ENSMUSG00000020268	chr11	Lyrm7	54826866	54827065	3597	-0.44943	3.789263	0.014924	0.036351	0.03628	-1	213	142	282	330	315	146	310	177	246	197
ENSMUSG00000074102	chr9	Rbm15b	1.07E+08	1.07E+08	6511	0.492936	2.986466	0.014936	0.036376	0.041235	1	67	64	143	106	156	143	197	204	170	117
ENSMUSG00000041057	chr17	Wdr43	71616215	71616485	3450	-0.36848	4.765561	0.014944	0.036389	0.025303	-1	441	405	690	437	469	346	590	382	503	360
ENSMUSG00000038126	chr5	Mphosph9	1.24E+08	1.24E+08	8544	-0.58747	1.880513	0.014956	0.036409	0.050219	-1	56	40	141	51	74	48	65	42	60	46
ENSMUSG00000051367	chr12	Six1	73040015	73040574	4383	-0.36102	6.031358	0.014979	0.036459	0.02546	-1	1028	900	1630	1128	1220	740	1255	958	1408	929
ENSMUSG00000035863	chr10	Palm	79793572	79793740	2651	0.430272	3.81485	0.014985	0.036467	0.033015	1	144	141	269	189	223	217	248	331	338	307
ENSMUSG00000034066	chr1	Farp2	93512079	93512184	5235	-0.44146	3.097966	0.015005	0.03651	0.031306	-1	114	92	264	174	165	103	144	136	166	109

ENSMUSG00000020928	chr11	Higd1b	1.03E+08	1.03E+08	847	0.704098	0.730829	0.015025	0.036551	0.053467	1	13	17	25	16	23	20	53	31	52	23
ENSMUSG00000025041	chr19	Nt5c2	46886831	46889051	4475	0.518788	2.724275	0.015029	0.036554	0.045013	1	54	47	116	124	96	105	167	155	162	112
ENSMUSG00000002017	chr17	Fam98a	75537086	75538861	3479	-0.33695	5.167615	0.015037	0.03656	0.021253	-1	532	435	966	578	772	448	756	504	732	489
ENSMUSG00000036469	chr8	March1	65617900	65618182	7146	0.72703	0.414119	0.015035	0.03656	0.061914	1	11	8	30	10	17	26	25	34	27	24
ENSMUSG00000024151	chr17	Msh2	87672330	87672806	5518	-0.37095	4.179468	0.015062	0.036615	0.024609	-1	242	242	376	347	430	227	379	247	371	231
ENSMUSG00000064363	chrMT	mt-Nd4	10167	11544	1378	-0.59266	12.57638	0.015087	0.036669	0.070675	-1	59849	51363	135534	173487	195271	64848	121364	77422	120407	70689
ENSMUSG00000053898	chr7	Ech1	28825217	28825412	2284	-0.6422	7.399355	0.015109	0.036714	0.082531	-1	1843	1743	2708	5855	4428	1728	3844	1955	3057	1815
ENSMUSG00000034429	chr15	Zfp707	75969123	75969404	3094	0.579092	1.642051	0.015132	0.036764	0.044315	1	44	27	56	26	41	50	95	59	84	46
ENSMUSG00000020827	chr11	Mink1	70562881	70563126	6286	-0.36265	4.994662	0.015218	0.036965	0.024625	-1	437	346	847	564	768	381	541	514	687	434
ENSMUSG00000045667	chr11	Smtnl2	72389164	72391413	3815	-0.50096	8.741357	0.015228	0.036985	0.050658	-1	9124	6183	10981	5290	8396	6137	7313	4578	10291	4554
ENSMUSG00000102918	chr18	PCDHGB6	37806364	37809743	5499	0.376654	5.707021	0.015236	0.036997	0.027726	1	555	499	1213	628	864	753	1163	1168	1221	1056
ENSMUSG00000060636	chr16	Rpl35a	33056453	33056510	3526	0.470922	6.874405	0.015258	0.037043	0.044261	1	1611	1520	1526	1332	1548	2265	3372	2070	3079	1789
ENSMUSG00000047371	chr7	Zfp768	1.27E+08	1.27E+08	2245	-0.34797	5.368408	0.015286	0.037099	0.023156	-1	680	499	911	746	881	548	780	547	885	576
ENSMUSG00000055413	chr17	H2-Q5	35394126	35394189	1591	0.911808	0.113443	0.015285	0.037099	0.081753	1	10	14	10	6	12	17	28	32	19	18
ENSMUSG00000001138	chr1	Cnnm3	36511867	36513153	6420	0.35857	3.93692	0.0153	0.037126	0.022327	1	154	146	321	218	254	252	385	307	341	275
ENSMUSG00000037826	chr6	Ppm1k	57506502	57510849	5560	-0.69629	3.942517	0.015343	0.037221	0.093468	-1	125	116	393	494	468	121	346	184	241	199
ENSMUSG00000063317	chr7	Usp31	1.22E+08	1.22E+08	10198	-0.43082	3.785071	0.015345	0.037221	0.032754	-1	187	155	453	197	330	149	229	237	266	188
ENSMUSG00000025486	chr7	Sirt3	1.41E+08	1.41E+08	1570	-0.58003	4.046537	0.015361	0.037252	0.064261	-1	209	142	315	471	479	174	349	160	315	228
ENSMUSG00000027678	chr2	Ncoa3	1.66E+08	1.66E+08	7895	-0.48586	4.358162	0.015364	0.037252	0.044451	-1	253	156	652	441	530	216	366	316	367	294
ENSMUSG00000038422	chr4	Hdhd3	62499008	62500093	1366	0.697868	1.325015	0.015383	0.037291	0.073623	1	23	14	39	30	44	41	48	80	42	52
ENSMUSG00000009681	chr10	Bcr	75060896	75062310	6537	0.489874	2.72486	0.01539	0.037302	0.039269	1	63	61	132	80	107	93	159	185	141	114
ENSMUSG00000001630	chr6	Stk38l	1.47E+08	1.47E+08	4571	-0.40868	3.685643	0.0154	0.037312	0.029363	-1	184	151	295	271	281	122	278	213	232	173
ENSMUSG00000031954	chr8	Cfdp1	1.12E+08	1.12E+08	1215	0.392924	4.300436	0.015399	0.037312	0.027696	1	240	233	302	264	296	354	531	415	446	292
ENSMUSG00000007880	chr4	Arid1a	1.34E+08	1.34E+08	11476	-0.40245	5.082714	0.015411	0.037332	0.030972	-1	493	325	1131	553	752	376	666	468	675	502
ENSMUSG00000038055	chr16	Dexi	10502531	10503914	3353	0.378093	5.098761	0.015449	0.037419	0.027098	1	488	370	618	396	493	590	760	619	968	603
ENSMUSG00000002210	chr7	Smg9	24399619	24399891	3702	0.349988	4.275116	0.015457	0.037431	0.021949	1	243	164	381	260	337	310	421	399	504	340
ENSMUSG00000028580	chr4	Pum1	1.31E+08	1.31E+08	6008	-0.36522	5.078146	0.015465	0.037442	0.025228	-1	468	383	998	598	698	391	562	574	684	484
ENSMUSG00000023852	chr17	Chd1	15704967	15705312	8721	-0.37099	3.930882	0.015474	0.037454	0.023866	-1	233	165	422	246	347	173	335	218	281	215
ENSMUSG00000027361	chr2	Gabpb1	1.27E+08	1.27E+08	7752	0.462755	2.664995	0.015478	0.037454	0.032809	1	58	75	117	78	93	105	154	121	147	129
ENSMUSG00000036323	chr5	Srp72	76974683	76974832	5717	-0.33684	5.547141	0.015476	0.037454	0.021823	-1	646	568	1287	841	934	563	958	747	908	627
ENSMUSG00000017707	chr2	Serinc3	1.64E+08	1.64E+08	3840	-0.39161	7.815396	0.015487	0.037468	0.031002	-1	4007	2914	5834	3248	4692	3457	3814	3286	4505	2671
ENSMUSG00000033088	chr15	Triobp	78947724	78948048	10681	-0.4638	5.040738	0.015491	0.037472	0.041761	-1	589	429	1001	426	675	428	478	685	538	362
ENSMUSG00000000486	chr7	Sept1	1.27E+08	1.27E+08	2060	0.896614	-0.06147	0.015511	0.037512	0.07179	1	7	9	6	13	11	21	19	21	19	18
ENSMUSG00000072893	chr11	4933439C10Rik	59505662	59506886	5616	0.658204	1.21875	0.015518	0.037523	0.054477	1	32	23	44	18	20	42	60	52	52	40
ENSMUSG00000078517	chr4	Emc1	1.39E+08	1.39E+08	6683	0.342715	5.581747	0.015532	0.03755	0.022715	1	555	456	964	659	807	766	1079	867	1399	821
ENSMUSG00000084910	chr4	C630043F03Rik	72201348	72202270	2581	-0.64929	1.452021	0.015535	0.03755	0.065906	-1	53	35	62	51	57	24	77	32	43	19
ENSMUSG00000057406	chr5	Whsc1	33820725	33820877	15898	-0.40092	3.377256	0.015542	0.03756	0.026831	-1	165	128	294	159	214	107	188	171	201	149
ENSMUSG00000022012	chr14	Enox1	77156763	77157042	3495	0.961762	-0.17535	0.015563	0.037597	0.084312	1	5	9	11	8	8	6	25	17	33	14
ENSMUSG00000098754	chr2	Gm28045	1.32E+08	1.32E+08	3370	-0.41412	3.20341	0.015561	0.037597	0.02775	-1	139	122	241	152	192	100	147	137	177	151
ENSMUSG00000037938	chr2	Chchd5	1.29E+08	1.29E+08	1727	0.412549	3.186898	0.015568	0.037603	0.026929	1	111	87	136	141	140	144	238	174	224	163
ENSMUSG00000027810	chr3	Eif2a	58525821	58526086	6118	-0.38766	5.495262	0.015581	0.037629	0.029475	-1	751	736	1093	697	754	595	957	635	842	565
ENSMUSG00000002221	chr5	Paxip1	27740667	27742503	5052	-0.441	3.000064	0.015595	0.037655	0.03129	-1	133	84	192	156	176	96	117	124	165	110
ENSMUSG00000035666	chr2	Gtf3c4	28822299	28826797	7230	-0.39831	4.372435	0.015617	0.037694	0.029122	-1	248	211	583	420	496	261	363	327	415	266
ENSMUSG00000083992	chr11	Gm11478	86630428	86631026	599	0.541872	2.73998	0.015616	0.037694	0.048415	1	77	88	124	56	78	108	196	154	148	109
ENSMUSG00000030393	chr7	Zik1	10487229	10491008	4199	-0.78726	0.277407	0.01563	0.037718	0.069303	-1	17	12	46	21	21	7	26	14	14	14
ENSMUSG00000031570	chr8	Ppapdc1b	25720061	25720151	2546	0.467973	2.42318	0.015642	0.037741	0.03313	1	63	46	105	58	88	74	140	113	122	109
ENSMUSG00000062997	chr2	Rpl35	39001580	39001765	1241	0.440585	6.798709	0.015652	0.037758	0.038971	1	1578	1368	1609	1380	1354	2116	2899	1974	2984	1801
ENSMUSG00000030701	chr7	Plekhb1	1.01E+08	1.01E+08	3554	-0.56791	6.746746	0.015661	0.037765	0.065132	-1	2033	2275	2904	1130	1595	1570	1743	1429	1963	1165
ENSMUSG00000048874	chr1	Phf3	30802339	30805942	14190	-0.35998	4.835052	0.015659	0.037765	0.02422	-1	354	349	831	495	621	342	560	476	519	389
ENSMUSG00000021711	chr13	Trappc13	1.04E+08	1.04E+08	5166	-0.35164	4.635039	0.015678	0.037792	0.022817	-1	402	290	639	449	477	336	540	385	435	303
ENSMUSG00000029998	chr6	Pcyox1	86386006	86389371	4797	-0.35429	6.179926	0.015675	0.037792	0.024823	-1	1108	858	1950	1208	1541	865	1275	1137	1453	1086
ENSMUSG00000024053	chr17	Emilin2	71252176	71253093	3910	0.475221	3.804739	0.015706	0.037853	0.042099	1	180	119	345	135	182	285	294	340	295	232
ENSMUSG00000022614	chr15	Lmf2	89351004	89351887	2906	0.400689	3.940714	0.015714	0.037866	0.029067	1	163	128	264	235	282	259	293	312	411	299
ENSMUSG00000027236	chr2	Eif3j1	1.22E+08	1.22E+08	5830	-0.42913	6.942827	0.015727	0.037891	0.037258	-1	2010	1979	3068	1817	2357	1608	2870	1305	2478	1511
ENSMUSG00000084416	chr1	Rpl10a-ps1	64993951	64994604	654	0.45022	4.642667	0.015739	0.037912	0.038338	1	367	299	367	300	295	484	670	474	650	363
ENSMUSG00000020329	chr10	Polrmt	79736123	79736283	4685	-0.38668	4.636026	0.015752	0.037938	0.028021	-1	397	252	653	462	547	273	382	415	546	355
ENSMUSG00000030101	chr6	Sumf1	1.08E+08	1.08E+08	3405	0.363979	4.054667	0.015811	0.038071	0.023342	1	221	161	311	212	259	275	390	377	366	282
ENSMUSG00000046056	chr7	Sbsn	30734739	30734768	3802	0.65787	1.813944	0.015814	0.038071	0.068058	1	39	39	65	29	39	67	77	110	80	43
ENSMUSG00000017929	chr2	B4galt5	1.67E+08	1.67E+08	4308	0.432791	3.853647	0.015842	0.038127	0.034662	1	138	105	352	209	222	213	448	310	332	228
ENSMUSG00000031960	chr8	Aars	1.11E+08	1.11E+08	9282	-0.38635	6.710669	0.015842	0.038127	0.030029	-1	1462	1051	2689	2191	2410	1378	1908	1390	2229	1435
ENSMUSG00000005873	chr18	Reep5	34344889	34347168	2894	0.349819	7.739251	0.01585	0.038138	0.024859	1	2556	2206	4115	2983	3300	3775	5021	4029	5633	3493
ENSMUSG00000029521	chr5	Chek2	1.11E+08	1.11E+08	2247	-0.60343	1.081462	0.015896	0.038243	0.040452	-1	30	27	51	41	48	29	32	34	30	20
ENSMUSG00000027088	chr2	Phospho2	69789623	69789956	4335	-0.35212	4.281898	0.015907	0.038262	0.022245	-1	294	271	468	324	389	270	381	307	316	270
ENSMUSG00000005718	chr16	Tfap4	4544661	4545747	2113	0.611847	2.145004	0.015911	0.038263	0.060198	1	71	44	77	30	48	88	102	98	106	77
ENSMUSG00000030522	chr7	Mtmr10	64287653	64287841	7474	-0.42129	4.208386	0.015929	0.038299	0.033267	-1	271	196	585	349	352	169	429	294	375	213

ENSMUSG00000039633	chr8	Lonrf1	36216064	36217601	3930	-0.57963	4.146607	0.015952	0.038349	0.065498	-1	342	338	529	171	293	203	233	262	427	184
ENSMUSG00000037885	chr2	Stk35	1.3E+08	1.3E+08	6195	-0.43771	3.28495	0.015993	0.03844	0.032274	-1	129	98	288	183	229	99	185	164	172	134
ENSMUSG00000037573	chr11	Tob1	94211454	94211731	2288	-0.47652	7.237294	0.016011	0.038478	0.046309	-1	2313	2330	3878	2403	3181	1378	3676	1499	2627	2572
ENSMUSG00000018541	chr11	Cwc25	97745481	97747469	5053	0.410312	3.081406	0.016017	0.038485	0.027083	1	104	83	178	86	134	136	212	176	202	147
ENSMUSG00000079499	chr2	6530402F18Rik	29245107	29248878	5511	0.553774	2.174242	0.016023	0.038493	0.050606	1	35	30	118	60	58	71	106	107	117	78
ENSMUSG00000015522	chr3	Arnt	95434388	95434561	8007	-0.34766	5.577852	0.016043	0.038525	0.023638	-1	692	572	1392	784	966	533	970	694	1000	689
ENSMUSG00000024579	chr18	Pcyox1l	61696837	61697976	2645	0.824899	0.704879	0.01604	0.038525	0.084423	1	27	13	11	14	19	24	37	45	45	26
ENSMUSG00000053877	chr7	Srcap	1.28E+08	1.28E+08	18791	-0.43048	5.656146	0.016057	0.038553	0.036765	-1	633	465	1637	886	1304	552	862	735	977	796
ENSMUSG00000068823	chr3	Csde1	1.03E+08	1.03E+08	4201	-0.37005	9.939084	0.016062	0.038556	0.0282	-1	16310	13904	23723	15798	18830	11904	20629	13296	18990	14179
ENSMUSG00000031734	chr8	Irx3	91798525	91798976	2611	-0.82086	2.224963	0.016081	0.038597	0.123056	-1	77	43	110	133	114	71	57	34	127	21
ENSMUSG00000100153	chr7	Gm5601	1.2E+08	1.2E+08	972	-0.5207	2.251028	0.016092	0.038615	0.044365	-1	84	72	108	71	104	46	107	51	105	52
ENSMUSG00000041308	chr8	Sntb2	1.07E+08	1.07E+08	4423	-0.61598	1.939005	0.016122	0.038679	0.059827	-1	40	34	139	71	102	45	73	47	72	36
ENSMUSG00000031357	chrX	Syap1	1.63E+08	1.63E+08	2351	-0.3494	4.980209	0.016186	0.038826	0.023417	-1	493	461	726	526	607	358	566	508	639	468
ENSMUSG00000055027	chr6	Smyd1	71213940	71215909	4546	-0.37505	9.079453	0.01621	0.038877	0.028995	-1	9523	6259	14824	8942	10296	6592	12033	7726	10612	6787
ENSMUSG00000036992	chr2	Nxt1	1.49E+08	1.49E+08	1116	0.476549	2.265201	0.016231	0.03892	0.032235	1	56	43	73	66	77	72	134	103	107	85
ENSMUSG00000034312	chr6	Iqsec1	90659598	90661025	7412	-0.52801	5.944792	0.016234	0.03892	0.056372	-1	706	485	1652	1538	1758	554	1065	942	1164	917
ENSMUSG00000040857	chr7	Erf	25242561	25245531	3607	0.435404	2.903307	0.016241	0.038931	0.030532	1	66	75	143	113	112	106	192	156	200	129
ENSMUSG00000029267	chr5	Mtf2	1.08E+08	1.08E+08	5263	-0.44051	3.287048	0.016245	0.038934	0.033664	-1	114	141	302	155	206	102	169	139	212	136
ENSMUSG00000020544	chr11	Cox11	90638173	90638552	1423	-0.3418	4.356499	0.016252	0.038944	0.021302	-1	344	266	467	346	405	257	384	292	426	293
ENSMUSG00000035171	chr19	1110059E24Rik	21581202	21581630	3067	0.444355	2.969802	0.016272	0.038985	0.031362	1	101	82	120	107	108	121	229	160	194	120
ENSMUSG00000029290	chr5	Zfp326	1.06E+08	1.06E+08	7217	-0.41132	3.069148	0.016279	0.038994	0.027079	-1	128	110	225	123	187	93	147	136	153	122
ENSMUSG00000072761	chr17	Gm6712	17294443	17294589	594	-0.87108	0.057014	0.016285	0.039002	0.085434	-1	13	22	28	16	18	14	19	4	15	9
ENSMUSG00000019528	chr3	Gyg	20122084	20122864	2344	-0.37696	8.49021	0.016334	0.039111	0.029311	-1	5975	5096	9352	5931	6233	4542	7336	4700	7575	4805
ENSMUSG00000001053	chr11	N4bp3	51643063	51644148	2728	0.62405	2.032023	0.01634	0.039119	0.063067	1	41	30	50	80	47	66	83	95	132	67
ENSMUSG00000008682	chrX	Rpl10	74270812	74270874	2053	0.43026	8.092235	0.016419	0.0393	0.038121	1	3886	3359	4598	2977	3322	4861	7143	5444	7311	4145
ENSMUSG00000032714	chr10	Syde1	78584503	78585911	3288	0.487795	2.847304	0.016429	0.039317	0.040772	1	64	67	138	104	108	117	190	183	125	133
ENSMUSG00000095123	chr10	Gm21781	4391587	4396424	4838	0.786039	0.848955	0.01645	0.03936	0.09131	1	19	14	38	10	21	34	25	41	38	50
ENSMUSG00000005610	chr7	Eif4g2	1.11E+08	1.11E+08	7348	-0.36257	9.364368	0.01646	0.03937	0.027241	-1	9893	7475	18458	11912	13332	7510	13569	9844	13334	9138
ENSMUSG00000038406	chr7	Scaf1	45002948	45003371	8368	-0.36215	5.464943	0.016459	0.03937	0.025792	-1	584	488	1209	841	982	493	801	643	949	669
ENSMUSG00000027667	chr3	Zfp639	32510259	32510589	5475	-0.3332	4.606663	0.016472	0.039384	0.020554	-1	371	311	603	416	491	343	513	348	454	313
ENSMUSG00000058900	chr13	Rsl1	67173207	67173253	1648	-0.74518	0.448579	0.01647	0.039384	0.066758	-1	27	19	26	32	21	12	30	16	14	15
ENSMUSG00000079435	chrX	Rpl36a	1.35E+08	1.35E+08	1655	0.515113	6.133411	0.016492	0.039427	0.05382	1	963	955	978	786	711	1464	2051	1333	1622	1076
ENSMUSG00000056673	chrY	Kdm5d	897788	898115	15164	-2.42115	2.842283	0.016502	0.039443	1.038835	-1	120	127	311	208	228	78	0	0	128	0
ENSMUSG00000025503	chr7	Taldo1	1.41E+08	1.41E+08	1998	0.41132	6.484224	0.016537	0.039518	0.034371	1	1263	1017	1459	1078	1216	1499	2002	2209	2160	1435
ENSMUSG00000036315	chr17	Znrd1	36954356	36954552	819	0.430882	3.790946	0.016544	0.039528	0.033066	1	168	175	207	182	181	267	349	232	359	234
ENSMUSG00000026102	chr1	Inpp1	52785427	52790217	6460	-0.55113	2.196828	0.016566	0.039566	0.048064	-1	51	59	101	96	128	41	79	71	74	68
ENSMUSG00000027303	chr2	Ptpra	1.3E+08	1.3E+08	3335	0.358002	4.235563	0.016565	0.039566	0.023545	1	212	173	385	279	291	314	458	427	393	321
ENSMUSG00000103436	chrX	RP23-135F22.6	7558602	7560883	5727	0.359376	4.30657	0.016581	0.039595	0.023883	1	241	171	375	298	317	373	428	353	517	342
ENSMUSG00000020250	chr10	Txnrd1	82859206	82859300	3417	-0.38356	6.306067	0.016601	0.039636	0.029888	-1	1106	871	2204	1514	1707	922	1900	1129	1544	922
ENSMUSG00000071650	chr19	Ganab	8898090	8898159	3862	0.359332	4.907327	0.016609	0.039648	0.024947	1	338	285	562	404	546	489	714	668	603	568
ENSMUSG00000040774	chr3	Cept1	1.07E+08	1.07E+08	3116	-0.43191	4.581377	0.01663	0.039685	0.036258	-1	449	368	644	286	445	299	461	415	362	310
ENSMUSG00000069045	chrY	Ddx3y	1260771	1263367	5199	-2.55325	5.214786	0.01663	0.039685	1.151867	-1	495	783	1859	936	1244	259	3	1	796	2
ENSMUSG00000078201	chr2	Tmem203	25255439	25256292	854	0.520949	2.942171	0.016635	0.039688	0.046264	1	122	81	113	84	85	127	192	125	229	149
ENSMUSG00000028080	chr3	Lrba	86224680	86224754	18270	-0.38262	5.297273	0.016638	0.039688	0.028828	-1	520	392	1055	780	948	489	720	510	868	555
ENSMUSG00000039234	chr3	Sec24d	1.23E+08	1.23E+08	3856	0.445745	3.022447	0.016642	0.039692	0.034629	1	82	62	164	94	162	115	211	170	184	166
ENSMUSG00000030147	chr6	Clec4b1	1.23E+08	1.23E+08	784	0.974722	-0.15098	0.016664	0.039736	0.110247	1	9	6	18	7	3	24	21	19	11	17
ENSMUSG00000042211	chr18	Fbxo38	62504069	62504880	4388	-0.3352	4.539831	0.016723	0.039871	0.020649	-1	355	275	599	376	509	313	441	329	446	342
ENSMUSG00000024642	chr19	Tle4	14448072	14449841	4640	-0.42431	4.223917	0.016753	0.039935	0.034506	-1	238	270	560	291	392	174	362	230	466	260
ENSMUSG00000042035	chr3	Igsf3	1.01E+08	1.01E+08	7389	0.529049	2.590617	0.016786	0.040006	0.048381	1	40	55	142	68	100	80	139	130	159	131
ENSMUSG00000000318	chr11	Clec10a	70156197	70156262	2899	0.878685	3.840801	0.016836	0.040117	0.153111	1	185	180	251	55	107	379	286	542	267	154
ENSMUSG00000038047	chr4	Haus6	86578855	86582018	6459	-0.48669	2.966425	0.016859	0.040165	0.041053	-1	116	101	273	111	148	73	162	122	123	112
ENSMUSG00000035923	chr10	Myf6	1.07E+08	1.07E+08	1248	0.422327	6.50316	0.016872	0.040189	0.036523	1	1292	998	1721	902	1263	1616	2746	1542	2426	1333
ENSMUSG00000027364	chr2	Usp50	1.27E+08	1.27E+08	3093	0.561775	1.369349	0.016892	0.040229	0.039787	1	31	17	43	38	32	40	65	57	57	49
ENSMUSG00000028495	chr4	Rps6	86854660	86854955	1586	0.40827	7.195313	0.016912	0.040269	0.034389	1	2045	1782	2344	1740	1913	2619	3845	2845	3696	2350
ENSMUSG00000036188	chr12	Ankmy2	36157124	36157423	2446	0.412288	3.01436	0.016917	0.040276	0.027359	1	91	84	137	111	125	150	194	160	176	144
ENSMUSG00000038538	chr6	Ubn2	38433950	38434598	21438	-0.41582	4.765282	0.016931	0.040301	0.033722	-1	386	302	964	362	609	321	477	428	564	349
ENSMUSG00000084790	chr16	Gm15879	4032839	4033052	1023	-0.95934	1.105503	0.016946	0.04033	0.154425	-1	55	45	73	18	24	37	30	21	29	10
ENSMUSG00000022759	chr16	Lrrc74b	17544465	17545642	3941	-0.78538	0.816728	0.016968	0.040367	0.086084	-1	26	23	52	34	37	16	32	16	11	34
ENSMUSG00000034192	chr6	Lsm3	91515928	91516078	1257	0.438818	3.889714	0.016965	0.040367	0.035153	1	181	175	203	222	192	280	428	249	349	247
ENSMUSG00000064120	chr17	Mocs1	49428362	49428564	3110	-0.3993	3.71374	0.016971	0.040368	0.028255	-1	196	155	373	193	307	173	254	233	207	157
ENSMUSG00000075054	chr13	Yae1d1	17986640	17989782	3436	-0.38662	3.346751	0.016991	0.040407	0.025605	-1	163	131	255	162	215	123	233	135	184	133
ENSMUSG00000031918	chr9	Mtmr2	13748410	13749400	4913	-0.36088	4.10101	0.017014	0.040454	0.023353	-1	247	172	474	320	377	220	333	255	317	243
ENSMUSG00000028773	chr4	Fabp3	1.3E+08	1.3E+08	823	-1.18081	8.021765	0.017024	0.040464	0.282091	-1	1464	1609	2307	15823	7915	1846	5604	1607	4045	2202
ENSMUSG00000062611	chr14	Rps3a2	88123017	88123808	792	0.575366	3.220409	0.017024	0.040464	0.060601	1	124	121	118	81	126	213	275	189	218	113
ENSMUSG00000010554	chr11	Mettl16	74770830	74770984	13817	-0.35142	4.342385	0.017043	0.040495	0.022843	-1	332	257	487	329	424	304	398	264	392	264

ENSMUSG00000026864	chr2	Hspa5	34771970	34772146	4229	0.376098	7.930545	0.017041	0.040495	0.029456	1	3447	2267	4640	3049	3734	4181	6203	5557	5228	3953
ENSMUSG00000025034	chr19	Trim8	46501648	46503013	3230	0.328585	4.981111	0.017052	0.040509	0.020624	1	390	322	610	445	485	497	728	649	823	523
ENSMUSG00000002345	chr8	2310045N01Rik	70139499	70139772	2743	0.416328	2.96061	0.017057	0.040514	0.027554	1	101	72	142	111	102	123	190	162	195	134
ENSMUSG00000062647	chr2	Rpl7a	26910764	26910830	1781	0.384308	8.066742	0.017066	0.040527	0.03076	1	3508	3177	4461	3538	3593	4741	6952	5207	6760	4251
ENSMUSG00000004473	chr7	Clec11a	44303770	44304986	1952	0.847661	2.063564	0.017081	0.040555	0.134811	1	16	26	51	39	113	58	117	82	75	135
ENSMUSG00000029559	chr5	2210016L21Rik	1.15E+08	1.15E+08	3303	0.379056	4.40657	0.017125	0.040654	0.026879	1	276	243	344	267	321	401	471	369	547	380
ENSMUSG00000027204	chr2	Fbn1	1.25E+08	1.25E+08	12128	0.472551	5.59146	0.017141	0.040683	0.045883	1	494	299	1164	602	877	660	990	940	1293	1198
ENSMUSG00000050812	chr4	AI314180	58798911	58800320	11447	-0.35268	8.108171	0.017163	0.040728	0.025981	-1	4008	3605	7821	4585	5290	3607	5524	4075	5674	3484
ENSMUSG00000021708	chr13	Rasgrf2	91880400	91884524	8810	-0.49655	2.220589	0.017166	0.040729	0.038689	-1	56	65	121	85	109	41	101	66	92	54
ENSMUSG00000024668	chr19	Sdhaf2	10500513	10503129	3096	-0.3972	5.27247	0.017187	0.040758	0.031696	-1	517	494	765	910	821	453	826	503	753	545
ENSMUSG00000027605	chr2	Acss2	1.56E+08	1.56E+08	10163	-0.69561	4.954433	0.017186	0.040758	0.098624	-1	377	187	573	1140	878	324	444	474	463	427
ENSMUSG00000028559	chr4	Osbpl9	1.09E+08	1.09E+08	7006	-0.36504	6.601711	0.017189	0.040758	0.027431	-1	1293	1448	2619	1662	1813	1287	1900	1451	1707	1389
ENSMUSG00000032500	chr9	Dclk3	1.11E+08	1.11E+08	3495	-0.85267	-0.10626	0.017191	0.040758	0.071005	-1	11	11	27	19	19	7	10	19	9	8
ENSMUSG00000006024	chr7	Napa	16098458	16098774	3786	0.384858	7.297625	0.017215	0.040808	0.030783	1	1725	1903	3092	1889	2327	2851	3584	2759	3882	3086
ENSMUSG00000020472	chr11	Zkscan17	59485520	59487817	4573	-0.33375	4.533082	0.01724	0.04086	0.020739	-1	330	271	613	414	480	276	424	364	483	329
ENSMUSG00000024493	chr18	Lars	42202350	42202718	3856	-0.34009	5.581971	0.017318	0.041038	0.023231	-1	717	620	1225	834	937	598	1105	655	970	599
ENSMUSG00000051977	chr17	Prdm9	15543079	15545360	4308	-0.59444	1.509069	0.017323	0.041041	0.050255	-1	38	43	67	55	63	38	56	45	28	31
ENSMUSG00000032120	chr9	C2cd2l	44309237	44311267	4334	-0.38205	4.026713	0.017365	0.041127	0.026821	-1	267	196	423	254	356	201	271	318	293	199
ENSMUSG00000054034	chrX	Tceal5	1.36E+08	1.36E+08	1263	0.57288	4.521008	0.017363	0.041127	0.065426	1	331	313	323	185	250	386	663	328	539	574
ENSMUSG00000059142	chr17	Zfp945	22846697	22852766	10173	-0.48375	2.771041	0.01737	0.041132	0.040137	-1	100	102	186	112	135	101	155	90	109	62
ENSMUSG00000079559	chr9	Gm684	51270258	51270925	1263	0.916496	-0.19412	0.017416	0.041233	0.079294	1	11	7	5	6	12	15	18	24	16	16
ENSMUSG00000002799	chr12	Jag2	1.13E+08	1.13E+08	4054	-0.43979	4.422946	0.017442	0.04128	0.037811	-1	307	226	594	410	501	183	397	275	417	396
ENSMUSG00000005716	chr15	Pvalb	78191114	78191694	1041	0.524705	13.97177	0.017442	0.04128	0.058022	1	242915	202711	263062	119608	194116	337609	360292	310810	434389	276977
ENSMUSG00000022797	chr16	Tfrc	32608920	32609036	6185	-0.63398	7.529875	0.017447	0.041284	0.084072	-1	2814	1195	4307	5021	5442	1652	4485	1558	3811	2286
ENSMUSG00000029545	chr5	Acads	1.15E+08	1.15E+08	2269	-0.49267	6.331852	0.017461	0.041309	0.050478	-1	1135	796	1463	2281	1915	886	1539	1219	1690	896
ENSMUSG00000008575	chr4	Nfib	82290173	82296811	14957	-0.36096	6.785046	0.017517	0.041436	0.027064	-1	1563	1557	3014	1803	2128	1366	1949	1529	2457	1582
ENSMUSG00000022617	chr15	Chkb	89416405	89416979	5805	-0.54915	8.167437	0.017528	0.041455	0.063388	-1	3669	2390	6125	8573	7370	3114	6193	3048	5806	3680
ENSMUSG00000036513	chr3	Commd2	57642904	57646876	4757	0.422388	3.476424	0.017536	0.041465	0.03079	1	128	143	177	130	164	190	312	207	277	177
ENSMUSG00000002580	chr11	Mien1	98437708	98438145	747	0.439319	4.725399	0.017554	0.0415	0.037843	1	368	349	396	284	332	494	716	495	650	426
ENSMUSG00000048581	chr3	E130311K13Rik	63914684	63915738	2398	-0.53123	2.180472	0.017579	0.041546	0.045769	-1	86	75	93	70	88	59	85	71	59	55
ENSMUSG00000062694	chr6	Cav3	1.12E+08	1.12E+08	1160	0.417502	5.910162	0.017579	0.041546	0.035759	1	797	572	903	870	945	1105	1578	882	1923	911
ENSMUSG00000033082	chr6	Clec1a	1.29E+08	1.29E+08	3268	-0.81368	1.145751	0.017615	0.041623	0.107708	-1	18	22	60	41	86	15	50	17	30	30
ENSMUSG00000014503	chr18	Pkd2l2	34409423	34409497	2666	-0.60859	0.681582	0.017654	0.041707	0.039732	-1	25	21	42	29	30	15	30	17	30	18
ENSMUSG00000029201	chr5	Ugdh	65413202	65414063	6799	0.495092	3.329897	0.017731	0.041882	0.045471	1	115	104	200	92	160	152	247	272	171	205
ENSMUSG00000073987	chr4	Ggh	20042052	20042282	1965	0.477004	3.042102	0.017789	0.042012	0.038843	1	122	93	130	92	95	144	212	180	199	130
ENSMUSG00000053062	chr16	Jam2	84774123	84774553	5872	-0.4446	4.93043	0.017796	0.042021	0.039812	-1	378	283	672	713	854	343	614	433	526	448
ENSMUSG00000042050	chr12	Wdr60	1.16E+08	1.16E+08	3725	-0.40434	4.128566	0.017856	0.042154	0.031171	-1	277	241	548	237	322	250	295	236	383	210
ENSMUSG00000054452	chr10	Aes	81559494	81559668	1411	-0.35783	9.360885	0.017885	0.042215	0.027229	-1	10949	8144	14304	12437	13345	8452	12967	9496	13516	8706
ENSMUSG00000037295	chr4	Ldlrap1	1.35E+08	1.35E+08	3829	0.445144	2.780327	0.017895	0.042232	0.033039	1	75	63	138	74	119	99	144	161	180	128
ENSMUSG00000042331	chr11	Specc1	61956779	61956889	13276	0.55208	1.754463	0.017909	0.042256	0.046525	1	30	28	68	41	50	46	78	80	67	79
ENSMUSG00000038216	chr11	Pnmt	98386450	98386866	1154	1.305396	0.932669	0.017935	0.042311	0.305741	1	8	7	19	22	27	16	21	14	168	29
ENSMUSG00000049038	chr10	Mterf2	85119435	85120814	1565	-0.46204	3.956339	0.017976	0.042399	0.041488	-1	237	175	292	368	363	206	351	156	266	216
ENSMUSG00000061273	chrX	Mmgt1	56585512	56589303	4234	-0.33949	5.69553	0.018005	0.042462	0.023397	-1	733	588	1412	950	1076	643	1120	715	961	764
ENSMUSG00000042116	chr4	Vwa1	1.56E+08	1.56E+08	3623	-0.45169	4.649223	0.018017	0.042482	0.041277	-1	474	432	647	316	407	336	456	306	551	302
ENSMUSG00000039831	chr3	Arhgap29	1.22E+08	1.22E+08	5088	-0.45349	3.962136	0.018032	0.04251	0.040103	-1	251	178	393	284	357	112	371	273	249	216
ENSMUSG00000018425	chr11	Dhx40	86768846	86770261	4233	-0.39303	4.240469	0.018095	0.042643	0.029833	-1	303	305	499	252	350	245	392	285	302	260
ENSMUSG00000089989	chr7	Flt3l	45131188	45131431	3712	0.49424	2.061428	0.018094	0.042643	0.037186	1	45	42	89	45	53	75	89	93	95	77
ENSMUSG00000030124	chr6	Lag3	1.25E+08	1.25E+08	2109	1.090969	-0.24052	0.018133	0.042717	0.150223	1	11	6	9	2	9	16	20	29	6	17
ENSMUSG00000042043	chr13	Tbca	94788943	94789002	503	0.433554	4.231396	0.018133	0.042717	0.036088	1	231	238	229	226	310	365	480	362	454	297
ENSMUSG00000012535	chr6	Tnpo3	29540827	29541866	10246	-0.32419	5.758339	0.018171	0.042798	0.021448	-1	815	692	1338	954	1065	690	1163	811	1061	707
ENSMUSG00000026839	chr2	Upp2	58567298	58567528	7053	0.690284	0.755698	0.018219	0.042905	0.05811	1	13	18	29	14	23	24	49	25	37	42
ENSMUSG00000017667	chr2	Zfp334	1.65E+08	1.65E+08	8205	-0.53467	2.230061	0.018243	0.042941	0.045848	-1	61	39	136	99	120	54	81	57	84	67
ENSMUSG00000018548	chr11	Trim37	87127077	87127494	7214	-0.40929	2.991492	0.018241	0.042941	0.028045	-1	115	103	230	136	149	88	142	114	159	117
ENSMUSG00000026657	chr2	Frmd4a	4017717	4018019	23350	0.548695	2.31276	0.018244	0.042941	0.053005	1	34	33	93	72	97	69	122	122	110	102
ENSMUSG00000090877	chr17	Hspa1b	34956436	34959238	2803	0.807823	1.830401	0.018266	0.042985	0.119247	1	29	26	24	33	90	68	51	82	97	91
ENSMUSG00000005506	chr2	Celf1	90940382	90940641	8446	-0.36961	6.448773	0.018275	0.042993	0.028621	-1	1457	974	2480	1317	1891	1047	1593	1248	2038	1138
ENSMUSG00000026005	chr1	Rpe	66700831	66701028	3113	-0.47149	3.396797	0.018279	0.042993	0.041754	-1	193	161	295	148	175	101	183	195	164	154
ENSMUSG00000027463	chr2	Slc52a3	1.52E+08	1.52E+08	2767	0.707775	0.392602	0.018279	0.042993	0.057746	1	13	7	29	11	15	28	25	29	32	20
ENSMUSG00000018923	chr11	Med11	70451919	70452063	1046	0.542367	2.288473	0.018312	0.043062	0.04706	1	49	68	68	47	72	93	130	95	113	84
ENSMUSG00000022560	chr15	Slc52a2	76538943	76539195	2700	0.5947	2.307741	0.018332	0.043103	0.063389	1	40	26	69	82	101	78	103	96	140	112
ENSMUSG00000036777	chr9	Anln	22331214	22333173	5421	-0.60804	1.437793	0.01834	0.043112	0.053142	-1	42	46	85	37	45	28	34	41	44	40
ENSMUSG00000062232	chr3	Rapgef2	79062516	79064561	14051	-0.4217	3.656441	0.018343	0.043112	0.032835	-1	146	146	372	213	321	141	269	162	221	192
ENSMUSG00000028328	chr4	Tmod1	46038935	46039309	3946	-0.34976	8.449726	0.018357	0.043138	0.026131	-1	5577	4131	9502	5697	7191	4699	6942	5046	6301	5068
ENSMUSG00000020873	chr11	Slc35b1	95384692	95385113	2223	0.337186	5.463839	0.018401	0.043219	0.022905	1	606	462	812	590	639	704	1145	817	1088	769
ENSMUSG00000025491	chr7	Ifitm1	1.41E+08	1.41E+08	1094	1.154443	-0.12563	0.018399	0.043219	0.183243	1	5	7	2	7	17	14	46	7	25	12

ENSMUSG00000076258	chr16	Gm23935	11144125	11144181	57	0.935023	6.986251	0.018399	0.043219	0.183447	1	2264	920	1978	1056	536	1765	2000	1267	6463	3980
ENSMUSG00000026544	chr1	Dusp23	1.73E+08	1.73E+08	1410	0.371698	5.753333	0.01844	0.0433	0.028636	1	669	426	898	841	983	911	1362	897	1340	1049
ENSMUSG00000040423	chr1	Rc3h1	1.61E+08	1.61E+08	11308	-0.40026	4.68842	0.018442	0.0433	0.031996	-1	438	326	779	367	487	307	406	489	522	305
ENSMUSG00000029471	chr5	Camkk2	1.23E+08	1.23E+08	4843	0.455113	2.872991	0.018472	0.043361	0.036061	1	73	61	121	87	157	116	179	168	189	115
ENSMUSG00000050447	chr2	Lypd6	50066429	50066584	3729	0.898172	0.861788	0.018481	0.043375	0.131979	1	2	22	23	22	26	33	55	32	31	48
ENSMUSG00000012117	chr4	Dhdds	1.34E+08	1.34E+08	3784	0.439192	3.490305	0.018486	0.04338	0.035598	1	102	113	162	199	178	169	259	241	287	215
ENSMUSG00000031448	chr8	Adprhl1	13235655	13235988	1820	0.461632	4.192933	0.018493	0.043388	0.042439	1	173	137	288	362	281	302	446	282	535	373
ENSMUSG00000056153	chr18	Socs6	88665224	88665382	8225	-0.34667	5.009582	0.018505	0.043409	0.023901	-1	433	382	931	536	696	372	622	452	673	488
ENSMUSG00000001436	chr10	Slc19a1	77032241	77032290	4644	0.46162	2.607484	0.018519	0.043435	0.034657	1	78	53	109	67	101	97	142	147	166	86
ENSMUSG00000003929	chr17	Zfp81	33329342	33335653	6639	-0.56676	1.699767	0.018531	0.043445	0.047358	-1	43	45	96	49	76	32	69	52	37	42
ENSMUSG00000036944	chr15	Tmem71	66526212	66527934	2931	0.600027	0.982132	0.018534	0.043445	0.044293	1	18	16	34	23	29	27	44	50	41	41
ENSMUSG00000038253	chr6	Hoxa5	52201754	52202831	1877	0.689417	0.709292	0.018529	0.043445	0.05419	1	15	16	18	20	23	24	46	24	38	39
ENSMUSG00000040564	chr7	Apoc1	19689484	19689636	537	1.639572	2.066772	0.018596	0.043584	0.518906	1	63	34	28	7	12	125	16	305	52	29
ENSMUSG00000064030	chr10	Wibg	1.29E+08	1.29E+08	1285	0.439461	3.360489	0.018619	0.04363	0.034369	1	127	126	164	125	136	202	250	183	284	153
ENSMUSG00000028621	chr4	Cyb5rl	1.07E+08	1.07E+08	7430	-0.40447	3.165825	0.018631	0.043651	0.028423	-1	134	103	199	181	203	96	168	142	198	106
ENSMUSG00000056144	chr7	Trim34a	1.04E+08	1.04E+08	4255	0.573233	1.491356	0.018642	0.043668	0.046357	1	29	26	48	31	41	46	64	80	53	48
ENSMUSG00000020741	chr11	Cluh	74649495	74649694	6502	-0.52141	7.110228	0.018646	0.043669	0.058026	-1	1739	1003	3392	3782	3722	1419	2496	1988	2654	1908
ENSMUSG00000030313	chr6	Dennd5b	1.49E+08	1.49E+08	10621	-0.52912	2.631241	0.018663	0.043701	0.050451	-1	70	65	179	110	181	49	130	93	127	70
ENSMUSG00000028538	chr4	St3gal3	1.18E+08	1.18E+08	2768	-0.37304	6.155531	0.018684	0.043742	0.029209	-1	1037	754	1776	1523	1491	812	1318	1013	1582	1015
ENSMUSG00000051107	chr13	Gm15440	51685529	51686246	1231	0.379564	5.925214	0.018689	0.043747	0.030012	1	847	626	1200	682	888	990	1441	1136	1877	930
ENSMUSG00000032643	chr4	Fhl3	1.25E+08	1.25E+08	1683	-0.47254	7.472912	0.018706	0.043779	0.047799	-1	2536	1738	5366	3356	4341	2493	2557	1869	4614	2199
ENSMUSG00000067629	chr17	Syngap1	26941384	26941518	6267	0.517917	1.70082	0.018714	0.04379	0.03733	1	30	34	63	36	46	55	70	78	76	56
ENSMUSG00000028601	chr4	Echdc2	1.08E+08	1.08E+08	2287	-0.39577	3.72862	0.018745	0.043856	0.028971	-1	221	182	318	211	269	208	244	217	209	150
ENSMUSG00000027194	chr2	Ttc17	94300767	94301867	8984	-0.3542	4.561152	0.018754	0.043869	0.024382	-1	315	307	732	358	471	308	474	343	445	324
ENSMUSG00000003617	chr3	Cp	19957054	19957429	9566	-0.50678	3.852765	0.018771	0.0439	0.050227	-1	201	168	518	214	320	215	211	285	185	160
ENSMUSG00000025229	chr19	Pitx3	46135685	46136605	1526	0.573753	2.156997	0.018813	0.043992	0.058762	1	41	22	83	60	86	54	99	94	152	84
ENSMUSG00000028447	chr4	Dctn3	41714798	41715238	1042	0.366549	4.589158	0.018869	0.044107	0.025979	1	303	294	387	332	328	397	600	455	627	403
ENSMUSG00000029591	chr5	Ung	1.14E+08	1.14E+08	2566	-0.63926	3.019642	0.018867	0.044107	0.080312	-1	104	57	148	250	244	79	165	105	149	87
ENSMUSG00000026640	chr1	Plxna2	1.95E+08	1.95E+08	17174	-0.49283	3.140261	0.018885	0.044136	0.044586	-1	98	85	310	171	203	94	198	127	140	111
ENSMUSG00000101102	chr1	Gm28609	1.33E+08	1.33E+08	463	-0.97165	0.599025	0.0189	0.044164	0.157281	-1	13	8	33	55	46	7	36	12	21	14
ENSMUSG00000098650	chr11	Gm28048	22834744	22837195	2746	0.425064	5.564885	0.01897	0.04432	0.037532	1	651	591	639	577	659	899	1374	784	1158	768
ENSMUSG00000032580	chr9	Rbm5	1.08E+08	1.08E+08	15434	0.345197	5.182281	0.018985	0.044347	0.024266	1	419	347	752	489	601	595	897	846	761	593
ENSMUSG00000031371	chrX	Haus7	73437315	73437565	1438	0.492563	3.532203	0.019005	0.044386	0.045593	1	145	162	196	107	131	212	254	259	300	193
ENSMUSG00000031119	chrX	Gpc4	52053021	52053726	2651	0.387611	4.06235	0.019011	0.044391	0.029304	1	169	145	390	219	273	239	463	289	377	359
ENSMUSG00000023805	chr17	Synj2	5941280	5941577	8342	-0.62911	4.598713	0.019021	0.044408	0.082461	-1	228	163	606	670	830	231	399	308	403	387
ENSMUSG00000025915	chr1	Sgk3	9798107	9798246	14311	-0.50137	2.750171	0.019042	0.044449	0.044209	-1	79	65	165	153	182	72	124	113	117	79
ENSMUSG00000099764	chr16	Rps10-ps2	20822145	20822640	496	0.561869	2.8631	0.019061	0.044486	0.057558	1	109	94	102	67	72	141	199	132	165	139
ENSMUSG00000026317	chr8	Cln8	14881335	14881860	7606	0.333998	4.493332	0.019219	0.044845	0.021687	1	236	214	424	339	404	372	512	446	562	393
ENSMUSG00000029146	chr5	Snx17	31193227	31193465	2791	0.324413	5.613342	0.019251	0.044913	0.021622	1	596	519	885	696	786	777	1120	970	1260	853
ENSMUSG00000098178	chr17	Yam1	39846958	39848788	1831	1.010189	11.65959	0.019258	0.04492	0.216967	1	42278	15994	55155	41972	18537	30894	47673	22480	165513	133555
ENSMUSG00000026825	chr2	Dnm1	32308471	32309064	5240	0.537332	3.201805	0.019269	0.04493	0.056948	1	70	72	212	111	160	114	176	234	209	235
ENSMUSG00000031373	chrX	Car5b	1.64E+08	1.64E+08	6354	1.315905	2.717547	0.019268	0.04493	0.347114	1	97	64	58	17	39	114	58	478	79	73
ENSMUSG00000061024	chr1	Rrs1	9545408	9547455	2048	0.373928	4.005079	0.019282	0.044953	0.026585	1	211	134	313	209	267	210	431	372	402	256
ENSMUSG00000003360	chr15	Ddx23	98645134	98646017	5452	-0.33231	6.273031	0.019304	0.044997	0.023362	-1	1158	968	1843	1393	1610	959	1483	1180	1624	1056
ENSMUSG00000037972	chr16	Snn	11066298	11066447	2902	0.578833	2.409239	0.019322	0.045031	0.058174	1	64	59	73	67	63	83	150	154	130	59
ENSMUSG00000034573	chr5	Ptpn13	1.03E+08	1.03E+08	8280	-0.74415	1.693128	0.019332	0.045046	0.096296	-1	23	23	118	70	106	37	51	45	46	33
ENSMUSG00000071662	chr19	Polr2g	8793129	8793404	868	0.358769	4.902481	0.019404	0.045205	0.025661	1	402	341	502	390	430	474	803	550	813	468
ENSMUSG00000018574	chr11	Acadvl	70010183	70010436	2686	-0.64213	8.306221	0.019432	0.045264	0.089337	-1	3162	2917	5201	11265	8851	3150	6355	3620	6256	3775
ENSMUSG00000020921	chr11	Tmem101	1.02E+08	1.02E+08	2021	0.388767	3.783092	0.019464	0.045331	0.028444	1	147	143	227	182	254	261	269	259	375	241
ENSMUSG00000022051	chr14	Bnip3l	66985239	66987775	3859	-0.34151	6.004404	0.019491	0.045383	0.024652	-1	1008	901	1565	1073	1200	787	1285	1026	1196	896
ENSMUSG00000039473	chr16	Ubn1	5050068	5050781	6455	-0.37097	5.4244	0.019504	0.045406	0.02867	-1	677	494	1360	620	868	457	775	678	926	617
ENSMUSG00000001833	chr9	Sept7	25252439	25252699	2538	-0.3594	6.244535	0.019528	0.045455	0.027576	-1	1137	1103	1925	1201	1488	797	1636	1179	1430	1100
ENSMUSG00000025856	chr5	Pdgfa	1.39E+08	1.39E+08	3119	0.392835	4.841263	0.019533	0.045458	0.03144	1	348	293	455	367	516	407	690	435	829	629
ENSMUSG00000017721	chr2	Pigt	1.64E+08	1.64E+08	3856	0.349339	5.403743	0.019554	0.045498	0.025282	1	465	430	773	624	711	658	834	868	1165	795
ENSMUSG00000007891	chr7	Ctsd	1.42E+08	1.42E+08	2519	0.370181	9.845316	0.019566	0.045519	0.029999	1	11398	9328	15517	13598	14306	15948	19598	21046	22757	15031
ENSMUSG00000052248	chr2	Zeb2os	45111138	45111302	1388	0.61482	1.139693	0.019595	0.04558	0.053365	1	30	18	40	19	26	44	51	49	38	44
ENSMUSG00000043962	chr4	Thrap3	1.26E+08	1.26E+08	9234	-0.35658	6.029825	0.019608	0.045601	0.026911	-1	940	697	1923	1128	1411	772	1293	933	1306	966
ENSMUSG00000057497	chr6	Fam136a	86365683	86365819	1605	-0.38224	3.843961	0.019613	0.045605	0.028072	-1	229	178	311	293	283	189	335	198	271	157
ENSMUSG00000022946	chr16	Dopey2	93711907	93712068	7313	-0.45234	4.887544	0.019617	0.045607	0.042567	-1	476	333	1137	361	581	353	503	513	584	338
ENSMUSG00000021418	chr13	Rpp40	35893472	35896925	6540	-0.43976	3.438578	0.019643	0.045657	0.037059	-1	202	168	280	140	197	138	247	152	176	128
ENSMUSG00000028541	chr4	B4galt2	1.18E+08	1.18E+08	5031	0.454366	2.289923	0.019667	0.045705	0.032124	1	46	50	94	57	81	73	110	98	128	96
ENSMUSG00000101249	chr1	Gm29216	24615706	24616197	492	-0.51612	3.987778	0.019719	0.045819	0.054403	-1	165	167	308	405	479	193	328	184	325	179
ENSMUSG00000070604	chr7	Vsig10l	43463151	43463272	3730	0.709042	0.555446	0.019727	0.04583	0.061632	1	19	5	20	19	20	18	37	26	40	33
ENSMUSG00000055041	chr15	Commd5	76899910	76899992	1060	0.436828	3.222904	0.019741	0.045853	0.03394	1	121	104	143	122	128	141	253	148	230	201
ENSMUSG00000096255	chr17	Dynlt1b	6430112	6430238	768	-1.46367	1.465519	0.019776	0.045927	0.419143	-1	79	52	51	25	103	36	45	43	3	1

ENSMUSG00000029501	chr5	Ankle2	1.1E+08	1.1E+08	5259	-0.33143	4.929613	0.019821	0.046022	0.022173	-1	434	379	828	489	648	349	633	429	615	459
ENSMUSG00000057605	chr19	Gm6807	45450308	45451195	888	0.932896	-0.06265	0.019858	0.046102	0.092775	1	7	13	7	12	5	19	30	19	21	12
ENSMUSG00000068686	chr2	Cd59b	1.04E+08	1.04E+08	1300	0.580943	1.847201	0.019955	0.046318	0.055546	1	58	24	43	45	51	70	95	73	71	68
ENSMUSG00000012705	chr8	Retn	3655770	3655843	1579	1.506973	4.662714	0.01996	0.046322	0.467609	1	400	269	143	45	56	488	219	1921	244	335
ENSMUSG00000027833	chr3	Shox2	66971727	66973907	3311	0.700138	1.586936	0.020011	0.046432	0.083309	1	31	35	57	18	36	51	54	88	54	70
ENSMUSG00000015804	chr5	Med28	45520221	45520484	5010	0.369669	5.281412	0.020017	0.046438	0.028256	1	522	474	604	481	571	691	988	762	947	619
ENSMUSG00000049940	chr3	Pgrmc2	41066326	41068724	3242	0.348607	5.152415	0.020029	0.046458	0.024966	1	480	386	663	410	561	542	812	803	845	626
ENSMUSG00000017376	chr11	Nlk	78567168	78568975	5447	-0.38975	3.511203	0.020052	0.046503	0.027768	-1	179	153	334	161	221	136	198	188	202	167
ENSMUSG00000020638	chr12	Cmpk2	26469204	26470026	3198	0.688128	1.699081	0.020058	0.046508	0.083318	1	37	25	58	31	44	49	125	78	35	65
ENSMUSG00000032549	chr9	Rab6b	1.03E+08	1.03E+08	5031	-0.50652	3.217609	0.020074	0.046538	0.048906	-1	103	106	291	167	241	100	174	193	130	98
ENSMUSG00000054978	chr9	Kbtbd13	65388684	65391652	2969	-0.62947	4.570571	0.020082	0.046548	0.084295	-1	279	172	527	719	700	197	519	209	446	369
ENSMUSG00000047793	chr1	Sned1	93235841	93236201	9491	0.548763	3.846437	0.020089	0.046556	0.062748	1	138	110	423	116	209	303	453	321	268	200
ENSMUSG00000041773	chr13	Enc1	97241105	97241529	4742	0.764217	1.518337	0.020117	0.046613	0.101401	1	23	21	20	40	58	35	79	93	54	54
ENSMUSG00000030403	chr7	Vasp	19256929	19257754	2438	0.524374	5.016631	0.020123	0.046618	0.05853	1	492	328	692	232	388	650	598	623	1095	518
ENSMUSG00000002342	chr8	Tmem161a	70172356	70172440	3673	0.339725	6.371912	0.020176	0.046733	0.024822	1	975	811	1543	1201	1384	1326	1862	1531	2284	1488
ENSMUSG00000021936	chr14	Mapk8	33377898	33382324	9255	-0.33649	5.193651	0.020179	0.046733	0.023427	-1	510	457	1027	632	717	431	793	496	740	528
ENSMUSG00000058704	chr17	Memo1	74200706	74201325	1513	-0.35654	5.003181	0.020192	0.046753	0.026512	-1	542	472	739	548	545	389	640	480	709	387
ENSMUSG00000095464	chr16	Gm21987	38347040	38347207	456	0.427463	6.091969	0.020202	0.046768	0.039281	1	966	845	924	837	909	1253	1941	1217	1715	1079
ENSMUSG00000063684	chr2	Gm13910	1.09E+08	1.09E+08	1428	-0.536	4.872581	0.020241	0.04685	0.061377	-1	313	300	565	897	739	300	662	353	567	354
ENSMUSG00000099689	chr7	Unspecified	29908223	29908651	3208	-0.46965	2.77603	0.020257	0.046879	0.038554	-1	94	79	207	108	164	63	123	98	118	116
ENSMUSG00000089837	chr15	Npcd	79789675	79789916	1453	-0.77078	0.949659	0.020261	0.046882	0.089671	-1	25	15	53	47	52	20	36	19	14	32
ENSMUSG00000022562	chr15	Oplah	76296597	76296781	5596	-0.4711	5.703168	0.02027	0.046894	0.047846	-1	690	457	1119	1481	1202	569	901	856	924	734
ENSMUSG00000050777	chr1	Tmem37	1.2E+08	1.2E+08	1311	0.607907	5.261692	0.020279	0.046905	0.07998	1	356	218	570	606	765	942	729	454	1512	605
ENSMUSG00000030189	chr6	Ybx3	1.31E+08	1.31E+08	1862	-0.41739	9.847541	0.020283	0.046906	0.038573	-1	16419	15516	22202	13133	15520	10692	17684	11824	20568	12517
ENSMUSG00000031633	chr8	Slc25a4	46206797	46207620	2353	-0.44469	11.85711	0.02032	0.046985	0.043829	-1	54067	40147	70499	90618	89702	42044	80916	42228	79901	48935
ENSMUSG00000024853	chr19	Sf3b2	5273923	5274527	3231	0.335314	6.759014	0.020341	0.047024	0.024404	1	1275	1096	1955	1629	1752	1815	2455	2126	2696	1928
ENSMUSG00000056383	chr7	AI987944	41372923	41375374	2671	-0.43609	3.382866	0.020382	0.047112	0.036239	-1	141	174	254	169	212	143	192	108	198	160
ENSMUSG00000048949	chrX	Gm6206	1.03E+08	1.03E+08	2199	-0.46376	2.558441	0.020399	0.047144	0.037576	-1	99	93	147	107	87	66	106	86	114	76
ENSMUSG00000031129	chr9	Slc9a9	94669909	94670236	5679	0.558719	2.3681	0.020452	0.047256	0.057964	1	59	35	119	57	70	125	94	108	100	103
ENSMUSG00000046380	chr15	Jrk	74702301	74707864	5853	-0.62927	1.234915	0.020491	0.047339	0.057698	-1	44	22	51	54	50	28	37	21	35	39
ENSMUSG00000004677	chr8	Myo9b	71272714	71272829	7297	0.430889	3.673689	0.020503	0.047358	0.036651	1	110	137	258	159	217	218	235	307	281	260
ENSMUSG00000032375	chr9	Aph1b	66775202	66779380	5163	-0.5059	2.058382	0.020521	0.047391	0.03931	-1	63	55	125	57	92	53	74	65	56	56
ENSMUSG00000028980	chr4	H6pd	1.5E+08	1.5E+08	5236	-0.39331	6.158136	0.020537	0.04742	0.033551	-1	1226	902	2248	978	1308	1050	1290	992	1461	854
ENSMUSG00000030523	chr7	Trpm1	64153835	64154106	11512	-0.98102	0.065995	0.020559	0.047463	0.146512	-1	19	3	25	21	36	4	24	6	18	8
ENSMUSG00000022559	chr15	Fbxl6	76535730	76535963	1712	0.415288	2.890689	0.020563	0.047463	0.029642	1	87	78	123	89	125	129	154	162	182	130
ENSMUSG00000040297	chr1	Suco	1.62E+08	1.62E+08	8928	-0.37875	3.421367	0.020602	0.047536	0.026449	-1	163	160	273	155	216	125	215	173	189	145
ENSMUSG00000075227	chr19	Znhit2	6061192	6062472	1281	0.483825	3.148001	0.020599	0.047536	0.043309	1	138	98	137	85	114	123	195	204	249	166
ENSMUSG00000003992	chr13	Ssbp2	91460283	91460447	7961	-0.374	3.838066	0.020608	0.047543	0.026989	-1	180	212	406	222	289	175	315	192	278	186
ENSMUSG00000038323	chr1	1700066M21Rik	57377620	57377946	3235	-0.5509	1.575781	0.020624	0.04757	0.045539	-1	38	54	87	45	52	36	52	41	46	38
ENSMUSG00000059540	chr2	Tcea2	1.82E+08	1.82E+08	2704	0.43727	2.40405	0.020627	0.04757	0.029489	1	65	52	93	70	73	82	123	104	145	93
ENSMUSG00000024911	chr19	Fibp	5460607	5460778	1240	0.389345	4.373058	0.020667	0.047645	0.030173	1	259	271	338	245	285	367	467	427	522	347
ENSMUSG00000056260	chr3	Lrif1	1.07E+08	1.07E+08	9192	-0.47963	2.884845	0.020665	0.047645	0.043658	-1	119	126	176	114	138	58	128	131	143	103
ENSMUSG00000074521	chr2	Gm14327	1.78E+08	1.78E+08	1451	-0.82544	0.206242	0.020671	0.047646	0.091091	-1	7	19	35	25	24	15	19	9	21	6
ENSMUSG00000040389	chr3	Wdr47	1.09E+08	1.09E+08	4394	-0.4409	2.697129	0.020683	0.047665	0.033293	-1	87	79	171	128	136	68	104	99	116	106
ENSMUSG00000034957	chr7	Cebpa	35119293	35121926	2634	1.100076	4.499259	0.020686	0.047666	0.257844	1	388	270	176	76	118	420	301	1258	362	347
ENSMUSG00000028070	chr3	Apoa1bp	88056520	88056776	908	0.334899	5.189178	0.020694	0.047674	0.023151	1	414	411	641	534	571	558	851	725	990	616
ENSMUSG00000029090	chr5	Gpr125	49959951	49961514	4475	-0.3514	4.154089	0.020703	0.047687	0.023838	-1	253	188	473	321	405	206	372	286	305	259
ENSMUSG00000009566	chr2	Fpgs	32682609	32683468	3802	0.432126	3.039848	0.020769	0.047831	0.032909	1	111	78	148	105	112	117	245	181	209	116
ENSMUSG00000020902	chr11	Ntn1	68209364	68213334	6277	-0.53946	3.904444	0.020789	0.047868	0.059753	-1	154	143	485	279	447	155	223	279	191	237
ENSMUSG00000028191	chr3	Bcl10	1.46E+08	1.46E+08	1760	0.394838	3.539933	0.020815	0.047914	0.029569	1	165	90	218	138	201	190	305	245	306	165
ENSMUSG00000038335	chr11	Tsr1	74898071	74898215	3837	-0.35474	4.952508	0.020816	0.047914	0.026147	-1	527	437	807	438	579	446	585	502	540	391
ENSMUSG00000055093	chr6	Gm8430	1.22E+08	1.22E+08	471	0.737941	2.232066	0.020866	0.048021	0.101663	1	65	62	46	47	37	121	152	65	127	62
ENSMUSG00000004626	chr8	Stxbp2	3630955	3631204	4159	0.591131	2.048854	0.020923	0.048128	0.060184	1	49	44	64	41	57	79	106	123	86	46
ENSMUSG00000020196	chr10	Cabin1	75646110	75646687	7460	0.425734	3.793307	0.020923	0.048128	0.037034	1	133	89	314	203	250	227	273	305	361	266
ENSMUSG00000079109	chr5	Pms2	1.44E+08	1.44E+08	8442	-0.54223	2.254607	0.020923	0.048128	0.053027	-1	79	94	116	57	91	56	101	58	73	62
ENSMUSG00000037463	chr7	Fbxo27	28692849	28692972	3062	1.063052	-0.19413	0.020946	0.048171	0.148293	1	16	3	10	3	7	22	15	9	21	24
ENSMUSG00000035704	chr7	Alg8	97371606	97371732	2794	0.58813	1.951387	0.020951	0.048176	0.058089	1	44	38	62	59	34	50	101	108	83	70
ENSMUSG00000000339	chr3	Rtca	1.16E+08	1.16E+08	1880	-0.32672	4.644064	0.020996	0.048268	0.021521	-1	381	317	654	395	511	340	490	355	537	316
ENSMUSG00000032633	chr11	Flcn	59791408	59792811	4322	-0.32717	5.674584	0.020999	0.048268	0.022774	-1	824	578	1322	889	1019	679	906	726	1071	754
ENSMUSG00000000359	chr2	Rem1	1.53E+08	1.53E+08	2156	0.570498	1.317595	0.021005	0.048273	0.043179	1	27	27	45	27	27	40	56	40	78	47
ENSMUSG00000041977	chr3	Arhgef11	87617559	87618792	7918	-0.46073	4.961844	0.021015	0.04828	0.045261	-1	394	234	996	665	784	340	499	447	656	459
ENSMUSG00000051007	chr7	Pddc1	1.41E+08	1.41E+08	2871	0.394865	3.051998	0.021014	0.04828	0.02661	1	96	93	150	111	115	147	204	155	207	137
ENSMUSG00000014856	chr8	Tmem208	1.05E+08	1.05E+08	1511	0.403824	4.236978	0.021024	0.048292	0.032619	1	274	229	307	192	264	356	450	343	472	324
ENSMUSG00000070643	chr1	Sox13	1.33E+08	1.33E+08	4312	-0.47924	2.781211	0.021027	0.048292	0.040975	-1	93	75	182	138	162	92	95	77	137	111
ENSMUSG00000032294	chr9	Pkm	59656368	59656649	2599	0.384056	11.97475	0.021108	0.048456	0.033147	1	56740	32851	78106	53898	62813	65968	87830	76645	127850	64081

ENSMUSG00000050953	chr10	Gja1	56377300	56377518	3105	0.444067	3.788095	0.021111	0.048456	0.039932	1	108	142	263	178	262	228	378	349	247	233
ENSMUSG00000071657	chr19	Bscl2	8837467	8837864	5897	0.594449	4.444724	0.021105	0.048456	0.075613	1	295	243	358	201	261	339	351	836	466	342
ENSMUSG00000086725	chr11	A630052C17Rik	29170909	29172951	2203	-0.70352	0.305094	0.021114	0.048456	0.054308	-1	24	17	34	20	18	11	18	21	19	10
ENSMUSG00000029209	chr5	Gnpda2	69573108	69573156	6858	-0.52625	1.961091	0.021159	0.048551	0.043616	-1	48	61	106	68	80	41	58	55	61	66
ENSMUSG00000034839	chr9	Larp6	60712989	60713405	2440	0.638788	1.372241	0.021186	0.048605	0.064254	1	18	26	35	36	40	62	69	36	50	53
ENSMUSG00000056498	chr3	Tmem154	84666192	84666415	4738	0.81158	0.322222	0.021189	0.048605	0.079095	1	16	8	16	16	9	20	31	39	29	13
ENSMUSG00000042804	chr4	Gpr153	1.52E+08	1.52E+08	3909	0.436484	2.95623	0.021207	0.048636	0.035619	1	63	69	155	100	151	136	166	153	185	156
ENSMUSG00000021794	chr14	Glud1	34310727	34311342	4089	-0.38883	6.943033	0.021216	0.048649	0.033516	-1	1478	1346	2903	2853	2867	1449	2462	1897	2305	1689
ENSMUSG00000034401	chr4	Spata6	1.12E+08	1.12E+08	5616	0.489099	1.917431	0.021222	0.048654	0.035406	1	45	32	54	54	59	62	105	77	81	66
ENSMUSG00000033022	chr18	Cdo1	46713205	46713961	1530	1.551789	5.170328	0.021274	0.048766	0.505508	1	571	362	212	49	82	683	281	2862	310	454
ENSMUSG00000061479	chr7	Snrpa	27187005	27187364	1754	0.352607	4.804783	0.021282	0.048767	0.025619	1	403	254	469	413	415	492	666	530	731	446
ENSMUSG00000062006	chr3	Rpl34	1.31E+08	1.31E+08	1179	0.431075	6.725086	0.021282	0.048767	0.041081	1	1460	1390	1566	1249	1268	2042	2829	1951	2662	1653
ENSMUSG00000094130	chr14	Rpp14	8090078	8090554	477	-0.3703	3.76496	0.021317	0.048839	0.026799	-1	226	198	329	228	233	173	305	204	250	157
ENSMUSG00000007867	chr12	Ift43	86082561	86082640	775	0.428177	2.836234	0.021322	0.048841	0.031464	1	79	81	121	76	124	120	202	125	169	125
ENSMUSG00000025737	chr17	Wdr24	25823627	25824686	3432	-0.35753	3.882102	0.021344	0.048882	0.024708	-1	240	167	363	276	290	151	279	222	306	227
ENSMUSG00000037089	chr17	Slc35b2	45563964	45564773	2326	0.342024	4.689057	0.021347	0.048882	0.023728	1	355	272	466	350	363	423	654	493	584	469
ENSMUSG00000021474	chr13	Sfxn1	54071845	54071932	2811	0.880742	2.806543	0.021357	0.048888	0.159945	1	106	84	82	37	57	160	113	304	107	98
ENSMUSG00000038733	chr1	Wdr26	1.81E+08	1.81E+08	7848	-0.34248	7.10969	0.021356	0.048888	0.026031	-1	2057	1643	3916	2138	2984	1779	2759	1956	2874	1861
ENSMUSG00000039427	chr16	Alg1	5233621	5233857	2682	0.346802	3.915879	0.021396	0.04896	0.022738	1	199	143	271	217	231	250	360	313	393	227
ENSMUSG00000042644	chr17	Itpr3	27057304	27057674	8990	-0.59282	2.044745	0.021393	0.04896	0.061553	-1	37	39	143	97	94	39	68	58	76	54
ENSMUSG00000021774	chr14	Ube2e1	18282722	18283439	4457	-0.40952	6.065957	0.021422	0.049011	0.037035	-1	1184	1127	1735	862	1134	775	1245	1016	1420	861
ENSMUSG00000022570	chr15	Tsta3	75924684	75924994	1311	-0.36912	4.271158	0.021439	0.049042	0.027822	-1	312	318	390	297	384	244	367	300	345	274
ENSMUSG00000022911	chr16	Arl13b	62793685	62795708	5087	-0.53902	1.824944	0.021447	0.049051	0.04636	-1	53	52	81	67	74	32	67	52	44	60
ENSMUSG00000021218	chr13	Gdi2	3538075	3538343	2681	0.331001	6.801939	0.021481	0.04912	0.024213	1	1336	1192	2185	1582	1658	1894	2649	2209	2679	1916
ENSMUSG00000039202	chr7	Abhd2	79273201	79273339	10571	0.53538	2.876598	0.02153	0.049224	0.057874	1	55	42	158	102	144	85	172	177	202	152
ENSMUSG00000024012	chr17	Mtch1	29332072	29332778	2878	0.389317	6.321739	0.021554	0.049271	0.033421	1	823	866	1125	1355	1309	1251	1949	1547	2063	1506
ENSMUSG00000043421	chr6	Hilpda	29272488	29272608	1103	0.555963	1.922472	0.02157	0.049298	0.048404	1	43	41	38	48	63	54	101	86	102	61
ENSMUSG00000002064	chr11	Sdf2	78245746	78246170	1515	0.381567	5.920127	0.021591	0.049339	0.031744	1	889	693	1031	676	849	1067	1589	1092	1604	958
ENSMUSG00000005533	chr7	Igf1r	67952859	67952952	4489	-0.74017	1.219053	0.021632	0.049423	0.091989	-1	18	21	90	44	66	16	35	23	44	35
ENSMUSG00000031967	chr8	Afg3l1	1.23E+08	1.23E+08	4757	-0.32286	5.893948	0.021648	0.049452	0.02263	-1	928	730	1388	1062	1225	774	1168	837	1228	844
ENSMUSG00000080836	chr5	Gm6444	1.23E+08	1.23E+08	458	0.603714	1.248732	0.021668	0.049489	0.052492	1	28	16	43	34	24	44	80	38	56	34
ENSMUSG00000030243	chr6	Recql	1.42E+08	1.42E+08	7510	-0.41298	2.777499	0.021679	0.0495	0.029309	-1	126	82	154	118	140	83	117	104	128	97
ENSMUSG00000030884	chr7	Uqcrc2	1.21E+08	1.21E+08	2506	-0.47626	8.771328	0.02168	0.0495	0.051181	-1	5856	4150	8757	11525	11250	4700	10181	5191	8551	5617
ENSMUSG00000031728	chr8	Zfp821	1.1E+08	1.1E+08	2127	0.444189	2.452458	0.021692	0.049519	0.032832	1	63	47	111	80	68	77	134	112	142	103
ENSMUSG00000020598	chr12	Nrcam	44328885	44329096	7581	0.718341	0.38358	0.021728	0.049593	0.060093	1	10	13	28	11	11	27	31	28	24	23
ENSMUSG00000061848	chr15	Gm5805	81972390	81972845	456	0.475745	2.293968	0.021786	0.049715	0.037105	1	60	52	84	63	60	92	129	107	112	69
ENSMUSG00000002320	chr14	Tm9sf1	55635965	55636612	3880	0.343654	4.373764	0.021791	0.049719	0.024025	1	233	168	390	317	384	317	509	431	525	343
ENSMUSG00000055489	chr7	Ano5	51511029	51511250	7785	-0.41223	7.724207	0.021798	0.049727	0.03827	-1	2799	2007	6472	4158	4901	2414	5191	2747	3564	2925
ENSMUSG00000022914	chr16	Brwd1	95992092	95993977	20280	-0.34851	4.952715	0.021852	0.04984	0.025425	-1	427	327	934	530	670	404	550	433	676	433
ENSMUSG00000060681	chrX	Slc9a6	56609757	56609820	4961	-0.32679	5.396232	0.021862	0.049856	0.022812	-1	588	550	1112	726	833	500	823	610	809	673
ENSMUSG00000061882	chr5	Ccdc62	1.24E+08	1.24E+08	4306	0.437492	2.309373	0.021909	0.049954	0.030496	1	53	47	87	64	82	77	113	114	125	81
ENSMUSG00000085665	chr11	Gm12059	23067998	23068406	3105	-0.62327	1.194545	0.021919	0.049967	0.058307	-1	39	46	46	32	45	32	37	25	32	30
ENSMUSG00000024544	chr18	Ldlrad4	67933257	67933388	2493	-0.64019	1.906968	0.021959	0.050051	0.072322	0	52	24	114	75	112	38	58	34	77	55
ENSMUSG00000022203	chr14	Efs	54916543	54917532	3571	0.589907	1.757558	0.021973	0.050074	0.059948	0	29	28	61	45	50	51	59	89	65	85
ENSMUSG00000058331	chr13	Zfp85	67747800	67749722	2312	-0.63018	0.843876	0.021986	0.050094	0.053816	0	37	20	47	33	29	16	37	16	30	24
ENSMUSG00000046314	chr12	Stxbp6	44852488	44855877	4855	-0.5105	2.613375	0.021994	0.050103	0.048616	0	73	97	164	106	134	71	73	117	126	66
ENSMUSG00000101655	chr6	2310040G24Rik	86483376	86483699	775	-0.4059	6.452152	0.022023	0.050161	0.036912	0	1562	1495	1892	1311	1510	1208	1909	1192	1569	1052
ENSMUSG00000015747	chr3	Vps45	95999832	96000151	3991	0.440865	3.271481	0.022066	0.050251	0.036375	0	117	124	150	116	127	175	256	214	205	151
ENSMUSG00000026926	chr2	Pmpca	26389339	26389432	4282	-0.33331	7.587113	0.0221	0.05032	0.025077	0	2974	2449	4884	3163	3935	2458	4112	2749	3972	2469
ENSMUSG00000032403	chr9	2300009A05Rik	63394447	63394675	2000	0.44119	2.736144	0.022134	0.050389	0.033783	0	78	59	119	107	84	107	167	121	199	105
ENSMUSG00000101970	chr7	RP23-32A8.1	73544036	73544410	3778	0.409807	2.812101	0.022157	0.050432	0.028481	0	85	70	132	93	98	98	163	146	185	132
ENSMUSG00000038552	chr5	Fndc4	31292255	31293486	2261	0.579361	0.976663	0.022205	0.050532	0.038971	0	22	18	28	20	31	33	55	42	43	30
ENSMUSG00000024048	chr17	Myl12a	70993656	70994784	3201	0.436462	7.591151	0.022226	0.050572	0.043162	0	1775	1723	2789	3830	3021	3011	5203	3345	5227	3707
ENSMUSG00000021591	chr13	Glrx	75839868	75840175	1345	-0.41179	3.967321	0.022237	0.050588	0.03473	0	226	156	323	373	364	202	326	190	315	201
ENSMUSG00000021901	chr14	Bap1	31251450	31251654	4682	-0.32039	5.859794	0.022243	0.050593	0.022418	0	850	658	1458	1064	1240	743	1113	884	1235	777
ENSMUSG00000057193	chr9	Slc44a2	21337828	21337962	3456	0.343961	8.189236	0.022255	0.050604	0.026898	0	3481	2578	6545	3889	4752	4896	6601	5318	7544	5460
ENSMUSG00000081406	chr2	Rps6-ps4	75191073	75191822	750	0.42573	4.105252	0.022255	0.050604	0.036791	0	222	232	249	194	234	335	464	320	415	261
ENSMUSG00000001521	chr6	Tulp3	1.28E+08	1.28E+08	6704	0.384673	3.348023	0.022283	0.050658	0.027516	0	118	101	195	125	170	140	244	188	252	220
ENSMUSG00000030726	chr7	Pold3	1E+08	1E+08	4134	0.429286	2.657695	0.022292	0.050671	0.032161	0	77	53	119	90	89	123	141	125	136	116
ENSMUSG00000056666	chr6	Retsat	72598475	72598796	3537	-0.58343	5.01244	0.022312	0.050707	0.075436	0	332	288	561	1103	864	348	582	455	556	425
ENSMUSG00000006717	chr13	Acot13	24817948	24818191	721	-0.43637	5.946907	0.022338	0.050758	0.042591	0	804	747	1173	1604	1346	779	1401	722	1160	795
ENSMUSG00000029185	chr5	Fam114a1	64970071	64970144	2964	0.40992	3.18629	0.022349	0.050773	0.032118	0	77	95	189	123	148	164	237	179	177	172
ENSMUSG00000074656	chr2	Eif2s2	1.55E+08	1.55E+08	6755	-0.42433	7.51812	0.022356	0.05078	0.040914	0	3110	3215	4324	2574	3255	2492	4242	2236	3382	2155
ENSMUSG00000026433	chr1	Rab29	1.32E+08	1.32E+08	1468	0.462987	2.402683	0.022373	0.050803	0.036029	0	62	58	78	55	94	92	122	95	147	93
ENSMUSG00000085408	chr4	C530005A16Rik	1.17E+08	1.17E+08	2436	-0.52908	1.753523	0.022373	0.050803	0.046721	0	46	52	75	75	60	41	64	45	70	29

ENSMUSG00000026473	chr1	Glul	1.54E+08	1.54E+08	3323	0.521532	8.867831	0.022475	0.051016	0.062083	0	3054	4222	12224	6013	7096	9399	10601	12085	7765	9023
ENSMUSG00000055850	chr6	Rnf181	72359714	72360642	2070	0.372564	5.408527	0.022473	0.051016	0.030099	0	608	512	734	470	581	728	1070	895	1006	679
ENSMUSG00000020747	chr11	2310067B10Rik	1.16E+08	1.16E+08	5920	-0.40681	6.206038	0.022523	0.051115	0.03708	0	1031	625	2027	1534	1835	774	1369	1128	1551	1045
ENSMUSG00000021018	chr16	Polr2h	20717665	20717994	1448	0.469136	3.250594	0.022545	0.051157	0.042033	0	125	116	120	128	121	179	208	205	262	143
ENSMUSG00000029455	chr5	Aldh2	1.22E+08	1.22E+08	4704	0.538229	7.368912	0.022595	0.051262	0.065964	0	1295	1147	2305	3180	3118	2295	3837	4899	3486	3232
ENSMUSG00000050164	chr15	Mchr1	81235499	81235855	2188	-1.06481	2.273499	0.022625	0.051321	0.242218	0	53	45	106	187	133	46	53	21	170	12
ENSMUSG00000026915	chr2	Strbp	37483228	37483845	18487	-0.38263	4.32519	0.022636	0.051337	0.03063	0	306	310	580	241	396	233	399	295	372	292
ENSMUSG00000033365	chr4	Ipo13	1.18E+08	1.18E+08	4207	-0.36871	7.801399	0.022696	0.051464	0.031048	0	2969	2559	5871	4623	4623	2580	4495	2884	5303	2929
ENSMUSG00000069678	chr6	Pcgf1	83077869	83078238	1471	0.473468	2.582721	0.022718	0.051505	0.039119	0	75	62	90	67	98	114	183	115	117	95
ENSMUSG00000009741	chr9	Ubp1	1.14E+08	1.14E+08	3850	-0.32476	4.473301	0.022738	0.051541	0.021359	0	337	234	583	388	483	287	435	357	437	289
ENSMUSG00000030279	chr6	C2cd5	1.43E+08	1.43E+08	4468	0.390456	3.448148	0.022746	0.051552	0.029513	0	99	98	203	168	198	187	304	222	247	167
ENSMUSG00000076240	chr5	Mir702	1.37E+08	1.37E+08	109	0.567298	1.353534	0.022758	0.05157	0.045819	0	28	19	39	39	33	37	49	50	81	50
ENSMUSG00000031461	chr8	Myom2	15057653	15057739	8853	0.370235	10.79531	0.022786	0.051624	0.031584	0	21790	14748	36227	24612	30176	24746	47745	29673	54771	30985
ENSMUSG00000041718	chrX	Alg13	1.44E+08	1.44E+08	5964	-0.50672	1.891645	0.022817	0.051686	0.040674	0	39	51	109	62	89	40	75	48	64	48
ENSMUSG00000042015	chr13	Wdr41	94976344	94976589	5029	-0.32933	4.911746	0.022828	0.051701	0.023144	0	464	445	737	482	545	361	593	454	609	431
ENSMUSG00000022217	chr14	Emc9	55581516	55581743	2465	0.371573	4.473314	0.022836	0.051712	0.028767	0	286	203	301	361	381	371	555	414	551	394
ENSMUSG00000038368	chr4	Focad	88094629	88094675	11311	-0.35815	3.751199	0.022857	0.051751	0.02462	0	195	139	371	245	292	161	231	208	285	191
ENSMUSG00000060373	chr14	Hnrnpc	52073380	52075160	2869	0.329524	6.285776	0.022873	0.051777	0.024259	0	962	802	1451	1120	1222	1292	1983	1518	1745	1390
ENSMUSG00000024293	chr18	Esco1	10566602	10567646	4572	-0.36855	3.621413	0.022902	0.051821	0.026816	0	187	177	313	193	240	140	244	173	292	146
ENSMUSG00000052560	chr15	Cpne8	90487482	90489175	4164	0.619944	2.019015	0.022901	0.051821	0.072393	0	30	35	64	41	85	70	142	105	63	57
ENSMUSG00000099083	chr15	Atf7	1.03E+08	1.03E+08	10988	-0.40573	5.511905	0.022904	0.051821	0.036486	0	585	406	1573	779	1100	515	934	635	935	616
ENSMUSG00000071866	chr11	Ppia	6415443	6415979	3508	0.487264	6.851431	0.022917	0.051832	0.054009	0	1677	1551	1779	1012	1375	2481	3075	2281	2766	1677
ENSMUSG00000074846	chr2	Gm10774	1.27E+08	1.27E+08	204	0.563356	1.201924	0.022916	0.051832	0.043122	0	27	15	35	35	30	36	49	51	53	47
ENSMUSG00000026718	chr2	Stam	14074098	14074336	8386	-0.37102	3.658296	0.022939	0.051874	0.026655	0	178	139	362	219	272	135	264	221	222	166
ENSMUSG00000044026	chr19	Slc35g1	38395980	38396301	3471	-0.60566	1.055081	0.022975	0.051938	0.054439	0	37	27	58	22	51	16	40	28	30	30
ENSMUSG00000086741	chr8	Gm15816	23138794	23139575	1688	0.861868	1.721008	0.022974	0.051938	0.155226	0	24	7	89	46	31	72	37	89	115	54
ENSMUSG00000071369	chr10	Map3k5	19934472	19935074	6262	0.44677	3.313174	0.022986	0.051954	0.040113	0	123	61	165	155	177	127	277	228	239	178
ENSMUSG00000027694	chr3	Gm8325	60877014	60877046	464	-0.64104	0.646	0.023002	0.051982	0.050224	0	19	24	35	26	40	20	26	13	24	21
ENSMUSG00000029404	chr5	Arl6ip4	1.24E+08	1.24E+08	1438	0.353961	5.022138	0.023037	0.052052	0.026708	0	448	380	509	419	478	564	782	592	829	560
ENSMUSG00000020917	chr11	Acly	1E+08	1E+08	5279	0.610497	4.623902	0.023061	0.052091	0.083345	0	286	193	523	252	355	456	312	960	465	413
ENSMUSG00000062077	chr5	Trim54	31116712	31117077	1436	-0.37306	8.441672	0.023063	0.052091	0.032059	0	5943	4671	8563	5668	6666	4534	5540	4651	8543	4668
ENSMUSG00000014158	chr5	Trpv4	1.15E+08	1.15E+08	4076	0.603489	0.977235	0.023098	0.052163	0.053051	0	22	12	41	20	26	34	51	50	33	34
ENSMUSG00000039621	chr2	Prex1	1.67E+08	1.67E+08	10266	0.460059	3.57518	0.023119	0.0522	0.044886	0	134	58	265	160	225	215	269	215	325	224
ENSMUSG00000002014	chrX	Ssr4	73787028	73787306	3096	0.396783	5.497323	0.023164	0.052285	0.034766	0	658	543	704	541	585	819	1329	780	1051	737
ENSMUSG00000033701	chr1	Acbd6	1.56E+08	1.56E+08	6453	0.362666	4.746297	0.023164	0.052285	0.027925	0	392	261	482	367	364	452	560	527	778	443
ENSMUSG00000024457	chr17	Trim26	36837134	36837264	6868	-0.31889	4.233936	0.023171	0.052291	0.020295	0	278	255	466	302	379	264	367	277	364	252
ENSMUSG00000003119	chr11	Cdk12	98203059	98204410	11730	-0.52496	2.933921	0.02318	0.052302	0.054165	0	116	56	238	160	180	103	149	124	92	91
ENSMUSG00000020258	chr9	Glyctk	1.06E+08	1.06E+08	4229	-0.75801	0.011718	0.023195	0.052327	0.058468	0	17	11	22	18	24	10	15	6	14	16
ENSMUSG00000020459	chr11	Mtif2	29526408	29526487	3868	-0.37121	4.594412	0.023199	0.052327	0.029511	0	418	270	468	489	528	322	555	310	447	306
ENSMUSG00000024181	chr17	Mrpl28	26123520	26123849	1274	0.369897	5.879304	0.023216	0.05234	0.030581	0	782	532	849	943	976	1007	1456	1108	1644	907
ENSMUSG00000026024	chr1	Als2	59162926	59164215	9496	-0.33963	4.80578	0.023212	0.05234	0.024499	0	382	333	802	503	546	331	605	372	540	423
ENSMUSG00000052296	chr7	Ppp6r1	4631501	4632244	3787	-0.34606	6.263038	0.023215	0.05234	0.026939	0	1057	857	1970	1467	1713	919	1447	1115	1465	1229
ENSMUSG00000098496	chr7	1810026B05Rik	73539801	73544382	5140	0.407146	2.78301	0.023225	0.052351	0.028569	0	82	72	121	88	104	98	156	149	177	127
ENSMUSG00000027133	chr2	Nop10	1.12E+08	1.12E+08	1109	0.421953	5.402301	0.023231	0.052355	0.039369	0	578	529	593	570	511	798	1242	747	1055	621
ENSMUSG00000085704	chr2	4921531C22Rik	1.8E+08	1.8E+08	1967	-0.75678	0.479875	0.023298	0.052497	0.080038	0	13	20	26	42	29	17	20	21	16	13
ENSMUSG00000039405	chr7	Prss23	89507785	89510870	3226	0.373503	6.680151	0.023315	0.052528	0.031762	0	1290	988	1870	1359	1708	1234	2437	1924	3257	1957
ENSMUSG00000020935	chr11	Dcakd	1.03E+08	1.03E+08	2556	0.593246	3.625142	0.023342	0.05257	0.076409	0	97	60	135	250	258	199	314	247	354	239
ENSMUSG00000030034	chr6	Ino80b	83121765	83122364	1503	0.394271	3.234459	0.023342	0.05257	0.028588	0	134	92	152	126	135	147	206	195	246	171
ENSMUSG00000023044	chr15	Csad	1.02E+08	1.02E+08	2265	0.8732	2.955038	0.023383	0.052653	0.163781	0	116	94	93	35	71	141	127	363	120	121
ENSMUSG00000020474	chr11	Polm	5827860	5829115	3658	0.586155	1.871915	0.023431	0.052753	0.062964	0	52	23	84	26	50	74	76	67	111	60
ENSMUSG00000079083	chr9	Jrkl	13242790	13245741	2952	-0.51511	1.524537	0.023465	0.052819	0.039163	0	36	47	81	43	58	36	50	35	51	37
ENSMUSG00000020515	chr11	Cnot8	58104153	58104208	2636	0.321132	5.583545	0.02348	0.052844	0.022636	0	615	476	887	710	734	767	1300	831	1222	798
ENSMUSG00000007783	chr7	Cpt1c	44959373	44959675	2793	0.615619	0.920464	0.023489	0.052856	0.045004	0	21	21	25	19	25	34	40	44	42	34
ENSMUSG00000087413	chr4	Gm11266	82508016	82508229	1271	0.522203	2.495197	0.023515	0.052906	0.049516	0	67	67	92	61	71	77	157	79	190	107
ENSMUSG00000026349	chr1	Ccnt2	1.28E+08	1.28E+08	12345	-0.35826	4.717975	0.023528	0.052925	0.027373	0	360	284	777	413	629	295	579	391	464	390
ENSMUSG00000029386	chr5	Tctn2	1.25E+08	1.25E+08	8318	0.598791	1.501779	0.023534	0.052931	0.059591	0	38	19	69	27	25	55	61	60	74	47
ENSMUSG00000087128	chr4	Gm12655	94460931	94461355	961	-0.58548	1.18095	0.023578	0.053021	0.049352	0	25	28	47	51	60	28	38	30	31	30
ENSMUSG00000036054	chr8	Sugp2	70234226	70234652	14428	-0.37249	5.295686	0.02359	0.053038	0.030642	0	479	401	1104	803	903	427	804	579	714	616
ENSMUSG00000024985	chr19	Tcf7l2	55741810	55742530	8739	0.542299	2.510088	0.023604	0.053057	0.055987	0	81	56	107	39	83	74	121	144	152	114
ENSMUSG00000036432	chr3	Siah2	58674938	58676443	2999	0.387452	3.480328	0.023606	0.053057	0.029364	0	139	87	214	175	165	165	266	205	340	187
ENSMUSG00000030682	chr7	Cdipt	1.27E+08	1.27E+08	1876	0.362509	5.214432	0.023623	0.053086	0.029131	0	466	280	715	552	648	651	763	716	1106	590
ENSMUSG00000019853	chr10	Hebp2	18540123	18541332	1910	0.859694	-0.18341	0.023631	0.053095	0.077417	0	8	6	11	12	6	9	28	22	14	17
ENSMUSG00000022558	chr15	Mroh1	76380261	76380342	16533	-0.44053	4.362261	0.023699	0.053238	0.042099	0	276	181	548	474	484	219	317	277	525	277
ENSMUSG00000021276	chr12	Cinp	1.11E+08	1.11E+08	2029	0.341208	4.144889	0.023707	0.053247	0.023389	0	215	187	339	231	279	315	488	308	452	254
ENSMUSG00000022064	chr14	Pibf1	99099433	99100129	3271	-0.44226	2.803772	0.023794	0.053434	0.037754	0	106	96	152	143	137	78	178	86	121	82

ENSMUSG00000015597	chr17	Zfp318	46383731	46384330	8594	-0.38214	3.644603	0.02384	0.053527	0.029359	0	166	178	350	195	258	167	296	162	233	142
ENSMUSG00000026094	chr1	Stk17b	53755506	53757770	5185	0.408345	3.410751	0.023851	0.053534	0.032431	0	119	133	218	102	155	175	240	220	269	191
ENSMUSG00000031197	chrX	Vbp1	75514299	75514428	2132	-0.34738	5.147257	0.023849	0.053534	0.026652	0	567	522	848	529	701	365	689	541	704	566
ENSMUSG00000048814	chr1	Lonrf2	38793645	38798223	7506	-0.82275	-0.09031	0.023862	0.05355	0.067674	0	11	11	27	13	26	11	9	16	10	8
ENSMUSG00000070705	chr7	Eid2b	28277706	28280129	2424	-0.40129	2.624715	0.023954	0.053749	0.027174	0	87	78	150	112	134	68	118	97	111	86
ENSMUSG00000027610	chr2	Gss	1.56E+08	1.56E+08	5915	0.476256	2.918362	0.023961	0.053753	0.043009	0	107	72	99	109	102	135	178	189	184	105
ENSMUSG00000008658	chr16	Rbfox1	6809222	6809248	4151	-0.41592	7.651993	0.023983	0.053794	0.040249	0	3244	2927	6642	2409	3656	2363	4003	2473	4283	2845
ENSMUSG00000002524	chr15	Puf60	76070184	76070627	1912	0.319351	5.928575	0.023989	0.053799	0.022894	0	739	609	1147	883	994	980	1454	1106	1588	1076
ENSMUSG00000033960	chr18	9430020K01Rik	4634929	4635031	6730	-0.47075	4.20401	0.023997	0.053809	0.047971	0	196	164	477	421	533	192	296	307	318	284
ENSMUSG00000016758	chr15	Bik	83526862	83526936	943	0.815339	-0.09552	0.02401	0.053827	0.061776	0	10	9	11	6	11	18	16	18	29	14
ENSMUSG00000007721	chr8	Ccdc124	70868227	70868645	911	0.360204	5.938898	0.024024	0.05385	0.029264	0	848	686	967	767	967	993	1411	1151	1787	1016
ENSMUSG00000031016	chr7	Wee1	1.1E+08	1.1E+08	1941	-0.59897	1.315538	0.024049	0.053896	0.051832	0	36	24	77	44	58	31	38	41	26	34
ENSMUSG00000035790	chr16	Cep19	32099800	32100111	1751	0.374533	4.068119	0.024056	0.053904	0.028612	0	240	188	321	190	216	293	424	298	455	264
ENSMUSG00000051355	chr11	Commd1	22896136	22900057	5936	0.41243	5.786164	0.024113	0.054022	0.038491	0	778	700	748	689	724	1065	1475	1019	1361	848
ENSMUSG00000022895	chr16	Ets2	95702075	95702644	4710	-0.374	5.561185	0.024142	0.054078	0.031471	0	544	499	1433	836	1174	581	1065	695	886	580
ENSMUSG00000051786	chr15	Tubgcp6	89098357	89100503	7965	-0.38855	3.876161	0.024163	0.054117	0.030579	0	188	162	467	248	320	179	259	263	235	210
ENSMUSG00000032246	chr9	Calml4	62858104	62858161	861	0.788713	1.169729	0.024187	0.054161	0.108793	0	20	20	23	39	20	62	36	36	82	29
ENSMUSG00000020413	chr11	Hus1	8993137	8996346	6450	-0.40857	3.451436	0.024198	0.054176	0.033094	0	129	114	317	199	277	122	244	152	212	137
ENSMUSG00000053390	chr17	Zfp952	32993129	32993258	4368	-0.44773	2.437117	0.024209	0.054192	0.034434	0	69	75	148	92	117	63	106	70	85	86
ENSMUSG00000038525	chr5	Armc10	21645813	21646235	3407	0.466785	2.524486	0.024249	0.054273	0.038701	0	80	60	114	61	64	97	157	113	147	89
ENSMUSG00000024387	chr17	Csnk2b	35116196	35116425	2067	0.333629	6.549304	0.024276	0.054317	0.025509	0	1168	1007	1751	1322	1385	1460	2174	1751	2632	1611
ENSMUSG00000029321	chr5	Slc10a6	1.04E+08	1.04E+08	2124	0.960168	0.811579	0.024281	0.054317	0.167112	0	12	23	22	11	19	61	56	40	27	10
ENSMUSG00000038763	chr7	Alpk3	81057600	81057772	6445	-0.5236	7.432354	0.024278	0.054317	0.063959	0	1807	1485	4306	5043	4355	1643	3320	2091	3755	2427
ENSMUSG00000027298	chr2	Tyro3	1.2E+08	1.2E+08	6198	0.848026	0.042781	0.02435	0.05446	0.107521	0	6	4	15	12	17	18	9	23	26	28
ENSMUSG00000045248	chr8	Med26	72494558	72497106	3040	0.428538	2.970687	0.024397	0.054556	0.035891	0	84	55	160	119	126	155	218	148	163	124
ENSMUSG00000073468	chr17	Sft2d1	8311102	8311285	3580	0.488297	2.428622	0.024413	0.054583	0.043108	0	77	52	101	46	77	97	136	127	121	80
ENSMUSG00000048732	chr11	Klhl11	1E+08	1E+08	2393	-0.7855	0.287614	0.024426	0.054602	0.078934	0	14	11	43	26	24	15	21	20	10	8
ENSMUSG00000030224	chr6	Strap	1.38E+08	1.38E+08	3090	-0.33559	6.889733	0.024451	0.054641	0.026138	0	1920	1684	2859	1974	2125	1510	2429	1689	2375	1650
ENSMUSG00000062627	chr4	Mysm1	94942040	94947123	8946	-0.53559	2.250318	0.024448	0.054641	0.052908	0	61	49	175	69	114	55	106	55	68	65
ENSMUSG00000025226	chr19	Fbxl15	46328184	46328526	1348	0.54177	1.880243	0.02446	0.054652	0.051279	0	50	22	52	53	57	72	76	90	87	57
ENSMUSG00000020541	chr11	Tom1l1	90643465	90646309	7749	-0.3869	3.530036	0.024479	0.054684	0.030249	0	196	178	304	150	213	146	233	176	211	146
ENSMUSG00000035984	chr18	Nme5	34562634	34562803	1154	0.723106	0.430777	0.024484	0.054687	0.059407	0	13	14	14	15	17	25	39	23	41	14
ENSMUSG00000029833	chr6	Trim24	37870811	37871474	8521	-0.35799	5.472194	0.02452	0.054759	0.028853	0	738	516	1221	703	899	679	773	579	1019	518
ENSMUSG00000049577	chr8	Zfpm1	1.22E+08	1.22E+08	3503	-0.70885	1.694846	0.024548	0.054812	0.097185	0	32	26	83	95	88	23	48	35	86	33
ENSMUSG00000024943	chr19	Smc5	23206441	23208968	5730	-0.36445	3.583182	0.024557	0.054822	0.026154	0	163	164	331	173	265	136	215	190	232	179
ENSMUSG00000049321	chr11	Zfp2	50898712	50901291	4019	-0.50579	2.454989	0.024574	0.054832	0.049392	0	74	99	143	96	91	52	130	73	80	77
ENSMUSG00000057003	chr11	Myh4	67238029	67238079	6016	-0.45938	15.39424	0.024568	0.054832	0.049817	0	842632	435638	1528795	534103	846089	515969	628732	616951	966108	597504
ENSMUSG00000070443	chr3	Gm10291	78917258	78918256	999	0.967779	0.129423	0.024574	0.054832	0.130092	0	14	8	20	9	1	16	34	15	41	15
ENSMUSG00000074874	chr13	Ctla2b	60895351	60896143	1147	0.672668	0.695889	0.024674	0.055047	0.061782	0	20	11	18	23	20	29	31	45	33	28
ENSMUSG00000022863	chr16	Btg3	78359860	78360538	1439	0.862402	0.364743	0.024709	0.055115	0.108746	0	5	11	13	17	20	7	46	28	33	27
ENSMUSG00000029098	chr5	Acox3	35583040	35583134	9093	-0.33816	4.717748	0.024724	0.05514	0.024596	0	363	279	606	537	611	342	511	397	494	375
ENSMUSG00000001289	chr15	Pfdn5	1.02E+08	1.02E+08	1394	0.411777	6.597866	0.024742	0.05517	0.039344	0	1342	1277	1404	1123	1256	1800	2539	1750	2486	1572
ENSMUSG00000035236	chr2	Scai	39066214	39075156	11668	-0.61101	1.419774	0.024771	0.055217	0.059895	0	33	29	74	42	81	29	27	43	45	39
ENSMUSG00000062115	chr11	Rai1	60105013	60105394	9591	-0.58138	4.093622	0.024768	0.055217	0.075614	0	171	112	462	458	532	142	315	268	284	244
ENSMUSG00000005501	chr1	Usp40	87945119	87948596	11871	-0.3335	3.697488	0.0248	0.055262	0.02162	0	192	160	299	239	271	158	253	197	249	188
ENSMUSG00000076281	chr9	Gm24270	56223715	56223771	57	0.956489	3.020763	0.024797	0.055262	0.203368	0	114	34	128	109	53	88	113	61	421	295
ENSMUSG00000085894	chr1	Gm15832	39547570	39547661	1832	0.569556	1.892932	0.024806	0.055266	0.056881	0	35	40	55	45	56	46	67	108	110	63
ENSMUSG00000027996	chr3	Sfrp2	83766321	83767043	2153	1.069587	2.840011	0.02484	0.055333	0.251462	0	35	111	169	15	34	146	102	275	136	174
ENSMUSG00000045140	chr11	Pigw	84876315	84878512	2733	-0.53605	2.331796	0.024849	0.055344	0.056372	0	95	93	115	60	96	43	94	88	79	67
ENSMUSG00000055322	chr1	Tns1	73910231	73914674	16010	-0.43335	8.259682	0.024872	0.055386	0.04433	0	4211	2477	8897	6661	7459	3659	5212	3897	7300	4102
ENSMUSG00000017491	chr14	Rarb	16430842	16432267	3034	-0.40887	3.337438	0.024929	0.055502	0.033544	0	135	115	315	167	220	93	203	137	214	153
ENSMUSG00000031227	chrX	Magee1	1.05E+08	1.05E+08	3550	0.616633	1.487913	0.024965	0.055575	0.069273	0	30	13	53	28	53	29	57	67	85	61
ENSMUSG00000072825	chr12	Cep170b	1.13E+08	1.13E+08	6642	0.351862	4.188217	0.024986	0.055611	0.026403	0	225	158	423	214	297	280	371	366	476	359
ENSMUSG00000036833	chr2	Pnpla7	24976033	24976313	7496	-0.32366	5.712069	0.025021	0.055672	0.023748	0	700	655	1393	1008	993	650	935	826	1096	755
ENSMUSG00000046707	chr8	Csnk2a2	95446096	95448418	3766	0.37206	3.472083	0.025023	0.055672	0.027015	0	145	101	218	154	157	180	264	259	264	168
ENSMUSG00000051498	chr5	Tlr6	64953106	64955593	2603	0.812172	-0.08153	0.025026	0.055672	0.07316	0	7	6	9	10	16	13	21	19	35	10
ENSMUSG00000022749	chr16	Tbc1d23	57168866	57170440	3648	-0.32476	4.094144	0.025123	0.05588	0.021649	0	260	235	446	250	340	204	345	263	339	238
ENSMUSG00000029851	chr6	Fam115c	42623019	42624615	4775	0.558482	1.276828	0.025129	0.055882	0.047186	0	16	24	41	27	44	36	55	52	53	53
ENSMUSG00000043088	chr6	Il17re	1.13E+08	1.13E+08	2992	-0.89883	0.583446	0.025133	0.055882	0.137886	0	37	27	25	16	38	29	9	16	23	10
ENSMUSG00000043587	chr9	Pxylp1	96823336	96825622	6148	0.649283	0.682852	0.025168	0.055952	0.056546	0	9	15	24	19	27	34	36	31	30	32
ENSMUSG00000060438	chr3	Rps10-ps1	95622278	95622775	498	0.579068	1.395013	0.025176	0.055959	0.04942	0	40	25	32	29	32	52	64	50	70	39
ENSMUSG00000025157	chr19	Zdhhc16	41933472	41933665	1830	-0.34097	4.262899	0.025188	0.055967	0.024635	0	302	262	418	322	405	279	343	251	428	246
ENSMUSG00000027613	chr2	Eif6	1.56E+08	1.56E+08	2702	0.325077	5.14457	0.025185	0.055967	0.023232	0	415	414	644	490	535	553	801	728	936	586
ENSMUSG00000027792	chr3	Bche	73635808	73640041	6741	-0.57293	2.697927	0.02521	0.056008	0.068874	0	133	76	139	119	145	43	121	150	84	75
ENSMUSG00000022449	chr15	Adamts20	94270163	94270389	8997	0.605895	1.670828	0.025217	0.056013	0.065721	0	22	33	58	29	57	38	99	67	57	77

ENSMUSG00000014329	chr10	Bicc1	70922832	70925378	7441	0.337815	4.132955	0.025238	0.056049	0.023864	0	183	184	397	213	288	273	431	382	388	305
ENSMUSG00000022604	chr16	Cep97	55899888	55905869	9163	-0.43015	2.558843	0.025247	0.056061	0.03292	0	85	63	156	93	153	64	115	92	104	79
ENSMUSG00000055013	chr1	Agap1	89454806	89455592	17469	0.34189	4.379683	0.025257	0.056072	0.02528	0	218	178	472	284	366	305	460	449	555	360
ENSMUSG00000053173	chr6	Rpl18-ps2	1.28E+08	1.28E+08	604	0.670524	0.961331	0.025267	0.056087	0.066837	0	19	21	37	18	18	23	54	28	72	34
ENSMUSG00000027860	chr3	Vangl1	1.02E+08	1.02E+08	4038	0.55897	1.124059	0.025286	0.05612	0.04608	0	16	17	48	25	32	37	54	54	46	33
ENSMUSG00000038002	chr17	Cramp1l	24961228	24964946	7517	-0.43581	3.29265	0.025292	0.056123	0.037586	0	148	93	304	160	230	131	186	173	139	119
ENSMUSG00000024360	chr18	Etf1	34902785	34905070	3709	-0.33526	6.939408	0.025364	0.056263	0.026439	0	1954	1688	2971	2038	2332	1596	2590	1599	2582	1668
ENSMUSG00000076060	chr6	Mir704	47803576	47803652	77	0.665925	0.412373	0.025362	0.056263	0.05318	0	10	11	21	15	19	27	34	30	20	23
ENSMUSG00000030878	chr7	Cdr2	1.21E+08	1.21E+08	2782	0.537895	2.011171	0.025464	0.056476	0.050292	0	57	35	44	48	68	59	91	102	103	69
ENSMUSG00000038544	chr4	Inip	59769637	59772459	5995	0.490715	2.035853	0.025469	0.056479	0.04226	0	40	30	77	52	74	55	113	105	91	65
ENSMUSG00000080848	chr9	Gm9385	1.16E+08	1.16E+08	472	0.461965	4.097568	0.025502	0.056541	0.046155	0	225	234	249	206	185	332	488	297	472	236
ENSMUSG00000014668	chr5	Chfr	1.1E+08	1.1E+08	3169	-0.32714	3.988399	0.025522	0.056576	0.021714	0	255	176	409	280	313	208	313	249	326	194
ENSMUSG00000093185	chr4	Gm25692	45396994	45397118	125	0.481876	2.326185	0.025549	0.056627	0.04169	0	65	49	89	50	76	102	108	103	143	66
ENSMUSG00000070284	chr9	Gmppb	1.08E+08	1.08E+08	2785	0.521368	2.446048	0.025571	0.056666	0.053105	0	37	42	83	97	99	95	170	96	128	91
ENSMUSG00000031732	chr8	Phlpp2	1.1E+08	1.1E+08	8449	-0.51352	2.219114	0.025596	0.056713	0.04697	0	60	43	145	80	123	50	89	76	64	63
ENSMUSG00000048087	chr16	Gm4737	46152997	46155077	2081	-0.59824	0.962248	0.025693	0.056918	0.048551	0	30	29	54	23	45	25	28	19	37	25
ENSMUSG00000033029	chr15	1700088E04Rik	79129349	79130537	5292	0.739777	0.223892	0.025716	0.056958	0.064942	0	12	9	23	6	14	14	31	28	35	14
ENSMUSG00000045427	chrX	Hnrnph2	1.35E+08	1.35E+08	4369	-0.36968	5.626172	0.025723	0.056964	0.031747	0	779	812	1231	673	928	515	1117	747	915	699
ENSMUSG00000052137	chr4	Rbm12b2	12089439	12089727	3468	0.564381	1.871948	0.025728	0.056966	0.05545	0	43	45	60	33	45	54	68	100	96	66
ENSMUSG00000022466	chr15	Rpap3	97675105	97675379	2260	-0.34635	4.044273	0.025761	0.05703	0.025154	0	249	233	421	288	285	223	353	217	291	238
ENSMUSG00000031962	chr8	Cdh15	1.23E+08	1.23E+08	2843	0.339183	4.474866	0.025768	0.057036	0.025059	0	271	179	442	350	357	367	537	366	563	430
ENSMUSG00000020248	chr10	Nfyb	82748701	82750447	5068	-0.32047	4.897347	0.025857	0.057223	0.022863	0	464	401	718	461	619	341	671	423	614	408
ENSMUSG00000033862	chr8	Cdk10	1.23E+08	1.23E+08	1643	0.394022	3.472594	0.025896	0.057291	0.030517	0	152	123	171	133	172	189	286	245	267	159
ENSMUSG00000079557	chr17	March2	33685692	33686398	5997	0.340862	6.570994	0.025893	0.057291	0.027262	0	1322	1032	1722	1247	1342	1634	2313	1738	2496	1575
ENSMUSG00000046818	chr3	Ddit4l	1.38E+08	1.38E+08	2916	-0.50542	8.574473	0.025913	0.057318	0.06119	0	7299	7326	9520	3872	6892	5148	7506	4185	8423	4085
ENSMUSG00000064368	chrMT	mt-Nd6	13552	14070	519	-0.92779	7.019921	0.025926	0.057337	0.20236	0	657	663	4225	3999	5502	668	1176	1726	3303	1550
ENSMUSG00000031841	chr8	Cdh13	1.18E+08	1.18E+08	11144	0.371162	6.635224	0.025935	0.057349	0.032646	0	919	875	2114	1581	1682	1495	2183	1794	2689	2086
ENSMUSG00000030232	chr6	Aebp2	1.41E+08	1.41E+08	8111	-0.3247	5.066381	0.025941	0.057351	0.023632	0	463	400	911	612	663	380	646	543	762	426
ENSMUSG00000024208	chr17	Uqcc2	27122663	27122840	837	0.38894	7.172852	0.025993	0.057439	0.035945	0	2164	1677	2277	1761	1860	2579	3775	2538	3823	2354
ENSMUSG00000028453	chr4	Fancg	43002343	43003092	3795	0.62052	1.186953	0.025987	0.057439	0.055733	0	24	29	30	27	23	40	44	48	52	51
ENSMUSG00000097530	chr7	Kansl2-ps	72672818	72674278	1461	-0.44917	2.21232	0.025991	0.057439	0.035278	0	72	68	121	80	80	61	96	69	76	50
ENSMUSG00000021048	chr12	Mthfd1	76255232	76255544	3324	-0.32582	5.301373	0.026016	0.057479	0.023948	0	590	413	1046	705	856	478	852	592	692	591
ENSMUSG00000000168	chr9	Dlat	50634633	50636554	4886	-0.49403	7.513427	0.026054	0.057553	0.058393	0	2277	1556	3814	5029	4952	1785	3937	2284	3791	2424
ENSMUSG00000020570	chr12	Sypl	32953891	32954018	7535	-0.36092	7.407165	0.026061	0.057561	0.031128	0	2735	2389	4750	2505	3072	1813	3602	2375	3615	2426
ENSMUSG00000022477	chr15	Aco2	81872309	81872548	3892	-0.48992	10.50091	0.026083	0.057599	0.057749	0	17823	12491	32023	40790	36663	15972	30225	16675	32067	18084
ENSMUSG00000025969	chr1	Nrp2	62703285	62704277	11842	0.391887	3.987042	0.026102	0.057632	0.033388	0	140	142	327	228	290	207	423	403	356	260
ENSMUSG00000028998	chr5	Tomm7	23838944	23839828	1125	0.404127	5.938068	0.026116	0.057635	0.038132	0	871	755	868	782	798	1134	1752	1141	1456	935
ENSMUSG00000037896	chr12	Rcor1	1.11E+08	1.11E+08	5684	-0.41713	3.473593	0.026117	0.057635	0.035751	0	156	102	332	206	259	114	215	197	177	160
ENSMUSG00000053830	chr10	Gm9923	72309225	72311848	2624	-0.88165	0.118972	0.026111	0.057635	0.124157	0	7	20	25	21	30	2	15	19	21	8
ENSMUSG00000020641	chr12	Rsad2	26442753	26445570	4328	0.719095	2.235164	0.026122	0.057636	0.11191	0	29	31	59	50	120	84	179	89	57	108
ENSMUSG00000000530	chr15	Acvrl1	1.01E+08	1.01E+08	4265	0.345326	3.974515	0.026137	0.05766	0.024836	0	159	164	269	213	309	259	349	325	385	275
ENSMUSG00000043629	chr1	1700019D03Rik	52922324	52925734	4330	-0.7568	0.46858	0.026168	0.057719	0.083323	0	28	18	49	15	22	12	22	27	16	10
ENSMUSG00000032777	chr7	Gtf3c1	1.26E+08	1.26E+08	6960	-0.35548	5.55248	0.026233	0.057853	0.02913	0	595	468	1351	874	1120	519	865	717	974	709
ENSMUSG00000082691	chr6	Dynlt1-ps1	1.35E+08	1.35E+08	342	-0.69728	1.773737	0.026238	0.057855	0.096415	0	59	50	90	68	63	57	88	38	28	21
ENSMUSG00000018286	chr11	Psmb6	70525367	70525495	1872	0.408622	7.417717	0.026268	0.057911	0.039922	0	2379	2247	2539	1922	2257	3044	4407	3195	4644	2693
ENSMUSG00000051978	chr8	Erich1	14027565	14028153	1579	-0.68289	0.81517	0.026281	0.057931	0.075148	0	30	32	37	17	47	18	22	19	41	18
ENSMUSG00000009563	chr2	Tor2a	32757234	32757450	3050	0.415799	2.819961	0.026291	0.057942	0.032306	0	92	61	124	98	105	110	183	171	160	105
ENSMUSG00000009545	chr7	Kcnq1	1.43E+08	1.43E+08	4093	0.797887	-0.07801	0.026369	0.058104	0.08243	0	9	2	19	11	9	10	24	26	18	18
ENSMUSG00000041035	chr19	Dpcd	45560615	45560707	1995	0.393643	3.781023	0.026396	0.058155	0.031867	0	196	168	196	159	200	227	347	263	338	243
ENSMUSG00000003228	chr19	Grk5	60889749	60890631	3165	0.481297	2.085776	0.026409	0.058173	0.040371	0	33	40	64	64	78	64	105	90	101	80
ENSMUSG00000022836	chr16	Mylk	34745210	34745370	10159	-0.36628	4.352966	0.026415	0.058177	0.02939	0	260	242	523	328	542	218	442	364	351	266
ENSMUSG00000015289	chrX	Lage3	74351276	74353002	2021	0.400029	4.495924	0.026427	0.058189	0.035319	0	334	273	390	266	250	392	594	421	602	349
ENSMUSG00000078515	chr4	Ddi2	1.42E+08	1.42E+08	9553	-0.39623	6.362602	0.026429	0.058189	0.037318	0	1207	1173	2796	1067	1479	988	1730	1045	1648	1158
ENSMUSG00000026436	chr1	Elk4	1.32E+08	1.32E+08	6407	0.334698	5.073544	0.026463	0.058253	0.025316	0	424	339	730	419	506	581	731	624	999	517
ENSMUSG00000066357	chr9	Wdr6	1.09E+08	1.09E+08	4163	0.385325	3.429993	0.026468	0.058254	0.030457	0	125	87	209	148	190	148	229	198	313	223
ENSMUSG00000004356	chr10	Utp20	88746607	88747059	8831	-0.38197	3.650408	0.026509	0.058335	0.030084	0	140	157	363	198	316	158	258	195	229	156
ENSMUSG00000020034	chr10	Tcp11l2	84576626	84577012	3438	0.317578	5.496214	0.026515	0.058335	0.023065	0	483	511	860	605	779	708	1176	796	1065	842
ENSMUSG00000024614	chr18	Tmx3	90510154	90510377	4611	-0.31743	4.574748	0.026517	0.058335	0.021964	0	320	328	624	379	493	269	501	368	463	349
ENSMUSG00000042138	chr9	Msantd2	37489321	37489833	2289	0.576569	1.036078	0.026524	0.058341	0.050978	0	23	17	40	14	33	34	51	51	39	35
ENSMUSG00000021371	chr13	Mcur1	43538412	43541729	4350	-0.37086	5.476684	0.026568	0.058416	0.032066	0	628	433	1039	996	1019	460	977	695	922	567
ENSMUSG00000027861	chr3	Casq2	1.02E+08	1.02E+08	2736	1.067306	5.147113	0.026566	0.058416	0.266777	0	98	87	174	920	589	532	1718	421	1051	827
ENSMUSG00000049299	chr11	Trappc1	69323980	69324066	1112	0.380546	5.1242	0.026587	0.05845	0.033048	0	445	427	540	475	476	727	877	620	826	529
ENSMUSG00000029101	chr5	Rgs12	34949445	34949524	7910	0.556299	1.860721	0.026634	0.058543	0.059236	0	34	21	70	53	58	58	73	59	87	99
ENSMUSG00000033931	chr8	Rbm34	1.27E+08	1.27E+08	3429	-0.39607	2.870377	0.026657	0.058584	0.02988	0	118	103	200	106	137	81	142	102	148	102
ENSMUSG00000087579	chr19	1500017E21Rik	36614052	36614481	3977	0.578271	2.045685	0.026725	0.058723	0.065531	0	44	23	62	67	66	53	144	54	129	74

ENSMUSG00000052293	chr13	Taf9	1.01E+08	1.01E+08	2120	-0.38187	4.899473	0.026751	0.05877	0.033775	0	516	480	620	459	567	389	726	384	574	336
ENSMUSG00000031133	chrX	Arhgef6	57231485	57233651	8552	-0.41824	5.506027	0.026783	0.058829	0.041184	0	563	417	1220	1022	1115	489	1071	509	929	637
ENSMUSG00000087331	chr15	1810021B22Rik	89071196	89071336	896	-0.55381	1.225429	0.026786	0.058829	0.046177	0	37	32	44	56	42	27	35	34	39	30
ENSMUSG00000080989	chr2	Gm14048	1.31E+08	1.31E+08	1268	-0.70951	0.113607	0.026791	0.058829	0.055846	0	13	13	32	25	16	8	16	15	17	12
ENSMUSG00000099519	chr1	Gm29253	75171731	75171988	5231	0.328718	7.401698	0.026844	0.058935	0.02603	0	1995	1552	3304	2520	2850	2668	3813	3158	4488	3128
ENSMUSG00000031548	chr8	Sfrp1	23411502	23412328	4372	0.639816	3.180787	0.026907	0.059054	0.092568	0	96	80	261	47	110	208	189	263	187	126
ENSMUSG00000039901	chr19	9130011E15Rik	45818144	45818978	2896	-0.34992	3.977335	0.026902	0.059054	0.02594	0	279	163	423	257	316	206	348	216	316	190
ENSMUSG00000037010	chrX	Apln	48025146	48027707	3149	0.829407	1.05133	0.026931	0.059098	0.130886	0	21	8	13	27	44	26	45	73	60	26
ENSMUSG00000022698	chr16	Naa50	44139830	44140111	4648	-0.41532	8.528269	0.026938	0.059103	0.041948	0	6572	6491	9018	4823	6181	4282	6807	5042	8529	4759
ENSMUSG00000031636	chr8	Pdlim3	45885485	45885672	1578	0.454525	9.126266	0.026963	0.059148	0.050246	0	7201	7086	12111	4755	6440	9852	15150	8632	16307	9920
ENSMUSG00000029153	chr5	Ociad2	73322199	73323847	2509	-0.34312	5.84163	0.026969	0.059151	0.027759	0	989	822	1478	769	1086	773	1108	890	1163	708
ENSMUSG00000060981	chr13	Hist1h4h	23531050	23531522	473	-0.56079	2.537428	0.027088	0.059403	0.065608	0	92	49	98	163	147	68	108	68	123	62
ENSMUSG00000020189	chr10	Osbpl8	1.11E+08	1.11E+08	7152	-0.42059	3.900805	0.027113	0.059448	0.038783	0	186	177	475	246	337	128	238	286	293	221
ENSMUSG00000056185	chr19	Snx32	5495278	5495648	1650	0.455392	3.333101	0.027118	0.059449	0.043674	0	153	108	166	89	150	208	198	188	274	174
ENSMUSG00000027397	chr2	Slc20a1	1.29E+08	1.29E+08	5580	0.404054	3.276663	0.027168	0.059544	0.032997	0	131	108	191	97	134	174	212	211	245	152
ENSMUSG00000060803	chr19	Gstp1	4035407	4035661	757	0.395193	6.53912	0.02717	0.059544	0.037419	0	1352	1167	1557	950	1244	1694	2191	1753	2500	1533
ENSMUSG00000013465	chr2	Nelfb	25199712	25200466	3432	0.311371	4.875982	0.027188	0.059571	0.021606	0	354	279	563	443	479	459	685	579	792	473
ENSMUSG00000020032	chr10	Nuak1	84370905	84375387	5625	-0.37773	4.454276	0.0272	0.059571	0.03202	0	327	284	557	384	450	227	362	278	447	417
ENSMUSG00000031701	chr8	Dnaja2	85537640	85539407	2839	-0.35478	7.891269	0.027195	0.059571	0.030627	0	3929	3639	5981	3632	4018	3012	4999	3216	4707	3290
ENSMUSG00000037341	chrX	Slc9a7	20105755	20106214	3819	-0.7891	0.827095	0.0272	0.059571	0.100466	0	19	12	76	29	47	19	22	26	16	25
ENSMUSG00000027412	chr2	Lpin3	1.61E+08	1.61E+08	3694	0.555045	1.982538	0.027273	0.05972	0.060824	0	43	23	73	57	60	99	71	89	91	57
ENSMUSG00000032254	chr9	Kif23	61917280	61917679	3423	0.914415	-0.2689	0.027324	0.059821	0.111465	0	10	5	10	3	12	23	9	17	16	17
ENSMUSG00000040287	chr10	Stac3	1.28E+08	1.28E+08	2543	-0.37381	8.255256	0.027336	0.059838	0.034116	0	5058	4898	7733	4247	5489	4446	6076	4026	5604	4138
ENSMUSG00000036206	chr1	Sh3bp4	89070415	89070597	5112	0.490074	2.415729	0.027355	0.05987	0.046243	0	40	54	83	79	95	82	108	95	157	115
ENSMUSG00000008683	chr7	Rps15a	1.18E+08	1.18E+08	6262	0.425281	7.210974	0.027374	0.0599	0.043823	0	1966	2021	2191	1760	1778	2842	4112	2730	3718	2221
ENSMUSG00000030120	chr6	Mlf2	1.25E+08	1.25E+08	1533	0.335321	7.615818	0.027418	0.059988	0.027298	0	2616	2226	3516	2498	2926	3265	4658	3735	5132	3305
ENSMUSG00000031204	chrX	Asb12	95470201	95470466	1258	-0.36964	4.790428	0.027478	0.06011	0.031461	0	343	329	720	550	615	310	600	315	661	372
ENSMUSG00000016831	chr14	Tox4	52279146	52279232	6940	-0.33837	6.17725	0.027488	0.060121	0.027302	0	1067	889	2132	1096	1478	898	1362	980	1584	1060
ENSMUSG00000030787	chr7	Lyve1	1.11E+08	1.11E+08	2607	-0.61595	2.880819	0.027526	0.060195	0.082625	0	77	85	260	109	220	119	117	137	90	51
ENSMUSG00000000531	chr15	Grasp	1.01E+08	1.01E+08	2013	0.44735	2.321852	0.02755	0.060236	0.03559	0	61	42	85	56	92	71	142	89	145	79
ENSMUSG00000021993	chr14	Mipep	60784566	60784870	2403	-0.31275	5.88289	0.027574	0.06027	0.023141	0	925	730	1349	1055	1205	747	1272	856	1244	756
ENSMUSG00000036062	chr4	N28178	42916660	42916829	7118	-0.85614	0.082022	0.027571	0.06027	0.089116	0	11	13	42	16	21	11	11	18	7	13
ENSMUSG00000031833	chr8	Mast3	70778117	70779937	5334	0.486723	2.27425	0.027616	0.06035	0.046246	0	53	33	108	58	75	102	98	116	104	75
ENSMUSG00000026064	chr1	Ptp4a1	30940302	30943323	5763	-0.32305	4.356714	0.027654	0.060425	0.022811	0	325	265	423	379	418	254	410	338	361	293
ENSMUSG00000023965	chr17	Fbxl17	63057452	63060411	5526	-0.36667	5.515783	0.027679	0.06046	0.031644	0	616	441	1508	791	996	524	875	627	960	693
ENSMUSG00000084929	chr4	Foxo6os	1.2E+08	1.2E+08	2291	-0.42582	4.11991	0.027678	0.06046	0.040694	0	207	179	353	420	463	220	341	267	264	249
ENSMUSG00000039629	chr6	Strip2	29917013	29917230	8328	-0.75281	0.305989	0.027822	0.060751	0.064924	0	17	10	36	22	33	14	12	18	13	18
ENSMUSG00000042772	chr1	Smg7	1.53E+08	1.53E+08	6341	-0.33642	5.730338	0.027817	0.060751	0.026666	0	792	500	1519	939	1189	703	981	852	1060	697
ENSMUSG00000033105	chr10	Lss	76531588	76531621	10787	-0.52286	1.565692	0.027873	0.060853	0.042824	0	48	27	89	46	70	36	40	46	53	38
ENSMUSG00000031840	chr8	Rab3a	70754679	70754868	2226	0.320054	5.000441	0.027882	0.060862	0.023405	0	366	292	585	484	584	462	800	567	848	596
ENSMUSG00000027959	chr3	Sass6	1.17E+08	1.17E+08	4241	0.677131	0.584859	0.027921	0.060938	0.074993	0	13	7	35	15	19	25	48	30	20	31
ENSMUSG00000086914	chr9	Gm16124	53667246	53667355	516	0.555932	2.389674	0.027926	0.060938	0.058708	0	69	73	53	58	62	83	141	103	137	97
ENSMUSG00000031987	chr8	Egln1	1.25E+08	1.25E+08	3515	-0.36516	8.015872	0.027953	0.060987	0.032782	0	3963	2775	5577	5787	5468	2982	5267	3589	5898	3361
ENSMUSG00000028101	chr3	Pias3	96696384	96696531	3918	0.385105	2.955018	0.027985	0.061036	0.028841	0	95	71	150	100	122	135	169	178	167	134
ENSMUSG00000074825	chr2	Itpripl1	1.27E+08	1.27E+08	3738	0.493319	2.139662	0.027982	0.061036	0.045368	0	35	46	75	56	77	87	104	107	84	70
ENSMUSG00000071281	chr13	Zfp65	67705306	67708929	4124	-0.48488	2.072744	0.028003	0.061066	0.043243	0	76	56	130	54	75	51	87	51	68	57
ENSMUSG00000002996	chr12	Hbp1	31926254	31927507	6167	-0.3337	6.602855	0.028008	0.061067	0.026982	0	1579	1290	2698	1494	1728	1255	2094	1377	1873	1324
ENSMUSG00000042770	chr6	Hebp1	1.35E+08	1.35E+08	1061	0.546053	2.637006	0.028023	0.06109	0.061872	0	89	64	92	76	68	112	109	188	125	112
ENSMUSG00000036427	chr7	Gpi1	34202122	34202549	4497	0.371295	9.915211	0.028047	0.061132	0.0341	0	13388	7899	19118	13312	14947	15912	21071	18718	30970	14442
ENSMUSG00000026342	chr1	Slc35f5	1.26E+08	1.26E+08	2956	-0.35173	4.484111	0.028098	0.061227	0.027906	0	305	232	568	461	492	283	492	283	494	274
ENSMUSG00000074513	chr3	Arfip1	84496093	84497891	2986	0.345043	4.051328	0.0281	0.061227	0.025221	0	205	197	306	198	252	236	370	334	439	312
ENSMUSG00000041341	chr12	Atg2b	1.06E+08	1.06E+08	10173	-0.32794	4.711734	0.028107	0.061232	0.024243	0	344	305	778	423	567	300	548	403	546	351
ENSMUSG00000033955	chr2	Tnks1bp1	85048022	85048135	6184	0.362756	4.714411	0.028168	0.061355	0.030481	0	275	237	483	375	503	429	465	587	671	506
ENSMUSG00000020895	chr11	Tmem107	69070806	69071033	1369	0.553582	1.582257	0.02818	0.061371	0.051089	0	43	30	42	24	46	48	69	75	63	55
ENSMUSG00000032802	chr2	Srxn1	1.52E+08	1.52E+08	2820	0.394355	5.170108	0.028187	0.061377	0.036793	0	396	312	598	592	615	728	1042	529	1000	485
ENSMUSG00000002565	chr12	Scin	40059769	40060627	2999	-0.60439	2.399259	0.028296	0.061603	0.077064	0	98	81	201	47	88	63	109	60	67	75
ENSMUSG00000017466	chr11	Timp2	1.18E+08	1.18E+08	3896	0.397	7.576562	0.028321	0.061649	0.03889	0	2020	1788	4843	1987	3168	3424	3703	4575	4527	3327
ENSMUSG00000025511	chr7	Tspan4	1.41E+08	1.41E+08	2178	0.38295	4.147356	0.028347	0.061694	0.032985	0	159	164	344	294	290	264	483	442	392	257
ENSMUSG00000035107	chr16	Dcbld2	58408443	58408951	8401	0.510956	2.609976	0.028379	0.061754	0.056179	0	52	38	123	69	135	84	127	143	143	140
ENSMUSG00000030527	chr7	Crtc3	80586627	80589951	9850	-0.35536	3.890178	0.028384	0.061756	0.026957	0	196	157	434	250	343	158	274	236	321	207
ENSMUSG00000032870	chr4	Smap2	1.21E+08	1.21E+08	3160	0.346494	4.472147	0.028425	0.061833	0.027142	0	227	191	376	377	413	333	534	426	591	395
ENSMUSG00000099681	chr11	1700052K11Rik	1.05E+08	1.05E+08	3708	-0.50423	1.836152	0.02843	0.061836	0.046803	0	70	44	82	70	59	31	83	50	58	45
ENSMUSG00000053746	chr2	Ptrh1	32775786	32775895	1135	0.57257	0.965884	0.028445	0.061857	0.043891	0	21	17	28	27	25	32	41	47	54	27
ENSMUSG00000028800	chr4	Hdac1	1.3E+08	1.3E+08	3445	0.34806	3.729247	0.028491	0.061926	0.025005	0	171	143	234	152	229	202	298	286	350	217
ENSMUSG00000029186	chr5	Pi4k2b	52741587	52741968	3751	0.673918	1.168703	0.02849	0.061926	0.078338	0	27	27	29	22	23	36	68	51	29	52

ENSMUSG00000035021	chr12	Baz1a	54892989	54894501	7159	0.54216	1.553426	0.028483	0.061926	0.051732	0	26	15	54	45	50	39	88	65	76	43
ENSMUSG00000073639	chr18	Rab18	6765205	6765332	2257	-0.32496	6.593879	0.028513	0.061965	0.025754	0	1435	1387	2357	1530	1921	1120	1994	1386	1993	1427
ENSMUSG00000028410	chr4	Dnaja1	40722150	40722435	8629	0.387383	5.380914	0.02853	0.061992	0.035648	0	515	541	696	445	638	781	1010	974	813	675
ENSMUSG00000053110	chr9	Yap1	7931999	7934732	9257	0.361001	5.990412	0.028605	0.062144	0.031641	0	683	484	1258	972	1212	860	1675	1156	1707	1223
ENSMUSG00000044807	chr11	Zfp354c	50811086	50815993	5596	-0.44878	2.153515	0.028679	0.062295	0.034477	0	71	52	106	75	104	55	71	79	69	59
ENSMUSG00000027805	chr3	Pfn2	57841895	57843314	3017	-0.37185	7.621515	0.028686	0.0623	0.034277	0	3235	3143	4783	2985	3449	2140	4010	2646	4603	2651
ENSMUSG00000103114	chr1	RP23-103B18.8	1.91E+08	1.91E+08	2385	-0.57617	1.334235	0.028701	0.062322	0.057083	0	45	22	53	56	59	28	59	36	35	22
ENSMUSG00000024325	chr17	Ring1	34020792	34021483	3243	0.346272	4.129502	0.028717	0.062337	0.025822	0	261	185	293	223	251	267	437	325	423	332
ENSMUSG00000041920	chr11	Slc16a6	1.09E+08	1.09E+08	4883	-0.61727	1.980371	0.028716	0.062337	0.077158	0	45	33	79	105	122	38	94	49	60	42
ENSMUSG00000034459	chr19	Ifit1	34640871	34640987	2656	0.839047	1.864729	0.028743	0.062382	0.15067	0	36	44	44	26	46	54	186	85	27	67
ENSMUSG00000059834	chr3	Sclt1	41626720	41627234	7569	-0.45023	1.991351	0.028771	0.062434	0.034068	0	53	53	101	78	78	42	80	66	68	46
ENSMUSG00000021577	chr13	Sdha	74322254	74323173	3883	-0.42234	9.909501	0.0288	0.062485	0.044503	0	12255	9581	20376	23317	24833	10716	21674	11977	20340	12298
ENSMUSG00000020377	chr11	Ltc4s	50236469	50236601	736	1.105923	0.830182	0.028809	0.062495	0.249786	0	22	15	28	8	11	41	11	92	33	21
ENSMUSG00000072946	chr12	Ptgr2	84285232	84285476	5929	-0.41886	5.998777	0.028853	0.062581	0.042877	0	910	604	1244	1629	1553	775	1397	826	1195	863
ENSMUSG00000075701	chr7	Vimp	66079649	66079789	1198	0.347438	5.08107	0.028885	0.062628	0.028061	0	416	431	644	403	461	535	936	657	741	599
ENSMUSG00000098708	chr7	Gm27252	63896533	63896559	717	-0.67456	0.210521	0.028883	0.062628	0.051721	0	16	20	31	20	17	11	18	12	17	16
ENSMUSG00000042590	chr13	Ipo11	1.07E+08	1.07E+08	7878	-0.31785	4.243941	0.028973	0.062809	0.021825	0	252	222	480	329	435	268	388	288	349	244
ENSMUSG00000025869	chr13	Nop16	54584185	54585424	1845	0.341826	4.417772	0.028995	0.062825	0.025871	0	270	260	350	279	321	381	519	429	493	345
ENSMUSG00000032459	chr9	Mrps22	98588730	98588926	3991	-0.3313	4.027683	0.028992	0.062825	0.024019	0	238	229	388	272	327	205	384	211	310	220
ENSMUSG00000059316	chr2	Slc27a4	29802634	29802960	4412	0.417471	3.833744	0.028999	0.062825	0.039576	0	126	111	245	263	247	244	273	324	391	241
ENSMUSG00000086584	chr11	Gm12002	12314514	12314667	2757	-0.71289	0.775958	0.028997	0.062825	0.086612	0	15	19	33	54	41	12	32	21	27	21
ENSMUSG00000021792	chr14	Fam213a	40993740	40994637	2948	-0.44185	4.856695	0.029033	0.062888	0.046751	0	489	460	562	524	569	357	438	659	423	329
ENSMUSG00000043415	chr2	Otud1	19657752	19660583	2832	0.850294	4.243976	0.029059	0.062934	0.173542	0	98	283	209	255	166	157	1242	248	436	315
ENSMUSG00000038524	chr18	Fchsd1	37957431	37959654	5473	0.64084	0.797191	0.029085	0.062979	0.058149	0	17	20	24	21	18	35	29	42	40	31
ENSMUSG00000022665	chr16	Ccdc80	45093402	45093597	4140	0.501708	5.494686	0.029129	0.063065	0.061429	0	679	508	757	389	596	916	814	1348	841	750
ENSMUSG00000006058	chr11	Snf8	96034885	96035067	2677	0.331959	4.56241	0.029143	0.063081	0.024691	0	288	285	411	283	391	426	566	466	581	359
ENSMUSG00000027770	chr3	Dhx36	62468013	62470747	10217	-0.32211	4.939268	0.029146	0.063081	0.024098	0	415	419	811	492	632	344	688	468	544	462
ENSMUSG00000021257	chr12	Angel1	86700502	86702441	4463	-0.368	3.665106	0.029164	0.063109	0.028402	0	179	130	371	232	266	162	197	195	256	190
ENSMUSG00000008604	chr3	Ubqln4	88553758	88553912	4147	-0.33802	6.862058	0.029215	0.06319	0.028219	0	1849	1255	2849	2254	2376	1503	2084	1655	2753	1504
ENSMUSG00000023170	chr11	Gps2	69913888	69914074	1604	-0.32229	4.801537	0.02921	0.06319	0.024003	0	398	386	671	526	498	343	509	397	598	421
ENSMUSG00000024537	chr18	Psmg2	67641599	67641735	1059	0.410031	4.691429	0.029215	0.06319	0.03916	0	367	340	413	292	299	485	689	452	588	462
ENSMUSG00000018974	chr5	Sart3	1.14E+08	1.14E+08	3586	0.355404	3.430632	0.029225	0.063202	0.025925	0	122	100	183	156	197	174	228	220	267	201
ENSMUSG00000083621	chrX	Gm14586	52772342	52772749	408	0.428435	3.426744	0.029274	0.063297	0.039116	0	162	116	185	134	117	195	316	197	262	157
ENSMUSG00000005566	chr7	Trim28	13024152	13025061	4044	0.317454	5.711801	0.029299	0.063331	0.024147	0	657	564	1073	663	807	841	1082	1103	1401	883
ENSMUSG00000073295	chrX	Nudt11	6047453	6048404	3036	-0.61657	0.402014	0.029299	0.063331	0.045472	0	16	17	40	22	26	10	24	18	24	13
ENSMUSG00000023235	chr8	Ccl25	4325210	4325288	2668	-0.57769	1.207252	0.029332	0.063392	0.057024	0	33	47	60	31	39	32	39	31	38	22
ENSMUSG00000052253	chr15	Zfp622	25984366	25985183	2803	0.35238	4.6136	0.029351	0.063421	0.028323	0	315	305	480	285	315	417	541	451	642	444
ENSMUSG00000030842	chr7	Lamtor1	1.02E+08	1.02E+08	1366	0.334846	6.788107	0.029438	0.0636	0.027676	0	1523	1042	1833	1682	1722	1885	2689	1973	2986	1814
ENSMUSG00000011658	chr7	Fuz	44896079	44896362	5003	0.327126	4.60802	0.029454	0.06361	0.02403	0	324	280	419	320	365	398	660	434	548	437
ENSMUSG00000022365	chr15	Derl1	57869502	57871906	3145	0.337029	6.583869	0.029454	0.06361	0.027951	0	1383	1028	1817	1121	1419	1602	2250	1974	2309	1637
ENSMUSG00000036057	chr9	Ptpn23	1.1E+08	1.1E+08	5336	0.370091	3.755104	0.029457	0.06361	0.030605	0	141	111	313	162	249	207	265	299	367	242
ENSMUSG00000074886	chr13	Grk6	55445334	55445560	3241	0.320724	4.055345	0.029497	0.063686	0.02248	0	216	139	347	215	289	270	378	335	427	273
ENSMUSG00000027454	chr2	Gins1	1.51E+08	1.51E+08	1516	0.679333	0.884869	0.029511	0.063706	0.074552	0	22	17	32	14	22	40	58	23	30	41
ENSMUSG00000018809	chr11	Smyd4	75348433	75348751	4329	-0.4487	2.484075	0.029519	0.063711	0.038506	0	81	54	157	99	136	70	113	59	107	79
ENSMUSG00000005950	chr11	P2rx5	73160421	73160733	2395	0.472742	3.853707	0.029559	0.06378	0.051981	0	144	93	183	305	245	242	390	286	338	270
ENSMUSG00000056413	chr5	Adap1	1.39E+08	1.39E+08	3232	0.628533	1.208233	0.02956	0.06378	0.069666	0	28	17	25	33	34	47	38	60	43	48
ENSMUSG00000060594	chr9	Layn	51056780	51057656	1786	0.779372	0.359367	0.029598	0.063851	0.097338	0	8	9	26	9	19	11	35	45	25	19
ENSMUSG00000028333	chr4	Anp32b	46450902	46451349	1716	0.352394	6.369057	0.029639	0.063929	0.030508	0	992	1044	1429	914	1374	1272	1955	1642	2280	1397
ENSMUSG00000020182	chr11	Ddc	11814101	11814517	4461	1.051587	-0.17405	0.02968	0.064007	0.155705	0	8	16	7	3	3	18	15	16	31	15
ENSMUSG00000041187	chr7	Prkd2	16842902	16843033	3757	0.50493	2.414046	0.029708	0.064057	0.050576	0	48	47	61	98	89	84	134	122	136	86
ENSMUSG00000003423	chr7	Pih1d1	45154303	45154420	2024	0.349778	5.063468	0.029748	0.064133	0.028702	0	507	365	520	442	466	528	799	674	883	554
ENSMUSG00000010307	chr7	Tmem86a	47050640	47050801	1791	0.611992	3.131209	0.029764	0.064147	0.08707	0	74	47	92	180	162	186	140	189	278	151
ENSMUSG00000022723	chr16	Crybg3	59490775	59493685	7488	-0.63069	4.524153	0.029762	0.064147	0.096934	0	225	123	567	703	755	193	457	323	418	287
ENSMUSG00000026770	chr2	Il2ra	11642807	11643064	5711	-0.72324	0.636184	0.029812	0.06424	0.081498	0	22	16	44	23	45	14	18	35	15	16
ENSMUSG00000026554	chr1	Dcaf8	1.72E+08	1.72E+08	12996	-0.33037	8.25887	0.029867	0.064348	0.027505	0	4840	4337	7940	4702	5653	3918	6056	4540	6665	3925
ENSMUSG00000029676	chr6	Pot1a	25743737	25744693	8669	-0.3494	3.633749	0.029889	0.064384	0.026334	0	182	188	304	194	239	169	257	165	261	149
ENSMUSG00000039007	chr15	Cpq	33083129	33083322	1923	0.371754	4.691966	0.029922	0.064444	0.032302	0	312	330	488	285	367	463	583	610	552	419
ENSMUSG00000047264	chr8	Zfp358	3493138	3493309	1999	-0.35482	5.173092	0.029974	0.064547	0.030331	0	532	488	897	692	641	474	562	529	923	433
ENSMUSG00000097061	chr12	9330151L19Rik	69197211	69197615	2546	0.490195	2.06684	0.029989	0.064569	0.044102	0	63	35	74	52	47	65	101	104	94	70
ENSMUSG00000043631	chr13	Ecm2	49504810	49505005	3596	-0.42749	4.252277	0.03008	0.064754	0.042371	0	197	192	535	365	546	265	330	256	301	303
ENSMUSG00000030103	chr6	Bhlhe40	1.09E+08	1.09E+08	3272	0.462602	7.278102	0.030117	0.064823	0.053834	0	1395	1726	3193	1840	2496	1771	5824	2107	4488	2976
ENSMUSG00000006299	chr1	Aamp	74279840	74280309	3458	0.357569	6.95505	0.030152	0.064887	0.031925	0	1585	1541	2085	1498	1853	2057	2673	2422	3626	2041
ENSMUSG00000083012	chr5	Fam220a	1.44E+08	1.44E+08	2734	-0.35276	6.290876	0.030157	0.064888	0.030874	0	1338	772	1964	1500	1605	1035	1595	1009	1778	966
ENSMUSG00000059839	chr13	Zfp874b	67471514	67474951	3743	-0.3562	3.430358	0.030175	0.064916	0.026878	0	159	165	275	157	209	128	228	155	205	148
ENSMUSG00000042423	chr7	Fbrs	1.27E+08	1.27E+08	2650	0.31456	4.330418	0.030194	0.064947	0.022092	0	252	198	428	280	291	326	438	372	525	367

ENSMUSG00000043131	chr6	Mob1a	83326016	83326267	4794	0.345239	4.468357	0.0302	0.064949	0.027565	0	217	236	482	299	354	313	537	540	482	383
ENSMUSG00000029217	chr5	Tec	72755718	72756379	3632	0.477349	2.552889	0.030216	0.064963	0.045736	0	76	63	96	55	94	78	134	100	158	142
ENSMUSG00000085455	chr5	1810059H22Rik	1.49E+08	1.49E+08	2897	0.81032	-0.0548	0.030212	0.064963	0.083041	0	6	5	8	18	12	19	16	17	25	20
ENSMUSG00000001280	chr15	Sp1	1.02E+08	1.02E+08	8325	0.315416	4.58436	0.030249	0.06501	0.023147	0	264	204	552	315	436	371	552	477	590	435
ENSMUSG00000033773	chr5	Rpap2	1.08E+08	1.08E+08	3893	-0.33224	4.195717	0.030261	0.06501	0.024809	0	310	264	458	264	331	251	329	294	355	243
ENSMUSG00000034867	chr7	Ankrd27	35586244	35586369	5258	-0.3238	4.017171	0.03025	0.06501	0.022599	0	210	193	418	313	330	224	320	253	293	216
ENSMUSG00000040280	chr10	Ndufa4l2	1.28E+08	1.28E+08	960	0.495387	2.931056	0.030262	0.06501	0.053487	0	55	73	112	115	151	104	176	119	253	163
ENSMUSG00000057113	chr11	Npm1	33152287	33152852	2665	0.368463	6.737466	0.030258	0.06501	0.033855	0	1263	1457	1853	1244	1479	1872	2852	1868	2665	1796
ENSMUSG00000028927	chr4	Padi2	1.41E+08	1.41E+08	5013	-1.21535	6.98686	0.030296	0.065066	0.360369	0	681	592	2516	6035	5227	317	1608	588	1078	3175
ENSMUSG00000031825	chr8	Crispld2	1.2E+08	1.2E+08	4777	-0.43037	4.976051	0.030298	0.065066	0.044678	0	311	343	943	567	886	493	464	418	566	455
ENSMUSG00000047996	chrX	Prrg1	78449613	78453172	11614	-0.68305	1.85889	0.030331	0.065126	0.100789	0	47	68	144	34	66	18	63	58	71	44
ENSMUSG00000033721	chr3	Vav3	1.09E+08	1.09E+08	6005	0.543099	1.625267	0.030338	0.06513	0.054537	0	16	25	56	50	52	54	83	65	66	53
ENSMUSG00000042185	chr9	Nfrkb	31386192	31386270	9953	-0.36051	3.564025	0.030356	0.065157	0.027533	0	176	128	353	181	258	136	207	188	260	157
ENSMUSG00000029338	chr5	Antxr2	97882783	97886600	5427	0.328503	4.478648	0.030476	0.065405	0.025118	0	227	208	538	293	369	329	526	438	529	437
ENSMUSG00000027163	chr2	Commd9	1.02E+08	1.02E+08	1602	0.336514	4.844358	0.030551	0.065556	0.026427	0	399	309	438	399	453	500	640	568	762	455
ENSMUSG00000031513	chr8	Leprotl1	34135572	34137838	2879	0.319998	4.383802	0.030603	0.065656	0.023094	0	213	229	411	310	332	328	459	414	554	360
ENSMUSG00000029291	chr5	Rufy3	88583574	88584317	3986	-0.45277	2.286398	0.030623	0.065689	0.037997	0	64	48	124	104	115	57	77	69	93	72
ENSMUSG00000033006	chr15	Sox10	79154913	79156641	2713	-0.58964	0.76673	0.030663	0.065763	0.049966	0	29	24	35	27	39	12	35	19	27	25
ENSMUSG00000042190	chr5	Cmklr1	1.14E+08	1.14E+08	3408	0.486188	3.728724	0.030704	0.065841	0.055843	0	157	112	240	162	222	226	187	422	280	246
ENSMUSG00000037697	chr14	Ddhd1	45593174	45595664	6759	0.494442	2.022543	0.030781	0.065996	0.047245	0	46	31	68	50	72	60	102	115	77	66
ENSMUSG00000018398	chr11	Sept8	53519257	53519451	6087	0.347922	4.098727	0.030795	0.066015	0.027823	0	180	151	368	228	312	269	368	428	382	286
ENSMUSG00000042410	chr2	Agps	75832177	75832511	9421	-0.32161	4.563559	0.030827	0.066073	0.023619	0	337	237	663	431	504	288	459	386	442	343
ENSMUSG00000047342	chr11	Zfp286	62753377	62753682	4735	-0.66105	1.011217	0.03084	0.06609	0.073603	0	20	34	46	41	48	22	27	32	18	33
ENSMUSG00000020846	chr11	Fam101b	76019194	76022240	3512	0.384199	3.837099	0.030854	0.06611	0.033455	0	151	121	207	225	293	229	393	311	306	234
ENSMUSG00000028389	chr4	Zfp37	62189540	62192689	3692	-0.67091	0.252868	0.030942	0.066277	0.055344	0	13	18	30	16	32	8	21	15	17	16
ENSMUSG00000032261	chr9	Sh3bgrl2	83548327	83548503	7865	0.606765	0.594757	0.030939	0.066277	0.052457	0	16	8	24	18	24	32	34	27	43	18
ENSMUSG00000026816	chr2	Gtf3c5	28566311	28567177	4560	0.354936	3.55653	0.030952	0.066287	0.026993	0	145	118	213	135	217	193	287	202	267	241
ENSMUSG00000034949	chr10	Zfr2	81233155	81233242	7483	-0.6375	1.412063	0.031005	0.06639	0.077085	0	52	38	52	37	70	33	25	24	51	47
ENSMUSG00000050989	chr4	Sepn1	1.35E+08	1.35E+08	3619	0.37576	3.818544	0.031018	0.066407	0.032119	0	170	126	288	185	227	210	294	368	280	273
ENSMUSG00000028969	chr5	Cdk5	24418250	24419462	2050	0.339195	3.756725	0.031106	0.066564	0.02444	0	159	145	233	210	198	228	326	282	329	207
ENSMUSG00000048755	chr15	Mcat	83546797	83547942	1893	-0.32731	4.304102	0.031101	0.066564	0.024747	0	284	253	413	410	392	226	402	302	432	257
ENSMUSG00000053985	chr7	Zfp14	30038053	30039416	1506	-0.59572	0.70418	0.031106	0.066564	0.050089	0	24	19	35	38	32	16	34	25	22	15
ENSMUSG00000039680	chr16	Mrps6	92058270	92058480	1053	0.390095	3.844718	0.03112	0.066582	0.033883	0	204	153	197	218	192	259	326	313	348	226
ENSMUSG00000000276	chr11	Dgke	89035179	89040911	8387	-0.43536	2.547561	0.03114	0.066604	0.038318	0	67	76	130	115	150	69	131	81	105	67
ENSMUSG00000046519	chr3	Golph3l	95588934	95589134	2841	-0.36753	3.827033	0.03114	0.066604	0.02973	0	225	161	406	206	313	212	292	202	208	200
ENSMUSG00000028945	chr5	Rheb	24802823	24803756	5540	-0.35276	5.906201	0.031189	0.066697	0.031137	0	1049	921	1519	837	1016	721	1297	841	1185	824
ENSMUSG00000082286	chr11	Pisd-ps1	3125904	3126058	1757	-0.46681	3.059394	0.031199	0.066708	0.047167	0	168	94	246	113	161	104	145	142	101	128
ENSMUSG00000035941	chr9	Ibtk	85687360	85688514	8628	-0.35228	6.726674	0.031226	0.066755	0.031321	0	1523	947	2916	2001	2546	1293	2056	1614	1980	1570
ENSMUSG00000020009	chr10	Ifngr1	19591949	19592197	2847	0.354342	5.028381	0.031243	0.06677	0.030605	0	371	303	674	453	537	611	700	824	653	498
ENSMUSG00000049233	chr13	Apoo-ps	1.07E+08	1.07E+08	903	-0.44392	2.736759	0.031238	0.06677	0.042022	0	122	108	166	96	108	78	154	96	117	72
ENSMUSG00000016252	chr2	Atp5e	1.74E+08	1.74E+08	1756	0.378078	8.369762	0.031306	0.066893	0.036626	0	4327	3599	4447	5195	4915	5228	9809	5718	8709	5376
ENSMUSG00000026097	chr1	Ormdl1	53297095	53297188	4711	-0.35785	3.53509	0.031326	0.066926	0.027758	0	186	162	277	182	230	150	267	177	175	154
ENSMUSG00000037661	chr3	Gpr160	30855950	30856057	4227	0.804341	0.129145	0.031337	0.066939	0.098975	0	13	3	25	9	9	22	18	26	35	12
ENSMUSG00000035095	chr14	Fam167a	63436394	63436632	4274	-1.05997	0.185229	0.031407	0.067077	0.211763	0	10	8	46	20	36	0	16	21	8	15
ENSMUSG00000022407	chr15	Adsl	80948490	80948700	4398	-0.35249	6.75333	0.03142	0.067094	0.031554	0	1623	1137	2372	2327	2365	1257	2493	1463	2270	1370
ENSMUSG00000037754	chr2	Ppp1r16b	1.59E+08	1.59E+08	8844	-0.53599	1.50943	0.031434	0.067113	0.052761	0	36	32	67	52	80	29	67	31	59	25
ENSMUSG00000037805	chr17	Rpl10a	28328471	28328618	2349	0.374625	7.144879	0.031448	0.067132	0.03569	0	1872	1848	2324	1731	1817	2446	3890	2635	3571	2208
ENSMUSG00000073616	chr1	Myeov2	92637145	92637403	1499	0.423953	5.613781	0.031629	0.067508	0.044732	0	710	669	653	562	587	886	1364	883	1269	767
ENSMUSG00000031851	chr8	Ntpcr	1.26E+08	1.26E+08	2673	0.356766	3.491357	0.031659	0.067561	0.026662	0	159	111	194	150	166	171	296	187	294	206
ENSMUSG00000026202	chr1	Tuba4a	75214228	75216593	3701	-0.34923	9.698874	0.031672	0.067579	0.031538	0	12458	12951	20660	13348	14840	11175	17121	10508	17412	11267
ENSMUSG00000024421	chr18	Lama3	12333819	12334308	10745	-0.82807	0.378347	0.031704	0.067636	0.123655	0	9	11	51	20	40	7	34	13	14	12
ENSMUSG00000034593	chr9	Myo5a	75071015	75071659	14803	0.437192	3.991242	0.031751	0.067726	0.045623	0	207	153	404	122	225	241	336	393	438	259
ENSMUSG00000038784	chr6	Cnot4	35022066	35023432	7185	-0.31272	4.392615	0.031802	0.067822	0.022551	0	288	292	557	337	408	240	443	328	412	299
ENSMUSG00000056493	chr5	Foxk1	1.42E+08	1.42E+08	7445	-0.39881	4.661539	0.031819	0.067847	0.038435	0	328	228	897	424	576	302	427	356	587	338
ENSMUSG00000027624	chr2	Epb4.1l1	1.56E+08	1.56E+08	11528	0.452789	3.652173	0.031827	0.067855	0.047754	0	166	127	208	130	212	212	206	369	274	226
ENSMUSG00000026827	chr2	Gpd2	57237635	57237988	6549	-0.42333	7.62018	0.03191	0.068021	0.046181	0	3657	3063	5986	2116	3343	2226	3887	3372	3484	2496
ENSMUSG00000031979	chr8	Cog2	1.25E+08	1.25E+08	4778	-0.32902	4.070428	0.031981	0.06816	0.024398	0	220	205	427	302	369	219	348	201	360	240
ENSMUSG00000056724	chr9	Nbeal2	1.11E+08	1.11E+08	9554	-0.41311	2.527313	0.032116	0.068438	0.03266	0	73	72	159	106	121	70	98	98	117	64
ENSMUSG00000024590	chr18	Lmnb1	56707813	56708474	2962	0.395892	2.975038	0.03213	0.068446	0.032362	0	96	87	162	90	104	144	172	164	169	145
ENSMUSG00000074247	chr8	Dda1	71469199	71469325	2846	0.315136	5.025853	0.032125	0.068446	0.023781	0	465	314	588	461	491	523	751	648	879	515
ENSMUSG00000100826	chr7	D7Ertd715e	59307924	59309726	26093	-0.5382	1.713212	0.032162	0.068503	0.055655	0	43	34	90	60	85	23	47	44	80	47
ENSMUSG00000021662	chr13	Arhgef28	97898595	97899816	6259	-0.64895	1.237957	0.032214	0.068602	0.080222	0	16	33	63	47	69	22	28	37	52	23
ENSMUSG00000028199	chr3	Cryz	1.55E+08	1.55E+08	6195	-0.33036	3.95337	0.032236	0.068638	0.024318	0	241	188	330	311	305	208	285	248	270	227
ENSMUSG00000033318	chr10	Gstt2	75831845	75832094	1370	0.533833	2.122163	0.032255	0.068656	0.057579	0	55	35	68	58	62	70	88	140	99	58
ENSMUSG00000034707	chr10	Gns	1.21E+08	1.21E+08	3855	0.335445	5.674978	0.03225	0.068656	0.028327	0	620	420	1206	679	822	802	1083	1178	1142	950

ENSMUSG00000075318	chr2	Scn2a1	65620857	65621015	9259	-0.76267	0.088169	0.032281	0.068701	0.09212	0	17	12	42	15	14	6	15	18	21	6
ENSMUSG00000060441	chr7	Trim5	1.04E+08	1.04E+08	3690	0.817129	0.140592	0.032339	0.068813	0.091479	0	16	12	11	10	6	21	28	27	16	21
ENSMUSG00000029381	chr5	Shroom3	92683435	92683831	7755	-0.69763	0.412459	0.03235	0.068815	0.085359	0	20	31	20	18	29	10	20	15	30	13
ENSMUSG00000055980	chr1	Irs1	82233101	82237604	9144	0.416256	6.491961	0.032348	0.068815	0.04458	0	1009	708	2293	993	1501	1044	1838	2175	2618	1803
ENSMUSG00000026192	chr1	Atic	71557150	71557274	7985	0.301914	5.016538	0.032428	0.068969	0.021884	0	420	330	649	438	498	514	719	657	747	603
ENSMUSG00000048264	chr13	Dip2c	9276528	9277066	8223	-0.37127	4.161221	0.032481	0.069072	0.03231	0	224	177	579	316	399	194	417	247	346	242
ENSMUSG00000024528	chr18	Srfbp1	52465693	52465785	1463	-0.39452	2.921844	0.032552	0.069204	0.032915	0	122	120	188	107	142	98	164	109	137	88
ENSMUSG00000026667	chr1	Uhmk1	1.7E+08	1.7E+08	8101	-0.32652	4.793845	0.032554	0.069204	0.02537	0	398	304	785	470	589	362	449	496	529	391
ENSMUSG00000025374	chr10	Nabp2	1.28E+08	1.28E+08	2507	0.314227	5.404705	0.032625	0.069344	0.024244	0	566	466	787	539	655	713	905	831	1172	677
ENSMUSG00000028959	chr5	Fastk	24438440	24439918	4372	-0.35507	7.349014	0.032649	0.069384	0.032672	0	2346	1854	3322	3609	3624	1951	3387	2159	3463	2297
ENSMUSG00000040520	chr4	Manea	26324506	26328308	4867	-0.51129	2.103933	0.032655	0.069384	0.055216	0	64	49	104	76	111	24	91	60	95	57
ENSMUSG00000024085	chr17	Man2a1	64600736	64601870	7223	0.394418	3.96349	0.03266	0.069385	0.037269	0	157	145	394	159	266	232	333	403	343	285
ENSMUSG00000075033	chr16	Nxpe3	55839953	55844726	6430	-0.60495	1.581944	0.032701	0.069461	0.070043	0	26	30	89	72	75	32	40	33	51	51
ENSMUSG00000048965	chr7	Mrgpre	1.44E+08	1.44E+08	3759	-0.57985	0.908792	0.032824	0.069711	0.04997	0	36	23	50	22	42	21	27	32	32	18
ENSMUSG00000040463	chr11	Mybbp1a	72441355	72441575	5803	-0.31761	6.058348	0.032868	0.069793	0.025535	0	935	713	1762	1206	1487	814	1270	1041	1415	922
ENSMUSG00000031585	chr8	Gtf2e2	33731833	33731988	2348	0.407022	3.20071	0.032901	0.069853	0.03487	0	117	117	150	110	119	150	235	150	268	155
ENSMUSG00000063358	chr16	Mapk1	16983382	16983739	7110	-0.30746	6.939804	0.032958	0.069962	0.02439	0	1815	1585	3130	2055	2434	1612	2595	1705	2487	1712
ENSMUSG00000013646	chr11	Sh3bp5l	58330724	58330802	6352	0.304739	4.588964	0.032996	0.070032	0.021816	0	304	227	440	347	417	381	529	424	650	444
ENSMUSG00000048027	chr17	Rgmb	15806253	15807801	2633	-0.32061	4.778556	0.033003	0.070035	0.024598	0	358	330	787	454	584	322	563	441	477	423
ENSMUSG00000027654	chr2	Fam83d	1.59E+08	1.59E+08	3991	-0.94875	2.420507	0.033068	0.070162	0.21842	0	129	163	162	26	42	62	74	30	96	70
ENSMUSG00000030868	chr7	Dctn5	1.22E+08	1.22E+08	2649	0.362737	4.322081	0.033158	0.070341	0.03093	0	257	261	332	229	287	383	441	400	470	332
ENSMUSG00000079022	chr15	Col22a1	71795795	71799520	9203	-0.61052	4.463635	0.033187	0.070391	0.094134	0	163	208	647	531	721	221	419	199	291	438
ENSMUSG00000047676	chr3	Rpsa-ps10	1.5E+08	1.5E+08	1031	0.485179	3.283462	0.033195	0.070398	0.05387	0	150	102	130	103	142	221	285	133	249	142
ENSMUSG00000029624	chr5	Ptcd1	1.45E+08	1.45E+08	3271	-0.39086	3.717244	0.033217	0.070432	0.035107	0	176	112	348	304	291	159	258	186	270	171
ENSMUSG00000006673	chr9	Qrich1	1.09E+08	1.09E+08	7728	-0.29714	5.005125	0.033253	0.070497	0.021355	0	429	391	831	597	637	394	631	501	662	457
ENSMUSG00000003031	chr6	Cdkn1b	1.35E+08	1.35E+08	4552	-0.32424	5.042368	0.033271	0.070524	0.025848	0	462	469	919	486	639	407	627	444	666	529
ENSMUSG00000026664	chr2	Phyh	4919019	4919144	1893	-0.50924	7.630099	0.033363	0.070709	0.067909	0	2470	1843	3306	5706	5595	2258	3998	2132	4522	2415
ENSMUSG00000049124	chr17	Gm8186	26098872	26099257	386	0.53472	1.662346	0.033394	0.070764	0.049978	0	46	37	43	34	34	50	82	64	68	64
ENSMUSG00000027384	chr2	Ndufaf5	1.4E+08	1.4E+08	1789	-0.41167	5.516023	0.033477	0.070928	0.043605	0	956	724	950	691	723	588	1048	754	778	463
ENSMUSG00000062867	chr9	Impdh2	1.09E+08	1.09E+08	3077	0.335627	5.473809	0.033518	0.071002	0.028098	0	570	558	786	537	645	740	1145	852	1196	648
ENSMUSG00000022022	chr14	Mtrf1	79397772	79398036	1862	-0.33725	3.723738	0.033524	0.071005	0.025738	0	186	165	310	257	267	155	321	183	253	167
ENSMUSG00000068922	chr3	Msto1	88905107	88905520	5418	0.391901	3.157732	0.033542	0.071031	0.033102	0	96	76	135	160	146	159	216	157	232	152
ENSMUSG00000053253	chr14	Ndfip2	1.05E+08	1.05E+08	11553	-0.31726	3.785313	0.033566	0.071071	0.021966	0	216	150	353	238	286	171	263	200	287	200
ENSMUSG00000027655	chr2	Dhx35	1.59E+08	1.59E+08	5170	-0.39269	3.377747	0.033579	0.071086	0.033984	0	157	99	296	195	223	147	200	113	219	140
ENSMUSG00000020576	chr12	Nbas	13269127	13269264	7239	-0.36675	4.444217	0.033597	0.071101	0.03234	0	270	200	682	381	537	257	399	320	462	307
ENSMUSG00000032040	chr9	Dcps	35124408	35124844	1451	0.390061	3.029668	0.033596	0.071101	0.031611	0	101	92	154	103	107	150	206	170	198	113
ENSMUSG00000073535	chr1	Gm5532	1.56E+08	1.56E+08	2206	-1.64395	1.108398	0.033621	0.071142	0.635425	0	2	3	15	149	87	3	28	7	37	21
ENSMUSG00000024617	chr18	Camk2a	60925618	60925840	7465	-0.3634	8.94773	0.033683	0.07125	0.034876	0	8548	5776	15258	6298	10120	6633	8649	6877	10557	6859
ENSMUSG00000028597	chr4	Gpx7	1.08E+08	1.08E+08	1289	0.424609	3.031769	0.033679	0.07125	0.038821	0	99	106	146	93	99	159	184	159	177	153
ENSMUSG00000037772	chr7	Mrpl23	1.43E+08	1.43E+08	1777	0.350646	5.257254	0.033727	0.071331	0.030533	0	531	477	596	496	513	643	985	680	1014	623
ENSMUSG00000075307	chr2	Klhl41	69670120	69671306	2529	0.339661	9.230083	0.033747	0.071362	0.030507	0	7229	6406	10842	9006	8933	8874	15752	9578	17257	10962
ENSMUSG00000025873	chr13	Faf2	54621784	54621903	5084	0.320652	3.872909	0.03376	0.071379	0.023346	0	195	124	311	187	243	234	347	303	328	261
ENSMUSG00000044791	chr9	Setd2	1.11E+08	1.11E+08	8350	-0.32642	5.003176	0.033797	0.071446	0.026172	0	437	325	964	573	675	372	669	523	599	451
ENSMUSG00000030983	chr7	Bccip	1.34E+08	1.34E+08	2038	-0.37174	6.042321	0.033877	0.071603	0.035893	0	1200	1090	1461	924	1134	817	1384	862	1339	906
ENSMUSG00000045968	chr1	Teddm2	1.54E+08	1.54E+08	4905	0.480776	2.768911	0.033915	0.071673	0.05259	0	46	69	167	78	107	129	127	123	216	118
ENSMUSG00000026803	chr2	Ttf1	29060262	29060303	6023	-0.37453	2.849785	0.033993	0.071814	0.028548	0	108	90	185	111	161	102	149	109	123	84
ENSMUSG00000075389	chr11	2810410L24Rik	1.2E+08	1.2E+08	3028	0.565823	1.562592	0.033993	0.071814	0.058495	0	46	28	48	28	31	57	94	58	66	37
ENSMUSG00000063808	chr7	Gpatch1	35276536	35276811	3295	-0.37002	3.025173	0.034008	0.071834	0.02856	0	111	110	214	135	168	95	170	122	129	125
ENSMUSG00000028618	chr4	Tmem59	1.07E+08	1.07E+08	2056	0.314662	6.609181	0.034022	0.071852	0.025645	0	1240	1139	1751	1267	1522	1537	2412	1924	2296	1736
ENSMUSG00000103409	chr9	RP23-456B9.23	1.08E+08	1.08E+08	369	-0.43604	3.132116	0.034038	0.071876	0.042565	0	157	83	207	155	214	116	223	105	124	111
ENSMUSG00000033031	chr16	C330027C09Rik	48994185	48994379	5688	-0.69126	0.15836	0.034048	0.071885	0.059768	0	21	16	27	10	27	14	16	13	14	13
ENSMUSG00000043059	chr5	Zfp513	31198981	31200147	2476	0.372183	2.800391	0.034054	0.071885	0.027415	0	84	63	117	106	111	112	173	130	168	125
ENSMUSG00000037235	chr5	Mxd4	34173887	34177149	3882	0.321364	5.53242	0.034073	0.071914	0.026308	0	531	408	952	683	798	758	923	1076	1091	802
ENSMUSG00000020621	chr12	Rdh14	10390780	10391226	1472	-0.32024	5.352797	0.034113	0.071988	0.026075	0	633	626	891	670	765	467	900	604	869	537
ENSMUSG00000049764	chr10	Zfp280b	76032654	76032749	5097	-0.35811	4.12414	0.034199	0.072156	0.030378	0	261	195	530	235	404	227	297	251	416	214
ENSMUSG00000026526	chr1	Fh1	1.76E+08	1.76E+08	3392	-0.37981	7.88356	0.034272	0.0723	0.038229	0	3349	2511	4707	5608	5425	2924	5364	3003	4952	2909
ENSMUSG00000027340	chr2	Slc23a2	1.32E+08	1.32E+08	7951	-0.43615	3.684154	0.034327	0.072404	0.045508	0	147	114	368	280	326	109	259	217	247	176
ENSMUSG00000015757	chr10	Ppil4	7792891	7793020	6450	-0.34076	3.643476	0.034351	0.072443	0.026072	0	182	166	288	215	267	165	293	187	195	164
ENSMUSG00000021458	chr13	2010111I01Rik	63014934	63015963	6349	0.397367	4.644418	0.034376	0.072484	0.039474	0	267	204	359	476	423	408	620	436	797	379
ENSMUSG00000090841	chr10	Myl6	1.28E+08	1.28E+08	665	0.409362	7.022887	0.034462	0.072655	0.044136	0	1932	1677	1690	1495	1759	2447	3208	2743	3027	2079
ENSMUSG00000028524	chr4	Sgip1	1.03E+08	1.03E+08	10136	-0.81208	-0.05865	0.034469	0.072658	0.083947	0	7	11	32	16	25	8	16	16	7	9
ENSMUSG00000051034	chr5	Zfp11	1.3E+08	1.3E+08	3929	-0.57823	1.47057	0.034488	0.072687	0.065347	0	35	27	76	51	77	23	66	21	54	37
ENSMUSG00000022419	chr15	Deptor	55112317	55112619	8874	-0.32985	6.993049	0.034514	0.07273	0.028646	0	1805	1816	3532	1717	2706	1626	2451	2077	2551	1665
ENSMUSG00000057278	chr6	Snrpg	86371583	86371614	350	0.418341	3.154689	0.034522	0.07273	0.037832	0	125	110	154	98	104	166	210	168	240	137
ENSMUSG00000063410	chr14	Stk24	1.21E+08	1.21E+08	2676	-0.34053	4.223143	0.034531	0.07273	0.027161	0	268	183	562	316	407	236	374	267	321	297

ENSMUSG00000092327	chr5	Gm20488	1.49E+08	1.49E+08	2996	0.396856	3.09869	0.034525	0.07273	0.035474	0	95	80	194	98	134	149	259	164	150	154
ENSMUSG00000041491	chr19	Cep78	15955774	15956403	2548	-0.48394	1.419207	0.034544	0.072746	0.039249	0	34	34	73	58	45	28	49	41	46	33
ENSMUSG00000033632	chr18	AW554918	25168999	25169086	7014	-0.47639	2.297128	0.034553	0.072755	0.046692	0	84	46	156	63	120	57	84	58	97	73
ENSMUSG00000042605	chr5	Atxn2	1.22E+08	1.22E+08	7161	-0.34845	5.250503	0.034569	0.072776	0.030691	0	495	348	1034	790	886	432	713	593	767	567
ENSMUSG00000024990	chr19	Rbp4	38116620	38116909	1297	1.292883	2.677349	0.034594	0.072818	0.410651	0	105	71	41	22	20	107	39	447	68	108
ENSMUSG00000032419	chr9	Tbx18	87702800	87705945	4718	0.568826	1.103344	0.034641	0.072904	0.057673	0	16	18	47	24	30	38	74	29	42	40
ENSMUSG00000061887	chr4	Ssbp3	1.07E+08	1.07E+08	6582	0.329391	4.259781	0.034735	0.073089	0.025973	0	222	168	357	283	348	288	402	455	487	310
ENSMUSG00000068141	chr17	Gm10232	3044014	3044733	720	0.575654	0.759885	0.034741	0.073089	0.045604	0	18	15	23	23	22	34	45	33	32	27
ENSMUSG00000071072	chr10	Ptges3	1.28E+08	1.28E+08	2217	0.358061	5.977176	0.034745	0.073089	0.033157	0	859	807	1056	712	883	996	1444	1278	1729	1057
ENSMUSG00000028497	chr4	Ptplad2	88396144	88398219	6756	0.434997	2.280169	0.034751	0.07309	0.038211	0	64	41	95	54	74	84	109	113	93	92
ENSMUSG00000023307	chr19	March5	37207543	37207904	2396	-0.34667	6.068936	0.03476	0.073097	0.031398	0	1127	996	1671	986	1213	928	1198	1056	1503	757
ENSMUSG00000025169	chr11	Ogfod3	1.21E+08	1.21E+08	1308	0.339214	3.663865	0.034787	0.073143	0.025595	0	155	142	239	159	195	234	272	218	327	225
ENSMUSG00000047260	chr11	Emc6	73175519	73176751	1415	0.351271	6.058	0.034808	0.073174	0.031996	0	1001	723	1096	893	884	1135	1623	1246	1836	1042
ENSMUSG00000026116	chr1	Tmem131	36792191	36793205	9413	-0.3999	4.866663	0.034973	0.073498	0.040693	0	369	245	846	651	673	277	653	435	562	411
ENSMUSG00000028639	chr4	Ybx1	1.19E+08	1.19E+08	2531	-0.32694	8.8575	0.03497	0.073498	0.028647	0	7696	6620	10239	8043	8297	6230	9375	6519	9447	6295
ENSMUSG00000032380	chr9	Dapk2	66158223	66158340	3512	-0.54639	3.125184	0.034986	0.073514	0.071271	0	76	64	266	215	256	111	139	124	132	125
ENSMUSG00000054792	chr9	Klhl18	1.1E+08	1.1E+08	4526	-0.33552	3.509718	0.035032	0.07359	0.024347	0	164	123	294	197	259	137	222	155	241	166
ENSMUSG00000066724	chr7	Gm10175	23946649	23947237	589	0.700368	1.358443	0.035033	0.07359	0.093271	0	23	41	29	27	21	46	76	39	89	34
ENSMUSG00000020755	chr11	Sap30bp	1.16E+08	1.16E+08	3708	0.334177	4.053574	0.035069	0.073653	0.026578	0	225	127	293	237	307	277	379	334	373	308
ENSMUSG00000026589	chr1	Sec16b	1.58E+08	1.58E+08	5410	0.518439	1.147135	0.035084	0.073674	0.041046	0	21	23	41	27	27	38	59	42	41	44
ENSMUSG00000034974	chr10	Dapk3	81183007	81183096	1766	0.334401	4.063993	0.035135	0.073769	0.025952	0	237	169	299	226	243	249	350	321	472	309
ENSMUSG00000038489	chr7	Polr2l	1.41E+08	1.41E+08	1650	0.38692	5.217624	0.03517	0.07383	0.038171	0	554	444	487	478	521	726	918	663	989	560
ENSMUSG00000022906	chr16	Parp9	35938470	35939060	4872	0.384932	3.064787	0.03519	0.073861	0.032376	0	106	76	154	101	144	147	244	173	153	136
ENSMUSG00000002825	chr9	Qtrt1	21411837	21412097	1319	0.412192	2.144776	0.035202	0.073872	0.029894	0	55	41	71	58	72	70	112	87	115	69
ENSMUSG00000014769	chr17	Psmb1	15475721	15476205	1036	0.400183	7.057198	0.035207	0.073872	0.042518	0	1829	1819	2052	1519	1622	2410	3696	2432	3447	2009
ENSMUSG00000004085	chr2	Zak	72285637	72285855	10175	-0.3252	8.158036	0.035235	0.07392	0.028329	0	4187	3534	7904	4542	5912	3853	5971	3545	6294	3820
ENSMUSG00000042705	chr18	Commd10	46958862	46958928	1561	0.415952	2.447755	0.035284	0.074011	0.033918	0	70	54	90	64	89	81	142	125	111	98
ENSMUSG00000024456	chr18	Diap1	37843601	37845498	6339	-0.37543	7.005667	0.035383	0.074206	0.03757	0	1960	1315	2871	2654	3046	1791	2220	1523	3234	1591
ENSMUSG00000050144	chr3	Slc25a44	88410498	88412897	3578	-0.2956	5.079956	0.03539	0.074211	0.021729	0	521	408	878	569	651	438	608	595	669	458
ENSMUSG00000045777	chr7	Ifitm10	1.42E+08	1.42E+08	4789	0.583323	1.986789	0.035416	0.074253	0.074789	0	49	41	77	26	56	83	57	75	138	66
ENSMUSG00000040612	chr1	Ildr2	1.66E+08	1.66E+08	8251	-0.59648	1.299994	0.035444	0.074299	0.064974	0	27	32	72	42	62	27	27	46	29	38
ENSMUSG00000044609	chr7	Gm9294	42953600	42954388	789	0.612222	0.623909	0.035453	0.074307	0.056871	0	17	15	30	12	17	26	29	42	36	23
ENSMUSG00000066900	chr5	Suds3	1.17E+08	1.17E+08	2418	-0.32721	6.347684	0.035471	0.074333	0.028236	0	1246	998	1612	1636	1754	1077	1486	1221	1769	1083
ENSMUSG00000039195	chr2	1110008P14Rik	32377097	32379533	2694	0.429523	4.427417	0.035549	0.074484	0.046126	0	357	252	318	239	242	413	450	399	631	352
ENSMUSG00000040824	chr7	Snrpd2	19149722	19149894	613	0.379909	5.298994	0.03557	0.074516	0.036944	0	545	517	562	500	507	697	1076	684	1039	609
ENSMUSG00000026123	chr1	Plekhb2	34849976	34850063	7987	-0.37008	6.302834	0.035579	0.074524	0.036221	0	1111	693	1854	1803	1886	969	1489	1120	1673	1093
ENSMUSG00000002944	chr5	Cd36	17781690	17783349	3927	-0.60453	7.855011	0.035606	0.074568	0.097936	0	2800	2208	3438	7884	6142	1924	4613	4892	3198	2368
ENSMUSG00000053769	chr3	Lysmd1	95134088	95134996	2394	0.451255	2.260426	0.03581	0.074983	0.040967	0	69	43	67	47	90	78	114	90	123	89
ENSMUSG00000050855	chr7	Zfp940	29833620	29835803	6090	-0.65637	0.555496	0.035816	0.074984	0.069561	0	24	20	29	27	34	12	40	11	18	18
ENSMUSG00000029127	chr5	Zbtb49	38189735	38192137	7715	-0.57484	0.663403	0.03583	0.07499	0.044937	0	28	17	46	23	31	14	22	23	30	20
ENSMUSG00000041168	chr17	Lonp1	56614301	56614563	2963	-0.31928	6.657073	0.03583	0.07499	0.027099	0	1412	1182	2196	2051	2227	1237	1939	1529	2260	1340
ENSMUSG00000025499	chr7	Hras	1.41E+08	1.41E+08	3733	0.348178	6.370454	0.035868	0.075059	0.032039	0	1221	934	1336	964	1275	1512	1938	1629	2116	1276
ENSMUSG00000001240	chr11	Ramp2	1.01E+08	1.01E+08	3301	0.319788	5.982782	0.036002	0.075326	0.02669	0	799	722	1057	911	961	1088	1486	1235	1599	1016
ENSMUSG00000026095	chr1	Asnsd1	53344617	53344979	3528	-0.31826	6.883279	0.036081	0.07548	0.027119	0	1763	1626	2732	2117	2251	1526	2594	1517	2515	1592
ENSMUSG00000026571	chr1	Dcaf6	1.65E+08	1.65E+08	6424	-0.31943	7.762607	0.036132	0.075574	0.027544	0	3288	2843	5911	3433	4154	2667	4928	2852	4550	2969
ENSMUSG00000061126	chr17	Cyp4f39	32468462	32468683	1599	-0.68643	3.179244	0.036177	0.075658	0.119152	0	104	165	225	191	199	60	110	205	61	168
ENSMUSG00000026648	chr2	Dclre1c	3424131	3424326	9316	-0.55499	1.149771	0.036254	0.075794	0.053464	0	38	26	66	28	49	30	44	36	26	20
ENSMUSG00000030811	chr7	Fbxl19	1.28E+08	1.28E+08	4293	0.499488	1.605877	0.036251	0.075794	0.042855	0	38	32	50	36	37	58	57	55	90	52
ENSMUSG00000002031	chr9	Ift46	44767908	44767927	5658	0.353035	3.604614	0.036277	0.07582	0.027735	0	144	154	202	162	173	201	301	230	276	224
ENSMUSG00000030695	chr7	Aldoa	1.27E+08	1.27E+08	2754	0.337242	14.3243	0.036278	0.07582	0.031038	0	291551	197973	389548	271000	308344	311353	457182	381596	635255	340671
ENSMUSG00000025026	chr19	Add3	53140445	53140714	4938	-0.34621	4.792267	0.036321	0.075898	0.030127	0	366	281	904	436	625	317	516	439	532	424
ENSMUSG00000004561	chr14	Mettl17	51884842	51885023	3970	0.33083	3.398056	0.03633	0.075904	0.023881	0	115	104	190	145	196	162	244	208	260	190
ENSMUSG00000055862	chr10	Izumo4	80702693	80702959	938	0.521644	1.063162	0.036349	0.075932	0.03974	0	23	20	36	18	34	33	56	42	42	39
ENSMUSG00000028522	chr4	Mier1	1.03E+08	1.03E+08	12513	-0.35395	4.073777	0.03638	0.075986	0.030207	0	204	202	466	328	348	180	262	304	343	254
ENSMUSG00000024132	chr17	Eci1	24426683	24426742	1091	-0.4633	6.319841	0.036527	0.076281	0.057784	0	983	901	1346	2372	1792	859	1848	1083	1340	1093
ENSMUSG00000040302	chr5	Rbm48	3583978	3584807	3071	-0.40948	2.548103	0.036641	0.076507	0.034309	0	93	73	175	86	111	71	123	78	94	86
ENSMUSG00000039063	chr2	Echdc3	6188465	6189651	2685	0.3768	3.264808	0.036655	0.076523	0.030964	0	132	95	142	146	139	137	261	199	233	161
ENSMUSG00000020216	chr10	Jsrp1	80808496	80809039	1333	0.361645	8.779951	0.036756	0.076722	0.035689	0	6188	5063	6945	5541	6475	7974	9087	7439	12701	7960
ENSMUSG00000040365	chr11	Trim41	48806404	48807846	3511	0.293684	4.818628	0.036791	0.076783	0.021453	0	373	286	589	352	450	465	633	546	694	490
ENSMUSG00000038546	chr13	Ranbp9	43402673	43403689	3064	-0.30641	5.341722	0.036822	0.076836	0.024187	0	646	429	1100	684	824	456	807	603	836	633
ENSMUSG00000028397	chr4	Kdm4c	74242497	74242640	5823	-0.3523	3.239346	0.036911	0.07701	0.027149	0	134	129	263	142	187	109	163	149	184	145
ENSMUSG00000033379	chr4	Atp6v0b	1.18E+08	1.18E+08	2051	0.346984	6.316054	0.037064	0.077316	0.032175	0	1171	907	1287	1035	1095	1452	1985	1429	2042	1269
ENSMUSG00000038866	chr1	Zcchc2	1.06E+08	1.06E+08	6774	-0.34632	3.392619	0.037082	0.077341	0.026765	0	182	131	278	158	195	146	179	159	213	139
ENSMUSG00000072623	chr6	Zfp9	1.18E+08	1.18E+08	3968	-0.41499	2.845753	0.037094	0.077354	0.038502	0	87	94	214	122	152	85	155	74	160	93
ENSMUSG00000041935	chr15	AW549877	3982036	3986479	5083	-0.34414	4.083602	0.037126	0.07741	0.02865	0	215	196	472	280	402	171	330	314	303	247

ENSMUSG00000027184	chr2	Caprin1	1.04E+08	1.04E+08	10219	-0.30402	5.92509	0.037267	0.077678	0.024443	0	901	732	1578	1015	1253	722	1147	1095	1142	864
ENSMUSG00000052698	chr9	Tln2	67217087	67221518	12193	-0.36838	6.281084	0.037263	0.077678	0.036533	0	939	740	2388	1686	1608	888	1505	1145	1717	1039
ENSMUSG00000019906	chr10	Lin7a	1.07E+08	1.07E+08	5952	-0.61777	1.376874	0.037305	0.077745	0.076443	0	23	46	73	32	74	39	48	32	40	21
ENSMUSG00000036533	chr17	Cdc42ep3	79334025	79335716	1967	-0.33089	4.854145	0.037394	0.07792	0.028332	0	467	383	719	446	580	274	644	394	635	441
ENSMUSG00000027933	chr3	Ints3	90391380	90391911	4460	-0.29936	4.536754	0.037433	0.077988	0.021818	0	356	251	599	384	505	315	402	370	475	329
ENSMUSG00000024773	chr19	Atg2a	6241668	6241966	7693	-0.40446	4.552107	0.037484	0.07807	0.042101	0	275	199	613	553	589	266	367	366	496	346
ENSMUSG00000025278	chr14	Flnb	7817957	7818443	9100	-0.42311	3.604063	0.037483	0.07807	0.043374	0	136	105	332	257	334	148	197	210	214	167
ENSMUSG00000020866	chr11	Cacna1g	94408391	94409876	10137	0.614585	1.198277	0.037532	0.078158	0.079617	0	12	19	54	18	42	26	60	47	50	57
ENSMUSG00000048240	chr10	Gng7	80948624	80951746	3786	-0.4427	2.012846	0.037565	0.078215	0.037867	0	73	48	105	55	88	46	79	68	61	51
ENSMUSG00000010406	chr14	Mrpl52	54426909	54426960	412	0.465948	4.828139	0.037627	0.078332	0.056861	0	407	420	332	280	351	587	698	541	694	463
ENSMUSG00000026788	chr2	Zbtb43	33450287	33455123	5225	-0.35174	3.5935	0.037643	0.078352	0.028146	0	159	129	323	217	283	170	220	176	198	187
ENSMUSG00000000253	chr13	Gmpr	45507444	45507743	1871	0.310846	7.652864	0.037675	0.078393	0.026424	0	2608	2116	3511	2943	3164	3086	5116	3693	5518	3258
ENSMUSG00000039382	chrX	Wdr45	7721973	7722230	2717	0.317168	4.953717	0.03767	0.078393	0.025603	0	353	334	478	505	518	508	694	614	805	518
ENSMUSG00000001175	chr12	Calm1	1E+08	1E+08	4698	-0.38975	9.220028	0.037705	0.07844	0.04194	0	10878	9605	16398	6994	10029	7875	12207	7905	11864	7765
ENSMUSG00000031622	chr8	Sin3b	72723288	72723408	4298	0.315297	4.707206	0.037709	0.07844	0.024805	0	297	316	512	345	387	416	602	510	737	400
ENSMUSG00000032217	chr9	Rnf111	70425429	70427107	5003	-0.38995	3.364619	0.037723	0.078458	0.035488	0	146	114	328	156	223	89	203	170	212	147
ENSMUSG00000033319	chr18	Fem1c	46501746	46506389	5726	-0.35774	4.101186	0.037782	0.078567	0.031743	0	228	175	541	309	354	182	399	216	368	236
ENSMUSG00000017485	chr14	Top2b	16365179	16365726	6355	-0.32525	5.341604	0.037818	0.07863	0.027861	0	555	568	1097	615	832	435	950	583	716	636
ENSMUSG00000022451	chr15	Twf1	94577951	94579990	3054	0.391025	3.29518	0.037828	0.078638	0.035927	0	130	80	172	137	161	152	270	233	170	176
ENSMUSG00000037408	chr1	Cnnm4	36471620	36473085	4829	-0.72268	3.367499	0.037904	0.078785	0.13607	0	71	67	184	361	385	91	178	111	182	149
ENSMUSG00000059772	chr7	Slx1b	1.27E+08	1.27E+08	3521	0.425954	2.203631	0.037962	0.078892	0.036914	0	53	35	88	60	78	59	103	107	115	88
ENSMUSG00000034757	chr11	Tmub2	1.02E+08	1.02E+08	2544	0.284043	4.599112	0.037981	0.078907	0.019778	0	325	237	477	323	400	391	582	465	598	397
ENSMUSG00000054939	chr16	Zfp174	3847268	3848274	5897	-0.47178	1.790789	0.037977	0.078907	0.043177	0	45	37	109	59	75	31	71	41	67	51
ENSMUSG00000022898	chr16	Dscr3	94497783	94499082	3670	0.312864	4.139076	0.037991	0.078915	0.023398	0	258	169	314	224	289	290	394	345	456	292
ENSMUSG00000005299	chr5	Letm1	33739673	33742612	9650	-0.42584	6.107346	0.038005	0.078925	0.049337	0	838	629	1344	1831	1832	803	1404	959	1329	935
ENSMUSG00000028882	chr4	Ppp1r8	1.33E+08	1.33E+08	2924	0.307523	4.212563	0.038007	0.078925	0.02246	0	255	201	325	240	293	297	412	362	494	306
ENSMUSG00000026792	chr2	Lrsam1	32925216	32926901	5145	-0.32725	3.811977	0.038054	0.078967	0.025255	0	220	147	337	264	299	154	305	204	261	217
ENSMUSG00000031775	chr8	Pllp	94674895	94676279	1889	-0.6608	0.100059	0.038056	0.078967	0.060954	0	10	15	24	23	24	8	16	9	21	15
ENSMUSG00000038722	chr5	Bud31	1.45E+08	1.45E+08	1609	0.402469	5.289355	0.038058	0.078967	0.042838	0	597	511	584	424	469	704	1127	697	993	587
ENSMUSG00000051451	chr7	Crebzf	90442729	90446104	4989	-0.34265	3.770571	0.038053	0.078967	0.028173	0	218	192	328	183	301	144	260	211	261	220
ENSMUSG00000078670	chr7	Fam174b	73740307	73740828	2678	0.673706	0.619974	0.038043	0.078967	0.073142	0	17	12	13	15	30	28	33	42	38	18
ENSMUSG00000001663	chr10	Gstt1	75783813	75784233	1528	0.418495	3.331254	0.038094	0.079018	0.041324	0	130	124	174	123	119	171	201	253	212	186
ENSMUSG00000020941	chr11	Map3k14	1.03E+08	1.03E+08	6550	0.428684	3.034891	0.038088	0.079018	0.043084	0	82	75	135	101	169	151	279	131	184	116
ENSMUSG00000092203	chr17	1110038B12Rik	34950238	34950475	1811	0.453701	2.815279	0.038164	0.079151	0.047583	0	111	61	126	83	86	149	153	141	198	90
ENSMUSG00000001964	chrX	Emd	74254687	74255033	2517	0.308337	4.950106	0.038192	0.079196	0.02428	0	422	323	599	428	434	561	698	546	819	496
ENSMUSG00000032059	chr9	Alg9	50775019	50775518	3889	0.361395	3.388269	0.038258	0.079322	0.030279	0	131	102	196	129	176	169	193	244	282	173
ENSMUSG00000027708	chr3	Dcun1d1	35892105	35895699	4563	-0.35356	5.520418	0.038308	0.079412	0.033549	0	705	756	1244	580	832	565	979	620	828	700
ENSMUSG00000032232	chr9	Cgnl1	71626509	71629392	7844	0.608041	3.218754	0.038351	0.079489	0.094606	0	96	93	146	119	128	103	153	388	152	192
ENSMUSG00000039480	chr10	Nt5dc1	34288288	34288562	3192	-0.46565	2.250132	0.038365	0.079505	0.048096	0	75	57	145	62	108	34	102	72	98	61
ENSMUSG00000030107	chr6	Usp18	1.21E+08	1.21E+08	1770	0.548898	2.043999	0.038402	0.079569	0.066934	0	60	36	87	28	54	86	122	76	67	78
ENSMUSG00000019916	chr10	P4ha1	59323296	59323476	4114	0.319391	5.804454	0.038437	0.079631	0.027366	0	683	615	1143	613	974	894	1207	1254	1230	1026
ENSMUSG00000024290	chr18	Rock1	10064401	10066051	6187	-0.39985	3.749901	0.038486	0.079719	0.039672	0	155	187	366	240	297	116	243	219	225	247
ENSMUSG00000076435	chr11	Acsf2	94557102	94558357	3432	0.634486	1.715009	0.038512	0.079761	0.091234	0	31	24	48	41	58	40	58	130	66	53
ENSMUSG00000066613	chr5	Zfp932	1.1E+08	1.1E+08	3272	-0.45603	2.454945	0.038567	0.079861	0.047164	0	104	97	110	73	102	74	101	69	95	75
ENSMUSG00000047215	chr5	Rpl9	65388364	65388441	3080	0.381208	7.766654	0.038643	0.080008	0.04024	0	3228	2787	3257	2504	2828	3837	6137	4168	5194	3367
ENSMUSG00000050382	chr7	Kif7	79698098	79698915	4581	0.718966	-0.16602	0.038677	0.080065	0.065065	0	6	7	17	4	14	16	16	18	20	17
ENSMUSG00000032178	chr9	Ilf3	21368019	21368099	4754	-0.30564	4.642886	0.038791	0.080288	0.02337	0	322	280	681	440	554	329	461	377	482	381
ENSMUSG00000024589	chr18	Nedd4l	64887756	64888095	8626	0.365826	4.975346	0.038807	0.080308	0.035716	0	366	230	626	409	649	435	756	478	931	668
ENSMUSG00000042557	chr9	Sin3a	57072040	57072063	5385	-0.29414	4.140542	0.038896	0.08048	0.020617	0	242	216	483	284	362	221	356	270	354	249
ENSMUSG00000031532	chr8	Saraf	34154563	34154836	1897	0.30619	7.732314	0.038913	0.080501	0.025998	0	2465	2244	3836	3332	3387	3427	5229	3780	5698	3563
ENSMUSG00000035949	chr2	Fbxw2	34804514	34805999	6661	-0.29637	5.749187	0.038918	0.080501	0.023604	0	840	767	1228	888	997	716	1148	771	1064	739
ENSMUSG00000028467	chr4	Gba2	43566928	43567467	4481	-0.38981	3.205099	0.038956	0.080566	0.034959	0	116	100	196	203	229	103	166	147	164	141
ENSMUSG00000039231	chrX	Suv39h1	8061171	8062983	5270	0.376441	2.825089	0.038978	0.080599	0.029234	0	87	76	120	105	95	110	186	140	166	121
ENSMUSG00000025425	chr18	St8sia5	77185853	77186225	2097	-0.3801	4.863549	0.03899	0.080611	0.038423	0	459	277	736	627	595	301	575	322	729	435
ENSMUSG00000085396	chrX	Firre	50555744	50555929	1439	0.532977	1.092412	0.038999	0.080619	0.046759	0	20	25	42	18	28	30	54	45	44	44
ENSMUSG00000045302	chr5	Preb	30950853	30955737	7176	0.311627	5.888752	0.039149	0.080915	0.026316	0	807	490	1137	863	1005	1029	1289	1090	1578	1006
ENSMUSG00000083863	chr2	Gm13341	22587291	22587962	672	-0.64915	1.053738	0.03919	0.080987	0.083826	0	21	17	68	46	51	12	24	31	44	30
ENSMUSG00000037032	chr7	Apbb1	1.06E+08	1.06E+08	4404	0.374788	3.33791	0.039248	0.081094	0.033579	0	103	76	178	176	180	152	235	184	285	185
ENSMUSG00000052419	chr6	2610001J05Rik	13867735	13870740	3784	0.322102	4.846138	0.039286	0.08116	0.026598	0	416	309	471	395	423	470	783	492	754	452
ENSMUSG00000015222	chr1	Map2	66175273	66175495	16449	-0.69213	0.652713	0.039314	0.081193	0.083977	0	14	12	46	38	42	15	28	12	22	25
ENSMUSG00000042901	chr1	Aida	1.83E+08	1.83E+08	6175	0.292145	4.497556	0.039309	0.081193	0.02105	0	273	254	429	303	365	369	585	437	497	378
ENSMUSG00000020585	chr12	Laptm4a	8921664	8922294	1773	0.320064	8.52422	0.039355	0.081256	0.028686	0	4513	4459	6789	4797	5469	5971	9562	6697	8373	6818
ENSMUSG00000030374	chr7	Strn4	16815889	16816634	7958	0.342508	4.039792	0.039357	0.081256	0.029277	0	182	146	310	270	264	263	343	396	431	241
ENSMUSG00000001383	chr18	Zmat2	36793923	36793959	2257	0.401182	6.441762	0.039399	0.081331	0.04439	0	1244	1146	1274	840	1293	1743	2365	1546	2066	1326
ENSMUSG00000032397	chr9	Tipin	64281607	64281652	1211	0.338804	3.196305	0.039424	0.08137	0.024819	0	106	98	174	122	145	154	255	169	215	139

ENSMUSG00000017404	chr11	Rpl19	98026710	98026762	1022	0.356999	7.646405	0.039462	0.081434	0.035539	0	2493	2706	3114	2624	2693	3452	5189	3911	4849	3253
ENSMUSG00000039033	chr2	Tasp1	1.4E+08	1.4E+08	3652	-0.37306	2.942951	0.039492	0.081484	0.031587	0	116	106	193	122	156	75	172	97	158	114
ENSMUSG00000017386	chr11	Traf4	78158499	78160948	3292	0.472362	2.372555	0.039511	0.081511	0.04924	0	70	47	82	70	69	89	99	149	115	79
ENSMUSG00000051185	chr1	Fam174a	95313623	95314250	4814	-0.335	5.79482	0.039556	0.081591	0.03071	0	916	809	1327	869	1009	540	1033	822	1294	865
ENSMUSG00000020251	chr10	Glt8d2	82650433	82651518	5773	-0.53908	1.339455	0.039685	0.081845	0.051186	0	36	39	74	35	50	42	36	33	34	32
ENSMUSG00000002289	chr17	Angptl4	33773750	33775568	3286	1.101417	3.328074	0.039739	0.081943	0.321489	0	161	160	40	20	47	167	593	227	140	158
ENSMUSG00000002308	chr17	Cd320	33843091	33843291	2592	0.344401	3.636078	0.039843	0.082146	0.028251	0	147	131	212	176	204	203	263	302	266	213
ENSMUSG00000022673	chr16	Mcm4	15623897	15624769	3589	0.399823	2.676894	0.039903	0.082256	0.034452	0	76	64	93	96	102	107	179	130	126	110
ENSMUSG00000079491	chr17	H2-T10	36115876	36117734	3419	0.595286	0.588132	0.039978	0.082397	0.049088	0	16	16	20	13	23	26	39	33	26	27
ENSMUSG00000018442	chr11	Derl2	71007164	71007347	8049	0.349981	3.896441	0.040003	0.082437	0.029914	0	196	168	268	177	228	202	333	377	358	248
ENSMUSG00000000317	chr11	Bcl6b	70224128	70226143	3719	0.497134	2.163012	0.040062	0.082531	0.05325	0	44	45	65	76	57	70	98	100	151	56
ENSMUSG00000048154	chr15	Kmt2d	98831669	98834592	19887	-0.36601	5.374477	0.04006	0.082531	0.03627	0	539	387	1416	655	983	471	709	617	938	601
ENSMUSG00000034903	chr2	Cobll1	65088339	65089557	8342	-0.6268	2.209717	0.040078	0.082552	0.096071	0	47	39	103	130	137	28	75	70	68	83
ENSMUSG00000027635	chr2	Dsn1	1.57E+08	1.57E+08	3354	-0.60989	0.748482	0.040108	0.082591	0.068182	0	33	30	48	19	22	19	28	17	31	20
ENSMUSG00000041346	chr11	Wrap53	69561758	69562019	2062	0.375581	2.673078	0.040115	0.082591	0.029382	0	80	56	106	96	101	100	153	120	178	102
ENSMUSG00000051184	chr7	Zfp524	5015501	5015560	1110	0.374274	3.267239	0.040116	0.082591	0.032229	0	133	93	163	132	141	168	199	218	262	136
ENSMUSG00000053801	chr7	Grwd1	45825227	45826093	2053	0.294996	4.119199	0.040129	0.082605	0.021182	0	201	171	330	246	312	308	399	335	425	272
ENSMUSG00000048106	chr3	4632415L05Rik	19894886	19895962	1077	-0.72548	0.204171	0.040192	0.082711	0.095529	0	20	11	27	23	25	10	35	6	12	11
ENSMUSG00000096780	chr17	Tmem181b-ps	6438524	6438843	4187	-1.15858	1.061418	0.040192	0.082711	0.331456	0	36	39	43	43	58	34	36	36	3	1
ENSMUSG00000032513	chr9	Gorasp1	1.2E+08	1.2E+08	3483	-0.29945	4.140082	0.040266	0.08285	0.021982	0	279	206	457	313	318	220	331	258	384	254
ENSMUSG00000029715	chr5	Pop7	1.38E+08	1.38E+08	1081	0.419239	2.752596	0.04028	0.082853	0.039989	0	95	52	90	105	110	119	147	125	186	116
ENSMUSG00000040605	chr16	Bace2	97356728	97357101	3736	0.495878	1.258031	0.040277	0.082853	0.042583	0	18	22	40	28	46	37	52	55	54	44
ENSMUSG00000026655	chr2	Fam107b	3613758	3613938	3762	0.576514	1.949816	0.040304	0.082889	0.073603	0	59	36	59	40	43	41	124	114	73	63
ENSMUSG00000022602	chr15	Arc	74669083	74669993	3057	0.719265	1.172205	0.04037	0.083011	0.122095	0	14	5	29	35	53	40	61	41	40	56
ENSMUSG00000022184	chr15	Fbxo4	3965445	3965792	2047	0.469419	1.829879	0.040413	0.083087	0.04442	0	40	28	67	41	60	50	83	99	74	58
ENSMUSG00000016946	chr17	Kctd5	24047734	24049444	2751	0.315808	3.466479	0.040459	0.083169	0.02287	0	127	107	227	162	170	184	267	208	254	195
ENSMUSG00000040249	chr10	Lrp1	1.28E+08	1.28E+08	17717	0.483129	6.712574	0.040479	0.083197	0.065858	0	891	579	2800	1201	2171	1517	2143	2942	2336	2096
ENSMUSG00000056836	chr7	Gm6851	40190935	40191324	390	0.769937	-0.17501	0.040519	0.083266	0.067736	0	5	10	9	10	11	18	20	18	14	17
ENSMUSG00000024525	chr18	Impa2	67289253	67289506	1661	0.662871	1.874173	0.040604	0.083424	0.10548	0	22	21	33	80	65	44	112	67	102	79
ENSMUSG00000074748	chr10	Atxn7l3b	1.13E+08	1.13E+08	3572	0.293573	4.476008	0.040608	0.083424	0.022002	0	254	226	492	273	388	362	507	459	502	391
ENSMUSG00000051705	chr9	Senp8	59734259	59737868	3792	-0.36695	2.912147	0.040699	0.083598	0.031146	0	112	119	172	118	146	98	155	109	154	84
ENSMUSG00000038880	chr17	Mrps34	24895116	24895488	2064	0.296437	5.530707	0.040756	0.083702	0.023657	0	608	470	774	711	741	757	1051	850	1142	843
ENSMUSG00000041202	chr4	Pla2g2d	1.39E+08	1.39E+08	2243	-0.70372	2.018323	0.040786	0.08375	0.123113	0	91	64	151	34	59	48	50	88	64	24
ENSMUSG00000002803	chr12	Btbd6	1.13E+08	1.13E+08	2088	-0.3874	4.104602	0.040818	0.083792	0.03914	0	226	182	375	418	376	187	317	198	377	288
ENSMUSG00000039384	chr1	Dusp10	1.84E+08	1.84E+08	3042	-0.68315	5.510512	0.040822	0.083792	0.130544	0	526	248	1432	1201	1441	310	684	350	1496	541
ENSMUSG00000047731	chr19	Wbp1l	46599084	46599293	4463	0.370948	6.608858	0.040825	0.083792	0.038701	0	1262	968	1988	1132	1560	2273	2068	2079	2070	1352
ENSMUSG00000032171	chr9	Pin1	20652130	20652197	3808	0.326949	5.40561	0.040907	0.083935	0.028862	0	608	417	637	675	625	683	1042	744	1161	715
ENSMUSG00000070283	chr9	Ndufaf3	1.09E+08	1.09E+08	1815	0.346217	4.147403	0.040907	0.083935	0.030649	0	209	157	259	287	335	281	456	294	407	363
ENSMUSG00000066278	chr5	Vps37b	1.24E+08	1.24E+08	2512	0.39855	2.970427	0.040975	0.08406	0.037144	0	95	64	114	107	159	138	165	135	201	158
ENSMUSG00000025270	chrX	Alas2	1.51E+08	1.51E+08	2403	0.487143	1.381605	0.041045	0.084179	0.043493	0	26	16	42	42	43	47	54	51	70	43
ENSMUSG00000067942	chr17	Zfp160	21008941	21008986	3791	-0.41491	2.196348	0.041043	0.084179	0.035039	0	61	60	110	88	96	53	98	58	73	70
ENSMUSG00000030847	chr7	Bag3	1.29E+08	1.29E+08	2591	0.4105	6.846974	0.04107	0.084217	0.047735	0	1077	744	1891	2266	2177	1803	2581	2282	3366	2065
ENSMUSG00000040111	chr9	Gramd1b	40293233	40298079	9721	0.432128	3.36558	0.041083	0.08423	0.047623	0	106	67	173	181	186	166	253	281	206	159
ENSMUSG00000002032	chr9	Tmem25	44793776	44795048	2902	-0.54162	3.172491	0.041105	0.084261	0.076359	0	104	74	167	260	264	100	182	86	209	105
ENSMUSG00000003970	chr15	Rpl8	76904071	76904109	862	0.343164	8.25236	0.04116	0.084361	0.033533	0	4018	3808	4734	4114	4301	5469	6978	5903	8034	4845
ENSMUSG00000041112	chr13	Elmo1	20090596	20090771	10113	0.54935	2.071501	0.041169	0.084366	0.073937	0	22	20	90	67	84	69	117	77	110	74
ENSMUSG00000022313	chr15	Utp23	51877429	51877710	2992	0.415924	2.315859	0.041195	0.084407	0.036734	0	58	49	104	56	72	99	133	93	96	83
ENSMUSG00000039765	chr5	Cc2d2a	43662379	43662559	6776	-0.40461	3.163843	0.041214	0.084423	0.038769	0	86	100	252	172	235	116	178	132	172	105
ENSMUSG00000040016	chr3	Ptger3	1.58E+08	1.58E+08	2107	1.116951	0.948381	0.041219	0.084423	0.302457	0	34	16	24	6	8	49	20	102	28	18
ENSMUSG00000089665	chr8	Fcor	3671188	3671396	366	1.412503	0.192382	0.041222	0.084423	0.432753	0	12	16	3	2	7	32	18	67	10	5
ENSMUSG00000019863	chr10	Qrsl1	43874188	43874706	3442	-0.41537	4.116899	0.041228	0.084423	0.0459	0	229	163	326	453	433	190	371	218	375	227
ENSMUSG00000059195	chr4	Gm12715	1.04E+08	1.04E+08	1128	0.520166	1.238688	0.041289	0.084535	0.052291	0	26	9	40	35	42	36	59	44	62	42
ENSMUSG00000037523	chr2	Mavs	1.31E+08	1.31E+08	3345	-0.39568	5.264087	0.041298	0.08454	0.043246	0	445	354	877	1018	898	408	779	580	807	506
ENSMUSG00000022074	chr14	Tnfrsf10b	69767472	69767791	3171	0.655285	0.692888	0.041377	0.084676	0.071298	0	14	18	11	19	29	23	45	39	39	23
ENSMUSG00000060904	chr10	Arl1	88730858	88730985	2369	-0.32531	6.713502	0.041373	0.084676	0.029909	0	1564	1722	2374	1608	1949	1288	2221	1534	1981	1539
ENSMUSG00000035202	chr9	Lars2	1.23E+08	1.23E+08	3881	0.72333	8.343645	0.04142	0.084751	0.148254	0	4646	1708	6016	4934	2619	3590	4915	3307	16143	9898
ENSMUSG00000032518	chr9	Rpsa	1.2E+08	1.2E+08	1861	0.360067	8.887521	0.041455	0.084796	0.037125	0	6700	5758	7025	6201	6554	8944	12720	8418	11398	7372
ENSMUSG00000053317	chr4	Sec61b	47474658	47474753	1271	0.475549	4.050273	0.041454	0.084796	0.060056	0	280	203	300	122	167	287	454	375	374	264
ENSMUSG00000036501	chr18	Fam13b	34442352	34442765	3343	-0.40913	2.490517	0.041486	0.084847	0.035811	0	79	66	163	88	124	67	118	98	82	69
ENSMUSG00000019782	chr10	Rwdd1	33996555	33996848	1136	-0.387	6.223876	0.041513	0.084888	0.042356	0	1260	1326	1486	1088	1409	1098	1575	872	1585	860
ENSMUSG00000079477	chr6	Rab7	87999106	88000530	2610	-0.31478	7.971984	0.041563	0.084978	0.028292	0	3961	2666	6960	3919	5534	3566	4889	3515	5387	3230
ENSMUSG00000026489	chr1	Adck3	1.8E+08	1.8E+08	5293	-0.82423	9.222545	0.041585	0.085009	0.191968	0	4003	3356	9672	26324	20303	4025	13738	4719	11718	7185
ENSMUSG00000032607	chr9	Amt	1.08E+08	1.08E+08	2437	0.672353	0.300165	0.041596	0.085018	0.074461	0	8	10	26	10	17	25	17	33	25	22
ENSMUSG00000104372	chr11	AL663030.1	1.21E+08	1.21E+08	495	-0.3846	2.957267	0.041638	0.085091	0.033713	0	133	75	202	124	181	92	147	143	132	95
ENSMUSG00000063888	chr17	Rpl7l1	46773907	46775736	2606	0.295809	5.300982	0.041654	0.085111	0.02352	0	492	397	642	596	702	633	1017	790	920	625

ENSMUSG00000028953	chr5	Abcf2	24565341	24566003	2573	-0.30772	7.301894	0.041724	0.08524	0.026967	0	2647	2059	3956	2430	2975	2081	3277	2212	3353	2105
ENSMUSG00000058396	chr10	Gpr182	1.28E+08	1.28E+08	3954	0.878937	0.289989	0.041781	0.085344	0.148916	0	12	9	8	18	14	34	21	43	19	10
ENSMUSG00000028978	chr5	Nos3	24364810	24365001	4132	0.431068	3.255366	0.04179	0.085349	0.046693	0	102	74	147	153	177	117	222	276	227	154
ENSMUSG00000030055	chr6	Rab43	87788853	87792840	5526	0.382824	3.217143	0.041801	0.085353	0.036376	0	88	88	215	124	144	179	169	215	228	147
ENSMUSG00000030339	chr6	Ltbr	1.25E+08	1.25E+08	2354	0.308051	4.700977	0.041817	0.085353	0.025105	0	311	220	494	388	482	450	663	505	669	360
ENSMUSG00000031776	chr8	Arl2bp	94666755	94666901	1905	0.326277	5.874538	0.041804	0.085353	0.029478	0	909	620	991	766	817	938	1354	1144	1592	971
ENSMUSG00000075284	chr2	Wipf1	73429610	73432465	5896	0.370835	3.690148	0.041813	0.085353	0.035629	0	125	110	283	161	251	193	292	302	247	268
ENSMUSG00000038984	chr15	Tspyl5	33683876	33687883	4008	0.593664	0.367637	0.041908	0.085524	0.049766	0	11	9	18	13	25	21	30	22	27	28
ENSMUSG00000028837	chr4	Psmb2	1.27E+08	1.27E+08	1204	0.304737	6.178362	0.041936	0.085568	0.025898	0	889	799	1323	1058	1105	1227	1667	1329	1988	1148
ENSMUSG00000042167	chr13	Papd4	93147400	93147665	1873	-0.42047	2.829133	0.042011	0.085709	0.041306	0	84	104	202	118	148	101	168	94	97	88
ENSMUSG00000030347	chr6	D6Wsu163e	1.27E+08	1.27E+08	2238	-0.39855	2.882704	0.042103	0.085883	0.036888	0	118	98	177	127	146	114	153	108	93	98
ENSMUSG00000031862	chr8	Atp13a1	69791163	69791641	3915	0.32375	4.134818	0.042115	0.085895	0.027422	0	219	140	411	226	291	300	356	355	402	340
ENSMUSG00000033938	chr8	Ndufb7	83566671	83566930	4522	0.356111	7.370648	0.042247	0.086151	0.036319	0	2177	1633	2160	2727	2733	2827	4218	2892	4524	2697
ENSMUSG00000019806	chr10	Aig1	13647054	13647706	9196	0.370286	3.146126	0.042271	0.086186	0.032343	0	95	75	132	136	180	136	221	175	202	167
ENSMUSG00000025404	chr10	R3hdm2	1.27E+08	1.27E+08	5987	-0.36068	6.855443	0.042317	0.086267	0.037128	0	1393	1058	3166	2492	2805	1304	2126	1728	2415	1752
ENSMUSG00000055240	chr17	Zfp101	33360507	33361258	7424	-0.46748	1.607981	0.042347	0.086315	0.043195	0	49	46	81	48	51	31	67	39	44	46
ENSMUSG00000009090	chr11	Ap1b1	4986824	4987051	4957	-0.29389	5.702705	0.042382	0.086354	0.023878	0	868	607	1355	787	1056	705	928	797	1170	693
ENSMUSG00000022552	chr15	Sharpin	76347040	76347185	3765	0.295819	4.711531	0.042385	0.086354	0.022888	0	328	259	463	392	444	451	595	475	717	407
ENSMUSG00000063108	chr9	Zfp26	20432972	20438660	9631	-0.43816	2.797446	0.042386	0.086354	0.04611	0	129	79	180	89	168	66	150	78	127	117
ENSMUSG00000027276	chr2	Jag1	1.37E+08	1.37E+08	5827	-0.38242	3.231281	0.042453	0.086477	0.035733	0	132	160	234	121	195	102	168	153	174	141
ENSMUSG00000073888	chr4	Ccl27a	41769467	41769654	2377	0.507254	2.455711	0.042477	0.086513	0.059386	0	92	55	80	72	45	104	148	103	133	89
ENSMUSG00000030960	chr7	Mettl10	1.33E+08	1.33E+08	1764	0.434058	2.218932	0.042516	0.08658	0.03806	0	62	53	72	49	70	68	132	97	104	79
ENSMUSG00000019189	chr11	Rnf145	44518964	44519274	7786	0.319416	3.790826	0.042545	0.086618	0.025114	0	156	140	264	182	251	200	311	329	325	230
ENSMUSG00000060181	chr10	Slc35e3	1.18E+08	1.18E+08	3482	0.375745	2.712451	0.042548	0.086618	0.029539	0	78	72	111	87	100	94	186	132	153	107
ENSMUSG00000014177	chr11	Tvp23b	62879455	62879595	2235	0.427115	2.460624	0.042558	0.086624	0.040398	0	72	53	91	63	90	78	115	133	115	117
ENSMUSG00000032570	chr9	Atp2c1	1.05E+08	1.05E+08	9689	-0.30724	4.820253	0.042564	0.086624	0.025242	0	439	330	830	429	539	318	575	402	609	426
ENSMUSG00000036214	chr17	Znrd1as	36958592	36958702	1360	-0.36002	3.955334	0.042598	0.086679	0.034337	0	260	276	312	220	281	186	319	240	305	197
ENSMUSG00000040591	chr2	1110051M20Rik	91275068	91277134	5202	0.319206	4.09019	0.042621	0.086714	0.025677	0	247	179	318	207	253	276	352	331	417	329
ENSMUSG00000046791	chr12	2410016O06Rik	83950608	83952953	2346	0.416853	1.921014	0.04265	0.086758	0.032042	0	40	37	70	53	54	56	85	82	90	70
ENSMUSG00000051243	chr9	Islr2	58196298	58199983	4933	0.653707	0.698348	0.042665	0.086775	0.086616	0	10	5	32	27	24	26	29	26	49	37
ENSMUSG00000078812	chr11	Eif5a	69916714	69917341	2377	0.365517	8.784586	0.042704	0.086841	0.038711	0	6248	5669	7657	4933	5583	7618	11278	8169	12306	6611
ENSMUSG00000021360	chr13	Gcnt2	40859768	40861273	7038	-0.44579	3.071956	0.042725	0.086871	0.050593	0	92	101	180	216	188	93	196	87	171	111
ENSMUSG00000099309	chr9	Mir7085	44400423	44400488	66	-0.65108	0.282732	0.042846	0.087105	0.064079	0	26	15	23	14	31	18	16	15	16	13
ENSMUSG00000026197	chr1	Zfand2b	75168646	75168707	1772	0.3707	3.768964	0.042864	0.087128	0.033992	0	170	183	195	168	202	211	343	250	393	217
ENSMUSG00000011877	chr11	Git1	77493562	77493634	4838	-0.35124	5.515391	0.042871	0.087128	0.034527	0	622	417	1102	1033	1054	526	793	661	1069	659
ENSMUSG00000095115	chr7	Itpripl2	1.18E+08	1.18E+08	6862	0.339449	4.257042	0.042881	0.087136	0.030876	0	160	165	391	285	396	312	433	383	454	353
ENSMUSG00000024143	chr17	Rhoq	86963082	86963747	4151	-0.32741	7.768622	0.042964	0.087276	0.031018	0	3533	2230	5826	3798	4612	2235	3932	3459	4946	3324
ENSMUSG00000039356	chr2	Exosc2	31670715	31670861	2888	0.405233	3.337101	0.042961	0.087276	0.040424	0	158	115	151	117	130	202	237	202	243	151
ENSMUSG00000074166	chr7	AW146154	41478880	41481499	3405	-0.45079	2.011309	0.042981	0.087297	0.044098	0	83	53	92	72	60	53	71	62	73	45
ENSMUSG00000053279	chr19	Aldh1a1	20601961	20602077	2053	-0.5086	7.71674	0.043006	0.087336	0.074885	0	2058	2026	5652	5124	5939	2251	4488	1543	4713	3261
ENSMUSG00000018572	chr11	Phf23	69995777	69996053	3273	0.31143	4.531142	0.043048	0.087383	0.025239	0	315	273	427	285	331	396	501	469	572	384
ENSMUSG00000020225	chr10	Tmbim4	1.2E+08	1.2E+08	2581	0.333959	5.381841	0.043046	0.087383	0.030741	0	581	514	693	496	606	750	949	780	1171	617
ENSMUSG00000026627	chr1	Tmem206	1.91E+08	1.91E+08	2246	0.566624	1.186623	0.043053	0.087383	0.063382	0	17	21	35	30	38	38	44	71	44	35
ENSMUSG00000032002	chr9	Dcun1d5	7184566	7184882	1201	-0.31447	5.468523	0.043056	0.087383	0.027721	0	690	657	961	739	838	571	1071	580	887	558
ENSMUSG00000032012	chr9	Pvrl1	43744576	43744722	5054	0.546289	1.264778	0.043087	0.087432	0.060333	0	23	22	52	19	37	56	44	40	71	35
ENSMUSG00000041975	chr2	Mettl8	70964561	70965679	5594	0.385956	2.561933	0.043173	0.087594	0.033297	0	74	50	124	70	93	112	158	108	120	99
ENSMUSG00000029247	chr5	Paics	76951307	76951835	3139	-0.29998	6.631867	0.043311	0.087861	0.025813	0	1673	1302	2254	1659	1852	1304	2138	1409	2038	1321
ENSMUSG00000001349	chr9	Cnn1	22099281	22099418	2368	0.977883	0.927134	0.043335	0.087896	0.221554	0	12	30	12	20	14	8	37	83	54	37
ENSMUSG00000011096	chr7	Akt1s1	44848991	44849348	3201	0.305353	6.954301	0.043351	0.087914	0.02679	0	1725	1239	2237	1785	1885	1936	2804	2302	3403	2165
ENSMUSG00000025078	chr19	Nhlrc2	56548261	56548860	3934	-0.56831	1.801444	0.043393	0.087987	0.072302	0	30	26	116	80	93	37	56	48	59	48
ENSMUSG00000086915	chr10	Gm16365	39558496	39558712	1408	0.742586	0.232935	0.043423	0.088034	0.080969	0	17	10	10	16	8	14	27	22	41	19
ENSMUSG00000027018	chr2	Hat1	71388958	71389304	2886	0.318316	4.227434	0.043443	0.088061	0.025818	0	250	204	301	269	290	309	538	317	411	325
ENSMUSG00000040229	chrX	Gpr34	13632089	13632197	2090	0.651787	0.692621	0.043467	0.088097	0.082256	0	12	17	38	11	18	28	23	31	42	40
ENSMUSG00000038507	chr6	Parp12	39086410	39087640	3995	0.364811	3.104246	0.043484	0.088117	0.03192	0	85	69	159	149	145	126	225	187	201	141
ENSMUSG00000040731	chr5	Eif4h	1.35E+08	1.35E+08	2425	0.292351	7.030053	0.043499	0.088134	0.0246	0	1543	1399	2361	1898	2244	2109	3075	2440	3269	2289
ENSMUSG00000026698	chr1	Pigc	1.62E+08	1.62E+08	4250	0.314643	4.237184	0.043521	0.088166	0.025248	0	266	214	352	202	302	283	485	343	472	333
ENSMUSG00000003476	chr6	Crhr2	55090049	55091418	5112	-0.45181	5.000341	0.043554	0.088219	0.057688	0	395	248	719	827	881	316	625	362	711	496
ENSMUSG00000020709	chr11	Adap2	80154105	80154309	1785	-0.69941	0.794905	0.043561	0.088219	0.098739	0	15	15	67	19	58	15	34	23	25	17
ENSMUSG00000027531	chr3	Impa1	10311956	10315301	5437	-0.30481	4.246115	0.043621	0.088327	0.024048	0	314	253	460	260	397	240	343	283	394	286
ENSMUSG00000027709	chr3	Mccc1	35959311	35960129	2977	-0.30321	5.494445	0.043657	0.088387	0.025622	0	639	486	1066	874	1002	513	994	777	797	631
ENSMUSG00000067148	chr17	Polr1c	46243920	46244220	2278	0.34751	3.489823	0.043665	0.08839	0.028514	0	128	135	195	153	168	163	298	241	293	161
ENSMUSG00000029036	chr4	Atad3a	1.56E+08	1.56E+08	3765	-0.35023	4.720553	0.043692	0.08843	0.033631	0	392	248	553	556	660	315	524	475	527	296
ENSMUSG00000056716	chr10	Gm5420	21686411	21686503	992	-0.97025	0.633478	0.043778	0.088592	0.231086	0	4	32	30	47	40	5	39	9	17	23
ENSMUSG00000029144	chr5	Gtf3c2	31156005	31157767	6359	-0.29432	4.903363	0.043793	0.088609	0.023245	0	454	326	852	476	609	377	610	508	545	416
ENSMUSG00000057054	chr11	Inca1	70688361	70688749	1377	-0.49996	1.435633	0.043862	0.088734	0.052205	0	31	34	56	60	66	21	61	40	51	29

ENSMUSG00000064068	chr3	Mtx1	89209081	89209421	3584	0.345819	3.946111	0.043887	0.088772	0.030453	0	226	160	228	216	232	273	316	320	411	242
ENSMUSG00000003527	chr16	Dgcr14	17900711	17902323	2819	0.340132	3.147517	0.044074	0.089135	0.026391	0	107	92	162	128	131	137	202	151	225	178
ENSMUSG00000015165	chr7	Hnrnpl	28808541	28808859	5953	0.296449	6.015068	0.0441	0.089175	0.024873	0	800	724	1132	935	1031	1093	1562	1226	1592	1054
ENSMUSG00000023915	chr17	Tnfrsf21	43016555	43017092	3626	-0.30693	4.920767	0.04418	0.089324	0.025747	0	453	331	729	480	752	334	590	550	626	396
ENSMUSG00000010047	chr9	Hyal2	1.08E+08	1.08E+08	3293	0.338782	3.704302	0.044238	0.089428	0.028968	0	155	116	206	207	236	205	271	293	335	215
ENSMUSG00000033392	chr9	Clasp2	1.14E+08	1.14E+08	5690	-0.32759	5.617941	0.044246	0.089429	0.030316	0	622	492	1424	915	1117	545	962	679	1021	799
ENSMUSG00000022792	chr16	Yars2	16302965	16303747	3149	-0.38206	3.623598	0.044302	0.089529	0.038023	0	194	139	242	267	269	134	310	167	186	184
ENSMUSG00000102627	chr7	Snurf	59995449	59995554	216	-0.35841	4.045518	0.044339	0.089591	0.034194	0	197	198	375	369	361	196	327	186	367	255
ENSMUSG00000048000	chr1	Gigyf2	87326998	87327092	14216	-0.30062	4.935407	0.044349	0.089597	0.024469	0	411	335	842	527	675	371	615	457	553	501
ENSMUSG00000074064	chr8	Mlycd	1.19E+08	1.19E+08	2968	-0.37132	6.166454	0.044384	0.089653	0.040008	0	1031	874	1306	1787	1431	801	1691	1037	1438	885
ENSMUSG00000021215	chr13	Net1	3882565	3884473	3734	-0.30261	5.596161	0.044451	0.089776	0.025835	0	586	699	1084	905	1011	640	890	774	909	722
ENSMUSG00000052914	chr4	Cyp2j6	96516138	96518205	3605	0.448601	2.345121	0.044559	0.089979	0.046426	0	37	48	85	68	106	90	150	93	125	72
ENSMUSG00000019932	chr10	Kera	97607205	97607377	1950	-0.99049	3.833526	0.044585	0.090019	0.276685	0	56	143	424	354	659	105	170	204	34	297
ENSMUSG00000018217	chr11	Pmp22	63128982	63129150	2354	0.310159	5.471738	0.044611	0.090043	0.027268	0	453	428	880	688	785	764	990	986	890	792
ENSMUSG00000019854	chr10	Reps1	18055861	18056115	5301	-0.30447	4.293001	0.044611	0.090043	0.024251	0	294	245	589	295	349	233	384	308	400	282
ENSMUSG00000022353	chr15	Mtss1	58941244	58944130	4965	-0.31609	3.827945	0.044618	0.090043	0.025099	0	188	155	360	263	322	149	279	243	289	201
ENSMUSG00000074506	chr3	Gm10705	87207545	87208005	461	-0.72447	0.123595	0.044676	0.090148	0.093453	0	10	20	34	24	11	6	18	11	20	14
ENSMUSG00000026019	chr1	Wdr12	60069785	60078241	11955	-0.316	4.633843	0.044698	0.090179	0.027315	0	376	377	656	354	442	351	501	364	524	292
ENSMUSG00000029490	chr5	Mfsd7a	1.08E+08	1.08E+08	2508	0.6969	1.46303	0.044777	0.090324	0.111201	0	49	30	30	28	15	55	79	70	64	32
ENSMUSG00000096983	chr11	2010015M23Rik	88039578	88040036	1199	0.696152	0.038235	0.044859	0.090476	0.064914	0	8	8	10	18	11	19	22	15	25	21
ENSMUSG00000006715	chr13	Gmnn	24751845	24752230	1465	-0.55775	2.294172	0.044964	0.090671	0.077463	0	61	39	91	150	126	64	92	48	87	65
ENSMUSG00000039218	chr17	Srrm2	23790662	23790945	10982	-0.36279	7.168323	0.04497	0.090671	0.038644	0	1918	1387	5118	2138	3282	1653	2738	2138	2874	2162
ENSMUSG00000079941	chr13	Gm11273	21501029	21501418	390	0.37841	3.357101	0.045046	0.09081	0.035114	0	114	110	169	179	127	165	278	187	283	151
ENSMUSG00000090000	chr18	Ier3ip1	76930017	76930216	1894	0.330254	5.558251	0.045052	0.09081	0.030808	0	615	603	756	643	635	849	1147	818	1249	749
ENSMUSG00000024277	chr18	Mapre2	23752333	23752420	10202	-0.28523	5.219104	0.045133	0.09096	0.022607	0	530	459	960	669	705	448	676	576	838	547
ENSMUSG00000059851	chr7	Suv420h2	4740115	4740181	4001	0.354426	2.977716	0.045167	0.091013	0.028732	0	83	84	136	98	150	127	190	170	190	122
ENSMUSG00000039347	chr6	Atp6v0e2	48537569	48537854	1832	0.303105	5.880914	0.045188	0.091028	0.026318	0	749	532	1068	985	916	970	1484	993	1492	1038
ENSMUSG00000060938	chr11	Rpl26	68901583	68901624	1444	0.353877	7.800619	0.045185	0.091028	0.036975	0	2976	2921	3479	2719	3123	4307	5931	3990	5277	3402
ENSMUSG00000024018	chr17	Ccdc167	29689378	29690046	4896	-0.45136	2.395122	0.045211	0.091061	0.046432	0	79	46	152	112	105	57	108	84	70	78
ENSMUSG00000036372	chr19	Tmem258	10204014	10204264	1611	0.366442	4.901228	0.045382	0.091391	0.037384	0	444	360	480	370	374	517	922	562	698	413
ENSMUSG00000025235	chr9	Bbs4	59321966	59322982	2542	-0.33898	3.155858	0.045505	0.091624	0.027652	0	136	117	191	151	196	136	169	114	181	112
ENSMUSG00000040124	chr1	Gorab	1.63E+08	1.63E+08	2855	-0.43708	1.537184	0.045519	0.09164	0.035719	0	38	42	72	53	55	28	51	44	52	43
ENSMUSG00000056427	chr11	Slit3	35121224	35121711	6067	-0.44063	3.652523	0.045535	0.091657	0.05205	0	170	167	459	145	267	193	171	189	279	132
ENSMUSG00000019897	chr10	Ccdc59	1.06E+08	1.06E+08	4314	0.364714	3.614877	0.045587	0.091748	0.033423	0	140	164	219	128	191	191	361	214	312	192
ENSMUSG00000050192	chr3	Eif5a2	28781276	28781413	5027	-0.63501	0.597262	0.045648	0.091856	0.06826	0	18	11	46	25	44	11	24	15	32	20
ENSMUSG00000038065	chr6	Mturn	54681624	54681931	5695	-0.36301	3.812975	0.045678	0.091903	0.034232	0	167	151	391	256	344	183	229	279	241	175
ENSMUSG00000046876	chr13	Atxn1	45549758	45557585	10605	-0.29257	5.404117	0.045696	0.091927	0.024113	0	524	510	1129	743	929	485	818	676	862	651
ENSMUSG00000039158	chr4	Akna	63367125	63368286	5765	0.467222	1.983902	0.045761	0.092043	0.050882	0	30	31	85	55	67	71	87	104	77	63
ENSMUSG00000025451	chr13	Paip1	1.19E+08	1.19E+08	3456	-0.32119	5.944439	0.045823	0.092154	0.030038	0	992	962	1425	940	1088	853	1371	862	1123	817
ENSMUSG00000028577	chr4	Plaa	94567514	94569909	6441	-0.28059	5.585648	0.04587	0.092219	0.022431	0	771	658	1152	740	897	643	948	725	1002	660
ENSMUSG00000036053	chr2	Fmnl2	52857860	52858259	6033	-0.39401	2.904188	0.045865	0.092219	0.037291	0	104	105	242	92	150	88	146	104	139	109
ENSMUSG00000084957	chr19	Bbip1	53929677	53931502	2488	-0.32652	4.864573	0.045882	0.092229	0.030081	0	453	462	677	410	567	374	694	382	521	408
ENSMUSG00000066068	chr2	Gm13611	32271845	32272162	318	0.64053	0.882017	0.045896	0.092243	0.072292	0	24	23	15	23	18	24	50	43	42	34
ENSMUSG00000022096	chr14	Hr	70552212	70552324	6919	-0.41199	5.922408	0.045958	0.092355	0.049613	0	867	444	1562	1421	1494	913	878	971	1098	808
ENSMUSG00000062198	chr12	2700097O09Rik	55045661	55045943	4939	0.368371	2.516216	0.046038	0.092501	0.029365	0	64	57	104	69	103	88	157	106	130	100
ENSMUSG00000015759	chr14	Cnih1	46775582	46776549	1570	0.324843	5.996296	0.04607	0.092551	0.030588	0	863	783	1230	732	882	1101	1402	1237	1652	1082
ENSMUSG00000028247	chr4	Coq3	21879673	21879796	2997	-0.33198	4.964886	0.046149	0.092695	0.031392	0	454	369	617	616	742	366	790	409	658	369
ENSMUSG00000072872	chr6	Rybp	1E+08	1E+08	4458	-0.49487	1.323113	0.046155	0.092695	0.047333	0	42	30	67	37	53	18	54	45	40	28
ENSMUSG00000062353	chr5	Gm15772	3236431	3236868	438	0.441368	2.359826	0.04618	0.09273	0.04424	0	60	60	94	50	77	93	154	110	110	65
ENSMUSG00000027108	chr2	Ola1	73092801	73093724	3561	-0.3253	5.528011	0.046205	0.092767	0.03067	0	815	712	1087	618	824	626	977	622	961	592
ENSMUSG00000069094	chr3	Pde7a	19223108	19227841	7748	0.341678	6.450533	0.046281	0.092906	0.034397	0	1276	895	2057	936	1095	1381	2330	1593	2219	1499
ENSMUSG00000021432	chr13	Slc35b3	38932140	38932916	2214	0.515307	1.125638	0.046294	0.092917	0.049252	0	18	25	42	18	35	37	56	34	66	32
ENSMUSG00000033161	chr3	Atp1a1	1.02E+08	1.02E+08	4487	0.293441	6.552753	0.046325	0.092966	0.025357	0	1241	819	2026	1243	1597	1487	2167	1749	2346	1709
ENSMUSG00000036733	chr7	Rbm42	30640994	30641220	2193	0.297053	5.096757	0.046417	0.093122	0.024556	0	419	394	613	468	550	541	704	662	969	578
ENSMUSG00000041219	chr2	Arhgap11a	1.14E+08	1.14E+08	5332	0.55493	1.011892	0.046417	0.093122	0.061251	0	14	16	36	28	32	39	44	56	43	23
ENSMUSG00000002329	chr14	Mdp1	55657879	55659074	1733	0.308912	4.70288	0.046426	0.093126	0.026195	0	342	250	427	407	428	472	574	498	699	387
ENSMUSG00000038954	chr17	Supt3	44777152	44777428	4121	-0.37362	3.408211	0.046436	0.093131	0.035785	0	213	135	241	141	220	159	164	161	208	138
ENSMUSG00000015354	chr9	Pcolce2	95637601	95637873	4625	-0.40142	3.673289	0.046556	0.093359	0.042938	0	166	196	370	178	266	177	174	252	192	178
ENSMUSG00000062933	chr9	Gm10123	96895658	96896147	490	0.435188	3.63015	0.046566	0.093365	0.050498	0	180	171	187	128	136	259	297	246	296	183
ENSMUSG00000014599	chr3	Csf1	1.08E+08	1.08E+08	5262	0.359057	4.184407	0.046596	0.09341	0.035923	0	157	176	444	184	371	279	493	390	435	280
ENSMUSG00000042396	chr9	Rbm7	48488709	48489988	1798	-0.34626	3.342329	0.046626	0.093456	0.030138	0	157	151	245	168	177	107	203	150	185	166
ENSMUSG00000037260	chr8	Hgsnat	25944459	25945315	2679	-0.28368	4.633983	0.046635	0.093459	0.021674	0	381	262	611	428	544	326	516	413	464	329
ENSMUSG00000010358	chr11	Ifi35	1.01E+08	1.01E+08	1727	0.363472	4.004895	0.046646	0.093469	0.035038	0	229	174	201	240	243	298	415	299	396	238
ENSMUSG00000040522	chrX	Tlr8	1.67E+08	1.67E+08	3586	0.686533	0.261317	0.046663	0.093489	0.088112	0	13	4	22	9	21	25	24	34	18	18
ENSMUSG00000051515	chr7	Fam181b	93079879	93080983	1836	0.723302	0.054294	0.046679	0.093507	0.073514	0	6	9	9	16	15	15	22	23	34	12

ENSMUSG00000042106	chr9	Fam212a	1.08E+08	1.08E+08	1156	0.557051	1.211957	0.046778	0.093684	0.063989	0	22	16	41	29	38	38	35	71	56	36
ENSMUSG00000057265	chr12	Ccdc176	84409071	84409255	2234	-0.59902	0.812372	0.046782	0.093684	0.064048	0	22	15	40	45	41	26	23	26	24	19
ENSMUSG00000025010	chr19	Ccnj	40831279	40831442	4355	-0.42673	1.900308	0.046792	0.09369	0.038853	0	49	48	82	79	78	35	78	62	67	45
ENSMUSG00000062797	chr7	l7Rn6	89917529	89919007	2933	-0.30314	5.432451	0.046829	0.09375	0.026574	0	748	630	975	653	766	532	918	605	881	626
ENSMUSG00000032449	chr9	Slc25a36	97074961	97079239	9594	-0.30384	4.722112	0.046871	0.093821	0.025466	0	471	257	664	463	519	354	546	422	486	350
ENSMUSG00000066058	chr4	Cldn19	1.19E+08	1.19E+08	4263	-0.59378	0.799291	0.046888	0.09384	0.062236	0	18	18	44	32	51	24	37	20	21	17
ENSMUSG00000018001	chr5	Cyth3	1.44E+08	1.44E+08	4682	0.290032	3.962673	0.046912	0.093873	0.021694	0	185	140	326	207	287	246	414	293	375	245
ENSMUSG00000033208	chr10	S100b	76253853	76253958	1484	-0.66539	0.510973	0.047065	0.094165	0.086331	0	16	17	33	39	26	5	30	23	24	14
ENSMUSG00000085888	chr11	Gm12224	54340369	54340684	1091	-0.33257	5.914426	0.047108	0.094237	0.03265	0	1112	822	1327	985	1072	806	1142	730	1452	810
ENSMUSG00000001918	chr7	Slc1a5	16781346	16782475	4156	0.821945	5.633409	0.047152	0.094308	0.199562	0	922	539	622	246	360	868	681	2550	686	747
ENSMUSG00000017132	chr11	Cyth1	1.18E+08	1.18E+08	3905	-0.32	5.257031	0.047158	0.094308	0.029316	0	461	388	943	845	861	502	769	554	759	534
ENSMUSG00000055775	chr11	Myh8	67277124	67277234	11772	0.75975	8.73684	0.047173	0.094324	0.172398	0	4047	1723	9537	3545	8884	1976	8070	14845	19653	6912
ENSMUSG00000050229	chr1	Pigm	1.72E+08	1.72E+08	7554	0.345286	2.834675	0.047304	0.094573	0.028212	0	83	64	156	82	124	108	162	143	175	131
ENSMUSG00000039103	chr3	Nexn	1.52E+08	1.52E+08	2562	-0.34154	8.61947	0.047314	0.094577	0.035317	0	6176	5621	9307	5998	8163	5558	8656	4068	8093	5643
ENSMUSG00000034118	chr5	Tpst1	1.3E+08	1.3E+08	2789	0.3707	3.449184	0.047385	0.094706	0.035442	0	135	123	216	124	160	180	276	280	206	166
ENSMUSG00000052707	chr7	Tnrc6a	1.23E+08	1.23E+08	8471	-0.30859	4.924658	0.047404	0.09473	0.026673	0	377	349	966	475	641	379	604	479	576	442
ENSMUSG00000014349	chr11	Ube2z	96047432	96050414	3997	0.283129	5.453224	0.047422	0.094748	0.023015	0	561	396	816	695	726	765	1039	813	1037	728
ENSMUSG00000059325	chr5	Hopx	77086988	77087816	1516	0.456605	1.432844	0.047428	0.094748	0.037507	0	33	26	43	29	44	37	59	61	75	43
ENSMUSG00000027086	chr2	Fastkd1	69686815	69687140	5853	-0.37004	3.655402	0.047456	0.094791	0.036087	0	152	123	294	302	288	158	230	179	235	193
ENSMUSG00000009030	chr2	Pdcl	37350074	37352382	3751	-0.37628	3.407243	0.047529	0.094921	0.037033	0	135	155	272	187	212	93	196	197	179	172
ENSMUSG00000056698	chr6	Elmod3	72565922	72566863	3560	-0.35558	3.09164	0.047601	0.095051	0.031351	0	132	106	175	162	184	119	158	140	179	85
ENSMUSG00000103974	chr13	AL589742.1	21500953	21501352	475	0.371938	3.359888	0.047608	0.095051	0.034805	0	116	110	169	179	128	165	278	187	283	151
ENSMUSG00000024851	chr19	Pitpnm1	4099998	4100213	6889	0.479432	2.114744	0.047688	0.095196	0.054027	0	38	50	68	66	58	71	75	120	104	73
ENSMUSG00000017778	chr13	Cox7c	86044816	86044908	1131	0.363925	7.787456	0.047821	0.095447	0.040084	0	2896	2226	2791	3671	3574	3585	6486	3614	6162	3393
ENSMUSG00000028461	chr4	Ccdc107	43492900	43493023	1547	0.379797	4.424896	0.047838	0.095467	0.040104	0	300	301	308	235	285	388	514	416	572	328
ENSMUSG00000021703	chr13	Serinc5	92611138	92611287	5316	0.480127	2.415533	0.047858	0.095478	0.059716	0	32	39	105	75	115	65	139	120	127	108
ENSMUSG00000034161	chr15	Scx	76457438	76458186	1136	0.524643	2.176687	0.047851	0.095478	0.066129	0	52	58	62	50	60	84	129	50	100	109
ENSMUSG00000089857	chr8	Zfp882	71908608	71908738	3569	-0.64636	0.80358	0.047865	0.095478	0.08197	0	28	19	47	32	38	25	44	10	17	21
ENSMUSG00000090262	chr5	Mpv17	31140660	31141850	3208	0.32971	4.959862	0.047874	0.095482	0.030888	0	425	320	507	472	456	505	989	539	621	532
ENSMUSG00000085741	chr2	5430405H02Rik	1.57E+08	1.57E+08	3851	0.650901	0.322915	0.047945	0.09561	0.065741	0	19	10	17	11	13	17	22	33	27	26
ENSMUSG00000031517	chr8	Gpm6a	54954728	54955315	3336	-0.69337	0.127625	0.047964	0.095632	0.076709	0	12	15	35	12	27	8	17	22	14	8
ENSMUSG00000036026	chr17	Tmem63b	45660171	45660980	5098	-0.34263	6.142141	0.047974	0.095638	0.035031	0	946	735	1515	1605	1631	857	1596	902	1486	951
ENSMUSG00000004221	chrX	Ikbkg	74393290	74393405	8110	-0.2872	4.510171	0.048011	0.095698	0.022534	0	292	270	599	396	496	279	515	335	476	295
ENSMUSG00000090077	chr2	Lime1	1.81E+08	1.81E+08	2304	0.334907	3.080308	0.048039	0.095738	0.027237	0	110	71	172	116	133	150	198	176	179	142
ENSMUSG00000050973	chr7	Gdpgp1	80232867	80233205	3132	-0.61438	0.602575	0.048096	0.095838	0.058753	0	19	18	49	20	36	25	21	17	19	18
ENSMUSG00000024742	chr19	Fen1	10199132	10201097	2422	0.409196	2.759265	0.048173	0.095976	0.040661	0	64	82	89	92	126	123	155	131	181	105
ENSMUSG00000054843	chr19	Atrnl1	57611034	57611643	6581	-0.4219	3.286847	0.04823	0.096077	0.046589	0	124	94	269	173	267	110	149	149	149	183
ENSMUSG00000050213	chr4	Snip1	1.25E+08	1.25E+08	2428	0.393729	2.832054	0.048306	0.096214	0.036244	0	97	78	92	104	103	120	187	132	169	121
ENSMUSG00000020134	chr11	Peli1	21091291	21091678	6553	-0.34479	3.252509	0.048346	0.096278	0.02935	0	123	102	231	193	217	107	188	150	169	147
ENSMUSG00000026773	chr2	Pfkfb3	11471433	11474543	7561	-0.71357	8.145924	0.048358	0.096287	0.153972	0	6414	4960	12090	2040	3172	2794	6025	2005	8044	2061
ENSMUSG00000050796	chr4	B3galt6	1.56E+08	1.56E+08	3184	0.468404	1.35941	0.048367	0.09629	0.041743	0	33	14	44	33	44	40	60	46	64	50
ENSMUSG00000031951	chr8	Tmem231	1.12E+08	1.12E+08	2887	0.548459	0.862271	0.048391	0.096324	0.053924	0	12	15	37	27	22	20	51	33	47	36
ENSMUSG00000027470	chr2	Mylk2	1.53E+08	1.53E+08	2951	-0.38097	10.05821	0.048474	0.096476	0.044487	0	19482	15954	29801	14555	16713	13456	19450	11998	21444	18189
ENSMUSG00000043099	chr11	Hic1	75164565	75167544	3750	0.443441	3.336216	0.048593	0.096697	0.054826	0	109	53	203	184	155	154	179	205	296	213
ENSMUSG00000053332	chr1	Gas5	1.61E+08	1.61E+08	3760	0.36149	5.186363	0.048653	0.096802	0.038015	0	547	465	596	387	479	711	919	689	867	543
ENSMUSG00000021701	chr13	Plk2	1.1E+08	1.1E+08	2802	0.386332	3.33671	0.048695	0.096872	0.039808	0	93	77	230	165	156	166	273	221	268	124
ENSMUSG00000032745	chr13	Gpbp1	1.11E+08	1.11E+08	3905	-0.29146	6.00452	0.048732	0.096931	0.025266	0	932	927	1450	1039	1298	867	1353	1018	1194	857
ENSMUSG00000031826	chr8	Usp10	1.2E+08	1.2E+08	5456	-0.27951	5.217148	0.048748	0.096947	0.022246	0	534	406	985	645	781	479	676	634	744	531
ENSMUSG00000006369	chr15	Fbln1	85205949	85206212	4368	0.555996	3.96164	0.048795	0.096954	0.091359	0	86	132	330	154	366	270	361	497	206	299
ENSMUSG00000032396	chr9	Dis3l	64306756	64307348	5458	-0.27593	5.064093	0.048764	0.096954	0.021541	0	463	380	827	633	683	424	692	503	659	495
ENSMUSG00000039987	chr5	Phtf2	20758663	20761075	6929	-0.32124	7.352839	0.048802	0.096954	0.03144	0	2374	1983	4658	2690	3230	1604	3650	2342	3369	2563
ENSMUSG00000040028	chr8	Elavl1	4284782	4289924	6030	0.296717	4.686892	0.048774	0.096954	0.024421	0	338	285	495	366	355	403	549	531	651	449
ENSMUSG00000040928	chr4	S100pbp	1.29E+08	1.29E+08	9448	0.34694	2.749761	0.048784	0.096954	0.027769	0	79	63	134	88	110	102	141	136	183	117
ENSMUSG00000071646	chr19	Mta2	8941875	8942382	4093	0.275006	5.215726	0.048767	0.096954	0.021655	0	418	366	787	562	607	590	886	679	991	599
ENSMUSG00000074358	chr7	Ccdc61	18890883	18891173	2122	0.414406	2.299182	0.048799	0.096954	0.037849	0	66	49	85	64	65	80	98	112	139	74
ENSMUSG00000007038	chr17	Neu1	34931253	34931547	3733	0.27949	4.428564	0.048861	0.097049	0.020918	0	275	233	393	286	368	360	546	393	518	342
ENSMUSG00000021830	chr14	Txndc16	45134448	45135970	10360	-0.29669	4.594163	0.048865	0.097049	0.024307	0	289	313	689	391	506	324	460	349	466	371
ENSMUSG00000021361	chr13	Tmem14c	41016250	41016398	945	0.298154	5.559621	0.048888	0.09708	0.025929	0	667	459	742	702	792	786	1239	825	1189	752
ENSMUSG00000024511	chr18	Rab27b	69979131	69985377	10679	0.517805	0.954954	0.048911	0.097098	0.047803	0	25	15	31	19	31	27	48	29	47	45
ENSMUSG00000028863	chr4	Meaf6	1.25E+08	1.25E+08	5211	0.409293	3.248823	0.048907	0.097098	0.043958	0	122	115	133	111	152	203	179	183	270	137
ENSMUSG00000030166	chr6	Rad52	1.2E+08	1.2E+08	3371	0.37173	2.720363	0.048922	0.097104	0.031485	0	91	66	110	84	100	90	166	115	183	122
ENSMUSG00000068205	chr2	Macrod2	1.4E+08	1.4E+08	10308	-0.44526	3.667875	0.049018	0.09728	0.056649	0	227	250	327	153	177	167	286	194	205	134
ENSMUSG00000020868	chr11	Xylt2	94663851	94664909	3979	0.369343	2.668868	0.049047	0.097294	0.031119	0	85	54	103	95	101	96	150	126	177	101
ENSMUSG00000036678	chr15	Aaas	1.02E+08	1.02E+08	1816	0.348274	2.889403	0.049039	0.097294	0.028233	0	82	85	135	103	109	129	165	149	182	120
ENSMUSG00000100783	chr5	2310047D07Rik	1.49E+08	1.49E+08	823	-0.44066	2.800686	0.04904	0.097294	0.051739	0	134	124	112	115	122	87	145	82	131	93

ENSMUSG00000056708	chr1	Ier5	1.55E+08	1.55E+08	3276	0.358338	3.812726	0.049078	0.097341	0.034799	0	138	138	231	228	252	248	412	268	362	168
ENSMUSG00000039630	chr1	Hnrnpu	1.78E+08	1.78E+08	8959	0.286192	6.909811	0.049138	0.097432	0.024766	0	1495	1379	2365	1592	1856	1897	2893	2346	2885	2082
ENSMUSG00000048200	chr7	Cracr2b	1.41E+08	1.41E+08	2764	0.4517	2.845895	0.049135	0.097432	0.054134	0	81	55	106	115	126	141	146	174	212	77
ENSMUSG00000025793	chr11	Hgs	1.2E+08	1.2E+08	2991	0.311405	4.536762	0.049159	0.097444	0.027074	0	281	258	470	304	349	329	440	500	653	422
ENSMUSG00000057894	chr7	Zfp329	12804977	12806592	6732	-0.45891	2.10794	0.049159	0.097444	0.049534	0	49	60	90	91	103	40	70	75	67	70
ENSMUSG00000033554	chr3	Dph5	1.16E+08	1.16E+08	4086	-0.37537	2.48913	0.049174	0.097458	0.032564	0	91	73	135	94	109	72	126	90	92	62
ENSMUSG00000076437	chr2	2700094K13Rik	84669215	84669397	1131	0.412211	3.171505	0.049193	0.097481	0.043581	0	123	116	127	88	142	174	192	202	215	137
ENSMUSG00000019261	chr8	Map1s	70905974	70906127	3271	0.349724	3.310016	0.049218	0.097518	0.031047	0	125	98	175	137	158	149	182	221	243	199
ENSMUSG00000036980	chr5	Taf6	1.38E+08	1.38E+08	3779	-0.29155	5.295298	0.049241	0.097534	0.024692	0	637	431	923	745	758	516	770	514	821	611
ENSMUSG00000038497	chr8	Tmco3	13288013	13288387	4533	-0.3288	3.74028	0.049236	0.097534	0.028744	0	167	162	325	252	302	126	263	222	266	209
ENSMUSG00000063412	chr8	Gm10131	34111143	34111736	594	0.487821	1.114165	0.049367	0.097767	0.041818	0	21	17	30	28	42	31	49	43	51	44
ENSMUSG00000002006	chrX	Pdzd4	73793359	73795920	3970	0.515571	0.941311	0.049453	0.097923	0.043036	0	17	21	29	22	30	24	43	42	47	38
ENSMUSG00000045257	chr17	Morn2	80290212	80290337	644	0.420555	2.258989	0.049517	0.098035	0.038809	0	58	56	65	72	62	80	119	87	122	82
ENSMUSG00000030177	chr6	Ccdc77	1.2E+08	1.2E+08	6685	-0.45576	1.906676	0.049541	0.098068	0.044712	0	47	43	109	66	84	50	82	58	45	45
ENSMUSG00000022526	chr15	Zfp251	76852148	76854614	3497	-0.32225	3.216654	0.049557	0.098086	0.025152	0	132	107	249	168	181	113	193	127	176	142
ENSMUSG00000001157	chr6	Gmcl1	86691768	86693051	3823	0.453727	1.953778	0.049605	0.098166	0.045359	0	40	35	75	52	56	50	91	109	95	55
ENSMUSG00000005483	chr8	Dnajb1	83608175	83608542	2263	0.373091	3.078038	0.049658	0.098257	0.035058	0	94	94	138	120	133	147	219	205	164	121
ENSMUSG00000026158	chr1	Ogfrl1	23366424	23370448	8109	-0.40094	3.068284	0.049825	0.098573	0.04269	0	118	134	261	114	140	85	144	158	166	105
ENSMUSG00000023156	chr14	Rpp14	8080367	8080512	2401	-0.28449	5.137637	0.049852	0.09861	0.023512	0	576	452	826	602	638	497	786	533	651	444
ENSMUSG00000049115	chr13	Agtr1a	30336441	30336589	2467	-0.45455	1.908861	0.049952	0.098794	0.046431	0	52	50	120	44	84	48	82	53	61	40
ENSMUSG00000003316	chr8	Glg1	1.11E+08	1.11E+08	7090	-0.33771	5.83897	0.04997	0.098801	0.034192	0	744	516	1900	977	1297	714	1082	827	1108	886
ENSMUSG00000020777	chr11	Acox1	1.16E+08	1.16E+08	5082	-0.33953	7.336674	0.049978	0.098801	0.035489	0	2179	1624	4031	3552	3482	1627	3474	2704	2945	2429
ENSMUSG00000031489	chr8	Adrb3	27225776	27226528	2893	1.165454	2.64614	0.049971	0.098801	0.391069	0	123	66	26	27	24	78	58	417	73	116
ENSMUSG00000038975	chr3	Rabggtb	1.54E+08	1.54E+08	1509	0.294919	5.792361	0.050165	0.099156	0.025836	0	762	601	949	816	812	964	1319	948	1445	919
ENSMUSG00000027210	chr2	Meis2	1.16E+08	1.16E+08	12043	0.630702	0.392944	0.050255	0.099291	0.063546	0	19	11	20	9	16	24	29	35	28	16
ENSMUSG00000038807	chr11	Rap1gap2	74383356	74387511	6632	0.474075	3.948162	0.050255	0.099291	0.066845	0	103	80	277	271	358	273	317	311	389	319
ENSMUSG00000051169	chr6	Rpusd3	1.13E+08	1.13E+08	2161	-0.40184	2.98171	0.050254	0.099291	0.042052	0	101	84	157	185	194	110	134	96	160	113
ENSMUSG00000041360	chr19	D19Bwg1357e	27388702	27390313	3462	0.295932	3.88586	0.050299	0.099362	0.022919	0	163	162	298	219	222	250	370	298	325	235
ENSMUSG00000081485	chr11	Gm12338	75599763	75599954	192	0.422569	5.837043	0.05031	0.099368	0.054245	0	823	602	684	856	814	1221	1842	817	1456	731
ENSMUSG00000073702	chr1	Rpl31	39367842	39367934	1662	0.339345	7.033521	0.050318	0.09937	0.035361	0	1893	1575	2162	1693	1714	2329	3732	2449	2886	2044
ENSMUSG00000001416	chr3	Cct3	88297116	88297266	6370	0.287331	6.616393	0.050413	0.099543	0.025128	0	1218	1063	1733	1397	1662	1684	2398	1944	2358	1499
ENSMUSG00000031451	chr8	Gas6	13465374	13465900	2593	0.346636	7.011002	0.050423	0.099547	0.037051	0	1286	1271	2314	2103	2233	1937	3263	3437	2711	1880
ENSMUSG00000029253	chr5	Cenpc1	86012043	86012327	3173	-0.53154	2.065478	0.05044	0.099557	0.072159	0	56	66	118	67	85	40	96	38	47	83
ENSMUSG00000074212	chr3	Dnajb14	1.38E+08	1.38E+08	12553	-0.32256	4.325522	0.050443	0.099557	0.029123	0	298	251	581	274	423	233	306	352	415	309
ENSMUSG00000048701	chr10	Ccdc6	70097121	70097581	6385	-0.28953	6.172576	0.050507	0.099668	0.025332	0	1120	833	2030	1105	1435	927	1352	1187	1493	992
ENSMUSG00000038146	chr17	Notch3	32120820	32122860	8044	-0.38519	4.628044	0.050533	0.099706	0.043613	0	324	203	719	435	688	213	504	419	514	343
ENSMUSG00000019039	chr9	Dalrd3	1.09E+08	1.09E+08	2458	0.317276	3.692224	0.050606	0.099834	0.026039	0	178	130	208	191	201	197	316	275	286	225
ENSMUSG00000073542	chr18	Cep76	67617397	67619372	3979	-0.37495	3.108005	0.050639	0.099885	0.036181	0	147	87	266	121	179	95	155	110	192	133
ENSMUSG00000097039	chr15	Pvt1	62037986	62038201	6996	0.571215	1.164594	0.050705	0.1	0.069425	0	37	20	28	16	34	42	66	49	39	35
ENSMUSG00000027534	chr3	Snx16	10417817	10419223	2632	-0.40598	2.461711	0.050795	0.100147	0.038551	0	72	64	163	88	124	56	88	97	95	87
ENSMUSG00000036208	chr16	BC027231	44724301	44724468	5741	-0.50841	1.375148	0.050795	0.100147	0.054154	0	32	40	89	34	46	27	47	38	36	39
ENSMUSG00000049517	chr13	Rps23	90923131	90923199	756	0.369304	7.522477	0.050833	0.100207	0.042297	0	2582	2485	2739	2088	2477	3425	5039	3460	4379	2741
ENSMUSG00000027257	chr2	Pacsin3	91255954	91256190	4327	0.336804	8.135072	0.050855	0.100237	0.035328	0	4118	3056	4597	3562	4290	5447	6159	4597	8150	4414
ENSMUSG00000020900	chr11	Myh10	68691559	68691842	10458	-0.58453	3.674673	0.050864	0.100239	0.10124	0	114	84	254	417	402	108	262	203	195	169
ENSMUSG00000000552	chr15	Zfp385a	1.03E+08	1.03E+08	2291	0.439105	3.204744	0.050959	0.100411	0.053756	0	110	80	163	113	163	122	136	277	256	161
ENSMUSG00000039176	chr7	Polg	79448791	79450037	6843	-0.30732	5.196125	0.050995	0.100467	0.027948	0	490	372	891	770	804	397	799	566	746	526
ENSMUSG00000021102	chr12	Glrx5	1.05E+08	1.05E+08	930	0.335993	5.715274	0.051045	0.100552	0.034112	0	663	483	735	938	864	857	1270	926	1563	816
ENSMUSG00000003273	chr7	Car11	45699843	45700339	1926	-0.42706	2.737725	0.051137	0.100718	0.04807	0	130	113	169	84	98	82	118	99	117	95
ENSMUSG00000033581	chr16	Igf2bp2	22059009	22060885	7131	0.624551	0.42746	0.051155	0.100738	0.071806	0	19	7	23	8	22	27	27	34	26	20
ENSMUSG00000020074	chr10	Ccar1	62743928	62744822	4478	-0.27256	4.58423	0.051178	0.100768	0.020972	0	359	321	571	396	458	312	542	375	453	314
ENSMUSG00000017652	chr2	Cd40	1.65E+08	1.65E+08	3406	0.703177	-0.1215	0.051248	0.100882	0.075617	0	6	4	10	18	11	16	27	15	19	14
ENSMUSG00000031347	chrX	Cetn2	72913532	72914293	1646	0.316529	4.80404	0.051251	0.100882	0.028857	0	405	341	498	310	402	486	678	504	671	481
ENSMUSG00000028156	chr3	Eif4e	1.39E+08	1.39E+08	2882	-0.29959	6.572381	0.051288	0.100941	0.027693	0	1430	1143	2156	1710	2057	1072	2208	1282	2109	1307
ENSMUSG00000087260	chr3	Lamtor5	1.07E+08	1.07E+08	881	0.313768	5.186097	0.051304	0.100957	0.028887	0	509	429	596	513	493	635	941	609	916	599
ENSMUSG00000022119	chr14	Rbm26	1.05E+08	1.05E+08	7649	-0.30674	4.182013	0.051344	0.100989	0.025895	0	247	220	533	288	361	212	387	280	303	294
ENSMUSG00000031729	chr8	Ist1	1.1E+08	1.1E+08	2341	0.287605	5.206528	0.051339	0.100989	0.024251	0	491	366	605	552	639	654	846	688	927	587
ENSMUSG00000035047	chr9	Kri1	21273457	21274248	4182	0.317887	3.369868	0.05133	0.100989	0.026202	0	116	94	196	147	190	189	269	193	225	161
ENSMUSG00000028159	chr3	Dapp1	1.38E+08	1.38E+08	3284	-0.77686	1.89782	0.051449	0.101164	0.168151	0	22	18	78	148	119	42	64	47	44	44
ENSMUSG00000039804	chr2	Ncoa5	1.65E+08	1.65E+08	4383	0.312947	3.616077	0.051447	0.101164	0.025879	0	141	120	224	175	218	228	259	262	281	190
ENSMUSG00000041974	chr16	Spidr	15889227	15889785	3279	0.54183	1.124644	0.051456	0.101164	0.055227	0	24	26	36	18	30	37	53	59	46	28
ENSMUSG00000030409	chr7	Dmpk	19083849	19084154	4330	0.429696	8.308701	0.051509	0.101255	0.057931	0	3099	1748	4962	6394	6167	4366	8148	6604	8778	5846
ENSMUSG00000024944	chr19	Arl2	6134374	6134801	2891	0.29257	5.43827	0.051523	0.101267	0.025295	0	545	501	702	657	669	686	1005	827	1166	704
ENSMUSG00000023456	chr6	Tpi1	1.25E+08	1.25E+08	2209	0.313697	11.44313	0.051591	0.101385	0.031061	0	40613	25847	47063	40015	45177	46905	74381	47406	75329	42434
ENSMUSG00000050234	chr4	Gja4	1.27E+08	1.27E+08	1685	0.393479	2.707305	0.051631	0.101449	0.036962	0	84	66	88	95	106	94	139	126	194	118
ENSMUSG00000028394	chr4	Pole3	62522649	62524110	2040	0.284612	4.541788	0.051689	0.101548	0.022587	0	317	245	425	306	384	389	593	398	621	354

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ENSMUSG00000096740	chr19	Lbhd1	8883732	8884079	3289	0.380613	3.436818	0.051797	0.101744	0.03886	0	176	107	167	132	152	213	288	169	242	191
ENSMUSG00000009097	chr16	Tbx1	18581713	18582456	1777	0.32652	4.996277	0.051902	0.101934	0.031835	0	371	282	592	528	520	453	574	664	888	647
ENSMUSG00000059743	chr3	Fdps	89093592	89093843	1241	0.300567	4.569159	0.051909	0.101934	0.025495	0	322	285	429	299	343	392	503	480	622	388
ENSMUSG00000097167	chr3	Gm16740	95217457	95218058	956	0.673221	0.015003	0.051984	0.102067	0.069544	0	9	10	15	10	11	10	15	23	29	23
ENSMUSG00000060143	chr14	Gm10076	1.06E+08	1.06E+08	384	0.486715	3.686588	0.052225	0.102525	0.068683	0	222	136	155	121	188	331	347	198	306	169
ENSMUSG00000066191	chr4	Anks6	47015669	47016816	5237	-0.54401	1.07629	0.052296	0.102648	0.058504	0	34	16	68	33	48	18	27	33	46	26
ENSMUSG00000006342	chr10	Susd2	75636619	75637370	3255	0.43038	1.967205	0.05232	0.102682	0.043253	0	35	38	81	47	64	52	73	94	106	73
ENSMUSG00000010025	chr11	Aldh3a2	61223417	61224686	5619	-0.31464	3.699991	0.052331	0.102687	0.026144	0	190	133	330	233	291	147	252	220	230	202
ENSMUSG00000027942	chr3	4933434E20Rik	90051636	90051693	6826	-0.29761	6.291541	0.052364	0.102738	0.027472	0	1303	1127	1643	1283	1467	965	1630	1143	1601	1136
ENSMUSG00000051022	chr5	Hs3st1	39613935	39615404	2230	0.622261	0.244092	0.052409	0.10281	0.050771	0	12	12	17	12	14	18	33	14	31	23
ENSMUSG00000049489	chr11	Fam58b	78750506	78751729	1224	0.323509	3.6972	0.052431	0.102838	0.027648	0	186	147	236	159	179	233	310	246	314	203
ENSMUSG00000027881	chr3	Prpf38b	1.09E+08	1.09E+08	4750	0.341245	4.393863	0.052477	0.102914	0.033937	0	269	234	437	209	345	312	426	539	473	370
ENSMUSG00000040383	chr2	Aqr	1.14E+08	1.14E+08	11805	-0.30491	4.004251	0.052522	0.102976	0.02528	0	230	176	461	243	353	205	326	288	284	205
ENSMUSG00000098973	chr9	Mir6236	1.1E+08	1.1E+08	123	0.690164	5.116603	0.052525	0.102976	0.147665	0	524	213	672	505	218	369	539	375	1653	1051
ENSMUSG00000076372	chr16	Mir568	43640655	43640737	83	-0.59461	0.631152	0.052592	0.103093	0.06893	0	31	15	35	24	36	11	34	29	16	16
ENSMUSG00000086324	chr16	Gm15564	35966752	35966870	821	0.703083	2.967339	0.052624	0.10314	0.147061	0	123	46	157	97	51	74	135	91	314	265
ENSMUSG00000022110	chr14	Sucla2	73525319	73525546	3988	-0.31868	8.976751	0.052672	0.103219	0.032261	0	7217	6444	10151	10282	10644	6613	11853	6592	10266	6386
ENSMUSG00000031153	chrX	Gripap1	7789765	7790068	5502	0.266181	4.602611	0.05268	0.103219	0.019911	0	296	253	444	345	434	398	597	439	572	414
ENSMUSG00000035545	chr7	Leng8	4137039	4137122	6391	0.299217	5.409326	0.052775	0.103375	0.027203	0	587	393	973	437	742	681	1052	841	970	737
ENSMUSG00000049232	chr6	Tigd2	59208870	59209181	3007	-0.31281	3.679816	0.052772	0.103375	0.026349	0	168	157	327	237	262	143	294	173	241	198
ENSMUSG00000008167	chr8	Fbxw9	85060055	85060536	3383	0.543632	1.44352	0.052888	0.103581	0.063392	0	21	37	32	35	41	47	45	57	75	55
ENSMUSG00000071477	chr6	Zfp777	48024188	48025818	3588	-0.28597	4.212392	0.052907	0.103604	0.022533	0	284	195	471	343	365	233	337	329	371	252
ENSMUSG00000007411	chr12	Mark3	1.12E+08	1.12E+08	3388	-0.27813	5.736011	0.052987	0.103714	0.023584	0	802	692	1311	880	1030	705	1180	715	998	817
ENSMUSG00000020166	chr10	Cnot2	1.16E+08	1.16E+08	3711	-0.26924	4.591412	0.052984	0.103714	0.020512	0	345	282	632	415	474	310	506	413	456	317
ENSMUSG00000041895	chr11	Wipi1	1.1E+08	1.1E+08	4410	-0.36164	6.063132	0.052978	0.103714	0.040787	0	807	623	1563	1549	1682	743	1404	884	1516	911
ENSMUSG00000024830	chr19	Rps6kb2	4156713	4157199	2445	0.268034	4.661263	0.053074	0.10387	0.020486	0	314	252	507	354	430	384	568	491	653	433
ENSMUSG00000041570	chr1	Camsap2	1.36E+08	1.36E+08	9195	-0.35429	3.315896	0.053108	0.103921	0.033615	0	140	116	297	147	218	100	201	191	169	135
ENSMUSG00000045790	chr5	Ccdc149	52374651	52376678	3317	0.592771	0.819587	0.053127	0.103943	0.068488	0	15	17	24	25	24	31	38	54	28	27
ENSMUSG00000030720	chr7	Cln3	1.27E+08	1.27E+08	5781	0.335412	2.971847	0.053199	0.104068	0.02825	0	101	68	153	119	113	131	178	165	177	134
ENSMUSG00000022724	chr16	Mina	59471775	59471945	5290	-0.28364	4.239202	0.053353	0.104353	0.022753	0	263	249	391	359	391	242	421	288	364	249
ENSMUSG00000031508	chr8	Ankrd10	11611583	11612947	3950	0.285154	4.112889	0.053527	0.104679	0.02249	0	233	166	389	210	269	254	423	339	433	292
ENSMUSG00000023795	chr17	Pisd-ps2	3076578	3076782	2108	-0.56717	1.211473	0.053557	0.104722	0.066317	0	40	17	69	33	62	25	38	36	25	36
ENSMUSG00000026705	chr1	Klhl20	1.61E+08	1.61E+08	12847	-0.3087	3.584884	0.053577	0.104731	0.025326	0	164	150	340	170	262	145	233	176	250	175
ENSMUSG00000027940	chr3	Tpm3	90072649	90072850	6085	0.555876	5.23964	0.053576	0.104731	0.096856	0	240	232	384	978	626	661	1098	877	838	635
ENSMUSG00000026928	chr2	Card9	26352176	26352411	2293	0.622746	0.004261	0.053614	0.104786	0.057909	0	6	6	16	13	16	19	24	20	16	18
ENSMUSG00000041781	chr12	Cpsf2	1.02E+08	1.02E+08	5315	-0.27989	4.732327	0.053664	0.10487	0.022833	0	357	322	662	479	551	333	611	366	505	393
ENSMUSG00000063052	chr3	Lrrc40	1.58E+08	1.58E+08	4575	-0.33375	2.877542	0.05372	0.104963	0.026715	0	114	82	198	124	144	92	156	103	140	100
ENSMUSG00000094365	chr7	Gm21982	30641001	30641220	3821	0.282313	5.22621	0.053867	0.105235	0.023796	0	458	430	683	523	598	601	775	713	1025	640
ENSMUSG00000027175	chr2	Tcp11l1	1.05E+08	1.05E+08	6877	-0.40177	2.032338	0.053953	0.105372	0.036955	0	54	65	97	63	86	56	74	60	83	43
ENSMUSG00000028607	chr4	Cpt2	1.08E+08	1.08E+08	2391	-0.41845	6.049654	0.053953	0.105372	0.055336	0	756	660	1205	1895	1628	692	1368	1026	1359	832
ENSMUSG00000039656	chr17	Rxrb	34031812	34032223	3698	-0.26766	5.469279	0.053973	0.105396	0.021733	0	608	579	1029	802	880	573	879	761	874	595
ENSMUSG00000028138	chr3	Adh5	1.38E+08	1.38E+08	2801	-0.28179	5.813544	0.054073	0.105576	0.024622	0	832	689	1240	1108	1086	677	1267	817	1186	764
ENSMUSG00000028032	chr3	Papss1	1.32E+08	1.32E+08	2599	0.376234	2.931095	0.054146	0.10568	0.037392	0	82	75	134	117	119	114	146	192	164	149
ENSMUSG00000036181	chr13	Hist1h1c	23738808	23740367	1560	-0.35167	7.072396	0.054151	0.10568	0.039439	0	2353	1484	3050	2396	2926	1803	2403	1466	3673	1691
ENSMUSG00000071533	chr16	Pcnp	56007245	56007482	3115	-0.28185	5.044234	0.054142	0.10568	0.023978	0	485	504	728	525	626	410	698	504	649	473
ENSMUSG00000053134	chr5	Supt7l	31514569	31515926	5347	-0.30434	3.461749	0.054202	0.105764	0.024289	0	165	118	290	202	214	131	234	172	211	153
ENSMUSG00000020267	chr11	Hint1	54866383	54866600	872	0.347542	7.025851	0.054266	0.105874	0.038363	0	1885	1674	2031	1538	1768	2263	3794	2315	3115	2000
ENSMUSG00000046096	chr7	BC030336	1.21E+08	1.21E+08	4842	-0.29812	3.92943	0.054296	0.105916	0.024518	0	251	156	359	287	305	174	311	261	283	219
ENSMUSG00000030265	chr6	Kras	1.45E+08	1.45E+08	5347	-0.32742	4.153359	0.05443	0.10616	0.030775	0	237	169	504	315	424	180	338	266	380	286
ENSMUSG00000042289	chr7	Hsd3b7	1.28E+08	1.28E+08	6154	0.296528	4.779237	0.054437	0.10616	0.02645	0	287	255	608	375	507	422	662	641	572	454
ENSMUSG00000034723	chr2	Tmx4	1.35E+08	1.35E+08	10907	-0.30327	4.092767	0.054526	0.106318	0.026117	0	215	203	424	326	366	178	381	246	331	270
ENSMUSG00000062729	chr1	Ppox	1.71E+08	1.71E+08	4515	0.310718	3.538624	0.054562	0.106372	0.025915	0	141	115	208	153	214	207	257	244	240	203
ENSMUSG00000026248	chr1	Mrpl44	79776018	79776311	1644	0.289041	5.107599	0.054615	0.106445	0.025218	0	417	307	601	575	605	542	818	597	946	587
ENSMUSG00000053460	chr6	Ggcx	72414308	72414449	3244	0.346988	3.314336	0.054607	0.106445	0.033407	0	107	80	187	139	200	143	235	221	201	200
ENSMUSG00000039713	chr4	Plekhg5	1.52E+08	1.52E+08	4945	0.346842	3.129959	0.054634	0.106467	0.032322	0	98	68	196	125	143	130	170	174	258	157
ENSMUSG00000083774	chr7	Gm7180	81222362	81222874	513	-0.60102	0.392806	0.05465	0.106482	0.063123	0	18	10	30	33	28	10	26	12	24	17
ENSMUSG00000062070	chrX	Pgk1	1.06E+08	1.06E+08	2244	0.312729	9.639662	0.054677	0.106519	0.03162	0	11786	7114	14241	10769	13444	12693	22121	13736	21793	12076
ENSMUSG00000027641	chr2	Rbl1	1.57E+08	1.57E+08	5993	-0.42718	1.714927	0.0547	0.106547	0.038851	0	52	49	92	45	57	38	64	49	52	45
ENSMUSG00000092595	chr17	Gm20427	34026034	34026225	3703	0.284333	6.742324	0.054716	0.106563	0.025554	0	1417	1206	1831	1503	1704	1772	2555	2005	2679	1771
ENSMUSG00000002908	chr8	Kcnn1	70842049	70844561	4054	-0.32173	4.579267	0.054738	0.106591	0.030659	0	336	213	564	532	534	317	485	327	466	347
ENSMUSG00000085208	chr11	Brip1os	86201370	86201552	6498	0.384541	3.094531	0.054794	0.106684	0.041582	0	83	66	151	135	166	140	165	204	174	173
ENSMUSG00000038290	chr11	Smg6	74925823	74926003	8453	-0.30043	4.64368	0.054835	0.106748	0.02662	0	326	271	712	440	535	300	428	403	595	336
ENSMUSG00000032192	chr9	Gnb5	75311395	75311520	1188	-0.55042	3.620952	0.054843	0.106749	0.092255	0	125	94	222	384	373	110	228	129	231	214
ENSMUSG00000031298	chrX	Gpr64	1.6E+08	1.6E+08	5278	-0.69599	0.643343	0.054975	0.10699	0.101074	0	13	29	45	26	34	18	15	35	15	16
ENSMUSG00000033196	chr11	Myh2	67171027	67171088	7137	-1.67661	9.480713	0.055045	0.10711	0.835255	0	988	321	8413	51630	30295	191	6760	5725	12567	7626

ENSMUSG00000090019	chr6	Gimap1	48739054	48739156	1872	0.578467	1.146848	0.055074	0.10715	0.076092	0	28	12	19	29	47	34	48	52	47	46
ENSMUSG00000020363	chr11	Gfpt2	49794178	49794243	5591	0.393053	3.357478	0.055151	0.107285	0.044944	0	105	85	251	114	180	176	239	284	198	146
ENSMUSG00000021576	chr13	Pdcd6	74303121	74304048	1524	0.291531	4.195506	0.055166	0.107298	0.023638	0	243	219	346	230	266	287	417	361	476	300
ENSMUSG00000097743	chr14	Gm16973	56696280	56698038	2421	0.547194	0.914315	0.055184	0.107318	0.059893	0	18	22	42	10	25	30	44	34	49	35
ENSMUSG00000063458	chr14	1700112E06Rik	22019712	22019908	2714	0.471317	1.771231	0.05529	0.107508	0.050473	0	38	36	51	51	43	58	105	74	55	57
ENSMUSG00000071172	chr17	Srsf3	29032673	29032786	5109	0.319823	5.645816	0.05532	0.10755	0.031761	0	677	663	872	573	698	909	1261	965	1179	764
ENSMUSG00000021692	chr13	Dimt1	1.07E+08	1.07E+08	2545	-0.42472	1.789238	0.055393	0.107676	0.040013	0	61	43	89	55	63	44	79	38	67	38
ENSMUSG00000030509	chr7	Asb7	66644565	66647925	6226	-0.30494	3.397738	0.05544	0.107752	0.024176	0	164	131	271	170	201	122	203	169	198	163
ENSMUSG00000036022	chrX	Fam122b	53243415	53246290	4409	-0.56891	1.074441	0.055492	0.107838	0.068627	0	21	40	52	29	51	34	33	21	29	28
ENSMUSG00000083240	chr2	Gm13453	40127504	40127860	357	0.394972	1.90432	0.055501	0.107839	0.03271	0	43	38	73	49	50	52	99	68	89	71
ENSMUSG00000030284	chr6	Creld1	1.13E+08	1.13E+08	3816	0.313082	5.797161	0.055567	0.107951	0.030784	0	839	587	1070	586	888	938	1103	1089	1508	971
ENSMUSG00000005982	chr16	Naa60	3872375	3872581	3815	-0.29485	5.481812	0.055593	0.107986	0.026875	0	617	437	1081	945	961	562	913	691	846	661
ENSMUSG00000052738	chr6	Suclg1	73248382	73248753	4617	-0.32709	8.071114	0.055612	0.108008	0.034723	0	3755	3239	5128	6055	5775	3479	6012	3483	5570	3588
ENSMUSG00000059409	chr17	Ppp2r5d	46682991	46684126	2926	-0.3009	5.080719	0.055627	0.108021	0.027561	0	456	350	902	669	701	390	570	530	750	534
ENSMUSG00000027411	chr2	Vps16	1.3E+08	1.3E+08	3727	0.295155	4.084338	0.055747	0.108238	0.024068	0	238	190	291	236	244	254	430	315	404	303
ENSMUSG00000032118	chr9	Fez1	36821939	36822375	4029	-0.36966	2.757409	0.055775	0.108276	0.034314	0	89	95	162	128	131	105	105	89	137	91
ENSMUSG00000040363	chrX	Bcor	12036740	12037917	7190	-0.37898	4.350209	0.055799	0.108306	0.043865	0	293	199	579	331	520	170	498	230	447	320
ENSMUSG00000021379	chr13	Id4	48261427	48261938	1660	0.696208	0.529354	0.055881	0.108451	0.092406	0	18	21	12	9	17	20	47	32	37	17
ENSMUSG00000100774	chr1	Gm7329	65095227	65095436	210	-0.71248	0.728735	0.055906	0.108484	0.122403	0	39	40	35	16	18	23	25	25	21	14
ENSMUSG00000007670	chr17	Khsrp	57021058	57022970	3990	0.282076	4.559168	0.05594	0.108524	0.023739	0	268	207	527	344	403	357	495	514	577	409
ENSMUSG00000019470	chr8	Xab2	3608421	3610219	4685	0.285484	3.835709	0.055944	0.108524	0.02231	0	191	130	277	191	249	205	325	289	353	256
ENSMUSG00000024581	chr18	Napg	62977836	62978024	5139	-0.28817	4.55085	0.056039	0.108641	0.02455	0	352	318	666	327	430	301	505	359	431	334
ENSMUSG00000041417	chr13	Pik3r1	1.02E+08	1.02E+08	10079	-0.39201	5.235024	0.056038	0.108641	0.048391	0	348	389	1080	764	1024	387	792	719	590	499
ENSMUSG00000043858	chr7	Nup62	44816088	44816483	2851	0.268046	4.689615	0.056034	0.108641	0.021232	0	309	241	525	384	445	436	603	463	659	417
ENSMUSG00000047126	chr11	Cltc	86694351	86695690	8499	-0.29347	7.282743	0.056045	0.108641	0.027807	0	2111	1787	4670	2521	3168	2005	3298	2401	2914	2224
ENSMUSG00000070822	chr7	Zscan18	12768092	12769745	3626	0.896533	0.332046	0.056013	0.108641	0.200653	0	10	1	5	23	25	11	45	28	26	27
ENSMUSG00000068699	chr6	Flnc	29433153	29433813	9543	-0.47461	8.934438	0.056164	0.108857	0.073436	0	5109	3069	14072	13030	13465	5374	9337	5977	10613	6756
ENSMUSG00000028709	chr4	Mob3c	1.16E+08	1.16E+08	2975	0.428975	2.070637	0.056174	0.10886	0.042282	0	51	44	80	49	56	65	137	72	111	54
ENSMUSG00000038034	chr1	Igsf8	1.72E+08	1.72E+08	5217	0.453342	3.730692	0.056254	0.108998	0.063219	0	98	76	225	280	245	205	262	305	355	257
ENSMUSG00000051456	chr13	Hspb3	1.14E+08	1.14E+08	781	0.354263	4.978998	0.056271	0.109016	0.038665	0	443	422	532	335	419	616	745	483	834	542
ENSMUSG00000058838	chr9	Rps27a-ps2	83409660	83410126	467	0.447717	3.63155	0.056422	0.109276	0.058818	0	186	173	138	124	167	245	366	212	262	209
ENSMUSG00000069844	chr11	Sco1	67052670	67052916	3925	-0.37256	2.897822	0.056418	0.109276	0.037336	0	110	78	138	156	189	92	162	105	139	94
ENSMUSG00000003847	chr8	Nfat5	1.07E+08	1.07E+08	18378	-0.33495	4.451277	0.056472	0.109348	0.033473	0	249	228	705	346	532	256	428	341	389	346
ENSMUSG00000022817	chr16	Itgb5	33829665	33830030	3362	-0.30479	6.662382	0.056476	0.109348	0.029903	0	1372	1180	2373	2102	2065	1406	1642	1430	2238	1535
ENSMUSG00000000711	chr10	Rab5b	1.29E+08	1.29E+08	3166	-0.27986	6.917691	0.056499	0.109378	0.025254	0	1818	1309	3238	2108	2431	1446	2510	1871	2496	1754
ENSMUSG00000039693	chr4	Msantd3	48539935	48539997	1973	0.309136	3.696202	0.056548	0.109456	0.025941	0	159	135	223	197	205	202	291	226	384	212
ENSMUSG00000035578	chr16	Iqcg	33015385	33017063	3462	-0.60272	2.04048	0.056575	0.109493	0.101084	0	63	30	54	133	109	47	72	48	59	63
ENSMUSG00000047757	chrX	Fancb	1.65E+08	1.65E+08	2983	-0.58757	0.255611	0.056639	0.1096	0.052748	0	23	17	28	14	23	13	21	14	14	17
ENSMUSG00000020589	chr12	Fam49a	12262139	12262238	4846	0.401075	2.30889	0.056679	0.109633	0.040606	0	51	55	107	50	77	96	119	97	93	91
ENSMUSG00000035824	chr8	Tk2	1.04E+08	1.04E+08	2400	0.375467	2.673547	0.056671	0.109633	0.034844	0	80	78	113	68	95	100	159	139	132	114
ENSMUSG00000096971	chr15	4930556M19Rik	10717144	10719429	4029	0.592933	1.108877	0.05668	0.109633	0.084124	0	18	13	27	33	41	39	53	21	79	36
ENSMUSG00000028779	chr4	Pef1	1.3E+08	1.3E+08	1915	0.294159	5.257588	0.056702	0.109658	0.026543	0	552	419	654	541	545	630	921	710	1048	575
ENSMUSG00000025066	chr19	Sfr1	47731756	47731821	1583	0.29797	6.414249	0.056719	0.10966	0.028401	0	1240	961	1596	1024	1259	1346	2287	1597	2140	1330
ENSMUSG00000030852	chr7	Tacc2	1.31E+08	1.31E+08	9537	-0.3603	8.809555	0.056711	0.10966	0.042594	0	5874	3991	13263	9278	10052	5072	9105	5452	11359	5911
ENSMUSG00000083773	chr2	Gm13394	28933610	28934609	1000	-0.70181	0.133316	0.056747	0.109698	0.090884	0	28	11	23	11	26	17	16	16	11	8
ENSMUSG00000021113	chr12	Snapc1	73964530	73964746	2125	0.312197	3.178785	0.056863	0.109895	0.024829	0	107	88	178	138	135	136	248	166	204	158
ENSMUSG00000021420	chr13	Fars2	36117411	36118005	2125	-0.38155	4.382352	0.056866	0.109895	0.045008	0	239	237	399	535	489	241	403	243	485	303
ENSMUSG00000084098	chr2	Gm13422	23235236	23235739	504	-0.64646	0.833074	0.056974	0.110088	0.100618	0	29	15	63	45	17	16	43	18	27	18
ENSMUSG00000028136	chr3	Snx27	94497550	94502065	6241	-0.26645	5.646851	0.05699	0.110104	0.02215	0	783	569	1371	758	1009	652	980	792	1025	718
ENSMUSG00000005583	chr13	Mef2c	83504034	83504376	6760	-0.29608	9.190038	0.057021	0.110146	0.028871	0	7541	7396	16035	10394	11449	7064	12553	7881	12424	8650
ENSMUSG00000034154	chr2	Ino80	1.19E+08	1.19E+08	6803	-0.2709	4.411085	0.05708	0.110245	0.021242	0	320	242	580	353	405	270	430	346	435	287
ENSMUSG00000037139	chr4	Myom3	1.36E+08	1.36E+08	6038	-1.58335	4.861895	0.057098	0.110264	0.761962	0	26	12	175	2110	1301	66	394	138	349	411
ENSMUSG00000062683	chr15	Atp5g2	1.03E+08	1.03E+08	1675	0.307929	6.955862	0.057122	0.110294	0.030769	0	1665	1242	2034	1968	1913	2021	3315	2165	3493	1798
ENSMUSG00000026107	chr1	Nabp1	51465862	51469086	8498	-0.47756	4.442324	0.057175	0.110379	0.072692	0	342	517	487	261	308	191	357	412	440	276
ENSMUSG00000049643	chr7	2310022A10Rik	27553233	27553353	4780	0.297416	6.315881	0.057215	0.110441	0.02841	0	1072	750	1370	1261	1272	1219	1869	1464	2309	1277
ENSMUSG00000032046	chr2	Abhd12	1.51E+08	1.51E+08	2823	0.274805	4.975474	0.057305	0.110598	0.023095	0	416	279	614	492	502	518	671	640	762	537
ENSMUSG00000023010	chr15	Tmbim6	99392882	99393040	3806	0.285858	8.032373	0.057347	0.110664	0.026824	0	3354	2921	5153	3490	4020	4035	5556	5275	6961	4542
ENSMUSG00000000739	chr8	Sult5a1	1.23E+08	1.23E+08	1764	0.600288	2.028078	0.057376	0.110703	0.100356	0	52	54	79	16	49	71	75	118	99	68
ENSMUSG00000031822	chr8	Gse1	1.2E+08	1.2E+08	8098	0.289246	4.981431	0.057392	0.110719	0.026068	0	359	294	751	391	557	524	668	552	760	637
ENSMUSG00000027488	chr2	Snta1	1.54E+08	1.54E+08	3094	0.336012	7.803335	0.057424	0.110763	0.037143	0	2742	1710	4007	3723	3957	3961	4532	3602	6919	3883
ENSMUSG00000058546	chr11	Rpl23a	78180932	78180997	847	0.319271	7.407334	0.057492	0.11088	0.033341	0	2329	2088	2686	2315	2375	3041	4390	3142	4075	2642
ENSMUSG00000026565	chr1	Pou2f1	1.66E+08	1.66E+08	16597	-0.43142	3.07513	0.057541	0.110958	0.052554	0	111	59	318	142	196	100	153	127	162	109
ENSMUSG00000029669	chr6	Tspan12	21771395	21772936	2626	-0.53678	3.102697	0.057583	0.111023	0.086792	0	102	78	141	235	265	65	142	169	117	136
ENSMUSG00000073530	chr1	Pappa2	1.59E+08	1.59E+08	10294	-1.06909	0.598634	0.057599	0.111038	0.309593	0	10	41	73	11	24	23	15	32	7	3
ENSMUSG00000067377	chrX	Tspan6	1.34E+08	1.34E+08	2060	0.465867	1.737408	0.057677	0.111171	0.05124	0	29	33	39	50	65	57	75	72	68	65

ENSMUSG00000026958	chr2	Dpp7	25352276	25352566	3337	0.312239	3.611643	0.057722	0.111243	0.027171	0	146	123	220	167	217	173	282	268	250	245
ENSMUSG00000024845	chr19	Tmem134	4125934	4126200	4601	0.30579	6.279961	0.057738	0.111256	0.030108	0	1101	880	1282	1123	1074	1381	1852	1431	1942	1250
ENSMUSG00000017615	chr11	Tnfaip1	78522850	78525541	3781	-0.27537	6.067735	0.057753	0.111268	0.024305	0	926	805	1694	1187	1383	853	1381	995	1496	892
ENSMUSG00000032363	chr9	Adamts7	90163069	90163314	6282	0.680199	0.515501	0.057776	0.111297	0.110866	0	4	8	25	26	21	30	19	29	32	33
ENSMUSG00000035530	chr11	Eif1	1E+08	1E+08	2098	0.301193	9.269097	0.057822	0.11137	0.030058	0	8018	6716	11032	9271	8965	9441	15814	10194	17432	10436
ENSMUSG00000003849	chr8	Nqo1	1.07E+08	1.07E+08	1553	-0.38744	4.767828	0.057867	0.11144	0.047929	0	491	465	669	401	384	372	512	405	662	245
ENSMUSG00000040265	chr1	Dnm3	1.62E+08	1.62E+08	24452	-0.57948	2.185442	0.057895	0.111479	0.096032	0	90	74	175	42	54	43	96	80	60	50
ENSMUSG00000025757	chr3	Hspa4l	40744495	40744785	11792	-0.44748	3.082365	0.057937	0.111526	0.05737	0	108	74	170	170	279	98	138	156	125	122
ENSMUSG00000038776	chr1	Ephx1	1.81E+08	1.81E+08	1950	0.30953	4.53208	0.057934	0.111526	0.029266	0	233	211	423	395	415	341	497	551	567	377
ENSMUSG00000025470	chr7	Zfp511	1.4E+08	1.4E+08	1100	0.394329	2.28642	0.057972	0.111578	0.037907	0	71	42	95	68	55	83	126	95	111	80
ENSMUSG00000000001	chr3	Gnai3	1.08E+08	1.08E+08	3262	0.296569	4.197501	0.057994	0.111604	0.025544	0	226	218	395	202	281	256	439	372	442	337
ENSMUSG00000024772	chr19	Ehd1	6276725	6277378	3705	0.277511	5.175971	0.058015	0.111629	0.023972	0	408	354	689	543	658	656	789	666	955	550
ENSMUSG00000027947	chr3	Il6ra	89869324	89871386	3343	-0.56608	1.744202	0.058113	0.111784	0.084203	0	33	24	91	81	98	35	46	68	48	39
ENSMUSG00000033565	chr15	Rbfox2	77078990	77084206	7358	0.346266	6.091819	0.058113	0.111784	0.039096	0	644	526	1294	1168	1340	878	1745	1171	1930	1363
ENSMUSG00000088559	chr1	Mir1981	1.85E+08	1.85E+08	82	0.556727	0.749966	0.058371	0.112265	0.054541	0	18	21	23	16	22	26	32	27	50	35
ENSMUSG00000034032	chr2	Rpap1	1.2E+08	1.2E+08	6636	-0.31999	4.442845	0.058387	0.11228	0.030834	0	264	216	585	415	526	264	368	313	454	359
ENSMUSG00000029231	chr5	Pdgfra	75152291	75152457	6737	0.331742	5.270355	0.058608	0.112687	0.035636	0	355	314	989	490	745	644	887	832	765	743
ENSMUSG00000026208	chr1	Des	75360329	75360992	3754	0.319743	11.87276	0.058634	0.112722	0.034196	0	48968	37658	67790	54786	58540	61016	78893	58880	122755	64514
ENSMUSG00000043190	chr13	Rfesd	76001535	76003088	2906	-0.39374	3.825545	0.058646	0.112728	0.048083	0	249	279	273	205	218	185	294	235	245	160
ENSMUSG00000020424	chr11	Gatsl3	4218225	4218426	1574	0.479199	1.485467	0.058671	0.11276	0.050799	0	24	32	42	31	51	42	49	69	70	53
ENSMUSG00000014633	chr8	Cmc2	1.17E+08	1.17E+08	2043	-0.31496	4.043093	0.058721	0.112839	0.029809	0	243	207	312	334	355	214	354	201	375	214
ENSMUSG00000021221	chr12	Dpf3	83213745	83215811	4225	-0.34674	3.118821	0.058739	0.112857	0.031786	0	122	86	231	144	215	115	172	108	157	138
ENSMUSG00000035847	chrX	Ids	70343069	70346673	5101	-0.37396	4.815883	0.058782	0.112923	0.044354	0	395	345	879	421	594	230	424	516	544	514
ENSMUSG00000031832	chr8	Taf1c	1.2E+08	1.2E+08	3386	-0.40637	2.893308	0.058804	0.112949	0.046944	0	132	122	198	90	124	108	110	118	153	85
ENSMUSG00000015461	chr17	Atf6b	34647146	34647316	2757	0.30716	3.434717	0.058912	0.11314	0.025199	0	124	115	194	160	176	174	241	239	253	173
ENSMUSG00000028890	chr4	Mtf1	1.25E+08	1.25E+08	8907	-0.28033	4.177279	0.058924	0.113147	0.022668	0	255	190	518	307	367	217	359	296	383	246
ENSMUSG00000024327	chr17	Slc39a7	34028267	34029068	2594	0.272761	6.063464	0.058953	0.113188	0.023985	0	875	692	1235	934	1130	1059	1517	1253	1682	1182
ENSMUSG00000033970	chr5	Rfc3	1.52E+08	1.52E+08	3611	0.476155	1.691983	0.059045	0.113344	0.052811	0	57	27	43	37	41	61	84	58	72	55
ENSMUSG00000040385	chr19	Ppp1ca	4192158	4192271	1379	0.299729	7.502774	0.059052	0.113344	0.029762	0	2437	2187	3317	2342	2578	3047	4268	3500	4739	2844
ENSMUSG00000017843	chr12	Ppp2r5c	1.1E+08	1.1E+08	4224	-0.28444	6.070184	0.059073	0.113369	0.026221	0	914	824	1779	1192	1321	779	1355	1026	1292	1096
ENSMUSG00000044148	chrX	1810030O07Rik	12654879	12656486	2699	0.303689	4.195964	0.059133	0.113466	0.026798	0	242	234	330	217	266	271	470	367	413	325
ENSMUSG00000009418	chr1	Nav1	1.35E+08	1.35E+08	17303	0.40073	3.993894	0.059143	0.11347	0.051029	0	143	110	425	157	341	219	344	375	378	323
ENSMUSG00000032468	chr9	Armc8	99478372	99480777	6531	-0.26972	5.637373	0.059172	0.113509	0.023245	0	720	584	1363	784	1019	603	1149	732	1053	658
ENSMUSG00000026425	chr1	Srgap2	1.31E+08	1.31E+08	12560	0.303965	4.127199	0.059185	0.113517	0.027781	0	209	179	430	181	284	319	388	336	418	285
ENSMUSG00000028081	chr3	Rps3a1	86137940	86138110	977	0.372882	8.500105	0.059208	0.113545	0.046446	0	4989	5178	5492	4023	4523	6780	10091	6595	8581	5513
ENSMUSG00000024101	chr17	Wash	66111546	66111649	2986	0.284035	4.520722	0.059263	0.113633	0.023898	0	287	276	396	325	349	397	540	440	575	348
ENSMUSG00000043284	chr11	Tmem11	60864452	60865348	1745	0.299655	5.429926	0.059369	0.113817	0.028474	0	622	469	699	634	615	764	1140	742	1069	657
ENSMUSG00000090084	chrX	Srpx	10037977	10039100	2652	0.444352	3.495712	0.059376	0.113817	0.060743	0	133	117	280	86	166	277	191	234	243	192
ENSMUSG00000040929	chr19	Rfx3	27761721	27768693	11034	-0.57522	1.214583	0.0594	0.113847	0.080143	0	19	24	75	48	57	14	37	27	55	33
ENSMUSG00000027603	chr2	Ggt7	1.55E+08	1.55E+08	3264	-0.50325	0.73413	0.059464	0.113953	0.045424	0	24	18	39	29	39	25	26	18	33	16
ENSMUSG00000008429	chr9	Herpud2	25108130	25109005	2744	-0.35171	5.365984	0.059504	0.114014	0.040293	0	708	634	1221	506	647	406	772	643	953	591
ENSMUSG00000015474	chr17	Ppt2	34616662	34617487	2614	0.277504	5.227314	0.059523	0.114033	0.024306	0	481	329	680	605	642	582	813	707	989	663
ENSMUSG00000054280	chr5	Prr14l	32789218	32793832	11004	-0.39174	2.587471	0.059534	0.114038	0.039778	0	80	59	197	91	138	61	116	100	119	77
ENSMUSG00000025981	chr1	Coq10b	55052770	55052990	4805	0.291833	4.366566	0.059579	0.114097	0.025117	0	277	225	344	273	352	294	578	346	519	360
ENSMUSG00000069020	chr2	Urm1	29820075	29820206	4275	0.329736	4.392975	0.059582	0.114097	0.03338	0	268	185	290	376	356	377	555	393	477	330
ENSMUSG00000037410	chr9	Tbc1d2b	90202027	90205222	8799	0.370175	3.688151	0.059615	0.114144	0.042292	0	110	96	324	199	212	190	306	329	265	222
ENSMUSG00000037339	chr5	Fam53a	33600351	33600880	9110	-0.29304	5.893297	0.059678	0.114247	0.027982	0	936	698	1332	1056	1262	805	1047	855	1505	731
ENSMUSG00000039956	chr16	Mrap	90738324	90738669	1464	1.198373	1.94963	0.059778	0.114422	0.438741	0	69	49	20	4	18	84	50	243	49	33
ENSMUSG00000036769	chrX	Wdr44	23693051	23693539	8353	-0.35035	4.380856	0.059817	0.114481	0.038244	0	265	256	576	318	511	196	421	252	417	394
ENSMUSG00000021824	chr14	Ap3m1	21031442	21036703	7015	-0.27436	4.487419	0.059859	0.114545	0.02249	0	343	225	538	424	471	293	458	334	451	322
ENSMUSG00000048232	chr4	Fbxo10	45034247	45036082	4691	0.433443	2.367403	0.059904	0.114615	0.051719	0	52	37	102	60	106	93	108	71	174	89
ENSMUSG00000030264	chr6	Thumpd3	1.13E+08	1.13E+08	3888	-0.3078	3.983507	0.059957	0.1147	0.028462	0	277	227	333	245	294	182	352	244	267	244
ENSMUSG00000020708	chr11	Psmc5	1.06E+08	1.06E+08	1394	0.331628	7.562741	0.05997	0.114708	0.036751	0	2486	2596	3093	2222	2618	3288	4592	3566	4996	2941
ENSMUSG00000042364	chr13	Snx18	1.14E+08	1.14E+08	4446	0.278049	4.052496	0.060041	0.114826	0.022512	0	212	152	327	224	300	236	368	350	400	300
ENSMUSG00000027848	chr3	Olfml3	1.04E+08	1.04E+08	4014	0.410982	3.796259	0.060055	0.114838	0.053488	0	104	93	262	213	325	221	385	273	255	293
ENSMUSG00000029014	chr5	Dnajc2	21757267	21757409	5029	-0.30392	4.77969	0.060095	0.114898	0.02928	0	379	447	551	480	523	391	586	373	547	357
ENSMUSG00000026851	chr2	BC005624	30972177	30973301	3280	0.318669	5.23795	0.060135	0.114956	0.03231	0	516	501	643	400	567	656	996	668	859	645
ENSMUSG00000003477	chr6	Inmt	55170626	55171277	1600	-0.67136	4.605323	0.060169	0.114997	0.147755	0	377	450	986	243	397	548	232	300	470	108
ENSMUSG00000038564	chr5	Ift172	31253280	31253424	5407	-0.31789	4.619437	0.060182	0.114997	0.031374	0	334	232	687	466	548	246	453	389	500	415
ENSMUSG00000075273	chr2	Ttc30b	75935849	75938585	2737	-0.44907	1.618956	0.060176	0.114997	0.044068	0	46	32	84	52	68	36	64	51	35	42
ENSMUSG00000021177	chr12	Tdp1	99884517	99884552	5464	0.42471	1.641712	0.060215	0.115043	0.040931	0	41	26	59	36	46	56	61	76	68	50
ENSMUSG00000087269	chr2	D330023K18Rik	31146457	31146785	1249	0.455871	1.821389	0.060298	0.115185	0.049	0	53	30	47	49	49	71	89	55	97	51
ENSMUSG00000034424	chr8	Gcsh	1.17E+08	1.17E+08	1579	-0.27261	5.033519	0.060328	0.115226	0.023484	0	492	478	699	537	634	450	682	466	650	466
ENSMUSG00000071647	chr19	Eml3	8929694	8929952	3161	0.3551	2.772788	0.060393	0.115334	0.033973	0	71	65	150	96	101	117	157	163	138	109
ENSMUSG00000022403	chr15	St13	81363669	81365578	3457	-0.29537	6.241834	0.060497	0.115516	0.028799	0	1061	994	1702	1418	1527	886	1258	1351	1482	1198

ENSMUSG00000096929	chr1	A330023F24Rik	1.95E+08	1.95E+08	9354	-0.49963	1.993381	0.060521	0.115545	0.068456	0	74	63	115	38	77	58	90	57	58	33
ENSMUSG00000027569	chr2	Mrgbp	1.81E+08	1.81E+08	3499	0.411979	2.242966	0.060575	0.115631	0.042941	0	66	44	91	57	61	62	105	106	100	105
ENSMUSG00000069114	chr3	Zbtb10	9250602	9252080	7414	-0.33995	2.938011	0.060798	0.116041	0.030636	0	122	80	217	112	168	88	143	109	173	105
ENSMUSG00000020070	chr10	Rufy2	62980223	62980332	8108	-0.41526	1.770532	0.060851	0.116125	0.038134	0	47	40	99	59	66	30	71	51	60	50
ENSMUSG00000023439	chr6	Gnb3	1.25E+08	1.25E+08	2632	-0.69953	0.030149	0.060894	0.116189	0.098205	0	18	21	22	8	21	14	9	18	14	8
ENSMUSG00000049751	chr12	Rpl36al	69182731	69183165	1353	0.420985	6.45281	0.061045	0.116462	0.059286	0	1311	1264	1308	821	997	1780	2454	1528	2287	1192
ENSMUSG00000078122	chrX	F630028O10Rik	96239926	96239996	3295	0.87838	-0.14553	0.061061	0.116475	0.166065	0	16	7	15	4	2	23	14	23	13	17
ENSMUSG00000031568	chr8	Rwdd4a	47533664	47533943	3352	-0.27447	4.472369	0.061094	0.116521	0.022976	0	316	244	511	406	499	253	459	334	503	310
ENSMUSG00000029863	chr6	Casp2	42264985	42265197	6986	0.364649	2.416238	0.061338	0.11697	0.035023	0	59	41	121	65	93	91	119	119	119	87
ENSMUSG00000036002	chr4	Fam214b	43032414	43033688	4129	0.288118	5.366279	0.061358	0.116974	0.026846	0	565	386	783	604	653	706	779	764	1168	712
ENSMUSG00000056880	chr9	Gadl1	1.16E+08	1.16E+08	3966	-0.79634	3.624799	0.061351	0.116974	0.207811	0	421	216	296	96	155	232	117	80	336	61
ENSMUSG00000035944	chr15	Ttc38	85832306	85832419	3842	-0.44376	2.921028	0.061405	0.117046	0.059019	0	74	72	176	213	175	75	159	100	151	104
ENSMUSG00000028483	chr4	Snapc3	83417724	83418054	6760	0.363108	2.41296	0.06143	0.117078	0.032677	0	65	53	106	61	85	91	145	106	128	71
ENSMUSG00000020422	chr11	Tns3	8431652	8434638	11182	0.435037	3.948954	0.061482	0.11716	0.061354	0	116	83	259	286	352	238	378	320	347	320
ENSMUSG00000030435	chr7	U2af2	5062143	5062336	2266	0.252764	5.577705	0.061491	0.117161	0.020558	0	590	503	977	646	813	774	1084	913	1176	798
ENSMUSG00000051343	chr6	Rab11fip5	85334963	85337226	4104	0.31215	5.110881	0.061503	0.117166	0.031661	0	369	286	776	596	512	575	775	620	1047	519
ENSMUSG00000025578	chr11	Cbx8	1.19E+08	1.19E+08	3675	0.432988	1.51683	0.061542	0.117225	0.038407	0	27	34	59	30	39	41	66	56	77	50
ENSMUSG00000040795	chr4	Iqcc	1.3E+08	1.3E+08	3188	0.359541	2.881131	0.061596	0.117309	0.036105	0	95	53	127	120	121	144	177	124	178	120
ENSMUSG00000026014	chr1	Raph1	60482292	60490321	20498	-0.34196	4.450451	0.061606	0.117312	0.037125	0	249	241	637	406	501	236	383	303	605	275
ENSMUSG00000058600	chr15	Rpl30	34440505	34440604	3020	0.363671	7.474019	0.06172	0.117512	0.044814	0	2503	2435	2712	2131	2175	3373	4965	3154	4298	2621
ENSMUSG00000028745	chr4	Capzb	1.39E+08	1.39E+08	3299	0.288148	8.387721	0.061783	0.117615	0.028287	0	4674	3703	6807	4133	4868	5653	7916	6029	8723	5515
ENSMUSG00000042303	chr15	Sgsm3	80977765	80977865	4358	-0.29174	4.048496	0.061805	0.117641	0.025427	0	296	199	386	272	301	250	303	234	350	215
ENSMUSG00000032939	chr8	Nup93	94214597	94214631	2882	0.320158	3.9358	0.061853	0.117715	0.03138	0	208	134	354	173	244	290	319	242	434	257
ENSMUSG00000036893	chr2	Ehmt1	24790769	24792130	7136	-0.2973	4.191291	0.061881	0.11773	0.026641	0	212	197	487	349	418	204	360	304	376	261
ENSMUSG00000053886	chr8	Sh2d4a	68276567	68276872	2718	0.410551	2.907223	0.061888	0.11773	0.049479	0	58	62	119	126	155	114	194	133	156	169
ENSMUSG00000072572	chr14	Slc39a2	51892889	51893914	3447	0.745898	0.237854	0.061886	0.11773	0.116888	0	9	14	17	10	13	18	31	44	12	15
ENSMUSG00000040195	chr10	Tmem194	1.28E+08	1.28E+08	7822	0.39643	2.296512	0.061904	0.117745	0.039871	0	58	49	113	56	62	93	111	74	133	87
ENSMUSG00000020387	chr11	Jade2	51813455	51817657	10760	-0.38728	2.920782	0.061928	0.117765	0.040998	0	95	73	246	119	183	100	125	137	139	89
ENSMUSG00000024639	chr19	Gnaq	16132831	16133461	6185	-0.32113	3.841303	0.061942	0.117765	0.030506	0	168	181	437	230	297	187	269	272	250	177
ENSMUSG00000031060	chrX	Rbm10	20617503	20618082	3714	0.282608	3.845864	0.061933	0.117765	0.023553	0	170	125	308	214	240	228	334	286	307	269
ENSMUSG00000054836	chr9	Elp6	1.1E+08	1.1E+08	2054	0.475988	1.887238	0.062028	0.117913	0.058941	0	43	31	42	61	61	58	66	91	80	79
ENSMUSG00000024937	chr19	Ehbp1l1	5707376	5708425	6440	-0.2844	9.075279	0.062087	0.118008	0.027707	0	8041	6441	13211	8981	11625	6981	9898	7293	12156	8357
ENSMUSG00000020745	chr11	Pafah1b1	74673949	74679614	9620	-0.27404	7.401127	0.062119	0.118052	0.025474	0	2531	2116	4460	2603	3387	2245	3534	2429	3476	2401
ENSMUSG00000069835	chr11	Sat2	69622024	69622332	1424	0.445664	1.874659	0.062208	0.118204	0.046617	0	55	39	45	46	50	60	82	72	83	74
ENSMUSG00000102070	chr1	Gm28661	24614885	24615565	681	-0.39277	3.877175	0.062219	0.118209	0.048757	0	161	170	268	311	442	190	327	166	321	174
ENSMUSG00000078923	chr2	Ube2v1	1.68E+08	1.68E+08	2721	-0.29993	5.219885	0.062297	0.11834	0.029298	0	560	428	749	739	828	500	673	459	854	574
ENSMUSG00000039706	chr5	Ldb2	44472133	44473512	2485	0.412046	2.035585	0.062345	0.118396	0.040539	0	48	47	86	47	47	66	101	80	117	57
ENSMUSG00000063882	chr4	Uqcrh	1.16E+08	1.16E+08	1237	0.343777	8.649461	0.06234	0.118396	0.040485	0	5347	4373	5250	6437	6237	6852	11692	6314	10924	6090
ENSMUSG00000024055	chr17	Cyp4f13	32924688	32924954	3330	0.508144	1.604113	0.062375	0.118436	0.068093	0	48	23	72	21	34	56	68	72	63	51
ENSMUSG00000021460	chr13	Auh	52835119	52835551	9580	-0.27185	5.458537	0.06244	0.118543	0.024211	0	635	554	929	852	881	580	983	631	936	559
ENSMUSG00000028158	chr3	Mttp	1.38E+08	1.38E+08	4410	-0.54713	1.311458	0.062463	0.118571	0.075504	0	53	36	55	50	28	28	34	31	36	45
ENSMUSG00000003032	chr4	Klf4	55527143	55528300	3049	0.297204	3.903863	0.062484	0.118593	0.026176	0	154	176	317	180	257	239	392	311	304	251
ENSMUSG00000004535	chr6	Tax1bp1	52713729	52713855	6609	-0.28183	6.468065	0.062527	0.118657	0.026768	0	1334	1304	2086	1433	1582	1184	1937	1330	1646	1236
ENSMUSG00000031328	chrX	Flna	74223461	74223977	9400	0.320922	6.251162	0.062556	0.118691	0.034864	0	721	634	1709	1054	1561	1052	1669	1655	1839	1502
ENSMUSG00000071649	chr19	B3gat3	8920374	8920648	1601	0.283189	5.456358	0.062563	0.118691	0.026011	0	633	468	700	617	711	761	1041	815	1124	675
ENSMUSG00000021973	chr14	Micu2	57916280	57917375	2310	0.288067	5.791137	0.062612	0.118768	0.027269	0	747	630	864	855	818	875	1407	989	1357	963
ENSMUSG00000059201	chr6	Lep	29060220	29060248	3354	-1.12751	3.18697	0.062687	0.118893	0.412084	0	302	280	211	37	69	55	29	266	46	96
ENSMUSG00000031425	chrX	Plp1	1.37E+08	1.37E+08	5551	-0.50168	1.882511	0.062715	0.118894	0.068112	0	39	62	116	61	65	32	92	46	46	58
ENSMUSG00000042541	chr6	Shfm1	6557294	6558491	1472	0.334508	6.276737	0.062714	0.118894	0.037563	0	1011	1094	1197	933	1061	1354	1950	1347	1950	1324
ENSMUSG00000066148	chr4	Prpf4	62408797	62408901	5671	-0.26416	4.946182	0.062709	0.118894	0.021873	0	418	353	844	484	674	423	636	495	578	425
ENSMUSG00000060427	chr8	Zfp868	69610857	69612455	2893	-0.37405	2.303436	0.062745	0.118936	0.034755	0	77	70	113	82	95	65	95	77	70	74
ENSMUSG00000050014	chr15	Apol10b	77584158	77585811	1986	0.462705	1.644535	0.062879	0.119171	0.050669	0	29	34	58	27	58	61	92	61	66	40
ENSMUSG00000027259	chr2	Adal	1.21E+08	1.21E+08	5317	-0.29287	4.453326	0.062926	0.119244	0.026813	0	332	255	561	386	424	275	549	280	376	330
ENSMUSG00000057335	chr1	Cep170	1.77E+08	1.77E+08	18049	-0.35955	3.601752	0.063017	0.119399	0.038734	0	170	153	428	159	221	168	210	211	197	167
ENSMUSG00000030493	chr7	C230052I12Rik	35392275	35393091	1824	0.637631	0.006818	0.063076	0.119495	0.058038	0	14	8	11	10	12	15	17	19	26	21
ENSMUSG00000060044	chr10	Tmem26	68723746	68724090	5052	-0.83918	0.426337	0.06317	0.119654	0.176399	0	29	23	49	10	19	27	7	20	17	7
ENSMUSG00000017446	chr11	C1qtnf1	1.18E+08	1.18E+08	3131	-0.36497	3.488088	0.063206	0.119706	0.039928	0	161	149	350	147	227	126	188	227	172	166
ENSMUSG00000099471	chr1	Gm8451	1.27E+08	1.27E+08	447	0.626644	0.513055	0.063226	0.119728	0.075219	0	17	16	23	16	9	28	38	27	41	13
ENSMUSG00000020385	chr11	Clk4	51261730	51261793	5797	-0.28129	4.9652	0.063264	0.119781	0.025606	0	526	432	793	460	530	377	579	479	687	465
ENSMUSG00000040865	chr1	Ino80d	62958418	62958632	17713	-0.3426	3.833738	0.06329	0.119813	0.035589	0	199	143	471	194	332	153	252	256	277	207
ENSMUSG00000093574	chr5	Gm20671	32737230	32737454	1731	-0.34819	3.511139	0.063317	0.119848	0.036396	0	160	118	228	258	262	143	265	186	201	126
ENSMUSG00000069089	chr13	Cdk7	1.01E+08	1.01E+08	7595	-0.30327	3.944728	0.063357	0.119906	0.027761	0	238	213	418	234	264	192	305	209	279	263
ENSMUSG00000024033	chr17	Rsph1	31255019	31255219	1164	0.584357	0.663674	0.063375	0.119924	0.074038	0	15	11	18	26	24	21	30	49	31	28
ENSMUSG00000020608	chr12	Smc6	11265886	11266288	5603	-0.26621	5.015161	0.063425	0.120002	0.022634	0	400	379	848	582	691	399	697	512	656	442
ENSMUSG00000001211	chr10	Agpat3	78269178	78273775	7577	-0.30971	6.619007	0.063501	0.120128	0.032682	0	1250	1060	2113	2285	2135	1251	1945	1444	2057	1382

ENSMUSG00000028584	chr4	Lrrc38	1.43E+08	1.43E+08	2324	-0.30293	5.446844	0.063547	0.120197	0.030156	0	671	430	1066	720	1084	635	698	691	779	697
ENSMUSG00000097412	chr10	1810014B01Rik	86685601	86685737	1661	-0.32019	3.193016	0.063637	0.120351	0.02923	0	140	103	194	175	200	98	210	129	168	139
ENSMUSG00000001656	chr15	Hoxc11	1.03E+08	1.03E+08	2021	0.465601	2.830932	0.063661	0.120379	0.063322	0	107	79	126	85	64	129	202	117	235	80
ENSMUSG00000017307	chr2	Acot8	1.65E+08	1.65E+08	1994	0.384806	2.490816	0.063689	0.12038	0.037802	0	70	61	85	76	87	102	131	81	144	110
ENSMUSG00000019173	chr11	Rab5c	1.01E+08	1.01E+08	2194	0.267727	5.323822	0.063688	0.12038	0.023301	0	512	405	731	617	649	664	1004	840	868	617
ENSMUSG00000034789	chr13	Rab24	55319223	55320214	1865	0.288676	5.235458	0.063674	0.12038	0.027043	0	537	412	600	547	573	670	886	631	953	639
ENSMUSG00000043183	chr13	Simc1	54503779	54504004	5675	-0.44694	1.747757	0.063774	0.120524	0.049351	0	38	38	113	58	67	30	65	61	61	38
ENSMUSG00000020978	chr12	Klhdc2	69296681	69297147	5438	-0.29624	7.14599	0.063787	0.120531	0.030181	0	2376	1990	3346	2145	2598	1992	3233	1935	2897	1719
ENSMUSG00000057751	chr4	Megf6	1.54E+08	1.54E+08	7877	0.599855	0.102837	0.063835	0.120605	0.053816	0	10	7	13	16	15	13	32	22	21	18
ENSMUSG00000022305	chr15	Lrp12	39870603	39872878	4574	0.385807	2.24397	0.063892	0.120677	0.038212	0	50	40	93	60	86	64	120	119	99	78
ENSMUSG00000039196	chr4	Orm1	63344560	63344714	775	1.385686	2.034816	0.063889	0.120677	0.605292	0	80	41	17	3	13	96	20	299	42	39
ENSMUSG00000061353	chr6	Cxcl12	1.17E+08	1.17E+08	8176	-0.29406	6.055649	0.063958	0.120786	0.029256	0	856	810	1573	1123	1634	743	1600	1062	1283	873
ENSMUSG00000033039	chr15	Micall1	79108972	79109429	6701	-0.30058	4.236048	0.063981	0.120812	0.027954	0	244	191	485	393	394	222	324	317	430	256
ENSMUSG00000021186	chr12	Fbln5	1.02E+08	1.02E+08	5829	0.310763	3.772363	0.064059	0.120941	0.028655	0	160	155	298	170	197	191	368	318	301	207
ENSMUSG00000062328	chr18	Rpl17	75000477	75000543	775	0.352907	7.320952	0.06408	0.120963	0.042908	0	2202	2220	2580	1881	1953	2994	4328	2980	3769	2387
ENSMUSG00000049832	chr17	Gm9840	35935624	35935950	327	0.626819	0.58983	0.064183	0.121142	0.080501	0	12	17	15	18	24	18	47	21	28	40
ENSMUSG00000054808	chr7	Actn4	28893248	28894387	5026	0.292489	5.447319	0.064223	0.121182	0.028529	0	486	393	843	690	789	610	955	1079	1043	706
ENSMUSG00000101316	chr11	Gm12663	16635109	16636066	958	-0.50332	0.837684	0.064215	0.121182	0.046149	0	26	18	48	31	39	23	35	16	27	26
ENSMUSG00000020653	chr12	Klf11	24651371	24651566	4228	0.588837	2.385096	0.064272	0.121258	0.103194	0	43	80	61	43	88	56	220	75	111	116
ENSMUSG00000026251	chr1	Chrnd	87190607	87190742	3288	0.579321	2.348399	0.064293	0.121279	0.103904	0	27	34	52	109	102	96	113	72	145	115
ENSMUSG00000098134	chr12	Rnf113a2	84417196	84418578	1383	-0.34831	3.015687	0.064358	0.121368	0.034919	0	128	135	177	120	146	109	162	101	160	113
ENSMUSG00000104049	chr12	AC120402.1	84417194	84418310	1383	-0.34831	3.015687	0.064355	0.121368	0.034918	0	128	135	177	120	146	109	162	101	160	113
ENSMUSG00000020717	chr11	Pecam1	1.07E+08	1.07E+08	6228	0.294603	5.831466	0.064429	0.121467	0.029271	0	582	530	946	960	1132	862	1431	1153	1450	894
ENSMUSG00000041765	chr14	Ubac2	1.22E+08	1.22E+08	2153	-0.28835	5.172075	0.064428	0.121467	0.027267	0	532	384	861	700	752	505	618	469	857	523
ENSMUSG00000058809	chr11	Gm12141	41498737	41500458	1722	-0.45117	2.006351	0.064463	0.121513	0.055	0	54	58	95	77	80	30	79	74	52	67
ENSMUSG00000002846	chr16	Timmdc1	38498347	38499083	1784	-0.2909	5.015948	0.064508	0.121582	0.027853	0	456	421	600	649	703	455	689	441	674	418
ENSMUSG00000062580	chr1	Timm17a	1.35E+08	1.35E+08	7893	-0.30421	6.558716	0.064564	0.12167	0.031785	0	1286	1052	2059	1963	2102	1207	1937	1199	2273	1238
ENSMUSG00000102644	chr5	THAP6	91962389	91962978	4119	-0.39154	2.273145	0.064605	0.121729	0.041259	0	69	83	116	76	83	46	93	82	96	62
ENSMUSG00000005621	chr7	Zfp592	80993681	80993762	7412	-0.29352	4.272141	0.064617	0.121734	0.026427	0	239	192	560	350	431	247	352	301	404	280
ENSMUSG00000050188	chr4	Lsm10	1.26E+08	1.26E+08	943	0.356687	2.76154	0.064657	0.121792	0.0334	0	83	86	130	79	87	107	169	135	157	117
ENSMUSG00000069727	chr7	Gm5595	42660105	42662996	3148	-0.44564	2.022108	0.064667	0.121795	0.053605	0	62	63	107	64	71	53	108	40	57	52
ENSMUSG00000032315	chr9	Cyp1a1	57697613	57697699	2619	-0.69149	0.711911	0.064816	0.122057	0.112576	0	13	12	58	40	38	18	18	35	17	16
ENSMUSG00000001909	chr8	Trmt1	84686307	84686699	6306	-0.29271	4.903595	0.064983	0.122338	0.028202	0	471	445	695	492	506	404	492	448	706	411
ENSMUSG00000065979	chr16	Cpped1	11803721	11805583	5205	-0.25747	5.622245	0.064978	0.122338	0.022046	0	744	564	1234	884	934	669	1083	725	988	665
ENSMUSG00000039886	chr5	Tmem120a	1.36E+08	1.36E+08	1553	0.510387	3.801074	0.065111	0.122561	0.085434	0	205	160	186	168	161	230	212	529	297	187
ENSMUSG00000026171	chr1	Rnf25	74593748	74594402	2181	0.315983	4.056287	0.065147	0.122596	0.030648	0	217	214	314	190	231	310	350	299	438	272
ENSMUSG00000036615	chr3	Rfxap	54803115	54804575	2242	0.282192	4.034651	0.065157	0.122596	0.023938	0	206	176	354	221	232	283	419	269	410	263
ENSMUSG00000078572	chr11	1810043H04Rik	1.2E+08	1.2E+08	834	0.304285	3.968502	0.065149	0.122596	0.027768	0	233	161	234	222	249	245	375	266	414	280
ENSMUSG00000025580	chr11	Eif4a3	1.19E+08	1.19E+08	2122	0.293037	4.963208	0.065182	0.122626	0.027846	0	466	349	559	382	460	563	827	515	758	485
ENSMUSG00000032295	chr9	Man2c1	57130690	57130889	7052	0.272416	4.3096	0.065237	0.122712	0.023068	0	226	193	363	300	368	312	406	382	495	370
ENSMUSG00000031388	chrX	Naa10	73916873	73917195	4132	0.275059	4.944072	0.065293	0.1228	0.024286	0	421	311	501	474	505	454	756	564	834	504
ENSMUSG00000026494	chr1	Kif26b	1.79E+08	1.79E+08	14696	-0.54082	0.708631	0.065422	0.123025	0.061033	0	22	20	62	21	26	15	32	18	29	21
ENSMUSG00000063334	chr10	Krr1	1.12E+08	1.12E+08	5958	-0.27564	5.028967	0.065485	0.123126	0.025004	0	518	476	784	479	592	444	705	486	587	473
ENSMUSG00000025733	chr17	Rhot2	25838457	25839494	4442	-0.38513	6.83769	0.065525	0.123165	0.051666	0	1420	972	2322	3128	2790	1246	2336	1616	2433	1585
ENSMUSG00000100455	chr1	Gm29170	1.44E+08	1.44E+08	3666	-0.39005	2.315706	0.065517	0.123165	0.042735	0	84	80	112	71	92	47	116	70	104	59
ENSMUSG00000023991	chr17	Foxp4	47867133	47868803	4926	0.316635	3.323885	0.06557	0.123233	0.029476	0	128	93	214	110	178	152	212	219	224	190
ENSMUSG00000047067	chr1	Dusp28	92906981	92907423	1314	0.31348	4.617961	0.065657	0.123379	0.031599	0	342	251	355	411	356	428	587	417	687	380
ENSMUSG00000040599	chr11	Mis12	71019611	71020189	3003	0.315851	2.961589	0.065696	0.123435	0.026799	0	88	84	165	101	117	127	193	159	167	131
ENSMUSG00000002266	chr7	Zim1	6675443	6678262	3641	-0.76552	0.447259	0.065706	0.123436	0.138059	0	13	12	50	21	39	13	26	3	17	25
ENSMUSG00000025231	chr19	Sufu	46396896	46397284	6945	0.322732	3.104734	0.065968	0.12391	0.030968	0	92	68	194	101	175	138	192	165	221	149
ENSMUSG00000020573	chr12	Pik3cg	32173473	32173969	6786	0.520402	1.095808	0.06598	0.123916	0.073084	0	23	10	55	16	37	41	41	46	43	42
ENSMUSG00000027254	chr2	Map1a	1.21E+08	1.21E+08	12166	0.568418	4.403484	0.066031	0.123995	0.111303	0	116	83	411	371	487	349	355	339	846	433
ENSMUSG00000020086	chr10	H2afy2	61738665	61739462	2175	0.562797	0.436861	0.066053	0.124018	0.067957	0	7	9	30	18	19	22	35	24	21	31
ENSMUSG00000038838	chr17	Vars2	35655634	35656652	5460	-0.37283	3.744295	0.066158	0.124197	0.044167	0	141	133	309	334	321	142	227	205	301	195
ENSMUSG00000015709	chr7	Arnt2	84246281	84250154	5988	-0.71489	1.991706	0.066185	0.12423	0.158027	0	22	31	103	110	145	53	63	49	26	65
ENSMUSG00000032179	chr9	Bmp5	75775364	75776582	4025	-0.48867	3.802173	0.066209	0.124257	0.079098	0	182	156	348	246	410	97	173	160	279	332
ENSMUSG00000017421	chr11	Zfp207	80383279	80383495	6658	-0.25671	5.663134	0.066308	0.124418	0.022236	0	776	681	1282	791	913	662	1079	804	987	706
ENSMUSG00000038437	chr11	Mllt6	97663414	97663680	7451	-0.32129	6.39459	0.066313	0.124418	0.035839	0	1057	820	2021	1811	2016	968	1826	1078	1773	1286
ENSMUSG00000026784	chr2	Pdss1	22895522	22895762	4248	-0.49888	2.674225	0.066334	0.12444	0.07704	0	75	52	113	195	165	65	146	94	94	82
ENSMUSG00000025780	chr2	Itih5	10153571	10153755	7900	0.356153	5.670735	0.066427	0.124596	0.043977	0	579	475	1355	496	839	748	1164	1238	899	1081
ENSMUSG00000028069	chr3	Gpatch4	88043108	88043179	2447	-0.27212	4.68711	0.066442	0.124607	0.024112	0	419	359	548	410	497	373	521	384	534	324
ENSMUSG00000022507	chr16	1810013L24Rik	8830100	8830685	4066	-0.30074	5.530935	0.066458	0.124618	0.030662	0	625	465	1506	756	942	540	934	638	1073	659
ENSMUSG00000001151	chr10	Pcnt	76351254	76351779	9530	-0.34537	6.13858	0.066489	0.12466	0.041302	0	820	592	2072	1537	1641	803	1404	1155	1275	1047
ENSMUSG00000021501	chr13	Caml	55623005	55623256	1755	0.362288	2.898511	0.066515	0.124691	0.036169	0	96	93	146	78	99	125	203	149	177	107
ENSMUSG00000092417	chr17	Gpank1	35121455	35121550	1879	0.327008	3.436865	0.066525	0.124692	0.03198	0	118	113	198	133	210	212	206	216	281	166

ENSMUSG00000015189	chr6	Casd1	4600840	4601301	4062	-0.27617	4.873902	0.0666	0.124815	0.024967	0	446	359	754	447	606	321	629	455	535	488
ENSMUSG00000037957	chr12	Wdr20	1.11E+08	1.11E+08	5593	-0.32672	2.902407	0.066629	0.124851	0.029204	0	105	79	179	125	187	97	160	105	146	96
ENSMUSG00000090157	chr2	Gm16534	32050086	32051219	1711	-0.50164	1.282858	0.066702	0.124971	0.059049	0	37	31	59	31	65	26	35	30	34	48
ENSMUSG00000025316	chr8	Banp	1.22E+08	1.22E+08	6632	0.482238	2.974874	0.06674	0.125018	0.07384	0	89	92	132	83	119	138	143	269	112	136
ENSMUSG00000026556	chr1	Vangl2	1.72E+08	1.72E+08	6990	0.641955	0.367642	0.066746	0.125018	0.09144	0	7	8	10	20	29	20	27	20	34	29
ENSMUSG00000031842	chr8	Pde4c	70723720	70723783	5545	-0.49422	1.293181	0.066981	0.125422	0.056296	0	30	23	65	51	58	33	35	21	54	35
ENSMUSG00000031955	chr8	Bcar1	1.12E+08	1.12E+08	3171	0.2847	3.654631	0.066974	0.125422	0.024083	0	151	116	282	174	201	173	287	264	326	214
ENSMUSG00000068396	chr6	Rpl34-ps1	71124610	71124963	354	0.556055	1.407769	0.066995	0.125431	0.075308	0	35	38	30	27	27	54	49	56	78	38
ENSMUSG00000098992	chr11	Gm27597	98029413	98029492	80	0.309898	6.850401	0.067048	0.125512	0.033559	0	1436	1565	1806	1550	1655	1950	3019	2182	2780	1816
ENSMUSG00000061816	chr1	Myl1	66924295	66924557	2074	-0.34123	13.18749	0.067097	0.125587	0.041527	0	195858	123220	241753	116407	155871	128501	185446	130282	203469	113364
ENSMUSG00000071335	chr10	G630090E17Rik	39946907	39948123	1787	-0.46021	1.369534	0.067162	0.125691	0.05325	0	40	38	51	52	47	22	68	34	39	32
ENSMUSG00000031647	chr8	Mfap3l	60632827	60633058	6837	-0.39064	3.252299	0.067214	0.12577	0.047587	0	149	97	240	185	206	65	185	147	182	175
ENSMUSG00000027944	chr3	Hax1	89995457	89995710	1117	0.287259	4.884216	0.067313	0.125932	0.026939	0	412	335	464	401	481	521	742	501	758	455
ENSMUSG00000055694	chr8	Gdf1	70329817	70330276	1349	0.351581	4.348641	0.067326	0.125932	0.041207	0	308	179	408	191	367	362	338	378	573	402
ENSMUSG00000068923	chr3	Syt11	88744700	88748010	5205	-0.34388	3.295982	0.067329	0.125932	0.035841	0	183	121	234	146	191	88	174	180	201	147
ENSMUSG00000022881	chr16	Rfc4	23113943	23114107	1534	-0.33421	2.924169	0.067345	0.125944	0.032661	0	143	100	164	127	129	95	167	104	143	102
ENSMUSG00000024906	chr19	Mus81	5482345	5483029	3567	0.278249	4.624272	0.067365	0.125964	0.025253	0	322	199	451	417	414	388	559	480	604	432
ENSMUSG00000047030	chr2	Spata2	1.67E+08	1.67E+08	4510	-0.27124	4.466734	0.067374	0.125964	0.023287	0	312	245	630	346	462	260	425	387	460	306
ENSMUSG00000036585	chr18	Fgf1	38838673	38842121	4648	-0.74266	4.03133	0.067404	0.126002	0.189736	0	87	102	254	692	558	129	359	150	215	269
ENSMUSG00000028719	chr4	Cmpk1	1.15E+08	1.15E+08	3420	0.274295	4.616373	0.067437	0.126045	0.0239	0	326	280	428	337	387	331	558	491	635	446
ENSMUSG00000033769	chr6	Exoc6b	84618487	84621511	11187	-0.29328	4.064073	0.067466	0.126082	0.026485	0	227	156	460	309	374	204	319	285	327	236
ENSMUSG00000039246	chr1	Lyplal1	1.86E+08	1.86E+08	1578	0.777161	0.681612	0.067538	0.126186	0.152761	0	28	16	11	14	14	26	27	64	25	26
ENSMUSG00000071653	chr19	1810009A15Rik	8888853	8888964	1444	0.359983	3.35423	0.067541	0.126186	0.03906	0	166	104	156	122	150	201	266	161	225	180
ENSMUSG00000054027	chr10	Nt5dc3	86779005	86779311	5952	-0.35502	7.147435	0.067589	0.126258	0.044585	0	2482	1246	4531	2117	3003	2228	2197	2089	3245	1598
ENSMUSG00000027550	chr3	Lrrcc1	14533788	14534022	7475	0.400642	3.360573	0.067641	0.126338	0.050796	0	72	92	167	195	188	131	283	175	275	209
ENSMUSG00000021713	chr13	Ppwd1	1.04E+08	1.04E+08	2367	-0.37934	2.088057	0.067731	0.126488	0.036581	0	76	60	97	55	88	51	86	56	81	58
ENSMUSG00000019699	chr1	Akt3	1.77E+08	1.77E+08	4980	-0.42375	2.853119	0.067783	0.126566	0.053546	0	73	69	184	179	173	77	129	118	111	117
ENSMUSG00000078584	chr4	AU022252	1.19E+08	1.19E+08	9570	-0.25189	4.809039	0.067823	0.126624	0.020441	0	377	332	692	491	590	364	555	443	563	413
ENSMUSG00000040396	chr8	Abhd13	9977707	9978019	5191	-0.29168	3.507818	0.067866	0.126687	0.024733	0	147	136	282	200	251	146	259	182	204	144
ENSMUSG00000030087	chr6	Klf15	90462576	90462725	2527	-0.29616	5.118557	0.067908	0.126729	0.029409	0	454	420	974	675	608	503	656	543	547	551
ENSMUSG00000084168	chr11	Atp5l2-ps	97768060	97768371	312	0.568394	1.614117	0.067899	0.126729	0.088335	0	33	33	48	47	25	61	92	36	109	33
ENSMUSG00000027341	chr2	Tmem230	1.32E+08	1.32E+08	3267	0.268475	4.614239	0.067967	0.126821	0.022924	0	357	256	461	337	357	362	628	463	615	396
ENSMUSG00000092544	chr8	Gm20422	69742862	69743269	1358	-0.46711	1.385554	0.067997	0.126859	0.052471	0	39	33	91	35	43	24	59	39	41	32
ENSMUSG00000104279	chr1	RP24-252K15.4	1.78E+08	1.78E+08	1870	0.599605	1.0227	0.068038	0.126918	0.086919	0	23	23	21	21	31	45	60	47	45	15
ENSMUSG00000045251	chr7	Zfp688	1.27E+08	1.27E+08	2734	0.580788	0.998488	0.068128	0.127067	0.075953	0	33	23	28	16	17	36	51	47	49	24
ENSMUSG00000030826	chr7	Bcat2	45570153	45570399	3899	-0.27771	6.566835	0.068188	0.127162	0.027093	0	1292	1297	2339	1620	1842	1285	1621	1728	1900	1266
ENSMUSG00000022656	chr16	Pvrl3	46387706	46395272	12747	0.387204	1.993131	0.068207	0.127179	0.037075	0	38	41	68	52	72	68	95	77	77	79
ENSMUSG00000023007	chr15	Prpf40b	99295087	99295273	4952	-0.25405	4.381407	0.068217	0.12718	0.020348	0	322	270	470	339	413	280	413	330	419	292
ENSMUSG00000026223	chr1	Itm2c	85894281	85894789	2491	0.331586	5.561605	0.068258	0.127239	0.03808	0	721	539	964	460	646	877	932	1064	1120	752
ENSMUSG00000030225	chr6	Dera	1.38E+08	1.38E+08	1742	-0.33534	2.6686	0.068274	0.12725	0.0309	0	117	80	138	101	122	77	111	99	135	86
ENSMUSG00000041632	chr13	Mrps27	99344786	99344875	1848	-0.32028	5.049299	0.06831	0.1273	0.035124	0	435	349	645	729	823	410	772	447	725	394
ENSMUSG00000066258	chr7	Trim12a	1.04E+08	1.04E+08	5781	0.400695	2.349529	0.06844	0.127525	0.043741	0	59	52	86	59	90	95	161	100	90	73
ENSMUSG00000021193	chr13	Pitrm1	6548157	6548229	3524	-0.26805	5.474044	0.068511	0.127608	0.024482	0	637	481	1159	826	877	594	1050	619	860	600
ENSMUSG00000042389	chr6	Tsen2	1.16E+08	1.16E+08	6437	0.330341	3.066455	0.068523	0.127608	0.030559	0	122	84	135	114	127	117	198	172	192	162
ENSMUSG00000048911	chr2	Rnf24	1.31E+08	1.31E+08	6801	0.484793	1.594174	0.068505	0.127608	0.064945	0	24	23	69	30	57	49	54	89	69	45
ENSMUSG00000049504	chr3	Proser1	53463666	53464319	5084	-0.35389	3.046355	0.068519	0.127608	0.036843	0	104	96	237	117	209	79	158	123	171	131
ENSMUSG00000014859	chr8	E2f4	1.05E+08	1.05E+08	1992	-0.2582	4.860015	0.068587	0.127709	0.021991	0	422	344	780	468	571	352	617	442	657	383
ENSMUSG00000075585	chr5	6330403L08Rik	1.39E+08	1.39E+08	5522	-0.31255	4.648772	0.068761	0.128015	0.032816	0	415	334	745	346	416	371	501	310	562	313
ENSMUSG00000039308	chr14	Ndst2	20723739	20724360	3305	0.319709	3.100879	0.068884	0.128226	0.030498	0	100	67	195	123	138	145	186	194	189	140
ENSMUSG00000062944	chr7	9130023H24Rik	1.28E+08	1.28E+08	3581	-0.44956	1.277467	0.068919	0.128272	0.043909	0	41	23	62	43	50	22	39	33	43	42
ENSMUSG00000036941	chr18	Elac1	73735038	73739300	4971	-0.26756	3.891236	0.069033	0.128467	0.021581	0	208	195	363	244	294	194	293	256	265	212
ENSMUSG00000024712	chr19	Rfk	17394043	17394392	2603	-0.27819	6.849681	0.069065	0.128508	0.027563	0	1791	1673	2697	1815	2100	1401	2597	1632	2318	1693
ENSMUSG00000026782	chr1	Abi2	60409619	60409919	8543	-0.37253	3.015514	0.069115	0.128562	0.04217	0	128	86	170	149	199	105	126	89	210	113
ENSMUSG00000027495	chr2	Fam210b	1.72E+08	1.72E+08	3617	0.296807	3.536352	0.06911	0.128562	0.02644	0	139	120	268	129	190	182	304	233	283	169
ENSMUSG00000062937	chr4	Mtap	89137122	89137524	3226	0.301549	4.568364	0.069123	0.128562	0.030002	0	352	258	509	232	356	386	609	479	582	349
ENSMUSG00000086782	chr4	E130102H24Rik	1.01E+08	1.01E+08	918	-0.67824	0.170553	0.06919	0.128669	0.099489	0	24	14	37	16	11	13	23	15	7	13
ENSMUSG00000020402	chr11	Vdac1	52360860	52361152	2620	-0.30187	10.20707	0.06921	0.12867	0.032983	0	16014	13369	24714	25321	26325	14981	22744	15860	27062	17194
ENSMUSG00000024127	chr17	Prepl	85063477	85064733	3830	-0.32202	3.835998	0.069208	0.12867	0.032908	0	193	161	478	213	276	147	309	255	271	187
ENSMUSG00000002428	chr3	Hltf	20057811	20058007	5931	-0.4646	2.398407	0.069261	0.128747	0.065157	0	54	59	116	95	173	57	123	87	63	68
ENSMUSG00000040746	chr11	Rnf167	70647235	70647313	3539	0.261949	5.364686	0.069273	0.128752	0.023125	0	521	494	784	574	604	675	1009	771	985	672
ENSMUSG00000020087	chr10	Tysnd1	61695514	61696742	2286	0.319353	3.814421	0.069376	0.128909	0.032113	0	174	151	266	196	210	225	253	345	385	207
ENSMUSG00000043008	chr16	Klhl6	19946499	19947292	2606	0.546627	0.778316	0.069377	0.128909	0.068476	0	9	14	31	22	31	36	46	39	30	21
ENSMUSG00000022803	chr16	Popdc2	38362209	38363147	2360	0.271279	6.322093	0.069411	0.128954	0.025938	0	1090	726	1501	1161	1393	1198	2028	1402	1922	1488
ENSMUSG00000023032	chr15	Slc4a8	1.01E+08	1.01E+08	13021	-0.54645	1.402127	0.069428	0.128966	0.079612	0	25	19	65	61	83	27	44	46	49	24
ENSMUSG00000026235	chr1	Epha4	77367185	77369671	8054	-0.60041	0.857284	0.069445	0.128981	0.081806	0	16	19	43	41	51	15	20	24	29	34

ENSMUSG00000003033	chr8	Ap1m1	72240018	72240243	3150	0.261802	4.524652	0.069492	0.128997	0.022191	0	302	202	419	357	410	352	571	419	547	406
ENSMUSG00000006019	chr7	Dhx34	16197147	16197422	4596	0.336968	2.67281	0.069499	0.128997	0.031722	0	87	52	129	78	106	102	134	133	144	121
ENSMUSG00000021143	chr12	Pacs2	1.13E+08	1.13E+08	5480	-0.2935	6.014701	0.069502	0.128997	0.030196	0	816	652	1610	1355	1443	836	1212	998	1254	994
ENSMUSG00000029577	chr5	Ube3b	1.14E+08	1.14E+08	5264	-0.28909	7.887204	0.069465	0.128997	0.030067	0	3443	2241	6306	4490	5130	3099	4371	3398	5333	3404
ENSMUSG00000054469	chr17	Lclat1	73107985	73108145	4689	-0.29156	4.235777	0.06948	0.128997	0.027195	0	274	175	505	319	445	228	416	251	378	285
ENSMUSG00000042032	chr11	Mat2b	40679314	40680194	5001	-0.2732	6.011349	0.069575	0.129113	0.026233	0	928	788	1462	1228	1287	827	1464	861	1359	900
ENSMUSG00000028573	chr4	Fggy	95557507	95557591	5844	0.317541	3.124863	0.069733	0.129388	0.02819	0	111	102	162	116	120	148	211	162	232	127
ENSMUSG00000031155	chrX	Pim2	7878262	7878556	2795	0.544096	0.730313	0.06975	0.129401	0.057998	0	13	17	29	21	21	25	47	20	55	24
ENSMUSG00000040225	chr1	Prrc2c	1.63E+08	1.63E+08	16092	-0.32792	5.193179	0.069856	0.129581	0.037081	0	438	340	1270	570	865	417	697	606	724	531
ENSMUSG00000074896	chr19	Ifit3	34583531	34583604	1745	0.51646	3.101402	0.069887	0.12962	0.087467	0	96	120	137	72	120	142	327	184	91	165
ENSMUSG00000025266	chrX	Gnl3l	1.51E+08	1.51E+08	5570	-0.27954	5.157023	0.069993	0.12978	0.02663	0	559	412	1000	533	705	402	695	514	717	619
ENSMUSG00000036560	chr7	Lgi4	31059342	31060190	4584	-0.43743	2.284043	0.069888	0.12978	0.05275	0	57	43	153	85	126	70	97	76	62	61
ENSMUSG00000021171	chr12	Esyt2	1.16E+08	1.16E+08	5539	-0.27963	5.571162	0.070036	0.129842	0.027031	0	635	494	1489	780	968	628	914	694	1043	668
ENSMUSG00000081051	chr1	Gm15427	95498621	95499151	531	0.328453	4.047845	0.070097	0.129937	0.03439	0	234	214	273	218	195	298	404	291	416	266
ENSMUSG00000066595	chr1	Mfsd7b	1.91E+08	1.91E+08	5177	-0.54035	3.639876	0.070169	0.130053	0.10089	0	90	134	395	212	429	91	325	105	301	150
ENSMUSG00000031343	chrX	Gabra3	72432681	72434984	3924	0.639241	0.263962	0.070218	0.130107	0.084146	0	6	13	15	14	20	15	19	37	25	23
ENSMUSG00000067547	chr15	Gm7666	6653923	6654741	819	-0.38215	3.411313	0.070211	0.130107	0.047446	0	158	108	180	243	272	146	254	128	205	118
ENSMUSG00000046879	chr11	Irgm1	48861968	48865209	5810	0.31578	4.176507	0.070283	0.130208	0.032383	0	209	200	349	242	291	250	638	338	383	261
ENSMUSG00000068742	chr2	Cry2	92403646	92405820	6320	-0.2866	5.763582	0.070315	0.130249	0.028875	0	759	705	1477	864	1067	659	896	757	1392	812
ENSMUSG00000001334	chr4	Fndc5	1.29E+08	1.29E+08	2763	-0.453	6.45511	0.070436	0.130455	0.073986	0	910	770	1543	2748	2311	902	1839	1067	1812	1274
ENSMUSG00000020534	chr11	Shmt1	60788104	60789316	3883	-0.34483	3.461889	0.070496	0.130548	0.037879	0	175	172	309	145	182	136	230	204	191	124
ENSMUSG00000024982	chr19	Zdhhc6	55298301	55298888	2284	-0.25012	4.65897	0.07053	0.13059	0.020506	0	400	308	581	419	498	325	535	402	489	361
ENSMUSG00000037455	chr10	Slc18b1	23796986	23797183	3258	0.449307	2.085575	0.070538	0.13059	0.056839	0	66	32	70	41	73	59	85	121	100	69
ENSMUSG00000052911	chr9	Lamb2	1.08E+08	1.08E+08	6082	0.339099	7.198907	0.070598	0.130683	0.041722	0	1391	1036	3357	2376	2782	1846	3539	2845	3791	3090
ENSMUSG00000015092	chr2	Edf1	25557847	25558029	1317	0.307645	6.458865	0.070615	0.130695	0.03376	0	1231	1061	1319	1225	1293	1611	1887	1638	2359	1388
ENSMUSG00000022901	chr16	Cd86	36603869	36605338	3661	0.563802	0.693332	0.070715	0.130863	0.061164	0	17	20	17	16	25	32	46	21	39	26
ENSMUSG00000006464	chr19	Bbs1	4886898	4890758	5581	-0.48586	1.433171	0.070731	0.130874	0.058824	0	32	21	61	67	69	33	40	35	56	34
ENSMUSG00000006050	chr18	Sra1	36666681	36667659	4684	-0.27909	5.539698	0.070773	0.130934	0.027301	0	856	613	1121	653	829	642	878	681	1019	634
ENSMUSG00000037349	chr19	Nudt22	6993018	6993202	1195	0.319959	2.858436	0.070792	0.130946	0.027968	0	83	71	134	100	127	101	165	134	207	126
ENSMUSG00000038369	chr2	Ncoa6	1.55E+08	1.55E+08	9744	-0.32979	4.146851	0.0708	0.130946	0.035684	0	192	162	567	339	407	215	331	279	379	236
ENSMUSG00000041740	chr5	Rnf10	1.15E+08	1.15E+08	4447	-0.26751	8.183243	0.070893	0.1311	0.026062	0	4197	3484	7207	5370	5547	3762	5502	4271	6613	4165
ENSMUSG00000041119	chr17	Pde9a	31386234	31386356	2834	0.634762	0.523468	0.070941	0.131171	0.09395	0	6	20	27	13	17	24	51	32	24	17
ENSMUSG00000051817	chr2	Sox12	1.52E+08	1.52E+08	4453	0.633803	0.627795	0.070953	0.131174	0.091957	0	9	19	24	19	18	24	25	44	52	15
ENSMUSG00000041220	chr3	Elovl6	1.3E+08	1.3E+08	5951	0.762087	1.015571	0.070982	0.131192	0.168309	0	25	22	23	19	21	27	31	92	19	42
ENSMUSG00000054814	chr5	Usp46	73998463	74002137	5533	-0.29766	3.708128	0.070973	0.131192	0.027752	0	155	181	371	215	250	142	277	214	254	188
ENSMUSG00000004896	chr3	Rrnad1	87922601	87923912	6342	0.342172	2.547224	0.070999	0.131205	0.033133	0	67	49	121	83	94	101	139	130	114	97
ENSMUSG00000022008	chr14	Gpalpp1	76086232	76090746	5448	-0.29304	3.581295	0.071053	0.13125	0.025941	0	183	130	307	217	231	178	266	169	213	152
ENSMUSG00000042320	chr12	Prox2	85086385	85087554	3335	-0.54583	0.548164	0.071037	0.13125	0.066178	0	17	24	27	24	37	13	36	22	21	11
ENSMUSG00000067235	chr17	H2-Q10	35470089	35470179	4348	1.232773	1.212502	0.071049	0.13125	0.481802	0	48	23	11	6	5	31	21	157	22	40
ENSMUSG00000026032	chr1	Ndufb3	58586384	58586670	763	0.347128	6.776806	0.071291	0.131672	0.043549	0	1415	1218	1369	1822	1686	1878	3457	1749	2812	1569
ENSMUSG00000071337	chr6	Tia1	86404219	86404522	12945	-0.31601	3.669125	0.071362	0.131784	0.031834	0	213	159	388	175	212	154	232	211	284	158
ENSMUSG00000020811	chr11	Wscd1	71749920	71750100	4287	-0.48057	1.182405	0.071619	0.132221	0.056421	0	26	25	44	58	51	20	40	29	50	29
ENSMUSG00000063428	chr10	Ddo	40630011	40630091	3000	-0.31136	5.151582	0.071618	0.132221	0.033913	0	553	386	779	684	783	497	887	391	596	538
ENSMUSG00000036249	chr2	Rbm43	51924448	51925934	2633	0.48674	1.476856	0.071639	0.13224	0.058808	0	34	35	48	19	41	60	59	58	59	44
ENSMUSG00000059939	chr4	9430015G10Rik	1.56E+08	1.56E+08	3695	0.422136	1.617885	0.071773	0.13247	0.040954	0	41	33	64	31	34	46	77	63	76	49
ENSMUSG00000026172	chr1	Bcs1l	74588289	74588393	2192	-0.28874	4.236574	0.072187	0.133215	0.027384	0	255	188	413	407	422	249	402	299	367	239
ENSMUSG00000024472	chr18	Dcp2	44380500	44380686	8643	-0.30303	3.765133	0.072202	0.133225	0.028698	0	167	142	369	258	301	172	223	247	279	183
ENSMUSG00000031200	chrX	Mtcp1	75410444	75411131	4478	-0.45027	1.319866	0.072213	0.133225	0.048843	0	37	36	78	38	36	29	34	40	52	30
ENSMUSG00000039357	chr14	Fut11	20694968	20695698	3344	0.406558	2.066285	0.072262	0.133297	0.047645	0	32	40	100	45	75	64	86	102	97	73
ENSMUSG00000028713	chr4	Cyp4b1	1.16E+08	1.16E+08	2256	0.400295	2.479223	0.072284	0.133319	0.047163	0	66	57	120	67	72	96	125	155	114	74
ENSMUSG00000024805	chr19	Pcgf5	36379067	36379159	1659	-0.29138	4.098503	0.072308	0.133345	0.027796	0	214	204	497	297	339	198	385	212	384	249
ENSMUSG00000031217	chrX	Efnb1	99136130	99137013	3452	0.364819	2.699118	0.072326	0.133349	0.038062	0	72	68	100	89	118	74	147	143	172	126
ENSMUSG00000079480	chrX	Pin4	1.02E+08	1.02E+08	651	0.365686	3.876051	0.07233	0.133349	0.043506	0	190	217	194	166	210	255	421	255	353	230
ENSMUSG00000073375	chr17	Lrrc30	67630965	67632723	1759	-0.29392	6.912607	0.072356	0.133378	0.031414	0	1657	1486	3175	2113	2417	2049	2024	1722	2121	1767
ENSMUSG00000004667	chr10	Polr2e	80035949	80036301	2670	0.272687	5.22086	0.072422	0.133463	0.02562	0	505	381	577	587	626	590	949	660	956	604
ENSMUSG00000025858	chr5	Get4	1.39E+08	1.39E+08	2431	0.263894	5.199397	0.072418	0.133463	0.023874	0	475	418	709	500	564	619	904	610	993	568
ENSMUSG00000032725	chr7	Folr2	1.02E+08	1.02E+08	1079	0.451201	3.612972	0.072438	0.133473	0.069804	0	153	140	287	101	151	266	219	343	192	210
ENSMUSG00000031839	chr8	Hsbp1	1.19E+08	1.19E+08	1163	0.285125	6.65684	0.072585	0.133726	0.029428	0	1420	1219	1759	1324	1434	1731	2533	1753	2505	1654
ENSMUSG00000018659	chr11	Pnpo	96937825	96939083	2925	-0.29118	4.444689	0.072595	0.133726	0.028766	0	378	275	432	373	440	342	408	296	487	257
ENSMUSG00000032463	chr9	Faim	98986373	98986512	5745	0.573263	0.902221	0.072617	0.133748	0.073044	0	28	19	15	22	25	25	44	45	36	40
ENSMUSG00000059208	chr17	Hnrnpm	33646233	33646659	4701	0.284237	6.419198	0.072633	0.133758	0.029166	0	1100	1071	1485	1029	1420	1529	1957	1564	1969	1507
ENSMUSG00000085795	chr8	Zfp703	26977336	26977611	3304	0.627173	4.895563	0.072649	0.13377	0.142639	0	112	133	333	705	667	440	822	549	689	774
ENSMUSG00000017713	chr11	Tha1	1.18E+08	1.18E+08	2910	-0.36071	2.741474	0.07267	0.13379	0.039102	0	104	74	138	138	143	100	127	100	143	62
ENSMUSG00000005628	chr3	Tmod4	95124476	95124578	1717	-0.32638	8.928917	0.072791	0.133991	0.039474	0	8415	8011	11050	6974	8047	7116	10861	6040	9633	6237
ENSMUSG00000016194	chr1	Hsd11b1	1.93E+08	1.93E+08	4251	-0.49696	3.101955	0.072813	0.133991	0.082835	0	146	116	209	145	185	203	96	77	164	81

ENSMUSG00000028318	chr4	Polr1e	45018583	45018792	3897	0.426959	1.846539	0.072809	0.133991	0.046554	0	51	43	57	36	47	66	79	70	101	50
ENSMUSG00000028431	chr4	Ikbkap	56749680	56751719	7399	-0.25597	5.12413	0.072819	0.133991	0.02251	0	525	379	956	582	675	468	694	544	768	452
ENSMUSG00000029234	chr5	Tmem165	76183880	76184352	2588	0.280809	3.935279	0.072951	0.134214	0.024659	0	210	170	304	191	225	233	389	329	355	228
ENSMUSG00000003269	chr7	Cyth2	45806637	45807848	3515	0.264243	4.030437	0.073015	0.134313	0.021626	0	209	182	296	235	257	259	373	320	414	260
ENSMUSG00000042380	chr4	Smim12	1.27E+08	1.27E+08	1022	0.275682	4.774832	0.073031	0.134324	0.025615	0	397	280	450	402	431	439	648	475	754	442
ENSMUSG00000087679	chr2	C330006A16Rik	26136814	26138913	2483	0.329029	4.156807	0.073084	0.134403	0.036848	0	161	160	285	347	320	302	366	373	456	301
ENSMUSG00000019818	chr10	Cd164	41519414	41519700	4449	-0.3111	7.404009	0.073105	0.134422	0.035705	0	2996	2451	4460	2098	3037	2269	2943	2520	3859	2296
ENSMUSG00000040557	chr5	Wbscr27	1.35E+08	1.35E+08	3342	0.51444	0.71932	0.073133	0.134456	0.056628	0	19	13	27	17	26	26	45	41	23	28
ENSMUSG00000024379	chr18	Tslp	32815383	32815403	1133	0.633478	0.15133	0.073185	0.134509	0.076974	0	18	8	17	9	10	17	20	32	27	14
ENSMUSG00000024381	chr18	Bin1	32377217	32377490	2451	0.31141	9.772426	0.073174	0.134509	0.036063	0	13121	9777	16214	10414	12393	15473	18987	14124	25943	14613
ENSMUSG00000024414	chr11	Mrpl27	94653767	94653841	985	0.278798	5.099188	0.073192	0.134509	0.026677	0	435	424	550	482	541	538	946	597	831	554
ENSMUSG00000101225	chr7	1700008J07Rik	1.28E+08	1.28E+08	2432	0.379009	1.717379	0.07332	0.134724	0.033218	0	39	33	58	35	58	54	83	62	82	49
ENSMUSG00000025154	chr19	Arhgap19	41766588	41770196	5140	-0.31575	4.003169	0.073349	0.134759	0.032924	0	188	157	495	314	331	180	378	241	305	216
ENSMUSG00000036632	chr3	Alg5	54735539	54735649	3537	0.312395	3.550979	0.073492	0.135004	0.030141	0	148	141	206	148	180	231	280	226	270	164
ENSMUSG00000027952	chr3	Pmvk	89459118	89459464	1514	0.300876	3.875898	0.073511	0.13502	0.028744	0	190	162	209	211	261	264	345	274	377	215
ENSMUSG00000020876	chr11	Snx11	96767555	96769322	4232	0.279954	3.831854	0.073653	0.135245	0.024422	0	194	147	245	213	219	248	342	287	312	223
ENSMUSG00000032305	chr9	Fam219b	57537528	57537834	3055	0.296178	4.035825	0.073654	0.135245	0.028419	0	235	188	284	188	267	298	381	343	364	247
ENSMUSG00000021504	chr13	B4galt7	55599896	55600192	2896	0.31547	2.779628	0.073776	0.135449	0.027756	0	90	62	132	93	111	97	154	133	175	128
ENSMUSG00000067344	chr6	Rps25-ps1	1.45E+08	1.45E+08	378	0.49386	1.497551	0.073913	0.135682	0.065351	0	42	28	59	27	24	55	87	41	68	41
ENSMUSG00000081249	chr11	Gm11517	96795439	96795825	387	0.516795	0.747799	0.073932	0.1357	0.053694	0	23	11	22	21	26	26	44	21	49	30
ENSMUSG00000048826	chr17	Dact2	14195231	14197311	2808	-0.59845	1.139806	0.07395	0.135713	0.094906	0	37	25	75	31	42	22	13	42	35	36
ENSMUSG00000073233	chr12	Gm9144	7859827	7860076	1265	-0.47056	0.659495	0.074048	0.135855	0.037558	0	21	19	37	29	33	16	27	22	26	22
ENSMUSG00000083380	chr15	Gm3244	73809507	73809896	390	-0.60506	0.081576	0.074041	0.135855	0.062682	0	21	12	21	19	19	17	17	8	18	9
ENSMUSG00000021279	chr12	Cdc42bpb	1.11E+08	1.11E+08	6718	-0.2899	4.416503	0.074244	0.136197	0.028157	0	266	209	589	405	482	248	409	348	408	338
ENSMUSG00000035168	chr2	Tanc1	59612042	59612196	14570	0.300076	3.18659	0.07426	0.136207	0.027086	0	97	83	158	144	173	147	224	172	200	163
ENSMUSG00000037400	chr3	Atp11b	35754138	35754410	4859	-0.27456	4.293794	0.074283	0.136211	0.024924	0	240	226	544	312	453	223	433	318	381	279
ENSMUSG00000051346	chr10	Spryd4	1.28E+08	1.28E+08	1570	-0.30485	5.076729	0.074279	0.136211	0.033062	0	516	337	704	684	785	479	703	403	805	410
ENSMUSG00000028010	chr3	Gar1	1.3E+08	1.3E+08	1714	0.348774	2.994319	0.07432	0.136227	0.036029	0	103	100	141	97	105	116	184	191	185	129
ENSMUSG00000033253	chr4	Szt2	1.18E+08	1.18E+08	11947	-0.34083	3.394506	0.074305	0.136227	0.03643	0	134	93	309	183	262	116	219	151	192	167
ENSMUSG00000037166	chr7	Ppp1r14a	29289320	29289535	531	0.60469	0.443838	0.074323	0.136227	0.068109	0	15	15	20	13	15	11	31	25	48	25
ENSMUSG00000095762	chr8	Gm16378	1.23E+08	1.23E+08	342	0.606319	-0.10986	0.074497	0.136527	0.059369	0	12	4	15	10	11	16	26	17	15	15
ENSMUSG00000026121	chr1	Sema4c	36548639	36550368	4593	0.348174	3.014737	0.074549	0.136605	0.03838	0	72	70	148	116	172	122	231	138	169	159
ENSMUSG00000033499	chr13	Larp4b	9093881	9094180	8464	-0.27489	6.476481	0.074617	0.136711	0.027703	0	1160	928	2372	1581	2056	1133	1721	1308	2026	1250
ENSMUSG00000027351	chr2	Spred1	1.17E+08	1.17E+08	6784	0.315873	3.646307	0.074759	0.136933	0.033181	0	108	116	280	184	230	180	344	260	243	233
ENSMUSG00000029047	chr4	Pex10	1.55E+08	1.55E+08	3298	-0.32055	3.073829	0.074759	0.136933	0.031394	0	141	84	188	172	163	101	171	110	181	121
ENSMUSG00000052593	chr12	Adam17	21323509	21325626	7154	0.319967	4.530085	0.074857	0.137093	0.036238	0	227	168	389	415	487	371	582	445	513	422
ENSMUSG00000086290	chr4	Snhg12	1.32E+08	1.32E+08	1626	0.414391	2.117121	0.07495	0.137244	0.046938	0	60	45	70	56	56	95	112	74	106	54
ENSMUSG00000027332	chr2	Ivd	1.19E+08	1.19E+08	5505	-0.26719	7.747807	0.075037	0.137385	0.026685	0	2776	2472	5234	4126	4616	2535	4631	3528	4300	3033
ENSMUSG00000026509	chr1	Capn2	1.82E+08	1.82E+08	6345	0.258099	6.142488	0.075095	0.137472	0.024325	0	826	687	1382	1103	1228	1159	1598	1318	1714	1231
ENSMUSG00000031672	chr8	Got2	95864134	95865251	2585	-0.49199	8.47317	0.075156	0.137565	0.09077	0	3825	2383	6797	11047	10515	3491	7639	3773	7624	5156
ENSMUSG00000002835	chr17	Chaf1a	56040416	56040551	3308	-0.43481	1.049316	0.075232	0.137666	0.042248	0	27	29	39	40	46	22	37	35	39	21
ENSMUSG00000039178	chr5	Tbc1d19	53809627	53809858	2688	-0.3527	4.115192	0.075226	0.137666	0.043617	0	305	288	451	197	294	273	353	238	348	180
ENSMUSG00000021241	chr12	Isca2	84773270	84773371	868	0.281956	4.791205	0.075252	0.137684	0.027416	0	347	288	437	445	466	433	752	426	732	466
ENSMUSG00000014867	chr2	Surf4	26920040	26922171	3281	0.258989	7.192972	0.07535	0.137843	0.024951	0	1772	1614	3130	1929	2357	2279	3546	2770	3768	2341
ENSMUSG00000022210	chr14	Dhrs4	55478758	55479033	1390	-0.49419	4.364602	0.075417	0.137948	0.088873	0	202	202	276	698	550	247	385	296	448	210
ENSMUSG00000038354	chr3	Ankrd35	96670131	96670449	3688	0.561533	0.238883	0.075443	0.137977	0.051501	0	12	9	18	16	14	18	23	22	39	15
ENSMUSG00000019256	chr12	Ahr	35497974	35500700	6163	-0.45128	1.465626	0.075472	0.138011	0.0494	0	36	24	71	50	74	35	65	32	47	29
ENSMUSG00000085566	chr2	A730017L22Rik	1.31E+08	1.31E+08	6012	-0.44645	1.257249	0.075485	0.138014	0.043459	0	32	36	57	35	53	28	31	43	40	33
ENSMUSG00000025868	chr13	Higd2a	54590207	54590419	648	0.283104	6.475643	0.075576	0.138162	0.029576	0	1274	882	1504	1354	1373	1487	2080	1563	2551	1350
ENSMUSG00000037846	chr10	Rtkn2	67979570	67979812	5547	0.715945	1.501044	0.075632	0.138245	0.159273	0	32	45	53	9	20	46	50	37	103	73
ENSMUSG00000040464	chr5	Gtpbp10	5537454	5539451	4744	-0.28391	3.72606	0.075663	0.138282	0.025987	0	173	158	330	242	276	170	296	164	300	173
ENSMUSG00000019297	chr14	Nop9	55745693	55746020	3694	0.259695	3.98018	0.075755	0.138431	0.021519	0	202	150	307	247	248	248	365	281	394	278
ENSMUSG00000071041	chr8	Gm15210	1E+08	1E+08	1545	0.382786	2.142915	0.07578	0.138458	0.03849	0	52	42	82	71	53	62	117	97	112	63
ENSMUSG00000070867	chr4	Trabd2b	1.14E+08	1.14E+08	6617	0.564453	2.355743	0.075838	0.138545	0.107337	0	60	48	93	41	87	56	84	175	72	139
ENSMUSG00000049502	chr16	Dtx3l	35926511	35929368	5724	-0.31873	3.488076	0.075891	0.138623	0.032369	0	149	109	319	200	253	135	269	138	217	160
ENSMUSG00000018547	chr11	Pip4k2b	97715157	97718939	5204	-0.26734	6.705539	0.075989	0.138784	0.02654	0	1434	1172	2930	1801	2081	1453	1991	1462	2372	1437
ENSMUSG00000027502	chr2	Rtfdc1	1.72E+08	1.72E+08	2644	0.259437	5.71411	0.076021	0.138823	0.024214	0	701	610	960	709	816	891	1186	932	1390	843
ENSMUSG00000055762	chr15	Eef1d	75894796	75895591	5897	0.280663	7.008131	0.076124	0.138991	0.029385	0	1624	1572	2076	1830	2051	2095	2882	2351	3489	2156
ENSMUSG00000002052	chr11	Supt6	78206746	78207769	7095	-0.26662	5.84355	0.076209	0.139127	0.025836	0	767	597	1626	973	1256	736	1049	908	1240	842
ENSMUSG00000029017	chr5	Pmpcb	21737141	21737276	5141	-0.296	6.206145	0.076225	0.139138	0.032635	0	1122	925	1384	1489	1551	888	1755	961	1618	972
ENSMUSG00000028331	chr4	5830415F09Rik	46376505	46377248	2271	0.443126	1.408588	0.07634	0.139329	0.045435	0	37	27	40	29	38	48	74	56	47	41
ENSMUSG00000043929	chrX	Klhl15	94234599	94234653	9741	0.437601	1.658937	0.076365	0.139354	0.052418	0	26	27	61	52	45	39	62	62	79	76
ENSMUSG00000032827	chr6	Ppp1r9a	4902917	4903031	14531	0.423769	1.684872	0.07641	0.139418	0.046939	0	42	25	72	29	50	43	81	77	84	44
ENSMUSG00000090659	chr13	Zfp493	67779754	67779819	4693	-0.48734	1.272648	0.076436	0.139447	0.065859	0	32	45	60	37	41	20	55	29	31	42
ENSMUSG00000026003	chr1	Acadl	66830839	66831527	2005	-0.56335	7.767319	0.076517	0.139555	0.119735	0	1861	1788	3128	8159	6244	1932	4969	2508	4707	2583

ENSMUSG00000030744	chr7	Rps3	99477896	99478951	4483	0.321971	8.231576	0.076512	0.139555	0.039248	0	4347	4012	4545	3592	4143	5368	7919	5593	7194	4613
ENSMUSG00000027630	chr3	Tbl1xr1	22076652	22076954	8362	0.265895	5.22543	0.076537	0.13957	0.025139	0	541	400	760	464	557	577	837	646	987	691
ENSMUSG00000036975	chr1	Tmem177	1.2E+08	1.2E+08	3341	-0.29166	4.048207	0.076546	0.13957	0.028676	0	211	189	339	326	407	217	355	214	357	226
ENSMUSG00000026463	chr1	Atp2b4	1.34E+08	1.34E+08	12248	-0.35738	4.158917	0.076704	0.139819	0.044329	0	228	199	558	268	423	206	277	380	248	283
ENSMUSG00000029152	chr5	Ociad1	73292794	73292976	4132	0.269589	6.746678	0.076699	0.139819	0.027081	0	1468	1278	2016	1425	1531	1767	2634	1982	2609	1776
ENSMUSG00000048930	chr6	Tada3	1.13E+08	1.13E+08	3883	0.272542	3.63833	0.076844	0.140056	0.02324	0	160	129	244	170	199	195	266	249	282	234
ENSMUSG00000025759	chr3	Mfsd8	40818070	40819720	3184	-0.26875	4.2023	0.076915	0.140166	0.024298	0	263	226	484	300	362	239	467	271	326	236
ENSMUSG00000013367	chr7	Iglon5	43472907	43474551	2619	0.598824	-0.04729	0.07694	0.140191	0.072016	0	5	7	19	7	18	13	16	17	25	22
ENSMUSG00000028034	chr3	Fubp1	1.52E+08	1.52E+08	6491	0.272341	4.290344	0.077019	0.140316	0.025076	0	211	210	403	283	326	246	494	415	432	370
ENSMUSG00000024205	chr11	Rpl36-ps2	76601319	76601629	311	0.667941	0.232085	0.07706	0.140371	0.115777	0	15	3	19	16	14	32	34	23	13	14
ENSMUSG00000026020	chr1	Nop58	59684971	59685226	10758	0.335896	4.083901	0.077107	0.140438	0.038893	0	235	192	335	171	262	297	580	287	336	243
ENSMUSG00000027353	chr2	Mcm8	1.33E+08	1.33E+08	3718	-0.52787	1.021077	0.077288	0.140748	0.068023	0	30	26	49	39	40	22	28	37	17	36
ENSMUSG00000032737	chr7	Inppl1	1.02E+08	1.02E+08	4981	-0.36362	7.091435	0.07748	0.141079	0.05016	0	1694	1009	3337	3305	3520	1555	2705	1905	2765	2064
ENSMUSG00000025857	chr5	Heatr2	1.39E+08	1.39E+08	3514	-0.27747	3.930505	0.077503	0.141101	0.025145	0	223	148	406	269	328	170	294	264	324	213
ENSMUSG00000040537	chr5	Adam22	8072352	8078706	12231	-0.46385	1.194476	0.077596	0.141252	0.053426	0	27	27	57	32	66	17	41	38	40	33
ENSMUSG00000051344	chr1	Plekhm3	64785983	64786587	10921	-0.33544	3.043624	0.077799	0.141602	0.034375	0	97	81	234	156	191	96	164	119	151	130
ENSMUSG00000004880	chr1	Lbr	1.82E+08	1.82E+08	4761	-0.265	4.325766	0.077845	0.141646	0.023611	0	301	220	567	309	402	249	418	285	388	323
ENSMUSG00000007458	chr6	M6pr	1.22E+08	1.22E+08	4170	0.253652	5.215757	0.07784	0.141646	0.022934	0	499	416	761	469	575	568	913	764	822	624
ENSMUSG00000090248	chr2	Gm14027	1.29E+08	1.29E+08	622	-0.7371	-0.03974	0.077956	0.141828	0.137215	0	10	15	33	12	19	3	26	3	19	11
ENSMUSG00000023089	chr6	Ndufa5	24518666	24518824	1032	0.336064	7.483484	0.077967	0.141829	0.043019	0	2279	2055	2292	2974	2700	3174	5222	2741	4690	2723
ENSMUSG00000041891	chr18	Lman1	65980754	65982710	6411	-0.27948	5.728317	0.077997	0.141864	0.028745	0	646	563	1468	926	1241	609	991	826	1062	887
ENSMUSG00000022568	chr15	Scrib	76047158	76047537	5736	-0.27068	4.76676	0.078028	0.141902	0.02569	0	360	281	652	555	587	369	490	406	581	403
ENSMUSG00000028901	chr4	Gmeb1	1.32E+08	1.32E+08	7857	-0.29939	3.33202	0.078049	0.14192	0.027869	0	125	112	271	197	201	136	192	162	212	121
ENSMUSG00000061288	chr5	Taok3	1.17E+08	1.17E+08	10952	0.338008	2.715988	0.078075	0.141947	0.036117	0	69	53	153	81	119	108	149	150	130	116
ENSMUSG00000041625	chr14	Ggact	1.23E+08	1.23E+08	1988	-0.31705	3.288026	0.078173	0.142107	0.032783	0	161	137	199	150	207	147	186	129	223	109
ENSMUSG00000011114	chr9	Tbrg1	37649182	37649503	3482	0.257795	4.934656	0.078201	0.142137	0.023446	0	378	354	647	384	478	490	751	494	742	566
ENSMUSG00000000078	chr13	Klf6	5861489	5861842	4217	0.35255	5.039106	0.078337	0.142345	0.045613	0	322	431	602	361	590	411	1231	595	698	531
ENSMUSG00000058192	chr9	Zfp846	20581325	20581678	2861	-0.43058	1.100157	0.078326	0.142345	0.039725	0	34	28	55	30	43	20	38	39	34	28
ENSMUSG00000022350	chr15	E430025E21Rik	59331998	59332359	4032	-0.27077	4.845934	0.078423	0.142449	0.025851	0	417	271	835	495	599	353	556	442	605	433
ENSMUSG00000025745	chr5	Hadha	30118301	30119960	5341	-0.47682	8.298151	0.078423	0.142449	0.087185	0	3158	2540	5467	10771	8030	3256	6832	3831	6727	4052
ENSMUSG00000043342	chr2	Hoxd9	74697727	74698833	2136	0.745947	2.810224	0.078426	0.142449	0.197851	0	124	94	120	27	23	142	162	168	264	71
ENSMUSG00000040918	chr1	Slc19a2	1.64E+08	1.64E+08	3838	-0.43222	2.53908	0.078458	0.142487	0.060558	0	75	50	130	136	150	48	141	69	102	93
ENSMUSG00000058317	chr14	Ube2e2	18573575	18574391	4671	0.385154	2.343932	0.078603	0.142732	0.042115	0	56	60	86	53	90	72	129	114	143	65
ENSMUSG00000032062	chr9	2310030G06Rik	50739691	50740749	1242	-0.55732	1.725504	0.078644	0.142787	0.102311	0	38	48	49	86	81	30	93	23	50	48
ENSMUSG00000024180	chr17	Tmem8	26113316	26113567	3464	0.508001	1.496733	0.078678	0.142828	0.075169	0	24	36	60	24	37	59	55	80	51	39
ENSMUSG00000007805	chr1	Twist2	91801461	91802149	3174	0.847776	-0.0292	0.078744	0.142928	0.179852	0	12	12	12	8	4	24	8	32	13	20
ENSMUSG00000057531	chr13	Dtnbp1	44922079	44922454	1334	-0.27329	5.184542	0.078825	0.143057	0.027421	0	527	455	716	782	682	448	753	578	787	476
ENSMUSG00000037568	chr1	Vash2	1.91E+08	1.91E+08	4314	0.663137	1.57068	0.078895	0.143164	0.138739	0	30	47	49	18	27	79	37	61	107	33
ENSMUSG00000005656	chr12	Snx6	54746349	54747059	1928	0.299617	4.672188	0.07892	0.14317	0.032068	0	359	300	540	246	384	459	588	524	607	379
ENSMUSG00000035051	chr17	Dhx57	80238304	80238930	5077	-0.29491	3.464163	0.078913	0.14317	0.027209	0	137	125	312	180	246	133	219	190	197	160
ENSMUSG00000069565	chr10	Dazap1	80261486	80261575	2944	0.260074	4.666691	0.078935	0.143178	0.023761	0	334	232	492	389	420	357	549	497	644	479
ENSMUSG00000036061	chr15	Smug1	1.03E+08	1.03E+08	3281	-0.28406	3.154934	0.078966	0.143215	0.023813	0	126	102	240	148	178	111	188	144	176	114
ENSMUSG00000000384	chr11	Tbrg4	6615598	6615766	3696	-0.33214	5.358487	0.079015	0.143284	0.041232	0	501	412	809	1033	958	451	816	559	943	601
ENSMUSG00000042408	chr4	Zmym6	1.27E+08	1.27E+08	7692	-0.32025	2.898192	0.079091	0.143401	0.0305	0	101	95	218	122	134	106	159	99	141	96
ENSMUSG00000035754	chr10	Wdr18	79960152	79960372	2954	-0.24651	5.18989	0.079184	0.143552	0.021938	0	563	435	876	633	692	515	708	546	818	479
ENSMUSG00000027006	chr2	Dnajc10	80315466	80315805	5004	-0.24233	5.171458	0.079273	0.143692	0.021077	0	498	438	913	599	734	457	807	552	686	530
ENSMUSG00000018474	chr11	Chd3	69343273	69344478	8443	0.355192	3.403572	0.079354	0.14382	0.043508	0	101	89	206	175	184	176	200	281	199	195
ENSMUSG00000027219	chr2	Slc28a2	1.22E+08	1.22E+08	4208	-0.32327	2.981812	0.079544	0.144144	0.031532	0	97	93	202	143	177	116	169	127	128	93
ENSMUSG00000079659	chr5	Tmem243	9100737	9100859	988	-0.39488	2.656101	0.079561	0.144144	0.051357	0	101	114	162	80	101	79	158	83	110	69
ENSMUSG00000084843	chr2	B230312C02Rik	1.8E+08	1.8E+08	1703	0.791346	3.34286	0.079566	0.144144	0.231585	0	97	93	350	31	61	133	315	243	492	57
ENSMUSG00000050628	chr11	Ubald2	1.16E+08	1.16E+08	1532	0.266449	4.099249	0.079594	0.144175	0.023737	0	250	164	340	225	270	285	433	341	412	242
ENSMUSG00000033577	chr9	Myo6	80165031	80165229	12078	-0.31345	3.08612	0.079685	0.14432	0.031075	0	125	114	216	119	182	88	142	153	175	128
ENSMUSG00000026519	chr1	Tmem63a	1.81E+08	1.81E+08	4492	-0.26923	5.080485	0.079755	0.144429	0.026254	0	522	390	961	494	672	444	555	513	783	507
ENSMUSG00000031392	chrX	Irak1	74013914	74015501	4716	-0.25374	5.665042	0.079804	0.144497	0.023908	0	741	596	1242	878	1031	591	1215	793	905	763
ENSMUSG00000024782	chr19	Ak3	29020833	29022946	3120	-0.2807	6.207763	0.079821	0.144507	0.029829	0	992	762	1682	1565	1627	895	1365	1230	1512	1107
ENSMUSG00000031520	chr8	Vegfc	54077532	54077925	1881	-0.38459	1.318969	0.079922	0.144672	0.032018	0	40	28	56	45	50	26	48	35	48	34
ENSMUSG00000029428	chr5	Stx2	1.29E+08	1.29E+08	4164	0.301696	3.278526	0.080033	0.144852	0.029918	0	92	89	205	131	194	141	209	203	254	166
ENSMUSG00000054604	chr16	Cggbp1	64851996	64852236	4522	0.266388	4.406364	0.08009	0.144935	0.02474	0	254	227	432	288	351	300	468	483	451	393
ENSMUSG00000029027	chr4	Dffb	1.54E+08	1.54E+08	2351	0.502017	0.586626	0.080148	0.145013	0.052648	0	20	12	21	15	24	26	28	25	32	35
ENSMUSG00000055817	chr17	Mta3	83706163	83706285	5319	-0.34484	2.939537	0.080155	0.145013	0.03687	0	109	63	208	149	177	106	128	116	161	99
ENSMUSG00000029920	chr6	Smarcad1	65042667	65042961	5099	-0.37204	2.756086	0.080182	0.145043	0.045061	0	84	109	187	83	148	71	156	106	103	98
ENSMUSG00000044548	chr12	Dact1	71309884	71310307	3761	0.36485	2.432531	0.080393	0.145404	0.041516	0	59	38	107	75	103	98	147	110	95	90
ENSMUSG00000085028	chr2	Slc2a4rg-ps	1.81E+08	1.81E+08	2976	0.504158	1.040956	0.080435	0.145461	0.05832	0	26	24	30	19	28	33	55	51	31	36
ENSMUSG00000051747	chr2	Ttn	76703980	76705329	116825	-0.38395	12.34084	0.080499	0.145556	0.057612	0	71151	40264	203440	80790	115684	55376	84497	73744	128898	75243
ENSMUSG00000089739	chr2	Gm20431	1.68E+08	1.68E+08	2367	-0.26863	5.456493	0.080608	0.145734	0.026826	0	660	461	948	867	953	589	818	587	997	662

ENSMUSG00000022337	chr15	Emc2	43477229	43477325	1245	-0.29998	6.117374	0.080664	0.145808	0.03452	0	1091	1103	1392	1200	1198	1015	1577	891	1344	900
ENSMUSG00000032504	chr9	Pdcd6ip	1.14E+08	1.14E+08	6903	0.249761	5.759562	0.080671	0.145808	0.023444	0	700	474	1231	726	949	801	1261	1064	1370	913
ENSMUSG00000027253	chr2	Lrp4	91457511	91457752	10504	-0.41036	3.497704	0.080976	0.146339	0.059238	0	135	96	274	260	300	114	253	147	150	211
ENSMUSG00000037710	chr10	Cisd1	71330480	71331126	1084	0.273694	7.360089	0.081003	0.146369	0.029008	0	2230	1782	2720	2484	2571	2676	4039	2798	4416	2678
ENSMUSG00000046688	chr3	Tifa	1.28E+08	1.28E+08	2527	0.464847	1.619211	0.081159	0.146629	0.058455	0	43	39	48	26	39	47	91	72	56	48
ENSMUSG00000031791	chr8	Tmem38a	72572103	72572227	2094	-0.25851	10.44051	0.08124	0.146756	0.026288	0	21126	16022	34401	24536	27174	19512	29038	19377	29502	19138
ENSMUSG00000038178	chr11	Slc43a2	75531694	75531822	10042	0.413675	4.48061	0.081269	0.146789	0.064424	0	170	153	293	505	432	335	514	433	675	392
ENSMUSG00000039050	chr2	Osbpl2	1.8E+08	1.8E+08	4187	-0.26288	4.725914	0.081336	0.14689	0.024537	0	348	276	638	512	591	384	524	390	505	383
ENSMUSG00000004071	chr16	Cdip1	4750348	4750601	5746	-0.26056	6.578018	0.081362	0.146906	0.026147	0	1359	1138	2502	1740	1753	1138	2047	1394	2162	1337
ENSMUSG00000071078	chr8	Nr2c2ap	70131333	70131599	1175	0.41085	2.409869	0.081367	0.146906	0.051212	0	73	73	84	51	67	95	120	124	123	78
ENSMUSG00000051359	chr15	Ncald	37366175	37368925	6987	0.356041	2.063541	0.081392	0.146931	0.0338	0	37	46	81	53	73	61	113	75	100	72
ENSMUSG00000033416	chr10	Gucd1	75351111	75352902	8206	-0.29731	5.800569	0.081425	0.14695	0.033567	0	699	546	1461	1243	1129	873	1115	780	1130	676
ENSMUSG00000040370	chr6	Lyrm5	1.45E+08	1.45E+08	2682	-0.27394	5.334552	0.081421	0.14695	0.028284	0	610	556	778	819	713	525	912	588	824	527
ENSMUSG00000067719	chr5	Gm10221	24581458	24581879	422	0.363665	4.836917	0.081535	0.147129	0.049607	0	381	215	423	529	448	498	885	409	869	361
ENSMUSG00000022185	chr14	Acin1	54642161	54643048	8649	0.253747	5.611441	0.081596	0.14722	0.024157	0	521	538	1036	717	809	792	1095	1073	1100	778
ENSMUSG00000087590	chr18	2410004N09Rik	33794892	33795124	430	0.470847	1.779475	0.081672	0.147336	0.062282	0	50	43	63	34	28	45	87	76	94	55
ENSMUSG00000040472	chr14	Rabggta	55715873	55716538	2630	0.266262	3.807253	0.081688	0.147345	0.024045	0	179	114	299	192	255	216	318	249	346	260
ENSMUSG00000021631	chr17	Mrps36-ps1	53866715	53867020	306	0.507473	0.826125	0.081754	0.147428	0.058984	0	18	11	24	23	35	23	56	25	51	27
ENSMUSG00000034254	chr17	Agpat1	34604262	34604490	3001	-0.25774	6.433292	0.081756	0.147428	0.025525	0	1316	1045	2058	1512	1679	1109	1469	1378	1919	1318
ENSMUSG00000029924	chr6	Slc37a3	39334770	39337284	4065	-0.27691	3.630985	0.081851	0.147579	0.025586	0	169	160	302	217	244	145	304	169	238	176
ENSMUSG00000001508	chr11	Sgca	94962791	94963080	1735	0.260659	7.758944	0.081917	0.147657	0.026572	0	2600	2376	4323	3107	3493	3360	4854	3801	6290	3543
ENSMUSG00000032388	chr9	Spg21	65460937	65461154	2690	0.366511	3.770783	0.081906	0.147657	0.047762	0	228	144	252	138	175	265	285	346	283	194
ENSMUSG00000099066	chr17	Mir6978	57217172	57217228	57	-0.63528	0.196686	0.081934	0.147667	0.093493	0	20	16	39	9	20	12	21	22	10	9
ENSMUSG00000038766	chr3	Gabpb2	95181766	95188975	15465	-0.26634	4.011984	0.08196	0.147695	0.023536	0	226	168	437	264	355	228	330	262	284	224
ENSMUSG00000028466	chr4	Creb3	43562332	43562959	2372	0.260711	4.940563	0.082049	0.147835	0.024518	0	396	375	523	378	540	509	707	551	759	526
ENSMUSG00000037257	chr9	Aagab	63602655	63602771	2600	-0.26346	4.587288	0.082106	0.147913	0.024966	0	351	352	533	413	428	356	438	336	486	362
ENSMUSG00000039759	chr4	Thap3	1.52E+08	1.52E+08	1334	0.311798	4.982444	0.082115	0.147913	0.035774	0	461	418	448	399	444	559	812	558	806	479
ENSMUSG00000002948	chr8	Map2k7	4238740	4239033	5359	-0.25026	6.47073	0.08217	0.147952	0.024085	0	1306	961	2250	1539	1847	1146	1712	1443	1901	1242
ENSMUSG00000026353	chr1	Ubxn4	1.28E+08	1.28E+08	4659	-0.25404	6.003976	0.082155	0.147952	0.024618	0	959	844	1631	1005	1206	926	1288	992	1326	833
ENSMUSG00000051375	chr18	Pcdh1	38185914	38189942	8797	0.340871	3.097679	0.082161	0.147952	0.039166	0	84	61	183	134	159	121	171	155	260	163
ENSMUSG00000021388	chr13	Aspn	49544443	49544717	2346	-0.48095	3.98468	0.082237	0.148033	0.086316	0	106	171	430	379	460	143	210	216	285	327
ENSMUSG00000047248	chr7	C2cd3	1E+08	1E+08	11706	-0.31202	3.329778	0.082236	0.148033	0.031378	0	130	111	299	155	224	150	184	172	188	116
ENSMUSG00000030814	chr7	Bcl7c	1.28E+08	1.28E+08	5331	0.298421	4.252766	0.082368	0.148249	0.031455	0	279	223	359	198	295	352	423	338	524	281
ENSMUSG00000029156	chr5	Sgcb	73632749	73635698	3709	-0.25787	7.048151	0.082446	0.148369	0.025948	0	1829	1697	3329	2163	2711	1700	2992	1795	2715	1940
ENSMUSG00000079610	chr1	Ankrd39	36537507	36539534	4654	0.33272	2.758378	0.082619	0.14866	0.033627	0	101	65	110	91	102	114	145	117	190	114
ENSMUSG00000056076	chr5	Eif3b	1.4E+08	1.4E+08	2966	0.253929	6.792708	0.082668	0.148729	0.02501	0	1480	1186	1999	1641	1770	1794	2520	2049	2879	1828
ENSMUSG00000000938	chr6	Hoxa10	52231197	52232780	3270	0.276379	4.088789	0.082713	0.148789	0.026186	0	226	166	283	247	306	215	452	297	432	322
ENSMUSG00000025170	chr11	Rab40b	1.21E+08	1.21E+08	2008	0.318052	4.85288	0.082786	0.148891	0.037687	0	416	344	625	285	382	450	614	465	855	555
ENSMUSG00000044556	chr4	Tex38	1.16E+08	1.16E+08	802	-0.60166	0.648587	0.082792	0.148891	0.097084	0	17	19	25	40	41	28	15	17	32	13
ENSMUSG00000014226	chr1	Cacybp	1.6E+08	1.6E+08	2390	-0.26788	5.780127	0.08282	0.148901	0.027551	0	965	769	1212	788	1026	633	1161	920	1043	823
ENSMUSG00000023019	chr15	Gpd1	99717515	99717648	2961	-0.27567	9.585753	0.082812	0.148901	0.030162	0	13753	9077	19772	10987	14720	10432	14522	12928	16116	9840
ENSMUSG00000033715	chr13	Akr1c14	4049011	4049132	2973	-0.66935	0.940743	0.082911	0.149045	0.138843	0	35	22	38	33	52	5	34	50	18	22
ENSMUSG00000093290	chr7	Mir3572	3655962	3656047	86	0.630136	0.119889	0.083079	0.149326	0.082055	0	15	7	8	14	16	27	24	16	27	13
ENSMUSG00000025016	chr19	Tm9sf3	41210842	41215139	6144	-0.26386	6.831198	0.083093	0.14933	0.027239	0	1791	1558	2894	1628	2148	1333	2156	1935	2366	1710
ENSMUSG00000030309	chr6	Caprin2	1.49E+08	1.49E+08	7656	0.352773	2.192256	0.083124	0.149366	0.03565	0	57	43	91	60	66	89	121	73	96	76
ENSMUSG00000086370	chrX	Ftx	1.04E+08	1.04E+08	7598	0.588934	0.507533	0.083302	0.149665	0.083053	0	15	12	28	11	19	13	39	33	20	37
ENSMUSG00000103104	chr17	Riok2	17374332	17374670	3196	-0.27539	4.039061	0.083372	0.149771	0.026995	0	226	212	329	297	375	179	385	240	358	220
ENSMUSG00000015023	chr8	Ddx19a	1.11E+08	1.11E+08	2957	-0.25308	4.27083	0.083411	0.149822	0.022255	0	261	220	527	337	374	238	425	273	405	281
ENSMUSG00000020526	chr11	Znhit3	84910950	84911648	2136	-0.31112	3.445016	0.083424	0.149824	0.033653	0	215	153	233	154	188	150	229	154	203	147
ENSMUSG00000006412	chr1	Pfdn2	1.71E+08	1.71E+08	1937	0.280526	5.927645	0.083458	0.149845	0.03015	0	841	728	1030	815	912	1057	1538	1057	1648	870
ENSMUSG00000028755	chr4	Cda	1.38E+08	1.38E+08	1035	0.768319	-0.1803	0.083448	0.149845	0.136269	0	2	7	12	17	7	4	28	21	22	15
ENSMUSG00000038520	chr7	Tbc1d17	44840901	44841420	3448	0.25239	5.612316	0.083573	0.150023	0.024015	0	700	546	957	629	729	804	1142	871	1248	809
ENSMUSG00000038697	chr8	Taf5l	1.24E+08	1.24E+08	3033	-0.27377	3.645287	0.08358	0.150023	0.024728	0	191	132	312	235	239	168	263	214	235	153
ENSMUSG00000057098	chr11	Ebf1	44617317	44618312	9756	-0.3262	3.389388	0.083664	0.150138	0.035842	0	122	149	266	144	265	119	193	190	179	158
ENSMUSG00000096687	chr10	AA474331	39890018	39892929	3833	-0.38596	2.089415	0.083666	0.150138	0.043848	0	54	44	114	86	90	48	79	44	101	62
ENSMUSG00000024683	chr19	Mrpl16	11770415	11770524	1122	-0.27384	5.360159	0.083738	0.150225	0.02865	0	563	522	816	812	883	561	966	530	881	514
ENSMUSG00000025532	chr5	Crcp	1.3E+08	1.3E+08	1579	-0.25837	4.194631	0.083728	0.150225	0.023278	0	299	237	412	258	391	272	370	269	351	252
ENSMUSG00000092274	chr19	Neat1	5824708	5845478	20771	0.363939	9.38451	0.083766	0.150255	0.052808	0	10068	8207	11683	5694	10415	11692	19679	9012	15076	13531
ENSMUSG00000038371	chr7	Sbf2	1.1E+08	1.1E+08	12127	-0.31799	3.346378	0.083795	0.150288	0.033091	0	133	94	268	202	231	127	208	169	162	151
ENSMUSG00000041236	chr13	Vps41	18717292	18717336	3195	-0.26369	6.038538	0.083938	0.150523	0.027021	0	1064	917	1578	990	1183	900	1320	1001	1458	831
ENSMUSG00000027957	chr3	Slc35a3	1.17E+08	1.17E+08	10173	-0.32892	2.842495	0.083951	0.150525	0.034004	0	89	90	163	144	152	86	112	130	134	107
ENSMUSG00000000296	chr10	Tpd52l1	31332380	31332969	1267	-0.24158	4.6286	0.084005	0.150602	0.020919	0	360	298	582	433	491	342	555	347	491	345
ENSMUSG00000002748	chr5	Baz1b	1.35E+08	1.35E+08	10794	-0.25405	5.84465	0.084033	0.150633	0.02467	0	787	607	1555	1021	1195	729	1099	1010	1122	828
ENSMUSG00000069049	chrY	Eif2s3y	1010543	1010685	4161	-1.79725	4.983935	0.084104	0.15074	1.155202	0	612	770	902	688	879	544	4	2	729	1
ENSMUSG00000006517	chr8	Mvd	1.22E+08	1.22E+08	1761	0.394729	2.512188	0.084154	0.150808	0.051729	0	61	33	98	104	101	75	124	129	165	94

ENSMUSG00000001029	chr11	Icam2	1.06E+08	1.06E+08	1904	0.362907	2.417286	0.084182	0.150827	0.038204	0	72	54	84	73	81	84	124	107	162	69
ENSMUSG00000021670	chr13	Hmgcr	96648967	96650633	7275	0.355746	2.253454	0.084207	0.150827	0.035525	0	57	40	82	70	82	63	139	92	125	69
ENSMUSG00000022099	chr14	Dmtn	70602184	70604854	4629	0.626041	1.363532	0.084221	0.150827	0.123186	0	44	24	28	27	26	30	40	101	54	44
ENSMUSG00000098188	chr10	Sowahc	59221953	59226434	4482	0.608542	1.395185	0.084218	0.150827	0.119526	0	31	27	41	27	33	44	46	87	23	65
ENSMUSG00000103578	chr10	AC153941.1	59221953	59222224	4477	0.608541	1.395185	0.084195	0.150827	0.119505	0	31	27	41	27	33	44	46	87	23	65
ENSMUSG00000034538	chr7	Zfp418	7171330	7171558	2725	-0.56074	-0.06122	0.084236	0.150832	0.067677	0	19	14	16	18	13	6	16	13	19	10
ENSMUSG00000031922	chr9	Cep57	13807792	13808840	4180	-0.38622	2.082187	0.084399	0.151064	0.041879	0	56	46	115	69	101	52	89	59	56	69
ENSMUSG00000053907	chr6	Mat2a	72432799	72434395	2804	-0.3085	7.234951	0.084395	0.151064	0.037815	0	2835	2062	3601	1955	2848	2517	3075	2128	2631	1858
ENSMUSG00000061897	chr2	Gm14292	1.79E+08	1.79E+08	456	-0.46147	1.111447	0.084392	0.151064	0.051066	0	27	18	68	41	45	23	51	29	33	24
ENSMUSG00000001891	chr11	Ugp2	21321138	21322129	3069	-0.32065	9.35674	0.084506	0.151215	0.041247	0	10469	7939	13796	13488	12520	6554	16715	7709	15425	8922
ENSMUSG00000018566	chr11	Slc2a4	69942539	69943572	3478	-0.30095	9.14917	0.0845	0.151215	0.036301	0	8105	5137	13557	12267	12643	7286	11240	7376	13025	8151
ENSMUSG00000044317	chr7	Gpr4	19212538	19212634	2884	0.44912	1.594857	0.08458	0.151327	0.058825	0	21	26	38	55	58	45	67	62	87	48
ENSMUSG00000021326	chr13	Trim27	21179445	21179556	4702	0.258173	4.421109	0.08461	0.151359	0.023601	0	272	243	431	299	313	375	481	428	521	317
ENSMUSG00000035623	chr7	Rsf1	97579896	97580105	12635	-0.28001	4.042714	0.084708	0.151515	0.027065	0	203	191	504	268	330	227	320	239	300	260
ENSMUSG00000092192	chr9	Dyx1c1	72958785	72958997	1975	-0.5159	0.648304	0.084741	0.151554	0.058712	0	28	12	45	33	23	16	34	19	24	18
ENSMUSG00000022220	chr14	Adcy4	55769058	55769287	3500	0.346394	2.984605	0.084782	0.151586	0.040504	0	71	65	124	142	158	116	212	151	187	139
ENSMUSG00000054312	chr3	Mrps21	95862634	95862932	1282	0.292358	6.123878	0.084779	0.151586	0.03326	0	1006	878	1137	911	952	1187	1747	1240	1816	1081
ENSMUSG00000087236	chr1	Gm1305	1.8E+08	1.8E+08	3449	0.425513	1.485734	0.084807	0.151609	0.047323	0	32	33	47	29	42	60	55	60	57	44
ENSMUSG00000020105	chr10	Lrig3	1.26E+08	1.26E+08	4050	-0.37568	1.896593	0.084882	0.151724	0.038746	0	45	57	93	57	79	40	68	52	67	61
ENSMUSG00000032563	chr9	Mrpl3	1.05E+08	1.05E+08	5961	-0.31148	5.239196	0.084943	0.151812	0.037405	0	509	370	758	901	855	477	900	483	706	545
ENSMUSG00000026249	chr1	Serpine2	79794197	79795042	8287	-0.27171	7.111284	0.085008	0.151887	0.029309	0	1864	1456	3533	2589	3038	2022	2793	1833	3054	1832
ENSMUSG00000038446	chr10	Cdc40	40831626	40833356	3361	-0.28963	3.193221	0.084997	0.151887	0.026539	0	119	119	208	164	195	116	190	150	149	137
ENSMUSG00000073125	chrX	Xlr3b	73192207	73192249	3780	1.210907	0.136925	0.085216	0.152238	0.510466	0	15	1	35	0	1	14	25	7	38	39
ENSMUSG00000040254	chr5	Sema3d	12383166	12383674	6521	-0.72667	0.561818	0.085306	0.152379	0.152654	0	5	21	59	29	31	16	15	32	13	15
ENSMUSG00000037606	chr7	Osbpl5	1.44E+08	1.44E+08	4915	0.244053	4.528354	0.085396	0.152519	0.021609	0	271	235	520	310	387	373	482	455	547	409
ENSMUSG00000020659	chr12	Cbll1	31484829	31487461	4007	-0.31331	3.403317	0.085426	0.152532	0.033097	0	160	126	320	139	216	115	201	153	205	182
ENSMUSG00000020778	chr11	Ten1	1.16E+08	1.16E+08	2728	0.33443	3.749312	0.085426	0.152532	0.039106	0	191	178	204	157	187	272	323	221	341	201
ENSMUSG00000093273	chr11	Mir3064	1.07E+08	1.07E+08	67	-0.3001	4.457191	0.085569	0.152766	0.033764	0	371	344	521	265	418	320	487	345	365	275
ENSMUSG00000004895	chr3	Prcc	87858903	87859346	2099	0.24408	5.35933	0.085636	0.152808	0.022596	0	501	408	753	668	694	694	925	748	985	700
ENSMUSG00000008200	chr2	Fnbp4	90745370	90745826	6583	0.293701	3.709544	0.085638	0.152808	0.030584	0	169	115	323	134	228	203	331	275	315	194
ENSMUSG00000009210	chr11	2310007L24Rik	1.06E+08	1.06E+08	1724	-0.37582	2.185802	0.085626	0.152808	0.042222	0	80	56	95	84	86	78	78	59	72	61
ENSMUSG00000021608	chr13	Lpcat1	73467197	73467517	4131	0.344589	2.51127	0.085633	0.152808	0.037317	0	64	45	108	79	108	106	109	125	137	89
ENSMUSG00000030825	chr7	Hsd17b14	45554893	45555066	2046	-0.89162	0.109681	0.085659	0.152824	0.232656	0	18	22	50	2	13	11	6	9	19	16
ENSMUSG00000024410	chr18	3110002H16Rik	12168717	12168902	5768	0.268346	3.769931	0.085689	0.152855	0.024355	0	203	120	264	194	211	219	344	245	329	223
ENSMUSG00000031382	chrX	Asb11	1.64E+08	1.64E+08	2847	0.32334	7.448615	0.085699	0.152855	0.04187	0	2333	2122	3333	2322	2146	2316	5681	2759	4963	2688
ENSMUSG00000025246	chrX	Tbl1x	77511013	77511269	7052	-0.28127	4.097142	0.085858	0.153118	0.028374	0	235	231	515	221	336	204	354	303	338	219
ENSMUSG00000031725	chr8	Ces1f	93256236	93256600	3285	1.183046	2.127581	0.085879	0.153134	0.515148	0	70	70	14	11	10	74	30	301	56	56
ENSMUSG00000098399	chr7	Gm27995	1.04E+08	1.04E+08	100	0.730201	0.00252	0.085921	0.153189	0.129105	0	19	8	11	4	10	24	23	26	19	8
ENSMUSG00000034042	chr4	Gpbp1l1	1.17E+08	1.17E+08	4158	-0.25909	4.545403	0.085936	0.153194	0.024359	0	289	255	626	432	494	284	477	329	505	359
ENSMUSG00000029686	chr6	Cul1	47453398	47453627	4058	-0.26027	6.491187	0.086015	0.153314	0.026846	0	1393	1213	2359	1348	1608	1240	1941	1254	1767	1309
ENSMUSG00000039086	chr2	Ss18l1	1.8E+08	1.8E+08	4343	-0.41699	1.667509	0.086051	0.153358	0.050538	0	39	44	83	50	71	20	71	46	66	44
ENSMUSG00000033707	chr15	Lrrc24	76715276	76716306	3912	-0.25964	4.982643	0.086105	0.153435	0.025593	0	470	386	618	642	627	399	592	511	722	424
ENSMUSG00000001415	chr3	Smg5	88336260	88336497	6956	-0.28944	6.130621	0.086159	0.153509	0.033058	0	1115	631	1741	1394	1456	968	1268	1275	1427	830
ENSMUSG00000029787	chr6	Avl9	56714927	56715214	7463	-0.39493	1.988793	0.086176	0.153519	0.045738	0	52	39	118	62	96	40	72	79	70	46
ENSMUSG00000073422	chr17	H2-Ke6	34026033	34026225	1533	0.283901	5.376186	0.086333	0.153779	0.030815	0	557	533	631	588	602	726	1071	763	1011	615
ENSMUSG00000058665	chr1	En1	1.21E+08	1.21E+08	2624	0.507872	2.272373	0.086467	0.153996	0.089598	0	42	26	48	106	92	77	119	85	162	73
ENSMUSG00000033502	chr3	Cdc14a	1.16E+08	1.16E+08	11335	-0.39656	4.332254	0.086501	0.154037	0.06057	0	294	276	472	319	484	180	327	547	264	249
ENSMUSG00000030157	chr6	Clec2d	1.29E+08	1.29E+08	1213	0.363637	5.881696	0.086528	0.154064	0.052366	0	891	807	1043	588	658	1225	1635	954	1426	838
ENSMUSG00000066839	chr9	Ecsit	22072246	22072580	1684	-0.292	6.452236	0.086551	0.154083	0.034045	0	1239	909	1764	2006	1872	1013	1739	1286	1997	1261
ENSMUSG00000053604	chr6	Rpia	70765720	70766648	5359	0.264426	4.744939	0.086617	0.154181	0.025646	0	375	310	502	363	378	362	633	540	699	459
ENSMUSG00000002550	chr2	Uck1	32255002	32256211	2751	0.371122	3.831498	0.086794	0.154476	0.050485	0	225	172	209	170	178	245	274	394	303	219
ENSMUSG00000043993	chr11	2900052L18Rik	1.2E+08	1.2E+08	1588	0.635364	-0.25556	0.086824	0.154508	0.076204	0	8	4	13	8	13	15	21	6	20	18
ENSMUSG00000103109	chr11	RP23-263M10.12	73080683	73083604	2922	-0.65183	-0.04272	0.086928	0.154672	0.093865	0	7	6	32	20	24	5	20	14	14	9
ENSMUSG00000044627	chr2	Swi5	32278816	32279131	5551	0.292077	6.580135	0.086944	0.154681	0.033987	0	1202	1308	1541	1280	1363	1590	2614	1692	2187	1597
ENSMUSG00000024875	chr19	Yif1a	5088538	5088748	1493	0.274504	5.001191	0.086963	0.154692	0.028744	0	367	283	547	588	552	501	836	537	843	522
ENSMUSG00000096942	chr12	Rps19-ps6	1.11E+08	1.11E+08	438	0.440853	2.444687	0.08698	0.154703	0.06262	0	100	54	73	64	59	80	156	128	134	72
ENSMUSG00000016409	chrX	Nkap	37126795	37127375	4326	-0.27563	3.495769	0.087109	0.15487	0.025175	0	140	132	287	189	260	131	217	176	240	168
ENSMUSG00000026663	chr1	Atf6	1.71E+08	1.71E+08	9231	-0.26515	5.221385	0.087092	0.15487	0.026823	0	495	365	1118	646	782	495	805	531	749	534
ENSMUSG00000048332	chr3	Lhfp	53041528	53041774	2108	0.302469	3.797863	0.087104	0.15487	0.033273	0	130	150	268	179	283	246	319	254	263	287
ENSMUSG00000047777	chr4	Phf13	1.52E+08	1.52E+08	3205	0.303396	2.919851	0.087129	0.154885	0.028591	0	77	85	158	112	108	130	178	137	183	125
ENSMUSG00000039201	chrX	Tbc1d25	8154472	8156066	2794	0.426261	1.994697	0.087155	0.15491	0.058977	0	47	24	54	78	63	74	81	83	109	58
ENSMUSG00000051989	chr16	Smim11	92301286	92301343	972	0.318268	5.117463	0.087246	0.155051	0.038924	0	508	454	476	466	466	618	935	589	899	510
ENSMUSG00000030521	chr7	Mphosph10	64376576	64376804	3651	-0.26151	4.105059	0.087517	0.155512	0.024773	0	257	262	390	268	306	237	366	281	321	222
ENSMUSG00000037960	chr13	1110007C09Rik	49202951	49203235	804	0.297756	5.888461	0.087713	0.15584	0.035217	0	779	520	952	1049	951	1000	1316	1011	1852	874
ENSMUSG00000041712	chr12	Ubr7	1.03E+08	1.03E+08	3247	-0.24403	4.562496	0.087831	0.156027	0.022029	0	380	292	595	347	457	288	535	352	501	324

ENSMUSG00000097047	chr17	1110020A21Rik	84954967	84955308	853	0.509205	0.842056	0.087842	0.156027	0.064054	0	18	18	24	24	26	38	50	20	52	22
ENSMUSG00000001323	chr11	Srr	74906359	74908843	4560	-0.38135	3.592297	0.087886	0.156084	0.053269	0	153	88	335	291	269	120	232	202	189	203
ENSMUSG00000031758	chr8	Cdyl2	1.17E+08	1.17E+08	8087	0.399811	2.319832	0.087899	0.156085	0.053348	0	50	36	134	62	72	76	125	83	171	66
ENSMUSG00000064346	chrMT	mt-Tw	4950	5016	67	-0.39516	6.71686	0.088085	0.156396	0.063519	0	1364	1069	2006	2475	2825	1410	2730	1220	2454	829
ENSMUSG00000006527	chr14	Sfmbt1	30714849	30714966	8629	-0.26218	3.823163	0.088127	0.156449	0.023392	0	189	160	395	239	282	203	299	197	278	196
ENSMUSG00000042207	chr1	Kdm5b	1.35E+08	1.35E+08	16555	0.274524	3.540658	0.088193	0.156546	0.026337	0	130	109	274	157	191	170	259	244	255	221
ENSMUSG00000032265	chr9	Fam46a	85320439	85325233	5703	0.430168	2.734604	0.088283	0.156684	0.064346	0	70	93	141	52	90	109	195	173	121	90
ENSMUSG00000037022	chr8	Mmaa	79266424	79268215	2843	-0.27217	3.895457	0.088486	0.157023	0.026173	0	199	179	299	283	346	181	284	232	282	243
ENSMUSG00000038522	chr10	AI317395	40001575	40003589	2729	-0.58035	1.965542	0.088518	0.15706	0.119926	0	61	22	66	117	106	33	78	27	89	59
ENSMUSG00000019158	chr7	Tmem160	16452779	16453170	814	0.299567	4.842458	0.088561	0.157115	0.034063	0	391	382	422	372	422	480	655	506	833	440
ENSMUSG00000021294	chr12	Kif26a	1.12E+08	1.12E+08	6918	-0.39954	2.136717	0.088654	0.157249	0.052503	0	45	51	96	106	100	42	97	60	99	50
ENSMUSG00000056328	chr11	Myh1	67200052	67200124	6353	-1.09212	11.80715	0.088661	0.157249	0.471753	0	13866	6438	51453	194143	148244	11422	75531	10731	44466	72005
ENSMUSG00000001482	chr8	Def8	1.23E+08	1.23E+08	3988	-0.28839	5.714975	0.088946	0.157712	0.033126	0	703	503	1105	1170	1238	674	1033	705	1148	789
ENSMUSG00000033751	chr8	Gadd45gip1	84831522	84832640	2494	0.274926	5.071502	0.088935	0.157712	0.029252	0	375	325	537	610	589	481	795	590	883	633
ENSMUSG00000031480	chr8	Thsd1	22227313	22227429	4422	0.483057	1.146323	0.089014	0.157813	0.061951	0	14	26	42	25	35	26	47	62	49	39
ENSMUSG00000092137	chr9	Gcom1	71479325	71479540	1726	-0.28131	5.766803	0.089035	0.157828	0.031554	0	749	527	1129	1161	1311	712	1193	745	1124	762
ENSMUSG00000028073	chr3	Pear1	87747890	87750297	6781	0.290238	3.355905	0.089088	0.157901	0.029659	0	112	81	208	135	220	170	245	197	246	164
ENSMUSG00000020601	chr12	Trib2	15791727	15794076	4290	0.332036	4.534384	0.089145	0.157971	0.042664	0	220	252	496	294	413	245	559	365	814	445
ENSMUSG00000029363	chr5	Rfc5	1.17E+08	1.17E+08	4669	0.463894	0.791632	0.089151	0.157971	0.050178	0	18	15	33	22	22	17	41	32	43	39
ENSMUSG00000005225	chr6	Plekha8	54595111	54595471	7005	-0.34499	2.205167	0.089194	0.158025	0.034473	0	74	59	127	63	88	68	83	64	87	60
ENSMUSG00000026584	chr1	Scyl3	1.64E+08	1.64E+08	5802	-0.36707	2.293814	0.089227	0.158063	0.041942	0	64	48	150	84	106	43	100	85	99	63
ENSMUSG00000035674	chr7	Ndufa3	3617373	3617407	858	0.300813	7.395079	0.089244	0.158072	0.037045	0	2196	1662	2481	3085	2483	2692	4577	2899	4540	2574
ENSMUSG00000033763	chr8	Mtss1l	1.11E+08	1.11E+08	5311	-0.31668	6.246275	0.089318	0.158182	0.04079	0	1231	1181	2082	1027	1213	940	1165	1084	1941	1097
ENSMUSG00000006373	chrX	Pgrmc1	36598206	36598614	1857	0.322984	3.792148	0.089411	0.158326	0.038276	0	162	166	231	165	250	205	287	355	254	271
ENSMUSG00000033060	chr14	Lmo7	1.02E+08	1.02E+08	11951	0.281867	6.383504	0.08943	0.158337	0.032307	0	879	674	1833	1265	1630	1166	2440	1420	2116	1403
ENSMUSG00000074141	chr7	Il4i1	44816370	44816483	4097	-0.45686	1.811467	0.089446	0.158344	0.068106	0	74	46	109	32	60	52	70	39	57	44
ENSMUSG00000075705	chr17	Msrb1	24736642	24736762	1258	0.333385	6.991834	0.089466	0.158359	0.045552	0	1685	1064	1935	2144	2208	2529	2653	2047	4179	1699
ENSMUSG00000019846	chr10	Lama4	38965515	38966149	12068	0.271783	4.830484	0.089678	0.158713	0.02896	0	317	230	656	400	541	408	695	541	592	588
ENSMUSG00000026027	chr1	Stradb	58973522	58973850	7256	-0.2422	6.804514	0.089726	0.158777	0.023855	0	1640	1297	2634	1956	2319	1488	2373	1614	2414	1564
ENSMUSG00000053137	chr15	Mapk11	89142486	89143817	2440	0.360677	1.790507	0.089757	0.158796	0.035812	0	35	33	67	48	55	63	67	69	76	64
ENSMUSG00000058407	chr1	Txndc9	37985189	37987779	9102	0.261685	5.000145	0.089761	0.158796	0.026147	0	441	361	552	451	497	567	865	522	750	496
ENSMUSG00000035227	chr7	Spcs2	99837569	99839883	2815	0.289535	6.117485	0.089785	0.158817	0.033718	0	983	875	1353	819	898	1141	1789	1341	1785	1001
ENSMUSG00000037822	chr5	Smim14	65446844	65450437	7460	0.237219	5.181732	0.089859	0.158907	0.02176	0	435	374	788	497	619	561	774	754	889	603
ENSMUSG00000084215	chr4	Gm11814	10438815	10439743	929	-0.57884	0.130482	0.089856	0.158907	0.061801	0	12	10	33	21	22	14	23	14	10	11
ENSMUSG00000056938	chr11	Acbd4	1.03E+08	1.03E+08	2937	0.333314	4.253264	0.089878	0.158919	0.041937	0	285	261	320	199	237	330	404	425	408	340
ENSMUSG00000103922	chr1	RP23-34E15.4	4771131	4772199	1069	-0.47532	0.983797	0.089904	0.158944	0.056354	0	31	15	55	46	32	22	28	26	39	28
ENSMUSG00000029769	chr6	Ccdc136	29396309	29396335	4298	-0.28888	3.374499	0.090166	0.159385	0.029436	0	142	144	228	193	198	130	209	138	255	129
ENSMUSG00000087412	chr7	Gm15501	93178983	93179669	687	0.399961	2.682803	0.090189	0.159405	0.054395	0	115	54	85	94	77	125	159	128	137	102
ENSMUSG00000052566	chr8	Hook2	84990595	84990752	2617	0.38873	2.45214	0.090201	0.159405	0.047316	0	72	74	90	60	67	103	126	110	146	72
ENSMUSG00000061787	chr7	Rps17	81342732	81342849	1274	0.315545	7.548895	0.090231	0.159436	0.041048	0	2673	2453	2719	2432	2603	3397	5431	3304	4120	2848
ENSMUSG00000045948	chr7	Mrps12	28739641	28739979	1040	0.28708	5.064815	0.090261	0.159447	0.031903	0	475	432	509	447	473	579	743	635	876	526
ENSMUSG00000070371	chr7	Prss36	1.28E+08	1.28E+08	3221	0.334012	2.711545	0.09026	0.159447	0.034842	0	88	70	108	101	84	97	179	134	158	96
ENSMUSG00000005683	chr10	Cs	1.28E+08	1.28E+08	2828	-0.33557	9.673706	0.090397	0.159666	0.046873	0	10838	6465	18710	19760	19876	9203	17151	11447	18000	11429
ENSMUSG00000052821	chrX	Cysltr1	1.07E+08	1.07E+08	5142	-0.48695	0.669822	0.090427	0.159697	0.050333	0	20	17	52	23	32	22	31	22	23	15
ENSMUSG00000034520	chr11	Gjc1	1.03E+08	1.03E+08	5003	0.416712	1.711833	0.090525	0.15985	0.052564	0	24	28	53	46	71	59	93	50	68	60
ENSMUSG00000039285	chr9	Azi2	1.18E+08	1.18E+08	6439	-0.25053	4.968782	0.090655	0.160058	0.024155	0	476	309	745	608	637	373	673	510	605	465
ENSMUSG00000030763	chr7	Lcmt1	1.23E+08	1.23E+08	1369	0.254811	4.727698	0.090683	0.160086	0.024306	0	347	321	508	351	389	421	668	439	675	445
ENSMUSG00000006378	chr15	Gcat	79030874	79031120	3851	-0.26785	3.659767	0.090704	0.160102	0.025291	0	186	156	265	250	241	175	271	172	256	173
ENSMUSG00000037572	chr14	Wdhd1	47240944	47241812	7192	0.604117	-0.00786	0.090772	0.160201	0.075745	0	15	3	11	12	15	22	21	16	23	14
ENSMUSG00000035234	chr5	Fam175a	1.01E+08	1.01E+08	3011	-0.39943	1.896581	0.090804	0.160235	0.050035	0	52	53	69	85	67	44	93	50	61	42
ENSMUSG00000074282	chr7	Zfp94	24301704	24303873	3510	-0.47847	1.111444	0.090822	0.160246	0.063722	0	23	22	50	45	57	32	50	21	38	18
ENSMUSG00000035007	chr11	Rundc1	1.01E+08	1.01E+08	3223	0.270289	3.676688	0.090877	0.160259	0.025099	0	176	131	258	180	180	174	295	259	324	224
ENSMUSG00000039842	chr8	Mcph1	18595131	18595635	7806	-0.34583	2.29596	0.090859	0.160259	0.034815	0	74	57	134	75	101	66	73	82	86	75
ENSMUSG00000041037	chr7	Irgq	24530648	24530904	6123	-0.26921	4.728128	0.090889	0.160259	0.027662	0	319	269	683	472	662	317	532	401	545	409
ENSMUSG00000073002	chr6	Vamp5	72368049	72369470	1648	-0.31637	6.199335	0.090879	0.160259	0.041202	0	1298	1213	1504	1190	1105	1046	1516	981	1692	837
ENSMUSG00000083044	chr4	Gm12416	84104895	84105902	1008	0.554725	0.308623	0.090843	0.160259	0.077164	0	13	5	32	11	15	12	28	20	36	27
ENSMUSG00000014353	chr2	Tmem87b	1.29E+08	1.29E+08	8395	-0.2411	4.287331	0.090955	0.160298	0.021395	0	293	258	476	296	378	245	449	300	383	269
ENSMUSG00000028334	chr4	Nans	46489248	46489490	4581	0.265212	4.116637	0.090927	0.160298	0.025046	0	247	192	292	246	264	268	384	331	477	274
ENSMUSG00000057672	chr8	Pkn1	83669762	83670368	7386	-0.2955	4.225178	0.09096	0.160298	0.032934	0	232	180	443	390	450	196	426	319	327	275
ENSMUSG00000066442	chr9	Mthfs	89210676	89210821	7498	0.439099	1.574603	0.090945	0.160298	0.052651	0	38	40	38	27	47	52	70	63	76	41
ENSMUSG00000033044	chr11	Dhrs7c	67798187	67798403	1880	0.269212	7.75901	0.091075	0.160437	0.030107	0	3140	1817	4474	3079	3522	3630	5784	4135	5398	2980
ENSMUSG00000049891	chr8	Gm7984	75398511	75398738	534	-0.61095	0.132952	0.091054	0.160437	0.072108	0	19	5	35	17	24	10	18	13	14	16
ENSMUSG00000096199	chr12	Ptrhd1	4234027	4234278	4013	-0.3286	2.970729	0.091074	0.160437	0.037415	0	166	89	168	130	132	111	152	112	148	104
ENSMUSG00000045294	chr5	Insig1	28071363	28071795	2697	0.443877	3.783399	0.091589	0.161321	0.07768	0	200	132	266	135	200	251	254	504	220	172
ENSMUSG00000019837	chr10	Gtf3c6	40249203	40249831	1020	-0.28047	4.080437	0.09166	0.161413	0.029993	0	262	273	333	258	323	232	387	224	330	228

ENSMUSG00000038503	chr7	Mesdc2	83884466	83884655	5081	0.245243	4.694186	0.091666	0.161413	0.022861	0	290	276	492	386	466	381	617	533	548	472
ENSMUSG00000090952	chr17	Gm17251	33759992	33760587	925	0.487641	1.665121	0.091766	0.161567	0.074817	0	52	33	56	25	35	41	92	84	81	35
ENSMUSG00000032342	chr9	Mto1	78448208	78448510	4078	-0.24097	4.612037	0.091792	0.161593	0.021998	0	368	271	562	453	488	326	564	366	502	311
ENSMUSG00000080921	chr6	Rpl38-ps2	1.41E+08	1.41E+08	213	0.364756	3.891324	0.09181	0.161603	0.049959	0	204	215	194	185	184	302	413	258	333	211
ENSMUSG00000010936	chr8	Vac14	1.11E+08	1.11E+08	3028	-0.33646	4.956682	0.091899	0.161737	0.045847	0	561	545	707	414	461	496	528	446	694	341
ENSMUSG00000034471	chr11	Caskin2	1.16E+08	1.16E+08	5177	-0.31035	4.182493	0.091916	0.161746	0.036565	0	199	171	423	424	438	228	334	279	362	272
ENSMUSG00000003955	chr16	Fam162a	36043844	36044091	635	0.261744	5.453102	0.092043	0.161948	0.027207	0	592	451	723	709	686	731	1213	753	1078	641
ENSMUSG00000024892	chr19	Pcx	4510472	4510581	4272	-0.41446	6.729142	0.092057	0.161952	0.07162	0	2166	1563	2605	1384	1877	1114	1772	2854	1632	933
ENSMUSG00000057229	chr7	Atp5sl	25619414	25619460	2916	-0.37135	4.88485	0.092237	0.162246	0.055781	0	354	218	629	796	759	315	586	415	655	417
ENSMUSG00000079243	chr9	Xirp1	1.2E+08	1.2E+08	5839	0.394129	6.48108	0.092255	0.162256	0.064819	0	764	482	1658	1706	1893	1424	2417	1341	2952	1393
ENSMUSG00000030612	chr7	Mrpl46	78775236	78775725	1392	-0.29917	4.394548	0.09227	0.162262	0.034796	0	299	245	365	446	494	321	465	269	395	272
ENSMUSG00000014905	chr12	Dnajb9	44205897	44207405	1865	-0.23895	5.265899	0.092319	0.162326	0.022497	0	539	479	1028	645	700	460	743	669	803	562
ENSMUSG00000090066	chr3	1110002E22Rik	1.38E+08	1.38E+08	9998	-0.31552	7.49953	0.092341	0.162344	0.041681	0	2482	1900	5937	2558	4090	1842	4269	2309	4330	2472
ENSMUSG00000022579	chr15	Gpihbp1	75596628	75596730	2554	0.321012	4.294529	0.09236	0.162355	0.0398	0	221	218	284	334	314	402	432	439	456	239
ENSMUSG00000020696	chr11	Rffl	82802449	82806189	5922	-0.33673	2.782241	0.09254	0.16265	0.038554	0	137	65	164	108	141	69	151	109	137	91
ENSMUSG00000020520	chr11	Galnt10	57645442	57645717	5965	-0.31347	3.345481	0.092644	0.162811	0.03442	0	122	105	228	191	274	118	194	168	183	157
ENSMUSG00000057604	chr6	Lmcd1	1.12E+08	1.12E+08	1730	0.694371	6.713898	0.092681	0.162855	0.200339	0	379	320	1095	2895	2006	1089	3450	1589	3471	2640
ENSMUSG00000058126	chr14	Tpm3-rs7	1.13E+08	1.13E+08	2106	0.593393	0.162819	0.092719	0.1629	0.085257	0	8	5	13	18	21	15	35	26	15	19
ENSMUSG00000021003	chr12	Galc	98202304	98204087	3822	0.365858	2.564575	0.092795	0.163012	0.046817	0	62	45	108	86	116	86	131	166	123	89
ENSMUSG00000074876	chr2	Spata5l1	1.23E+08	1.23E+08	1547	-0.33406	2.138637	0.093155	0.163622	0.031723	0	71	52	113	76	77	57	97	64	77	55
ENSMUSG00000062778	chr3	Chia1	1.06E+08	1.06E+08	1903	-0.52351	0.412814	0.093204	0.163687	0.0667	0	21	20	31	20	24	11	19	9	32	22
ENSMUSG00000042055	chr7	Wdr11	1.3E+08	1.3E+08	10372	-0.23909	4.861364	0.093266	0.163774	0.022166	0	424	338	782	449	584	335	627	463	626	414
ENSMUSG00000024026	chr17	Glo1	30592866	30593074	1935	-0.25234	6.771156	0.093294	0.163784	0.026547	0	1776	1510	2540	1685	1963	1534	2304	1553	2184	1566
ENSMUSG00000029823	chr6	Luc7l2	38551334	38551908	12084	-0.26341	6.664305	0.093296	0.163784	0.028829	0	1519	1218	2917	1334	2152	1221	1997	1702	1950	1564
ENSMUSG00000034931	chr11	Dhx8	1.02E+08	1.02E+08	5032	-0.26637	4.028983	0.093342	0.163842	0.025943	0	219	204	408	302	306	199	287	284	289	275
ENSMUSG00000027981	chr3	Rnpc3	1.14E+08	1.14E+08	6627	-0.35483	2.474316	0.093418	0.163954	0.042946	0	82	84	148	97	80	63	123	96	106	57
ENSMUSG00000055302	chr5	Mrfap1	36794867	36795944	1648	0.283303	7.632801	0.093483	0.164047	0.033748	0	2832	2453	2951	2474	3279	3409	4849	3482	5047	3230
ENSMUSG00000054641	chr6	Mmrn1	60924976	60925042	5868	0.406325	2.357219	0.093555	0.164152	0.059231	0	50	39	119	52	102	103	127	128	104	57
ENSMUSG00000037344	chr5	Slc12a9	1.37E+08	1.37E+08	5020	0.370612	2.369337	0.093662	0.164317	0.04556	0	83	49	104	41	79	81	133	100	129	82
ENSMUSG00000037553	chr4	Zdhhc18	1.34E+08	1.34E+08	5382	0.261149	5.037517	0.093722	0.1644	0.027172	0	388	309	640	500	591	507	627	671	975	508
ENSMUSG00000061458	chr12	Nol10	17348458	17348619	3020	0.26782	3.529335	0.094078	0.165004	0.024158	0	135	134	199	162	200	162	289	221	283	197
ENSMUSG00000020219	chr10	Timm13	80899450	80900259	1225	0.283569	5.93088	0.094126	0.165065	0.032975	0	888	742	907	865	873	984	1529	1078	1648	952
ENSMUSG00000030603	chr7	Psmc4	28041707	28041920	2169	0.262058	6.659158	0.094166	0.165114	0.02859	0	1277	1252	1739	1452	1527	1691	2287	1756	2724	1665
ENSMUSG00000051906	chr8	Cd209f	4102787	4103249	1528	-0.73914	2.820758	0.094307	0.16534	0.217762	0	170	142	259	35	90	126	68	159	51	48
ENSMUSG00000045827	chr13	Serpinb9	33003250	33003344	3494	0.316182	2.902142	0.094321	0.165342	0.032365	0	108	83	144	86	103	110	202	153	175	114
ENSMUSG00000025381	chr10	Cnpy2	1.28E+08	1.28E+08	1017	0.28702	4.890813	0.09458	0.165772	0.032508	0	401	406	483	352	435	530	772	531	678	465
ENSMUSG00000027176	chr2	Cstf3	1.05E+08	1.05E+08	5879	0.301225	2.830888	0.094591	0.165772	0.029709	0	99	70	123	83	130	114	176	127	159	130
ENSMUSG00000026576	chr1	Atp1b1	1.64E+08	1.64E+08	3081	-1.00786	6.731135	0.094695	0.165924	0.418874	0	238	296	1318	5621	4522	548	2132	432	2312	1397
ENSMUSG00000048234	chr1	Rnf149	39551296	39552515	2838	0.295731	3.159708	0.094703	0.165924	0.030704	0	92	81	175	142	158	127	206	216	208	136
ENSMUSG00000083443	chr6	Gm15519	1.13E+08	1.13E+08	1566	-0.46258	0.868267	0.094784	0.166044	0.052225	0	26	24	50	39	22	21	32	28	28	23
ENSMUSG00000056665	chr15	Them6	74721204	74721807	1784	-0.25742	3.60726	0.094892	0.166212	0.0234	0	180	147	285	212	242	156	219	180	289	171
ENSMUSG00000000440	chr6	Pparg	1.15E+08	1.15E+08	1984	0.725111	2.656645	0.094954	0.166297	0.206966	0	77	105	58	55	46	125	68	301	87	92
ENSMUSG00000020691	chr11	Mettl2	1.05E+08	1.05E+08	3399	-0.33085	2.406731	0.095	0.166356	0.034549	0	79	61	135	90	108	70	132	66	91	67
ENSMUSG00000042451	chr1	Mybph	1.34E+08	1.34E+08	2329	1.078086	8.68478	0.09514	0.166579	0.478315	0	7069	5579	5951	224	415	7989	12399	17406	6490	6027
ENSMUSG00000041777	chr2	Cir1	73283105	73285035	3159	-0.26859	3.499177	0.095253	0.166755	0.025908	0	162	149	274	178	229	140	274	148	215	164
ENSMUSG00000029029	chr4	Wrap73	1.54E+08	1.54E+08	4335	0.275	3.636323	0.095281	0.166783	0.026756	0	176	127	214	163	213	190	271	268	330	183
ENSMUSG00000072964	chrX	Bhlhb9	1.36E+08	1.36E+08	2978	0.472245	2.247813	0.095427	0.167016	0.077635	0	51	72	102	43	38	65	109	106	100	108
ENSMUSG00000058594	chr2	Fbxo18	11742573	11742808	5115	-0.24691	4.86576	0.09548	0.167087	0.023888	0	416	325	821	465	579	416	654	454	526	388
ENSMUSG00000075376	chr2	Rc3h2	37370069	37375428	11688	-0.27292	5.501654	0.095495	0.167091	0.030797	0	810	620	1159	590	792	622	804	704	1065	577
ENSMUSG00000008035	chrX	Mid1ip1	10715013	10715067	2128	-0.45039	5.380061	0.095537	0.167142	0.085636	0	481	393	870	1139	1057	420	1301	369	964	363
ENSMUSG00000028600	chr4	Podn	1.08E+08	1.08E+08	4270	0.298918	4.111138	0.095555	0.167142	0.035159	0	184	161	362	249	310	271	294	454	437	264
ENSMUSG00000031753	chr8	Cog4	1.11E+08	1.11E+08	4053	-0.2446	6.317227	0.095562	0.167142	0.025027	0	1127	1014	1876	1468	1484	1026	1528	1212	1709	1216
ENSMUSG00000025666	chrX	Tmem47	81070698	81070817	4025	0.319757	2.912454	0.095677	0.167322	0.035281	0	70	78	153	113	124	91	182	131	202	155
ENSMUSG00000022760	chr16	Thap7	17527982	17528740	1880	0.279617	3.333963	0.095712	0.16736	0.026256	0	146	106	175	136	155	164	238	179	261	163
ENSMUSG00000006021	chr7	Kptn	16119895	16120181	3341	-0.26913	3.735808	0.095806	0.167503	0.02693	0	178	177	252	246	304	176	289	185	279	179
ENSMUSG00000081999	chr2	Gm13461	41987473	41988017	662	0.340288	2.380393	0.095871	0.167594	0.034395	0	60	64	77	73	81	79	135	95	125	89
ENSMUSG00000028312	chr4	Smc2	52439243	52439334	5478	0.455406	0.969065	0.095899	0.167605	0.057399	0	16	18	43	28	22	31	40	45	33	42
ENSMUSG00000037818	chr3	3110057O12Rik	40846970	40847136	5433	-0.57654	2.778609	0.095902	0.167605	0.132327	0	56	39	149	223	214	44	178	81	121	90
ENSMUSG00000020231	chr10	Dip2a	76259429	76259722	8215	-0.36224	2.557154	0.096097	0.167922	0.045694	0	59	67	163	111	141	52	105	94	123	93
ENSMUSG00000085088	chr11	4931413K12Rik	75589665	75590708	1282	0.566536	1.549922	0.096137	0.167971	0.10889	0	45	36	53	22	21	70	50	47	103	37
ENSMUSG00000024134	chr17	Six2	85684277	85685513	2119	-0.60517	3.478317	0.096252	0.168149	0.148951	0	128	159	437	82	338	174	66	145	143	219
ENSMUSG00000018599	chr11	Mief2	60728398	60728567	2716	0.292933	6.719234	0.096382	0.168355	0.03656	0	1191	822	1751	1998	1945	1455	2608	1906	2869	1910
ENSMUSG00000051147	chr8	Nat2	67494867	67494902	1509	0.583376	-0.06279	0.096452	0.168454	0.069821	0	7	7	13	17	10	15	19	25	16	16
ENSMUSG00000065399	chr18	Mir133a-1	10782899	10782985	87	0.556432	1.2007	0.096473	0.168469	0.098757	0	31	30	33	18	26	55	25	50	61	40
ENSMUSG00000020628	chr12	Trappc12	28690629	28691557	4257	-0.25929	3.966843	0.096489	0.168474	0.025138	0	213	183	330	311	331	181	310	233	323	253

ENSMUSG00000020532	chr11	Acaca	84129672	84130130	15155	0.535742	4.456431	0.096535	0.168533	0.12058	0	268	181	478	258	282	354	267	1015	310	317
ENSMUSG00000030275	chr6	Etnk1	1.43E+08	1.43E+08	6429	-0.27078	5.129194	0.096554	0.168544	0.029763	0	471	317	912	671	809	384	694	623	701	513
ENSMUSG00000074340	chr3	Ovgp1	1.06E+08	1.06E+08	3561	0.513162	1.367199	0.096568	0.168546	0.081331	0	37	33	52	14	25	46	74	53	48	43
ENSMUSG00000032688	chr18	Malt1	65430963	65431398	5073	-0.46793	1.754527	0.096588	0.168558	0.071232	0	36	26	119	76	65	53	64	41	62	31
ENSMUSG00000024037	chr17	Wdr4	31494323	31496928	5432	-0.30507	2.839555	0.096992	0.169219	0.031771	0	112	88	199	107	131	80	138	136	137	90
ENSMUSG00000031386	chrX	Hcfc1	73942792	73944477	8360	-0.31286	5.846898	0.096979	0.169219	0.041139	0	741	441	1980	1001	1316	759	1177	843	1134	798
ENSMUSG00000025979	chr1	Mob4	55131231	55131359	4855	-0.23461	5.671601	0.09714	0.169427	0.022837	0	786	697	1223	745	973	655	1109	756	1046	745
ENSMUSG00000038695	chr7	Josd2	44467980	44468190	2466	0.267984	5.022922	0.097149	0.169427	0.028937	0	464	392	542	397	525	556	668	558	835	603
ENSMUSG00000039252	chr5	Lgi2	52537864	52538780	1950	-0.59459	0.900822	0.097131	0.169427	0.10794	0	25	18	72	23	42	31	36	32	17	10
ENSMUSG00000028348	chr4	Murc	48663514	48664029	2054	0.270869	7.329895	0.097166	0.169433	0.031473	0	2176	1883	3274	1999	2326	2742	4381	2455	4025	2647
ENSMUSG00000024667	chr19	Tmem216	10533865	10533955	1977	0.423241	1.285258	0.097211	0.16949	0.044053	0	28	24	40	32	35	27	62	59	65	34
ENSMUSG00000028717	chr4	Tal1	1.15E+08	1.15E+08	4379	0.465732	0.654273	0.097294	0.169612	0.052416	0	17	9	31	15	29	24	48	31	32	21
ENSMUSG00000030672	chr7	Mylpf	1.27E+08	1.27E+08	885	0.294573	13.66771	0.097368	0.169719	0.037783	0	213968	144773	234430	135037	196754	231309	309562	231989	338431	205406
ENSMUSG00000048379	chr14	Socs4	47276931	47277221	6873	-0.30486	3.018381	0.097429	0.169803	0.032416	0	109	104	220	132	158	81	150	156	148	121
ENSMUSG00000026848	chr2	Tor1b	30952959	30953223	5327	0.245691	5.25671	0.097446	0.16981	0.024585	0	534	425	820	467	565	650	875	726	846	663
ENSMUSG00000031879	chr8	Fam96b	1.05E+08	1.05E+08	1075	0.267768	4.154165	0.097581	0.17001	0.026959	0	258	187	306	246	282	271	535	311	422	261
ENSMUSG00000061028	chr7	Clasrp	19581044	19581158	2153	0.323599	3.093013	0.097586	0.17001	0.036905	0	125	88	131	105	145	181	182	147	200	135
ENSMUSG00000052180	chr13	Serpinb6c	33879816	33880332	1391	0.708559	0.212963	0.097661	0.170119	0.128315	0	16	16	9	9	10	33	24	13	35	13
ENSMUSG00000022668	chr16	Gtpbp8	44736768	44739368	3527	-0.28971	3.056058	0.097681	0.17013	0.028972	0	118	120	186	146	152	112	179	111	148	126
ENSMUSG00000005763	chr1	Cd247	1.66E+08	1.66E+08	5329	-0.50658	0.547861	0.097695	0.170133	0.069907	0	17	19	24	29	39	16	35	18	27	9
ENSMUSG00000040078	chr6	Gm9769	85843980	85844459	480	-0.33306	2.691435	0.097714	0.170143	0.038679	0	83	105	167	91	125	93	146	83	110	84
ENSMUSG00000009378	chr19	Slc16a12	34668403	34670893	4051	-0.58653	0.346511	0.097922	0.170483	0.082289	0	12	13	35	16	41	18	24	19	12	11
ENSMUSG00000022987	chr15	Zfp641	98285588	98289220	4254	-0.26502	4.619587	0.098047	0.170677	0.027576	0	318	254	656	424	569	376	441	326	484	388
ENSMUSG00000036278	chr19	Macrod1	7056768	7057182	1274	0.257655	7.753197	0.098067	0.17069	0.028698	0	2957	2441	3648	3233	3254	3437	5269	3650	5759	3585
ENSMUSG00000000915	chr5	Hip1r	1.24E+08	1.24E+08	5022	-0.53445	3.321764	0.098267	0.170994	0.118433	0	264	201	207	107	101	142	169	115	260	75
ENSMUSG00000028811	chr4	Yars	1.29E+08	1.29E+08	5943	-0.24098	5.489261	0.098263	0.170994	0.023931	0	615	491	1043	871	943	648	812	697	976	624
ENSMUSG00000025893	chr9	Kbtbd3	4309743	4309934	2310	-0.33282	2.880784	0.098297	0.171024	0.041807	0	119	106	146	136	133	93	178	79	167	86
ENSMUSG00000028565	chr4	Nfia	97772734	97772911	10891	0.250041	5.023032	0.098488	0.171333	0.025469	0	406	343	707	385	577	457	670	697	880	537
ENSMUSG00000046667	chr4	Rbm12b1	12140264	12140605	3122	0.455356	0.995978	0.098703	0.171663	0.049046	0	26	21	25	25	28	37	47	42	50	23
ENSMUSG00000057234	chr2	Mettl15	1.09E+08	1.09E+08	2275	-0.42767	1.787487	0.098698	0.171663	0.060462	0	34	41	85	83	71	25	77	59	60	45
ENSMUSG00000037752	chr4	Xkr8	1.33E+08	1.33E+08	4312	0.417675	1.303425	0.098756	0.171731	0.05112	0	34	19	56	24	32	33	45	58	67	43
ENSMUSG00000039634	chr4	Zfp189	49521176	49521251	3006	-0.38908	1.794371	0.09894	0.172006	0.046702	0	60	45	103	51	51	47	50	60	63	44
ENSMUSG00000060601	chr7	Nr1h2	44549616	44550131	3366	-0.23161	5.046879	0.098928	0.172006	0.021803	0	513	441	727	533	634	467	702	493	635	478
ENSMUSG00000015932	chr2	Dstn	1.44E+08	1.44E+08	1911	0.254013	4.783108	0.098979	0.172053	0.025999	0	307	312	537	380	486	376	567	619	647	511
ENSMUSG00000047554	chr7	Tmem41b	1.1E+08	1.1E+08	5316	-0.25984	3.911418	0.099152	0.17233	0.025374	0	205	170	393	288	277	173	304	213	313	249
ENSMUSG00000046562	chr5	Unc119b	1.15E+08	1.15E+08	4603	0.244816	4.228447	0.099257	0.17249	0.022716	0	251	199	380	248	299	251	475	325	454	359
ENSMUSG00000025332	chrX	Kdm5c	1.52E+08	1.52E+08	7110	0.310372	4.821877	0.099279	0.172506	0.040573	0	314	216	636	418	515	330	696	608	541	660
ENSMUSG00000030231	chr6	Plekha5	1.4E+08	1.4E+08	5133	-0.37318	2.307629	0.099307	0.172532	0.046635	0	54	45	138	93	129	70	99	80	82	55
ENSMUSG00000065887	chr4	n-R5s185	53860652	53860770	119	-0.48812	1.639207	0.099337	0.172562	0.084904	0	56	39	110	37	48	23	87	28	56	43
ENSMUSG00000001761	chr6	Smo	29735694	29736353	3779	0.357305	2.701665	0.099473	0.172774	0.048755	0	58	45	138	81	150	97	144	145	134	130
ENSMUSG00000002108	chr2	Nr1h3	91184061	91184482	2515	0.271888	4.276128	0.099506	0.172806	0.028761	0	233	218	342	303	296	298	505	452	438	252
ENSMUSG00000053644	chr18	Aldh7a1	56509687	56509982	5181	0.246851	5.172026	0.099517	0.172806	0.025343	0	374	354	807	544	630	526	879	769	737	649
ENSMUSG00000030556	chr7	Lrrc28	67513411	67515178	4834	-0.24222	4.119194	0.099697	0.173096	0.022404	0	279	193	401	319	322	234	351	249	386	240
ENSMUSG00000040007	chr2	Bahd1	1.19E+08	1.19E+08	4664	0.284817	3.247745	0.099734	0.173137	0.028615	0	118	103	206	120	139	121	225	210	242	155
ENSMUSG00000041133	chrX	Smc1a	1.52E+08	1.52E+08	5769	0.236267	5.263297	0.099747	0.173137	0.022974	0	450	418	791	514	686	636	1072	681	855	579
ENSMUSG00000027710	chr3	Acad9	36066000	36066270	3913	-0.24787	5.312204	0.099792	0.173193	0.02558	0	548	426	922	771	850	544	933	541	831	514
ENSMUSG00000003534	chr17	Ddr1	35681567	35682518	4774	0.307137	4.391051	0.099805	0.173194	0.038708	0	221	189	427	324	372	251	408	348	691	443
ENSMUSG00000056692	chr17	D17Wsu92e	27751232	27753995	4250	-0.2528	8.580815	0.099848	0.173245	0.028108	0	5263	4385	8593	7356	8254	4723	7693	5493	8824	5619
ENSMUSG00000063952	chr17	Brpf3	28801090	28801361	7194	-0.29777	3.548256	0.099886	0.173289	0.033579	0	175	129	330	166	259	135	207	246	224	142
ENSMUSG00000036568	chr17	Gltscr1l	46798116	46801829	6579	-0.27878	3.331542	0.099931	0.173343	0.027603	0	121	125	294	174	187	121	203	156	210	141
ENSMUSG00000020368	chr11	Canx	50293961	50296335	4693	0.238712	6.367813	0.099955	0.173362	0.024491	0	979	800	1721	1244	1442	1210	1891	1705	2003	1391
ENSMUSG00000021905	chr14	Dph3	32080566	32081269	3555	-0.26669	5.747029	0.100037	0.173481	0.030515	0	918	810	1130	860	876	737	1203	721	1092	740
ENSMUSG00000022178	chr14	Ajuba	54567469	54569056	3503	0.355047	1.739653	0.100118	0.173546	0.037914	0	43	25	67	38	59	50	66	71	83	60
ENSMUSG00000027834	chr3	Serpini1	75557547	75557642	7286	-0.62894	0.154458	0.100101	0.173546	0.113768	0	4	14	23	28	31	8	20	10	25	11
ENSMUSG00000041117	chr7	Ccdc8	16992708	16997516	4809	0.398428	1.701141	0.100126	0.173546	0.04992	0	30	33	74	38	47	40	58	73	82	71
ENSMUSG00000092981	chr17	Mir5125	23823291	23823369	79	0.523719	1.042207	0.100098	0.173546	0.077491	0	26	32	33	12	21	39	53	38	50	30
ENSMUSG00000088609	chr13	Gm24187	9834469	9834525	57	0.688644	2.673039	0.100182	0.17362	0.194338	0	107	30	87	103	52	72	76	53	298	213
ENSMUSG00000101856	chr5	1700096K18Rik	25530013	25531466	1454	-0.38372	1.402989	0.100414	0.174	0.040055	0	33	45	63	43	46	31	46	39	51	35
ENSMUSG00000028836	chr4	Slc30a2	1.34E+08	1.34E+08	3564	-1.15093	4.651295	0.100559	0.174228	0.556585	0	623	236	673	575	715	492	55	17	865	23
ENSMUSG00000038239	chr7	Hrc	45335290	45337374	2410	0.252848	10.30969	0.100583	0.174247	0.028358	0	14540	11378	24735	20429	23833	20239	27696	23497	33037	22035
ENSMUSG00000042962	chr12	Gm5436	84258332	84258973	642	0.379524	2.755178	0.100604	0.174261	0.052768	0	72	57	87	127	118	80	206	125	195	102
ENSMUSG00000021007	chr12	Spata7	98628157	98628334	4642	-0.37542	1.597609	0.100626	0.174276	0.040311	0	50	39	58	56	60	44	58	35	49	45
ENSMUSG00000025925	chr1	Terf1	15805646	15805957	4608	0.433857	1.794208	0.100653	0.174299	0.062049	0	47	41	46	36	54	73	99	72	53	51
ENSMUSG00000026511	chr1	Srp9	1.82E+08	1.82E+08	5541	0.27645	5.78785	0.100722	0.174396	0.03246	0	774	731	990	675	736	937	1443	1023	1375	801
ENSMUSG00000039220	chr17	Ppp1r10	35916434	35916598	5623	-0.27124	4.045376	0.100777	0.174468	0.028233	0	204	190	491	293	310	208	297	305	293	248

ENSMUSG00000027835	chr3	Pdcd10	75516490	75517601	2939	-0.31021	3.328531	0.100874	0.174614	0.036878	0	186	146	248	127	171	119	235	139	181	146
ENSMUSG00000081094	chr8	Rpl19-ps11	19492906	19493623	718	0.288958	3.965399	0.100955	0.174723	0.032071	0	228	193	256	200	217	293	405	285	330	241
ENSMUSG00000097052	chr2	Snhg7	26637177	26637633	2465	0.467691	0.803083	0.100964	0.174723	0.054447	0	17	18	23	24	27	39	33	31	34	32
ENSMUSG00000059554	chr10	Ccdc28a	18213676	18214178	2964	0.305485	2.800187	0.101033	0.17482	0.031467	0	98	65	108	105	113	112	177	116	167	123
ENSMUSG00000002379	chr17	Ndufa11	56717762	56717942	2661	0.30638	7.110855	0.101049	0.174825	0.041246	0	1725	1211	1903	2696	2292	2249	3514	2338	3923	2164
ENSMUSG00000028439	chr4	Fam219a	41517691	41520395	3724	-0.25541	5.247391	0.101151	0.174979	0.027499	0	555	545	1047	478	727	478	758	584	842	529
ENSMUSG00000051980	chr16	Casr	36493696	36495974	4718	-0.46344	2.746676	0.10124	0.175109	0.084465	0	103	86	285	87	84	66	158	97	76	110
ENSMUSG00000037921	chr8	Ddx60	61928087	61928276	6931	-0.65044	0.286112	0.101311	0.175198	0.118752	0	21	14	37	8	33	9	18	19	8	23
ENSMUSG00000085348	chr11	Gm12300	67211256	67211846	2027	-0.36049	6.321515	0.101317	0.175198	0.057091	0	1112	1648	2047	1172	991	1150	1424	1056	1517	1201
ENSMUSG00000075279	chr2	Mrpl23-ps1	74591330	74591909	580	0.3548	3.285094	0.101405	0.175326	0.046928	0	140	130	139	126	117	183	274	158	248	136
ENSMUSG00000024831	chr19	Ighmbp2	3260924	3261635	4101	-0.3238	2.274828	0.101418	0.175327	0.032824	0	83	56	106	76	104	61	106	64	84	71
ENSMUSG00000020775	chr11	Mrpl38	1.16E+08	1.16E+08	2550	0.25746	5.615146	0.101452	0.175363	0.028282	0	571	437	839	868	895	756	1088	933	1363	778
ENSMUSG00000037300	chr8	Ttc13	1.25E+08	1.25E+08	10190	0.233533	4.350126	0.101634	0.175655	0.021367	0	277	194	436	294	315	342	457	375	487	341
ENSMUSG00000002413	chr6	Braf	39603237	39610404	13862	-0.29087	3.103639	0.101773	0.175872	0.028757	0	104	100	252	142	177	110	165	137	151	133
ENSMUSG00000074802	chr10	Gas2l3	89408823	89414492	6748	0.584112	0.200366	0.101914	0.176092	0.098013	0	6	4	19	22	17	13	26	33	29	13
ENSMUSG00000037791	chr11	Phf12	77982754	77983377	4909	-0.25493	3.88099	0.102286	0.176712	0.024515	0	202	153	390	260	310	169	289	271	297	203
ENSMUSG00000029703	chr5	Lrwd1	1.36E+08	1.36E+08	6650	0.290603	2.754439	0.102392	0.176848	0.027976	0	87	61	124	92	120	113	163	138	152	102
ENSMUSG00000094410	chr1	Zbed6	1.34E+08	1.34E+08	10156	-0.27091	7.066517	0.102384	0.176848	0.032438	0	2144	1626	4152	1665	2533	1757	2728	2049	2739	1893
ENSMUSG00000091580	chr16	Gm6467	21896506	21896931	609	0.468043	1.183462	0.10263	0.177237	0.058665	0	29	28	47	21	19	33	57	44	66	32
ENSMUSG00000053929	chr15	Cyhr1	76643395	76646574	6210	-0.24031	6.761153	0.102699	0.177333	0.025398	0	1700	1258	2333	1937	2235	1581	2052	1728	2319	1423
ENSMUSG00000019929	chr10	Dcn	97479500	97479789	2084	-0.27099	9.179575	0.102828	0.177532	0.032918	0	6646	7780	16199	8940	12777	7654	10155	10126	10701	8970
ENSMUSG00000027318	chr2	Adam33	1.31E+08	1.31E+08	5394	0.459983	2.053835	0.102937	0.177698	0.078003	0	59	48	78	27	60	100	72	96	77	68
ENSMUSG00000022680	chr16	Pdxdc1	13833148	13834846	7973	-0.23609	5.798555	0.102956	0.177707	0.02398	0	713	656	1261	1114	1137	723	1140	882	1172	783
ENSMUSG00000028268	chr3	Gbp3	1.43E+08	1.43E+08	3239	0.443855	2.380729	0.102969	0.177707	0.07504	0	56	46	72	75	98	79	176	140	62	79
ENSMUSG00000049305	chr9	Ccdc71	1.08E+08	1.08E+08	3267	0.23938	4.063617	0.102985	0.177712	0.021542	0	207	176	298	258	285	247	426	315	410	264
ENSMUSG00000007379	chr3	Dennd2c	1.03E+08	1.03E+08	6858	0.375495	3.165145	0.103032	0.177746	0.056228	0	125	89	202	65	151	134	201	128	222	223
ENSMUSG00000032952	chr3	Ap4b1	1.04E+08	1.04E+08	2907	-0.24805	4.007987	0.103029	0.177746	0.02359	0	261	176	346	276	345	226	343	234	288	243
ENSMUSG00000028576	chr4	Ift74	94614491	94614651	2656	-0.34105	2.891495	0.103061	0.177774	0.044531	0	125	118	166	117	119	119	172	88	122	90
ENSMUSG00000034274	chr11	Thoc5	4895320	4895378	2861	0.248595	4.13537	0.103103	0.177819	0.023743	0	235	208	344	232	255	308	396	312	429	286
ENSMUSG00000034463	chr14	Scara3	65919395	65921188	3405	0.248349	4.028652	0.103114	0.177819	0.023997	0	181	181	381	216	252	248	373	352	367	269
ENSMUSG00000023262	chr9	Acy1	1.06E+08	1.06E+08	2966	0.35895	2.683385	0.103276	0.178028	0.047943	0	53	59	110	118	109	73	157	154	158	113
ENSMUSG00000025227	chr19	Tmem180	46341121	46341170	2804	0.410786	1.078761	0.10326	0.178028	0.040779	0	32	16	37	25	28	34	54	35	55	32
ENSMUSG00000050856	chr5	Atp5k	1.08E+08	1.08E+08	616	0.307662	7.767402	0.10327	0.178028	0.042327	0	2643	1953	2842	4282	3735	3428	5804	3850	5953	3380
ENSMUSG00000026586	chr1	Prrx1	1.63E+08	1.63E+08	11066	-0.33178	5.822372	0.103345	0.178123	0.048384	0	555	558	1368	1347	1411	555	1258	791	1081	947
ENSMUSG00000076609	chr6	Igkc	70726435	70726757	323	0.914768	1.405754	0.103396	0.178188	0.336089	0	64	11	53	7	4	56	53	91	80	22
ENSMUSG00000038398	chr8	Upf3a	13785615	13785884	1402	0.275517	3.629739	0.103418	0.178203	0.028187	0	168	146	214	158	195	172	257	264	306	228
ENSMUSG00000031536	chr8	Polb	22628119	22628369	1227	-0.25514	5.63396	0.103538	0.178364	0.028405	0	722	769	958	888	894	636	1102	724	1034	686
ENSMUSG00000039782	chr5	Cpeb2	43233463	43235088	7122	-0.34804	4.772818	0.103534	0.178364	0.052289	0	353	288	937	363	656	216	558	363	740	396
ENSMUSG00000028642	chr4	4930538K18Rik	1.19E+08	1.19E+08	1452	-0.41352	1.164581	0.103556	0.178371	0.045645	0	32	23	61	36	49	32	35	26	54	22
ENSMUSG00000054793	chr7	Cadm4	24482023	24482162	2161	-0.42694	1.29423	0.103766	0.17871	0.056545	0	32	26	56	55	50	16	56	30	47	38
ENSMUSG00000024576	chr18	Csnk1a1	61555274	61555873	10502	-0.25429	7.709619	0.103907	0.17893	0.029018	0	3243	3004	5279	2968	3793	2676	4265	2980	4742	2995
ENSMUSG00000024065	chr17	Ehd3	73804841	73805469	3658	0.336048	2.880133	0.104051	0.179154	0.041588	0	81	81	163	86	111	139	221	136	170	83
ENSMUSG00000004099	chr9	Dnmt1	20907206	20907561	6304	0.292241	3.436806	0.104096	0.179208	0.034216	0	116	78	238	156	217	154	230	216	256	219
ENSMUSG00000031963	chr9	Bmper	23223076	23223773	3793	0.343659	3.226868	0.104123	0.179233	0.046914	0	92	102	241	90	152	214	210	156	206	145
ENSMUSG00000013236	chr17	Ptprs	56412431	56413393	6970	0.326917	4.93603	0.104188	0.179321	0.046841	0	283	184	681	497	654	395	861	512	771	613
ENSMUSG00000026568	chr1	Mpc2	1.65E+08	1.65E+08	7344	-0.29325	7.450461	0.10425	0.179404	0.038693	0	2565	2146	3172	3862	3557	2063	4210	2249	4017	2233
ENSMUSG00000062929	chr12	Cfl2	54858817	54861237	2940	-0.25973	8.665832	0.104278	0.179429	0.030485	0	5968	5844	9568	6640	7357	4600	8681	5549	9299	6251
ENSMUSG00000035629	chr16	1700021K19Rik	32821703	32824146	7478	-0.23749	5.109698	0.104307	0.179456	0.023553	0	488	359	975	601	663	459	673	522	728	517
ENSMUSG00000024424	chr18	Ttc39c	12599926	12600003	5197	0.3467	1.67177	0.104334	0.179478	0.033418	0	34	28	60	45	53	52	66	70	78	48
ENSMUSG00000034160	chrX	Ogt	1.02E+08	1.02E+08	8045	-0.25966	6.845307	0.104554	0.179834	0.030088	0	1825	1537	3199	1437	2209	1456	2284	1945	2197	1690
ENSMUSG00000059323	chr15	Tonsl	76622088	76622350	5815	0.258983	5.891199	0.10461	0.179906	0.029173	0	820	733	1046	759	900	1037	1538	962	1479	931
ENSMUSG00000047153	chr14	Khnyn	55884969	55885142	3876	-0.36538	2.829571	0.104655	0.179961	0.050711	0	84	67	183	137	187	72	198	100	110	92
ENSMUSG00000041671	chr6	Pyroxd1	1.42E+08	1.42E+08	4933	-0.28461	3.573017	0.10473	0.180067	0.031825	0	204	172	297	159	205	178	253	160	239	148
ENSMUSG00000025630	chrX	Hprt	52988137	52988250	1289	0.273341	4.935558	0.104799	0.180162	0.031209	0	428	412	508	400	401	464	754	605	744	504
ENSMUSG00000024897	chr19	Apba1	23758876	23759091	6632	0.455357	1.292273	0.104903	0.180293	0.073331	0	21	17	70	30	28	32	42	57	56	56
ENSMUSG00000101304	chr9	Plet1os	50488795	50489487	1245	-0.35444	3.065928	0.104892	0.180293	0.049979	0	98	140	169	180	144	102	208	104	126	128
ENSMUSG00000026034	chr1	Clk1	58410189	58412340	8132	0.295488	4.838005	0.104919	0.180298	0.036923	0	432	352	516	371	332	510	772	585	595	412
ENSMUSG00000024425	chr18	Ndfip1	38418975	38419176	930	-0.22505	5.246511	0.105204	0.180764	0.021526	0	563	482	893	593	771	447	788	636	760	581
ENSMUSG00000001366	chr9	Fbxo9	78081499	78082088	3103	-0.23454	5.38772	0.10523	0.180785	0.023755	0	613	553	1003	743	717	534	982	612	819	601
ENSMUSG00000056592	chr7	Zfp658	43562256	43562421	3495	0.618701	-0.19551	0.105278	0.180845	0.113192	0	2	6	28	5	10	15	19	18	19	12
ENSMUSG00000051721	chr12	BC068281	4843303	4843451	3131	-0.47944	1.666918	0.10535	0.180921	0.080635	0	34	26	95	62	85	25	61	73	42	34
ENSMUSG00000103651	chr19	RP24-245M20.4	4762103	4765171	3069	-0.69738	-0.27209	0.105346	0.180921	0.116992	0	15	4	30	8	18	5	16	16	7	6
ENSMUSG00000000579	chr17	Dynlt1c	6601671	6601836	3777	0.550559	0.757607	0.105489	0.181138	0.082382	0	19	20	23	13	26	37	51	16	47	22
ENSMUSG00000025172	chr19	Ankrd2	42036038	42036122	1100	-1.30592	4.95108	0.105543	0.181183	0.728143	0	40	33	175	2152	1235	85	624	60	805	235
ENSMUSG00000033965	chrX	Slc16a2	1.04E+08	1.04E+08	4244	0.341806	2.949818	0.105538	0.181183	0.045983	0	63	56	156	124	162	93	211	149	189	147

ENSMUSG00000024188	chr17	Luc7l	26252910	26253091	7509	0.270606	3.794098	0.105572	0.181209	0.028856	0	178	159	300	159	212	245	293	301	280	237
ENSMUSG00000032415	chr9	Ube2cbp	86307306	86307876	1790	0.402144	1.636615	0.105588	0.181213	0.049246	0	34	40	54	35	42	56	77	70	50	54
ENSMUSG00000025086	chr19	Trub1	57452906	57453196	6395	-0.29944	2.535218	0.10561	0.181227	0.030297	0	70	75	153	92	125	67	117	94	112	80
ENSMUSG00000022545	chr16	Ercc4	13109684	13110141	6730	-0.29968	2.718668	0.106016	0.181883	0.031936	0	90	79	166	108	142	66	129	90	155	100
ENSMUSG00000087497	chr11	2810001G20Rik	64079484	64079777	1057	0.465791	0.716022	0.10602	0.181883	0.049091	0	23	15	19	24	20	28	39	31	40	24
ENSMUSG00000011267	chr7	Zfp296	19577287	19577628	1530	0.639012	-0.00647	0.106294	0.182295	0.111433	0	14	9	17	5	10	17	14	33	24	9
ENSMUSG00000044285	chr14	Gm1821	46084126	46084815	690	-0.81735	4.072492	0.106301	0.182295	0.295616	0	485	504	149	232	99	233	399	309	114	63
ENSMUSG00000061130	chr17	Ppm1b	84956741	84956887	4971	-0.2823	7.087747	0.106284	0.182295	0.036107	0	1781	1338	3052	2873	3227	1455	2910	1899	3240	1973
ENSMUSG00000050379	chrX	Sept6	36911326	36913254	9882	0.358007	1.796807	0.106517	0.182641	0.039227	0	45	33	58	41	60	58	70	79	69	64
ENSMUSG00000024487	chr18	Yipf5	40204865	40206400	2329	0.260935	3.526153	0.106585	0.182735	0.024757	0	132	139	222	160	179	178	298	194	266	206
ENSMUSG00000035042	chr11	Ccl5	83525778	83526064	960	0.792338	0.020416	0.106736	0.182946	0.237013	0	4	0	14	20	18	31	14	27	16	11
ENSMUSG00000097290	chr16	1300002E11Rik	21794347	21794446	3955	0.342288	2.36151	0.106722	0.182946	0.039593	0	75	51	73	69	83	79	139	108	99	88
ENSMUSG00000009647	chr10	Mcu	59446984	59448858	6936	0.244824	5.26443	0.106764	0.18297	0.025885	0	416	409	851	574	616	619	996	589	1075	590
ENSMUSG00000042520	chr3	Ubap2l	89999589	90000253	5446	-0.24915	6.087712	0.106789	0.18299	0.02754	0	916	702	2003	1114	1432	852	1327	1112	1469	959
ENSMUSG00000091985	chr4	Gm17354	1.09E+08	1.09E+08	3039	-0.31926	2.354511	0.106826	0.18303	0.033876	0	78	63	128	87	95	73	85	69	121	62
ENSMUSG00000034121	chr11	Mks1	87853215	87853329	4044	-0.41964	1.000358	0.106864	0.183071	0.045111	0	31	25	55	34	31	23	37	33	25	29
ENSMUSG00000074781	chr10	Ube2n	95515162	95515237	3851	0.237329	5.748163	0.106917	0.183138	0.024604	0	750	610	1060	660	868	883	1346	927	1384	823
ENSMUSG00000061758	chr6	Akr1b10	34384218	34384407	3535	-0.27486	5.746572	0.106998	0.183254	0.033556	0	785	510	1129	1177	1181	731	1193	668	1049	819
ENSMUSG00000066152	chr4	Slc31a2	62262562	62262623	2033	-0.28659	3.125112	0.107026	0.183278	0.029321	0	135	102	240	131	168	135	143	147	164	114
ENSMUSG00000004631	chr6	Sgce	4674350	4674632	3086	0.300774	3.504427	0.107086	0.183316	0.035039	0	147	137	216	135	168	173	281	284	210	180
ENSMUSG00000079509	chrX	Zfx	94074631	94079979	7755	-0.29382	4.056504	0.10709	0.183316	0.035299	0	198	177	543	259	361	169	326	273	309	285
ENSMUSG00000093470	chr11	Gm20645	23736847	23740357	3511	0.352193	1.973747	0.107075	0.183316	0.039704	0	57	39	76	45	52	64	111	67	78	71
ENSMUSG00000026662	chr2	Sephs1	4881564	4881860	5925	-0.22737	4.669479	0.107108	0.183323	0.021351	0	351	320	661	396	505	314	506	398	544	387
ENSMUSG00000011263	chr7	Exoc3l2	19489056	19489174	2201	0.423403	1.169416	0.107165	0.183398	0.046504	0	23	26	38	33	25	33	48	43	70	32
ENSMUSG00000039942	chr15	Ptger4	5206661	5209784	6648	0.468646	1.320957	0.107278	0.183567	0.071197	0	22	23	57	30	32	34	97	54	47	27
ENSMUSG00000041506	chr9	Rrp9	1.06E+08	1.06E+08	2788	-0.24557	3.9386	0.107392	0.183738	0.024246	0	229	197	324	250	329	187	308	266	352	181
ENSMUSG00000097239	chr11	Gm27029	1.01E+08	1.01E+08	2079	0.255843	6.694406	0.107525	0.183942	0.02956	0	1607	1085	1730	1397	1655	1828	2461	1763	2495	1745
ENSMUSG00000046329	chr17	Slc25a23	57043711	57045663	5294	0.278979	4.205597	0.107636	0.184109	0.032899	0	218	133	345	309	360	243	509	323	416	365
ENSMUSG00000035150	chrX	Eif2s3x	94188707	94190922	3812	-0.30818	5.36887	0.107664	0.184133	0.042357	0	606	486	1096	709	841	374	1133	647	563	695
ENSMUSG00000039740	chr4	Alg2	47465067	47465418	3450	0.268354	4.250601	0.107776	0.1843	0.03022	0	242	160	394	269	346	236	538	391	370	368
ENSMUSG00000036305	chr15	Rpl39-ps	1.03E+08	1.03E+08	355	0.386537	1.847598	0.107807	0.184329	0.047655	0	54	39	60	41	45	74	94	56	86	51
ENSMUSG00000015467	chr17	Egfl8	34613349	34613581	1761	-0.51068	0.401407	0.107904	0.184472	0.071276	0	22	15	26	31	20	9	27	14	18	24
ENSMUSG00000022237	chr15	Ankrd33b	31291479	31297984	8706	-0.43632	4.997509	0.108032	0.184667	0.085329	0	227	229	980	834	892	438	583	326	654	475
ENSMUSG00000028996	chr4	Rbp7	1.49E+08	1.49E+08	718	0.508442	1.135298	0.108092	0.184745	0.080046	0	34	27	27	21	24	41	40	63	45	31
ENSMUSG00000039263	chr2	Npepl1	1.74E+08	1.74E+08	2998	-0.23997	6.688774	0.108176	0.184866	0.026176	0	1554	1367	2131	1866	1974	1463	1980	1633	2275	1338
ENSMUSG00000036880	chr18	Acaa2	74779197	74779265	1515	-0.59393	7.090709	0.10826	0.184962	0.161324	0	931	905	1785	5791	4020	1309	3011	1455	2793	1673
ENSMUSG00000070423	chr7	Olfr558	1.03E+08	1.03E+08	2915	-0.40358	1.789604	0.108254	0.184962	0.058692	0	32	55	79	61	82	25	75	49	75	47
ENSMUSG00000047412	chr9	Zbtb44	31030644	31030958	8857	-0.24285	5.460931	0.108307	0.185017	0.02598	0	694	482	1224	744	765	561	870	660	1068	580
ENSMUSG00000027698	chr3	Nceh1	27182965	27183215	5253	-0.61081	4.218876	0.10834	0.18505	0.167166	0	152	75	250	718	675	203	368	233	331	222
ENSMUSG00000032965	chr16	Ift57	49699233	49699549	2862	0.344675	2.408132	0.108373	0.185082	0.040111	0	66	69	102	50	78	87	144	101	116	85
ENSMUSG00000023939	chr17	Mrpl14	45686322	45686427	949	0.328844	5.626041	0.108494	0.185217	0.048591	0	651	471	550	939	806	869	1354	794	1392	700
ENSMUSG00000025357	chr10	Dgka	1.29E+08	1.29E+08	2808	0.251673	3.659283	0.10847	0.185217	0.024443	0	137	133	275	188	199	205	340	238	264	202
ENSMUSG00000097162	chr7	2310010J17Rik	90124858	90125032	451	0.387821	1.47998	0.108488	0.185217	0.046287	0	35	26	44	35	46	51	45	61	59	55
ENSMUSG00000097073	chr9	9430037G07Rik	88595325	88598247	3767	-0.65103	-0.0124	0.108524	0.185246	0.10431	0	7	10	19	21	32	17	13	13	14	5
ENSMUSG00000033918	chr16	Parl	20279820	20280085	3892	0.257169	5.04154	0.108584	0.185323	0.02848	0	400	355	569	580	476	541	806	544	915	505
ENSMUSG00000004897	chr3	Hdgf	87906321	87906714	2873	0.260834	8.482449	0.108609	0.185342	0.03143	0	5086	4346	6630	4657	4972	5708	7957	6549	9790	5898
ENSMUSG00000024384	chr18	Iws1	32067734	32068039	9623	-0.23568	4.546066	0.108631	0.185356	0.023053	0	272	285	576	398	536	295	482	369	502	325
ENSMUSG00000044646	chr18	Zbtb7c	75820178	75820365	4729	0.584243	0.763263	0.108723	0.185489	0.125314	0	3	12	28	30	32	26	43	20	40	43
ENSMUSG00000014039	chr16	Prdm15	97791467	97794656	10547	-0.32204	2.738844	0.108834	0.185655	0.036656	0	96	75	200	109	123	90	129	118	94	97
ENSMUSG00000031389	chrX	Arhgap4	73891442	73894963	8105	0.246692	4.217756	0.108899	0.185742	0.024348	0	266	188	303	275	317	295	479	313	482	289
ENSMUSG00000025129	chr11	Ppp1r27	1.21E+08	1.21E+08	771	0.410432	6.140191	0.108917	0.185749	0.076896	0	1148	761	916	935	904	960	2502	1325	2395	608
ENSMUSG00000027221	chr2	Chst1	92599707	92600148	2680	0.862988	2.754515	0.109127	0.186059	0.321809	0	113	101	68	23	36	134	74	394	81	65
ENSMUSG00000032329	chr9	Hmg20a	56418644	56418931	3691	-0.22648	4.253942	0.10912	0.186059	0.02086	0	280	250	461	298	365	239	423	288	386	278
ENSMUSG00000016528	chr1	Mapkapk2	1.31E+08	1.31E+08	3041	-0.29721	7.929692	0.109262	0.186264	0.040949	0	3264	2291	5167	5886	5351	2841	4921	3257	5884	3481
ENSMUSG00000015127	chr17	Unkl	25188397	25188492	5673	-0.40635	1.398499	0.109323	0.186345	0.04883	0	36	38	81	29	53	32	37	41	51	37
ENSMUSG00000025178	chr19	Pi4k2a	42090435	42090936	3771	0.231978	4.578318	0.109413	0.186474	0.022848	0	272	218	521	371	417	406	493	438	613	396
ENSMUSG00000028914	chr4	Casp9	1.42E+08	1.42E+08	5197	0.340181	2.440518	0.109642	0.186842	0.044759	0	66	35	122	69	99	83	105	113	117	117
ENSMUSG00000055745	chr15	Ldoc1l	84553398	84557823	4426	-0.2704	3.289457	0.10972	0.18695	0.027409	0	143	103	250	158	217	107	182	151	224	147
ENSMUSG00000029311	chr5	Hsd17b11	1.04E+08	1.04E+08	3265	0.273901	3.598547	0.109884	0.187206	0.030494	0	143	105	231	167	245	185	262	290	245	209
ENSMUSG00000032527	chr9	Pccb	1.01E+08	1.01E+08	2771	-0.23735	6.666777	0.11021	0.187736	0.025831	0	1409	1130	2201	2018	2156	1326	2125	1598	2099	1434
ENSMUSG00000036655	chr12	Colec11	28594173	28595048	1383	0.664605	-0.0333	0.110323	0.187904	0.109978	0	19	10	11	6	5	10	25	23	26	14
ENSMUSG00000031578	chr8	Mak16	31159468	31160577	1857	-0.26055	3.596757	0.11034	0.187909	0.026828	0	196	169	258	187	231	170	252	205	199	167
ENSMUSG00000036940	chr4	Kdm1a	1.37E+08	1.37E+08	5179	0.232879	4.75928	0.110377	0.187949	0.022914	0	331	288	496	431	446	442	641	439	708	453
ENSMUSG00000000881	chrX	Dlg3	1.01E+08	1.01E+08	5844	0.467985	1.667105	0.110405	0.187972	0.080701	0	25	30	68	48	39	31	78	106	59	51
ENSMUSG00000027438	chr2	Napb	1.49E+08	1.49E+08	7051	0.293201	3.428403	0.110541	0.188155	0.033859	0	150	125	224	101	171	165	257	187	246	215

ENSMUSG00000037787	chr12	Apopt1	1.12E+08	1.12E+08	3945	0.23856	5.092877	0.110529	0.188155	0.0246	0	505	378	592	450	554	584	824	609	807	548
ENSMUSG00000016496	chr19	Cd274	29367455	29367506	3622	-0.42904	1.866136	0.110706	0.188412	0.070829	0	40	62	77	56	91	35	99	65	44	38
ENSMUSG00000042462	chr7	Dctpp1	1.27E+08	1.27E+08	676	0.270762	3.991975	0.110791	0.188533	0.029297	0	230	198	246	213	233	256	382	322	384	242
ENSMUSG00000078765	chr7	U2af1l4	30563301	30563349	3804	0.236595	4.858769	0.111044	0.188938	0.02384	0	402	316	486	442	461	479	672	544	716	457
ENSMUSG00000091989	chr7	Gm17257	80507787	80508254	468	0.552886	0.187574	0.111138	0.189075	0.070639	0	18	4	13	18	13	17	30	21	28	16
ENSMUSG00000022747	chr16	St3gal6	58468125	58470727	6080	-0.25633	7.327512	0.111187	0.189109	0.030659	0	2652	2182	4225	2343	2670	1880	3459	2383	3377	2439
ENSMUSG00000058318	chr2	Phf21a	92093117	92093153	8561	-0.23536	4.098682	0.111179	0.189109	0.022153	0	250	197	480	251	340	234	328	276	367	232
ENSMUSG00000040264	chr3	Gbp5	1.42E+08	1.42E+08	5844	-0.45946	1.686623	0.111514	0.189641	0.080607	0	31	56	77	45	83	21	75	66	48	35
ENSMUSG00000029433	chr5	Diablo	1.24E+08	1.24E+08	6155	0.250632	5.756942	0.11157	0.189712	0.028296	0	695	582	825	898	905	857	1429	915	1387	848
ENSMUSG00000023707	chr5	Ogfod2	1.24E+08	1.24E+08	2260	0.283239	4.020334	0.111629	0.189788	0.032859	0	237	187	225	216	275	234	351	325	472	255
ENSMUSG00000040997	chr14	Abhd4	54254129	54254471	2749	0.230803	4.730797	0.111774	0.19001	0.023207	0	300	237	556	415	494	421	591	525	592	471
ENSMUSG00000024975	chr19	Pdcd4	53892231	53892456	2556	0.255259	4.021486	0.111938	0.190265	0.026198	0	207	209	302	203	246	241	365	343	367	285
ENSMUSG00000034105	chr8	Tldc1	1.2E+08	1.2E+08	2574	-0.35146	2.032649	0.111995	0.190313	0.04443	0	49	47	97	79	94	40	106	49	82	52
ENSMUSG00000037916	chr19	Ndufv1	4007497	4007665	2521	-0.34501	8.422374	0.111992	0.190313	0.056131	0	4246	3210	6011	9244	8455	3945	7220	4386	8225	4531
ENSMUSG00000019927	chr10	Ube2d1	71254980	71255874	4371	0.322998	7.945079	0.112094	0.190456	0.049076	0	3749	3393	4851	2125	3008	3864	5890	4854	6673	4004
ENSMUSG00000038457	chr8	Tmem255b	13435459	13435667	1224	0.450548	1.418086	0.112141	0.190511	0.070226	0	21	21	28	52	51	39	80	56	55	42
ENSMUSG00000031482	chr8	Slc25a15	22375554	22377981	3451	-0.28722	4.101667	0.112333	0.190813	0.035126	0	239	144	381	373	410	212	361	221	371	257
ENSMUSG00000022681	chr16	Ntan1	13819251	13819436	2174	0.243648	4.620961	0.112396	0.190896	0.025315	0	320	257	483	360	388	401	735	382	579	371
ENSMUSG00000039908	chr11	Slc26a11	1.19E+08	1.19E+08	3610	0.372946	2.407782	0.112502	0.191052	0.053618	0	78	56	106	35	91	90	133	86	121	104
ENSMUSG00000029125	chr5	Stx18	38038742	38039499	4194	0.243133	3.821258	0.112584	0.191167	0.022811	0	181	166	259	202	216	230	354	246	339	228
ENSMUSG00000021285	chr12	Ppp1r13b	1.12E+08	1.12E+08	4658	-0.28779	3.282392	0.11264	0.191237	0.0315	0	149	99	214	190	208	134	153	150	186	160
ENSMUSG00000001444	chr11	Tbx21	97098071	97099378	2488	-0.58538	-0.01542	0.112724	0.191356	0.074173	0	15	9	19	19	24	10	10	11	12	20
ENSMUSG00000026768	chr2	Itga8	12106632	12109201	7368	-0.51964	1.096765	0.112752	0.191379	0.08992	0	29	23	66	42	38	10	29	39	30	43
ENSMUSG00000029250	chr5	Polr2b	77310147	77310630	4667	-0.23275	5.72065	0.112816	0.191463	0.024613	0	741	653	1366	870	1009	690	1282	741	956	792
ENSMUSG00000021595	chr13	Nsun2	69533746	69533910	5737	-0.22544	5.624467	0.11286	0.191512	0.023011	0	679	634	1068	908	977	698	990	712	1082	692
ENSMUSG00000042595	chrX	Fam199x	1.37E+08	1.37E+08	8299	-0.36821	2.663686	0.112929	0.191606	0.053743	0	84	74	211	88	131	44	114	108	148	94
ENSMUSG00000025810	chr8	Nrp1	1.28E+08	1.28E+08	5907	-0.3722	5.077899	0.112981	0.191643	0.063658	0	293	290	817	818	986	320	675	643	575	487
ENSMUSG00000030732	chr7	Chrdl2	1E+08	1E+08	1728	-0.745	-0.41355	0.112981	0.191643	0.137355	0	9	5	9	17	26	14	6	7	6	9
ENSMUSG00000086040	chr6	Wipf3	54429603	54429860	7114	-0.35602	4.275118	0.112995	0.191643	0.056821	0	214	190	466	415	514	211	399	163	488	319
ENSMUSG00000002831	chr17	Plin4	56100591	56102330	5777	-0.31665	7.696973	0.113036	0.191689	0.047391	0	3396	2175	5813	3828	3693	2837	3444	4840	2938	2515
ENSMUSG00000050705	chr17	2310061I04Rik	35892677	35892966	2414	-0.27689	5.868483	0.113153	0.191862	0.035496	0	808	622	1113	1262	1364	779	1058	773	1472	802
ENSMUSG00000024104	chr6	Fam21	1.16E+08	1.16E+08	4294	-0.26156	5.119768	0.113216	0.191936	0.030869	0	597	480	974	429	577	473	727	548	655	486
ENSMUSG00000024870	chr19	Rab1b	5099207	5100572	1835	0.240609	7.090597	0.113225	0.191936	0.027142	0	1739	1371	2372	2254	2276	2122	3026	2603	3505	2290
ENSMUSG00000047409	chr9	Ctdspl	1.19E+08	1.19E+08	5190	0.409892	2.908455	0.11325	0.191954	0.070562	0	93	84	130	85	115	95	118	247	133	158
ENSMUSG00000092868	chr15	Mir5113	80940039	80940120	82	0.349331	1.741114	0.1134	0.192182	0.035283	0	42	33	60	47	46	45	84	59	96	52
ENSMUSG00000019777	chr10	Hdac2	36974544	36974803	4474	0.256884	6.060072	0.113419	0.19219	0.030366	0	948	806	1229	801	1029	1083	1831	1069	1631	1095
ENSMUSG00000020523	chr11	Fam114a2	57482993	57484140	3075	-0.22983	6.088153	0.113469	0.192235	0.02438	0	1013	886	1546	1134	1317	961	1511	1028	1309	936
ENSMUSG00000021832	chr14	Psmc6	45329824	45329932	1564	-0.28196	6.725975	0.113474	0.192235	0.037503	0	1688	1822	2466	1451	1672	1409	2437	1538	2105	1354
ENSMUSG00000020847	chr11	Rph3al	75830999	75832214	3814	-0.26579	3.520904	0.113498	0.19225	0.028795	0	145	132	246	243	241	127	246	180	246	160
ENSMUSG00000026790	chr2	Odf2	29889221	29889278	9919	0.267695	3.158767	0.113569	0.192347	0.027662	0	97	89	210	125	136	163	201	154	198	158
ENSMUSG00000001089	chr4	Luzp1	1.36E+08	1.36E+08	8112	-0.34362	3.979091	0.113726	0.192587	0.051676	0	163	121	380	357	456	168	305	265	314	222
ENSMUSG00000033096	chr2	Apmap	1.51E+08	1.51E+08	2428	0.231489	5.047707	0.113894	0.192825	0.023567	0	437	375	633	462	520	564	792	687	701	502
ENSMUSG00000039585	chr9	Myo9a	59750896	59751345	13034	-0.27766	3.94724	0.113895	0.192825	0.03205	0	228	161	526	220	275	213	312	250	280	211
ENSMUSG00000029110	chr5	Rnf4	34336289	34336541	7287	0.226023	4.568594	0.114002	0.192957	0.021637	0	314	249	488	318	394	316	573	501	558	399
ENSMUSG00000031628	chr8	Casp3	46617449	46617496	1455	0.515538	0.306913	0.113998	0.192957	0.062463	0	12	12	23	17	10	12	30	32	26	21
ENSMUSG00000046556	chr8	Zfp319	95326137	95329812	4106	-0.31071	2.465625	0.114208	0.19328	0.033474	0	75	59	153	86	124	56	106	86	112	86
ENSMUSG00000004054	chr19	Map3k11	5689131	5689266	3801	0.28106	3.941604	0.114372	0.193509	0.0342	0	163	117	284	282	285	206	323	322	396	288
ENSMUSG00000021385	chr13	Ippk	49421311	49421466	2776	-0.28655	2.833655	0.114358	0.193509	0.032051	0	107	102	159	108	143	83	145	94	175	93
ENSMUSG00000025646	chr9	Atrip	1.09E+08	1.09E+08	6725	0.240436	4.754116	0.114577	0.19383	0.025153	0	370	289	555	370	400	445	741	415	674	422
ENSMUSG00000012848	chr7	Rps5	12922290	12922388	1734	0.271352	8.244445	0.114868	0.194249	0.035186	0	4335	3875	5038	4125	4042	5265	7916	5532	7318	4518
ENSMUSG00000022994	chr15	Adcy6	98589994	98592475	6017	0.249567	5.029217	0.114851	0.194249	0.028151	0	374	295	604	507	651	420	687	695	843	604
ENSMUSG00000067928	chr17	Zfp760	21707741	21707893	4209	0.465806	0.702593	0.11486	0.194249	0.070519	0	15	12	35	17	26	20	24	40	33	40
ENSMUSG00000000942	chr6	Hoxa4	52189671	52190688	1594	0.381502	1.662811	0.115054	0.194538	0.04474	0	36	42	52	40	39	44	72	69	89	45
ENSMUSG00000040888	chr17	Gfer	24693191	24694442	1775	-0.27694	4.663173	0.115126	0.194635	0.03484	0	518	358	562	332	406	322	505	387	530	357
ENSMUSG00000017478	chr8	Zc3h18	1.22E+08	1.22E+08	9190	-0.22199	4.753067	0.115251	0.194823	0.021245	0	391	285	700	440	568	351	546	454	552	377
ENSMUSG00000097835	chr18	Gm26910	67773712	67773954	698	-0.49953	0.358622	0.115494	0.195208	0.056253	0	19	13	40	24	17	17	26	13	18	15
ENSMUSG00000031723	chr8	Txnl4b	1.1E+08	1.1E+08	1892	0.272933	3.462278	0.115639	0.195428	0.02902	0	146	119	202	164	158	200	294	194	261	150
ENSMUSG00000041559	chr1	Fmod	1.34E+08	1.34E+08	3306	-0.69219	7.284385	0.115672	0.195459	0.227176	0	569	1181	4295	3730	7142	1519	2329	2398	816	3268
ENSMUSG00000041879	chr1	Ipo9	1.35E+08	1.35E+08	8233	-0.22267	4.982773	0.115716	0.19547	0.021795	0	445	337	879	523	625	410	664	510	630	460
ENSMUSG00000051234	chr9	Rnf7	96470937	96471852	1328	0.241802	6.627464	0.115694	0.19547	0.027544	0	1410	1081	1707	1335	1673	1627	2563	1650	2526	1535
ENSMUSG00000078552	chr4	Dcdc2b	1.3E+08	1.3E+08	1371	0.506047	0.21192	0.115723	0.19547	0.069292	0	11	7	22	11	20	25	25	24	14	21
ENSMUSG00000087117	chr11	Gm11523	96862997	96863571	1095	0.586385	-0.15914	0.115871	0.195696	0.080452	0	14	7	14	4	11	14	18	17	14	21
ENSMUSG00000024955	chr19	Esrra	6910977	6912010	2539	-0.34576	6.690555	0.116046	0.195967	0.057195	0	1456	829	1779	2731	2611	1279	1983	1307	2468	1409
ENSMUSG00000062619	chr17	2310039H08Rik	46772635	46773407	773	0.296848	3.988615	0.116077	0.195993	0.037215	0	244	198	221	216	215	257	379	252	435	278
ENSMUSG00000024767	chr19	Otub1	7198202	7199239	2545	0.227412	5.285903	0.116204	0.196136	0.023275	0	531	415	725	582	617	641	860	691	1057	613

ENSMUSG00000034120	chr11	Srsf2	1.17E+08	1.17E+08	2958	0.238913	6.159289	0.116195	0.196136	0.026675	0	897	868	1433	958	1080	1037	1673	1515	1700	1175
ENSMUSG00000058881	chr18	Zfp516	82910879	82910992	7817	-0.27375	4.265797	0.116206	0.196136	0.032679	0	237	213	604	284	422	198	415	275	389	325
ENSMUSG00000025393	chr10	Atp5b	1.28E+08	1.28E+08	4237	-0.32409	11.36376	0.116323	0.196284	0.050896	0	32676	24820	49430	67741	64139	30096	60170	34633	59992	34646
ENSMUSG00000035372	chr19	1810055G02Rik	3708333	3708436	1882	0.328316	2.655033	0.116311	0.196284	0.041682	0	66	54	119	94	116	78	214	121	144	90
ENSMUSG00000035203	chr7	Epn1	5080235	5080477	2807	-0.26145	7.347361	0.116346	0.196285	0.032806	0	2293	1771	3470	3442	3404	2107	2815	2407	4006	2321
ENSMUSG00000036835	chr7	Psenen	30561868	30562134	648	0.280054	5.632052	0.116353	0.196285	0.036317	0	696	692	783	610	678	890	1251	846	1270	741
ENSMUSG00000034168	chr12	Irf2bpl	86880703	86884814	4112	0.248252	5.12689	0.116396	0.196332	0.027827	0	430	399	612	479	629	444	939	576	837	703
ENSMUSG00000031539	chr8	Ap3m2	22787354	22789453	3467	0.293644	3.070208	0.116434	0.196347	0.034761	0	105	83	184	95	142	123	153	172	196	180
ENSMUSG00000039952	chr9	Dag1	1.08E+08	1.08E+08	6357	-0.27477	7.910952	0.116422	0.196347	0.036366	0	3236	2187	7716	4162	5012	2653	5223	3492	4943	3841
ENSMUSG00000020392	chr11	Cdkn2aipnl	51967661	51967957	1958	-0.28884	4.784444	0.116622	0.196639	0.038469	0	494	412	761	345	403	395	529	408	623	326
ENSMUSG00000027189	chr2	Trim44	1.02E+08	1.02E+08	5645	-0.23556	4.553246	0.116639	0.196642	0.02416	0	288	302	611	400	466	281	463	439	434	347
ENSMUSG00000026575	chr1	Nme7	1.64E+08	1.64E+08	5876	0.424972	0.959041	0.116717	0.196729	0.050364	0	30	16	26	24	28	24	43	47	46	32
ENSMUSG00000032392	chr9	Parp16	65214690	65214863	2483	-0.28883	2.783342	0.11672	0.196729	0.031	0	114	77	160	132	118	87	127	101	133	109
ENSMUSG00000022469	chr15	Rapgef3	97744770	97745666	6336	-0.29531	3.147959	0.11718	0.197478	0.033634	0	112	83	197	172	233	118	167	143	168	123
ENSMUSG00000039148	chr19	Sart1	5377523	5380135	5091	0.230601	4.994812	0.117233	0.197542	0.023707	0	392	371	564	480	524	525	652	596	820	539
ENSMUSG00000027559	chr3	Car3	14863512	14863605	2865	0.632126	10.70749	0.117276	0.197558	0.192179	0	28938	28490	22094	9193	5576	17786	48715	46487	40171	35125
ENSMUSG00000035296	chr14	Sgcg	61221059	61221776	1878	-0.27675	7.00347	0.117273	0.197558	0.036856	0	1705	1302	3160	2644	2762	1575	3111	1441	2627	2019
ENSMUSG00000056770	chr12	Setd3	1.08E+08	1.08E+08	6035	-0.2396	7.218172	0.117287	0.197558	0.027658	0	2365	2067	3509	2265	2681	2003	3003	2144	3382	2073
ENSMUSG00000038201	chr7	Kcna7	45405960	45407015	3494	-0.34514	7.735816	0.11758	0.198026	0.057794	0	2741	1642	4558	5405	5412	2071	4752	2679	4553	3461
ENSMUSG00000020893	chr11	Per1	69095217	69095303	5631	0.261047	4.962571	0.117637	0.198094	0.031589	0	295	336	742	411	554	589	659	695	653	462
ENSMUSG00000026696	chr1	Vamp4	1.63E+08	1.63E+08	4565	-0.2532	3.800665	0.117659	0.198094	0.026968	0	189	180	316	247	283	146	260	210	304	241
ENSMUSG00000034522	chr14	Zfp395	65358676	65358755	4229	0.23885	4.086949	0.117665	0.198094	0.024229	0	234	156	359	207	312	223	441	333	394	298
ENSMUSG00000030870	chr7	Ubfd1	1.22E+08	1.22E+08	9629	0.219658	4.999632	0.117834	0.198354	0.021619	0	411	337	719	435	496	526	773	582	780	494
ENSMUSG00000042549	chr11	Map2k3os	60920917	60921905	1291	0.490811	1.822574	0.117956	0.198534	0.097467	0	26	26	38	73	65	58	137	44	87	50
ENSMUSG00000014837	chr8	4931428F04Rik	1.05E+08	1.05E+08	3552	0.460007	0.691336	0.117979	0.198547	0.057535	0	19	14	16	24	27	30	28	35	39	25
ENSMUSG00000031432	chrX	Prps1	1.4E+08	1.4E+08	1993	0.245577	5.568544	0.118198	0.198866	0.027982	0	659	585	977	550	686	755	1259	929	1090	706
ENSMUSG00000073478	chr1	D730003I15Rik	1.91E+08	1.91E+08	1687	0.537669	0.511697	0.118186	0.198866	0.076583	0	17	19	27	6	16	19	30	31	42	21
ENSMUSG00000000402	chrX	Egfl6	1.67E+08	1.67E+08	2704	-0.75945	0.119186	0.118279	0.198977	0.193412	0	3	19	25	25	29	10	15	17	3	19
ENSMUSG00000025193	chr19	Cutc	43752996	43753220	1422	-0.23345	4.214573	0.118364	0.199094	0.023763	0	270	268	424	294	339	231	428	266	355	284
ENSMUSG00000056412	chr4	Gm12396	40775259	40775564	306	0.441827	2.198358	0.118424	0.19917	0.074814	0	74	64	60	47	44	98	114	68	104	83
ENSMUSG00000006471	chr2	Ndor1	25244821	25247854	5835	-0.29478	2.764998	0.118512	0.199267	0.031621	0	105	73	172	119	133	89	120	115	109	110
ENSMUSG00000073680	chr4	Tmem88b	1.56E+08	1.56E+08	3471	0.571467	0.661261	0.118497	0.199267	0.100943	0	26	18	17	11	19	17	36	19	50	40
ENSMUSG00000078126	chr14	Rpl23a-ps3	34170655	34171168	514	0.454453	0.920793	0.118685	0.199533	0.054921	0	26	23	24	15	30	24	48	39	50	29
ENSMUSG00000032577	chr9	Mapkapk3	1.07E+08	1.07E+08	5542	-0.24654	5.664713	0.118855	0.199794	0.028508	0	847	442	1415	847	1016	659	1021	752	1073	755
ENSMUSG00000009927	chr9	Rps25	44407714	44407757	683	0.291816	7.7991	0.118875	0.199803	0.041511	0	3222	3089	3732	2622	2831	4121	5835	3994	5371	3213
ENSMUSG00000040112	chr6	Mrps35	1.47E+08	1.47E+08	5543	0.284507	4.171679	0.118929	0.199843	0.036112	0	195	158	284	331	338	304	549	275	436	266
ENSMUSG00000071547	chr14	Nt5dc2	31134853	31134923	1407	0.637753	0.892531	0.118917	0.199843	0.172125	0	10	3	17	42	41	35	31	46	43	34
ENSMUSG00000022122	chr14	Ednrb	1.04E+08	1.04E+08	4037	-0.28163	3.264235	0.118979	0.199902	0.031282	0	113	108	257	149	240	125	193	172	180	118
ENSMUSG00000030801	chr7	Kat8	1.28E+08	1.28E+08	1573	0.232124	4.425024	0.1191	0.200078	0.023084	0	255	256	407	333	318	318	534	416	502	354
ENSMUSG00000040093	chr2	Bmf	1.19E+08	1.19E+08	5253	0.342832	2.234638	0.119175	0.20018	0.044193	0	53	41	102	46	93	73	147	92	99	65
ENSMUSG00000079168	chr8	Cd209g	4134733	4134787	1088	-0.83994	1.442293	0.119224	0.200237	0.306633	0	80	54	77	13	40	53	18	65	19	8
ENSMUSG00000040158	chr11	Tax1bp3	73177083	73177342	2989	0.337928	2.21735	0.119316	0.200341	0.040269	0	59	42	64	66	90	65	123	102	98	77
ENSMUSG00000049439	chr1	Cyp20a1	60343323	60343457	2286	0.289061	2.867034	0.119314	0.200341	0.034303	0	70	63	188	97	123	113	181	145	154	129
ENSMUSG00000003721	chr1	Insig2	1.21E+08	1.21E+08	3473	-0.22875	5.99456	0.119516	0.200651	0.024877	0	952	732	1440	1096	1357	866	1362	867	1357	949
ENSMUSG00000029836	chr6	Cbx3	51470360	51470431	3229	-0.24266	4.172566	0.11963	0.200816	0.025945	0	277	252	372	265	386	218	407	251	342	293
ENSMUSG00000040652	chr9	Oaz2	65668001	65668177	2990	0.247351	7.732589	0.119705	0.200917	0.029901	0	2806	2648	3724	2790	3403	3707	5082	3504	5631	3329
ENSMUSG00000041958	chr11	Pigs	78328415	78328508	2501	0.240029	4.626438	0.119752	0.200971	0.026118	0	362	222	500	328	421	446	478	448	617	425
ENSMUSG00000039108	chr2	Lsm14b	1.8E+08	1.8E+08	2892	-0.21179	5.628412	0.119841	0.201094	0.02101	0	715	602	1154	867	949	654	1015	803	1086	665
ENSMUSG00000042523	chr12	Dnal1	84114366	84114399	6938	-0.31333	2.886513	0.11996	0.201268	0.038267	0	106	65	221	122	163	95	153	93	131	122
ENSMUSG00000009733	chr15	Tfcp2	1.01E+08	1.01E+08	3250	-0.28413	3.219245	0.120044	0.201315	0.031692	0	150	79	254	165	190	128	171	148	169	139
ENSMUSG00000031154	chrX	Otud5	7841364	7841400	5200	0.22148	4.222407	0.120028	0.201315	0.020829	0	214	209	402	273	291	311	423	341	451	302
ENSMUSG00000041351	chr4	Rap1gap	1.38E+08	1.38E+08	6429	-0.5141	2.803701	0.120048	0.201315	0.117707	0	79	37	137	239	179	105	107	128	81	82
ENSMUSG00000051391	chr5	Ywhag	1.36E+08	1.36E+08	5500	-0.23239	8.291418	0.120021	0.201315	0.026576	0	4945	3621	8099	4710	6298	3955	6283	4940	7319	4212
ENSMUSG00000048142	chr5	Nat8l	33995984	33997210	6529	1.167357	1.655693	0.12013	0.201426	0.60103	0	68	37	4	11	7	51	16	208	40	52
ENSMUSG00000020010	chr10	Vnn3	23851462	23851796	1811	1.23234	-0.06606	0.120405	0.201863	0.573887	0	16	13	3	2	1	10	7	66	7	15
ENSMUSG00000056999	chr19	Ide	37268743	37270837	5823	-0.2415	6.914671	0.120593	0.202152	0.028448	0	1602	1293	3435	2123	2397	1395	2481	1835	2804	1752
ENSMUSG00000050786	chr6	Ccdc126	49319274	49319480	2421	-0.38553	1.226361	0.120663	0.202244	0.044149	0	40	21	66	39	42	21	39	37	46	35
ENSMUSG00000044139	chr7	Prss53	1.28E+08	1.28E+08	2134	0.382929	1.45813	0.120679	0.202245	0.048314	0	42	24	44	30	43	50	59	57	47	54
ENSMUSG00000032199	chr9	Polr2m	71478437	71479540	2424	-0.26893	7.446554	0.120944	0.202664	0.035612	0	2313	1678	3716	3892	4003	2183	3525	2460	3729	2673
ENSMUSG00000068917	chr3	Clk2	89164795	89165106	5299	0.242453	3.835658	0.121089	0.20288	0.024001	0	192	171	278	188	206	235	351	258	343	223
ENSMUSG00000031381	chrX	Piga	1.64E+08	1.64E+08	6379	0.447836	0.883261	0.121154	0.202965	0.061241	0	29	13	42	17	18	25	51	37	47	25
ENSMUSG00000014301	chr16	Pam16	4616464	4616633	857	0.296311	4.793628	0.121194	0.202999	0.040464	0	391	405	407	339	360	485	709	511	691	408
ENSMUSG00000068264	chr2	Ap5s1	1.31E+08	1.31E+08	1660	0.262445	3.775509	0.121205	0.202999	0.029727	0	175	113	218	233	259	224	302	237	348	244
ENSMUSG00000021725	chr13	Parp8	1.17E+08	1.17E+08	3088	-0.23917	3.855724	0.12124	0.203026	0.023948	0	199	153	369	246	316	184	324	194	311	209
ENSMUSG00000058638	chr7	Zfp110	12834761	12835164	4116	-0.23769	4.003401	0.121252	0.203026	0.02419	0	215	176	377	305	336	186	375	250	302	239

ENSMUSG00000072647	chr5	Adam1a	1.22E+08	1.22E+08	3120	0.498286	0.117069	0.121332	0.203134	0.062225	0	12	5	21	11	17	22	20	13	29	19
ENSMUSG00000067430	chr17	Zfp763	33016863	33019969	3557	-0.49537	1.284614	0.121423	0.203261	0.090913	0	44	13	72	45	54	17	65	27	34	37
ENSMUSG00000031355	chrX	Arhgap6	1.69E+08	1.69E+08	12128	-0.33092	2.349542	0.121607	0.203543	0.04039	0	55	64	162	80	102	59	89	90	98	69
ENSMUSG00000033849	chr1	B3galt2	1.44E+08	1.44E+08	9288	0.585752	2.247905	0.121727	0.203719	0.15232	0	78	52	35	67	46	70	67	192	73	90
ENSMUSG00000002010	chrX	Idh3g	73778963	73779171	2701	-0.29024	8.21413	0.1218	0.203763	0.0419	0	4038	2923	5682	7097	6748	3702	6785	3909	6798	3795
ENSMUSG00000032026	chr9	Rexo2	48468514	48468946	1075	0.267826	5.715409	0.121777	0.203763	0.034293	0	781	697	983	581	688	887	1332	997	1251	800
ENSMUSG00000036934	chr8	4921524J17Rik	85408759	85409890	1595	-0.27185	3.272656	0.121794	0.203763	0.030973	0	131	135	266	132	190	100	221	155	200	131
ENSMUSG00000030022	chr6	Adamts9	92772699	92774576	12527	0.325909	2.451453	0.121848	0.203793	0.040313	0	63	56	102	56	110	93	166	95	124	74
ENSMUSG00000101878	chr6	Gm8203	1.16E+08	1.16E+08	387	0.391018	1.228709	0.121836	0.203793	0.041413	0	29	29	37	24	34	43	57	38	52	40
ENSMUSG00000021461	chr13	Fancc	63304709	63305868	7884	0.379984	1.852126	0.121987	0.203953	0.054547	0	54	28	79	39	48	54	79	99	68	58
ENSMUSG00000031527	chr8	Eri1	35465265	35469370	5067	0.283946	2.877725	0.12199	0.203953	0.030834	0	99	83	122	102	112	122	187	135	148	131
ENSMUSG00000044150	chrX	A830080D01Rik	1.6E+08	1.6E+08	4869	-0.42701	0.426193	0.121979	0.203953	0.045142	0	17	18	36	25	19	15	27	18	22	15
ENSMUSG00000025959	chr1	Klf7	64029447	64035764	8131	-0.28583	3.445765	0.122042	0.204013	0.035063	0	128	126	303	179	249	99	265	174	213	158
ENSMUSG00000041645	chr12	Ddx24	1.03E+08	1.03E+08	3157	-0.22546	6.112535	0.122307	0.204405	0.02454	0	940	795	1656	1291	1391	941	1380	1039	1416	1056
ENSMUSG00000067653	chr1	Ankrd23	36530188	36531641	2697	-0.29417	11.33907	0.122305	0.204405	0.043344	0	35301	34488	49367	56626	50782	32530	67704	29291	46292	40052
ENSMUSG00000023000	chr15	Dhh	98893031	98894560	2363	-0.55096	0.05819	0.122453	0.204571	0.093633	0	9	8	23	28	23	8	16	11	28	8
ENSMUSG00000026797	chr2	Stxbp1	32787602	32789637	4991	0.335264	1.951554	0.122438	0.204571	0.041655	0	36	34	91	50	64	46	85	82	94	77
ENSMUSG00000028330	chr4	Ncbp1	46138613	46138886	3386	0.212788	4.584231	0.12244	0.204571	0.020002	0	325	240	485	338	404	371	565	478	571	371
ENSMUSG00000020471	chr11	Pold2	5872180	5872418	1896	-0.23092	4.826302	0.122473	0.204579	0.02475	0	433	395	677	414	533	408	592	378	634	387
ENSMUSG00000059005	chr2	Hnrnpa3	75659261	75659389	5396	0.222357	6.548881	0.122612	0.204785	0.024114	0	1197	1057	1872	1267	1559	1527	2359	1631	2211	1532
ENSMUSG00000002486	chr5	Tchp	1.15E+08	1.15E+08	3851	0.346267	1.915118	0.122722	0.204941	0.041124	0	46	30	57	57	70	44	94	76	94	70
ENSMUSG00000033487	chr14	Fndc3a	72537946	72540481	9944	-0.30664	3.117076	0.122736	0.204941	0.039541	0	131	104	238	126	179	81	168	151	135	162
ENSMUSG00000034269	chr6	Setd5	1.13E+08	1.13E+08	12481	-0.23333	4.85524	0.122943	0.205261	0.024962	0	405	314	858	439	578	342	575	490	591	440
ENSMUSG00000002885	chr8	Cd97	83723251	83723902	3757	0.278727	4.495799	0.122984	0.205303	0.036834	0	225	160	457	398	450	296	517	487	514	438
ENSMUSG00000087385	chr4	AA415398	1.2E+08	1.2E+08	2760	-0.36645	1.474345	0.123323	0.205844	0.045066	0	37	46	58	49	49	28	50	49	44	42
ENSMUSG00000028086	chr3	Fbxw7	84815268	84815769	7046	-0.22311	4.861645	0.12334	0.205846	0.023101	0	378	410	684	449	599	368	644	426	595	434
ENSMUSG00000033916	chr7	Chmp2a	13032006	13032202	927	0.272808	6.065781	0.123505	0.206095	0.036274	0	881	918	1020	891	992	1160	1837	1092	1586	1070
ENSMUSG00000022214	chr14	Dcaf11	55560006	55560121	8070	-0.22681	7.583341	0.123523	0.206099	0.025688	0	2810	2466	4428	3318	3620	2588	4075	2847	4319	2535
ENSMUSG00000026078	chr1	Pdcl3	38985608	38987849	4219	0.221458	5.418779	0.12364	0.206269	0.023079	0	565	472	870	592	674	640	1064	706	1183	678
ENSMUSG00000055407	chr7	Map6	99267447	99269313	6958	0.428674	2.036194	0.123699	0.206341	0.077194	0	35	23	50	91	77	58	98	82	94	85
ENSMUSG00000038346	chr6	Zfp384	1.25E+08	1.25E+08	6421	-0.22851	4.663007	0.123794	0.206474	0.023854	0	391	270	691	413	475	346	565	370	549	324
ENSMUSG00000031029	chr7	Eif3f	1.09E+08	1.09E+08	2891	0.23512	7.11662	0.12397	0.206742	0.027455	0	1757	1644	2637	2084	2019	2294	3107	2485	3517	2334
ENSMUSG00000031303	chrX	Map3k15	1.6E+08	1.6E+08	4348	-0.83468	1.25147	0.124025	0.206807	0.306766	0	18	10	96	88	39	4	12	52	47	33
ENSMUSG00000090641	chr13	Zfp712	67038594	67042232	3970	-0.56582	0.162756	0.124252	0.207159	0.082784	0	7	17	33	15	28	17	14	18	13	11
ENSMUSG00000020752	chr11	Recql5	1.16E+08	1.16E+08	6986	-0.2662	3.216751	0.124274	0.207171	0.029564	0	158	114	205	154	174	123	167	116	210	149
ENSMUSG00000044134	chr5	Fam109a	1.22E+08	1.22E+08	2335	0.302413	3.08455	0.124421	0.20739	0.037587	0	118	81	143	123	135	149	173	146	275	113
ENSMUSG00000049107	chr6	Ntf3	1.26E+08	1.26E+08	1427	0.407528	0.974023	0.12445	0.207412	0.052977	0	30	11	43	23	23	28	47	31	52	36
ENSMUSG00000054580	chr2	Pla2r1	60417543	60420302	9618	0.351673	1.923549	0.124482	0.207439	0.047574	0	30	40	82	39	76	71	79	63	88	72
ENSMUSG00000094483	chr11	Purb	6467599	6475917	8319	-0.22588	5.387694	0.124513	0.207464	0.024347	0	653	451	1151	612	850	488	844	694	942	598
ENSMUSG00000021806	chr14	Nid2	19751257	19751565	4884	0.28603	4.083355	0.124651	0.207641	0.038999	0	184	133	457	200	312	317	291	335	405	313
ENSMUSG00000039735	chr3	Fnbp1l	1.23E+08	1.23E+08	5408	-0.29898	2.221813	0.124635	0.207641	0.031752	0	62	68	104	71	100	56	87	75	92	65
ENSMUSG00000024201	chr17	Kdm4b	56326062	56326229	4895	-0.24854	4.557566	0.124808	0.207852	0.028331	0	289	239	700	447	451	295	429	361	545	345
ENSMUSG00000052534	chr1	Pbx1	1.68E+08	1.68E+08	13844	-0.23715	4.346102	0.124799	0.207852	0.025313	0	264	225	527	395	386	223	413	333	412	329
ENSMUSG00000015749	chr3	Anp32e	95929246	95929650	3566	-0.23286	6.729671	0.12493	0.207976	0.027014	0	1537	1518	2524	1525	2106	1464	1933	1586	2315	1615
ENSMUSG00000015942	chr5	Gtf2ird2	1.34E+08	1.34E+08	5572	-0.28502	2.933446	0.124916	0.207976	0.031347	0	112	74	218	110	176	96	142	117	163	107
ENSMUSG00000025409	chr10	Mbd6	1.27E+08	1.27E+08	4455	0.251221	4.005877	0.1249	0.207976	0.028616	0	179	142	363	220	304	197	338	334	421	306
ENSMUSG00000029458	chr5	Brap	1.22E+08	1.22E+08	6284	-0.21293	5.171711	0.124975	0.208025	0.021367	0	542	440	900	572	681	473	710	532	819	534
ENSMUSG00000014980	chr1	Tsen15	1.52E+08	1.52E+08	4195	0.27662	3.545067	0.125194	0.208363	0.031897	0	165	137	183	151	189	182	338	194	242	208
ENSMUSG00000051615	chr14	Rap2a	1.2E+08	1.2E+08	4174	0.281788	3.131193	0.125292	0.208501	0.03407	0	78	90	197	132	145	138	215	205	174	134
ENSMUSG00000020083	chr10	2010107G23Rik	62107655	62109123	2981	-0.53887	0.519539	0.125318	0.208518	0.111039	0	26	33	34	9	21	11	31	16	22	21
ENSMUSG00000025730	chr17	Rab40c	25882114	25883908	3094	0.254136	3.270921	0.125436	0.208688	0.026013	0	106	99	218	127	164	158	232	185	248	135
ENSMUSG00000083061	chr11	Gm12191	49678710	49679057	348	0.412743	1.690131	0.125638	0.208998	0.058984	0	46	42	49	35	36	52	109	57	64	47
ENSMUSG00000061979	chr5	Wbscr16	1.34E+08	1.34E+08	2874	-0.24198	4.759498	0.12576	0.209174	0.027862	0	431	286	563	546	531	310	593	420	640	349
ENSMUSG00000002546	chr2	Golga2	32287384	32287470	5500	-0.22427	6.297095	0.125855	0.209279	0.024902	0	1144	891	1918	1326	1637	968	1474	1245	1809	1181
ENSMUSG00000059923	chr11	Grb2	1.16E+08	1.16E+08	2916	0.223969	6.248808	0.125841	0.209279	0.024746	0	1007	851	1592	985	1218	1166	1708	1419	1932	1291
ENSMUSG00000020015	chr10	Cdk17	93160876	93161200	3643	0.294467	2.589335	0.125885	0.209304	0.03223	0	69	60	112	89	99	80	183	110	136	96
ENSMUSG00000078922	chr11	Tgtp1	48985327	48987894	3205	0.63715	-0.02195	0.126121	0.209669	0.125954	0	9	6	7	14	18	19	39	19	10	10
ENSMUSG00000045316	chr17	Fahd1	24848896	24850302	1407	-0.23839	5.217321	0.126295	0.209932	0.027721	0	572	534	649	637	767	477	755	554	813	540
ENSMUSG00000070420	chr5	Zscan25	1.45E+08	1.45E+08	1996	-0.3021	2.397901	0.126879	0.210877	0.034446	0	84	57	121	94	107	50	109	81	102	85
ENSMUSG00000063931	chr7	Pepd	34912379	34912454	3079	0.268657	5.183235	0.126902	0.210888	0.034993	0	494	425	587	514	572	577	771	956	773	521
ENSMUSG00000030513	chr7	Pcsk6	65861734	65861766	5144	-0.33777	4.622451	0.127044	0.211098	0.055036	0	319	197	794	426	605	298	310	511	407	406
ENSMUSG00000004633	chr6	Chn2	54039554	54040155	5745	0.499194	0.408203	0.127109	0.211179	0.062225	0	9	17	15	21	17	22	29	31	28	19
ENSMUSG00000020803	chr11	Txndc17	72207547	72207768	1324	0.2839	5.143612	0.127218	0.211308	0.039021	0	535	481	548	414	478	665	924	636	798	519
ENSMUSG00000027966	chr3	Col11a1	1.14E+08	1.14E+08	9657	-0.81312	1.560079	0.127214	0.211308	0.298577	0	8	27	94	72	114	32	41	19	10	73
ENSMUSG00000024429	chr17	Gnl1	35979851	35980247	3077	0.248051	5.24762	0.127402	0.211587	0.029632	0	506	484	659	499	582	598	727	713	1069	659

ENSMUSG00000028173	chr3	Wls	1.6E+08	1.6E+08	3304	-0.24263	5.194477	0.127431	0.211608	0.028435	0	608	372	928	570	772	425	686	529	763	657
ENSMUSG00000022779	chr16	Top3b	16870736	16870829	8340	-0.22556	3.808633	0.127481	0.211664	0.02159	0	214	156	369	228	260	181	290	217	296	198
ENSMUSG00000010453	chr1	Kansl3	36335730	36337651	6742	-0.26357	5.554673	0.127515	0.211694	0.034241	0	568	418	1199	1041	1035	559	981	823	863	687
ENSMUSG00000045519	chr9	Zfp560	20345136	20349159	4981	0.353226	2.868023	0.127555	0.211734	0.05323	0	100	104	143	76	71	138	167	127	169	130
ENSMUSG00000080268	chr19	Brms1	5041404	5041490	1338	0.247297	3.949947	0.127659	0.211881	0.02634	0	199	189	234	227	256	251	376	283	377	243
ENSMUSG00000028405	chr4	Aco1	40143081	40143541	4496	0.292461	4.62224	0.127701	0.211924	0.041549	0	314	245	459	349	412	409	455	728	457	370
ENSMUSG00000026456	chr1	Cyb5r1	1.34E+08	1.34E+08	4437	0.229478	6.621778	0.127726	0.211939	0.026426	0	1366	1104	1809	1328	1624	1520	2420	1690	2683	1539
ENSMUSG00000035376	chr16	Ptplb	35022421	35022635	3603	0.578111	2.434141	0.127841	0.212103	0.155913	0	99	65	71	35	54	108	81	220	74	74
ENSMUSG00000029641	chr5	Rasl11a	1.47E+08	1.47E+08	1126	0.730152	-0.19927	0.127867	0.21212	0.1516	0	13	7	10	5	9	7	26	26	27	3
ENSMUSG00000035778	chr2	Ggta1	35400179	35402802	4709	0.292895	3.224119	0.127901	0.21215	0.036892	0	93	104	173	129	173	145	309	177	179	133
ENSMUSG00000055994	chr8	Nod2	88647315	88647409	5014	0.502064	0.25416	0.127918	0.212151	0.07804	0	15	8	27	13	10	27	22	23	17	23
ENSMUSG00000026201	chr1	Stk16	75210838	75211052	4518	0.231677	4.123714	0.12801	0.212251	0.023658	0	250	191	335	236	262	298	392	350	406	262
ENSMUSG00000028420	chr4	Tmem38b	53826045	53826220	3807	-0.2616	6.067454	0.128007	0.212251	0.034527	0	1064	766	1728	1073	1336	760	1669	761	1619	937
ENSMUSG00000020519	chr11	Sap30l	57801637	57802289	1151	-0.23131	4.417143	0.128106	0.21237	0.024929	0	334	293	490	353	363	287	365	344	484	310
ENSMUSG00000038291	chr8	Snx25	46033261	46033822	4440	-0.28945	2.545161	0.128114	0.21237	0.031511	0	80	59	149	107	124	63	124	94	110	85
ENSMUSG00000021236	chr12	Entpd5	84373857	84377380	6039	-0.25193	4.304113	0.128146	0.212396	0.02931	0	231	236	429	395	447	255	353	385	360	278
ENSMUSG00000043716	chr1	Rpl7	16101295	16101359	2687	0.262502	8.272107	0.128205	0.212468	0.035385	0	4201	4081	5237	4052	4393	5494	8542	5326	7007	4662
ENSMUSG00000073678	chr1	Pgap1	54472994	54480844	16611	-0.34693	1.966849	0.128241	0.212502	0.042168	0	54	40	127	50	86	52	75	60	68	51
ENSMUSG00000035901	chr7	Dennd5a	1.1E+08	1.1E+08	8677	-0.2503	5.481998	0.128341	0.212641	0.030889	0	524	434	1084	961	1009	525	959	709	915	657
ENSMUSG00000010048	chr9	Ifrd2	1.08E+08	1.08E+08	2637	-0.22406	5.159329	0.128378	0.212675	0.024412	0	573	397	749	649	726	429	778	635	756	452
ENSMUSG00000060600	chr11	Eno3	70657202	70657267	1739	0.260289	12.63306	0.12854	0.212916	0.035108	0	96896	46331	122240	96586	110245	97671	154716	116316	176217	97909
ENSMUSG00000039556	chrX	Ppp1r3f	7557296	7560886	5153	-0.33777	2.121332	0.128599	0.212989	0.043134	0	55	45	100	90	98	57	75	47	101	65
ENSMUSG00000021109	chr12	Hif1a	73901375	73901498	5896	-0.25703	4.202841	0.128702	0.213105	0.031043	0	246	211	492	302	394	162	418	345	400	240
ENSMUSG00000086350	chr1	B230369F24Rik	1.78E+08	1.78E+08	2560	0.505859	0.39414	0.128688	0.213105	0.058861	0	17	16	17	10	18	21	30	21	41	17
ENSMUSG00000083179	chr4	Gm12693	94935621	94936103	483	-0.35073	1.768384	0.128719	0.213108	0.048552	0	58	59	69	45	60	38	63	44	78	46
ENSMUSG00000020409	chr11	Slu7	43433744	43433819	4050	-0.21281	5.053503	0.128848	0.213293	0.02172	0	470	428	841	532	614	443	765	499	663	462
ENSMUSG00000032267	chr9	Usp28	48985385	48985537	4220	-0.23874	5.84829	0.128964	0.213433	0.028523	0	838	564	1524	995	1241	653	1303	823	1385	783
ENSMUSG00000079614	chr18	Seh1l	67774876	67775120	3516	0.234783	4.804669	0.128961	0.213433	0.026197	0	421	294	618	319	417	444	715	516	643	450
ENSMUSG00000042293	chr9	Gm5617	48495345	48495964	620	0.406549	1.955247	0.12899	0.213449	0.065364	0	59	35	42	62	55	81	80	68	72	81
ENSMUSG00000036840	chr8	Siah1a	86723940	86725856	2107	0.261881	3.305397	0.129082	0.213575	0.027955	0	127	115	183	139	145	130	218	204	253	175
ENSMUSG00000036534	chr8	Slc38a7	95835920	95837671	4144	0.259715	3.090287	0.129242	0.213787	0.028373	0	105	68	173	132	149	140	193	175	177	147
ENSMUSG00000058298	chr10	Mcm9	53536329	53538767	4868	0.51436	0.451723	0.12924	0.213787	0.085968	0	13	9	16	13	33	23	38	33	17	22
ENSMUSG00000094936	chr19	Rbm4	4784293	4785567	4940	0.278026	3.162648	0.129379	0.213986	0.032718	0	97	79	145	147	181	142	256	161	205	133
ENSMUSG00000035062	chrX	Zc4h2	95639193	95640651	2257	0.477025	0.535082	0.129471	0.214111	0.072945	0	14	13	36	13	16	36	28	23	25	26
ENSMUSG00000031958	chr8	Ldhd	1.12E+08	1.12E+08	5328	-0.28187	5.8009	0.129553	0.214221	0.040269	0	757	515	1064	1277	1369	692	1325	764	1249	677
ENSMUSG00000032855	chr17	Pkd1	24549950	24550477	14170	-0.30214	5.212536	0.129579	0.214236	0.045348	0	384	322	1080	712	979	412	599	687	729	588
ENSMUSG00000014602	chr1	Kif1a	93015464	93018499	9330	-0.72998	0.207945	0.12967	0.214306	0.202359	0	13	4	31	36	25	3	27	26	9	8
ENSMUSG00000021253	chr12	Tgfb3	86056744	86057938	3384	0.219055	5.198707	0.129645	0.214306	0.023233	0	424	382	700	618	608	542	892	679	831	666
ENSMUSG00000030407	chr7	Qpctl	19140217	19141299	2100	0.335429	1.522198	0.12966	0.214306	0.035004	0	39	30	53	30	44	45	66	58	61	50
ENSMUSG00000022855	chr16	Senp2	22009484	22009742	4499	-0.22209	5.282014	0.129742	0.214387	0.024041	0	620	470	957	578	767	611	841	592	718	509
ENSMUSG00000025171	chr19	Ubtd1	41981763	41982008	1527	0.242725	4.067347	0.129751	0.214387	0.026525	0	261	171	285	205	296	275	393	285	389	305
ENSMUSG00000101599	chr1	Gm20342	63117118	63126837	9720	0.56995	0.19121	0.129803	0.214447	0.100367	0	9	14	28	9	7	16	23	35	21	16
ENSMUSG00000003123	chr7	Lipe	25379527	25380173	4518	0.621965	5.599236	0.129846	0.214482	0.19716	0	926	596	474	385	433	832	567	2454	664	608
ENSMUSG00000030423	chr7	Pop4	38262820	38263309	1214	0.272481	3.341445	0.129857	0.214482	0.031615	0	137	117	161	147	155	179	239	206	194	173
ENSMUSG00000020877	chr11	Scrn2	97029938	97030055	2050	0.246218	3.725064	0.129924	0.214566	0.026246	0	193	125	209	205	225	210	302	241	328	223
ENSMUSG00000020333	chr11	Acsl6	54303798	54303922	9914	-0.2197	4.940798	0.129962	0.214602	0.023058	0	418	362	809	519	592	453	684	413	631	423
ENSMUSG00000017314	chr11	Mpp2	1.02E+08	1.02E+08	4807	-0.47767	0.913758	0.130002	0.214642	0.07958	0	25	22	47	42	32	12	24	46	32	22
ENSMUSG00000001016	chr3	Ilf2	90476201	90476245	1973	0.23056	4.977209	0.13026	0.215041	0.025304	0	477	365	573	405	468	492	794	583	763	493
ENSMUSG00000020163	chr10	Uqcr11	80402997	80403155	641	0.261827	7.846442	0.130341	0.215147	0.035528	0	3022	2364	3244	4099	3778	3573	6234	3906	6004	3611
ENSMUSG00000007850	chr11	Hnrnph1	50376990	50377147	5842	0.222964	6.531431	0.130407	0.21523	0.02529	0	1258	1016	1936	1185	1489	1358	2377	1827	2057	1540
ENSMUSG00000032806	chrX	Slc10a3	74369217	74371011	2023	0.336858	1.771476	0.130509	0.215345	0.041958	0	38	24	65	53	59	44	75	81	86	53
ENSMUSG00000073700	chr4	Klhl21	1.52E+08	1.52E+08	3986	-0.24358	7.769825	0.130509	0.215345	0.030778	0	3238	2066	5259	4093	4843	2780	4375	3028	5310	3063
ENSMUSG00000055943	chr2	Emc7	1.12E+08	1.12E+08	5826	0.209162	5.650794	0.130546	0.215379	0.021516	0	683	560	987	683	821	770	1251	891	1178	854
ENSMUSG00000024833	chr19	Pola2	5940543	5941017	2872	-0.25922	3.392612	0.130617	0.21547	0.028464	0	145	131	213	206	214	155	179	156	208	160
ENSMUSG00000022982	chr16	Sod1	90220742	90220929	646	0.269537	7.311166	0.130862	0.215745	0.037578	0	2178	2082	2435	2183	2307	2829	3460	3254	4136	2223
ENSMUSG00000037608	chr10	Bclaf1	20312469	20312604	8426	-0.23346	5.385226	0.130811	0.215745	0.027006	0	584	530	1245	572	787	505	931	667	777	645
ENSMUSG00000064254	chr7	Ethe1	24587543	24587807	1484	0.271601	4.556904	0.130866	0.215745	0.035903	0	256	200	351	447	462	381	551	393	670	376
ENSMUSG00000071655	chr19	Ubxn1	8871559	8871585	1068	0.271242	7.395124	0.130817	0.215745	0.038104	0	2514	1941	2689	2221	2615	2996	3495	2945	5187	2379
ENSMUSG00000079139	chr1	Gm4204	1.35E+08	1.35E+08	1231	0.30963	3.173406	0.130864	0.215745	0.041779	0	112	127	186	80	128	124	214	189	212	165
ENSMUSG00000035392	chr2	Dennd1a	37798991	37801250	5740	-0.23801	4.63489	0.131058	0.216035	0.026714	0	356	225	671	443	534	306	458	411	509	393
ENSMUSG00000036104	chr1	Rab3gap1	1.28E+08	1.28E+08	11718	-0.21217	5.176122	0.131079	0.216044	0.021707	0	506	382	913	649	730	503	718	568	739	530
ENSMUSG00000006958	chr16	Chrd	20733127	20733295	5838	-0.37712	1.977417	0.131238	0.216279	0.053786	0	50	38	117	72	84	60	46	71	64	56
ENSMUSG00000019303	chr11	Psmc3ip	1.01E+08	1.01E+08	1818	0.392415	0.970216	0.131274	0.216311	0.048199	0	18	13	34	26	40	28	41	45	40	36
ENSMUSG00000042046	chr1	Dstyk	1.32E+08	1.32E+08	9345	-0.23382	4.206428	0.131591	0.216807	0.02487	0	228	188	478	336	416	254	343	281	419	255
ENSMUSG00000056204	chr8	Pgpep1	70646436	70650785	4882	0.242269	4.244809	0.131689	0.21694	0.027425	0	203	186	312	332	361	274	450	340	471	344

ENSMUSG00000028830	chr4	AU040320	1.27E+08	1.27E+08	6259	-0.23247	5.208595	0.131843	0.217141	0.026458	0	470	366	995	685	799	478	724	559	729	607
ENSMUSG00000067274	chr5	Rplp0	1.16E+08	1.16E+08	1659	0.23925	9.299385	0.131833	0.217141	0.030073	0	8846	7297	10395	9121	9926	10241	16481	11252	14534	10264
ENSMUSG00000045973	chr4	Slc25a51	45395923	45400179	5510	-0.22165	6.3065	0.131913	0.217229	0.025116	0	1183	911	1890	1344	1597	1110	1435	1303	1806	1049
ENSMUSG00000026104	chr1	Stat1	52119440	52119623	7105	0.267718	4.456382	0.132049	0.217398	0.034862	0	289	214	373	311	409	350	608	498	340	370
ENSMUSG00000038542	chr8	Pcid2	13077189	13078289	3084	0.240909	3.631114	0.13204	0.217398	0.024745	0	166	149	246	148	192	197	288	222	296	214
ENSMUSG00000085322	chr2	Gm14261	1.69E+08	1.69E+08	1429	-0.37608	1.319965	0.132132	0.217509	0.054002	0	49	37	40	43	42	29	42	35	59	28
ENSMUSG00000052373	chr11	Mpp3	1.02E+08	1.02E+08	9385	-0.27299	4.089951	0.132188	0.217574	0.034801	0	275	139	424	300	398	234	340	210	318	293
ENSMUSG00000032470	chr9	Mras	99385420	99388504	5134	0.273646	3.137018	0.13222	0.2176	0.031697	0	105	97	153	120	156	181	198	142	216	128
ENSMUSG00000097571	chrX	Jpx	1.03E+08	1.03E+08	4785	0.461313	0.452992	0.132263	0.217643	0.061846	0	15	10	26	14	21	11	36	29	26	31
ENSMUSG00000048376	chr13	F2r	95601804	95604937	3307	0.388576	2.506386	0.13232	0.217709	0.069196	0	36	42	88	124	105	99	120	100	140	113
ENSMUSG00000024234	chr18	Mtpap	4375592	4375778	2651	-0.22607	3.804244	0.132373	0.21771	0.02255	0	219	170	348	209	268	180	287	251	275	182
ENSMUSG00000030094	chr6	Xpc	91489305	91490266	5490	-0.25685	3.543156	0.132341	0.21771	0.028523	0	161	115	341	185	248	134	215	205	240	173
ENSMUSG00000097042	chr8	Gm17491	22480291	22482054	2309	0.558986	0.276105	0.132385	0.21771	0.09345	0	21	12	20	7	10	30	27	21	26	14
ENSMUSG00000104139	chr14	AC102815.1	1.03E+08	1.03E+08	3805	-0.34306	3.098759	0.132358	0.21771	0.052949	0	98	101	285	112	203	81	199	149	117	138
ENSMUSG00000057778	chr11	Cyb5d2	72777232	72778952	5143	-0.21502	4.632933	0.132439	0.21777	0.022295	0	383	331	520	429	451	319	548	382	508	353
ENSMUSG00000103661	chr1	ANKRD23	36530193	36531641	2327	-0.28625	11.31367	0.132482	0.217814	0.043299	0	34708	33976	48242	55244	49765	32190	66756	28809	45650	39341
ENSMUSG00000032498	chr9	Mlh1	1.11E+08	1.11E+08	4818	-0.26429	2.876945	0.132648	0.218045	0.028372	0	107	104	167	119	136	102	128	122	141	105
ENSMUSG00000050147	chr8	F2rl3	72761880	72762014	1751	0.410884	1.429271	0.132655	0.218045	0.061489	0	38	21	41	38	39	31	68	32	81	61
ENSMUSG00000089736	chr8	Tgfbr3l	4248214	4248352	1870	0.647687	-0.20443	0.132722	0.218127	0.144161	0	1	7	25	5	12	17	21	22	11	11
ENSMUSG00000031930	chr8	Wwp2	1.07E+08	1.07E+08	4280	0.225304	4.210964	0.132886	0.218343	0.023399	0	206	188	343	312	324	300	440	298	462	322
ENSMUSG00000039703	chr11	Nploc4	1.2E+08	1.2E+08	4776	-0.24131	6.687133	0.132878	0.218343	0.030269	0	1502	1182	2761	1791	1904	1402	1798	1599	2696	1256
ENSMUSG00000021290	chr12	2010107E04Rik	1.12E+08	1.12E+08	365	0.271816	7.520694	0.132961	0.218423	0.038733	0	2485	1994	2737	3092	2764	3088	5459	2827	4717	2646
ENSMUSG00000049521	chr15	Cdc42ep1	78842647	78842725	2542	0.257864	3.607641	0.132967	0.218423	0.02992	0	175	103	217	174	222	170	254	280	310	194
ENSMUSG00000061665	chr17	Cd2ap	42792951	42796369	5399	-0.27422	3.774126	0.133053	0.218537	0.035267	0	171	186	364	208	287	132	311	277	222	192
ENSMUSG00000019850	chr10	Tnfaip3	19000910	19003015	7226	0.293823	2.603226	0.133104	0.218573	0.036637	0	83	40	118	83	117	84	147	116	146	111
ENSMUSG00000042111	chr1	Ccdc115	34436670	34437610	2543	0.229086	4.148844	0.133108	0.218573	0.023797	0	243	196	360	250	253	303	439	286	439	282
ENSMUSG00000075010	chr19	AW112010	11047617	11048093	770	0.370287	3.024522	0.133125	0.218573	0.062483	0	115	95	128	93	120	152	253	203	112	103
ENSMUSG00000029119	chr5	Man2b2	36806921	36807210	3528	0.265657	3.377077	0.13318	0.218637	0.03246	0	97	100	243	151	182	174	210	233	219	178
ENSMUSG00000007589	chr14	Tinf2	55679083	55679409	1736	0.235148	3.85855	0.133257	0.218735	0.02491	0	196	131	273	218	254	257	375	248	346	207
ENSMUSG00000036528	chr7	Ppfibp2	1.08E+08	1.08E+08	4729	-0.34804	3.17145	0.133305	0.21876	0.055179	0	102	73	197	190	271	138	180	152	142	100
ENSMUSG00000037991	chr16	Rmi2	10835059	10835390	4495	-0.40133	1.960774	0.1333	0.21876	0.067192	0	85	40	115	43	70	54	73	75	61	35
ENSMUSG00000087090	chr7	Nctc1	1.43E+08	1.43E+08	3438	0.262474	6.828755	0.133466	0.218998	0.036071	0	1809	1071	2288	1387	1778	2364	2745	1752	2492	1859
ENSMUSG00000020946	chr11	Gosr2	1.04E+08	1.04E+08	3266	-0.22278	6.2209	0.133529	0.219047	0.025608	0	1149	936	1909	1154	1361	1048	1607	1065	1632	1000
ENSMUSG00000021395	chr13	Spin1	51100880	51100990	4434	-0.22207	4.361965	0.133525	0.219047	0.023043	0	285	236	544	302	450	249	403	350	465	280
ENSMUSG00000008668	chr17	Rps18	33951999	33952118	2491	0.253336	7.748064	0.133703	0.219306	0.033785	0	3017	2770	3464	2905	3142	3763	5636	3955	4981	3160
ENSMUSG00000066842	chr1	Hmcn1	1.51E+08	1.51E+08	21191	-0.45708	1.072561	0.133721	0.219308	0.069664	0	28	17	53	37	57	32	50	16	30	26
ENSMUSG00000009772	chr1	Nuak2	1.32E+08	1.32E+08	3920	0.493091	0.455771	0.133742	0.219311	0.066892	0	9	16	18	20	20	21	43	20	22	28
ENSMUSG00000039130	chr6	Zc3hc1	30366380	30366745	4601	0.213671	4.222806	0.133761	0.219311	0.020857	0	232	195	360	277	325	326	442	308	438	308
ENSMUSG00000053754	chr14	Chd8	52198151	52199152	12599	-0.23658	5.08569	0.133773	0.219311	0.027612	0	497	308	1027	551	692	422	705	536	689	509
ENSMUSG00000061175	chr3	Fnip2	79455974	79459741	8364	0.319085	2.523525	0.133891	0.219478	0.042858	0	69	52	120	69	101	68	128	144	114	115
ENSMUSG00000050945	chr18	Zfp438	5210031	5211198	3209	-0.32804	2.366869	0.134142	0.219863	0.044885	0	60	72	100	110	108	53	112	81	82	83
ENSMUSG00000016487	chr6	Ppfibp1	1.47E+08	1.47E+08	9790	0.24528	5.375444	0.134317	0.220123	0.030604	0	453	491	1104	462	614	623	1053	776	1017	679
ENSMUSG00000040331	chr7	Nsmce4a	1.31E+08	1.31E+08	2597	0.250733	5.123152	0.134427	0.220274	0.031198	0	470	441	605	519	453	533	999	589	772	594
ENSMUSG00000053091	chr7	Lins	66689889	66690023	5886	-0.3013	2.922288	0.134491	0.220352	0.038838	0	132	69	169	119	187	91	167	133	116	106
ENSMUSG00000039783	chr1	Kmo	1.76E+08	1.76E+08	4724	0.590534	-0.32231	0.134546	0.220415	0.073298	0	12	7	8	7	9	14	19	16	10	15
ENSMUSG00000012483	chr6	Rpa3	8255936	8256247	1136	0.368213	1.912118	0.134666	0.220558	0.049841	0	50	48	49	44	58	62	103	83	69	58
ENSMUSG00000074578	chr2	1500012F01Rik	1.67E+08	1.67E+08	2929	0.328639	3.30787	0.134666	0.220558	0.049235	0	145	134	148	125	118	205	240	202	204	136
ENSMUSG00000104357	chr3	TTC14	33800279	33800436	2145	-0.32465	2.359296	0.13475	0.220668	0.042119	0	64	70	134	81	107	69	121	85	65	67
ENSMUSG00000049960	chr14	Mrps16	20391231	20391460	566	0.250757	5.415416	0.13486	0.220821	0.031781	0	572	466	639	738	644	681	1150	671	1129	668
ENSMUSG00000022000	chr14	Zc3h13	75284373	75284665	6151	-0.25344	3.867392	0.134888	0.22084	0.029541	0	178	149	357	262	360	162	268	227	326	235
ENSMUSG00000035765	chr18	Dym	75018772	75018984	2471	-0.23064	6.490678	0.134922	0.220868	0.027833	0	1262	1110	2304	1655	1544	1177	1685	1305	2182	1289
ENSMUSG00000004789	chr12	Dlst	85110833	85110959	2767	-0.34603	8.15309	0.135013	0.22099	0.063785	0	3237	2205	5454	7928	7476	3231	6064	3798	6412	3889
ENSMUSG00000001520	chr6	Nrip2	1.28E+08	1.28E+08	3602	0.414145	1.273845	0.135114	0.221128	0.058853	0	21	19	43	37	41	23	77	45	72	32
ENSMUSG00000048285	chr12	Frmd6	70825514	70825573	4660	0.239635	4.43973	0.135163	0.221181	0.028257	0	267	177	519	287	401	276	517	382	607	392
ENSMUSG00000024798	chr19	Htr7	35958734	35960399	3399	-0.51112	0.055538	0.135275	0.221336	0.070847	0	16	10	29	14	21	12	28	13	11	7
ENSMUSG00000057863	chr17	Rpl36	56613395	56613448	404	0.264467	6.734593	0.135582	0.221811	0.036802	0	1577	1331	1490	1543	1534	1932	2547	1901	2493	1723
ENSMUSG00000075000	chr10	Nrbf2	67266689	67268166	1860	-0.268	3.399285	0.135669	0.221926	0.033275	0	165	127	252	184	195	120	273	119	221	154
ENSMUSG00000021585	chr13	Cast	74694286	74694833	2894	-0.24832	6.113296	0.13586	0.222186	0.032211	0	823	727	1696	1417	1533	792	1456	987	1459	1139
ENSMUSG00000056536	chr1	Pign	1.06E+08	1.06E+08	13595	-0.32966	2.423857	0.135861	0.222186	0.045005	0	79	46	169	80	119	56	119	97	92	67
ENSMUSG00000062014	chr14	Gmfb	46808149	46811823	4446	-0.21386	4.768967	0.135989	0.222367	0.022227	0	369	361	651	442	537	378	539	477	490	403
ENSMUSG00000028243	chr4	Ubxn2b	6191098	6191213	6642	-0.36813	1.093835	0.136021	0.222392	0.042093	0	28	31	53	31	42	27	39	40	30	25
ENSMUSG00000039686	chr2	Zer1	30097283	30098843	9784	-0.23505	5.481024	0.13605	0.222412	0.028135	0	576	432	1150	845	1000	551	866	642	956	742
ENSMUSG00000031176	chrX	Dynlt3	9654267	9656063	2576	-0.20778	5.72639	0.136075	0.222425	0.022197	0	801	701	1127	888	1007	715	1130	838	1041	775
ENSMUSG00000024044	chr17	Epb4.1l3	69156810	69156910	4109	0.409384	1.046012	0.136193	0.222591	0.058881	0	16	17	46	22	38	21	49	35	50	49
ENSMUSG00000005069	chr6	Pex5	1.24E+08	1.24E+08	3943	0.217044	5.07545	0.136302	0.222689	0.023669	0	418	298	652	558	609	500	747	614	837	614

ENSMUSG00000007564	chr17	Ppp2r1a	20945311	20945583	3375	0.220535	7.059349	0.136317	0.222689	0.025801	0	1650	1238	2728	2140	2293	2086	3225	2253	3414	2250
ENSMUSG00000031583	chr8	Wrn	33234384	33236459	6372	-0.3639	1.521269	0.136273	0.222689	0.044024	0	53	23	74	43	63	38	51	47	47	37
ENSMUSG00000031731	chr8	Ap1g1	1.1E+08	1.1E+08	7681	-0.22124	5.663043	0.136337	0.222689	0.024987	0	635	515	1365	901	1117	636	1066	819	1005	766
ENSMUSG00000043090	chr8	Zfp866	69761326	69763495	5601	-0.24339	3.610477	0.136321	0.222689	0.026247	0	155	130	354	202	252	140	264	194	249	179
ENSMUSG00000024304	chr18	Cdh2	16588877	16590353	8066	0.551468	0.743212	0.136503	0.222906	0.111298	0	6	27	17	18	31	27	34	25	42	40
ENSMUSG00000031711	chr8	Zfp330	82763621	82764491	1675	-0.22327	4.242969	0.13649	0.222906	0.024106	0	286	269	400	314	343	259	444	278	367	255
ENSMUSG00000004035	chr3	Gstm7	1.08E+08	1.08E+08	1601	-0.48254	1.376895	0.136699	0.22315	0.101867	0	30	27	42	89	43	18	55	42	45	34
ENSMUSG00000026305	chr1	Lrrfip1	90998737	90998893	6469	0.278252	7.229319	0.136703	0.22315	0.041291	0	2309	1991	2910	1463	1965	2514	3613	2792	3791	2399
ENSMUSG00000062456	chr19	Rpl9-ps6	32465885	32466575	691	0.401135	2.399111	0.136675	0.22315	0.068593	0	81	70	69	60	61	88	185	96	120	61
ENSMUSG00000009876	chr2	Cox4i2	1.53E+08	1.53E+08	788	0.466258	1.115193	0.136847	0.223357	0.078724	0	19	21	27	32	38	21	56	30	86	33
ENSMUSG00000041353	chrX	Tmem29	1.5E+08	1.5E+08	7621	-0.36858	1.418018	0.136868	0.223364	0.04507	0	46	26	68	45	51	43	48	45	40	27
ENSMUSG00000006457	chr19	Actn3	4861223	4861503	2894	-0.31409	13.07053	0.136942	0.223406	0.053313	0	148864	146774	248021	89281	125805	113119	146281	140257	185764	116973
ENSMUSG00000026111	chr1	Unc50	37430139	37430282	1579	0.281071	3.808578	0.13693	0.223406	0.036681	0	202	177	207	171	224	229	424	268	286	201
ENSMUSG00000028651	chr4	Ppie	1.23E+08	1.23E+08	1719	0.241936	3.950058	0.136944	0.223406	0.026722	0	229	175	286	181	251	257	387	270	402	221
ENSMUSG00000021868	chr14	Ppif	25694154	25694423	3641	-0.40175	5.277938	0.137199	0.223794	0.085363	0	389	278	654	1243	1063	414	874	487	835	515
ENSMUSG00000023832	chr17	Acat2	12942890	12944032	2544	0.418244	2.846384	0.137247	0.223812	0.085624	0	96	61	120	104	106	103	98	272	135	113
ENSMUSG00000024968	chr19	Rcor2	7267325	7267424	3135	0.615993	0.008911	0.137294	0.223812	0.100161	0	14	15	12	7	6	13	21	28	19	17
ENSMUSG00000035575	chr11	Utp6	79932321	79932714	4517	-0.23425	5.592116	0.137245	0.223812	0.028603	0	777	722	1194	628	834	629	1058	796	922	665
ENSMUSG00000037997	chr6	Parp11	1.27E+08	1.27E+08	5720	0.293866	2.273602	0.137287	0.223812	0.034229	0	59	44	98	62	83	96	110	93	104	69
ENSMUSG00000039463	chr2	Slc9a8	1.67E+08	1.67E+08	9095	-0.21214	5.239639	0.137283	0.223812	0.0225	0	526	403	968	651	782	511	701	587	790	598
ENSMUSG00000086968	chr3	4933431E20Rik	1.08E+08	1.08E+08	6821	-0.32951	1.991134	0.137314	0.223817	0.04159	0	47	53	105	50	100	52	81	59	81	44
ENSMUSG00000000561	chr3	Wdr77	1.06E+08	1.06E+08	6644	0.206083	5.316608	0.137339	0.223831	0.021344	0	545	417	788	564	662	621	1023	748	873	646
ENSMUSG00000032637	chr7	Atxn2l	1.26E+08	1.26E+08	4782	0.234501	5.166656	0.137402	0.223848	0.028537	0	473	281	857	451	686	579	795	736	766	638
ENSMUSG00000034265	chr17	Zdhhc14	5492600	5493691	3115	0.372252	2.276932	0.137387	0.223848	0.058716	0	81	41	90	58	60	74	119	118	137	49
ENSMUSG00000038403	chr3	Hfe2	96525185	96525330	2021	-0.2313	9.584855	0.137425	0.223848	0.028973	0	11882	10500	17533	12500	13838	11333	14692	11234	17409	10244
ENSMUSG00000068749	chr3	Psma5	1.08E+08	1.08E+08	1321	0.280071	6.035011	0.137435	0.223848	0.041238	0	851	973	1270	708	818	1106	1569	1144	1763	1038
ENSMUSG00000079415	chr19	Cntf	12763660	12764380	1073	-0.41016	0.723554	0.13741	0.223848	0.053638	0	27	15	29	35	36	19	36	17	32	19
ENSMUSG00000027316	chr2	Gfra4	1.31E+08	1.31E+08	2165	-0.46497	0.701224	0.137647	0.224166	0.07638	0	37	21	35	22	25	19	27	35	24	12
ENSMUSG00000028409	chr4	Smu1	40736542	40737395	3119	0.212378	5.661554	0.137806	0.224398	0.023081	0	683	602	988	667	798	824	1262	882	1171	837
ENSMUSG00000036555	chr5	Iqce	1.41E+08	1.41E+08	12037	0.338964	1.557128	0.137992	0.224673	0.041846	0	26	31	64	38	45	39	66	66	58	58
ENSMUSG00000049422	chr10	Chchd10	75935573	75936004	939	0.298349	8.949176	0.13803	0.224708	0.048278	0	6134	3375	8437	9532	8745	8231	9862	8168	15960	8171
ENSMUSG00000029063	chr4	Nadk	1.56E+08	1.56E+08	3747	0.274657	4.574188	0.138142	0.224862	0.038356	0	328	233	454	328	388	413	460	667	489	314
ENSMUSG00000061330	chr13	Gm11361	28257636	28258094	459	0.538939	0.006152	0.138394	0.225245	0.081708	0	13	9	19	10	7	19	33	18	13	13
ENSMUSG00000013822	chr9	Elof1	22112989	22113679	1092	0.246804	4.897149	0.138421	0.225261	0.03042	0	452	366	463	379	464	497	793	520	686	469
ENSMUSG00000037174	chr3	Elf2	51252720	51256985	9563	-0.20268	5.274288	0.138511	0.225379	0.020764	0	522	447	959	681	768	504	794	614	843	554
ENSMUSG00000096617	chr5	Gm5559	95861714	95862715	1002	0.58692	-0.18447	0.138785	0.225798	0.081323	0	8	11	13	10	6	16	23	9	27	10
ENSMUSG00000032249	chr9	Anp32a	62341293	62341351	3166	0.230413	5.658403	0.138924	0.225997	0.027665	0	568	556	785	846	947	844	1137	988	1151	838
ENSMUSG00000029402	chr5	Snrnp35	1.24E+08	1.24E+08	1347	0.217848	4.166995	0.139169	0.226367	0.021995	0	231	217	353	231	290	305	415	321	422	291
ENSMUSG00000016619	chr15	Nup50	84923428	84923650	4741	0.210522	4.312604	0.139242	0.22643	0.020818	0	259	223	421	262	315	325	483	361	473	306
ENSMUSG00000024732	chr19	Ccdc86	10941481	10943289	5774	-0.22554	4.419203	0.139237	0.22643	0.024926	0	357	272	565	297	368	285	405	349	449	310
ENSMUSG00000041939	chr5	Mvk	1.14E+08	1.14E+08	2674	0.26484	3.243123	0.139393	0.226648	0.032297	0	110	83	161	158	177	141	202	158	234	196
ENSMUSG00000022336	chr15	Eif3e	43250040	43250237	1541	-0.29026	6.939601	0.139441	0.226671	0.045733	0	2009	2246	2757	1651	1804	1766	2857	1655	2337	1569
ENSMUSG00000052539	chr3	Magi3	1.04E+08	1.04E+08	6773	-0.42734	1.481375	0.139428	0.226671	0.072975	0	29	42	100	31	55	22	52	53	43	40
ENSMUSG00000031467	chr8	Agpat5	18846277	18846778	10783	0.211413	4.883356	0.139643	0.226972	0.022244	0	416	309	609	392	475	459	720	600	661	456
ENSMUSG00000024949	chr19	Sf1	6363690	6364118	6211	0.233983	6.135188	0.140074	0.227644	0.02929	0	1005	630	1642	858	1177	1011	1549	1523	1710	1168
ENSMUSG00000029528	chr5	Pxn	1.16E+08	1.16E+08	8195	0.221881	6.314802	0.140331	0.228034	0.026391	0	1013	783	1916	1046	1286	1278	1997	1315	1884	1390
ENSMUSG00000025867	chr13	Cplx2	54371349	54371575	4928	-0.53066	0.266569	0.140775	0.228727	0.077143	0	7	14	28	23	35	14	16	21	17	13
ENSMUSG00000026159	chr1	Agfg1	82839483	82839889	8384	-0.22404	4.946271	0.140868	0.228851	0.025519	0	409	367	928	477	562	357	636	518	624	475
ENSMUSG00000042029	chr12	Ncapg2	1.16E+08	1.16E+08	6604	-0.39312	1.236186	0.141091	0.229185	0.054236	0	45	24	59	25	56	30	44	36	31	35
ENSMUSG00000089703	chr1	Gm15833	44212162	44213118	957	-0.56116	0.295698	0.141143	0.229241	0.115834	0	29	8	21	18	32	19	12	17	29	6
ENSMUSG00000029513	chr5	Prkab1	1.16E+08	1.16E+08	3066	0.249569	3.326116	0.141209	0.229319	0.027284	0	147	102	182	128	168	173	261	169	234	153
ENSMUSG00000024219	chr17	Anks1	27909340	27909646	7143	-0.36438	3.569866	0.141356	0.229446	0.067408	0	109	94	266	352	279	130	223	208	235	153
ENSMUSG00000042492	chr7	Tbc1d10b	1.27E+08	1.27E+08	4690	0.233652	5.305344	0.141351	0.229446	0.028761	0	475	357	767	570	804	632	727	763	1148	640
ENSMUSG00000049191	chrX	Rgag4	1.02E+08	1.02E+08	4761	0.421845	0.79503	0.141334	0.229446	0.057492	0	26	14	35	17	20	39	36	29	36	27
ENSMUSG00000053477	chr18	Tcf4	69344146	69345025	12250	-0.2399	5.287271	0.141325	0.229446	0.030122	0	443	425	1019	688	935	405	816	705	828	560
ENSMUSG00000020107	chr10	Anapc16	59987409	59988838	4890	0.237151	5.376047	0.141529	0.2297	0.029438	0	613	469	810	533	606	808	965	799	926	578
ENSMUSG00000037461	chr1	Ints7	1.92E+08	1.92E+08	7319	0.296887	2.826936	0.141633	0.22984	0.041208	0	67	67	151	86	148	116	143	177	146	114
ENSMUSG00000078815	chr7	Cacng6	3424195	3424992	1977	-0.23362	7.604665	0.141744	0.229991	0.029989	0	3073	2798	4543	2878	3473	2675	3729	2655	4390	2973
ENSMUSG00000043885	chr9	Slc36a4	15709738	15709837	5563	0.33916	2.191297	0.14198	0.230318	0.050549	0	38	37	96	70	85	67	118	109	74	83
ENSMUSG00000087598	chr7	Zfp111	24193947	24200042	10160	-0.35256	1.354162	0.141971	0.230318	0.038577	0	35	29	70	37	55	27	45	39	42	43
ENSMUSG00000029674	chr5	Limk1	1.35E+08	1.35E+08	7154	0.339266	1.651038	0.142043	0.230392	0.046945	0	31	19	64	46	62	50	57	64	83	54
ENSMUSG00000040339	chr3	Fam102b	1.09E+08	1.09E+08	5702	-0.24251	3.697374	0.142075	0.230415	0.026834	0	174	148	351	205	272	166	228	239	229	206
ENSMUSG00000029464	chr5	Gpn3	1.22E+08	1.22E+08	2508	-0.24312	4.05798	0.142123	0.230466	0.029444	0	307	210	398	248	273	211	408	238	305	239
ENSMUSG00000073374	chr17	C030034I22Rik	69417402	69421632	4231	-0.40987	0.347373	0.142221	0.230597	0.050975	0	19	20	27	21	19	13	23	17	29	11
ENSMUSG00000057315	chr5	Arhgap24	1.02E+08	1.02E+08	8791	0.32715	3.27142	0.142414	0.230882	0.053434	0	78	66	155	181	221	136	243	180	228	188

ENSMUSG00000031935	chr9	Med17	15260352	15262438	3899	0.261979	3.29911	0.142486	0.23097	0.031708	0	104	102	239	146	135	137	257	161	233	190
ENSMUSG00000035198	chr11	Tubg1	1.01E+08	1.01E+08	2266	-0.21836	4.853575	0.142801	0.231452	0.024392	0	370	347	637	574	580	392	526	466	655	406
ENSMUSG00000000805	chr11	Car4	84957786	84958050	1966	0.342463	2.463375	0.142847	0.231498	0.050957	0	60	51	63	102	102	94	146	103	140	75
ENSMUSG00000021327	chr13	Zkscan3	21387013	21388706	7817	-0.23198	3.912971	0.14291	0.231573	0.025307	0	223	167	409	236	294	187	300	293	262	214
ENSMUSG00000013539	chr16	Tango2	18300825	18301552	7040	-0.36975	5.026651	0.143009	0.231704	0.074036	0	350	265	717	919	784	390	717	282	868	423
ENSMUSG00000022940	chr16	Pigp	94358763	94359174	1888	-0.26035	6.287455	0.143067	0.231769	0.037168	0	1334	1274	1715	1148	1167	1087	1766	1136	1448	1086
ENSMUSG00000024608	chr18	Rps14	60774510	60774686	1384	0.291063	8.191791	0.143098	0.231792	0.046951	0	4511	4031	4119	3570	3878	5365	7645	5067	7499	4122
ENSMUSG00000018661	chr11	Cog1	1.14E+08	1.14E+08	4987	0.226793	4.356672	0.143214	0.231952	0.026048	0	245	173	451	316	365	327	406	404	570	313
ENSMUSG00000020642	chr12	Rnf144a	26306797	26310789	5163	0.314354	2.258103	0.1433	0.232006	0.04176	0	46	43	82	81	86	73	107	118	106	69
ENSMUSG00000024620	chr18	Pdgfrb	61045150	61045572	5478	0.296366	5.273411	0.143285	0.232006	0.047759	0	337	276	759	615	927	533	882	597	1088	819
ENSMUSG00000070003	chr8	Ssbp4	70597491	70597768	1474	0.239025	3.563472	0.143277	0.232006	0.026085	0	148	128	198	177	208	196	255	250	257	193
ENSMUSG00000051726	chr12	Kcnf1	17172100	17176888	4789	-0.52947	2.371138	0.143353	0.232062	0.140067	0	76	63	254	32	94	63	47	96	124	48
ENSMUSG00000028476	chr4	Reck	43875530	43875705	4779	-0.44299	2.547382	0.143481	0.232242	0.093833	0	54	60	219	95	141	68	72	129	60	98
ENSMUSG00000031925	chr9	Maml2	13619990	13621675	6138	-0.31594	2.275149	0.143714	0.23259	0.040669	0	51	57	115	82	128	52	102	83	87	65
ENSMUSG00000014771	chr17	Pdcd2	15519208	15520364	2582	0.30886	3.40371	0.143767	0.232648	0.044495	0	167	134	167	131	127	189	309	167	251	155
ENSMUSG00000032475	chr9	Nck1	1E+08	1E+08	4792	-0.2064	4.428046	0.143831	0.232724	0.021157	0	296	281	487	372	413	266	474	350	420	321
ENSMUSG00000002102	chr2	Psmc3	91054009	91054331	2607	0.247338	7.884904	0.143996	0.232962	0.03396	0	3095	3271	4076	3052	3381	3878	5412	4230	6363	3751
ENSMUSG00000024182	chr17	Axin1	26138688	26139041	3828	-0.20871	4.348791	0.144049	0.232996	0.021199	0	290	243	516	342	380	267	391	374	405	284
ENSMUSG00000030446	chr13	Zfp273	67813740	67813896	3799	-0.49184	0.530976	0.144053	0.232996	0.081971	0	20	24	46	19	18	20	33	16	13	19
ENSMUSG00000029614	chr5	Rpl6	1.21E+08	1.21E+08	2433	0.237922	7.49484	0.144076	0.232998	0.031318	0	2398	2377	3204	2388	2631	2927	4319	3341	4564	2819
ENSMUSG00000081087	chr2	Rps15a-ps7	1.52E+08	1.52E+08	392	0.404582	1.845147	0.144089	0.232998	0.063168	0	42	56	47	49	35	56	84	78	91	55
ENSMUSG00000026083	chr1	Eif5b	37998010	37998324	9753	-0.22554	7.149273	0.144245	0.233222	0.028199	0	2082	2105	3124	2216	2625	1932	2703	2230	3232	1945
ENSMUSG00000070319	chr9	Eif3g	20894352	20894442	1075	0.231938	5.911463	0.144394	0.233434	0.028929	0	836	753	1043	802	919	1041	1365	1012	1520	1002
ENSMUSG00000022037	chr14	Clu	65968483	65968688	3438	-0.26691	6.52035	0.144492	0.233558	0.039208	0	1368	880	1907	1536	2554	1259	1424	1759	1721	1344
ENSMUSG00000044461	chr14	Shisa2	59625281	59626400	3144	-0.23828	6.562638	0.144506	0.233558	0.031369	0	1464	1163	2422	1392	1886	962	2379	1378	2154	1298
ENSMUSG00000030315	chr6	Vgll4	1.15E+08	1.15E+08	4133	-0.26571	3.874247	0.144528	0.233565	0.034925	0	228	155	419	212	303	135	300	277	257	245
ENSMUSG00000039206	chr5	Daglb	1.43E+08	1.43E+08	5677	0.219141	4.412151	0.144677	0.233779	0.024582	0	255	183	463	319	395	317	446	445	481	385
ENSMUSG00000032788	chr10	Pdxk	78436744	78440913	5124	-0.25631	3.972609	0.144728	0.233832	0.031979	0	182	170	403	288	363	203	262	313	270	236
ENSMUSG00000035069	chr4	Oma1	1.03E+08	1.03E+08	2144	-0.23397	4.656444	0.144853	0.234006	0.028588	0	338	286	501	540	523	292	583	394	543	339
ENSMUSG00000024958	chr19	Gpr137	6938069	6938529	2768	0.273161	3.224522	0.144881	0.234023	0.035453	0	105	73	151	175	175	149	204	188	221	160
ENSMUSG00000048277	chr11	Syngr2	1.18E+08	1.18E+08	1776	0.234212	7.816217	0.145027	0.23423	0.030613	0	2995	2656	4584	2966	3372	3595	4785	3570	6548	3948
ENSMUSG00000003435	chr7	Supt5	28314898	28315270	3509	-0.22124	6.343635	0.145064	0.234235	0.026806	0	1019	955	2064	1473	1654	1044	1522	1223	1918	1201
ENSMUSG00000025809	chr8	Itgb1	1.29E+08	1.29E+08	4081	0.210713	7.76912	0.145066	0.234235	0.024764	0	2515	2318	4275	3254	4051	3329	5158	3810	5408	3809
ENSMUSG00000028809	chr4	Srrm1	1.35E+08	1.35E+08	7299	0.21691	5.614476	0.145089	0.234244	0.02545	0	553	488	1181	606	925	710	1067	920	1208	908
ENSMUSG00000037971	chr9	1110032A03Rik	50762828	50764016	5293	-0.2455	3.778325	0.145176	0.234355	0.029958	0	246	196	284	189	253	198	303	193	264	186
ENSMUSG00000021567	chr13	Nkd2	73818534	73821537	4728	-0.42004	1.215083	0.145198	0.234362	0.065984	0	24	28	67	25	68	18	45	38	42	32
ENSMUSG00000101556	chr17	Gm28869	15061069	15061182	811	0.468664	0.400007	0.145239	0.234401	0.06024	0	10	17	19	9	26	20	28	26	34	20
ENSMUSG00000034473	chr16	Sec22a	35311131	35314287	5221	0.27857	3.029769	0.145419	0.234663	0.035178	0	112	89	165	90	131	152	219	157	181	102
ENSMUSG00000029776	chr6	Hibadh	52546228	52547062	2226	-0.24096	7.135593	0.145532	0.234816	0.032415	0	1862	1623	2904	2957	2949	1686	3511	2269	2743	1798
ENSMUSG00000047084	chr7	Ngrn	80261215	80261423	1714	0.237343	4.489182	0.14559	0.234881	0.028122	0	341	276	388	287	320	360	565	393	563	350
ENSMUSG00000003346	chr10	Abhd17a	80583654	80584063	1547	0.214712	5.885109	0.145695	0.235022	0.024835	0	830	653	1031	827	1011	877	1328	1063	1529	1033
ENSMUSG00000030590	chr7	Fam98c	29152511	29152847	2712	0.255564	3.652888	0.145746	0.235076	0.030898	0	173	120	195	214	203	194	289	229	362	184
ENSMUSG00000037999	chr5	Arap2	62602445	62604656	8716	-0.41885	0.848669	0.145765	0.235077	0.058331	0	28	24	52	16	39	18	38	29	25	23
ENSMUSG00000045160	chr6	Bola3	83349147	83349237	3211	-0.23876	6.273995	0.145784	0.235081	0.031565	0	1215	897	1471	1608	1475	970	1832	1099	1642	1056
ENSMUSG00000038615	chr11	Nfe2l1	96817414	96820516	5441	-0.26016	9.45454	0.14588	0.235206	0.038216	0	9013	6424	16169	15989	15450	8573	13928	9968	15873	10662
ENSMUSG00000029710	chr5	Ephb4	1.37E+08	1.37E+08	4640	0.221529	4.090057	0.145922	0.235246	0.024417	0	197	149	336	271	328	268	352	323	456	274
ENSMUSG00000010205	chr9	Raver1	21074168	21075496	3440	0.217652	4.662594	0.146025	0.235354	0.024462	0	329	213	495	404	465	354	573	490	657	428
ENSMUSG00000033361	chrX	Prrg3	71962624	71962779	6087	-0.36373	2.442401	0.146013	0.235354	0.058809	0	55	50	170	101	132	86	73	69	98	90
ENSMUSG00000005804	chr2	Bloc1s6	1.23E+08	1.23E+08	3899	0.224959	4.643445	0.14608	0.235414	0.02554	0	331	282	451	346	425	353	681	392	684	397
ENSMUSG00000039156	chr5	Stim2	53998417	53999034	5215	-0.29893	5.309663	0.146232	0.23563	0.049221	0	715	664	1083	432	562	507	666	671	935	493
ENSMUSG00000085558	chr4	4930412C18Rik	9770585	9770821	6148	0.507086	0.278519	0.146371	0.235825	0.09902	0	9	3	14	26	22	16	29	26	23	23
ENSMUSG00000006931	chr11	Leprel4	1E+08	1E+08	2178	0.36415	2.337441	0.14664	0.236231	0.063512	0	52	34	79	114	70	91	106	84	114	106
ENSMUSG00000022391	chr15	Rangap1	81704248	81705258	3211	0.204716	5.295792	0.146724	0.236338	0.02222	0	515	433	811	517	666	659	819	746	907	678
ENSMUSG00000054874	chr19	Pcnxl3	5664635	5665247	8757	-0.25801	3.959888	0.146811	0.236449	0.032512	0	225	134	455	257	342	224	247	239	320	245
ENSMUSG00000028847	chr4	Trappc3	1.26E+08	1.26E+08	1737	0.215726	4.309494	0.146847	0.236478	0.022792	0	278	219	341	272	345	327	441	386	480	305
ENSMUSG00000030062	chr6	Rpn1	88084473	88084794	3642	0.214115	6.40881	0.146914	0.236557	0.025347	0	1128	882	1572	1214	1535	1507	1813	1579	2026	1368
ENSMUSG00000032381	chr9	Fam96a	66126611	66126970	1240	-0.2069	5.174412	0.146986	0.236619	0.022873	0	595	454	733	617	673	477	748	563	785	509
ENSMUSG00000040860	chr4	Crocc	1.41E+08	1.41E+08	8266	0.376567	1.437912	0.146988	0.236619	0.049368	0	46	27	43	25	38	44	60	43	71	50
ENSMUSG00000018906	chr11	P4ha2	54100095	54100168	6239	0.269362	4.81725	0.14704	0.236674	0.039438	0	292	210	533	541	523	437	519	523	726	578
ENSMUSG00000027562	chr3	Car2	14886273	14886371	2422	-0.44021	2.78738	0.147063	0.236682	0.09919	0	66	51	127	200	204	62	195	94	98	91
ENSMUSG00000032977	chr10	Fam207a	77486656	77488473	2427	0.269247	3.357671	0.147322	0.237013	0.033184	0	153	127	172	134	135	168	234	175	262	176
ENSMUSG00000051403	chr7	Ppp1r37	19530967	19531426	2971	-0.22138	6.011625	0.147316	0.237013	0.027018	0	964	740	1313	1260	1297	803	1249	1002	1419	998
ENSMUSG00000097577	chr14	6230400D17Rik	20687236	20688613	1554	-0.39757	1.791711	0.147302	0.237013	0.074901	0	40	65	63	64	67	28	102	41	65	40
ENSMUSG00000085133	chr14	B930095G15Rik	1.21E+08	1.21E+08	2792	0.426049	1.108031	0.147418	0.237138	0.077184	0	14	16	48	16	53	32	45	35	65	38
ENSMUSG00000034292	chr1	Traf3ip1	91494647	91494888	3712	-0.28568	2.413918	0.147658	0.237484	0.03305	0	69	58	131	106	105	74	110	79	88	78

ENSMUSG00000034334	chr13	Fam151b	92449622	92450252	1381	0.411013	1.055077	0.147669	0.237484	0.05782	0	20	30	38	19	27	30	53	50	37	34
ENSMUSG00000036099	chr10	Vezt	93939165	93939300	20631	-0.21419	5.147145	0.14771	0.237521	0.024626	0	478	512	901	559	607	487	735	550	786	463
ENSMUSG00000025477	chr7	Inpp5a	1.39E+08	1.39E+08	3529	-0.22761	6.588167	0.147778	0.237602	0.028959	0	1572	1072	2409	1613	1767	1291	1686	1375	2395	1412
ENSMUSG00000005043	chr11	Sgsh	1.19E+08	1.19E+08	4414	-0.28581	2.771842	0.147859	0.237704	0.035386	0	85	74	199	108	149	81	110	123	130	107
ENSMUSG00000046985	chr5	Tapt1	44175164	44177182	3487	-0.2207	5.922627	0.147884	0.237714	0.026758	0	876	616	1638	1062	1198	724	1390	889	1250	928
ENSMUSG00000018040	chr15	Rrp7a	83113433	83116971	5411	0.240082	5.175196	0.147922	0.237718	0.030616	0	533	474	608	459	504	597	861	688	870	563
ENSMUSG00000071604	chr19	Fam189a2	23972751	23973631	2547	0.23536	5.117177	0.147911	0.237718	0.029854	0	398	326	674	546	652	419	909	562	852	722
ENSMUSG00000020694	chr11	Tlk2	1.05E+08	1.05E+08	8070	-0.19837	5.569656	0.14801	0.237775	0.021183	0	655	581	1196	803	889	671	1025	730	961	668
ENSMUSG00000026941	chr2	Mamdc4	25563115	25563369	4630	-0.24798	5.823339	0.147976	0.237775	0.034349	0	976	838	1022	915	1038	789	1310	749	1286	683
ENSMUSG00000065954	chr8	Tacc1	25154552	25159820	7695	0.270347	4.168355	0.148011	0.237775	0.03915	0	181	128	445	287	325	228	391	450	408	312
ENSMUSG00000036241	chr4	Ube2r2	41135743	41136246	4189	-0.22121	7.782181	0.148187	0.238029	0.027793	0	3509	3032	4866	3497	3949	3020	4971	3718	4195	2814
ENSMUSG00000026200	chr1	Glb1l	75198236	75198354	5905	0.422632	0.630255	0.148214	0.238043	0.052795	0	24	16	25	16	16	24	36	35	29	25
ENSMUSG00000060860	chr7	Ube2s	4808155	4808484	858	0.259048	5.087602	0.14842	0.238345	0.035955	0	475	477	609	411	433	600	719	634	913	516
ENSMUSG00000031584	chr8	Gsr	33652523	33652570	2754	0.212114	4.493144	0.148494	0.238435	0.022517	0	313	249	459	309	338	349	567	379	582	350
ENSMUSG00000029207	chr5	Apbb2	66298861	66302709	10551	-0.24467	5.228028	0.148524	0.238455	0.03257	0	489	373	952	706	839	446	772	444	956	574
ENSMUSG00000022515	chr16	Anks3	4941415	4941797	2483	0.298255	3.552232	0.148595	0.23854	0.044776	0	201	117	213	139	157	177	218	307	264	194
ENSMUSG00000024246	chr17	Thumpd2	81026327	81026970	1856	0.386337	1.077763	0.148675	0.238624	0.048229	0	22	27	38	24	27	40	49	27	52	38
ENSMUSG00000026176	chr1	Ctdsp1	74391509	74391964	3334	0.222107	6.796629	0.148683	0.238624	0.027817	0	1319	965	2289	1886	1955	1566	2501	2100	2793	2032
ENSMUSG00000006678	chrX	Pola1	93304767	93305816	8813	-0.40735	0.739112	0.148855	0.23887	0.052168	0	16	24	44	31	30	16	34	21	25	27
ENSMUSG00000063810	chr6	Alms1	85587531	85588026	9986	-0.60514	0.062902	0.148933	0.238967	0.112738	0	18	5	40	13	20	15	11	17	8	14
ENSMUSG00000028099	chr3	Polr3c	96711490	96712060	3386	-0.21461	4.631856	0.148989	0.239012	0.024105	0	365	321	477	445	506	345	443	401	549	353
ENSMUSG00000052423	chr1	B4galt3	1.71E+08	1.71E+08	5467	0.258811	3.256186	0.148997	0.239012	0.030789	0	141	103	160	111	171	173	238	167	219	144
ENSMUSG00000097989	chr15	Gm4335	93196595	93197598	1004	0.565025	0.410266	0.149019	0.239018	0.100176	0	14	21	13	16	10	14	45	20	40	18
ENSMUSG00000035139	chr13	Secisbp2	51651697	51651820	4626	-0.22885	3.41943	0.149173	0.239236	0.023881	0	168	129	247	185	192	154	217	166	200	153
ENSMUSG00000027895	chr3	Kcnc4	1.07E+08	1.07E+08	3013	0.276024	6.501719	0.14922	0.239283	0.043186	0	972	806	1782	1546	1605	1125	2061	1472	2010	2330
ENSMUSG00000019857	chr10	Asf1a	53596961	53597298	2180	-0.25327	3.596394	0.149317	0.23938	0.032331	0	170	194	316	162	204	153	282	183	233	161
ENSMUSG00000033083	chr14	Tbc1d4	1.01E+08	1.01E+08	7676	-0.22993	5.429849	0.149313	0.23938	0.028974	0	546	500	1127	862	765	526	1081	701	755	600
ENSMUSG00000052429	chr7	Prmt1	44975989	44976983	2521	0.217005	6.418332	0.149453	0.239569	0.02625	0	1142	1009	1622	1211	1309	1355	2152	1434	2204	1352
ENSMUSG00000061607	chr17	Mdc1	35841515	35841679	7421	-0.27973	2.66485	0.149589	0.239758	0.034018	0	85	84	150	98	138	82	136	116	92	87
ENSMUSG00000039741	chr11	Bahcc1	1.2E+08	1.2E+08	11118	-0.31454	2.903172	0.149627	0.23979	0.046413	0	90	62	236	151	151	76	127	130	157	114
ENSMUSG00000050890	chr4	Pdik1l	1.34E+08	1.34E+08	5810	-0.35335	1.108498	0.149698	0.239846	0.042606	0	27	26	41	39	53	25	34	32	50	25
ENSMUSG00000085037	chr4	4933421O10Rik	33027142	33030521	3847	-0.39649	1.178076	0.149691	0.239846	0.063344	0	35	33	56	42	30	16	31	40	47	37
ENSMUSG00000047193	chr9	Dync2h1	6928503	6929623	16161	-0.3332	1.614768	0.149805	0.239988	0.04123	0	43	33	95	40	63	31	56	44	63	47
ENSMUSG00000062012	chr17	Zfp13	23575845	23577111	2439	-0.41208	0.785044	0.149829	0.239997	0.057101	0	17	26	39	25	43	20	41	17	27	23
ENSMUSG00000018559	chr11	Ctdnep1	69981156	69981585	2182	0.217278	7.490492	0.150035	0.240299	0.026937	0	2343	1747	3505	2859	3000	2571	4110	3196	4632	3284
ENSMUSG00000020863	chr11	Luc7l3	94287890	94291578	7278	0.235497	5.543464	0.150212	0.240554	0.030258	0	657	634	779	580	685	748	1150	879	1068	768
ENSMUSG00000001986	chrX	Gria3	41400854	41401257	9859	0.421555	0.67431	0.150251	0.240587	0.066238	0	14	16	35	13	26	23	24	40	32	33
ENSMUSG00000024269	chr18	Tpgs2	25127223	25129903	6840	-0.2414	3.325386	0.150304	0.240643	0.027397	0	160	99	219	173	225	118	217	170	195	139
ENSMUSG00000029761	chr6	Cald1	34598500	34598665	7687	0.23791	4.929134	0.150433	0.24082	0.03098	0	288	294	614	457	647	408	652	603	713	621
ENSMUSG00000029141	chr5	Slc4a1ap	31526995	31527684	4759	0.216222	4.091035	0.150588	0.241039	0.022709	0	219	206	336	205	292	255	437	299	415	275
ENSMUSG00000036139	chr15	Hoxc9	1.03E+08	1.03E+08	2430	0.252369	3.377675	0.15073	0.241237	0.029458	0	123	129	182	131	184	181	218	171	275	176
ENSMUSG00000026860	chr2	Sh3glb2	30344809	30345427	3990	0.283954	4.685042	0.150776	0.241282	0.043621	0	417	312	470	277	339	426	497	645	638	357
ENSMUSG00000024491	chr18	Rbm27	42275353	42275592	6431	-0.24454	3.662449	0.150882	0.241422	0.029507	0	151	151	302	209	306	129	244	219	274	196
ENSMUSG00000036504	chr2	Phpt1	25573430	25573699	1074	-0.24789	5.818543	0.150913	0.241442	0.034834	0	979	835	1019	906	1033	789	1315	744	1280	675
ENSMUSG00000030725	chr7	Lipt2	1E+08	1E+08	1663	-0.26257	2.468212	0.151055	0.241641	0.028973	0	89	68	120	96	102	76	108	85	101	80
ENSMUSG00000020375	chr11	Rufy1	50389286	50389958	2764	-0.2081	5.012213	0.151257	0.241916	0.023369	0	415	449	737	564	606	450	614	503	732	445
ENSMUSG00000025375	chr11	Aatk	1.2E+08	1.2E+08	7159	-0.30698	2.506413	0.151264	0.241916	0.04002	0	69	55	146	109	132	76	103	95	86	90
ENSMUSG00000044938	chr9	Klhl31	77636500	77636787	6494	0.272723	8.730148	0.151432	0.242157	0.043061	0	7044	5196	8335	4353	5328	6854	10861	7456	11516	6436
ENSMUSG00000056019	chr8	Zfp709	71882068	71882208	4234	-0.43041	0.740276	0.151456	0.242165	0.063811	0	22	25	51	26	22	17	37	29	19	20
ENSMUSG00000034211	chr5	Mrps17	1.3E+08	1.3E+08	2330	0.225426	4.868228	0.151681	0.242496	0.026923	0	362	338	480	465	484	491	742	512	753	405
ENSMUSG00000019505	chr11	Ubb	62551171	62551595	1675	0.217242	8.858614	0.151743	0.242566	0.027367	0	6293	5364	9431	6090	7245	7577	11054	8165	12028	7204
ENSMUSG00000078931	chr8	Pdf	1.07E+08	1.07E+08	1704	-0.21232	5.687076	0.152137	0.24315	0.025194	0	874	616	1085	858	983	772	1175	740	1012	682
ENSMUSG00000097287	chr5	D130017N08Rik	1.44E+08	1.44E+08	4122	-0.31781	1.825084	0.152145	0.24315	0.040423	0	59	43	71	53	81	48	74	38	77	46
ENSMUSG00000054612	chr7	Mgmt	1.37E+08	1.37E+08	818	0.373765	2.432881	0.152394	0.243518	0.064028	0	85	69	81	70	50	109	102	119	131	78
ENSMUSG00000025260	chrX	Hsd17b10	1.52E+08	1.52E+08	1298	0.23823	5.740538	0.152464	0.2436	0.031589	0	675	694	854	804	807	888	1457	937	1350	732
ENSMUSG00000046792	chr7	Zfp787	6131489	6133171	1899	-0.21054	4.439926	0.152665	0.243892	0.023047	0	303	237	472	427	441	262	446	359	454	324
ENSMUSG00000049657	chr4	Zbtb5	44991242	44995386	5606	-0.31117	2.081437	0.152808	0.244092	0.039568	0	65	42	123	72	75	52	74	81	83	48
ENSMUSG00000020918	chr11	Kat2a	1.01E+08	1.01E+08	3480	0.203383	4.163389	0.153017	0.244396	0.020868	0	237	167	363	259	323	275	410	366	413	283
ENSMUSG00000085783	chr16	Gm9816	62717037	62718450	1414	-0.31945	2.087528	0.153149	0.244578	0.042098	0	69	56	103	63	80	74	77	48	74	60
ENSMUSG00000064337	chrMT	mt-Rnr1	70	1024	955	0.313526	9.073386	0.153238	0.24469	0.057486	0	4388	4667	7806	11699	10385	9098	13337	11769	13735	7173
ENSMUSG00000049241	chr5	Hcar1	1.24E+08	1.24E+08	3285	0.954361	1.011133	0.153517	0.245105	0.45904	0	37	26	17	7	7	18	21	144	13	26
ENSMUSG00000051256	chr6	Jagn1	1.13E+08	1.13E+08	1201	0.224993	4.711452	0.153553	0.245133	0.026743	0	389	318	506	331	362	425	626	476	640	416
ENSMUSG00000060149	chr17	BC002059	16951539	16951708	1964	-0.33498	1.388278	0.153616	0.245204	0.044619	0	44	43	51	37	46	34	54	40	41	34
ENSMUSG00000003131	chr9	Pafah1b2	45965311	45968966	4241	0.206636	4.368249	0.15374	0.245344	0.021956	0	272	214	422	283	355	299	464	449	477	329
ENSMUSG00000027429	chr2	Sec23b	1.45E+08	1.45E+08	6302	0.221289	3.872401	0.15374	0.245344	0.024848	0	200	128	338	191	248	209	328	313	356	233

ENSMUSG00000065990	chr4	Aurkaip1	1.56E+08	1.56E+08	1766	0.247471	5.973124	0.153783	0.245383	0.034689	0	991	765	964	847	892	1061	1540	1085	1568	1006
ENSMUSG00000022528	chr16	Hes1	30064384	30064536	2037	0.409008	3.555536	0.153947	0.245586	0.091019	0	102	133	116	241	185	119	486	173	286	207
ENSMUSG00000081769	chr11	Gm12216	53783418	53783678	2647	0.526294	0.053473	0.153931	0.245586	0.093601	0	8	12	19	10	12	14	10	28	21	24
ENSMUSG00000025220	chr19	Mgea5	45750261	45752280	5024	-0.22374	6.127143	0.154096	0.245765	0.02865	0	1093	937	1927	974	1169	964	1430	1102	1488	943
ENSMUSG00000025997	chr1	Ikzf2	69531214	69539492	11613	-0.28056	2.899316	0.154081	0.245765	0.037228	0	115	95	202	88	161	83	126	111	168	122
ENSMUSG00000007812	chr5	Zfp655	1.45E+08	1.45E+08	4514	-0.2591	3.414476	0.154172	0.245849	0.034121	0	143	138	270	204	176	108	273	164	190	159
ENSMUSG00000033953	chr11	Ppp3r1	17159263	17159542	3228	-0.24015	7.511007	0.154186	0.245849	0.033703	0	2692	2764	4833	2473	3104	2300	3776	2494	3952	2887
ENSMUSG00000044716	chr5	Dok7	35056813	35056988	4228	0.277659	4.068432	0.154275	0.24596	0.042649	0	186	101	334	302	333	270	326	295	422	343
ENSMUSG00000025722	chr7	Wdr73	80890723	80891909	3721	0.279196	2.500839	0.154621	0.246483	0.034947	0	55	63	109	86	92	104	117	98	125	105
ENSMUSG00000055681	chr8	Cope	70302518	70302932	3353	0.220791	6.308942	0.154641	0.246486	0.027847	0	1047	975	1416	1118	1233	1358	1823	1365	2015	1259
ENSMUSG00000020272	chr11	Stk10	32533305	32533559	5187	0.30464	2.093209	0.155081	0.247158	0.044308	0	43	26	101	61	81	67	104	89	88	71
ENSMUSG00000026254	chr1	Eif4e2	87213914	87214019	7497	-0.20334	5.847253	0.155209	0.247331	0.023441	0	873	680	1223	967	1220	845	1208	832	1218	804
ENSMUSG00000024054	chr17	Smchd1	71344489	71345365	19319	-0.22996	3.638008	0.155275	0.247359	0.026058	0	164	146	311	212	258	135	276	224	222	189
ENSMUSG00000031216	chrX	Stard8	99003248	99003511	5499	-0.23829	4.432484	0.155282	0.247359	0.029941	0	266	220	568	369	514	287	423	313	376	387
ENSMUSG00000098557	chr14	Kctd12	1.03E+08	1.03E+08	6057	0.269347	4.087209	0.155255	0.247359	0.039647	0	174	178	410	199	308	200	353	424	345	352
ENSMUSG00000016552	chr15	Foxred2	77940522	77943392	5939	-0.47603	1.076042	0.15533	0.247376	0.0888	0	25	27	80	24	40	32	29	41	20	26
ENSMUSG00000020400	chr11	Tnip1	54910785	54911571	3539	-0.21291	6.397833	0.155323	0.247376	0.026141	0	1269	966	1973	1418	1725	1219	1555	1373	1977	1057
ENSMUSG00000046010	chr11	Zfp830	82764345	82765935	1591	-0.22675	3.291341	0.15543	0.247506	0.024291	0	149	127	216	159	188	125	219	145	191	142
ENSMUSG00000044468	chr3	Fam46c	1E+08	1E+08	6097	0.437525	1.300201	0.155475	0.247547	0.086259	0	17	27	74	20	29	28	50	43	77	51
ENSMUSG00000044056	chr11	Efcab9	32522751	32522983	1043	-0.49643	-0.10243	0.155555	0.247644	0.076535	0	16	14	15	18	13	15	17	8	17	6
ENSMUSG00000059995	chr11	Atxn7l3	1.02E+08	1.02E+08	4121	0.211251	4.42764	0.1556	0.247687	0.023449	0	307	217	461	288	335	328	440	402	571	366
ENSMUSG00000085589	chr6	A430078I02Rik	86470805	86472489	2233	-0.49219	-0.13604	0.155659	0.24775	0.058147	0	15	12	26	12	11	8	16	13	13	11
ENSMUSG00000030779	chr7	Rbbp6	1.23E+08	1.23E+08	8752	-0.20673	4.878113	0.155737	0.247816	0.023142	0	371	346	787	485	599	349	616	521	603	421
ENSMUSG00000041609	chr5	Ccdc64	1.16E+08	1.16E+08	5932	-0.3223	1.536539	0.155727	0.247816	0.039381	0	50	32	73	40	58	28	50	42	64	45
ENSMUSG00000050549	chr3	5730508B09Rik	1.28E+08	1.28E+08	1603	0.332578	1.586513	0.155785	0.247861	0.038176	0	45	30	52	37	40	40	80	61	69	47
ENSMUSG00000020738	chr11	Sumo2	1.16E+08	1.16E+08	1736	-0.22772	4.529961	0.155851	0.247937	0.02871	0	381	315	479	377	416	281	615	331	444	306
ENSMUSG00000050288	chr11	Fzd2	1.03E+08	1.03E+08	3663	0.410503	1.664114	0.155891	0.247971	0.078042	0	33	24	48	42	67	27	67	59	74	90
ENSMUSG00000062995	chr6	Ica1	8630527	8630797	3243	0.457714	0.734841	0.15603	0.248162	0.067413	0	19	17	25	26	16	19	44	37	51	17
ENSMUSG00000068079	chr2	Tcf15	1.52E+08	1.52E+08	980	0.334249	2.311883	0.156083	0.248217	0.05501	0	62	34	84	73	98	91	101	59	153	92
ENSMUSG00000020692	chr11	Nle1	82900768	82901050	3233	0.273781	2.975475	0.156226	0.248415	0.037082	0	118	65	140	98	148	154	197	146	170	107
ENSMUSG00000025395	chr10	Prim1	1.28E+08	1.28E+08	3868	0.475689	0.382162	0.156275	0.248463	0.076889	0	8	12	14	27	18	22	32	21	23	27
ENSMUSG00000025791	chr4	Pgm2	99929414	99929811	2921	-0.24042	10.54753	0.156629	0.248995	0.034465	0	26892	21164	36655	19127	25346	21258	29207	24055	31628	19767
ENSMUSG00000057367	chr9	Birc2	7818227	7818943	4580	-0.21438	4.835362	0.156686	0.249033	0.02544	0	475	366	595	443	560	431	656	395	568	374
ENSMUSG00000090778	chr8	Gm3235	91621448	91622006	695	-0.47974	0.871013	0.15669	0.249033	0.092313	0	21	10	32	51	51	20	33	20	34	25
ENSMUSG00000031398	chrX	Plxna3	74329066	74329215	7880	0.423994	0.374385	0.156949	0.249385	0.056923	0	9	8	25	19	22	13	32	25	27	27
ENSMUSG00000040139	chr7	9430038I01Rik	1.37E+08	1.37E+08	5752	-0.31478	1.626309	0.156942	0.249385	0.042125	0	49	42	55	52	65	27	69	49	60	42
ENSMUSG00000057388	chr17	Mrpl18	12911349	12911749	1398	-0.23926	6.340008	0.156978	0.249401	0.03353	0	1108	1028	1439	1679	1715	1049	1872	1084	1672	1193
ENSMUSG00000021519	chr13	Mterf3	66906968	66907183	4652	-0.22478	3.903935	0.157059	0.249501	0.026453	0	230	218	352	228	250	188	335	259	264	212
ENSMUSG00000054920	chr5	Klhl5	65107568	65107861	4866	0.255704	2.956416	0.157267	0.2498	0.030561	0	90	93	163	83	136	129	175	157	182	118
ENSMUSG00000024007	chr17	Ppil1	29250803	29251725	2163	0.244619	3.300188	0.157418	0.250011	0.028165	0	130	113	150	138	176	161	242	170	239	158
ENSMUSG00000024986	chr19	Hhex	37434810	37435233	1918	0.388365	1.058554	0.157545	0.250182	0.046416	0	22	27	39	23	25	24	53	37	58	35
ENSMUSG00000047989	chr18	Ino80c	24104757	24106658	2828	-0.20294	5.37797	0.157565	0.250184	0.023354	0	590	596	978	632	763	544	820	636	935	616
ENSMUSG00000021428	chr13	Riok1	38036989	38037531	2744	0.295011	2.834031	0.157593	0.250198	0.040397	0	97	94	109	83	111	126	202	123	145	112
ENSMUSG00000005338	chr1	Cadm3	1.73E+08	1.73E+08	7248	-0.26738	3.45387	0.157624	0.250217	0.036231	0	122	145	303	167	241	128	239	218	170	147
ENSMUSG00000025364	chr10	Pa2g4	1.29E+08	1.29E+08	2751	0.205856	5.812816	0.157807	0.250418	0.024054	0	744	678	995	824	889	864	1362	1035	1338	927
ENSMUSG00000053289	chr9	Ddx10	53098454	53099262	3368	-0.24284	3.529668	0.157788	0.250418	0.030553	0	144	192	266	174	212	159	244	180	231	150
ENSMUSG00000063172	chr4	Hspb11	1.07E+08	1.07E+08	2071	-0.42178	1.346023	0.157774	0.250418	0.081093	0	47	48	49	27	47	33	53	20	42	43
ENSMUSG00000040234	chr6	Tm7sf3	1.47E+08	1.47E+08	3438	0.216667	3.640114	0.158012	0.250713	0.023061	0	147	134	282	182	185	191	292	243	282	208
ENSMUSG00000002763	chr17	Pex6	46711463	46712384	3796	0.278196	4.89754	0.158061	0.25072	0.044353	0	299	261	497	566	559	328	612	664	738	638
ENSMUSG00000037845	chr9	Fdxacb1	50768236	50768455	3256	0.2886	2.666736	0.158072	0.25072	0.037683	0	65	79	112	76	119	82	160	102	162	127
ENSMUSG00000095832	chr3	Supt20	54692823	54692859	2112	0.297507	2.558805	0.158073	0.25072	0.041499	0	89	64	123	57	84	84	140	127	119	110
ENSMUSG00000045799	chr14	Gm9800	8799589	8800294	914	0.425298	1.082939	0.158098	0.25073	0.071505	0	27	21	22	20	46	49	50	34	42	32
ENSMUSG00000020362	chr11	Cnot6	49671503	49675405	6610	-0.2309	3.613375	0.158177	0.250825	0.026177	0	148	142	283	220	279	157	240	215	217	188
ENSMUSG00000021417	chr13	Eci2	34977748	34978066	2615	-0.25231	5.811629	0.158236	0.250888	0.037363	0	702	721	1007	1282	1137	664	1365	869	1242	663
ENSMUSG00000027014	chr2	Cwc22	77881159	77881490	6822	-0.23119	3.284906	0.158295	0.250922	0.02597	0	144	127	236	140	197	113	217	143	195	151
ENSMUSG00000044337	chr1	Ackr3	90203980	90204087	3348	0.227226	4.435987	0.158278	0.250922	0.028738	0	233	197	524	278	425	339	602	383	419	385
ENSMUSG00000045969	chr8	Ing1	11556066	11557045	2813	-0.25716	3.617475	0.158339	0.250962	0.033764	0	137	118	303	259	282	144	244	184	250	197
ENSMUSG00000003438	chr7	Timm50	28305516	28306030	2684	0.214557	5.368772	0.158365	0.250973	0.026154	0	545	385	731	678	740	686	829	809	1090	638
ENSMUSG00000024891	chr19	Slc29a2	5024006	5024277	2472	0.444182	2.499212	0.158516	0.251182	0.110745	0	28	22	120	108	126	75	141	83	159	129
ENSMUSG00000025609	chr6	Mkln1	31398735	31398954	22296	-0.2066	6.303948	0.158589	0.251269	0.02489	0	1074	931	2141	1222	1598	1036	1692	1177	1693	1162
ENSMUSG00000001158	chr6	Snrnp27	86675221	86675580	1767	0.236754	5.589689	0.158965	0.25178	0.032037	0	676	629	768	648	722	815	1340	773	1136	740
ENSMUSG00000020321	chr11	Mdh1	21556787	21557568	2567	-0.37454	9.204022	0.158964	0.25178	0.084218	0	6067	4840	9265	18381	15812	6345	14168	7170	12083	8340
ENSMUSG00000035776	chrX	Cd99l2	71420060	71422749	4902	-0.20803	6.948378	0.158969	0.25178	0.025599	0	1949	1487	3146	1788	2402	1738	2514	1861	2467	1886
ENSMUSG00000020287	chr11	Mpg	32226505	32226717	3752	0.303448	2.629773	0.159035	0.251855	0.044093	0	75	78	136	51	100	103	126	113	172	101
ENSMUSG00000018189	chr1	Uchl5	1.44E+08	1.44E+08	2921	0.223011	4.629123	0.159144	0.251998	0.026819	0	349	307	445	323	373	429	649	446	545	366

ENSMUSG00000055884	chr12	Fancm	65075606	65076177	7775	-0.44565	0.438738	0.159248	0.252132	0.062741	0	21	16	43	11	28	17	26	19	17	17
ENSMUSG00000005469	chr8	Prkaca	83972978	83973232	2293	0.209996	7.107156	0.159268	0.252133	0.026179	0	1812	1369	2575	2237	2299	2085	3168	2427	3546	2379
ENSMUSG00000046671	chr4	Mtfr1l	1.35E+08	1.35E+08	5370	-0.21303	7.10848	0.159319	0.252184	0.027026	0	2247	1694	3002	2425	2472	2002	2694	2102	3057	1876
ENSMUSG00000092072	chr3	Gm4540	1.06E+08	1.06E+08	395	-0.46576	0.725387	0.15939	0.252266	0.095029	0	23	41	26	27	20	20	28	23	24	24
ENSMUSG00000021815	chr14	Mss51	20482864	20483241	1829	0.366516	6.001381	0.159476	0.252372	0.079807	0	912	801	1106	666	902	1427	1193	548	1686	1562
ENSMUSG00000096403	chr6	Gm9825	7981829	7983430	1602	0.37712	1.294425	0.159541	0.252445	0.0559	0	25	24	36	37	41	53	51	53	58	25
ENSMUSG00000031924	chr8	Cyb5b	1.07E+08	1.07E+08	4294	-0.2321	6.12678	0.159561	0.252447	0.031696	0	968	689	1506	1478	1512	860	1408	1230	1572	880
ENSMUSG00000034442	chr12	Trmt5	73280410	73280632	1669	-0.27238	2.574969	0.159733	0.252689	0.03567	0	94	89	131	87	109	85	140	83	110	71
ENSMUSG00000039457	chr16	Ppl	5086291	5089828	6277	-0.40305	3.086587	0.159812	0.252783	0.087101	0	81	115	304	125	182	130	70	145	126	157
ENSMUSG00000025208	chr19	Mrpl43	45005014	45005940	1213	0.228982	5.238123	0.160107	0.25322	0.029861	0	523	366	553	646	665	600	980	621	905	637
ENSMUSG00000043909	chr2	Trp53bp1	1.21E+08	1.21E+08	14164	-0.20841	4.486553	0.160251	0.253417	0.023246	0	334	257	604	320	452	306	402	344	501	342
ENSMUSG00000024533	chr18	Spire1	67488209	67491549	5178	-0.22748	3.57446	0.160361	0.253561	0.025871	0	168	165	301	175	221	162	204	206	239	178
ENSMUSG00000038375	chr2	Trp53inp2	1.55E+08	1.55E+08	5257	-0.29263	9.082986	0.160573	0.253866	0.05188	0	7140	4036	11731	12547	14234	7175	10024	6955	12714	8059
ENSMUSG00000075053	chr13	Vdac3-ps1	18030324	18031629	1306	-0.49725	5.572436	0.160751	0.254117	0.148193	0	974	941	1536	456	449	384	1518	377	1269	365
ENSMUSG00000048458	chr3	Fam212b	1.06E+08	1.06E+08	4781	-0.34426	2.772952	0.160867	0.25427	0.062302	0	72	75	117	167	179	68	168	118	103	92
ENSMUSG00000009907	chr1	Vps4b	1.07E+08	1.07E+08	8905	-0.20761	4.403996	0.160919	0.254321	0.023427	0	277	291	522	329	410	260	467	380	399	294
ENSMUSG00000019295	chr5	Tmem129	33653216	33654614	2740	0.233633	3.437157	0.160976	0.254382	0.027598	0	129	95	208	168	205	174	279	226	226	158
ENSMUSG00000022295	chr15	Atp6v1c1	38661904	38662083	2097	0.200335	5.032982	0.161166	0.254652	0.022222	0	420	387	607	482	526	504	802	623	716	550
ENSMUSG00000026988	chr2	Wdsub1	59852364	59852961	3598	-0.26084	3.831671	0.161268	0.254782	0.037281	0	263	194	367	152	265	203	294	235	292	161
ENSMUSG00000032998	chr4	Foxj3	1.2E+08	1.2E+08	10973	-0.20524	5.276883	0.161338	0.254863	0.023976	0	516	459	1103	546	808	515	823	614	841	526
ENSMUSG00000053119	chr6	Chmp3	71543797	71544033	3250	0.220292	5.94815	0.161601	0.255248	0.028408	0	860	735	999	882	1012	1072	1503	1130	1378	977
ENSMUSG00000012296	chr17	Tjap1	46257851	46259483	2595	0.204535	4.684704	0.161632	0.255266	0.023191	0	352	228	521	393	445	376	551	493	667	434
ENSMUSG00000000355	chrX	Mcts1	38600578	38600778	1571	0.278422	4.957913	0.161789	0.255483	0.044634	0	506	400	570	333	376	592	804	588	759	383
ENSMUSG00000025776	chr1	Crispld1	17727045	17727134	4515	0.38281	1.336769	0.161913	0.25565	0.065709	0	14	23	49	36	51	36	66	53	40	52
ENSMUSG00000036860	chr11	Mrpl55	59202486	59202659	1027	-0.24421	4.873443	0.161965	0.255689	0.034557	0	445	335	517	667	551	370	574	400	688	440
ENSMUSG00000037286	chr9	Stag1	1.01E+08	1.01E+08	11781	-0.20535	4.734383	0.161984	0.255689	0.023361	0	338	337	720	438	493	359	611	427	494	374
ENSMUSG00000039914	chr10	Coq10a	1.28E+08	1.28E+08	2502	-0.29265	8.303486	0.162001	0.255689	0.052176	0	4125	2774	5772	8225	7410	3804	7225	4018	7163	4331
ENSMUSG00000074364	chr7	Ehd2	15946977	15950792	5100	0.256075	6.044593	0.162015	0.255689	0.039201	0	850	602	1187	1041	1185	940	1103	1729	1608	1122
ENSMUSG00000045411	chr7	2410002F23Rik	44246722	44246823	5233	0.265439	2.739988	0.162187	0.255929	0.032667	0	96	66	143	76	103	104	186	106	151	114
ENSMUSG00000026748	chr2	Plxdc2	16356304	16357237	6947	0.242052	4.562235	0.162267	0.255994	0.03393	0	196	220	566	372	448	378	530	431	488	478
ENSMUSG00000038236	chr6	Hoxa7	52214491	52216030	3761	0.245933	3.143322	0.162262	0.255994	0.02892	0	107	88	159	148	140	113	207	156	232	166
ENSMUSG00000053646	chr9	Plxnb1	1.09E+08	1.09E+08	9545	-0.42599	0.634045	0.162301	0.256018	0.064743	0	14	19	25	33	43	19	27	20	23	23
ENSMUSG00000039849	chr2	Pcif1	1.65E+08	1.65E+08	6544	-0.20844	4.799322	0.162335	0.256041	0.024514	0	349	381	680	462	537	343	600	383	602	448
ENSMUSG00000038893	chr11	Fam117a	95337018	95337261	3029	0.328277	2.40387	0.16237	0.256066	0.052998	0	63	52	114	79	64	77	102	155	116	74
ENSMUSG00000031137	chrX	Fgf13	59062145	59063669	4019	-0.20912	4.988318	0.162559	0.256333	0.024883	0	444	366	852	511	616	363	640	449	778	497
ENSMUSG00000029815	chr6	Malsu1	49073795	49074103	3079	-0.25814	4.967426	0.1626	0.256367	0.039415	0	494	581	625	438	481	402	678	455	643	444
ENSMUSG00000028068	chr3	Iqgap3	88081971	88082092	11384	0.536468	0.035425	0.163048	0.257044	0.111504	0	5	4	21	7	26	11	20	18	22	26
ENSMUSG00000028619	chr4	Tceanc2	1.07E+08	1.07E+08	7193	-0.21576	3.823976	0.163074	0.257054	0.023759	0	231	150	364	208	285	207	278	227	297	184
ENSMUSG00000018669	chr11	Cdk5rap3	96907426	96908122	3812	0.257854	4.81512	0.163351	0.25746	0.037883	0	385	415	529	304	360	435	617	584	702	460
ENSMUSG00000025995	chr1	Wdr75	45795166	45795604	4900	-0.21102	3.887963	0.163383	0.25748	0.023087	0	209	185	358	229	301	184	341	240	256	229
ENSMUSG00000037287	chr9	Tbcel	42412316	42416149	5556	-0.22671	4.297474	0.163692	0.257906	0.028329	0	250	216	450	360	453	259	493	249	366	299
ENSMUSG00000047238	chrX	Mageh1	1.53E+08	1.53E+08	1410	0.314703	1.973115	0.163681	0.257906	0.041909	0	56	42	63	49	60	72	81	57	97	76
ENSMUSG00000029484	chr5	Anxa3	96793385	96793563	1597	0.257513	3.686254	0.163854	0.25813	0.035436	0	170	159	254	145	201	220	288	311	235	200
ENSMUSG00000020923	chr11	Ubtf	1.02E+08	1.02E+08	6552	0.203777	5.899055	0.163877	0.258135	0.02442	0	851	684	1119	772	994	908	1391	1081	1472	1010
ENSMUSG00000020513	chr11	Tubd1	86544991	86545336	2070	-0.23818	3.066654	0.16394	0.258204	0.027256	0	142	97	208	125	154	115	167	147	155	110
ENSMUSG00000038646	chr7	Fam103a1	81762925	81763056	1741	-0.24097	3.865558	0.164058	0.258328	0.032392	0	197	249	311	206	275	178	344	222	275	207
ENSMUSG00000044068	chr11	Zrsr1	22973215	22976496	3282	-0.21582	3.80378	0.164056	0.258328	0.024226	0	213	163	358	217	264	173	334	235	244	196
ENSMUSG00000007987	chr5	Ift22	1.37E+08	1.37E+08	911	0.326859	1.663667	0.164102	0.258337	0.043785	0	45	29	51	34	59	56	73	46	69	64
ENSMUSG00000027954	chr3	Efna1	89271733	89272604	1830	0.250244	3.50101	0.164091	0.258337	0.032602	0	161	103	204	175	181	171	268	166	353	178
ENSMUSG00000053963	chr1	6330403A02Rik	1.8E+08	1.8E+08	6552	0.475765	0.803155	0.164224	0.258498	0.084691	0	16	28	28	18	16	23	58	39	38	19
ENSMUSG00000041477	chr6	Dcp1b	1.19E+08	1.19E+08	6339	-0.29256	1.891541	0.164353	0.25867	0.035699	0	46	50	82	75	66	51	70	52	75	49
ENSMUSG00000097624	chr17	Gm5091	15231585	15232411	1179	-0.54253	0.366818	0.164376	0.258676	0.122138	0	31	26	24	16	11	23	18	11	22	14
ENSMUSG00000045092	chr3	S1pr1	1.16E+08	1.16E+08	3029	0.282612	4.444808	0.164414	0.258704	0.046169	0	221	272	344	260	469	356	677	407	333	395
ENSMUSG00000026799	chr2	Med27	29346819	29347047	3310	0.256238	3.20877	0.164467	0.258758	0.031442	0	118	106	152	144	140	116	262	180	205	158
ENSMUSG00000033065	chr15	Pfkm	98092589	98092665	2957	0.230202	12.21697	0.164534	0.258832	0.032843	0	62615	38363	95335	78367	84640	68252	106784	79795	138041	83655
ENSMUSG00000078941	chr13	Ak6	1.01E+08	1.01E+08	2769	-0.23614	5.749101	0.164875	0.259338	0.033718	0	942	798	1119	794	907	751	1352	731	1088	664
ENSMUSG00000022757	chr16	Tfg	56690332	56691153	2292	-0.20243	5.701409	0.165001	0.259505	0.024362	0	853	654	1323	756	907	622	1117	846	1106	773
ENSMUSG00000061143	chr3	Maml3	51685907	51690854	10486	0.341556	1.858719	0.165053	0.259526	0.057946	0	22	28	86	65	58	66	78	64	88	61
ENSMUSG00000087080	chr11	Gm12199	50717670	50717976	517	-0.50567	1.835474	0.16505	0.259526	0.137645	0	92	73	71	28	46	72	41	46	60	37
ENSMUSG00000053398	chr3	Phgdh	98313170	98313457	2486	0.667042	2.93821	0.16511	0.259585	0.257551	0	143	135	56	40	35	140	98	334	145	106
ENSMUSG00000100755	chr3	Rps23-ps	37714740	37715164	425	0.285458	4.039463	0.165268	0.259802	0.045211	0	272	216	247	189	211	311	402	243	425	264
ENSMUSG00000030498	chr7	Gas2	51862015	51862444	4993	-0.33917	1.069815	0.165402	0.259982	0.040402	0	37	21	40	38	43	27	34	33	42	25
ENSMUSG00000029587	chr5	Zfp12	1.43E+08	1.43E+08	5821	-0.23676	3.201886	0.16551	0.260121	0.027972	0	142	106	230	145	179	94	207	164	171	136
ENSMUSG00000001962	chrX	Fam50a	74313033	74313325	2288	0.212549	4.396001	0.165645	0.260302	0.024519	0	275	258	388	295	326	359	460	356	541	342
ENSMUSG00000031969	chr9	Acad8	26974135	26975760	4143	-0.20683	5.433691	0.165672	0.260314	0.02541	0	621	544	841	796	892	597	953	611	987	566

ENSMUSG00000039041	chr2	Adrm1	1.8E+08	1.8E+08	4457	0.215659	6.361494	0.165831	0.260501	0.028109	0	1135	948	1676	1095	1232	1215	1722	1567	2297	1340
ENSMUSG00000046836	chr1	Brox	1.83E+08	1.83E+08	5010	-0.20376	4.589182	0.165825	0.260501	0.022845	0	335	240	635	411	503	312	515	424	447	345
ENSMUSG00000010045	chr9	Tmem115	1.08E+08	1.08E+08	2194	0.196123	4.422622	0.165911	0.260565	0.021222	0	280	209	451	314	365	330	453	406	500	387
ENSMUSG00000102158	chr1	RP23-433P9.4	1.85E+08	1.85E+08	335	0.527619	-0.08466	0.165901	0.260565	0.069704	0	9	15	13	7	9	13	23	14	25	15
ENSMUSG00000005354	chr15	Txn2	77915047	77915857	4208	0.255997	7.776333	0.166207	0.260986	0.040613	0	2545	1898	3074	4327	4190	3396	5595	3767	5764	3580
ENSMUSG00000030088	chr6	Aldh1l1	90486427	90486531	4512	0.36919	3.948529	0.166218	0.260986	0.08103	0	186	133	305	213	258	238	252	579	198	255
ENSMUSG00000027378	chr2	Nphp1	1.28E+08	1.28E+08	2708	-0.22138	5.135759	0.166281	0.261054	0.029154	0	561	523	825	506	584	496	717	484	839	461
ENSMUSG00000054723	chr17	Vmac	56713932	56715817	2276	0.386143	1.940654	0.166376	0.261172	0.068344	0	57	53	65	44	31	69	86	57	112	64
ENSMUSG00000002343	chr8	Armc6	70220172	70220877	3262	0.24521	3.344768	0.166469	0.261288	0.030733	0	146	108	174	138	167	151	204	213	217	200
ENSMUSG00000033099	chr15	Nol12	78934933	78935075	4317	0.260737	4.480033	0.1665	0.261305	0.03857	0	338	316	350	239	320	391	482	421	553	360
ENSMUSG00000022324	chr15	Matn2	34306680	34306908	3583	0.360813	2.842648	0.166763	0.261686	0.07388	0	53	51	136	120	157	93	180	158	104	177
ENSMUSG00000046020	chr2	Pofut1	1.53E+08	1.53E+08	9912	0.208814	4.431845	0.166813	0.261734	0.02456	0	248	199	450	367	365	297	539	418	465	394
ENSMUSG00000061374	chr7	Fiz1	5007057	5009205	2834	-0.20745	4.380561	0.166841	0.261747	0.023565	0	278	229	488	394	424	294	369	318	453	321
ENSMUSG00000025732	chr17	Fam195a	25863698	25864039	816	-0.33007	4.773648	0.166915	0.261832	0.065643	0	347	207	446	815	652	295	543	439	580	381
ENSMUSG00000051043	chr11	Gprc5c	1.15E+08	1.15E+08	5245	0.231495	6.292169	0.166985	0.261911	0.03292	0	945	746	1996	846	1485	1331	1857	1247	2100	1258
ENSMUSG00000036437	chr8	Npy1r	66697422	66697522	3007	-0.3718	1.663737	0.167072	0.262017	0.061714	0	43	35	99	48	62	54	62	58	44	24
ENSMUSG00000048096	chr1	Lmod1	1.35E+08	1.35E+08	3948	-0.36002	2.945085	0.167099	0.262028	0.07192	0	79	99	133	180	196	59	136	108	143	162
ENSMUSG00000032109	chr9	Nlrx1	44252713	44253539	3980	-0.21085	4.449989	0.167122	0.262033	0.024786	0	311	222	576	373	446	254	413	337	526	336
ENSMUSG00000030879	chr7	Mrpl17	1.06E+08	1.06E+08	4153	0.205241	5.440633	0.167152	0.262049	0.024804	0	575	436	730	716	766	713	1091	754	1055	664
ENSMUSG00000042079	chr6	Hnrnpf	1.18E+08	1.18E+08	3047	0.204294	4.805916	0.167214	0.262116	0.023516	0	409	299	507	418	430	452	659	520	687	425
ENSMUSG00000020719	chr11	Ddx5	1.07E+08	1.07E+08	5775	-0.21665	8.323535	0.167257	0.262121	0.029301	0	5086	4464	7914	4277	5933	4146	7046	5279	6037	4701
ENSMUSG00000039660	chr2	D2Wsu81e	30173453	30174185	3010	0.258076	3.019872	0.167238	0.262121	0.033279	0	105	100	149	105	120	143	167	176	164	135
ENSMUSG00000023909	chr17	Paqr4	23736186	23737999	2507	0.407267	2.440773	0.167296	0.262152	0.091327	0	23	51	80	120	97	72	119	122	124	114
ENSMUSG00000028218	chr4	Fam92a	12153409	12153978	4683	0.268071	2.673984	0.167366	0.262229	0.031947	0	75	76	109	94	99	91	174	117	164	91
ENSMUSG00000030352	chr6	Tspan9	1.28E+08	1.28E+08	4732	-0.19981	4.690939	0.167468	0.262359	0.022373	0	340	271	666	435	563	345	566	398	535	365
ENSMUSG00000009535	chr18	Rnmt	68300355	68300425	7339	-0.22736	5.349548	0.167625	0.262542	0.031153	0	695	573	1053	526	672	568	941	552	862	547
ENSMUSG00000033059	chr2	Pygb	1.51E+08	1.51E+08	4809	0.342903	3.725746	0.167612	0.262542	0.067482	0	226	162	204	136	168	196	229	416	267	211
ENSMUSG00000061032	chr10	Rrp1	78400362	78400984	2008	0.210988	6.023157	0.167724	0.262667	0.026947	0	776	722	1141	1054	1124	1039	1362	1159	1658	1149
ENSMUSG00000040236	chr8	Trappc5	3676299	3676603	2546	-0.21818	5.124308	0.167838	0.262783	0.028124	0	560	374	662	704	695	493	674	499	719	549
ENSMUSG00000045237	chrX	1110012L19Rik	70385877	70386151	1094	-0.21641	4.244286	0.167835	0.262783	0.026795	0	317	270	357	301	349	260	415	273	392	266
ENSMUSG00000015478	chr17	Rnf5	34601091	34601666	1483	0.209805	4.536916	0.167934	0.262872	0.024589	0	316	226	381	379	414	347	552	446	597	349
ENSMUSG00000028952	chr4	Zbtb48	1.52E+08	1.52E+08	3199	-0.30179	1.557743	0.167934	0.262872	0.036533	0	42	40	54	47	68	32	61	44	55	42
ENSMUSG00000022551	chr15	Cyc1	76343523	76343692	1194	-0.3161	8.613568	0.168074	0.26306	0.062677	0	5110	3080	6788	10704	9783	4574	9116	5029	8740	5225
ENSMUSG00000098907	chr9	Mir7082	21075497	21075588	92	0.354881	0.966187	0.168128	0.263113	0.042897	0	19	19	36	32	24	27	38	39	52	33
ENSMUSG00000043279	chr5	Trim56	1.37E+08	1.37E+08	9281	-0.24447	3.817853	0.168305	0.263359	0.032765	0	181	166	362	203	342	163	338	268	218	192
ENSMUSG00000044881	chr7	Coa4	1.01E+08	1.01E+08	1425	-0.30519	2.0737	0.168381	0.263447	0.042576	0	67	46	73	91	85	55	88	62	68	62
ENSMUSG00000019738	chr7	Polr2i	30231948	30232404	1212	0.248201	4.496113	0.16846	0.263501	0.034946	0	330	292	360	320	294	399	582	395	571	305
ENSMUSG00000026974	chr2	Zmynd19	24949792	24950047	4168	-0.20193	4.381713	0.168457	0.263501	0.023055	0	333	271	497	303	383	286	455	331	450	262
ENSMUSG00000031311	chrX	Nono	1.01E+08	1.01E+08	4375	0.191308	5.782683	0.168475	0.263501	0.021822	0	719	637	1108	762	895	849	1333	1032	1273	894
ENSMUSG00000021731	chr13	Mrps30	1.18E+08	1.18E+08	1590	0.212186	4.848788	0.168537	0.263567	0.025928	0	372	280	512	488	488	445	713	511	797	402
ENSMUSG00000044017	chr5	Gpr133	1.29E+08	1.29E+08	8321	0.324287	3.758286	0.16858	0.263603	0.063065	0	144	107	419	126	228	248	202	346	323	217
ENSMUSG00000041040	chr1	Fam117b	59913006	59913752	7290	0.259782	2.900798	0.168784	0.263891	0.033373	0	82	85	150	102	122	133	147	172	159	113
ENSMUSG00000037552	chr7	Plekhg2	28359604	28361261	6797	0.294759	2.527305	0.168962	0.264138	0.04551	0	40	53	113	97	116	99	126	107	144	93
ENSMUSG00000030278	chr6	Cidec	1.13E+08	1.13E+08	1856	0.909038	5.589312	0.169073	0.26428	0.501551	0	1006	674	381	118	153	816	269	3439	422	438
ENSMUSG00000032599	chr9	Ip6k2	1.09E+08	1.09E+08	4067	0.240693	3.385975	0.169274	0.264563	0.030285	0	114	112	192	139	213	155	275	151	268	188
ENSMUSG00000004980	chr6	Hnrnpa2b1	51460434	51463254	4086	0.214197	9.026992	0.169603	0.265045	0.02899	0	6976	6291	8643	7201	9103	8114	12805	9390	13194	8251
ENSMUSG00000031023	chr7	Akip1	1.1E+08	1.1E+08	1305	0.326618	3.317771	0.169695	0.265158	0.059415	0	161	132	139	100	143	219	198	200	254	123
ENSMUSG00000080242	chr6	Gm15487	37806086	37806550	465	0.371388	1.401553	0.169754	0.265219	0.058859	0	24	21	38	54	40	36	54	51	83	40
ENSMUSG00000027649	chr2	Ctnnbl1	1.58E+08	1.58E+08	2705	0.229442	3.457761	0.169805	0.265267	0.028115	0	107	103	237	176	202	149	263	226	250	191
ENSMUSG00000048776	chr6	Pthlh	1.47E+08	1.47E+08	1603	-0.5777	0.085142	0.169946	0.265456	0.149098	0	21	11	7	20	31	5	19	8	18	21
ENSMUSG00000036403	chr5	Cep135	76588698	76588924	7188	-0.37108	0.667061	0.170248	0.265897	0.041929	0	25	17	35	28	30	21	27	20	24	25
ENSMUSG00000039509	chr8	Nup133	1.24E+08	1.24E+08	5808	-0.19749	4.541308	0.170501	0.266261	0.021907	0	287	257	571	415	508	311	500	356	487	336
ENSMUSG00000024078	chr17	Ttc27	74717750	74718011	2820	-0.23759	3.394165	0.170723	0.266577	0.030613	0	164	153	234	178	164	164	198	156	211	141
ENSMUSG00000024370	chr18	Cdc23	34630951	34631301	9500	-0.19895	4.32154	0.170895	0.266813	0.021829	0	285	238	503	305	406	269	444	326	346	307
ENSMUSG00000033075	chr15	Senp1	98038744	98042952	11873	-0.23255	3.208511	0.170993	0.266935	0.026407	0	123	106	261	139	187	116	166	150	197	141
ENSMUSG00000032202	chr9	Rab27a	73044854	73045011	3879	0.417213	0.860757	0.171025	0.266953	0.067949	0	21	19	25	22	29	35	32	52	35	21
ENSMUSG00000024454	chr18	Hdac3	37935844	37937683	4026	-0.25374	6.196394	0.171269	0.267272	0.040479	0	1264	1233	1649	949	1126	1066	1433	1100	1653	906
ENSMUSG00000036167	chr15	Pphln1	93398350	93398461	4264	-0.2292	3.491661	0.171255	0.267272	0.027796	0	152	136	286	173	238	117	239	186	210	191
ENSMUSG00000021619	chr13	Atg10	90935349	90936245	1609	-0.27893	3.273137	0.1713	0.267289	0.043177	0	119	98	177	232	223	118	228	129	189	137
ENSMUSG00000040987	chr7	Mill2	18839966	18840091	1121	-0.54952	0.211299	0.1715	0.267568	0.109954	0	13	13	44	15	20	22	20	14	6	13
ENSMUSG00000017405	chr11	Nek8	78166106	78166777	5222	0.457982	0.26322	0.171569	0.267633	0.06891	0	12	13	16	13	19	18	16	25	23	30
ENSMUSG00000031351	chrX	Zfp185	72987339	72987519	3707	0.556815	0.642778	0.171581	0.267633	0.146301	0	19	15	20	13	27	34	26	52	10	28
ENSMUSG00000031537	chr8	Ikbkb	22659212	22660459	19078	0.198069	4.227235	0.17167	0.267739	0.021529	0	251	190	352	290	313	266	439	368	411	336
ENSMUSG00000031781	chr8	Ciapin1	94819818	94823207	5691	0.294859	4.663156	0.171821	0.267913	0.053131	0	237	199	334	577	480	419	609	436	650	439
ENSMUSG00000053453	chr14	Thoc7	13949014	13949327	883	-0.22353	6.003099	0.171819	0.267913	0.031268	0	1038	939	1315	1047	1090	870	1558	887	1254	897

ENSMUSG00000029076	chr4	Sdf4	1.56E+08	1.56E+08	6115	0.19584	6.818358	0.17195	0.268069	0.024028	0	1394	1233	2260	1765	1821	1768	2685	1976	2710	1917
ENSMUSG00000030978	chr7	Rrm1	1.02E+08	1.02E+08	3997	-0.21854	5.450303	0.171962	0.268069	0.029067	0	567	478	997	795	1009	555	1059	614	742	729
ENSMUSG00000020456	chr11	Ogdh	6291633	6291693	5456	-0.31196	9.878401	0.172082	0.268193	0.062296	0	10177	7043	21232	24994	23658	10361	18722	12729	22822	13719
ENSMUSG00000099227	chr1	Mir8114	1.54E+08	1.54E+08	111	-0.34395	4.608502	0.172075	0.268193	0.072051	0	210	205	905	436	616	319	514	444	270	375
ENSMUSG00000054252	chr5	Fgfr3	33721724	33721928	6907	0.379319	1.194277	0.172119	0.268219	0.057237	0	18	27	39	30	38	28	42	35	72	49
ENSMUSG00000001999	chr2	Blvra	1.27E+08	1.27E+08	2446	0.225232	3.60438	0.172234	0.268367	0.026439	0	161	149	216	159	198	207	299	226	245	204
ENSMUSG00000005360	chr15	Slc1a3	8634124	8636339	8537	0.73976	2.834657	0.17233	0.268486	0.329847	0	145	83	101	26	40	68	98	455	70	87
ENSMUSG00000024571	chr18	Gm16286	80206765	80206901	3075	0.205389	5.983724	0.172418	0.268591	0.025929	0	878	718	1163	930	982	977	1497	1236	1578	952
ENSMUSG00000042508	chr5	Dmtf1	9118801	9120138	11041	-0.25445	2.937978	0.172707	0.269009	0.03372	0	87	116	196	116	152	95	168	136	140	96
ENSMUSG00000021067	chr12	Sav1	69965012	69966347	2524	-0.25589	5.970352	0.172915	0.269302	0.041314	0	945	1005	1819	729	989	718	1281	918	1463	923
ENSMUSG00000030057	chr6	Cnbp	87842615	87844156	2536	-0.24157	9.260719	0.172938	0.269306	0.037542	0	10147	9670	14018	8611	9867	8500	13422	7814	13744	8580
ENSMUSG00000063049	chr8	Ing2	47667178	47669336	3019	0.29098	3.940482	0.172975	0.269332	0.048842	0	250	208	301	139	174	254	395	244	409	249
ENSMUSG00000028567	chr4	Txndc12	1.09E+08	1.09E+08	2253	0.250858	3.272037	0.173143	0.269562	0.032167	0	128	120	178	115	153	128	227	218	203	172
ENSMUSG00000031090	chr7	Nadsyn1	1.44E+08	1.44E+08	3306	-0.32771	1.367195	0.173399	0.269929	0.041804	0	28	41	63	36	55	30	49	34	53	36
ENSMUSG00000066415	chr9	Msl2	1.01E+08	1.01E+08	5627	-0.19534	4.755773	0.173493	0.270043	0.022232	0	346	313	685	475	537	324	548	428	589	424
ENSMUSG00000037275	chr11	Gemin5	58120002	58121784	6618	-0.20117	3.967574	0.1736	0.270178	0.021819	0	223	167	386	254	335	209	353	263	299	208
ENSMUSG00000030996	chr7	Art1	1.02E+08	1.02E+08	1417	-0.22059	8.498401	0.173684	0.270273	0.03133	0	5505	4069	7597	6868	7333	4977	8034	4403	8041	5434
ENSMUSG00000075266	chr10	Cenpw	30196011	30197226	1510	0.558454	-0.1276	0.173702	0.270273	0.093571	0	13	14	11	4	8	17	17	17	24	12
ENSMUSG00000019659	chr9	Ccdc12	1.11E+08	1.11E+08	818	0.224229	5.107463	0.17376	0.270332	0.030153	0	499	423	528	495	534	605	730	612	888	548
ENSMUSG00000024049	chr17	Myom1	71019521	71019651	5672	-0.22562	10.55541	0.174017	0.2707	0.032956	0	21469	15762	40718	27378	28531	16652	32867	20907	38233	21560
ENSMUSG00000022246	chr15	Rai14	10568979	10570774	5008	0.325435	3.388597	0.174111	0.270814	0.0626	0	93	68	144	216	233	166	235	164	309	189
ENSMUSG00000031848	chr8	Lsm4	70673248	70673457	1038	0.21215	5.386096	0.174237	0.270978	0.02719	0	591	525	714	591	615	678	1020	697	1059	672
ENSMUSG00000010651	chr9	Acaa1b	1.19E+08	1.19E+08	1962	1.086269	-0.03392	0.174314	0.271024	0.593706	0	18	14	5	0	2	13	5	63	13	11
ENSMUSG00000026483	chr1	Fam129a	1.52E+08	1.52E+08	7380	-0.2503	4.090753	0.174298	0.271024	0.036117	0	175	176	486	302	408	182	319	258	363	299
ENSMUSG00000038806	chr1	Sde2	1.81E+08	1.81E+08	3471	0.237733	3.396909	0.174327	0.271024	0.03068	0	123	91	256	156	166	133	303	202	241	171
ENSMUSG00000031485	chr8	Prosc	27042555	27042713	4534	-0.2238	5.072437	0.174415	0.271074	0.030441	0	413	338	752	716	747	420	711	459	704	554
ENSMUSG00000036180	chr8	Gatad2a	69907069	69909974	5502	0.189164	4.746983	0.17439	0.271074	0.021078	0	315	274	561	382	511	445	601	516	611	428
ENSMUSG00000050663	chr10	Trhde	1.14E+08	1.14E+08	8065	-0.54581	0.196078	0.174421	0.271074	0.134926	0	16	24	29	11	18	10	29	24	6	9
ENSMUSG00000027198	chr2	Ext2	93661028	93661681	7328	-0.21757	5.149369	0.174577	0.271285	0.028789	0	494	437	900	614	650	404	631	597	661	672
ENSMUSG00000037907	chr11	Ankrd13b	77470485	77471823	3839	-0.2132	3.877525	0.174793	0.271589	0.025509	0	189	182	327	290	277	189	288	264	326	181
ENSMUSG00000083477	chr5	Gm5555	49552257	49553270	1014	0.565682	-0.08272	0.174868	0.271672	0.114774	0	13	9	15	8	8	23	17	22	24	4
ENSMUSG00000038578	chr4	Susd1	59314683	59315409	4766	0.573067	0.306806	0.174893	0.27168	0.141872	0	14	14	26	7	12	30	25	40	13	11
ENSMUSG00000038530	chr1	Rgs4	1.7E+08	1.7E+08	3098	0.272451	3.324671	0.175121	0.272003	0.041504	0	84	101	177	172	197	137	281	190	282	129
ENSMUSG00000060862	chr4	Zbtb40	1.37E+08	1.37E+08	10710	-0.2336	3.282569	0.175277	0.272213	0.028724	0	138	113	265	163	173	114	170	181	190	152
ENSMUSG00000090733	chr3	Rps27	90212725	90212753	255	0.317755	7.324761	0.175357	0.272305	0.065095	0	2553	2417	2407	1710	1707	3247	4533	2773	3659	2124
ENSMUSG00000020564	chr12	Atxn7l1	33147693	33147915	12523	-0.23628	3.782103	0.175554	0.27258	0.031139	0	176	130	377	222	332	160	320	185	287	212
ENSMUSG00000003444	chr7	Med29	28386146	28387024	1281	0.219457	3.934367	0.175668	0.272693	0.026473	0	199	187	274	222	230	277	357	240	354	259
ENSMUSG00000020495	chr11	Smg8	87077732	87078150	3218	-0.22336	3.247337	0.175662	0.272693	0.026032	0	127	112	227	169	189	120	230	130	192	132
ENSMUSG00000028416	chr4	Bag1	40936398	40936676	1349	0.2087	7.288749	0.175773	0.272824	0.027968	0	2053	1842	2727	2441	2418	2446	3854	2749	3833	2559
ENSMUSG00000086688	chr11	Gm11560	99932162	99933109	948	-0.42047	0.048101	0.175878	0.272954	0.054872	0	13	14	20	20	18	7	17	12	21	16
ENSMUSG00000022833	chr16	Ccdc14	34690616	34690831	4107	-0.29391	1.622357	0.17598	0.27308	0.032522	0	47	30	76	51	64	40	59	51	53	41
ENSMUSG00000027374	chr2	Mrps5	1.28E+08	1.28E+08	6578	-0.21653	5.056245	0.176108	0.273247	0.028836	0	452	358	672	686	720	465	766	440	733	443
ENSMUSG00000026213	chr1	Stk11ip	75521529	75521642	5743	0.223166	4.097446	0.176353	0.273596	0.028299	0	213	200	372	251	226	272	363	278	500	278
ENSMUSG00000097316	chr1	Gm10516	1.92E+08	1.92E+08	2788	0.350938	1.311022	0.176558	0.273882	0.051402	0	21	24	38	38	47	38	60	54	68	26
ENSMUSG00000025608	chr6	Podxl	31519488	31523219	5488	-0.30123	5.475939	0.176895	0.274373	0.05798	0	416	403	950	1062	1254	445	1132	603	945	621
ENSMUSG00000040043	chr10	Rbms2	1.28E+08	1.28E+08	5609	-0.21004	5.914183	0.177062	0.2746	0.027839	0	772	616	1369	1194	1352	799	1140	970	1336	882
ENSMUSG00000042202	chr4	Slc35e2	1.56E+08	1.56E+08	6574	0.303701	2.174348	0.177218	0.274808	0.049209	0	55	27	101	58	88	64	118	105	82	75
ENSMUSG00000020390	chr11	Ube2b	51985497	51986810	2126	-0.23728	8.949915	0.17725	0.274818	0.036936	0	8203	7650	11621	7088	7650	6224	12076	6812	10113	6987
ENSMUSG00000026811	chr2	St6galnac6	32599709	32599836	4815	0.225459	6.124894	0.177265	0.274818	0.032276	0	1069	854	1295	907	930	1196	1701	1236	1666	1092
ENSMUSG00000071317	chr10	Bves	45335762	45335881	1607	0.192097	5.616368	0.177364	0.27494	0.022811	0	657	539	1010	717	755	693	1138	872	1303	824
ENSMUSG00000038212	chr13	Hiatl1	65064663	65066861	3925	-0.24724	3.439275	0.177606	0.275277	0.034156	0	144	157	259	179	198	123	193	213	178	182
ENSMUSG00000055692	chr16	Tmem191c	17276300	17276468	2441	0.5087	-0.02313	0.177624	0.275277	0.065741	0	12	11	10	14	9	19	23	19	21	11
ENSMUSG00000041303	chr1	Gtf3c3	54396004	54398002	4925	-0.23504	3.47361	0.177699	0.275361	0.02962	0	151	106	261	176	292	145	225	170	223	165
ENSMUSG00000027800	chr3	Tm4sf1	57285611	57287770	3355	0.293873	4.160904	0.177748	0.275406	0.051959	0	202	208	245	279	327	194	676	275	452	275
ENSMUSG00000057667	chr7	Bloc1s3	19505814	19507610	1824	0.276567	2.721755	0.177839	0.275515	0.037723	0	84	91	107	71	109	99	147	132	168	106
ENSMUSG00000058833	chr8	2810428I15Rik	70504292	70504509	1822	0.265621	5.979453	0.177913	0.275597	0.045054	0	955	930	982	698	821	1105	1435	1159	1636	973
ENSMUSG00000041560	chr7	Gltscr2	15937838	15937889	1555	0.197441	5.803351	0.178007	0.27571	0.02447	0	688	621	1017	917	911	903	1180	1000	1439	931
ENSMUSG00000022024	chr14	Sugt1	79587691	79587866	1951	-0.22779	6.136417	0.17803	0.275714	0.03353	0	1084	1122	1685	989	1117	911	1643	1029	1404	999
ENSMUSG00000018160	chr11	Med1	98152154	98152963	8753	-0.20303	4.417932	0.178114	0.275748	0.023761	0	289	212	539	371	472	270	453	364	401	325
ENSMUSG00000037570	chr15	Mcrs1	99242818	99243220	1915	0.204807	4.557944	0.178109	0.275748	0.024707	0	272	241	427	377	446	344	659	379	589	368
ENSMUSG00000044405	chr2	Adig	1.59E+08	1.59E+08	810	0.861937	3.051951	0.178073	0.275748	0.463513	0	67	71	24	171	107	107	52	639	56	60
ENSMUSG00000012609	chr12	Ttll5	85824659	85824731	15833	-0.32514	2.157951	0.178501	0.276296	0.052308	0	57	31	106	82	130	54	83	70	88	60
ENSMUSG00000097413	chr18	A830052D11Rik	32359057	32359435	1130	0.312297	2.543587	0.17851	0.276296	0.05017	0	84	77	113	56	73	100	136	102	173	76
ENSMUSG00000040188	chr9	Scamp2	57560944	57561110	2341	0.213939	5.752177	0.178658	0.276492	0.029132	0	814	546	1237	579	886	897	1218	1078	1299	802
ENSMUSG00000032332	chr9	Col12a1	79598991	79601179	15228	-0.58313	3.841261	0.178777	0.276645	0.2155	0	46	104	464	312	587	133	227	242	88	303

ENSMUSG00000022607	chr15	Ptk2	73205105	73206260	4991	-0.19757	4.736613	0.178842	0.276713	0.023156	0	387	280	734	397	553	348	509	445	583	388
ENSMUSG00000029722	chr5	Agfg2	1.38E+08	1.38E+08	3802	0.324361	2.388418	0.178863	0.276713	0.058047	0	50	54	91	75	99	113	95	124	79	91
ENSMUSG00000022684	chr16	Bfar	13671858	13672078	4451	-0.18532	5.835188	0.178887	0.276718	0.021664	0	847	705	1298	929	1116	833	1148	871	1182	842
ENSMUSG00000030002	chr6	Dusp11	85942268	85947776	7639	0.204744	4.713704	0.178955	0.276791	0.025753	0	309	250	697	330	439	396	648	516	616	404
ENSMUSG00000031378	chrX	Abcd1	73716597	73717930	4192	0.223176	4.999028	0.17902	0.276859	0.031268	0	311	273	625	606	605	476	720	595	829	541
ENSMUSG00000071654	chr19	Uqcc3	8880016	8880616	829	0.239728	5.403427	0.179113	0.276971	0.036106	0	668	527	722	522	588	779	973	715	1166	580
ENSMUSG00000016664	chr15	Pacsin2	83375607	83377730	3885	-0.24473	5.761275	0.179227	0.277106	0.038369	0	649	470	1134	1228	1372	755	1081	845	1120	746
ENSMUSG00000071419	chr6	Rps15-ps2	58017506	58017943	438	0.240604	3.747596	0.179242	0.277106	0.032526	0	197	156	274	185	159	209	380	248	277	214
ENSMUSG00000073481	chr1	Marc2	1.85E+08	1.85E+08	6629	0.221088	5.979807	0.1793	0.277162	0.031217	0	959	758	1167	765	954	1065	1374	1266	1580	928
ENSMUSG00000081824	chr16	BC002163	42955631	42955949	319	0.295235	3.381069	0.1794	0.277285	0.049082	0	147	121	137	180	132	185	310	177	252	131
ENSMUSG00000032251	chr9	Irak1bp1	82829540	82830339	2158	-0.33242	1.541228	0.180002	0.278183	0.050996	0	51	47	59	37	53	35	43	37	65	47
ENSMUSG00000041264	chr5	Uspl1	1.49E+08	1.49E+08	6648	-0.19476	5.326251	0.180023	0.278183	0.023784	0	671	515	959	586	699	552	846	624	787	607
ENSMUSG00000052406	chr2	Rexo4	26953563	26954596	3662	0.197461	4.210333	0.180241	0.278488	0.022716	0	239	183	389	279	303	330	447	359	382	273
ENSMUSG00000031755	chr8	Bbs2	94067954	94068382	3194	0.256913	2.412731	0.180402	0.278704	0.031361	0	69	51	101	75	88	79	144	109	106	83
ENSMUSG00000036916	chrX	Zfp280c	48541625	48543289	5236	-0.37424	1.651306	0.180552	0.27887	0.065723	0	43	30	86	30	99	36	50	51	56	47
ENSMUSG00000061751	chr16	Kalrn	33974258	33976079	18660	-0.32197	3.693734	0.180535	0.27887	0.063876	0	161	102	326	289	314	128	267	118	370	196
ENSMUSG00000037007	chr5	Zfp113	1.38E+08	1.38E+08	6754	-0.28712	2.104994	0.180611	0.278929	0.042073	0	54	65	84	62	105	50	94	76	78	51
ENSMUSG00000058799	chr10	Nap1l1	1.11E+08	1.11E+08	4086	0.240642	6.57986	0.180889	0.279293	0.037868	0	1332	1336	1973	970	1305	1506	2172	1874	2389	1560
ENSMUSG00000084106	chr1	Gm6136	86908793	86909683	891	0.261977	3.793741	0.180874	0.279293	0.039345	0	186	207	209	169	195	237	365	244	290	234
ENSMUSG00000035469	chr14	Rcbtb1	59201209	59201304	6010	-0.21264	4.125387	0.180943	0.279344	0.02663	0	234	243	457	230	353	225	383	235	356	280
ENSMUSG00000044475	chr10	Ascc1	60002805	60002907	1578	0.216155	4.312493	0.181006	0.279409	0.027186	0	283	242	402	252	277	319	501	335	527	287
ENSMUSG00000043923	chr9	Ccdc84	44410160	44410364	1158	0.404171	0.887732	0.181052	0.279448	0.064617	0	29	21	36	13	20	34	38	30	52	27
ENSMUSG00000025781	chr2	Atp5c1	10056016	10056161	1908	-0.24938	9.286681	0.181081	0.279459	0.041529	0	8656	6882	11128	14433	13223	8324	15230	7876	13361	8384
ENSMUSG00000089875	chr13	Etohd2	59769965	59770133	3136	0.381147	0.652421	0.181146	0.279527	0.048346	0	15	14	22	21	30	30	38	31	31	20
ENSMUSG00000041915	chr18	Ammecr1l	31759824	31760194	4769	-0.23826	3.302325	0.181186	0.279557	0.030998	0	116	104	256	190	207	113	177	164	234	140
ENSMUSG00000004609	chr7	Cd33	43527456	43529008	2571	0.436196	0.287407	0.181322	0.279734	0.082773	0	6	11	29	14	18	27	24	12	26	25
ENSMUSG00000034932	chr10	Mrpl54	81264713	81264997	825	0.223221	5.703703	0.18145	0.279899	0.031711	0	755	692	822	719	740	858	1292	900	1286	823
ENSMUSG00000030881	chr7	Arfip2	1.06E+08	1.06E+08	4902	0.275586	2.942608	0.181491	0.27993	0.041426	0	105	80	129	124	106	138	170	188	147	107
ENSMUSG00000039828	chr15	Wdr70	7873055	7873253	2151	-0.27687	4.290098	0.181741	0.280283	0.04857	0	322	354	513	190	305	267	380	320	402	248
ENSMUSG00000011837	chr8	Snapc2	4253102	4253304	1513	0.205022	3.897794	0.181785	0.280318	0.02363	0	191	152	298	221	251	234	322	301	401	204
ENSMUSG00000035919	chr9	Bbs9	22475715	22476055	6243	0.224887	2.91432	0.181879	0.28043	0.025633	0	99	75	163	100	120	116	176	133	172	135
ENSMUSG00000024869	chr19	Nudt8	4000580	4000847	4298	-0.28813	3.554535	0.181944	0.280498	0.050756	0	130	144	179	307	258	143	240	184	248	155
ENSMUSG00000000326	chr16	Comt	18406886	18408040	2532	0.193251	5.430235	0.18198	0.28052	0.023719	0	558	393	863	734	714	686	934	812	1041	722
ENSMUSG00000027367	chr2	Stard7	1.27E+08	1.27E+08	5567	-0.27381	7.511891	0.18216	0.280766	0.050045	0	2183	1696	3719	4525	4238	2025	4215	2241	4422	2620
ENSMUSG00000020739	chr11	Nup85	1.16E+08	1.16E+08	3385	0.198452	4.771698	0.18226	0.280887	0.02389	0	383	313	531	367	432	451	689	500	551	460
ENSMUSG00000024993	chr19	Fam45a	60811585	60811673	6242	-0.26373	2.83882	0.182376	0.281034	0.038059	0	104	90	192	118	122	81	181	133	112	86
ENSMUSG00000019891	chr10	Dcbld1	52233619	52233835	7282	0.387978	1.161243	0.182414	0.281059	0.073978	0	19	11	33	42	46	33	64	50	39	34
ENSMUSG00000031256	chrX	Cstf2	1.34E+08	1.34E+08	9180	-0.23102	2.990841	0.18253	0.281206	0.027881	0	110	106	171	128	167	93	155	147	162	107
ENSMUSG00000027074	chr2	Slc43a3	84936579	84936644	4464	-0.31159	4.450045	0.182661	0.281375	0.061291	0	228	215	688	398	517	428	349	414	339	199
ENSMUSG00000026858	chr2	Fam73b	30364233	30364305	6249	-0.28203	3.929049	0.182732	0.28145	0.048663	0	208	137	310	348	354	164	293	329	216	235
ENSMUSG00000029162	chr5	Khk	30921556	30922007	1670	0.23473	4.054159	0.182782	0.281496	0.032649	0	208	212	332	227	227	335	389	243	395	261
ENSMUSG00000024112	chr17	Cacna1h	25374285	25376146	9763	0.319331	1.26932	0.183168	0.282056	0.044265	0	20	20	49	28	52	35	60	38	65	38
ENSMUSG00000028744	chr4	Pqlc2	1.39E+08	1.39E+08	3516	0.235413	2.972589	0.183287	0.282208	0.030295	0	102	69	179	98	137	148	176	144	175	118
ENSMUSG00000059796	chr11	Eif4a1	69666936	69667617	4334	0.20872	6.536023	0.183348	0.282268	0.02864	0	1246	1135	1865	1255	1352	1480	2477	1803	2076	1337
ENSMUSG00000032006	chr9	Pdgfd	6168612	6168918	3119	-0.33847	1.436159	0.183429	0.28236	0.050676	0	42	37	76	42	38	31	51	55	38	34
ENSMUSG00000026817	chr2	Ak1	32621758	32621877	2593	0.213837	10.96647	0.18352	0.282455	0.030937	0	30428	20401	36086	28091	33040	35018	45373	35310	53617	28635
ENSMUSG00000029192	chr5	Tbc1d14	36490604	36493114	9802	-0.20122	4.211691	0.183554	0.282455	0.023503	0	271	184	490	318	363	270	417	261	363	264
ENSMUSG00000068874	chr3	Selenbp1	94933056	94933162	2273	0.251202	4.847904	0.183541	0.282455	0.04053	0	289	287	555	533	461	364	638	726	529	566
ENSMUSG00000028821	chr4	Syf2	1.35E+08	1.35E+08	2043	0.218817	5.542041	0.183622	0.282527	0.030559	0	637	651	824	559	693	746	1129	843	1176	717
ENSMUSG00000026637	chr1	Traf5	1.92E+08	1.92E+08	4566	0.330965	1.348451	0.183663	0.282556	0.046666	0	23	23	42	45	41	35	55	60	50	46
ENSMUSG00000078974	chr11	Sec61g	16500530	16501807	2464	0.305477	5.339427	0.184009	0.283056	0.060833	0	668	592	652	435	402	773	1169	631	987	567
ENSMUSG00000027323	chr2	Rad51	1.19E+08	1.19E+08	6649	0.422741	0.727067	0.184093	0.283152	0.076683	0	18	20	41	12	16	22	33	39	30	35
ENSMUSG00000018846	chr11	Pank3	35769484	35769947	7376	-0.30237	4.849359	0.184457	0.283679	0.059542	0	486	376	808	397	512	307	390	779	438	394
ENSMUSG00000029168	chr5	Dpysl5	30711564	30712002	6867	-0.40843	0.715599	0.184576	0.283829	0.066065	0	25	22	45	17	34	23	19	25	40	14
ENSMUSG00000024713	chr19	Pcsk5	17432832	17433775	9346	0.356752	1.777684	0.184673	0.283946	0.068653	0	28	36	79	34	64	66	63	93	55	54
ENSMUSG00000040710	chr1	St8sia4	95587682	95591964	20091	-0.31905	2.071488	0.184753	0.284036	0.052814	0	46	43	96	77	114	41	83	82	92	42
ENSMUSG00000006307	chr7	Kmt2b	30568858	30569436	9596	-0.23965	4.447761	0.184821	0.284074	0.035205	0	267	204	683	356	481	263	371	410	401	360
ENSMUSG00000030613	chr7	Ccdc90b	92561149	92561635	1801	-0.19843	4.126562	0.184813	0.284074	0.023677	0	275	242	376	271	313	237	394	250	343	262
ENSMUSG00000052056	chr2	Zfp217	1.7E+08	1.7E+08	6139	0.247458	3.39828	0.184967	0.284266	0.036265	0	115	106	294	105	179	157	278	206	239	165
ENSMUSG00000039917	chr5	Rhbdd2	1.36E+08	1.36E+08	7478	0.216263	3.386415	0.185204	0.284566	0.026307	0	119	99	211	165	187	162	208	219	245	178
ENSMUSG00000079017	chr12	Ifi27l2a	1.03E+08	1.03E+08	463	0.805826	5.627809	0.185205	0.284566	0.427258	0	1164	740	262	118	162	1118	673	2658	494	488
ENSMUSG00000033885	chr14	Pxk	8098213	8098416	2840	-0.20512	3.7261	0.185492	0.284974	0.023261	0	171	147	319	218	300	192	276	221	250	177
ENSMUSG00000016481	chr1	Cr1l	1.95E+08	1.95E+08	10349	-0.19166	5.178314	0.185714	0.28526	0.02341	0	530	432	900	564	712	489	899	582	665	480
ENSMUSG00000040105	chr19	Ppapdc2	28963953	28966811	2859	0.348043	1.912685	0.185721	0.28526	0.059361	0	57	42	60	46	48	60	85	107	73	47
ENSMUSG00000027222	chr2	Pex16	92374676	92374821	1775	0.22387	4.240421	0.185773	0.285306	0.030289	0	268	223	330	271	278	318	349	429	433	301

ENSMUSG00000015134	chr7	Aldh1a3	66390892	66392761	4615	0.448922	1.310735	0.185941	0.285532	0.108487	0	25	27	56	25	30	39	64	87	27	29
ENSMUSG00000029175	chr5	Slc35f6	30647933	30648098	3311	0.210709	4.038654	0.185984	0.285565	0.027176	0	192	131	351	277	298	261	335	310	430	269
ENSMUSG00000041633	chrX	Kctd12b	1.54E+08	1.54E+08	4906	-0.28625	2.134476	0.186023	0.285591	0.039852	0	68	46	84	77	106	48	96	80	72	59
ENSMUSG00000035725	chrX	Prkx	77761411	77763891	5807	0.21415	3.509405	0.186062	0.285618	0.025669	0	140	122	267	131	196	161	288	225	271	175
ENSMUSG00000031671	chr8	Setd6	95715915	95715963	1869	0.231271	3.451784	0.186404	0.286109	0.030079	0	137	131	189	127	214	183	247	227	260	154
ENSMUSG00000021911	chr14	Parg	32201949	32202465	5778	-0.18805	4.38516	0.186508	0.286236	0.021406	0	318	258	488	324	402	300	455	301	451	285
ENSMUSG00000060288	chr4	Ppih	1.19E+08	1.19E+08	1894	0.307059	2.674539	0.186571	0.2863	0.050082	0	88	87	103	84	74	102	205	105	127	102
ENSMUSG00000034616	chr19	Ssh3	4261668	4262632	2740	0.311743	2.017073	0.186608	0.286323	0.048948	0	34	51	89	44	68	54	81	98	105	62
ENSMUSG00000032077	chr9	Bud13	46283008	46283173	3980	0.253264	2.875256	0.18663	0.286324	0.033462	0	80	96	142	101	107	113	183	118	163	141
ENSMUSG00000032290	chr9	Ptpn9	56994968	56995656	4054	0.245701	2.976033	0.186788	0.286533	0.033615	0	94	85	152	86	160	117	170	179	165	134
ENSMUSG00000026098	chr1	Pms1	53189187	53189498	7542	-0.37283	1.348671	0.186898	0.286669	0.071806	0	32	40	66	33	52	29	75	23	53	22
ENSMUSG00000031660	chr8	Brd7	88331039	88331442	5244	-0.19737	6.327599	0.186923	0.286674	0.026139	0	1175	1130	1697	1309	1507	1093	1764	1200	1710	1131
ENSMUSG00000026455	chr1	Klhl12	1.34E+08	1.34E+08	11395	-0.18686	5.136649	0.18709	0.286898	0.02245	0	559	421	786	562	682	483	783	526	799	453
ENSMUSG00000026279	chr1	Thap4	93701935	93705655	6519	-0.21145	4.874115	0.187161	0.28694	0.028623	0	381	299	616	613	649	373	672	430	645	398
ENSMUSG00000030747	chr7	Dgat2	99153663	99154700	2251	-0.57173	5.539847	0.187158	0.28694	0.220014	0	820	456	504	1560	991	599	248	1565	419	393
ENSMUSG00000054302	chr12	Eapp	54670340	54673850	4448	-0.21155	4.358952	0.187343	0.287185	0.028	0	311	304	486	291	357	317	467	293	382	274
ENSMUSG00000022425	chr15	Enpp2	54838898	54839536	3473	-0.21713	4.678083	0.187479	0.287294	0.029364	0	366	289	657	420	515	412	399	483	451	366
ENSMUSG00000027845	chr3	Dclre1b	1.04E+08	1.04E+08	8152	-0.32725	1.633111	0.187478	0.287294	0.048369	0	40	39	78	50	65	56	65	34	44	41
ENSMUSG00000030357	chr6	Fkbp4	1.28E+08	1.28E+08	2795	-0.19698	6.994821	0.187473	0.287294	0.026288	0	1768	1519	2654	2499	2511	1707	2629	2086	2694	1808
ENSMUSG00000026749	chr2	Nek6	38511643	38511793	4149	-0.4478	4.455785	0.187513	0.287313	0.134536	0	563	437	561	143	216	374	434	248	471	183
ENSMUSG00000099966	chr14	2810402E24Rik	20641009	20644048	3040	-0.33547	2.114488	0.187585	0.28739	0.065693	0	82	69	68	64	83	52	93	40	114	53
ENSMUSG00000038467	chr2	Chmp4b	1.55E+08	1.55E+08	2027	0.207282	7.174936	0.187637	0.287404	0.029104	0	2061	1655	2542	2121	2238	2366	3401	2395	3865	2263
ENSMUSG00000067279	chr19	Ppp1r3c	36731737	36734354	2719	-0.3654	7.694232	0.18763	0.287404	0.091344	0	3460	3073	6745	2114	3693	4516	4664	2970	2453	1581
ENSMUSG00000035390	chr7	Brsk1	4690604	4690720	3594	0.467087	-0.20267	0.187718	0.287461	0.06458	0	5	7	17	7	16	14	13	18	19	15
ENSMUSG00000054099	chr5	Slc25a40	8422850	8423039	2777	-0.28228	2.020909	0.187717	0.287461	0.041516	0	62	54	107	69	58	40	84	56	85	65
ENSMUSG00000025198	chr19	Erlin1	44034944	44037148	4961	0.237906	3.047492	0.187851	0.287632	0.030926	0	119	84	167	103	131	126	175	193	178	131
ENSMUSG00000030287	chr6	Itpr2	1.46E+08	1.46E+08	13484	-0.29875	2.855399	0.188088	0.287961	0.05028	0	65	72	176	151	192	80	155	126	121	105
ENSMUSG00000020973	chr12	Dnaaf2	69189087	69190394	3390	0.288864	1.830386	0.188199	0.288065	0.034459	0	40	44	67	46	51	58	92	59	84	55
ENSMUSG00000074818	chr19	Pdzd7	45026906	45027974	4089	0.39648	2.728853	0.188188	0.288065	0.096871	0	122	67	151	28	86	125	181	117	122	125
ENSMUSG00000078908	chr8	Mon1b	1.14E+08	1.14E+08	5156	-0.24727	2.424327	0.188561	0.288586	0.030047	0	74	69	129	79	113	70	105	89	92	82
ENSMUSG00000022849	chr16	Hspbap1	35770386	35770539	4590	0.284632	2.040037	0.188645	0.288681	0.035533	0	56	47	63	53	67	60	110	77	99	60
ENSMUSG00000032648	chr19	Pygm	6384399	6384721	3218	-0.22603	12.81268	0.188794	0.288876	0.035425	0	132936	82079	197670	97303	121635	96731	140580	113572	172586	91121
ENSMUSG00000026938	chr2	Fcna	25624666	25625088	1374	-0.48238	1.786553	0.189022	0.289191	0.135734	0	68	49	119	25	60	60	35	81	43	27
ENSMUSG00000028411	chr4	Aptx	40682382	40686713	5886	-0.20984	4.421654	0.189084	0.289252	0.027615	0	340	285	521	289	410	355	432	324	441	256
ENSMUSG00000009739	chr15	Pou6f1	1.01E+08	1.01E+08	6987	-0.19614	4.380086	0.18936	0.289642	0.023512	0	319	206	533	376	381	277	440	313	457	296
ENSMUSG00000024403	chr17	Atp6v1g2	35233660	35233890	2510	0.422709	0.991991	0.189534	0.289875	0.075084	0	22	29	26	18	30	19	44	31	61	44
ENSMUSG00000018995	chr7	Nars2	96951505	96951944	4213	-0.27878	2.815948	0.189558	0.289877	0.044868	0	83	61	161	150	175	72	161	98	149	104
ENSMUSG00000023353	chr5	Agap3	24452177	24452534	3207	0.192308	5.373312	0.18994	0.290429	0.024373	0	545	367	829	687	716	665	859	825	1017	663
ENSMUSG00000035443	chr9	Thyn1	26999677	26999765	959	0.239383	3.915258	0.190115	0.290662	0.034069	0	215	185	214	218	241	256	412	254	380	202
ENSMUSG00000021270	chr12	Hsp90aa1	1.11E+08	1.11E+08	3931	0.221759	5.578281	0.190303	0.290917	0.032964	0	584	532	779	624	1017	832	1075	1087	894	746
ENSMUSG00000022721	chr16	Trmt2a	18248679	18250033	4952	0.211649	3.526437	0.190605	0.291344	0.025653	0	158	130	238	134	193	190	254	215	246	206
ENSMUSG00000023266	chr17	Frs3	47689030	47689098	3128	-0.27536	2.184042	0.190806	0.291518	0.039353	0	64	50	80	92	105	53	85	67	103	63
ENSMUSG00000026127	chr1	Imp4	34439851	34439927	8553	0.212304	3.695794	0.190807	0.291518	0.027161	0	155	110	242	220	244	222	271	238	307	217
ENSMUSG00000027243	chr2	Harbi1	91710852	91710975	5588	-0.26295	2.656938	0.190782	0.291518	0.039639	0	108	85	139	89	120	75	165	82	103	96
ENSMUSG00000068290	chr2	Ddrgk1	1.31E+08	1.31E+08	2084	0.205032	6.482705	0.19076	0.291518	0.028514	0	1227	1123	1496	1251	1433	1482	2039	1651	2165	1425
ENSMUSG00000059439	chr11	Bcas3	85353167	85353233	6085	0.21204	5.115438	0.191073	0.291891	0.029888	0	395	279	747	584	647	448	785	605	979	626
ENSMUSG00000025092	chr19	Hspa12a	58795751	58799998	5733	-0.29719	2.736485	0.191275	0.292099	0.051016	0	107	54	136	131	164	73	142	133	94	95
ENSMUSG00000026646	chr2	Suv39h2	3455815	3458729	4410	-0.40389	0.70817	0.191246	0.292099	0.069272	0	28	22	42	25	23	30	35	15	20	19
ENSMUSG00000090698	chr6	Apold1	1.35E+08	1.35E+08	3284	0.698511	1.51979	0.191273	0.292099	0.301305	0	16	41	22	20	61	17	219	28	47	30
ENSMUSG00000022962	chr16	Gart	91621186	91621748	3992	-0.18053	5.809108	0.191331	0.292123	0.021777	0	852	663	1415	874	1036	739	1186	905	1221	791
ENSMUSG00000026620	chr1	Mark1	1.85E+08	1.85E+08	4356	-0.37531	1.399892	0.191334	0.292123	0.071275	0	23	21	65	72	56	32	46	42	55	28
ENSMUSG00000020439	chr11	Smtn	3517523	3517827	4380	0.222687	6.420882	0.191364	0.292134	0.034121	0	1104	671	1705	1400	1617	1310	1910	1253	2482	1564
ENSMUSG00000009281	chr6	Rarres2	48569698	48569805	708	0.346082	4.775615	0.191468	0.292258	0.080478	0	491	396	462	200	285	528	651	689	527	367
ENSMUSG00000021427	chr13	Ssr1	37971401	37979806	9306	0.190246	5.667549	0.191489	0.292258	0.024134	0	623	614	1106	631	858	872	1159	908	1101	872
ENSMUSG00000044043	chr18	Pcdhb14	37447656	37456350	8695	0.415778	0.313394	0.191631	0.292441	0.066116	0	8	13	24	11	23	13	27	23	24	30
ENSMUSG00000024743	chr19	Syt7	10389090	10389513	6966	-0.53153	0.650922	0.191849	0.292638	0.142291	0	8	11	26	48	50	13	22	17	35	23
ENSMUSG00000030822	chr7	Prr14	1.27E+08	1.27E+08	3456	0.204308	4.070898	0.191838	0.292638	0.02619	0	195	142	363	279	299	276	375	363	367	250
ENSMUSG00000040136	chr7	Abcc8	46104523	46104761	4952	0.378864	1.391495	0.191841	0.292638	0.079546	0	33	20	70	24	35	40	34	49	64	66
ENSMUSG00000053964	chr7	Lgals4	28833854	28834226	2315	0.420742	0.672424	0.191838	0.292638	0.069582	0	21	14	23	18	25	19	35	48	38	16
ENSMUSG00000022257	chr15	Laptm4b	34238026	34238422	1897	-0.21882	5.226164	0.192178	0.293107	0.032259	0	719	511	878	513	558	500	758	598	782	532
ENSMUSG00000084846	chr3	A730011C13Rik	94994410	94996108	2234	0.481677	-0.06819	0.19223	0.293153	0.072671	0	12	8	19	3	15	16	24	13	19	17
ENSMUSG00000025525	chrX	Apool	1.12E+08	1.12E+08	3486	-0.21372	5.05172	0.192337	0.293282	0.03063	0	456	415	622	719	611	382	798	521	686	464
ENSMUSG00000031283	chrX	Chrdl1	1.43E+08	1.43E+08	6755	-0.35271	2.345727	0.192382	0.293316	0.073018	0	65	74	115	69	130	44	100	113	53	85
ENSMUSG00000025369	chr10	Smarcc2	1.28E+08	1.28E+08	5027	-0.18928	5.637189	0.192405	0.293318	0.023819	0	668	505	1217	880	1097	611	1006	869	1016	760
ENSMUSG00000030499	chr7	Kctd15	34639014	34640449	2991	-0.21552	6.39575	0.192444	0.293344	0.032033	0	1472	1031	2117	1178	1502	1139	1576	1116	2084	1268

ENSMUSG00000097375	chr13	6720427I07Rik	48535523	48537822	2300	0.419756	0.32198	0.192556	0.29348	0.057026	0	10	10	18	23	17	18	29	30	27	15
ENSMUSG00000024913	chr19	Lrp5	3584828	3585291	9738	-0.26641	4.441685	0.192593	0.293503	0.046513	0	238	187	506	510	523	217	423	413	395	351
ENSMUSG00000025269	chrX	Apex2	1.51E+08	1.51E+08	8744	0.285786	2.320043	0.19268	0.293603	0.043616	0	47	51	74	76	107	80	122	93	137	65
ENSMUSG00000049482	chr8	Ctu2	1.22E+08	1.22E+08	5164	0.2596	3.009644	0.192893	0.293893	0.037441	0	103	90	107	122	149	124	175	135	234	131
ENSMUSG00000014850	chr13	Msh3	92211872	92212546	11254	-0.21003	3.72108	0.19295	0.293946	0.02603	0	155	164	325	221	284	188	315	200	237	176
ENSMUSG00000031812	chr8	Map1lc3b	1.22E+08	1.22E+08	7517	0.199501	7.860944	0.193023	0.293991	0.027805	0	2945	2850	4574	3307	3585	3355	6121	3863	5991	3780
ENSMUSG00000047098	chr14	Rnf31	55591708	55592072	4838	0.247215	3.847292	0.193024	0.293991	0.039449	0	143	110	298	239	297	180	412	236	305	298
ENSMUSG00000027080	chr2	Med19	84678402	84678661	2059	0.221881	3.306936	0.193293	0.294368	0.028317	0	149	99	204	124	153	175	206	181	243	155
ENSMUSG00000029442	chr5	Wdr66	1.23E+08	1.23E+08	7583	0.355487	1.034777	0.193552	0.294729	0.059039	0	16	14	32	41	35	34	59	35	44	28
ENSMUSG00000071014	chr4	Ndufb6	40270591	40270847	659	0.218837	6.768564	0.193705	0.294927	0.033249	0	1521	1065	1790	1902	1739	1661	2967	1650	2940	1716
ENSMUSG00000040102	chr6	Klhl42	1.47E+08	1.47E+08	6267	0.285918	1.912792	0.193895	0.295183	0.041955	0	33	40	87	45	66	59	84	88	84	52
ENSMUSG00000019494	chr5	Cops6	1.38E+08	1.38E+08	2525	0.199114	6.391464	0.19392	0.295187	0.027209	0	1202	963	1489	1217	1319	1358	2000	1444	2137	1321
ENSMUSG00000036572	chrX	Upf3b	37091678	37092661	3999	0.209934	4.225719	0.19395	0.295198	0.027467	0	286	206	346	217	324	323	425	392	398	277
ENSMUSG00000053293	chr5	Pom121	1.35E+08	1.35E+08	5581	-0.22859	4.037195	0.19422	0.295575	0.032324	0	204	162	503	254	360	191	279	266	380	264
ENSMUSG00000019143	chr18	Hars2	36783008	36783494	4279	-0.19632	4.348867	0.194253	0.295577	0.023949	0	257	233	464	347	471	281	470	321	358	301
ENSMUSG00000098950	chr2	Gm28036	1.56E+08	1.56E+08	5823	-0.18348	5.388302	0.194265	0.295577	0.022364	0	565	472	1009	684	914	589	958	690	847	529
ENSMUSG00000049892	chr11	Rasd1	59963181	59964366	1611	0.776037	2.019942	0.194312	0.295614	0.392074	0	82	66	29	11	17	93	34	213	55	40
ENSMUSG00000028950	chr4	Tas1r1	1.52E+08	1.52E+08	4776	0.342405	1.271027	0.194458	0.295801	0.051086	0	26	23	46	34	35	33	60	26	75	45
ENSMUSG00000053334	chr5	Ficd	1.14E+08	1.14E+08	3154	-0.21596	3.589942	0.194573	0.295943	0.027853	0	203	129	317	179	221	132	268	186	243	192
ENSMUSG00000041124	chr9	Msantd4	4383535	4384142	2731	-0.17815	5.298071	0.194702	0.296105	0.021145	0	529	496	904	680	760	500	868	616	853	569
ENSMUSG00000029287	chr5	Tgfbr3	1.07E+08	1.07E+08	6545	-0.23091	5.073914	0.194848	0.296294	0.035632	0	461	392	1076	427	679	459	539	681	648	470
ENSMUSG00000005370	chr17	Msh6	87975050	87975405	4254	0.249486	2.772424	0.195109	0.296597	0.032096	0	94	81	121	83	110	102	179	141	154	97
ENSMUSG00000040913	chr19	Fbxw4	45578254	45578925	3158	-0.18981	4.831878	0.195087	0.296597	0.023526	0	405	333	622	538	542	392	528	421	674	422
ENSMUSG00000062515	chr3	Fabp4	10204088	10204570	4489	0.491653	8.224247	0.195115	0.296597	0.170337	0	5419	4826	2271	2528	2763	4801	5530	12435	5057	3467
ENSMUSG00000074826	chr13	Gm10767	66904914	66905342	2274	-0.45872	0.104244	0.19518	0.296663	0.070673	0	11	9	26	14	33	7	22	14	17	15
ENSMUSG00000026377	chr1	Nifk	1.18E+08	1.18E+08	1965	0.233508	4.422392	0.195233	0.296708	0.034765	0	313	287	365	236	337	330	625	401	485	300
ENSMUSG00000011427	chr7	Zfp790	29816072	29816289	4525	-0.22511	3.061259	0.19533	0.296787	0.028794	0	113	115	209	140	140	112	197	129	159	105
ENSMUSG00000027274	chr2	Mkks	1.37E+08	1.37E+08	3227	-0.21958	5.597286	0.195323	0.296787	0.033428	0	865	698	938	767	795	730	1118	669	1022	590
ENSMUSG00000002728	chr2	Naa20	1.46E+08	1.46E+08	3705	-0.20698	5.079616	0.195358	0.296797	0.029091	0	624	418	636	559	615	466	809	496	684	443
ENSMUSG00000027669	chr3	Gnb4	32580332	32585226	12692	0.261195	2.954273	0.195413	0.296846	0.041531	0	100	49	170	114	145	121	203	109	218	124
ENSMUSG00000025155	chr11	Dus1l	1.21E+08	1.21E+08	3758	-0.18073	4.758715	0.195647	0.297167	0.021264	0	399	343	566	478	507	363	553	442	576	389
ENSMUSG00000033902	chr2	Mapkbp1	1.2E+08	1.2E+08	7584	-0.24668	3.466935	0.1957	0.297213	0.036661	0	132	113	361	162	237	118	206	195	243	163
ENSMUSG00000020904	chr11	Cfap52	67924806	67925233	2320	0.435411	0.149401	0.195848	0.297405	0.085458	0	13	5	25	13	14	26	26	12	16	22
ENSMUSG00000032842	chr17	Abcc10	46303221	46303652	6856	0.313822	1.750937	0.195959	0.297505	0.053344	0	30	26	66	54	63	46	62	70	68	78
ENSMUSG00000068882	chr2	Ssb	69861562	69861739	2160	0.210862	5.791838	0.195938	0.297505	0.030347	0	724	765	1024	655	874	888	1484	1008	1171	897
ENSMUSG00000058402	chr7	Zfp420	29859979	29860093	4238	-0.28075	1.375906	0.196035	0.297586	0.033266	0	35	37	61	40	47	31	52	37	48	38
ENSMUSG00000041231	chr11	Ublcp1	44454571	44455615	2542	-0.19769	4.057958	0.196167	0.297719	0.024256	0	248	173	390	295	338	218	417	260	326	211
ENSMUSG00000086119	chr9	Gm2415	1.19E+08	1.19E+08	3735	0.462977	0.355192	0.19615	0.297719	0.078255	0	16	11	10	19	21	15	21	33	27	26
ENSMUSG00000054619	chr15	Mettl7a1	1E+08	1E+08	1883	-0.27406	5.322589	0.196284	0.297862	0.052248	0	641	589	944	627	673	395	653	1057	636	537
ENSMUSG00000022175	chr14	Lrp10	54464164	54464611	4201	0.202486	5.389331	0.196368	0.297956	0.028138	0	489	335	848	738	794	620	894	840	1070	686
ENSMUSG00000035649	chr4	Zcchc7	44755877	44756034	9612	0.217078	3.703349	0.196418	0.297971	0.028546	0	143	158	318	154	203	183	348	246	297	210
ENSMUSG00000047879	chr18	Usp14	9995432	9996248	5974	-0.19201	5.426693	0.196423	0.297971	0.025195	0	651	609	1077	625	710	540	903	697	924	631
ENSMUSG00000054611	chr19	Kdm2a	4314419	4319281	14294	-0.19597	5.661653	0.19653	0.298099	0.026046	0	649	561	1474	748	1069	661	963	888	987	793
ENSMUSG00000031712	chr8	Il15	82331637	82332024	1908	0.426436	3.297978	0.196699	0.298321	0.123704	0	60	46	129	234	220	96	371	201	202	179
ENSMUSG00000031683	chr8	Lsm6	78804865	78808245	4076	0.276512	5.727329	0.196807	0.298451	0.053142	0	683	872	871	559	677	840	1531	965	953	998
ENSMUSG00000054021	chr13	Sirt5	43370710	43370868	1367	-0.31259	3.236818	0.196837	0.298462	0.063173	0	95	84	173	264	228	110	199	130	225	114
ENSMUSG00000039307	chr11	Hexdc	1.21E+08	1.21E+08	4723	0.244481	3.161286	0.196934	0.298542	0.035506	0	139	92	195	98	129	169	201	146	187	162
ENSMUSG00000069208	chr13	Zfp825	74480517	74481150	822	-0.32131	2.217912	0.196917	0.298542	0.062266	0	84	77	108	71	56	61	123	54	76	61
ENSMUSG00000004032	chr3	Gstm5	1.08E+08	1.08E+08	1278	-0.21744	6.014345	0.196979	0.298545	0.033197	0	1106	943	1388	988	1037	993	1310	1053	1366	759
ENSMUSG00000021810	chr14	Ecd	20319859	20320951	3125	-0.17805	5.348486	0.196981	0.298545	0.021234	0	617	469	999	640	789	572	910	603	829	594
ENSMUSG00000064307	chr7	Lrrc51	1.02E+08	1.02E+08	1210	0.317843	1.069755	0.19741	0.299161	0.044041	0	22	15	38	34	35	35	36	41	48	39
ENSMUSG00000038072	chr5	Galnt11	25222882	25223031	2993	-0.21855	3.590383	0.197505	0.29927	0.02829	0	156	121	270	228	279	146	239	204	223	196
ENSMUSG00000035642	chr7	Aamdc	97550331	97550741	1615	0.280386	7.204654	0.197537	0.299285	0.056006	0	2348	2178	2576	1424	1703	2900	3402	2520	3697	2234
ENSMUSG00000099210	chr7	Mir7051	43457497	43457569	73	0.355233	1.79333	0.197786	0.299627	0.06423	0	31	45	40	64	49	41	99	66	77	65
ENSMUSG00000029625	chr5	Cpsf4	1.45E+08	1.45E+08	3598	0.255539	2.88711	0.197957	0.299852	0.037452	0	116	74	141	97	103	144	158	149	166	102
ENSMUSG00000018565	chr11	Elp5	69968222	69968540	2294	0.190138	4.985277	0.198103	0.300039	0.023892	0	445	308	559	515	539	515	760	553	804	472
ENSMUSG00000024330	chr17	Col11a2	34039437	34039736	6831	-0.36898	2.637521	0.198238	0.30021	0.082991	0	60	80	129	112	185	89	76	86	78	137
ENSMUSG00000037905	chr5	Bri3bp	1.25E+08	1.25E+08	6975	0.272965	2.259742	0.19853	0.300582	0.039061	0	69	50	92	57	72	63	94	114	114	82
ENSMUSG00000096188	chr8	Cmtm4	1.04E+08	1.04E+08	7734	-0.27321	3.560415	0.198511	0.300582	0.047098	0	125	98	310	266	274	121	216	226	239	172
ENSMUSG00000030269	chr6	Mtmr14	1.13E+08	1.13E+08	2874	-0.20116	4.566869	0.198639	0.300713	0.026431	0	323	269	617	477	370	331	445	370	502	358
ENSMUSG00000082284	chrX	H3f3a-ps1	1.02E+08	1.02E+08	410	-0.48962	0.21247	0.198673	0.30073	0.111681	0	22	27	14	11	20	17	25	13	15	11
ENSMUSG00000015542	chr11	Nat9	1.15E+08	1.15E+08	2066	0.220648	3.676899	0.198875	0.301001	0.028679	0	147	167	218	201	192	195	321	218	325	202
ENSMUSG00000045064	chr12	Zc2hc1c	85288591	85288785	4482	-0.35787	1.022603	0.199023	0.301191	0.053104	0	21	27	65	28	38	24	29	25	44	32
ENSMUSG00000017119	chr11	Nbr1	1.02E+08	1.02E+08	6871	-0.19139	6.576494	0.199275	0.301538	0.025933	0	1248	1140	2640	1501	1853	1179	1882	1629	2097	1413
ENSMUSG00000020123	chr10	Avpr1a	1.22E+08	1.22E+08	2671	0.482886	0.007546	0.199336	0.301596	0.118502	0	15	4	22	2	19	22	21	18	18	14

ENSMUSG00000054051	chr14	Ercc6	32513521	32513599	8422	-0.26055	2.786331	0.199362	0.301602	0.039511	0	93	63	207	126	129	77	162	124	117	91
ENSMUSG00000028631	chr4	Kcnq4	1.21E+08	1.21E+08	4024	-0.26194	4.376755	0.199548	0.301848	0.046291	0	268	160	429	510	491	278	367	289	495	301
ENSMUSG00000024678	chr19	Ms4a4d	11536801	11537160	1513	0.270167	3.188846	0.199685	0.302021	0.046501	0	98	107	235	88	145	173	236	200	167	119
ENSMUSG00000033735	chr6	Spr	85133678	85134288	1230	-0.19989	5.193483	0.199867	0.302262	0.027489	0	520	453	670	697	773	450	714	561	766	619
ENSMUSG00000021991	chr14	Cacna2d3	28904943	28905357	3695	-0.44852	0.18743	0.200017	0.302454	0.096394	0	22	21	17	20	12	13	10	18	25	14
ENSMUSG00000031591	chr8	Asah1	41340197	41341685	3390	0.200112	4.399785	0.200124	0.302581	0.02685	0	233	199	486	294	407	346	467	472	423	330
ENSMUSG00000040859	chr4	Bsdc1	1.29E+08	1.29E+08	5630	-0.17818	5.691821	0.200149	0.302584	0.022089	0	755	659	1237	849	919	644	1120	790	1143	780
ENSMUSG00000017167	chr11	Cntnap1	1.01E+08	1.01E+08	5875	0.418497	0.661783	0.20064	0.303293	0.089617	0	17	10	36	11	31	21	26	50	30	24
ENSMUSG00000020728	chr11	Cep112	1.08E+08	1.08E+08	6175	-0.46725	0.109831	0.200692	0.303336	0.091529	0	9	15	17	28	21	17	16	8	24	10
ENSMUSG00000020227	chr10	Irak3	1.2E+08	1.2E+08	3676	0.302232	2.300747	0.200787	0.303446	0.053039	0	58	52	108	58	75	88	129	126	73	65
ENSMUSG00000038527	chr6	C1rl	1.24E+08	1.24E+08	3010	0.475092	0.192874	0.200843	0.303474	0.087452	0	15	17	15	9	11	23	17	28	21	18
ENSMUSG00000054676	chr7	1600014C10Rik	38183217	38183521	3931	-0.18521	5.385181	0.200852	0.303474	0.02354	0	570	461	878	790	901	561	857	750	829	580
ENSMUSG00000043969	chr19	Emx2	59458372	59459624	3002	0.599244	0.434504	0.20093	0.303523	0.206073	0	6	19	23	10	22	40	17	47	12	13
ENSMUSG00000056947	chr3	Mab21l1	55782510	55785285	2776	-0.49447	0.87505	0.200917	0.303523	0.146997	0	34	32	66	9	23	15	30	35	43	12
ENSMUSG00000026049	chr1	Tex30	44086613	44087063	1926	-0.33392	1.339203	0.201471	0.304246	0.063329	0	42	44	51	37	38	24	46	51	56	23
ENSMUSG00000027322	chr2	Siglec1	1.31E+08	1.31E+08	7143	0.440248	1.840538	0.201458	0.304246	0.123954	0	43	36	95	28	42	74	56	117	37	63
ENSMUSG00000091460	chr9	Gm7808	19927896	19928282	387	0.336156	1.009579	0.201477	0.304246	0.046056	0	24	20	31	30	29	40	52	27	47	28
ENSMUSG00000025199	chr19	Chuk	44073335	44074540	5087	-0.20689	3.729006	0.201846	0.304768	0.025967	0	184	135	332	218	294	177	287	250	239	168
ENSMUSG00000001300	chr8	Efnb2	8617434	8620976	4324	-0.25154	2.791864	0.201926	0.304854	0.036869	0	91	73	156	132	154	67	120	126	158	104
ENSMUSG00000021468	chr13	Sptlc1	53332716	53333977	2606	0.202009	3.843929	0.202061	0.305023	0.02564	0	211	133	319	182	237	230	360	290	319	203
ENSMUSG00000075229	chr16	Ccdc58	36071660	36072137	1225	0.258427	3.335884	0.202714	0.305974	0.040185	0	134	143	153	134	142	186	247	169	258	140
ENSMUSG00000026315	chr1	Serpinb8	1.08E+08	1.08E+08	4795	0.386397	1.311822	0.202805	0.306077	0.088178	0	24	25	71	16	36	38	60	65	34	44
ENSMUSG00000038347	chr17	Tcte2	13482553	13483004	8560	0.383308	0.746146	0.20288	0.306144	0.070771	0	27	13	34	14	22	39	33	34	33	20
ENSMUSG00000038533	chr2	Cbfa2t2	1.54E+08	1.54E+08	8650	-0.20604	4.199478	0.202896	0.306144	0.027454	0	275	198	553	240	363	250	383	258	414	262
ENSMUSG00000032252	chr9	Glce	62057248	62061035	6828	-0.24896	3.104684	0.202937	0.306171	0.038465	0	110	109	207	120	210	80	194	164	145	133
ENSMUSG00000022032	chr14	Scara5	65666403	65666746	6093	-0.22709	4.740581	0.203118	0.306409	0.035043	0	353	317	884	339	515	420	476	470	478	370
ENSMUSG00000025512	chr7	Chid1	1.41E+08	1.41E+08	10799	0.267903	3.042291	0.203397	0.306773	0.044846	0	102	67	114	157	151	114	189	168	170	166
ENSMUSG00000056429	chr6	Tgoln1	72608432	72612110	5013	-0.18374	5.696491	0.203405	0.306773	0.023669	0	717	603	1344	823	1029	666	1121	973	924	751
ENSMUSG00000078184	chr1	B020018G12Rik	1.76E+08	1.76E+08	1338	0.480027	0.112633	0.203437	0.306786	0.083096	0	9	18	17	11	8	12	29	22	19	21
ENSMUSG00000031483	chr8	Erlin2	27023799	27023906	3943	-0.21173	3.673823	0.20354	0.306907	0.027553	0	174	135	359	209	248	145	225	226	288	195
ENSMUSG00000034768	chr11	Asb16	1.02E+08	1.02E+08	2843	-0.18512	6.767112	0.203632	0.30701	0.024858	0	1633	1336	2786	1713	1940	1460	2217	1679	2519	1534
ENSMUSG00000079317	chrX	Trappc2	1.66E+08	1.66E+08	3643	-0.19874	3.891734	0.203679	0.307047	0.025754	0	264	179	305	237	271	173	339	239	309	212
ENSMUSG00000005609	chr7	Ctr9	1.11E+08	1.11E+08	6544	-0.17826	4.5461	0.20385	0.307269	0.021035	0	338	294	547	349	473	287	485	423	495	323
ENSMUSG00000024164	chr17	C3	57203970	57204154	5143	0.375723	7.865495	0.203887	0.30729	0.103936	0	2975	2471	6602	1639	3236	5222	4390	7497	4312	2061
ENSMUSG00000023277	chr9	Twf2	1.06E+08	1.06E+08	2129	-0.29097	6.483033	0.204203	0.307731	0.062016	0	1055	736	1780	2463	2036	1153	1974	946	2184	1255
ENSMUSG00000021114	chr12	Atp6v1d	78842989	78843610	1403	0.2152	6.392932	0.204286	0.307787	0.033384	0	1126	1149	1413	1143	1234	1433	2120	1360	2044	1340
ENSMUSG00000030471	chr7	Zdhhc13	48789003	48789137	2410	-0.26633	2.411958	0.204283	0.307787	0.039882	0	103	60	111	92	88	82	111	75	102	64
ENSMUSG00000024812	chr19	Tjp2	24094523	24095590	4591	0.273132	2.517603	0.204471	0.308031	0.044476	0	62	42	99	89	126	66	153	118	139	95
ENSMUSG00000024462	chr17	Gabbr1	37045966	37046289	7764	0.254812	2.517768	0.204727	0.308381	0.036111	0	56	52	106	95	109	72	145	116	129	101
ENSMUSG00000028729	chr4	Ebna1bp2	1.19E+08	1.19E+08	3553	0.20281	5.125687	0.204971	0.308713	0.028249	0	498	461	647	430	513	573	858	596	837	559
ENSMUSG00000046605	chr11	B3gntl1	1.22E+08	1.22E+08	3518	-0.34099	1.0888	0.205025	0.308724	0.051857	0	28	25	36	45	47	26	36	43	32	25
ENSMUSG00000101645	chr2	Gm28635	84601439	84602903	4734	-0.20251	5.25944	0.205017	0.308724	0.028533	0	492	343	1022	670	899	465	770	676	782	572
ENSMUSG00000074415	chr9	2610203C20Rik	41376397	41376676	12655	0.289829	2.191829	0.205264	0.309049	0.048789	0	56	45	120	41	70	71	85	82	112	94
ENSMUSG00000018476	chr11	Kdm6b	69398508	69399849	6954	-0.21594	4.635566	0.205293	0.309058	0.031978	0	310	235	640	426	612	245	531	426	557	374
ENSMUSG00000025209	chr19	Peo1	45006558	45008375	3488	-0.22185	4.894441	0.205394	0.309175	0.034457	0	378	295	583	646	699	365	660	561	532	399
ENSMUSG00000003072	chr10	Atp5d	80138632	80138855	1928	0.25337	8.451386	0.205532	0.309333	0.047747	0	4049	2716	5128	7112	6837	5115	8082	5745	10699	5821
ENSMUSG00000078713	chr4	Tomm5	45105208	45105644	868	0.229422	4.991137	0.205546	0.309333	0.036449	0	444	402	448	479	496	538	895	494	824	435
ENSMUSG00000022136	chr14	Dnajc3	1.19E+08	1.19E+08	5190	-0.19722	5.240373	0.205589	0.309363	0.027075	0	537	417	1029	572	772	531	771	748	634	509
ENSMUSG00000020549	chr11	Elac2	64979038	64979331	3479	-0.17751	4.650957	0.205637	0.3094	0.021135	0	388	283	608	421	457	326	532	425	546	340
ENSMUSG00000026031	chr1	Cflar	58711508	58711592	12669	-0.20907	4.90922	0.205725	0.309498	0.02995	0	390	266	919	490	651	382	598	507	606	454
ENSMUSG00000038909	chr11	Kat7	95274259	95275887	5536	0.183035	4.808001	0.205841	0.309637	0.023151	0	381	238	642	410	483	453	640	499	678	452
ENSMUSG00000029610	chr5	Aimp2	1.44E+08	1.44E+08	1654	-0.19521	7.026343	0.205918	0.309717	0.028121	0	2010	1816	2615	2003	2594	1920	2749	2160	2662	1662
ENSMUSG00000043831	chr7	Lysmd4	67222544	67222629	3383	-0.20611	3.554052	0.206405	0.310384	0.026731	0	166	139	239	204	259	158	256	150	265	171
ENSMUSG00000054733	chr14	Msra	64122623	64123353	1862	-0.19278	4.326399	0.206408	0.310384	0.024897	0	277	245	367	393	419	272	403	320	416	296
ENSMUSG00000039456	chr16	Morc3	93832121	93832348	4178	-0.20456	3.666003	0.206445	0.310404	0.025931	0	163	154	338	184	271	176	303	196	230	172
ENSMUSG00000054435	chr6	Gimap4	48684549	48684623	1837	0.275284	2.179204	0.206897	0.311049	0.040365	0	55	46	72	68	79	65	133	94	80	72
ENSMUSG00000027716	chr3	Trpc3	36620482	36621397	5419	-0.40594	1.947316	0.20707	0.311274	0.101901	0	35	24	77	98	124	31	87	48	70	63
ENSMUSG00000013846	chr15	St3gal1	67102875	67106830	4985	0.221017	4.710399	0.207201	0.31133	0.034897	0	389	192	624	293	512	402	599	580	566	416
ENSMUSG00000023030	chr15	Slc11a2	1E+08	1E+08	6354	-0.19199	5.13857	0.207195	0.31133	0.025632	0	515	335	931	580	747	487	635	581	827	484
ENSMUSG00000033961	chr7	Zfp446	12977848	12978112	5801	-0.27491	1.814335	0.207199	0.31133	0.03623	0	48	38	101	56	65	41	80	57	58	48
ENSMUSG00000064202	chr19	4430402I18Rik	28893042	28894565	5420	-0.42492	0.105261	0.2072	0.31133	0.072707	0	19	17	16	19	16	14	15	19	21	7
ENSMUSG00000025651	chr9	Uqcrc1	1.09E+08	1.09E+08	4135	-0.2947	9.454714	0.207382	0.311535	0.065203	0	8386	5798	12150	19245	17577	8664	14953	8649	17669	9146
ENSMUSG00000066798	chr2	Zbtb6	37425500	37429923	5080	-0.2568	2.243067	0.207385	0.311535	0.036464	0	67	56	106	67	115	47	100	68	106	71
ENSMUSG00000001305	chr1	Rrp15	1.87E+08	1.87E+08	3239	-0.2133	3.243946	0.207678	0.31194	0.028161	0	137	143	199	139	182	122	185	161	181	143
ENSMUSG00000020111	chr10	Micu1	59702477	59702687	9234	0.196428	6.213415	0.207822	0.31212	0.028175	0	819	809	1410	1286	1242	1121	1745	1243	2024	1198

ENSMUSG00000026499	chr1	Acbd3	1.81E+08	1.81E+08	6780	-0.20591	3.755828	0.207845	0.31212	0.027302	0	169	169	348	216	274	134	278	230	288	221
ENSMUSG00000028419	chr4	Chmp5	40948407	40948676	1519	0.208346	4.980096	0.207876	0.312132	0.029919	0	450	433	545	399	453	470	778	616	754	491
ENSMUSG00000048058	chr2	Ldlrad3	1.02E+08	1.02E+08	6023	0.33058	2.623541	0.207901	0.312135	0.072071	0	42	41	96	122	143	76	130	137	162	114
ENSMUSG00000052533	chr2	Nup188	30286397	30286470	6241	-0.2767	3.101761	0.20799	0.312232	0.048547	0	106	59	235	193	188	95	161	149	189	115
ENSMUSG00000033983	chr11	Coil	88970252	88970272	3520	-0.27116	2.13175	0.2081	0.312362	0.040561	0	63	68	104	58	82	63	102	67	69	54
ENSMUSG00000026047	chr1	Kdelc1	44106546	44107104	3199	0.272999	2.179819	0.208323	0.312662	0.042154	0	64	43	94	56	67	72	109	105	74	77
ENSMUSG00000053580	chr11	Tanc2	1.06E+08	1.06E+08	16494	-0.22759	3.050434	0.208382	0.312714	0.030018	0	108	93	241	117	174	102	151	147	172	119
ENSMUSG00000022300	chr15	Dcaf13	39112865	39113051	1551	0.207352	3.935201	0.208424	0.312715	0.027719	0	222	164	311	214	220	268	422	272	324	211
ENSMUSG00000050947	chr3	Amigo1	1.08E+08	1.08E+08	5540	-0.20761	5.704466	0.20843	0.312715	0.031212	0	804	554	1495	710	1068	810	899	761	1287	676
ENSMUSG00000027651	chr2	Rprd1b	1.58E+08	1.58E+08	6499	0.183783	5.371243	0.208852	0.313291	0.024201	0	546	352	879	650	748	613	1096	691	987	679
ENSMUSG00000103970	chr9	RP23-250G8.14	1.09E+08	1.09E+08	1146	-0.31874	1.271866	0.208861	0.313291	0.051454	0	31	34	59	47	35	30	59	41	33	26
ENSMUSG00000070372	chr3	Capza1	1.05E+08	1.05E+08	3532	-0.20975	3.629098	0.208914	0.313336	0.027935	0	184	118	309	220	252	150	313	197	229	167
ENSMUSG00000022412	chr15	Mief1	80234080	80234181	5541	-0.18698	4.392572	0.209119	0.313607	0.023425	0	273	243	560	366	385	250	412	343	485	316
ENSMUSG00000007030	chr17	Vwa7	35016579	35016767	4313	-0.18333	4.454853	0.209165	0.313641	0.022852	0	332	270	520	370	380	296	427	316	527	320
ENSMUSG00000038022	chr6	Fam188b	55203383	55203569	4270	0.297742	1.461255	0.209396	0.313916	0.042274	0	31	28	44	33	55	33	67	57	55	54
ENSMUSG00000078656	chr11	Vps25	1.01E+08	1.01E+08	1642	0.193178	5.522865	0.209374	0.313916	0.026547	0	643	578	805	652	693	765	1116	820	1111	689
ENSMUSG00000098530	chr12	Gm28051	1.03E+08	1.03E+08	445	-0.37683	1.08199	0.209427	0.313927	0.083208	0	34	26	33	49	37	13	62	25	38	28
ENSMUSG00000098702	chr18	1500015A07Rik	61726390	61728254	2296	0.341959	1.315556	0.20946	0.313942	0.054808	0	29	34	37	27	38	43	49	45	78	30
ENSMUSG00000042308	chr7	Setd1a	1.28E+08	1.28E+08	6795	-0.21914	4.400551	0.209585	0.314094	0.032769	0	246	197	638	359	471	230	430	371	426	332
ENSMUSG00000037965	chr16	Zc3h7a	11136592	11137485	9160	0.210616	4.074566	0.209926	0.314569	0.029398	0	207	217	357	193	273	277	455	340	330	244
ENSMUSG00000058761	chr7	Rnf169	99920257	99926483	7647	0.224601	3.06382	0.210151	0.31487	0.030475	0	94	79	195	125	133	107	199	149	244	131
ENSMUSG00000051483	chr16	Cbr1	93607837	93608254	1237	0.197124	4.300542	0.21018	0.314878	0.025578	0	251	244	326	285	340	286	460	425	429	316
ENSMUSG00000031904	chr8	Slc7a6	1.06E+08	1.06E+08	3730	-0.21805	3.426965	0.210326	0.315062	0.029901	0	131	123	320	155	226	138	230	183	233	129
ENSMUSG00000028023	chr3	Pitx2	1.29E+08	1.29E+08	4726	-0.54964	3.223628	0.210362	0.315079	0.217353	0	57	63	214	318	276	79	88	61	139	284
ENSMUSG00000032733	chr9	Snx33	56917200	56918704	4564	0.25572	2.725122	0.210426	0.315135	0.041827	0	69	64	160	92	104	107	115	164	163	94
ENSMUSG00000038462	chr13	Uqcrfs1	30540308	30541341	1363	-0.24493	8.614043	0.21047	0.315135	0.045634	0	5000	3824	7249	9378	9036	4679	9538	5154	9048	5244
ENSMUSG00000040034	chr10	Nup43	7667503	7667681	2560	0.299778	2.18712	0.210464	0.315135	0.050527	0	66	54	78	46	72	77	149	69	86	71
ENSMUSG00000035125	chr6	Gcfc2	81923669	81923938	7571	0.326144	1.02129	0.210512	0.315163	0.043664	0	24	24	28	24	35	27	54	36	40	38
ENSMUSG00000037190	chr9	Cyb561d2	1.08E+08	1.08E+08	1974	0.291452	1.898391	0.210616	0.315282	0.043039	0	48	46	63	51	49	71	88	60	72	68
ENSMUSG00000098253	chr18	Mir7219	68260920	68260973	54	-0.31999	2.320642	0.211013	0.31584	0.064431	0	49	47	89	125	134	55	117	66	104	64
ENSMUSG00000034936	chr11	Arl4d	1.02E+08	1.02E+08	1382	0.305154	2.246516	0.211205	0.316092	0.055641	0	44	51	57	92	84	94	109	81	104	76
ENSMUSG00000034863	chr8	Ano8	71476023	71476921	3753	-0.22136	4.35183	0.211464	0.316444	0.033917	0	265	195	444	416	476	226	377	319	411	379
ENSMUSG00000020889	chr11	Nr1d1	98767932	98768419	3077	0.209993	6.743922	0.211509	0.316477	0.033366	0	1241	840	2580	1572	2103	1313	2479	2066	2878	1922
ENSMUSG00000032850	chr5	Rnft2	1.18E+08	1.18E+08	5593	-0.36314	0.754374	0.211607	0.316539	0.049582	0	31	16	42	22	34	25	29	17	32	23
ENSMUSG00000036461	chr14	Elf1	79481194	79481637	4314	0.246047	2.701529	0.211623	0.316539	0.035367	0	76	68	153	86	95	100	155	153	144	85
ENSMUSG00000098798	chr8	Gm27288	19493189	19493268	80	0.290004	2.325803	0.211593	0.316539	0.047696	0	75	59	70	61	81	100	135	81	97	77
ENSMUSG00000032571	chr9	Pik3r4	1.06E+08	1.06E+08	9660	-0.19913	3.871238	0.211679	0.316588	0.025365	0	173	166	344	247	347	194	293	220	289	240
ENSMUSG00000025436	chr10	Xrcc6bp1	1.27E+08	1.27E+08	1362	0.354986	0.635023	0.211713	0.316602	0.044096	0	15	17	33	20	17	22	33	32	33	27
ENSMUSG00000023336	chr8	Wfdc1	1.2E+08	1.2E+08	1213	0.210648	6.063347	0.211841	0.316758	0.033004	0	1094	630	1285	888	1077	1133	1747	1036	1780	957
ENSMUSG00000040479	chr2	Dgkz	91932824	91933525	6270	0.186267	5.632346	0.211966	0.31691	0.025668	0	682	418	1183	660	897	786	1117	837	1196	885
ENSMUSG00000047205	chr11	Dusp18	3895240	3895517	4632	0.295837	3.830246	0.212051	0.317001	0.062313	0	133	104	217	340	232	170	338	237	457	256
ENSMUSG00000007080	chr5	Pole	1.1E+08	1.1E+08	11160	-0.41298	1.254179	0.212129	0.317059	0.098991	0	13	21	67	58	60	16	46	38	47	34
ENSMUSG00000020265	chr10	Sumo3	77606097	77606341	3826	0.195888	5.979648	0.212138	0.317059	0.028331	0	877	727	1220	910	948	1132	1528	1157	1486	869
ENSMUSG00000034518	chr8	Hmgxb4	74993356	74993749	5227	-0.2412	2.896404	0.212162	0.317059	0.034723	0	110	71	184	132	157	91	179	96	130	123
ENSMUSG00000074030	chr8	Exoc8	1.25E+08	1.25E+08	7406	0.221479	3.272616	0.212277	0.317195	0.030602	0	106	99	196	164	150	130	191	206	253	164
ENSMUSG00000028700	chr4	Pomgnt1	1.16E+08	1.16E+08	5463	0.183245	6.109346	0.212313	0.317214	0.024853	0	982	697	1393	1036	1099	1018	1688	1188	1694	1175
ENSMUSG00000015672	chr13	Mrpl32	14610301	14610740	768	-0.20949	4.342562	0.212451	0.317385	0.031685	0	330	324	386	297	353	244	480	306	431	280
ENSMUSG00000100309	chr1	Gm6644	55444074	55445024	951	-0.27379	2.353919	0.213002	0.318171	0.046034	0	106	62	104	67	97	70	106	74	117	54
ENSMUSG00000028793	chr4	Rnf19b	1.29E+08	1.29E+08	2872	0.181043	4.911506	0.213139	0.31834	0.022929	0	413	321	595	408	532	456	686	585	804	420
ENSMUSG00000043153	chr12	Ispd	36381519	36382024	2690	-0.29155	1.563186	0.213175	0.318358	0.049034	0	54	42	70	47	36	31	63	45	62	37
ENSMUSG00000024563	chr18	Smad2	76241580	76241979	3549	-0.20064	3.533446	0.213219	0.318388	0.025486	0	162	154	282	179	215	156	235	221	205	157
ENSMUSG00000040651	chr14	Fam208a	27428847	27429384	7574	-0.25583	2.920571	0.213257	0.318409	0.040425	0	88	91	228	102	169	86	143	151	127	113
ENSMUSG00000037262	chr2	Kin	10080593	10080744	1705	0.260463	2.364896	0.213374	0.318512	0.038571	0	62	53	114	63	82	78	139	73	152	72
ENSMUSG00000075012	chr2	Fjx1	1.02E+08	1.02E+08	3134	0.454613	0.29329	0.213352	0.318512	0.103697	0	12	4	18	20	23	27	37	11	19	22
ENSMUSG00000017764	chr2	Zswim1	1.65E+08	1.65E+08	2781	0.227658	3.082623	0.213655	0.318896	0.032915	0	96	100	195	99	137	149	154	157	197	156
ENSMUSG00000002983	chr7	Relb	19606217	19606941	3885	0.284658	3.431378	0.213723	0.318961	0.054658	0	161	156	189	95	149	206	257	179	308	134
ENSMUSG00000053835	chr17	H2-T24	36005695	36006789	2182	0.321596	1.019372	0.214004	0.319345	0.045562	0	22	14	33	34	35	27	42	47	45	33
ENSMUSG00000044768	chr1	D1Ertd622e	97606318	97646361	41324	-0.29548	3.955289	0.214154	0.319497	0.064208	0	339	262	374	141	205	175	318	232	317	236
ENSMUSG00000046434	chr15	Hnrnpa1	1.03E+08	1.03E+08	1918	0.190087	6.288291	0.214154	0.319497	0.027066	0	1062	911	1400	1102	1331	1232	2052	1237	1819	1327
ENSMUSG00000030752	chr7	Kdm8	1.25E+08	1.25E+08	2385	-0.21399	3.459045	0.214472	0.3199	0.029597	0	176	113	289	153	233	141	255	141	228	168
ENSMUSG00000044857	chr17	Lemd2	27189601	27190790	2595	0.179857	5.096996	0.214456	0.3199	0.022927	0	434	397	606	523	593	551	818	657	803	502
ENSMUSG00000031949	chr8	Adat1	1.12E+08	1.12E+08	4399	0.293213	1.587153	0.214536	0.319958	0.045037	0	36	32	75	27	43	49	70	63	70	40
ENSMUSG00000071342	chr12	Lsmem1	40176386	40177228	1213	-0.23482	5.297215	0.214711	0.320183	0.041458	0	596	648	895	514	696	584	896	402	801	627
ENSMUSG00000036693	chr5	Nop14	34638532	34638651	2734	-0.18525	4.401946	0.215192	0.320865	0.023967	0	304	286	503	292	424	291	472	289	452	312
ENSMUSG00000001440	chr11	Kpnb1	97159714	97162681	6590	-0.17725	6.778951	0.215328	0.321032	0.023963	0	1649	1277	2716	1714	2135	1452	2463	1865	2261	1473

ENSMUSG00000081600	chr11	Gm12286	63312310	63313311	1002	0.355487	1.091485	0.215394	0.321094	0.066464	0	22	14	52	34	24	30	53	40	68	21
ENSMUSG00000025337	chr5	Sbds	1.3E+08	1.3E+08	2033	0.195575	4.749443	0.21548	0.321186	0.026902	0	332	327	442	440	433	423	699	480	556	460
ENSMUSG00000051149	chr2	Adnp	1.68E+08	1.68E+08	5350	-0.17496	5.13072	0.215711	0.321495	0.021987	0	542	367	898	560	672	456	746	540	745	535
ENSMUSG00000019795	chr10	Pcmt1	7629373	7630976	4718	-0.19336	7.022813	0.215846	0.321659	0.028836	0	1992	1828	3155	1960	2156	1830	2781	1913	2958	1734
ENSMUSG00000030780	chr7	BC017158	1.28E+08	1.28E+08	5526	0.265968	1.825468	0.215958	0.321754	0.035464	0	36	39	64	46	67	52	80	76	72	61
ENSMUSG00000040250	chr6	Asun	1.47E+08	1.47E+08	3968	-0.19087	3.517282	0.215947	0.321754	0.023071	0	171	127	256	199	228	135	251	178	248	169
ENSMUSG00000022858	chr16	Tra2b	22244549	22246866	5383	-0.18448	4.869882	0.216533	0.322575	0.024596	0	451	406	674	411	540	413	575	517	550	427
ENSMUSG00000037096	chr3	Gm9762	78966359	78966799	441	-0.31384	1.338629	0.216594	0.322619	0.044704	0	41	32	74	32	40	39	47	36	41	33
ENSMUSG00000051065	chr16	Mb21d2	28826176	28829009	3080	-0.2221	3.80603	0.216612	0.322619	0.033938	0	168	179	343	232	299	214	261	154	360	194
ENSMUSG00000041135	chr4	Ripk2	16122733	16123891	2816	0.284694	1.676504	0.216722	0.322746	0.036488	0	38	39	49	47	47	51	79	54	69	56
ENSMUSG00000021559	chr13	Dapk1	60601947	60602110	5934	0.358445	2.856435	0.216877	0.322942	0.090865	0	109	79	165	43	112	150	118	208	161	81
ENSMUSG00000004637	chr8	Wwox	1.14E+08	1.14E+08	10173	-0.233	2.668568	0.216931	0.322986	0.031222	0	82	67	138	122	142	87	130	109	112	87
ENSMUSG00000029642	chr5	Polr1d	1.47E+08	1.47E+08	1985	0.231446	5.913672	0.217106	0.323209	0.040541	0	904	824	869	795	872	1069	1431	1045	1623	832
ENSMUSG00000042854	chr2	Trp53rk	1.67E+08	1.67E+08	5755	0.268766	1.836128	0.217131	0.32321	0.035126	0	35	40	74	46	60	56	94	57	92	51
ENSMUSG00000030079	chr6	Ruvbl1	88465409	88465668	1899	0.20419	4.541892	0.217393	0.323565	0.029236	0	335	307	448	270	343	398	557	386	581	359
ENSMUSG00000034842	chr5	Art3	92331827	92331912	3932	0.199256	7.602677	0.217598	0.323825	0.030921	0	2467	2318	4176	2505	3118	3075	5150	2740	4706	3494
ENSMUSG00000054766	chr2	Set	30057378	30057401	4070	0.192841	6.330857	0.217617	0.323825	0.028307	0	1128	1009	1441	1054	1299	1322	1852	1382	2004	1311
ENSMUSG00000032673	chr11	Prorsd1	29511757	29513676	2128	-0.21499	3.798103	0.217673	0.323872	0.032841	0	240	218	289	186	231	188	314	203	276	196
ENSMUSG00000031446	chr8	Cul4a	13105621	13105903	6408	-0.17912	6.655099	0.217929	0.324216	0.024692	0	1390	1144	2656	1639	1963	1239	2214	1549	2250	1502
ENSMUSG00000044122	chr11	Proca1	78193392	78193766	2088	0.56694	0.610338	0.218132	0.324482	0.17605	0	22	26	16	12	9	22	28	60	20	22
ENSMUSG00000040310	chr2	Alx4	93642384	93643088	7060	-0.46195	0.462977	0.218291	0.324682	0.102393	0	10	12	42	27	33	14	25	22	9	25
ENSMUSG00000033111	chr14	3830406C13Rik	12284209	12284257	2477	-0.21718	3.405787	0.218376	0.324772	0.032094	0	175	163	217	158	174	133	236	173	194	155
ENSMUSG00000033126	chr10	Ybey	76459569	76463319	4520	0.213612	3.090574	0.218488	0.324903	0.027728	0	100	97	157	144	124	136	199	152	194	144
ENSMUSG00000054708	chr10	Ankrd24	81628540	81628640	8142	-0.2231	3.043266	0.218569	0.324986	0.032819	0	132	120	187	121	138	95	202	123	157	119
ENSMUSG00000023050	chr15	Map3k12	1.02E+08	1.03E+08	8986	0.276877	1.756989	0.21862	0.324996	0.045392	0	27	33	85	46	54	52	65	72	73	62
ENSMUSG00000074643	chr2	Cpne1	1.56E+08	1.56E+08	4507	-0.22696	3.778907	0.218624	0.324996	0.034936	0	178	118	411	218	317	177	313	251	253	165
ENSMUSG00000037465	chr15	Klf10	38294413	38296164	3045	0.531566	4.291909	0.218683	0.325047	0.214988	0	198	416	208	115	214	164	1176	203	308	394
ENSMUSG00000028234	chr4	Rps20	3831334	3834683	4080	0.241108	7.553295	0.218744	0.325101	0.045518	0	2960	2675	3150	2132	2335	3434	4531	3365	4271	2953
ENSMUSG00000034487	chr9	Kdelc2	53384023	53384286	3644	0.22307	3.21642	0.218925	0.32526	0.033192	0	106	101	220	117	150	164	211	202	161	153
ENSMUSG00000043445	chr17	Pgp	24470473	24471149	1027	-0.21401	4.934098	0.218949	0.32526	0.034389	0	407	315	551	688	679	358	692	488	697	399
ENSMUSG00000085653	chr1	Gm15179	75368212	75368431	867	0.238039	3.767689	0.218901	0.32526	0.040744	0	163	107	243	221	282	209	373	193	258	298
ENSMUSG00000095403	chr8	Gm21092	20550331	20550428	4132	-0.26475	1.922384	0.218892	0.32526	0.037747	0	53	52	97	49	76	51	90	53	73	43
ENSMUSG00000067873	chrX	Htatsf1	57053583	57053765	4879	-0.20212	7.250449	0.218975	0.325262	0.032032	0	2343	2308	3457	2141	2663	2318	3195	2135	3290	2066
ENSMUSG00000028657	chr4	Ppt1	1.23E+08	1.23E+08	3674	0.18091	4.8191	0.219028	0.325304	0.023785	0	357	289	526	447	508	472	623	533	564	509
ENSMUSG00000030245	chr6	Golt1b	1.42E+08	1.42E+08	2818	0.191838	4.396103	0.219136	0.325428	0.025838	0	331	227	427	246	339	351	471	380	492	345
ENSMUSG00000032478	chr9	Nme6	1.1E+08	1.1E+08	1014	0.179507	4.418469	0.219163	0.325432	0.022205	0	285	230	382	330	371	360	513	369	493	335
ENSMUSG00000024505	chr18	Dtwd2	49696145	49698500	3520	-0.27089	2.276473	0.219243	0.325514	0.045802	0	88	68	131	56	74	63	102	83	85	61
ENSMUSG00000022884	chr16	Eif4a2	23107444	23107820	5338	-0.20402	8.453732	0.219305	0.32557	0.032918	0	5339	5523	7307	5367	5911	4616	8169	5222	7413	4798
ENSMUSG00000092607	chr3	Scnm1	95129536	95129883	1885	0.195222	4.738562	0.219431	0.325721	0.02704	0	370	341	455	385	397	427	665	436	645	439
ENSMUSG00000029916	chr6	Agk	40325478	40325530	2225	0.242399	2.569161	0.219469	0.325741	0.03602	0	58	67	130	87	92	100	163	107	109	97
ENSMUSG00000028412	chr4	Slc44a1	53440413	53440716	6945	0.177422	5.439154	0.219517	0.325776	0.023315	0	544	537	897	606	670	709	966	756	1062	713
ENSMUSG00000025510	chr7	Cd151	1.41E+08	1.41E+08	2010	0.179516	6.887561	0.2196	0.325792	0.025021	0	1522	1294	2278	1856	1964	1850	2718	2304	2938	1762
ENSMUSG00000034220	chr1	Gpc1	92831645	92832097	5159	0.20565	8.392734	0.219571	0.325792	0.033442	0	4517	2854	6986	5265	5964	5910	6958	5356	9915	5041
ENSMUSG00000062127	chr3	Cttnbp2nl	1.05E+08	1.05E+08	5000	0.23237	2.604221	0.219602	0.325792	0.031985	0	62	71	127	78	108	95	159	100	126	110
ENSMUSG00000081810	chr4	Gm11878	22519628	22520027	400	0.369132	0.874448	0.21972	0.325931	0.05641	0	22	27	29	16	24	29	39	28	52	30
ENSMUSG00000035597	chr12	Prpf39	65036333	65036468	4401	-0.226	3.745843	0.219815	0.326035	0.036197	0	205	219	344	185	186	191	257	214	254	200
ENSMUSG00000028456	chr4	Unc13b	43058953	43059285	13497	-0.32058	1.457509	0.219855	0.326058	0.058511	0	29	37	61	49	62	28	76	49	40	26
ENSMUSG00000038957	chr9	Edc3	57708540	57708699	5804	0.198418	3.848358	0.219887	0.326068	0.027299	0	193	147	350	165	238	262	311	267	339	213
ENSMUSG00000033904	chr7	Ccp110	1.19E+08	1.19E+08	8256	-0.31586	1.661418	0.219914	0.326073	0.053742	0	41	33	90	37	82	50	46	49	69	34
ENSMUSG00000029171	chr5	Pgm1	64092936	64093088	2608	0.301037	1.161173	0.220087	0.326293	0.043828	0	24	16	50	29	38	30	62	48	49	28
ENSMUSG00000057596	chr7	Trim30d	1.04E+08	1.04E+08	3758	0.361868	0.766091	0.220203	0.326428	0.070637	0	20	12	41	17	25	28	39	44	21	28
ENSMUSG00000041241	chr4	Mul1	1.38E+08	1.38E+08	4000	-0.17205	5.389805	0.220354	0.326616	0.022139	0	595	455	909	763	879	554	942	671	900	573
ENSMUSG00000055485	chr2	Soga1	1.57E+08	1.57E+08	7984	-0.31962	1.752033	0.220506	0.326804	0.062001	0	33	35	97	63	74	22	71	48	79	52
ENSMUSG00000037519	chr7	Ppfia1	1.44E+08	1.44E+08	10105	-0.19429	4.557048	0.220578	0.326874	0.027045	0	303	230	616	438	487	259	489	371	503	395
ENSMUSG00000003604	chr2	Aven	1.12E+08	1.12E+08	5001	0.195541	4.017172	0.220614	0.326891	0.025495	0	233	197	310	203	250	232	369	335	398	247
ENSMUSG00000001569	chr5	Nom1	29434664	29435643	4895	-0.18193	4.050729	0.220713	0.327001	0.022743	0	241	212	398	269	293	247	356	227	354	234
ENSMUSG00000025340	chr5	Rabgef1	1.3E+08	1.3E+08	4168	-0.1918	6.621262	0.22076	0.327028	0.02872	0	1660	1047	2567	1418	1902	1395	1946	1406	2334	1388
ENSMUSG00000040957	chr18	Cables1	11839220	11840533	3397	0.406565	1.137006	0.22078	0.327028	0.094066	0	23	24	25	38	31	43	25	63	45	35
ENSMUSG00000020740	chr11	Gga3	1.16E+08	1.16E+08	6245	0.198361	3.938484	0.220981	0.327252	0.028514	0	188	116	371	213	298	238	326	322	354	246
ENSMUSG00000029319	chr5	Coq2	1.01E+08	1.01E+08	2624	-0.18277	6.190383	0.220968	0.327252	0.026004	0	1166	950	1568	1175	1326	979	1711	1144	1506	984
ENSMUSG00000027746	chr3	Ufm1	53855212	53857995	4122	-0.18864	4.855672	0.22106	0.327296	0.02665	0	430	438	635	425	509	410	672	436	554	407
ENSMUSG00000062329	chr5	Cytl1	37735519	37735709	974	0.487086	1.717124	0.221055	0.327296	0.152108	0	44	49	29	48	26	17	68	81	98	81
ENSMUSG00000087574	chr11	C030037D09Rik	88718645	88719017	4199	0.314415	1.578054	0.221286	0.327594	0.056887	0	32	25	57	43	52	33	81	37	69	73
ENSMUSG00000028688	chr4	Toe1	1.17E+08	1.17E+08	2979	-0.21089	3.216408	0.221407	0.327737	0.02971	0	158	109	186	150	187	115	227	124	203	125
ENSMUSG00000034850	chr2	Tmem127	1.27E+08	1.27E+08	4811	-0.18004	5.875064	0.221526	0.327876	0.025035	0	887	829	1314	858	1079	845	1186	894	1272	843

ENSMUSG00000006587	chr8	Snai3	1.22E+08	1.22E+08	1589	0.388998	3.808262	0.221566	0.327899	0.116172	0	98	72	170	350	300	164	355	171	447	332
ENSMUSG00000021271	chr12	Zfp839	1.11E+08	1.11E+08	3725	-0.21384	3.369194	0.221696	0.328019	0.031023	0	123	139	228	185	212	120	204	137	250	166
ENSMUSG00000039367	chr14	Sec24c	20674321	20674388	4446	-0.18618	6.186376	0.221673	0.328019	0.026809	0	1020	728	2027	1263	1386	1004	1574	1217	1493	977
ENSMUSG00000054893	chr7	Zfp667	6286579	6286654	4755	-0.25355	2.608522	0.222208	0.328738	0.040826	0	99	95	143	76	106	94	136	83	107	80
ENSMUSG00000025465	chr7	Echs1	1.4E+08	1.4E+08	5274	-0.25257	6.667296	0.222267	0.328755	0.050607	0	1073	1038	1873	2648	2338	1096	2426	1680	2012	1419
ENSMUSG00000034663	chr5	Bmp2k	96997689	96998096	8480	-0.23749	3.483381	0.222268	0.328755	0.039003	0	176	145	347	148	166	134	191	217	234	155
ENSMUSG00000019986	chr10	Ahi1	20952547	20952752	5093	0.352514	0.447832	0.222357	0.32882	0.054729	0	18	7	26	15	24	27	27	25	24	23
ENSMUSG00000020925	chr11	Ccdc43	1.03E+08	1.03E+08	3341	-0.18456	6.259219	0.222369	0.32882	0.026635	0	1309	921	1813	1093	1428	1044	1725	1136	1585	1113
ENSMUSG00000032537	chr9	Ephb1	1.02E+08	1.02E+08	6487	0.421314	0.308577	0.222386	0.32882	0.076629	0	8	7	24	20	20	19	34	22	36	9
ENSMUSG00000025428	chr18	Atp5a1	77773729	77774110	3135	-0.27045	11.05622	0.222488	0.328933	0.058744	0	24932	18210	39135	55967	52448	24758	47279	27013	52618	29475
ENSMUSG00000025933	chr1	Tmem14a	21218575	21218889	1351	0.383449	0.959561	0.223015	0.329638	0.063839	0	19	33	30	17	25	26	46	38	50	31
ENSMUSG00000062931	chr10	Zfp938	82224850	82226593	2128	-0.25157	2.803077	0.223013	0.329638	0.044366	0	122	115	147	105	94	93	147	102	149	89
ENSMUSG00000026896	chr2	Ifih1	62595798	62598088	8165	-0.28735	2.35937	0.223144	0.329792	0.053124	0	51	63	146	77	123	53	138	71	77	80
ENSMUSG00000023072	chr7	Cep89	35397035	35397206	5087	-0.22622	2.810567	0.223223	0.329872	0.033358	0	102	100	170	114	111	106	127	114	152	84
ENSMUSG00000001100	chr11	Poldip2	78512193	78512472	3783	-0.19395	6.732158	0.223344	0.330015	0.029823	0	1507	1103	2307	2225	2053	1437	2417	1545	2411	1400
ENSMUSG00000030410	chr7	Dmwd	19076249	19076701	2534	-0.18078	5.39584	0.223433	0.33007	0.024927	0	584	520	958	754	786	539	714	684	1006	666
ENSMUSG00000034994	chr10	Eef2	81176631	81176729	3098	-0.18538	10.3547	0.223445	0.33007	0.02775	0	18370	18278	30033	21833	22904	16654	26029	21075	29831	19441
ENSMUSG00000044982	chr18	Sft2d3	31909094	31911903	2810	0.332045	1.06023	0.223456	0.33007	0.057096	0	29	21	38	24	28	47	34	38	38	38
ENSMUSG00000019715	chr2	Gle1	29935426	29935598	6087	0.169073	5.270699	0.223502	0.330102	0.021385	0	461	420	823	613	621	580	967	708	856	635
ENSMUSG00000032959	chr5	Pebp1	1.17E+08	1.17E+08	1771	0.20395	7.768518	0.223726	0.330395	0.033303	0	3363	2457	3876	2914	3435	3872	4599	3515	6153	3315
ENSMUSG00000049755	chr11	Zfp672	58315114	58317534	6674	-0.18487	4.637308	0.223844	0.330528	0.024832	0	347	247	536	494	526	331	524	390	491	389
ENSMUSG00000091154	chr8	Proscos	27042377	27043042	666	-0.41677	0.50529	0.223866	0.330528	0.096819	0	18	15	22	42	22	10	23	17	40	16
ENSMUSG00000015126	chr17	Tsr3	25240170	25240364	1192	0.201413	4.173217	0.223951	0.33058	0.028408	0	265	215	318	251	269	313	402	265	458	315
ENSMUSG00000048388	chr2	Fam171b	83812636	83812977	5744	0.278497	1.299483	0.223928	0.33058	0.040395	0	21	22	57	34	41	41	52	53	51	37
ENSMUSG00000020783	chr11	1200014J11Rik	73047783	73048082	8140	0.209585	3.267076	0.224041	0.330604	0.029049	0	130	99	202	107	181	169	214	158	248	147
ENSMUSG00000030213	chr6	Atf7ip	1.37E+08	1.37E+08	19678	-0.17726	5.146537	0.224036	0.330604	0.02337	0	450	383	946	606	716	491	747	506	742	556
ENSMUSG00000057572	chr4	Zbtb8os	1.29E+08	1.29E+08	4500	-0.20384	3.840282	0.224066	0.330604	0.030025	0	215	232	291	214	243	210	290	213	294	202
ENSMUSG00000075271	chr2	Ttc30a1	75978247	75981967	3721	-0.32713	0.990732	0.224067	0.330604	0.055831	0	38	20	51	35	25	18	39	29	34	33
ENSMUSG00000003378	chr7	Grik5	25009853	25010794	3836	0.27408	1.861976	0.224217	0.330766	0.045572	0	53	29	81	42	56	59	70	76	68	73
ENSMUSG00000082935	chr1	Gm7658	21511933	21513056	1124	0.343559	0.929627	0.224227	0.330766	0.047824	0	16	24	40	26	21	25	46	35	50	29
ENSMUSG00000034022	chr15	Cpsf1	76595809	76595932	4515	-0.17791	4.66202	0.224478	0.331101	0.022836	0	348	259	585	466	534	339	483	422	535	386
ENSMUSG00000030871	chr7	Ears2	1.22E+08	1.22E+08	5152	-0.19901	3.277254	0.22456	0.331185	0.025747	0	163	112	211	147	193	140	200	139	206	135
ENSMUSG00000029111	chr5	Nelfa	33896936	33898909	4927	0.200077	3.184093	0.224823	0.331536	0.024754	0	116	93	168	141	155	151	203	178	216	131
ENSMUSG00000022330	chr15	Osr2	35296098	35296467	1723	0.426308	0.323063	0.224909	0.331625	0.073705	0	16	16	24	8	13	14	31	21	41	15
ENSMUSG00000094446	chr13	Gm6344	55085777	55086259	483	0.290033	2.002085	0.225081	0.331842	0.049335	0	68	36	60	50	64	70	107	67	105	48
ENSMUSG00000022035	chr14	Ccdc25	65837302	65837484	2227	-0.18188	4.9674	0.225404	0.332281	0.025158	0	473	423	627	451	674	423	699	564	581	416
ENSMUSG00000033705	chr2	Stard9	1.21E+08	1.21E+08	19408	-0.28298	2.598371	0.225482	0.33236	0.051281	0	60	52	187	97	161	76	129	107	106	75
ENSMUSG00000056014	chr5	A430033K04Rik	1.39E+08	1.39E+08	3900	-0.32094	1.745922	0.225804	0.332797	0.063323	0	47	44	63	60	75	35	85	30	52	64
ENSMUSG00000020069	chr10	Hnrnph3	63014664	63015714	3151	0.18199	4.381403	0.225995	0.333028	0.023993	0	278	216	398	290	388	385	506	341	450	326
ENSMUSG00000029147	chr5	Ppm1g	31202668	31203284	2165	-0.16921	5.261613	0.226061	0.333028	0.021732	0	507	428	888	685	800	504	792	602	887	545
ENSMUSG00000048796	chr3	Cyb561d1	1.08E+08	1.08E+08	5086	-0.20861	2.817629	0.226038	0.333028	0.02738	0	112	90	165	104	129	92	150	117	145	90
ENSMUSG00000067608	chr19	Pcna-ps2	9283238	9284494	1257	0.346688	0.27329	0.226024	0.333028	0.044084	0	11	10	28	13	17	16	27	21	26	22
ENSMUSG00000021520	chr13	Uqcrb	66900617	66900826	876	0.207299	8.165201	0.226226	0.333191	0.034858	0	3721	3360	4522	4870	4495	4690	8065	4421	7105	4307
ENSMUSG00000042903	chrX	Foxo4	1.01E+08	1.01E+08	3485	-0.1775	7.555255	0.226243	0.333191	0.025474	0	2594	2344	4314	3351	3504	2406	3886	2969	4129	2868
ENSMUSG00000067567	chrX	Hdac8	1.02E+08	1.02E+08	4839	0.251249	2.240328	0.226247	0.333191	0.03784	0	53	41	102	80	68	84	126	83	93	72
ENSMUSG00000015488	chr2	Cacfd1	27009926	27010105	4693	0.1791	6.142841	0.226418	0.333405	0.025343	0	912	716	1388	950	1424	1019	1628	1345	1823	1112
ENSMUSG00000093593	chr17	Gm20683	25834465	25835197	2790	-0.23712	6.602867	0.226508	0.333501	0.045323	0	1316	804	1874	2404	2185	1135	2293	1490	2017	1362
ENSMUSG00000024098	chr17	Twsg1	65923066	65926466	4046	-0.17098	5.381161	0.226648	0.33364	0.022216	0	572	418	1048	712	888	547	888	677	867	620
ENSMUSG00000050605	chr7	Zfp61	24291039	24292504	3431	-0.30731	1.19435	0.226653	0.33364	0.04618	0	30	25	41	43	56	26	41	28	43	40
ENSMUSG00000021782	chr14	Dlg5	24133953	24135673	8491	-0.32899	2.253544	0.226748	0.33372	0.067821	0	73	33	163	59	116	57	71	96	78	70
ENSMUSG00000056919	chr9	Cep162	87189577	87192922	11607	-0.252	1.905743	0.226758	0.33372	0.030969	0	48	44	95	65	71	49	70	60	68	56
ENSMUSG00000021614	chr13	Vcan	89655312	89657358	14462	0.248128	3.011133	0.226811	0.333762	0.044637	0	88	66	190	92	173	112	179	137	165	188
ENSMUSG00000037369	chrX	Kdm6a	18162575	18163172	8158	-0.29131	3.590223	0.226848	0.333779	0.063578	0	129	153	377	197	239	98	340	195	147	213
ENSMUSG00000021079	chr12	Timm9	71123173	71123686	1018	0.195636	3.735203	0.226886	0.333798	0.025187	0	172	163	239	202	201	206	307	259	332	194
ENSMUSG00000024038	chr17	Ndufv3	31520115	31520261	2490	0.204032	6.748711	0.227058	0.333978	0.033479	0	1408	1022	1840	2016	1708	1661	2558	1893	3083	1518
ENSMUSG00000034271	chr12	Jdp2	85599105	85599227	1881	0.250898	2.123099	0.227055	0.333978	0.037341	0	47	45	77	58	87	78	84	93	95	67
ENSMUSG00000039770	chr17	Ypel5	72836704	72836791	2869	0.240983	5.728528	0.227109	0.334014	0.045853	0	831	767	851	562	724	960	1247	967	1424	691
ENSMUSG00000015837	chr11	Sqstm1	50199366	50200947	3356	0.219607	9.392457	0.227337	0.334313	0.039512	0	9501	8153	14564	8433	8954	11197	12962	11698	20996	9972
ENSMUSG00000055917	chr12	Zfp277	40315046	40315903	2454	-0.20361	3.29253	0.227374	0.334331	0.029009	0	137	149	222	151	168	123	222	146	211	133
ENSMUSG00000036943	chr9	Rab8b	66843672	66847811	4743	0.201092	3.657959	0.227424	0.334337	0.028433	0	174	133	303	139	203	199	305	236	252	226
ENSMUSG00000047867	chr6	Gimap6	48701582	48702823	3496	-0.24166	3.694049	0.227429	0.334337	0.042888	0	121	145	291	267	323	145	297	240	270	146
ENSMUSG00000097333	chr13	Zfp87	67515781	67518112	2865	0.279447	1.909708	0.22759	0.334537	0.04297	0	44	40	70	59	51	43	112	61	101	58
ENSMUSG00000054770	chr1	Kctd18	57955101	57956820	12973	-0.2589	2.41595	0.227824	0.334844	0.043656	0	69	92	129	63	103	70	114	89	95	69
ENSMUSG00000017221	chr11	Psmd3	98682554	98682937	4967	0.175279	6.983458	0.227917	0.334943	0.024782	0	1634	1342	2566	1956	2097	1929	2801	2282	3329	2023
ENSMUSG00000057110	chr2	Cntrl	35109492	35109629	10334	-0.22792	3.067984	0.228055	0.335109	0.034008	0	108	90	245	136	163	98	203	126	137	137

ENSMUSG00000028121	chr3	Bcar3	1.22E+08	1.22E+08	3298	0.270641	2.454878	0.228188	0.335267	0.04659	0	94	63	94	54	79	89	134	105	106	99
ENSMUSG00000017737	chr2	Mmp9	1.65E+08	1.65E+08	3539	-0.49072	2.020946	0.228269	0.335349	0.176022	0	95	52	160	29	45	52	81	104	36	25
ENSMUSG00000068328	chr6	Aup1	83054653	83054832	1509	0.177953	5.946744	0.228329	0.335401	0.024983	0	848	715	1188	860	1007	973	1316	1148	1414	1098
ENSMUSG00000019873	chr10	Reep3	67009189	67013786	5473	0.189074	4.167856	0.228375	0.33543	0.026328	0	215	180	414	251	311	268	419	424	348	276
ENSMUSG00000001065	chr8	Zfp276	1.23E+08	1.23E+08	5530	-0.22993	2.746267	0.228432	0.335457	0.034006	0	85	90	146	103	153	70	137	124	123	104
ENSMUSG00000025505	chr7	Tmem80	1.41E+08	1.41E+08	3178	0.18123	3.837646	0.228444	0.335457	0.021955	0	180	155	270	211	256	195	351	246	360	243
ENSMUSG00000038780	chr5	Smurf1	1.45E+08	1.45E+08	6336	-0.25382	4.033268	0.228519	0.335531	0.048298	0	192	113	383	361	438	184	333	287	338	229
ENSMUSG00000036281	chr2	Snapc4	26362765	26363020	6622	0.257313	2.13062	0.22859	0.335597	0.042389	0	51	36	99	63	71	72	102	92	69	83
ENSMUSG00000059277	chr7	R74862	1.43E+08	1.43E+08	3889	0.395596	0.136024	0.228647	0.335645	0.060056	0	12	11	23	9	14	20	17	23	19	21
ENSMUSG00000027313	chr2	Chac1	1.19E+08	1.19E+08	1637	-0.39431	6.182769	0.228736	0.335738	0.127025	0	723	1583	2029	817	1387	617	1887	400	2229	977
ENSMUSG00000020910	chr11	Adprm	67037905	67038445	1977	0.263342	2.47039	0.228784	0.335771	0.042912	0	62	66	82	75	108	80	168	100	102	95
ENSMUSG00000030970	chr7	Ctbp2	1.33E+08	1.33E+08	6220	-0.24821	3.070323	0.228856	0.335839	0.045287	0	129	130	220	119	122	101	223	138	164	85
ENSMUSG00000001420	chr3	Tmem79	88328655	88329932	2912	-0.34869	0.947847	0.228941	0.33589	0.077288	0	33	35	25	34	30	14	42	28	38	28
ENSMUSG00000045725	chr6	Prr15	54327012	54327310	1381	0.523641	0.933401	0.228935	0.33589	0.1664	0	23	37	28	13	9	41	68	35	36	17
ENSMUSG00000028271	chr3	Gtf2b	1.43E+08	1.43E+08	1271	-0.20274	3.731113	0.229176	0.336197	0.030284	0	224	199	280	191	217	180	307	211	256	175
ENSMUSG00000023932	chr17	Cdc5l	45391892	45392304	2989	0.171853	5.669773	0.229315	0.336333	0.023185	0	710	536	1036	734	838	886	1196	805	1185	846
ENSMUSG00000058706	chr6	0610030E20Rik	72347317	72347515	4632	-0.17805	3.979221	0.229319	0.336333	0.021902	0	254	179	375	240	301	218	301	274	308	238
ENSMUSG00000023572	chr2	Ccndbp1	1.21E+08	1.21E+08	3469	0.214576	5.118136	0.22941	0.336427	0.035687	0	469	500	734	386	439	567	805	634	881	534
ENSMUSG00000034135	chr9	Sik3	46012820	46013130	7102	-0.18499	5.363093	0.229434	0.336427	0.026569	0	549	421	1138	655	875	523	749	622	1001	645
ENSMUSG00000079662	chr17	Ntn3	24203848	24206947	4894	0.388133	-0.02306	0.229563	0.336578	0.060409	0	10	8	18	12	13	17	26	18	11	17
ENSMUSG00000017858	chr2	Ift52	1.63E+08	1.63E+08	2802	-0.19186	4.035121	0.229808	0.336865	0.02702	0	246	244	329	237	320	251	313	275	321	223
ENSMUSG00000031878	chr8	Nae1	1.05E+08	1.05E+08	7792	-0.19779	4.719134	0.229796	0.336865	0.030703	0	411	413	557	385	439	343	623	353	552	392
ENSMUSG00000067870	chr15	Rpl31-ps8	90764279	90764656	378	0.247543	4.762255	0.229859	0.336902	0.047573	0	442	341	402	331	400	565	754	398	635	346
ENSMUSG00000020536	chr11	Llgl1	60699723	60699941	4862	0.17221	4.161266	0.230423	0.337691	0.021433	0	226	170	403	251	324	253	389	358	445	289
ENSMUSG00000027075	chr2	Slc43a1	84838850	84839681	5716	0.255862	4.322189	0.230475	0.337729	0.051142	0	271	215	519	204	280	432	596	300	444	223
ENSMUSG00000026649	chr1	1700009P17Rik	1.71E+08	1.71E+08	1774	0.357907	0.638993	0.230699	0.338021	0.051388	0	13	21	28	19	20	17	37	26	43	27
ENSMUSG00000057666	chr6	Gapdh	1.25E+08	1.25E+08	4133	0.210184	12.64995	0.230734	0.338035	0.036832	0	98453	50683	118929	101976	113845	94832	151845	112130	193573	92378
ENSMUSG00000049287	chr11	Iba57	59155369	59158659	4885	-0.22182	3.866708	0.230771	0.338051	0.037076	0	192	169	235	320	329	199	329	197	325	191
ENSMUSG00000033767	chr3	D930015E06Rik	83897655	83898613	10572	0.316302	2.766485	0.230843	0.338119	0.074092	0	41	52	102	156	137	97	184	135	168	104
ENSMUSG00000006154	chr7	Eps8l1	4460674	4461024	4953	-0.64859	1.448103	0.231297	0.338747	0.318923	0	0	42	72	78	73	12	61	50	36	32
ENSMUSG00000028496	chr4	Mllt3	87769925	87774146	12004	-0.20923	6.99438	0.231323	0.338748	0.036218	0	1906	2019	3129	1790	1998	1535	2880	1706	2961	1926
ENSMUSG00000020099	chr10	Unc5b	60762610	60765373	5852	0.303848	2.463666	0.231488	0.338925	0.067339	0	46	33	127	88	115	60	126	86	191	98
ENSMUSG00000086567	chr13	Gm2830	54499705	54500089	385	0.251526	4.915603	0.231495	0.338925	0.04967	0	460	445	507	348	351	564	816	453	781	412
ENSMUSG00000032892	chr11	Rangrf	68972484	68972741	1269	-0.19279	4.779945	0.231681	0.339159	0.029203	0	389	324	541	565	518	368	594	407	685	330
ENSMUSG00000043964	chr7	Orai3	1.28E+08	1.28E+08	2141	0.181802	4.008202	0.231777	0.339262	0.023558	0	215	184	358	195	261	265	333	294	394	264
ENSMUSG00000021715	chr13	Cwc27	1.05E+08	1.05E+08	2873	-0.20322	3.64552	0.231888	0.339387	0.030443	0	171	191	247	221	218	187	257	174	281	163
ENSMUSG00000029554	chr5	Mad1l1	1.4E+08	1.4E+08	3390	0.255166	2.638986	0.23206	0.339554	0.042251	0	65	70	99	100	112	76	126	109	162	136
ENSMUSG00000074479	chr3	Gm10704	88576410	88577139	730	0.315079	1.790298	0.232079	0.339554	0.058519	0	39	55	63	33	44	54	77	78	87	45
ENSMUSG00000075486	chr14	Commd6	1.02E+08	1.02E+08	1322	0.261297	2.458508	0.23204	0.339554	0.041825	0	80	70	90	72	72	77	150	113	109	90
ENSMUSG00000022131	chr14	Gpr180	1.18E+08	1.18E+08	2877	-0.16386	4.958094	0.23221	0.339692	0.020559	0	474	378	747	451	606	427	647	488	685	444
ENSMUSG00000042121	chr5	Ssh1	1.14E+08	1.14E+08	8892	-0.20959	3.078113	0.232224	0.339692	0.028309	0	130	80	205	149	169	130	171	123	175	110
ENSMUSG00000043323	chr5	Fbrsl1	1.1E+08	1.1E+08	4947	-0.21974	3.703162	0.232277	0.339732	0.034353	0	194	104	292	243	316	168	252	195	255	219
ENSMUSG00000028436	chr4	Dcaf12	41291300	41293214	3442	0.173789	5.560191	0.232437	0.339853	0.024171	0	569	416	973	775	902	668	1096	829	1187	823
ENSMUSG00000059895	chr15	Ptp4a3	73723145	73723515	4619	0.24288	9.428855	0.23239	0.339853	0.0494	0	7458	5703	13119	13905	11401	9633	18932	10537	22787	9153
ENSMUSG00000078249	chr11	Hmga1-rs1	1.21E+08	1.21E+08	1626	-0.31647	0.832866	0.232437	0.339853	0.044434	0	30	16	42	23	41	23	31	23	38	22
ENSMUSG00000073147	chr5	5031425E22Rik	23382308	23382529	5142	0.195736	3.770372	0.232489	0.339855	0.026034	0	181	172	246	186	216	201	297	239	374	222
ENSMUSG00000090210	chr3	Itga10	96645584	96645686	5186	0.409473	0.324	0.232469	0.339855	0.089303	0	11	4	22	18	26	12	40	23	19	25
ENSMUSG00000047250	chr2	Ptgs1	36230426	36230569	3884	0.292172	1.51917	0.23254	0.339892	0.050519	0	29	28	62	40	43	38	43	68	82	46
ENSMUSG00000021932	chr14	Rnaseh2b	62292589	62292654	6243	0.279416	2.648533	0.232599	0.33994	0.052661	0	102	62	89	105	77	131	153	107	134	88
ENSMUSG00000027387	chr2	Zc3h8	1.29E+08	1.29E+08	1624	-0.20126	3.473089	0.232658	0.339989	0.029536	0	203	147	220	166	194	142	240	168	235	159
ENSMUSG00000055839	chr17	Tceb2	23824740	23824979	508	0.249915	7.095474	0.232697	0.340009	0.051789	0	2402	1871	2322	1402	1604	2424	3171	2477	3464	2080
ENSMUSG00000019794	chr10	Katna1	7726000	7726123	2195	0.181373	4.076668	0.232863	0.340214	0.023539	0	232	191	358	191	300	261	377	299	432	270
ENSMUSG00000099647	chr7	Gm5776	54412158	54412478	321	-0.33003	1.648494	0.233223	0.340703	0.076927	0	51	55	59	61	35	41	82	31	63	35
ENSMUSG00000049295	chr14	Zfp219	52006077	52007147	3262	0.203486	4.096382	0.233355	0.340857	0.031073	0	221	178	323	281	265	323	294	356	417	252
ENSMUSG00000051373	chr2	Ppapdc3	32095528	32096262	2078	0.180277	7.359484	0.233381	0.340857	0.02702	0	2239	1631	3435	2396	2802	2496	4006	2537	4325	2776
ENSMUSG00000038429	chr6	Usp5	1.25E+08	1.25E+08	4621	0.17124	6.195466	0.233448	0.340919	0.023899	0	885	750	1500	1133	1337	1090	1602	1421	1792	1209
ENSMUSG00000099041	chr2	Gm28035	30240567	30240677	4238	-0.29233	4.13016	0.2335	0.340957	0.067819	0	240	168	316	425	401	347	286	197	445	157
ENSMUSG00000021116	chr12	Eif2s1	78861819	78862180	3405	-0.18964	5.289843	0.233547	0.340988	0.028899	0	581	548	858	601	730	574	1010	554	657	555
ENSMUSG00000020964	chr12	Sel1l	91806043	91810053	8555	-0.18909	6.013751	0.233848	0.34139	0.029045	0	853	658	1880	1015	1345	789	1233	1034	1462	1029
ENSMUSG00000030086	chr6	Chchd6	89383146	89383348	1126	0.290382	2.299871	0.233919	0.341456	0.05427	0	91	49	88	50	65	83	96	115	104	80
ENSMUSG00000048647	chr2	Exd1	1.2E+08	1.2E+08	6042	-0.3534	1.726564	0.234108	0.341694	0.082639	0	49	60	84	34	60	54	42	73	51	32
ENSMUSG00000098462	chr19	Gm27694	5799000	5799085	86	-0.33625	2.664874	0.234303	0.341941	0.082473	0	110	81	196	37	154	91	109	114	96	86
ENSMUSG00000051675	chr4	Trim32	65604986	65605069	3229	-0.18811	3.518052	0.234351	0.341973	0.023436	0	145	128	285	188	248	149	226	185	230	181
ENSMUSG00000034064	chr16	Poglut1	38525137	38526781	4658	0.180549	3.923333	0.234572	0.342258	0.023168	0	207	173	332	188	241	250	364	276	321	249
ENSMUSG00000038459	chr7	Abhd17c	84109356	84110801	2415	0.206628	3.340295	0.234721	0.342438	0.029142	0	127	108	191	145	179	153	182	220	265	160

ENSMUSG00000045672	chr4	Col27a1	63214004	63214404	13022	0.307041	1.868966	0.234747	0.342439	0.06476	0	32	38	89	30	75	62	74	72	61	80
ENSMUSG00000036186	chr2	Fam69b	26628457	26628699	2476	-0.61741	0.873692	0.234869	0.342579	0.268649	0	8	9	15	85	53	18	26	37	23	19
ENSMUSG00000090137	chr8	Uba52	70508263	70508528	1498	0.198615	7.318232	0.235103	0.342883	0.033028	0	2097	1747	2421	2817	2648	2626	3988	2626	3877	2578
ENSMUSG00000012422	chr13	Tmem167	90089123	90089783	10807	-0.18908	4.678657	0.235371	0.343235	0.027972	0	398	355	661	319	462	358	553	449	467	353
ENSMUSG00000027203	chr2	Dut	1.25E+08	1.25E+08	2410	0.268209	3.02477	0.23546	0.343316	0.049096	0	111	123	116	102	108	147	216	145	157	133
ENSMUSG00000043015	chr1	Tmem194b	52630703	52630851	7078	0.372756	0.265217	0.235478	0.343316	0.056817	0	15	10	24	11	17	22	26	20	17	25
ENSMUSG00000035517	chr4	Tdrd7	45965334	45965476	3958	-0.21296	4.043388	0.235508	0.343321	0.035072	0	268	267	370	200	283	241	317	298	297	225
ENSMUSG00000042570	chr10	Mier2	79540245	79541199	4497	-0.17727	4.143735	0.235665	0.343513	0.022815	0	264	205	405	285	353	274	308	306	378	235
ENSMUSG00000025816	chr2	Sec61a2	5870987	5872021	4572	-0.16921	5.271326	0.235731	0.343572	0.022524	0	537	449	973	605	774	545	819	561	738	643
ENSMUSG00000029472	chr5	Anapc5	1.23E+08	1.23E+08	2750	-0.20869	9.520724	0.236305	0.34437	0.037122	0	12271	10989	19047	9134	11383	10157	15877	11233	15169	10300
ENSMUSG00000042978	chr7	Sbk1	1.26E+08	1.26E+08	4092	0.19426	5.337991	0.236437	0.344518	0.030951	0	446	349	882	671	766	592	827	621	1110	800
ENSMUSG00000066149	chr4	Cdc26	62383654	62384538	7180	0.197552	4.442041	0.236459	0.344518	0.029545	0	342	252	419	271	316	370	544	365	560	298
ENSMUSG00000037355	chr5	Uvssa	33378549	33379325	8666	-0.28257	1.854362	0.236515	0.344562	0.047597	0	43	37	119	49	76	36	85	52	69	52
ENSMUSG00000022890	chr16	Atp5j	84827866	84827995	3130	-0.21027	8.409897	0.236703	0.344799	0.037664	0	4917	3963	6038	7340	6778	4485	8729	4583	7151	4490
ENSMUSG00000029426	chr5	Scarb2	92443873	92444284	2110	-0.19258	5.977683	0.236773	0.344824	0.030612	0	740	654	1576	1192	1398	768	1467	894	1296	1007
ENSMUSG00000083844	chr11	2210015D19Rik	5762129	5762240	3102	-0.18017	5.927784	0.236769	0.344824	0.026795	0	902	654	1425	1139	1129	840	1445	868	1352	794
ENSMUSG00000054203	chr1	Ifi205	1.74E+08	1.74E+08	4177	0.418589	3.213715	0.236911	0.344988	0.141173	0	102	103	231	65	148	239	304	244	95	61
ENSMUSG00000001052	chr3	Sec24b	1.3E+08	1.3E+08	6020	-0.17683	4.47055	0.237191	0.34532	0.023527	0	315	238	609	331	444	272	432	412	464	323
ENSMUSG00000050064	chr3	Zfp697	98382481	98382578	5163	0.387449	0.124304	0.237178	0.34532	0.066818	0	13	6	20	13	17	20	13	24	29	14
ENSMUSG00000061079	chr7	Zfp143	1.1E+08	1.1E+08	3013	-0.19764	3.220248	0.237324	0.345476	0.025618	0	137	95	228	152	196	121	203	127	206	137
ENSMUSG00000066150	chr4	Slc31a1	62360727	62360843	4280	-0.19475	4.229026	0.237478	0.345662	0.028395	0	246	158	476	368	409	252	414	299	378	260
ENSMUSG00000026036	chr1	Nif3l1	58445151	58445634	7763	-0.17668	3.667135	0.237591	0.34577	0.021559	0	179	152	312	213	230	177	265	205	251	185
ENSMUSG00000044447	chr14	Dock5	67751928	67756522	10335	0.354659	0.996759	0.237604	0.34577	0.07774	0	21	11	34	28	42	18	31	47	56	41
ENSMUSG00000049588	chr11	Ccdc69	55049731	55050558	1848	0.242056	2.80479	0.237847	0.346085	0.040498	0	110	59	113	79	148	92	173	141	167	115
ENSMUSG00000061461	chr5	Smim20	53267106	53267358	6494	0.192096	6.016646	0.237873	0.346085	0.030481	0	924	699	1047	1039	1070	1026	1819	1069	1480	991
ENSMUSG00000043889	chr13	Gm8399	81064684	81064992	1119	0.404183	-0.09304	0.237948	0.346155	0.076969	0	15	4	20	8	11	20	17	16	16	15
ENSMUSG00000032578	chr9	Cish	1.07E+08	1.07E+08	6419	-0.83204	4.492878	0.238084	0.346316	0.570327	0	80	119	890	422	1103	29	316	51	1270	62
ENSMUSG00000025008	chr19	Tctn3	40596446	40597542	3273	0.273782	1.299703	0.238159	0.346388	0.041254	0	24	16	57	33	47	36	55	45	55	44
ENSMUSG00000039637	chr16	Coro7	4626133	4627499	7420	0.193625	3.780106	0.238317	0.346579	0.028846	0	148	114	353	204	246	206	284	251	362	233
ENSMUSG00000085945	chr7	2310014F06Rik	1.13E+08	1.13E+08	659	-0.47978	0.39959	0.238396	0.346656	0.156752	0	16	15	31	19	34	13	37	3	38	7
ENSMUSG00000052794	chr8	1700030K09Rik	72443880	72443989	2970	-0.27456	1.905842	0.238424	0.346658	0.041493	0	55	31	97	70	76	50	62	66	63	57
ENSMUSG00000027540	chr2	Ptpn1	1.68E+08	1.68E+08	5533	0.182508	4.382724	0.238532	0.346739	0.025879	0	257	202	469	294	375	365	585	355	436	291
ENSMUSG00000063564	chr11	Col23a1	51289920	51290387	5736	0.317167	1.935204	0.238528	0.346739	0.072113	0	22	27	81	64	84	56	77	60	93	87
ENSMUSG00000025986	chr1	Slc39a10	46807544	46810111	6095	-0.283	2.667049	0.238729	0.346988	0.055777	0	55	54	190	124	160	71	142	107	107	91
ENSMUSG00000024914	chr19	Drap1	5422805	5423025	1741	0.243175	8.713198	0.238983	0.347319	0.050815	0	7012	5794	7195	4291	5390	7853	9660	7078	11237	5982
ENSMUSG00000037795	chr5	N4bp2	65763521	65763590	9871	0.252478	2.195911	0.239187	0.347578	0.043782	0	43	39	90	76	87	66	114	94	79	88
ENSMUSG00000063802	chr7	Hspbp1	4660521	4660845	1488	0.184601	4.722363	0.239445	0.347914	0.026822	0	397	258	427	407	474	461	595	447	611	435
ENSMUSG00000035478	chr10	Mbd3	80392539	80393018	1987	0.181826	6.770752	0.2396	0.348101	0.027978	0	1558	1167	2000	1634	1812	1716	2136	1988	2992	1804
ENSMUSG00000062762	chr9	Ei24	36779159	36780269	3459	-0.17206	6.672034	0.23987	0.348456	0.025161	0	1556	1333	2282	1625	1849	1395	2262	1496	2290	1426
ENSMUSG00000010911	chr2	Apip	1.03E+08	1.03E+08	1000	-0.18699	4.529912	0.239998	0.348603	0.028323	0	370	329	425	372	430	323	558	359	470	283
ENSMUSG00000019813	chr10	Cep57l1	41718840	41719907	7526	-0.30397	1.413244	0.240072	0.348673	0.052989	0	23	34	67	42	67	38	55	34	59	26
ENSMUSG00000002588	chr6	Pon1	5168090	5168496	2898	0.681751	1.356086	0.240226	0.348858	0.362174	0	51	34	28	8	20	72	27	124	17	20
ENSMUSG00000067825	chr6	Pex26	1.21E+08	1.21E+08	5667	-0.2516	2.551413	0.240269	0.348882	0.042829	0	90	60	156	91	118	66	94	127	131	66
ENSMUSG00000026991	chr2	Pkp4	59160850	59161128	5707	-0.21002	3.816672	0.240325	0.348925	0.033182	0	168	142	339	282	306	204	339	248	250	155
ENSMUSG00000020397	chr11	Med7	46436925	46437009	2871	0.20957	3.553896	0.240355	0.348927	0.030782	0	167	152	207	162	160	173	278	241	255	194
ENSMUSG00000035566	chr14	Pcdh17	84443563	84448653	9509	-0.43682	0.004083	0.240401	0.348927	0.07876	0	8	7	31	20	20	7	24	14	13	12
ENSMUSG00000041629	chr11	Fam104a	1.14E+08	1.14E+08	2619	0.180481	5.512788	0.240405	0.348927	0.026684	0	693	508	940	595	684	784	1019	752	1190	701
ENSMUSG00000038070	chr4	Cntln	84884309	84884824	7102	-0.29953	1.261994	0.240453	0.348958	0.04825	0	26	32	67	39	43	25	49	44	32	37
ENSMUSG00000017417	chr11	Plxdc1	97923238	97924607	4836	0.314477	2.122879	0.2405	0.348988	0.070529	0	27	46	73	60	104	44	94	81	125	91
ENSMUSG00000039048	chr9	Foxred1	35204206	35205123	4064	-0.18842	4.51412	0.240669	0.349194	0.028405	0	332	238	432	458	495	271	517	341	538	317
ENSMUSG00000016534	chrX	Lamp2	38401357	38402281	9552	0.190465	6.480699	0.24116	0.34987	0.030898	0	984	1025	2077	1239	1485	1061	1963	1871	2172	1683
ENSMUSG00000030647	chr7	Ndufc2	97400003	97400357	754	0.196485	6.820758	0.241204	0.349896	0.032924	0	1568	1261	1774	1893	1803	1810	3113	1780	2851	1668
ENSMUSG00000020496	chr11	Rnf187	58932288	58933396	1949	0.172253	6.458258	0.241255	0.349923	0.025058	0	1163	1011	1691	1312	1430	1354	1841	1688	2189	1449
ENSMUSG00000037892	chr3	Pcdh18	49743296	49745274	5366	-0.34194	2.094182	0.241276	0.349923	0.08073	0	25	48	136	85	100	46	65	86	72	63
ENSMUSG00000004568	chr8	Arhgef18	3393006	3393102	8395	-0.20996	3.32381	0.241388	0.350047	0.030949	0	131	99	258	151	245	120	178	180	220	146
ENSMUSG00000053838	chr11	Nudcd3	6105691	6108355	6496	-0.16976	7.014827	0.241419	0.350054	0.024674	0	1773	1521	3143	2116	2618	1730	2548	2009	3044	1888
ENSMUSG00000005907	chr5	Pex1	3596066	3596517	7740	-0.23001	2.441005	0.241471	0.350091	0.033095	0	77	62	142	94	94	83	110	93	100	62
ENSMUSG00000039191	chr5	Rbpj	53555779	53555903	5817	0.171571	4.852111	0.241563	0.350186	0.023877	0	338	266	707	399	541	399	738	531	664	485
ENSMUSG00000015750	chr3	Aph1a	95893969	95894283	2863	0.184638	4.489052	0.241788	0.350473	0.026972	0	247	211	436	391	423	314	478	396	642	372
ENSMUSG00000048756	chr10	Foxo3	42181841	42186295	7571	0.19222	4.880463	0.241815	0.350475	0.030706	0	287	290	800	421	497	446	697	607	583	516
ENSMUSG00000020412	chr11	Ascc2	4637747	4637822	4964	0.170349	4.83269	0.24185	0.350488	0.023039	0	383	278	582	454	468	406	591	544	757	470
ENSMUSG00000015653	chr5	Steap2	5664831	5673696	12142	0.34629	0.578567	0.241941	0.350581	0.064152	0	7	11	30	28	24	25	33	29	34	20
ENSMUSG00000007097	chr1	Atp1a2	1.72E+08	1.72E+08	7038	-0.26143	10.44286	0.242053	0.350665	0.059668	0	13695	11409	30319	37534	33163	16118	27375	20344	31680	21604
ENSMUSG00000034255	chr11	Arhgap27	1.03E+08	1.03E+08	6415	0.30378	2.141607	0.242079	0.350665	0.068534	0	39	30	61	90	94	86	79	74	106	82
ENSMUSG00000034681	chr17	Rnps1	24414675	24414734	1920	0.167397	5.386712	0.242029	0.350665	0.02288	0	569	431	868	646	663	659	938	677	1111	684

ENSMUSG00000084896	chr11	Gm11632	98084457	98085076	674	-0.29389	1.320039	0.24214	0.350715	0.04398	0	29	25	60	42	61	32	61	29	42	34
ENSMUSG00000022160	chr14	Mettl3	52294668	52295093	3987	0.181289	3.568911	0.242293	0.350899	0.022949	0	150	134	245	152	211	182	289	195	279	203
ENSMUSG00000049872	chr10	Fam26e	34091352	34092515	1786	0.322612	1.251796	0.242395	0.350969	0.06199	0	19	20	38	48	38	38	62	49	36	43
ENSMUSG00000079884	chr9	Gm10698	33728247	33728850	604	-0.24498	2.123984	0.242393	0.350969	0.038927	0	71	53	106	66	77	45	113	65	74	64
ENSMUSG00000035239	chr7	Neu3	99811439	99814307	3341	-0.25843	2.081423	0.242628	0.351269	0.043657	0	51	58	81	68	104	50	86	52	81	75
ENSMUSG00000051319	chr2	1500011K16Rik	1.28E+08	1.28E+08	800	-0.20579	5.886126	0.242757	0.351417	0.03638	0	1025	941	1140	885	912	829	1292	805	1239	881
ENSMUSG00000019797	chr10	1700021F05Rik	43525121	43525408	1339	0.221712	5.622543	0.242809	0.351455	0.041853	0	520	404	727	949	1094	706	1179	804	1341	873
ENSMUSG00000022247	chr15	Brix1	10474779	10476596	2731	0.212131	4.052632	0.242857	0.351485	0.033771	0	221	242	266	221	236	269	423	274	405	260
ENSMUSG00000015790	chr2	Surf1	26913381	26913658	1753	0.177615	4.722088	0.242935	0.351561	0.024491	0	372	323	478	379	400	384	603	493	676	418
ENSMUSG00000025758	chr3	Plk4	40800019	40800283	5863	-0.41186	-0.04201	0.243082	0.351721	0.068015	0	18	11	14	20	15	10	12	16	14	15
ENSMUSG00000029687	chr6	Ezh2	47530274	47530601	6197	0.249503	2.167285	0.243126	0.351721	0.03817	0	53	48	75	65	80	84	123	77	85	65
ENSMUSG00000034820	chr19	Cpsf7	10525244	10525327	3604	0.163261	4.450549	0.243116	0.351721	0.02057	0	287	224	477	318	364	340	542	402	461	360
ENSMUSG00000099364	chr1	5730419F03Rik	78595031	78596859	2092	0.350361	0.559366	0.243303	0.351939	0.059275	0	19	8	21	19	30	24	28	29	42	17
ENSMUSG00000027820	chr3	Mme	63241537	63241566	11542	-0.23638	3.072208	0.243419	0.352003	0.039865	0	102	89	224	159	168	87	135	173	158	140
ENSMUSG00000036273	chr15	Lrrk2	91673375	91673437	11834	-0.25297	2.625531	0.243412	0.352003	0.043514	0	83	56	181	105	126	63	140	83	110	113
ENSMUSG00000056612	chr19	Ppp1r14b	6975048	6975506	919	0.257503	5.931338	0.243427	0.352003	0.056781	0	1050	786	940	696	805	1207	1187	1036	1929	755
ENSMUSG00000044465	chr7	Fam160a2	1.05E+08	1.05E+08	11569	-0.17431	4.151471	0.243502	0.352074	0.022767	0	264	182	443	286	364	240	331	269	424	264
ENSMUSG00000015202	chr10	Cnksr3	7119063	7120586	3837	0.299588	1.906836	0.24361	0.352121	0.063956	0	38	21	67	66	78	77	71	83	80	50
ENSMUSG00000031916	chr8	Cog8	1.07E+08	1.07E+08	4637	-0.17752	6.108814	0.243598	0.352121	0.026927	0	1140	812	1486	1145	1284	1039	1579	1028	1423	892
ENSMUSG00000089782	chr1	Gm3531	97948901	97949389	489	0.267954	2.74547	0.243615	0.352121	0.050249	0	84	102	125	76	81	119	177	102	177	92
ENSMUSG00000018882	chr11	Mrpl45	97315716	97315939	2596	-0.20685	5.937849	0.243713	0.352225	0.036638	0	823	592	1128	1280	1515	847	1374	850	1389	814
ENSMUSG00000035513	chr2	Ntng2	29194541	29195053	3990	0.240386	3.124735	0.243962	0.352546	0.045226	0	85	58	169	151	195	105	205	169	229	156
ENSMUSG00000020937	chr11	Plcd3	1.03E+08	1.03E+08	3393	0.24507	2.45257	0.244009	0.352576	0.040948	0	80	57	122	62	76	87	102	90	136	112
ENSMUSG00000044172	chr17	Ptx4	25120760	25120991	1582	-0.60828	-0.08451	0.244072	0.352629	0.236227	0	2	4	13	28	37	5	23	9	12	12
ENSMUSG00000038296	chr7	Galnt18	1.11E+08	1.11E+08	2575	0.273272	2.084946	0.244164	0.352723	0.049993	0	40	33	71	80	81	70	118	87	83	57
ENSMUSG00000031938	chr9	4931406C07Rik	15283337	15284991	2981	0.304746	3.632621	0.244636	0.353366	0.076278	0	192	115	231	148	199	159	225	463	212	165
ENSMUSG00000000876	chr2	Pxmp4	1.55E+08	1.55E+08	3114	0.181095	4.13281	0.244745	0.353486	0.025327	0	240	184	362	254	279	262	374	400	349	295
ENSMUSG00000042660	chr18	Wdr55	36760239	36760480	1498	-0.19818	3.883206	0.244872	0.35363	0.0315	0	226	226	292	219	271	219	346	191	322	186
ENSMUSG00000036873	chr3	2410004B18Rik	1.46E+08	1.46E+08	2029	-0.1923	4.043524	0.244927	0.353671	0.029782	0	269	256	325	228	294	220	318	256	373	239
ENSMUSG00000025068	chr19	Gsto1	47854970	47855122	1968	0.19041	4.762503	0.245058	0.353821	0.029495	0	332	261	495	528	414	438	653	477	703	393
ENSMUSG00000074088	chr4	Snrnp40	1.3E+08	1.3E+08	3987	0.176262	3.787852	0.245132	0.353851	0.022581	0	180	159	285	193	218	233	296	247	314	232
ENSMUSG00000100725	chr1	Gm28062	1.78E+08	1.78E+08	3030	0.168043	6.602946	0.24512	0.353851	0.024297	0	1220	1164	1999	1376	1590	1453	2373	1788	2209	1620
ENSMUSG00000022992	chr15	Kansl2	98518821	98519547	2417	-0.17048	5.588762	0.245233	0.353959	0.02477	0	739	637	1041	779	863	666	1116	733	1093	595
ENSMUSG00000039183	chr17	Nubp2	24882611	24883314	1430	0.197507	3.262862	0.245447	0.354229	0.02619	0	140	109	177	132	146	145	228	168	223	165
ENSMUSG00000040181	chr1	Fmo1	1.63E+08	1.63E+08	6304	0.270433	4.175576	0.245496	0.354234	0.061154	0	207	177	307	296	326	260	347	619	301	240
ENSMUSG00000064369	chrMT	mt-Te	14071	14139	69	-0.94269	2.938767	0.245504	0.354234	0.736616	0	8	3	335	354	193	7	19	142	221	95
ENSMUSG00000031575	chr8	Ash2l	25816191	25817508	5236	0.187794	4.672247	0.245561	0.354277	0.028638	0	321	239	468	444	448	433	579	415	724	353
ENSMUSG00000049878	chr4	Rlf	1.21E+08	1.21E+08	6990	-0.18096	3.816518	0.245631	0.35434	0.024455	0	204	170	388	212	242	204	292	211	318	184
ENSMUSG00000025978	chr1	Rftn2	55170159	55172082	5871	0.28455	1.632798	0.245914	0.354608	0.050428	0	29	29	61	40	62	64	63	56	83	34
ENSMUSG00000031431	chrX	Tsc22d3	1.41E+08	1.41E+08	4341	0.275759	8.12224	0.245887	0.354608	0.067192	0	3625	4335	4618	2944	3917	6905	7395	4600	4779	3667
ENSMUSG00000036613	chr12	Tssc1	28751828	28752004	1692	-0.20531	2.969575	0.245924	0.354608	0.030896	0	119	115	167	129	126	104	160	128	171	99
ENSMUSG00000042787	chr9	Exog	1.19E+08	1.19E+08	3887	0.271746	1.732076	0.245871	0.354608	0.047357	0	47	29	67	41	52	59	64	70	54	66
ENSMUSG00000020812	chr11	1810032O08Rik	1.17E+08	1.17E+08	2776	0.325483	0.570863	0.246021	0.35471	0.043257	0	17	18	25	18	19	25	37	22	30	25
ENSMUSG00000035722	chr10	Abca7	79996494	79996588	6752	-0.21776	4.018131	0.246275	0.355038	0.037439	0	206	123	436	329	360	182	319	257	387	237
ENSMUSG00000099875	chr1	Gm15453	1.5E+08	1.5E+08	465	0.367658	0.428139	0.246501	0.355324	0.059611	0	15	16	23	12	20	26	32	19	38	13
ENSMUSG00000070738	chr1	Dgkd	87853287	87853456	6850	-0.17152	5.466504	0.24654	0.355342	0.024758	0	623	447	1064	824	874	502	978	733	943	686
ENSMUSG00000022781	chr16	Pak2	32016290	32020266	6795	0.164622	4.839176	0.246681	0.355507	0.022028	0	364	288	608	438	491	420	630	616	640	452
ENSMUSG00000020611	chr11	Gna13	1.09E+08	1.09E+08	6421	0.165043	4.797394	0.247081	0.356011	0.022193	0	344	253	604	445	498	394	675	491	703	449
ENSMUSG00000074682	chr2	Zcchc3	1.52E+08	1.52E+08	3073	0.374278	0.170204	0.247084	0.356011	0.055204	0	8	9	26	18	11	19	23	19	26	17
ENSMUSG00000062257	chr9	Opcml	27790775	27790900	13120	-0.31101	1.198966	0.247114	0.356014	0.048358	0	28	22	72	36	44	25	40	37	35	40
ENSMUSG00000063146	chr5	Clip2	1.34E+08	1.34E+08	4995	0.260235	2.272113	0.247174	0.356063	0.04872	0	55	37	94	55	115	59	117	85	107	103
ENSMUSG00000022362	chr15	9130401M01Rik	58028243	58029044	1732	-0.17544	4.02857	0.24734	0.356263	0.024523	0	255	223	325	266	295	213	381	272	325	216
ENSMUSG00000069808	chr11	Fam57a	76179671	76179986	6615	0.289548	0.904091	0.247606	0.356608	0.04353	0	25	12	42	22	29	26	37	35	47	32
ENSMUSG00000031556	chr8	Tm2d2	25017211	25017592	1280	0.168717	5.485246	0.247911	0.356933	0.02385	0	682	489	857	587	752	713	1067	781	1111	687
ENSMUSG00000035378	chr6	Shq1	1.01E+08	1.01E+08	2182	0.353122	0.895255	0.247913	0.356933	0.071077	0	23	18	25	19	38	24	40	48	26	38
ENSMUSG00000049641	chr10	Vgll2	52022502	52022803	1650	0.515368	5.25269	0.247875	0.356933	0.233423	0	126	109	472	1074	869	263	1125	563	1263	1015
ENSMUSG00000024150	chr17	Mcfd2	87254658	87256057	2612	0.166155	5.323552	0.247982	0.356993	0.023112	0	569	400	743	629	684	613	864	796	894	682
ENSMUSG00000034157	chr12	Cipc	86947043	86947250	4863	-0.1675	5.660605	0.24809	0.35711	0.023825	0	708	502	1197	940	1037	660	993	853	1158	720
ENSMUSG00000038583	chr10	Pln	53337686	53337795	2480	-0.36637	0.840243	0.248376	0.357484	0.087786	0	17	19	42	39	38	9	41	18	49	23
ENSMUSG00000039983	chr2	Ccdc32	1.19E+08	1.19E+08	2214	0.241241	2.639674	0.248741	0.357932	0.038794	0	88	78	113	77	88	115	156	112	148	78
ENSMUSG00000053965	chr3	Pde5a	1.23E+08	1.23E+08	6728	0.271128	1.633506	0.248726	0.357932	0.048623	0	31	20	58	41	75	46	66	59	79	50
ENSMUSG00000040414	chr19	Slc25a28	43663822	43664643	1514	-0.18951	4.508063	0.248853	0.358054	0.029703	0	349	267	505	409	413	347	389	347	604	267
ENSMUSG00000055725	chr5	Paqr3	97082329	97082608	7566	-0.30594	0.85114	0.249259	0.358599	0.04255	0	24	17	39	33	40	24	29	30	37	19
ENSMUSG00000032715	chr2	Trib3	1.52E+08	1.52E+08	2125	0.391337	0.644792	0.249289	0.358604	0.086161	0	17	16	19	28	19	35	26	40	23	22
ENSMUSG00000023110	chr14	Prmt5	54507187	54507947	3958	-0.16003	5.410665	0.249364	0.358673	0.021799	0	643	510	950	742	758	567	881	726	952	574

ENSMUSG00000091537	chr9	Tma7	1.09E+08	1.09E+08	1359	-0.23864	6.166483	0.250137	0.359744	0.050901	0	1304	1290	1511	848	1027	991	1667	972	1530	946
ENSMUSG00000029440	chr5	Psmd9	1.23E+08	1.23E+08	4562	0.174119	4.692303	0.250185	0.359775	0.024216	0	351	319	438	388	414	394	604	472	610	425
ENSMUSG00000021243	chr12	Fcf1	84970897	84970965	1117	0.209216	3.688987	0.250268	0.359855	0.033398	0	162	169	234	166	210	238	359	231	251	176
ENSMUSG00000004996	chr8	Mri1	84249906	84251711	3273	0.189315	4.048609	0.250326	0.3599	0.027508	0	226	193	275	265	255	224	351	304	414	312
ENSMUSG00000032867	chr5	Fbxw8	1.18E+08	1.18E+08	4978	0.164223	5.323931	0.250423	0.36	0.022926	0	480	383	805	665	741	558	894	781	986	668
ENSMUSG00000000568	chr5	Hnrnpd	99958426	99961333	4863	-0.17122	5.289436	0.250504	0.360078	0.0251	0	512	545	959	539	795	496	852	563	869	611
ENSMUSG00000066637	chr12	Ttc32	9029997	9030196	1000	-0.21613	3.780494	0.250599	0.360175	0.039239	0	244	228	259	185	220	181	290	205	320	175
ENSMUSG00000025421	chr18	Hdhd2	76930126	76930216	4822	-0.16414	5.73164	0.25067	0.360238	0.02325	0	801	620	1170	910	1021	826	1181	789	1034	746
ENSMUSG00000028221	chr4	Tmem55a	14864076	14864437	2339	-0.16904	4.881625	0.250709	0.360255	0.023669	0	418	341	655	491	619	363	550	460	644	513
ENSMUSG00000024011	chr17	Pi16	29318877	29319391	3987	0.348739	5.456285	0.25078	0.360279	0.108257	0	605	561	1086	406	433	999	737	1473	596	491
ENSMUSG00000091561	chr18	Gm6665	31819862	31819921	258	0.451316	0.523798	0.250761	0.360279	0.129043	0	16	18	36	8	13	14	24	33	22	43
ENSMUSG00000025102	chr7	3110040N11Rik	81782182	81782581	1231	0.220615	3.592232	0.250814	0.360289	0.036562	0	163	152	167	203	173	204	307	209	285	178
ENSMUSG00000091509	chr14	Gm17066	1.05E+08	1.05E+08	1113	0.280471	2.215709	0.251201	0.360806	0.054267	0	65	52	97	50	65	47	86	111	137	79
ENSMUSG00000002797	chr6	Ggct	54982580	54986001	4437	-0.21731	3.020914	0.251314	0.360895	0.035034	0	133	80	151	153	177	104	192	139	151	99
ENSMUSG00000085723	chr10	Gm15915	93674218	93674589	908	0.657912	-0.22209	0.251318	0.360895	0.259736	0	4	2	2	24	13	16	26	11	27	5
ENSMUSG00000019822	chr10	Smpd2	41485642	41486609	4468	0.179667	3.33424	0.251407	0.360984	0.023035	0	125	104	214	140	179	144	229	176	255	172
ENSMUSG00000048100	chr3	Taf13	1.09E+08	1.09E+08	3155	0.216447	4.631583	0.251463	0.361025	0.03887	0	367	362	434	259	354	416	566	454	657	352
ENSMUSG00000024826	chr19	Dpf2	5896516	5898631	6501	0.175016	5.701125	0.251566	0.361135	0.02697	0	691	407	1173	839	925	848	1094	957	1299	840
ENSMUSG00000021115	chr12	Vrk1	1.06E+08	1.06E+08	3796	0.242743	2.343008	0.251685	0.361141	0.04132	0	70	38	87	84	89	95	123	85	98	86
ENSMUSG00000021764	chr13	Ndufs4	1.14E+08	1.14E+08	1534	-0.2118	7.460627	0.251672	0.361141	0.040586	0	2717	2178	2815	3659	3506	2532	4284	2223	3801	2321
ENSMUSG00000022550	chr15	Adck5	76576358	76576494	3452	0.254663	2.040636	0.25169	0.361141	0.039354	0	58	36	69	70	59	68	92	70	112	59
ENSMUSG00000025403	chr10	Shmt2	1.28E+08	1.28E+08	2305	0.190447	4.912692	0.251707	0.361141	0.031034	0	347	262	520	533	623	424	617	552	825	528
ENSMUSG00000039953	chr4	Clstn1	1.5E+08	1.5E+08	4662	-0.22708	5.087898	0.251683	0.361141	0.044532	0	338	295	805	767	854	400	619	617	663	550
ENSMUSG00000086228	chr9	Ubap1l	65361060	65361087	1381	0.542276	-0.22528	0.252192	0.361798	0.18256	0	7	0	14	20	9	16	22	11	9	20
ENSMUSG00000050332	chrX	Amer1	95420318	95428598	8496	-0.26582	2.680549	0.252369	0.361973	0.050534	0	65	64	227	86	147	81	149	91	125	84
ENSMUSG00000063362	chr8	Alg11	22060721	22060770	4960	-0.18983	3.141032	0.25236	0.361973	0.02501	0	118	112	234	134	160	121	185	148	165	126
ENSMUSG00000023079	chr5	Gtf2ird1	1.34E+08	1.34E+08	4834	-0.21788	2.900209	0.252403	0.361983	0.032112	0	90	70	192	128	179	96	161	115	145	109
ENSMUSG00000089872	chr1	Rps6kc1	1.91E+08	1.91E+08	9741	0.190228	4.947022	0.252448	0.362009	0.031191	0	403	338	781	348	488	533	550	597	803	494
ENSMUSG00000038900	chr2	Rpl12	32961559	32961839	3598	0.222673	7.274119	0.252603	0.362192	0.044757	0	2252	2292	2499	1798	2161	2843	4100	2673	3134	2444
ENSMUSG00000016520	chr5	Lnx2	1.47E+08	1.47E+08	4557	0.269198	2.127168	0.252755	0.36237	0.053034	0	49	25	75	71	99	68	114	84	109	56
ENSMUSG00000052658	chr9	5830454E08Rik	1.21E+08	1.21E+08	727	-0.32405	0.634188	0.252791	0.362383	0.060473	0	16	25	27	27	33	13	40	22	28	17
ENSMUSG00000032652	chr6	Crebl2	1.35E+08	1.35E+08	3923	-0.18099	4.065742	0.253602	0.363506	0.025712	0	211	176	461	300	316	195	347	259	354	281
ENSMUSG00000087138	chr7	Gm15545	44986900	44987370	1976	0.360227	0.453337	0.253868	0.363848	0.061353	0	12	7	25	24	22	20	34	17	41	19
ENSMUSG00000016554	chr15	Eif3d	77958998	77959122	1910	0.158033	5.867432	0.254347	0.364455	0.021882	0	768	614	1136	900	1027	914	1357	1059	1346	957
ENSMUSG00000087687	chr8	Pet100	3621551	3621611	1189	0.213913	4.08586	0.254342	0.364455	0.036408	0	248	238	248	231	241	280	439	270	419	264
ENSMUSG00000028861	chr4	Mrps15	1.26E+08	1.26E+08	1693	0.185521	5.679904	0.25453	0.364679	0.030063	0	749	660	831	709	794	888	1199	816	1238	842
ENSMUSG00000042178	chr7	Armc5	1.28E+08	1.28E+08	3834	0.195606	3.786554	0.254739	0.364938	0.030769	0	173	160	341	143	228	199	277	282	329	246
ENSMUSG00000021286	chr12	Zfyve21	1.12E+08	1.12E+08	1310	0.186257	3.479325	0.254916	0.365154	0.026592	0	131	112	255	180	165	179	277	214	222	181
ENSMUSG00000015341	chr8	Golga7	23241353	23242631	2383	0.174642	5.003314	0.255018	0.365219	0.025731	0	437	360	551	529	506	456	670	606	817	561
ENSMUSG00000102101	chr16	2310061J03Rik	55973268	55974617	1350	0.327751	1.470624	0.254992	0.365219	0.066018	0	50	27	33	32	42	36	64	52	90	35
ENSMUSG00000025488	chr7	Cox8b	1.41E+08	1.41E+08	362	-0.20208	8.356125	0.255385	0.365707	0.037669	0	5099	4475	5972	6552	5348	4687	7582	4252	7520	4288
ENSMUSG00000031939	chr9	Taf1d	15306214	15306283	1361	0.25015	2.364479	0.255463	0.365766	0.042223	0	77	48	95	69	81	75	162	100	110	63
ENSMUSG00000039345	chr16	Mettl22	8470788	8470865	2665	-0.17719	6.507005	0.255482	0.365766	0.028529	0	1361	1289	1900	1506	1580	1337	2097	1291	1888	1250
ENSMUSG00000044991	chr2	1110034G24Rik	1.33E+08	1.33E+08	2117	0.252175	2.268166	0.255554	0.36583	0.040771	0	63	63	76	69	66	80	106	73	129	81
ENSMUSG00000028889	chr4	Yrdc	1.25E+08	1.25E+08	1981	0.22634	3.142966	0.25576	0.366086	0.038746	0	133	78	136	157	135	149	228	131	190	161
ENSMUSG00000004393	chr11	Ddx56	6258919	6259258	2533	0.21752	3.848128	0.255846	0.366169	0.038308	0	153	147	227	280	251	176	405	225	389	246
ENSMUSG00000024940	chr19	Ltbp3	5740904	5740985	5190	-0.18551	5.917298	0.256101	0.366447	0.03075	0	837	786	1591	803	1234	785	992	1070	1224	1038
ENSMUSG00000028211	chr4	Trp53inp1	11156431	11156547	6475	-0.19493	3.498058	0.256096	0.366447	0.028638	0	159	147	265	146	254	145	216	192	205	190
ENSMUSG00000050373	chr2	Snx21	1.65E+08	1.65E+08	4760	0.182246	4.746753	0.256123	0.366447	0.028403	0	395	248	504	424	448	460	501	465	739	432
ENSMUSG00000030400	chr7	Ercc2	19382010	19382059	4170	-0.17365	4.158305	0.256449	0.366874	0.02384	0	250	202	485	265	348	246	309	326	387	255
ENSMUSG00000030766	chr7	Arhgap17	1.23E+08	1.23E+08	3583	0.178618	4.252907	0.256614	0.36703	0.026642	0	249	194	481	214	331	278	396	361	500	316
ENSMUSG00000091957	chr18	Rps2-ps10	61259008	61259972	965	-0.31792	2.014992	0.256595	0.36703	0.082554	0	81	81	60	58	49	58	80	57	86	44
ENSMUSG00000026134	chr1	Prim2	33453810	33454304	5938	0.357774	0.259608	0.25666	0.367057	0.069314	0	13	9	31	15	10	17	22	31	22	18
ENSMUSG00000028423	chr4	Nfx1	40970906	40971059	8564	-0.15852	5.202	0.256805	0.367184	0.021765	0	543	473	918	537	665	494	778	612	770	535
ENSMUSG00000028703	chr4	Lrrc41	1.16E+08	1.16E+08	3713	0.179059	4.246562	0.256797	0.367184	0.026922	0	240	163	443	306	307	261	388	410	472	309
ENSMUSG00000024962	chr19	Vegfb	6982473	6982867	1605	-0.27637	6.437749	0.256972	0.367384	0.070226	0	939	664	1465	2528	2177	969	1747	1295	2075	1215
ENSMUSG00000035799	chr12	Twist1	33957671	33958638	1616	-0.37446	1.212535	0.257011	0.3674	0.097543	0	20	35	80	22	52	25	35	56	33	25
ENSMUSG00000029993	chr6	Nfu1	87009236	87009389	2078	0.187665	5.365341	0.257124	0.367513	0.030661	0	536	556	656	607	650	705	1009	660	1044	618
ENSMUSG00000035356	chr16	Nfkbiz	55811375	55812783	5018	0.346006	0.940439	0.257146	0.367513	0.070444	0	25	22	31	14	35	23	67	38	34	26
ENSMUSG00000051314	chr7	Ffar2	30818348	30820287	2790	0.7631	0.593246	0.257477	0.367946	0.462215	0	38	20	7	4	5	45	12	68	17	12
ENSMUSG00000035211	chr7	Xrra1	99859218	99859230	2631	-0.67116	0.177527	0.257667	0.368179	0.328334	0	31	23	38	0	8	19	10	10	22	11
ENSMUSG00000037526	chr14	Atg14	47540894	47543143	3450	-0.1822	3.316668	0.257834	0.368378	0.023926	0	132	126	246	153	196	138	184	163	215	145
ENSMUSG00000089911	chr3	Hiat1	1.17E+08	1.17E+08	4087	-0.17747	3.804759	0.257918	0.368459	0.024709	0	197	171	346	211	274	158	255	250	300	230
ENSMUSG00000096232	chr16	0610012G03Rik	31948024	31948353	417	0.191603	5.028925	0.257961	0.368481	0.032075	0	438	312	487	596	588	537	742	519	882	519
ENSMUSG00000040220	chr8	Gas8	1.24E+08	1.24E+08	1679	0.25945	1.813651	0.25802	0.368485	0.041749	0	39	44	74	31	63	55	75	68	81	59

ENSMUSG00000073555	chr18	Gm4951	60212080	60212169	2645	0.469428	0.031608	0.258004	0.368485	0.109696	0	14	13	17	5	11	14	35	25	12	11
ENSMUSG00000048897	chr7	Zfp710	80024814	80024986	4803	-0.21743	4.371198	0.258342	0.368905	0.041113	0	281	173	397	471	489	218	489	343	437	290
ENSMUSG00000009828	chr9	Ick	78109192	78109481	11524	0.215601	2.739379	0.258831	0.369563	0.035008	0	80	60	142	96	120	102	122	156	140	117
ENSMUSG00000029670	chr6	Ing3	21949571	21949793	4806	0.218736	2.492612	0.258941	0.369665	0.032299	0	64	65	104	79	98	76	116	122	131	97
ENSMUSG00000032548	chr9	Slco2a1	1.03E+08	1.03E+08	13545	0.253171	2.229328	0.258958	0.369665	0.04457	0	41	48	94	68	91	54	147	88	103	73
ENSMUSG00000020156	chr10	Mum1	80226434	80226704	10361	0.157919	4.142078	0.259077	0.369795	0.019706	0	231	186	359	257	310	262	416	329	389	299
ENSMUSG00000059291	chr4	Rpl11	1.36E+08	1.36E+08	2697	0.20624	6.932697	0.259302	0.370076	0.039273	0	1723	1775	1950	1571	1736	2205	3077	2102	2678	1890
ENSMUSG00000027752	chr3	Exosc8	54728678	54728893	3968	0.204188	2.986607	0.259441	0.370235	0.029811	0	119	81	156	109	118	125	204	124	178	137
ENSMUSG00000024165	chr17	Hn1l	24942156	24944678	2933	0.209081	2.767413	0.259541	0.370258	0.032528	0	88	63	145	106	103	119	128	127	148	125
ENSMUSG00000027634	chr2	Ndrg3	1.57E+08	1.57E+08	8388	-0.16192	5.32302	0.259504	0.370258	0.022952	0	495	459	980	745	770	594	839	649	823	549
ENSMUSG00000074576	chr2	Mocs3	1.68E+08	1.68E+08	1973	0.26482	1.622419	0.259514	0.370258	0.043324	0	37	32	51	44	52	49	60	43	73	68
ENSMUSG00000019710	chr3	Mrpl24	87919506	87919705	2255	0.177694	5.47104	0.259961	0.370818	0.0278	0	558	610	749	641	699	700	1043	782	1092	704
ENSMUSG00000030691	chr7	Fchsd2	1.01E+08	1.01E+08	9199	-0.19422	2.799182	0.260017	0.370858	0.026334	0	100	81	160	107	147	83	142	111	144	108
ENSMUSG00000061859	chr4	Inadl	98395785	98395837	13086	0.291228	1.11884	0.260599	0.371648	0.047093	0	24	15	35	39	37	32	49	31	61	36
ENSMUSG00000104348	chr1	RP23-59N15.4	1.93E+08	1.93E+08	2573	0.365265	2.224609	0.260662	0.371698	0.116197	0	28	20	98	105	87	55	113	79	86	129
ENSMUSG00000028076	chr3	Cd1d1	86995834	86996601	2570	0.68643	2.38197	0.261026	0.372177	0.411619	0	106	87	44	20	19	66	63	323	36	65
ENSMUSG00000040725	chr7	Hnrnpul1	25721498	25722363	3589	-0.16428	5.997854	0.261082	0.372216	0.024596	0	817	750	1598	1076	1286	807	1324	1002	1488	947
ENSMUSG00000020774	chr11	Aspa	73304992	73305633	5954	0.231723	3.457743	0.261186	0.372325	0.043257	0	128	103	146	231	186	178	285	195	263	163
ENSMUSG00000028636	chr4	Ppcs	1.19E+08	1.19E+08	1605	0.227239	2.606067	0.261474	0.372695	0.037506	0	78	50	99	104	114	110	146	101	150	85
ENSMUSG00000027671	chr3	Actl6a	32706298	32706428	3886	-0.1712	3.838632	0.26169	0.372909	0.023548	0	214	187	367	210	239	201	297	237	295	196
ENSMUSG00000039361	chr7	Picalm	90130232	90130702	4174	-0.16869	6.41771	0.261709	0.372909	0.026357	0	1355	920	2037	1344	1714	1010	2069	1455	1715	1216
ENSMUSG00000068220	chr15	Lgals1	78926725	78926804	800	0.283681	8.515578	0.261667	0.372909	0.076049	0	6682	5355	5689	3205	4075	8217	7233	6351	8917	5423
ENSMUSG00000040624	chr10	Plekhg1	3740364	3740540	8739	0.264959	1.781385	0.261769	0.372955	0.048044	0	29	33	68	42	77	56	91	71	61	52
ENSMUSG00000001786	chr10	Fbxo7	86021972	86022144	6180	0.206028	3.59434	0.261818	0.372985	0.034168	0	148	162	236	157	180	235	251	248	242	178
ENSMUSG00000021013	chr12	Ttc8	98920574	98920783	2749	-0.29531	1.843189	0.261979	0.373174	0.060617	0	58	38	120	51	51	39	46	67	76	56
ENSMUSG00000033216	chr6	Eefsec	88257334	88258391	2679	0.203521	2.536496	0.262604	0.374025	0.029506	0	75	52	116	88	99	99	127	111	125	92
ENSMUSG00000026114	chr1	Cnga3	37214434	37214522	3957	-0.39432	-0.00693	0.262653	0.374054	0.076641	0	12	9	14	23	23	13	23	8	18	9
ENSMUSG00000022105	chr14	Rb1	73183673	73184055	6015	-0.17901	4.072599	0.262858	0.374307	0.026441	0	229	178	393	287	369	176	336	304	340	285
ENSMUSG00000017176	chr11	Nt5c3b	1E+08	1E+08	3420	0.220511	2.864944	0.263297	0.374891	0.035902	0	70	79	125	127	133	109	194	130	186	99
ENSMUSG00000024436	chr17	Mrps18b	35910379	35910956	2089	-0.17522	4.408254	0.263504	0.375105	0.026433	0	298	219	437	411	455	261	445	302	499	331
ENSMUSG00000074221	chr7	Zfp568	29983955	29984228	7183	0.186473	3.874045	0.263489	0.375105	0.030227	0	153	125	399	203	267	217	307	266	387	248
ENSMUSG00000026339	chr1	Ccdc93	1.21E+08	1.21E+08	11445	-0.19814	3.733057	0.263538	0.375113	0.031221	0	168	119	361	233	298	186	295	237	220	184
ENSMUSG00000021917	chr14	Spcs1	30999826	31000222	1546	0.20975	6.309354	0.263764	0.375395	0.040968	0	1204	1152	1295	909	1109	1339	1993	1390	1928	1178
ENSMUSG00000034449	chr11	Dhrs11	84820856	84821301	1603	-0.25671	4.435595	0.263847	0.375473	0.059799	0	283	148	410	561	529	281	452	266	551	283
ENSMUSG00000032679	chr2	Cd59a	1.04E+08	1.04E+08	1811	0.18965	5.517171	0.264009	0.375662	0.032812	0	572	449	675	855	855	638	1178	821	1214	690
ENSMUSG00000049680	chr11	Urgcp	5713417	5718263	5871	-0.16531	5.480166	0.264197	0.37589	0.024637	0	605	427	1058	842	947	577	919	741	974	657
ENSMUSG00000002968	chr7	Med25	44879391	44879514	2297	-0.17653	5.773362	0.264283	0.375971	0.028667	0	853	567	1398	889	1045	737	876	895	1399	801
ENSMUSG00000071757	chr15	Zhx2	57694665	57695004	4434	0.158119	5.039298	0.26432	0.375983	0.022059	0	452	354	675	464	556	514	661	611	776	583
ENSMUSG00000045438	chr5	Cox19	1.39E+08	1.39E+08	3539	0.171466	4.624794	0.264501	0.37616	0.025162	0	300	274	424	435	410	397	604	403	600	392
ENSMUSG00000090626	chr9	Tex9	72450394	72451875	8798	-0.32134	0.989973	0.264486	0.37616	0.071031	0	30	33	37	34	30	34	42	22	43	14
ENSMUSG00000052748	chr1	Swt1	1.51E+08	1.51E+08	12865	-0.24123	2.1641	0.264571	0.37622	0.039456	0	68	50	103	84	78	72	97	62	66	66
ENSMUSG00000001844	chr5	Zdhhc4	1.43E+08	1.43E+08	2864	0.173364	4.562538	0.264816	0.376418	0.025656	0	327	261	483	356	347	376	516	428	667	322
ENSMUSG00000021681	chr13	Aggf1	95350683	95351702	3697	-0.15503	4.734658	0.264779	0.376418	0.020934	0	370	324	593	440	534	331	611	426	544	405
ENSMUSG00000025083	chr19	Afap1l2	56912361	56913408	5591	0.265944	1.579705	0.264852	0.376418	0.042863	0	29	31	60	45	47	31	89	54	70	49
ENSMUSG00000028958	chr5	Tmub1	24445458	24446273	1879	0.172388	4.137695	0.264833	0.376418	0.02436	0	278	182	339	240	278	279	385	315	450	274
ENSMUSG00000031399	chrX	Fam3a	74384719	74385435	2485	0.159388	4.19322	0.264743	0.376418	0.021127	0	249	182	398	268	300	279	377	353	428	313
ENSMUSG00000027580	chr2	Helz2	1.81E+08	1.81E+08	11529	0.250795	2.666334	0.265266	0.376966	0.053729	0	66	36	158	89	135	95	169	140	114	101
ENSMUSG00000024081	chr17	Cebpz	78919006	78920017	4074	-0.17174	4.728167	0.265418	0.377142	0.026113	0	350	387	678	401	436	382	544	441	500	395
ENSMUSG00000054690	chr3	Emcn	1.37E+08	1.37E+08	5409	0.216309	3.449209	0.265511	0.377233	0.038025	0	127	108	164	195	207	157	332	213	216	159
ENSMUSG00000020869	chr11	Lrrc59	94629767	94630109	3073	-0.1566	5.144314	0.265866	0.377697	0.021704	0	521	356	885	600	693	476	754	601	724	510
ENSMUSG00000043687	chr8	1190005I06Rik	1.21E+08	1.21E+08	1083	0.601883	0.0448	0.265966	0.377798	0.248788	0	21	4	2	11	19	23	10	32	14	18
ENSMUSG00000037493	chr9	Cib2	54544794	54545484	1433	-0.27245	7.537663	0.26622	0.378118	0.071465	0	4059	3231	4180	1624	2554	2911	3760	2838	3520	2321
ENSMUSG00000024302	chr18	Dtna	23415415	23415625	6587	-0.19513	6.481603	0.266271	0.378151	0.036119	0	1164	838	2359	1710	1857	999	2215	1135	1947	1470
ENSMUSG00000005374	chr5	Tbl2	1.35E+08	1.35E+08	5968	0.182954	3.502983	0.266735	0.378752	0.026673	0	166	108	245	150	186	178	248	247	249	168
ENSMUSG00000040543	chr11	Pitpnm3	72047528	72051360	9815	-0.32437	1.823462	0.266751	0.378752	0.076368	0	35	29	93	62	103	32	77	48	49	71
ENSMUSG00000010492	chr2	Uckl1os	1.82E+08	1.82E+08	2522	-0.1894	5.861935	0.266937	0.378895	0.033875	0	842	607	1132	1169	1248	720	1464	713	1324	855
ENSMUSG00000025147	chr7	Mob2	1.42E+08	1.42E+08	1456	0.169106	5.954588	0.26692	0.378895	0.026519	0	843	755	1107	879	1041	1057	1406	1113	1499	930
ENSMUSG00000034152	chr13	Exoc3	74169805	74172244	4596	-0.16405	5.610616	0.266915	0.378895	0.024632	0	655	479	1162	922	1023	656	1047	746	992	777
ENSMUSG00000070304	chr9	Scn2b	45117876	45118093	4562	-0.39652	0.379801	0.266983	0.378918	0.090764	0	9	11	36	19	39	12	35	18	21	10
ENSMUSG00000020257	chr9	Wdr82	1.06E+08	1.06E+08	6338	0.166256	4.943552	0.267035	0.378952	0.025309	0	355	269	675	479	614	459	691	649	644	514
ENSMUSG00000029505	chr5	Ep400	1.11E+08	1.11E+08	13971	-0.20323	4.292165	0.267339	0.379342	0.035802	0	229	170	648	321	412	237	364	344	438	285
ENSMUSG00000051768	chr7	Xrcc1	24547150	24547359	2155	0.174658	4.138872	0.267541	0.379589	0.025543	0	255	188	344	275	253	280	344	339	447	285
ENSMUSG00000028475	chr4	5430416O09Rik	43730034	43730164	4086	-0.33409	0.57047	0.267679	0.379744	0.067229	0	19	21	19	25	38	18	30	25	29	11
ENSMUSG00000039670	chr11	Oxld1	1.2E+08	1.2E+08	813	-0.24219	3.104258	0.26781	0.379889	0.051044	0	109	100	130	211	181	104	206	105	193	119
ENSMUSG00000041945	chr1	Mfsd9	40772038	40774546	5125	0.390232	0.074572	0.267859	0.379918	0.054587	0	17	8	17	10	13	14	23	15	29	17

ENSMUSG00000079037	chr2	Prnp	1.32E+08	1.32E+08	2343	0.175957	7.074119	0.267971	0.380037	0.029719	0	1815	1615	2905	1736	2094	2024	2619	2646	3129	2539
ENSMUSG00000032624	chr17	Eml4	83350931	83351239	5445	0.237643	1.957932	0.268165	0.38027	0.040942	0	43	32	93	44	76	56	95	77	73	71
ENSMUSG00000028850	chr4	Gpatch3	1.34E+08	1.34E+08	2086	0.262779	1.862768	0.268239	0.380334	0.045539	0	62	31	59	45	59	46	92	62	81	72
ENSMUSG00000004018	chr11	Fancl	26386135	26387310	3372	0.286565	1.93404	0.268455	0.380584	0.056609	0	71	43	69	35	45	53	90	74	98	61
ENSMUSG00000059734	chr19	Ndufs8	3908870	3909074	963	-0.219	6.960852	0.268478	0.380584	0.046384	0	1571	1197	2150	3031	2888	1543	3052	1688	2694	1757
ENSMUSG00000063698	chr19	Sfxn4	60837277	60839050	2975	0.26528	1.205011	0.268501	0.380584	0.037972	0	23	25	39	35	38	31	53	48	45	41
ENSMUSG00000026199	chr1	Ankzf1	75192151	75194284	5142	0.20995	2.640383	0.268533	0.380589	0.033321	0	69	67	146	74	110	111	121	119	135	107
ENSMUSG00000028842	chr4	Ago3	1.26E+08	1.26E+08	16571	-0.2231	3.235993	0.268629	0.380685	0.038926	0	110	92	312	126	213	136	186	150	174	137
ENSMUSG00000030730	chr7	Atp2a1	1.26E+08	1.26E+08	3483	0.182353	15.09818	0.268868	0.380983	0.032595	0	425683	322606	844652	509400	623751	472705	673189	655059	940903	675590
ENSMUSG00000001333	chr4	Sync	1.29E+08	1.29E+08	2862	-0.18592	4.881121	0.26896	0.381041	0.031301	0	430	273	745	495	647	364	615	364	656	530
ENSMUSG00000006705	chr17	Pknox1	31564749	31564888	6892	-0.18635	3.361823	0.268967	0.381041	0.026562	0	155	100	265	156	218	151	216	145	215	147
ENSMUSG00000031379	chrX	Pir	1.64E+08	1.64E+08	5553	0.248106	2.452395	0.269013	0.381066	0.043484	0	64	80	103	71	68	82	126	113	141	75
ENSMUSG00000003198	chr17	Zfp959	55892120	55892186	2028	-0.26201	1.295992	0.269157	0.381229	0.042745	0	38	28	60	45	36	28	59	41	44	26
ENSMUSG00000030123	chr6	Plxnd1	1.16E+08	1.16E+08	7192	-0.17299	5.471839	0.269641	0.381834	0.027709	0	644	432	1245	731	847	621	781	698	1103	627
ENSMUSG00000037601	chr11	Nme1	93956979	93959513	3342	0.204676	5.255872	0.269627	0.381834	0.039186	0	423	394	513	759	723	676	916	649	950	559
ENSMUSG00000026357	chr1	Rgs18	1.45E+08	1.45E+08	2031	0.43986	0.070307	0.269727	0.381915	0.081875	0	14	14	15	9	10	10	29	27	23	11
ENSMUSG00000014786	chr8	Slc9a5	1.05E+08	1.05E+08	5222	0.279607	1.007273	0.269913	0.382096	0.04135	0	23	20	42	25	29	21	44	39	48	39
ENSMUSG00000032905	chr18	Atg12	46732417	46734509	2492	-0.16082	5.068712	0.269912	0.382096	0.023709	0	559	424	763	483	603	493	737	556	656	454
ENSMUSG00000021876	chr14	Rnase4	51091077	51091253	1996	0.178054	5.634219	0.270155	0.382397	0.03018	0	583	553	1257	603	837	924	1069	1003	958	783
ENSMUSG00000032263	chr9	Bckdhb	83925145	83925359	1805	-0.16582	4.678854	0.27036	0.382647	0.024705	0	345	303	561	488	481	295	549	460	500	406
ENSMUSG00000078816	chr7	Prkcg	3303532	3303959	3112	0.400952	0.159478	0.270671	0.383047	0.067043	0	12	15	14	11	16	13	29	12	27	24
ENSMUSG00000014361	chr2	Mertk	1.29E+08	1.29E+08	4336	0.294767	1.779772	0.270748	0.383114	0.067621	0	40	29	77	42	58	54	55	107	60	51
ENSMUSG00000005813	chr3	Metap1	1.38E+08	1.38E+08	2549	-0.16899	6.282719	0.270854	0.383223	0.027552	0	1205	1102	1807	1097	1359	1017	1602	1230	1760	1145
ENSMUSG00000020737	chr11	Hn1	1.15E+08	1.15E+08	2149	0.262338	5.813863	0.270929	0.383289	0.06617	0	841	952	983	447	670	1096	1183	989	1354	924
ENSMUSG00000019787	chr10	Trdn	33083483	33083745	4514	-0.19047	10.47023	0.27116	0.383493	0.035848	0	19315	20505	38556	18069	26418	23561	26523	19859	30648	19935
ENSMUSG00000020078	chr10	Vps26a	62454843	62456858	3252	-0.1552	5.519771	0.271146	0.383493	0.022491	0	650	593	1175	696	799	627	983	786	934	649
ENSMUSG00000063904	chr19	Dpp3	4907229	4907797	2683	0.170878	4.613035	0.271141	0.383493	0.025762	0	345	271	420	356	435	413	503	392	667	392
ENSMUSG00000028035	chr3	Dnajb4	1.52E+08	1.52E+08	4318	-0.18505	5.676435	0.271327	0.383688	0.032883	0	599	641	1121	1001	1034	542	1342	701	1169	746
ENSMUSG00000025785	chr9	Exosc7	1.23E+08	1.23E+08	1843	0.194982	3.954943	0.271381	0.383723	0.031715	0	207	215	252	194	258	241	434	279	328	234
ENSMUSG00000036552	chr17	Ermard	14978864	14978899	6352	0.228302	2.29272	0.271414	0.383729	0.036215	0	70	53	99	56	77	95	106	85	107	75
ENSMUSG00000068250	chr6	Amn1	1.49E+08	1.49E+08	4300	0.305544	1.534153	0.271873	0.384337	0.060999	0	40	35	38	45	36	52	83	52	43	49
ENSMUSG00000103171	chr3	DNAJC19	34078662	34078845	393	0.201133	5.396781	0.272034	0.384523	0.03792	0	670	557	715	496	609	713	1206	656	998	598
ENSMUSG00000020307	chr10	Cdc34	79682195	79682590	1262	-0.17871	8.02779	0.27215	0.384615	0.031533	0	4774	3436	5477	3758	4456	3754	5265	3988	5803	3684
ENSMUSG00000036957	chr7	Lrfn3	30355514	30356103	2861	-0.29652	2.320621	0.272156	0.384615	0.068419	0	57	29	143	95	136	68	69	80	110	71
ENSMUSG00000006445	chr4	Epha2	1.41E+08	1.41E+08	4674	0.264084	1.559322	0.272316	0.3848	0.049684	0	24	25	53	49	60	33	74	57	62	58
ENSMUSG00000020108	chr10	Ddit4	59949675	59951029	1685	0.332504	3.338215	0.272719	0.385287	0.100125	0	108	154	98	139	176	165	418	130	138	184
ENSMUSG00000051238	chr9	Swsap1	21955753	21956004	1846	0.26273	1.808811	0.272694	0.385287	0.048226	0	46	38	49	53	58	55	64	82	66	65
ENSMUSG00000021809	chr14	Nudt13	20294690	20294792	2523	0.204939	4.256842	0.273407	0.386217	0.038742	0	198	148	318	385	396	295	497	320	481	294
ENSMUSG00000036282	chr14	Naa30	49172226	49172377	6970	-0.16405	4.629336	0.273483	0.386251	0.024547	0	350	352	576	357	454	308	477	469	506	368
ENSMUSG00000039795	chr3	Zfand1	10339953	10340905	6267	-0.22003	2.727428	0.273489	0.386251	0.039478	0	92	95	135	137	95	89	128	115	138	83
ENSMUSG00000103441	chr3	RP24-179O3.1	21753529	21753959	975	0.506957	-0.17004	0.273526	0.386262	0.159299	0	16	7	15	3	10	25	18	9	26	5
ENSMUSG00000035305	chr4	Ror1	1E+08	1E+08	5762	0.332646	0.727877	0.273574	0.386289	0.081782	0	13	7	47	24	25	25	41	36	24	29
ENSMUSG00000042613	chr3	Pbxip1	89436706	89436780	4674	-0.17373	8.801576	0.27372	0.386454	0.030057	0	6833	5819	11413	6450	7731	6029	8661	6275	10535	7077
ENSMUSG00000025410	chr10	Dctn2	1.27E+08	1.27E+08	1918	0.165496	6.854454	0.273959	0.38675	0.026724	0	1569	1434	2143	1678	1814	1878	2664	2029	2806	1842
ENSMUSG00000036864	chr7	Proser3	30539134	30539578	3512	0.272606	1.678363	0.274208	0.387061	0.058408	0	29	20	64	43	78	36	79	65	68	62
ENSMUSG00000042506	chr11	Usp22	61151785	61154513	4886	-0.17056	4.375973	0.274739	0.387769	0.025584	0	280	206	541	327	463	247	396	334	486	330
ENSMUSG00000085479	chr11	9430073C21Rik	67195680	67197472	2173	-0.91014	0.908198	0.274952	0.388028	0.764709	0	6	4	15	111	50	3	5	3	97	16
ENSMUSG00000034951	chr7	Cog7	1.22E+08	1.22E+08	3328	0.154167	4.675793	0.275048	0.388123	0.021214	0	317	276	495	394	464	394	553	487	631	396
ENSMUSG00000021639	chr13	Gtf2h2	1E+08	1E+08	4372	-0.18505	3.781195	0.275198	0.388292	0.030441	0	201	190	317	226	227	204	360	198	248	170
ENSMUSG00000039474	chr5	Wfs1	36966104	36968678	3564	-0.37686	6.405229	0.275312	0.388413	0.140955	0	604	435	1310	2870	2811	950	1511	1056	1921	1358
ENSMUSG00000003344	chr10	Btbd2	80642617	80643691	3586	-0.16774	4.948708	0.275425	0.38853	0.026002	0	395	309	701	642	618	401	633	489	650	488
ENSMUSG00000095690	chr19	Rab11b-ps2	7398421	7399077	657	0.214325	2.271022	0.275697	0.388873	0.032232	0	71	41	104	68	71	70	114	88	112	81
ENSMUSG00000031988	chr9	Vps26b	27004503	27010037	6872	-0.14902	5.466993	0.275994	0.389251	0.02093	0	650	485	1077	733	843	585	931	769	937	630
ENSMUSG00000030007	chr6	Cct7	85451505	85452127	2452	0.168064	7.239467	0.276064	0.389308	0.02799	0	2150	1853	2702	2064	2487	2439	3497	2706	3655	2377
ENSMUSG00000027618	chr2	Nfs1	1.56E+08	1.56E+08	3612	-0.15764	6.805632	0.276141	0.389374	0.024579	0	1650	1279	2341	1973	2265	1567	2463	1784	2416	1522
ENSMUSG00000058655	chr15	Eif4b	1.02E+08	1.02E+08	3853	-0.18112	8.12563	0.276227	0.389454	0.03297	0	4008	4333	6962	3942	4394	3824	5685	4351	6439	3864
ENSMUSG00000040877	chr12	Wdr25	1.09E+08	1.09E+08	4398	0.242298	2.019357	0.27658	0.389911	0.040685	0	38	50	72	59	71	47	110	82	92	65
ENSMUSG00000024529	chr18	Lox	52516069	52519233	4810	0.281918	4.383415	0.27681	0.390193	0.077916	0	178	255	650	152	351	461	323	418	427	378
ENSMUSG00000085622	chr12	3110056K07Rik	70991615	70992055	1504	0.315095	0.532209	0.276916	0.390302	0.051853	0	14	11	20	22	29	21	24	26	35	28
ENSMUSG00000031258	chrX	Xkrx	1.34E+08	1.34E+08	3024	-0.36836	0.648736	0.277051	0.390388	0.078667	0	18	7	43	34	36	12	26	26	31	22
ENSMUSG00000037736	chr5	Limch1	66745835	66746005	7411	-0.18234	6.646589	0.277065	0.390388	0.032951	0	1170	1016	2846	1774	2106	1229	2380	1386	2006	1661
ENSMUSG00000086765	chr4	Gm11827	11122805	11122915	1368	0.413239	0.27252	0.277065	0.390388	0.075761	0	16	19	19	10	9	17	22	22	31	22
ENSMUSG00000021704	chr13	Mtx3	92844787	92844867	6275	-0.21172	2.777622	0.277162	0.390471	0.035123	0	111	81	180	79	142	79	140	117	131	107
ENSMUSG00000025217	chr19	Btrc	45363734	45363886	6323	-0.16138	4.612868	0.277183	0.390471	0.023559	0	280	283	624	415	520	342	504	382	571	327
ENSMUSG00000034194	chr14	R3hcc1	69697305	69697602	2768	0.172749	4.034968	0.277223	0.390485	0.025735	0	244	175	302	216	290	281	356	266	434	248

ENSMUSG00000021768	chr14	Dusp13	21733394	21733851	2744	-0.16352	6.959331	0.277299	0.39055	0.026667	0	1835	1606	3108	1859	2224	1845	2637	1789	2811	1726
ENSMUSG00000024299	chr17	Adamts10	33524204	33524258	5453	0.215314	2.700691	0.277367	0.390605	0.037336	0	94	65	134	76	110	109	134	152	121	103
ENSMUSG00000029020	chr4	Mfn2	1.48E+08	1.48E+08	5194	-0.21208	9.165809	0.277867	0.391268	0.045606	0	7584	4415	13320	13229	12634	7275	11047	8350	14606	8146
ENSMUSG00000032186	chr9	Tmod2	75565621	75574123	10391	-0.29635	2.657605	0.27796	0.391357	0.073172	0	53	54	208	110	163	81	92	136	93	95
ENSMUSG00000079184	chr14	Mphosph8	56668248	56668564	3586	-0.16896	3.931295	0.278108	0.391524	0.02507	0	200	221	340	218	309	227	325	216	309	228
ENSMUSG00000025432	chr10	Avil	1.27E+08	1.27E+08	3398	0.32669	1.881974	0.278258	0.391693	0.081436	0	42	59	55	43	46	51	79	115	65	51
ENSMUSG00000005150	chr8	Wdr83	85075035	85075343	2818	0.186047	4.60857	0.278291	0.391698	0.03169	0	344	279	338	408	412	409	557	434	630	350
ENSMUSG00000039607	chr9	Rbms3	1.17E+08	1.17E+08	10413	0.218947	2.677738	0.278324	0.391704	0.038966	0	63	76	146	83	106	86	138	129	124	135
ENSMUSG00000021974	chr14	Fgf9	58070547	58070647	4266	-0.42585	0.213718	0.278463	0.391816	0.100181	0	5	16	25	22	31	16	19	17	10	18
ENSMUSG00000029165	chr5	Agbl5	30888694	30888842	7053	-0.26141	1.546995	0.278461	0.391816	0.046013	0	48	27	77	52	47	37	52	42	76	31
ENSMUSG00000059602	chr10	Syn3	86055125	86055664	12282	-0.85294	0.01271	0.278511	0.391842	0.607333	0	3	0	55	33	13	2	1	26	10	15
ENSMUSG00000055553	chr8	Kxd1	70508272	70508528	3176	0.178903	7.736274	0.278696	0.39206	0.03231	0	2815	2288	3302	3843	3582	3426	5223	3451	5330	3445
ENSMUSG00000010476	chr7	Ebf3	1.37E+08	1.37E+08	5021	-0.21629	3.161107	0.278846	0.39223	0.040512	0	135	119	262	99	164	113	207	172	160	103
ENSMUSG00000022967	chr16	Ifnar1	91485238	91485416	5879	0.182424	3.520217	0.279001	0.392407	0.029285	0	115	111	256	180	216	174	313	218	216	187
ENSMUSG00000070610	chr4	Gm13127	1.45E+08	1.45E+08	1389	-0.25564	1.033213	0.279499	0.393064	0.041415	0	30	24	38	40	37	21	39	29	49	26
ENSMUSG00000020929	chr11	Eftud2	1.03E+08	1.03E+08	8395	0.153924	4.867513	0.27961	0.393177	0.022173	0	365	278	592	483	525	471	703	499	689	455
ENSMUSG00000074170	chr7	Plekhf1	38220654	38222158	1559	0.19995	3.365557	0.279667	0.393177	0.035802	0	130	89	219	148	194	174	268	161	173	209
ENSMUSG00000083626	chr7	Gm4459	1.4E+08	1.4E+08	468	0.247744	1.873674	0.279646	0.393177	0.042941	0	44	31	68	63	57	65	97	56	94	45
ENSMUSG00000050244	chr13	Heatr1	12395398	12395470	6537	-0.1994	3.563703	0.279805	0.393328	0.034573	0	175	134	361	154	215	157	248	236	224	138
ENSMUSG00000060098	chr8	Prmt7	1.06E+08	1.06E+08	6125	-0.15171	5.491087	0.279842	0.393339	0.022347	0	641	520	949	786	920	550	973	707	1036	675
ENSMUSG00000026753	chr2	Ppp6c	39194354	39197589	4219	0.163026	6.101535	0.280056	0.393556	0.026171	0	934	822	1461	914	1062	1016	1599	1152	1756	1160
ENSMUSG00000034771	chr10	Tle2	81574561	81575691	6221	-0.24595	2.320257	0.280053	0.393556	0.047722	0	78	75	121	56	96	66	88	70	84	95
ENSMUSG00000043300	chr3	B3galnt1	69574158	69575960	2028	0.285179	1.757763	0.280299	0.393856	0.057811	0	53	42	60	37	40	43	76	76	60	70
ENSMUSG00000020886	chr11	Dlg4	70017085	70017233	4982	-0.28567	1.96438	0.280379	0.393927	0.069518	0	73	64	94	39	60	33	64	61	90	68
ENSMUSG00000035473	chr17	Galm	80127471	80127905	2476	0.283515	1.798738	0.280428	0.393954	0.062417	0	40	46	71	38	48	56	64	100	61	51
ENSMUSG00000028251	chr4	Tstd3	21757382	21758475	1588	-0.19332	4.098188	0.280481	0.393987	0.034973	0	268	176	282	341	387	236	422	224	354	237
ENSMUSG00000022436	chr15	Sh3bp1	78899667	78899961	4649	0.220556	2.691744	0.280529	0.394013	0.042168	0	77	65	154	79	107	128	108	141	134	100
ENSMUSG00000036867	chr9	Smad6	63953076	63954056	3205	0.27007	2.114837	0.280561	0.394016	0.057568	0	44	42	65	77	79	41	90	78	122	95
ENSMUSG00000024952	chr19	Rps6ka4	6829085	6829738	3119	0.160659	3.730156	0.28095	0.39452	0.02164	0	150	144	275	199	243	198	308	224	324	224
ENSMUSG00000091277	chr12	Gm1818	48554182	48556344	2399	-0.27172	1.6588	0.281003	0.394552	0.04652	0	43	30	82	55	65	56	70	41	47	37
ENSMUSG00000038268	chr11	Ovca2	75175942	75178387	2670	0.193985	2.870179	0.281126	0.394684	0.029983	0	100	67	145	113	119	132	152	121	179	116
ENSMUSG00000038252	chr6	Ncapd2	1.25E+08	1.25E+08	6267	-0.20273	3.214089	0.281241	0.394804	0.033176	0	120	86	221	162	224	127	152	138	218	145
ENSMUSG00000026260	chr1	Ndufa10	92439010	92439907	3331	-0.22209	7.969037	0.28155	0.395195	0.050661	0	3009	2374	4287	6322	5868	3122	5644	3484	6105	3291
ENSMUSG00000040270	chr4	Bach2	32238804	32239089	9940	0.323378	0.903688	0.281808	0.395515	0.073584	0	11	25	48	19	25	26	51	39	30	32
ENSMUSG00000018740	chr11	Slc25a35	68968131	68969037	3677	-0.2373	2.74386	0.281886	0.395541	0.046347	0	98	54	148	144	141	64	121	124	138	109
ENSMUSG00000031730	chr8	Dhodh	1.1E+08	1.1E+08	6326	-0.1825	3.645276	0.281866	0.395541	0.029868	0	186	136	233	257	245	142	270	193	276	195
ENSMUSG00000027001	chr2	Dusp19	80617045	80617606	2992	-0.19047	2.983757	0.281941	0.395576	0.030058	0	124	108	165	116	151	108	181	104	163	116
ENSMUSG00000101166	chr7	Gm28496	44246726	44246808	2991	-0.32914	0.340444	0.282443	0.396238	0.05895	0	21	15	29	18	21	11	30	23	13	17
ENSMUSG00000045930	chr12	Clec14a	58264720	58269258	4539	-0.20194	2.798728	0.282574	0.396381	0.033881	0	97	90	165	110	131	68	124	130	155	110
ENSMUSG00000022283	chr15	Pabpc1	36595661	36596099	5768	-0.18117	6.093153	0.282821	0.396685	0.033177	0	1102	954	1724	848	1195	962	1281	1330	1344	907
ENSMUSG00000087614	chr4	Gm12514	55131208	55131676	1026	-0.48201	-0.30287	0.28291	0.396768	0.140371	0	12	14	26	6	8	5	24	4	11	11
ENSMUSG00000039031	chr10	Arhgap18	26753421	26753502	3884	0.189715	2.967195	0.282964	0.396802	0.029299	0	93	84	163	97	150	127	174	168	173	109
ENSMUSG00000085586	chr11	Gm11613	97644184	97644557	1971	0.291561	2.570114	0.283082	0.396925	0.074223	0	59	56	58	140	98	78	155	100	151	110
ENSMUSG00000050592	chr2	Fam78a	32050055	32050912	5973	-0.18219	5.206323	0.283181	0.397022	0.032575	0	547	376	1045	557	725	421	749	466	896	661
ENSMUSG00000045761	chr17	Fam179a	71673261	71673499	5624	-0.48394	1.927198	0.283395	0.39728	0.221718	0	24	15	71	139	112	22	98	23	87	63
ENSMUSG00000036822	chr4	Topors	40259601	40263081	3856	-0.20165	3.252313	0.283504	0.397391	0.033787	0	120	115	285	137	178	112	196	168	159	163
ENSMUSG00000098332	chr9	5031420N21Rik	73039718	73039865	2999	0.262646	2.319858	0.283661	0.39757	0.053877	0	74	63	63	83	59	89	121	95	101	78
ENSMUSG00000040152	chr2	Thbs1	1.18E+08	1.18E+08	6073	-0.45145	3.896443	0.283727	0.397619	0.204391	0	54	89	217	407	695	142	416	190	195	218
ENSMUSG00000037624	chr1	Kcnk2	1.89E+08	1.89E+08	4943	0.272219	1.348119	0.283848	0.397706	0.054421	0	22	20	66	42	33	40	43	55	60	43
ENSMUSG00000064372	chrMT	mt-Tp	15356	15422	67	-0.41542	0.512229	0.283843	0.397706	0.117866	0	8	8	39	31	42	23	25	23	22	9
ENSMUSG00000038225	chr8	Primpol	46575579	46576721	6309	-0.25727	1.20791	0.283954	0.397812	0.041686	0	42	28	43	36	42	34	44	39	40	26
ENSMUSG00000030058	chr6	Copg1	87887814	87888072	10905	0.149461	5.609527	0.28399	0.39782	0.022176	0	600	471	1016	760	933	758	1177	893	1026	829
ENSMUSG00000026927	chr2	Sdccag3	26382802	26383694	3587	0.16103	4.359316	0.284133	0.397978	0.023773	0	247	207	358	345	399	317	500	382	457	323
ENSMUSG00000029003	chr4	Mad2l2	1.48E+08	1.48E+08	2622	0.216288	3.1882	0.284443	0.398371	0.039089	0	147	105	167	97	146	143	189	175	269	120
ENSMUSG00000002372	chr17	Ranbp3	56673225	56673411	2511	0.150093	5.616649	0.284691	0.398675	0.022113	0	692	550	963	700	816	812	1126	870	1120	781
ENSMUSG00000028603	chr4	Scp2	1.08E+08	1.08E+08	3478	-0.16417	7.05509	0.284961	0.399012	0.027853	0	2009	1834	2682	2169	2436	1748	2816	2437	2561	1922
ENSMUSG00000022538	chr16	Lsg1	30560494	30561862	5555	-0.16409	4.032661	0.285055	0.399101	0.024427	0	245	216	416	230	283	247	356	237	341	227
ENSMUSG00000093157	chr6	Mir3098	1.25E+08	1.25E+08	87	0.29787	0.553625	0.285339	0.399457	0.045323	0	13	15	24	20	26	24	34	18	37	24
ENSMUSG00000026270	chr1	Capn10	92934376	92935014	4346	0.208135	2.635788	0.285528	0.399636	0.035479	0	85	60	137	76	104	83	139	137	117	118
ENSMUSG00000031823	chr8	Zdhhc7	1.2E+08	1.2E+08	3472	0.152361	5.057629	0.285524	0.399636	0.022413	0	453	312	673	513	609	451	759	624	856	543
ENSMUSG00000039318	chr1	Rab3gap2	1.85E+08	1.85E+08	10800	-0.1591	4.627087	0.286167	0.40049	0.023498	0	352	254	700	374	475	355	484	388	548	358
ENSMUSG00000024735	chr19	Prpf19	10895231	10895468	7278	-0.16019	7.55587	0.28622	0.40052	0.026752	0	2495	2564	4454	3106	3358	2461	4235	2876	4060	2790
ENSMUSG00000005774	chr3	Rfx5	94954075	94954192	5497	0.197978	3.147119	0.286504	0.400876	0.033591	0	113	103	224	94	132	128	231	152	187	160
ENSMUSG00000102340	chr9	RP24-496O17.2	21275069	21277764	2696	-0.36757	0.452269	0.286554	0.400903	0.077237	0	15	8	40	18	39	17	20	13	29	21
ENSMUSG00000025159	chr19	Mms19	41941086	41944580	10415	0.151869	4.313153	0.286651	0.400997	0.021447	0	271	192	450	284	334	313	408	380	471	327

ENSMUSG00000026209	chr1	Dnpep	75307896	75308709	4289	0.149722	5.40661	0.287041	0.4015	0.021973	0	570	464	777	637	771	668	951	716	1065	690
ENSMUSG00000037847	chr19	Nmrk1	18631950	18631999	3345	-0.21843	2.159067	0.287443	0.401977	0.035776	0	66	62	105	77	65	66	90	66	89	58
ENSMUSG00000056749	chr13	Nfil3	52967209	52969021	2026	0.176786	4.04725	0.28744	0.401977	0.029832	0	169	171	377	250	302	333	368	286	373	224
ENSMUSG00000025141	chr11	Myadml2	1.21E+08	1.21E+08	992	-0.16366	6.211839	0.287537	0.402067	0.027526	0	1057	829	1708	1303	1465	1064	1577	966	1807	1054
ENSMUSG00000066800	chr1	Rnasel	1.54E+08	1.54E+08	6641	0.330355	1.819421	0.287685	0.402231	0.094645	0	44	46	86	25	44	72	87	94	49	40
ENSMUSG00000030815	chr7	Phkg2	1.28E+08	1.28E+08	3998	0.192937	3.16931	0.287862	0.402419	0.030271	0	129	109	146	116	156	141	177	167	218	159
ENSMUSG00000047221	chr5	Fam185a	21424958	21425576	3894	-0.19457	3.68803	0.28788	0.402419	0.035594	0	151	145	248	266	296	161	335	183	276	161
ENSMUSG00000025577	chr11	Cbx2	1.19E+08	1.19E+08	4257	0.378626	0.279142	0.287988	0.402527	0.097804	0	10	5	17	23	23	8	22	27	32	25
ENSMUSG00000031447	chr8	Lamp1	13159135	13159434	2255	0.155931	9.284245	0.288082	0.402594	0.025719	0	7910	7119	12835	9388	10255	9994	14132	11159	14526	10311
ENSMUSG00000039662	chr4	Icmt	1.52E+08	1.52E+08	5287	-0.15056	5.328275	0.288096	0.402594	0.022324	0	539	440	985	656	844	535	840	580	910	635
ENSMUSG00000025538	chr5	Sumf2	1.3E+08	1.3E+08	2667	0.198151	2.996125	0.288304	0.402799	0.033158	0	102	86	186	101	122	122	146	178	200	121
ENSMUSG00000091512	chr3	Lamtor3	1.38E+08	1.38E+08	1295	0.168767	4.910862	0.288279	0.402799	0.027296	0	420	370	525	448	465	482	747	470	795	447
ENSMUSG00000052456	chr8	Asna1	85017934	85018255	1250	-0.15248	5.357521	0.288402	0.402894	0.023234	0	575	477	815	779	813	544	866	664	851	631
ENSMUSG00000086784	chr7	Isoc2a	4877053	4877193	1088	-0.18196	4.934711	0.288596	0.403123	0.033579	0	449	468	601	504	522	349	587	657	590	433
ENSMUSG00000066406	chr7	Akap13	75455534	75455748	15203	-0.19823	6.081472	0.288716	0.403248	0.0406	0	774	569	1975	1306	1498	730	1347	1071	1563	1117
ENSMUSG00000028373	chr4	Astn2	65380803	65381689	4959	-0.44298	0.294512	0.28892	0.40349	0.115491	0	21	7	40	20	20	13	9	25	13	23
ENSMUSG00000026150	chr1	Mff	82724890	82725084	9757	-0.15425	6.794587	0.289183	0.403796	0.024897	0	1704	1371	2449	1841	2011	1513	2529	1652	2453	1573
ENSMUSG00000036009	chr10	Mettl25	1.06E+08	1.06E+08	2688	0.25522	1.50625	0.2892	0.403796	0.038809	0	34	32	39	38	55	47	64	53	60	46
ENSMUSG00000028016	chr3	Ints12	1.33E+08	1.33E+08	7257	-0.17884	3.293104	0.289307	0.403903	0.027131	0	149	118	238	164	163	152	192	138	216	135
ENSMUSG00000083282	chr19	Ctsf	4855129	4855486	1975	0.169131	4.948604	0.289391	0.403978	0.028259	0	329	323	578	599	507	456	697	530	794	524
ENSMUSG00000010362	chr11	Rdm1	1.02E+08	1.02E+08	1575	0.197436	4.753047	0.289565	0.404178	0.038094	0	408	391	479	303	363	467	673	494	610	388
ENSMUSG00000031286	chr3	Glt28d2	85869849	85872190	2732	-0.20696	2.983177	0.289634	0.404232	0.036949	0	83	98	220	126	165	83	162	133	197	102
ENSMUSG00000072582	chr11	Ptrh2	86683985	86684123	3132	0.182473	3.97844	0.289728	0.40432	0.029856	0	226	207	292	210	220	257	426	279	343	228
ENSMUSG00000002416	chr6	Ndufb2	39592574	39592712	5628	0.182607	7.196148	0.289818	0.4044	0.035062	0	2058	1617	2227	2569	2329	2290	3923	2284	3722	2261
ENSMUSG00000018169	chr15	Mfng	78755882	78756644	2839	0.385561	2.395689	0.289846	0.4044	0.140219	0	102	69	75	44	50	89	97	198	66	69
ENSMUSG00000036646	chr2	Man1b1	25332338	25332582	5391	0.150191	4.692854	0.289977	0.404497	0.021688	0	333	271	562	408	406	399	545	485	598	444
ENSMUSG00000038119	chr9	Cdon	35421128	35421183	7715	-0.20502	4.184784	0.289961	0.404497	0.040132	0	236	176	621	248	365	203	316	287	389	338
ENSMUSG00000078427	chr10	Sarnp	1.29E+08	1.29E+08	1062	0.210136	4.772843	0.290019	0.404514	0.043484	0	394	413	444	326	369	458	802	437	639	378
ENSMUSG00000032135	chr9	Mcam	44134469	44134756	3350	0.187877	5.003287	0.290097	0.404581	0.035161	0	511	394	587	340	533	472	695	750	743	461
ENSMUSG00000092341	chr19	Malat1	5795690	5802672	6983	-0.25253	7.559656	0.290487	0.405081	0.067778	0	2702	2182	6292	1336	4923	2879	3677	2905	3385	2745
ENSMUSG00000026203	chr1	Dnajb2	75236406	75236589	4249	-0.15914	6.368041	0.290619	0.405223	0.02647	0	1337	1070	1757	1232	1551	1226	1601	1390	1761	1147
ENSMUSG00000026179	chr1	Pnkd	74284930	74285137	7832	0.168811	4.880637	0.290706	0.405302	0.028104	0	409	278	475	484	573	462	676	481	798	456
ENSMUSG00000031422	chrX	Morf4l2	1.37E+08	1.37E+08	3135	0.166443	7.028879	0.290777	0.405359	0.029124	0	1819	1635	2518	1693	2109	2047	3287	2018	3082	2267
ENSMUSG00000037373	chr5	Ctbp1	33247724	33248686	2288	-0.15328	7.414494	0.290867	0.405441	0.024887	0	2420	2036	3912	2908	3261	2172	3568	2764	3706	2656
ENSMUSG00000030145	chr6	Zfp248	1.18E+08	1.18E+08	5039	-0.33288	0.734892	0.291014	0.405603	0.06368	0	17	23	52	23	28	23	21	26	24	29
ENSMUSG00000023968	chr17	Crip3	46428926	46428993	1520	0.445821	1.348831	0.291293	0.405949	0.174737	0	63	28	25	15	24	56	26	49	75	46
ENSMUSG00000103988	chr3	Dnajc19	34077454	34077524	333	0.191364	5.433734	0.291378	0.406024	0.037194	0	688	571	739	517	624	725	1228	673	1021	618
ENSMUSG00000023286	chr4	Ube2j2	1.56E+08	1.56E+08	4409	0.159287	5.400118	0.291495	0.406102	0.025296	0	560	549	813	579	656	686	1025	728	1036	623
ENSMUSG00000028848	chr4	Gpn2	1.34E+08	1.34E+08	1482	0.200614	2.665551	0.291473	0.406102	0.031434	0	96	62	102	91	112	98	141	122	141	106
ENSMUSG00000036144	chr12	Meox2	37108540	37109344	2360	-0.21772	3.54023	0.29169	0.406332	0.044811	0	112	131	236	258	275	121	244	178	229	208
ENSMUSG00000034101	chr2	Ctnnd1	84600071	84602903	7319	0.160384	5.279828	0.291801	0.406444	0.026549	0	446	334	938	584	751	555	801	805	943	643
ENSMUSG00000041757	chr1	Plekha6	1.33E+08	1.33E+08	10827	0.23544	3.63708	0.291863	0.406488	0.056446	0	132	71	277	187	294	160	330	246	213	264
ENSMUSG00000052763	chr6	Zfp212	47920476	47920749	3002	0.185259	3.401999	0.292237	0.406966	0.029282	0	133	135	209	117	192	148	235	183	267	190
ENSMUSG00000094595	chr4	Fsbp	11579665	11580107	4358	-0.4456	0.507705	0.292446	0.407214	0.14408	0	11	21	62	11	24	23	30	11	13	22
ENSMUSG00000038702	chr1	Dsel	1.12E+08	1.12E+08	5763	0.229861	1.954656	0.292748	0.407586	0.042698	0	37	36	79	53	80	55	98	88	69	61
ENSMUSG00000043372	chr11	Hexim2	1.03E+08	1.03E+08	2373	-0.25011	1.69153	0.292775	0.407586	0.047133	0	58	30	63	54	69	35	57	41	85	47
ENSMUSG00000070808	chr7	Gltscr1	15971262	15972889	5360	-0.20719	3.012869	0.293672	0.408792	0.036989	0	105	67	193	151	193	96	143	130	182	128
ENSMUSG00000047368	chr19	Abhd17b	21653309	21653593	2475	-0.17475	3.914945	0.2938	0.408928	0.029704	0	202	214	387	217	265	148	345	257	331	230
ENSMUSG00000033295	chr4	Ptprf	1.18E+08	1.18E+08	9130	-0.34084	1.208996	0.2939	0.409024	0.078607	0	20	17	63	52	55	33	38	36	27	39
ENSMUSG00000064371	chrMT	mt-Tt	15289	15355	67	-0.44057	1.391455	0.294284	0.409515	0.170135	0	16	21	31	87	82	34	23	41	49	43
ENSMUSG00000008305	chr4	Tle1	72117142	72118391	8711	-0.17765	4.13029	0.294642	0.409971	0.031619	0	267	196	422	302	314	179	448	303	422	195
ENSMUSG00000024346	chr18	Pfdn1	36403679	36404460	1077	0.181726	6.405822	0.294674	0.409971	0.03497	0	1284	1083	1424	1163	1248	1539	2093	1289	2076	1274
ENSMUSG00000071847	chr18	Apcdd1	62922327	62922721	2799	-0.41033	2.648119	0.294713	0.409983	0.169037	0	103	94	205	64	111	55	46	229	69	68
ENSMUSG00000031169	chrX	Porcn	8193848	8194277	3000	0.211158	2.272139	0.295027	0.410353	0.035758	0	60	47	99	58	93	78	92	76	120	94
ENSMUSG00000054474	chr6	Thnsl2	71128166	71128852	2071	0.198251	3.560658	0.295041	0.410353	0.035708	0	177	159	240	125	160	188	250	222	284	196
ENSMUSG00000039754	chr5	Alkbh4	1.36E+08	1.36E+08	2117	0.217156	2.36659	0.295259	0.410614	0.036511	0	62	60	93	76	82	91	92	85	130	93
ENSMUSG00000039497	chr10	Dse	34151394	34153974	4224	0.211084	3.291849	0.295307	0.410636	0.043076	0	134	86	240	118	164	174	201	245	166	146
ENSMUSG00000048833	chr12	Slc39a9	80644215	80644976	5229	-0.16586	3.785293	0.295672	0.411101	0.024455	0	189	129	352	247	279	178	287	232	278	209
ENSMUSG00000042354	chr14	Gnl3	31012434	31012634	1883	-0.19174	4.728168	0.295912	0.411392	0.03848	0	462	419	583	332	412	388	649	428	490	319
ENSMUSG00000008373	chr7	Prpf31	3629985	3630056	5439	0.148985	4.404867	0.296193	0.41174	0.021174	0	284	217	406	309	401	338	495	353	513	338
ENSMUSG00000047547	chr13	Cltb	54592401	54594042	4868	0.168274	6.829746	0.296442	0.412042	0.03033	0	1537	1505	2026	1556	1804	1771	2624	1979	3104	1669
ENSMUSG00000021356	chr13	Irf4	30749226	30749295	4715	-0.40993	1.388807	0.296671	0.412189	0.154339	0	40	40	95	21	41	32	30	78	41	14
ENSMUSG00000039428	chr7	Tmem135	89139723	89141970	6104	-0.18684	4.64227	0.296647	0.412189	0.036435	0	438	372	578	288	423	316	546	470	529	295
ENSMUSG00000043505	chr6	Gimap5	48746197	48746430	2353	-0.41602	0.074422	0.296657	0.412189	0.10236	0	7	6	31	21	26	13	26	16	12	7
ENSMUSG00000061536	chr9	Sec22c	1.22E+08	1.22E+08	6301	-0.16955	3.900608	0.296609	0.412189	0.026809	0	209	181	389	208	299	182	257	234	344	260

ENSMUSG00000021975	chr14	Ints9	64950045	64950367	2677	0.161879	3.807038	0.29671	0.4122	0.02374	0	182	148	289	213	228	202	281	279	374	214
ENSMUSG00000029430	chr5	Ran	1.29E+08	1.29E+08	2646	0.164063	6.713261	0.296847	0.412346	0.028821	0	1475	1345	1842	1386	1753	1759	2501	1834	2530	1561
ENSMUSG00000063801	chr7	Ap3s2	79875332	79880612	5797	-0.14065	5.669547	0.296948	0.412443	0.020488	0	739	568	1205	856	968	709	1088	828	1069	745
ENSMUSG00000058806	chr10	Col13a1	61838236	61838708	4605	-0.42347	0.169288	0.29703	0.412513	0.109586	0	13	9	22	19	33	10	21	7	13	27
ENSMUSG00000035172	chr11	Plekhh3	1.01E+08	1.01E+08	3582	-0.16692	4.73827	0.29715	0.412638	0.028326	0	389	284	563	516	523	293	496	527	585	404
ENSMUSG00000020652	chr12	Cenpo	4196004	4197106	7263	-0.2886	1.161415	0.297351	0.412835	0.054755	0	43	24	59	22	43	32	40	33	33	35
ENSMUSG00000028948	chr4	Nol9	1.52E+08	1.52E+08	4956	-0.17034	3.755321	0.297354	0.412835	0.027163	0	206	164	348	202	233	171	318	252	226	190
ENSMUSG00000090958	chr7	Lrrc32	98494222	98494308	3817	0.212557	2.841426	0.297585	0.413112	0.038629	0	76	71	149	107	132	78	194	146	201	95
ENSMUSG00000001127	chrX	Araf	20797814	20797881	6541	-0.15405	6.408638	0.297791	0.413355	0.025536	0	1191	1060	1818	1458	1662	1149	1866	1183	1818	1374
ENSMUSG00000031015	chr7	Swap70	1.1E+08	1.1E+08	4032	0.169435	3.454195	0.297999	0.413514	0.027228	0	131	98	236	154	223	164	249	232	221	181
ENSMUSG00000034930	chr6	Rtkn	83135463	83135585	3943	0.151601	4.115153	0.297992	0.413514	0.021064	0	237	201	351	234	288	271	406	291	416	281
ENSMUSG00000047604	chr19	Frat2	41845978	41848132	2155	0.253096	3.516655	0.297994	0.413514	0.065364	0	99	93	188	167	312	101	339	231	301	192
ENSMUSG00000019969	chr12	Psen1	83688203	83688293	3114	0.146296	4.992911	0.298105	0.413617	0.021695	0	387	342	701	478	546	485	660	644	783	485
ENSMUSG00000014606	chr11	Slc25a11	70644196	70644921	2120	-0.23087	8.044998	0.298182	0.413681	0.058667	0	3044	2362	4397	7055	6298	3114	6618	3670	5702	3643
ENSMUSG00000025158	chr11	Rfng	1.21E+08	1.21E+08	2489	0.155063	4.213454	0.298273	0.41372	0.023161	0	265	182	353	283	324	315	365	329	450	308
ENSMUSG00000025872	chr13	Thoc3	54458837	54460237	2428	0.15851	3.908335	0.298253	0.41372	0.02342	0	207	155	271	220	280	259	347	262	309	251
ENSMUSG00000014232	chr16	Cluap1	3908801	3908864	2279	0.170585	3.474997	0.2986	0.41409	0.025257	0	158	124	227	147	177	172	290	175	254	183
ENSMUSG00000054309	chr12	Cpsf3	21286297	21286544	2560	0.146929	4.411145	0.298602	0.41409	0.020695	0	290	215	439	332	350	314	514	378	496	346
ENSMUSG00000037370	chr10	Enpp1	24637914	24641976	10257	0.289555	2.305791	0.298937	0.414512	0.084558	0	34	28	101	82	124	54	122	94	95	118
ENSMUSG00000017781	chr11	Pitpna	75588097	75588352	4129	0.201582	7.08395	0.29898	0.414528	0.044441	0	2508	1568	2594	1522	1704	2134	3416	2619	3426	1853
ENSMUSG00000003575	chr8	Crtc1	70382355	70386335	11182	-0.18994	3.729923	0.299158	0.414731	0.034162	0	163	131	396	188	304	163	241	231	336	170
ENSMUSG00000016918	chr1	Sulf1	12692277	12692684	11294	-0.24857	3.638372	0.299442	0.415082	0.061143	0	112	105	357	249	318	138	242	268	174	198
ENSMUSG00000027508	chr3	Pag1	9687479	9694129	9580	-0.22712	2.146164	0.299509	0.415131	0.043227	0	70	50	127	51	86	42	90	76	100	62
ENSMUSG00000087611	chr5	4930458D05Rik	1.01E+08	1.01E+08	3055	0.384979	-0.06032	0.299884	0.415607	0.062976	0	15	8	12	11	12	10	23	23	20	12
ENSMUSG00000082575	chr4	Gm13050	1.43E+08	1.43E+08	1345	0.268901	1.607711	0.300002	0.415728	0.052859	0	39	39	58	41	34	41	50	67	71	61
ENSMUSG00000078490	chr4	C030017K20Rik	1.55E+08	1.55E+08	9951	-0.31839	0.68868	0.300391	0.416222	0.058972	0	16	21	39	28	32	26	23	14	32	26
ENSMUSG00000007837	chr7	Prrg2	45053613	45054197	2091	0.202596	3.288342	0.30079	0.416732	0.037084	0	169	96	149	133	163	150	224	208	232	136
ENSMUSG00000005674	chr1	Tomm40l	1.71E+08	1.71E+08	5135	-0.19617	5.554617	0.30091	0.416855	0.041656	0	603	443	798	1132	1073	581	1121	707	936	702
ENSMUSG00000081214	chr1	Rpl35a-ps2	1.81E+08	1.81E+08	333	0.4143	0.416526	0.301089	0.41706	0.122872	0	29	11	22	11	9	31	34	13	34	16
ENSMUSG00000046447	chr4	Camk2n1	1.38E+08	1.38E+08	4444	0.20105	3.277316	0.301124	0.417064	0.040202	0	107	94	233	118	188	172	161	212	187	181
ENSMUSG00000006675	chr9	P4htm	1.09E+08	1.09E+08	3890	-0.21965	1.668154	0.301194	0.417118	0.033733	0	37	39	71	58	63	38	55	52	68	47
ENSMUSG00000051255	chr19	Gm6563	23675844	23676712	869	0.235728	2.949985	0.301383	0.417335	0.048765	0	99	113	116	92	125	129	234	109	191	105
ENSMUSG00000027165	chr2	B230118H07Rik	1.02E+08	1.02E+08	4289	-0.20478	6.162093	0.301432	0.41736	0.04641	0	1206	1267	1329	984	1089	1104	1698	1016	1411	896
ENSMUSG00000040003	chr5	Magi2	19227046	19227589	7239	0.37566	0.286158	0.301524	0.417444	0.076225	0	14	12	9	22	18	13	28	26	34	15
ENSMUSG00000020650	chr12	Bcap29	31595354	31596377	2008	-0.16168	5.185034	0.301585	0.417485	0.027872	0	539	545	830	489	647	493	787	514	762	588
ENSMUSG00000032718	chr6	Mansc1	1.35E+08	1.35E+08	2373	-0.31115	0.273699	0.301881	0.417851	0.055621	0	16	14	27	17	25	6	22	18	26	19
ENSMUSG00000050668	chr17	Gpatch11	78835516	78835678	4198	-0.16292	3.982447	0.302036	0.418022	0.026106	0	234	200	314	246	336	248	342	206	352	215
ENSMUSG00000002949	chr8	Timm44	4259731	4260255	3664	-0.19029	5.985976	0.302197	0.418157	0.039757	0	838	621	1104	1455	1429	813	1505	914	1391	878
ENSMUSG00000071151	chr10	Gm4799	82954344	82955000	657	0.322279	0.511454	0.302171	0.418157	0.0558	0	11	22	22	19	18	20	35	28	32	19
ENSMUSG00000032724	chr2	Abtb2	1.04E+08	1.04E+08	6032	-0.38613	3.37554	0.302312	0.418273	0.158119	0	83	41	175	307	381	90	273	103	229	149
ENSMUSG00000063568	chr6	Jazf1	52768797	52770380	2536	-0.4604	-0.29421	0.302713	0.418784	0.086211	0	7	7	15	17	21	14	6	10	13	10
ENSMUSG00000042507	chr12	Elmsan1	84149176	84152561	7611	-0.21309	3.635381	0.302864	0.418925	0.044973	0	132	105	311	239	325	118	294	209	252	190
ENSMUSG00000098543	chr19	Gm27533	5844286	5844437	152	0.194837	5.670852	0.302878	0.418925	0.041403	0	793	583	975	492	957	861	1312	666	1075	1027
ENSMUSG00000020346	chr11	Mgat1	49244191	49244339	4733	0.145891	5.556054	0.303001	0.419052	0.022438	0	635	528	862	700	844	714	999	882	1188	746
ENSMUSG00000025007	chr19	Aldh18a1	40550257	40551329	4072	0.246047	2.502193	0.30312	0.419172	0.059952	0	63	29	94	99	137	96	123	109	128	92
ENSMUSG00000046947	chr6	Adck2	39573873	39575206	4095	0.176957	7.065602	0.30327	0.419336	0.034752	0	1910	1458	2054	2350	2121	2097	3552	2075	3407	2066
ENSMUSG00000044348	chrX	Slc25a53	1.37E+08	1.37E+08	7963	-0.32458	0.517773	0.303458	0.419552	0.066145	0	9	18	38	28	28	14	31	14	30	20
ENSMUSG00000062646	chr2	Ganc	1.2E+08	1.2E+08	9096	-0.16394	5.308416	0.303505	0.419573	0.028943	0	652	559	968	505	655	606	804	632	822	544
ENSMUSG00000027955	chr3	Fam198b	79884533	79884690	9598	-0.17133	3.983729	0.303555	0.419599	0.028159	0	179	166	425	269	347	186	303	303	324	240
ENSMUSG00000024070	chr17	Prkd3	78949405	78952030	11017	-0.17236	3.661288	0.303885	0.41988	0.027434	0	144	141	338	218	259	162	269	234	226	188
ENSMUSG00000051331	chr6	Cacna1c	1.19E+08	1.19E+08	21191	-0.37731	1.251237	0.303829	0.41988	0.126857	0	15	18	82	43	63	11	55	50	36	31
ENSMUSG00000057506	chr19	Bloc1s2	44139266	44139713	878	0.205634	3.425804	0.303804	0.41988	0.040152	0	183	131	176	136	145	192	280	175	222	171
ENSMUSG00000058351	chr14	Smim4	31088869	31089026	592	0.325507	2.421128	0.303885	0.41988	0.10474	0	62	38	49	118	102	109	93	70	193	73
ENSMUSG00000020844	chr11	Nxn	76257198	76258747	3239	0.171419	5.852059	0.304172	0.420206	0.032103	0	778	541	1015	962	1081	888	1278	832	1747	933
ENSMUSG00000099492	chr1	Gm5525	29484604	29485915	1312	-0.27743	0.80935	0.304184	0.420206	0.04736	0	25	23	40	29	28	18	24	25	40	29
ENSMUSG00000027620	chr2	Rbm39	1.56E+08	1.56E+08	6946	-0.15148	6.094207	0.304286	0.420303	0.025194	0	962	923	1569	1087	1220	973	1493	1169	1309	973
ENSMUSG00000025104	chr7	Hdgfrp3	81881251	81886083	9575	-0.23843	1.504558	0.304326	0.420314	0.03611	0	34	37	67	44	58	37	50	51	46	43
ENSMUSG00000021037	chr12	Ahsa1	87266746	87266921	1347	0.15774	6.964003	0.304513	0.420485	0.027661	0	1850	1366	2145	1866	2145	2041	3038	2301	2764	1916
ENSMUSG00000041921	chr2	Metap1d	71453276	71453398	4537	-0.15768	4.856565	0.304499	0.420485	0.026177	0	384	336	532	558	637	398	607	491	631	388
ENSMUSG00000026135	chr1	Zfp142	74565127	74567347	11355	-0.28229	3.053202	0.304665	0.42065	0.078534	0	63	55	237	175	245	84	166	121	168	141
ENSMUSG00000026608	chr1	Kctd3	1.89E+08	1.89E+08	8129	-0.16487	3.527168	0.304932	0.420975	0.02543	0	132	140	283	208	224	148	250	181	265	155
ENSMUSG00000028609	chr4	Magoh	1.08E+08	1.08E+08	770	0.191925	3.725174	0.304992	0.421014	0.035164	0	211	153	219	199	178	234	359	215	286	191
ENSMUSG00000021710	chr13	Nln	1.04E+08	1.04E+08	3780	0.204594	2.956926	0.305153	0.421193	0.038476	0	90	67	124	154	138	120	200	149	177	110
ENSMUSG00000048578	chr5	Mlec	1.15E+08	1.15E+08	6010	-0.15816	8.027098	0.306225	0.422628	0.028353	0	3989	3024	6802	3564	5162	3819	4697	4637	5334	3891
ENSMUSG00000025176	chr19	Hoga1	42045610	42046110	2259	-0.3283	0.76308	0.306277	0.422656	0.07458	0	29	23	41	16	34	20	28	12	42	28

ENSMUSG00000025408	chr10	Ddit3	1.27E+08	1.27E+08	1713	-0.25993	3.303062	0.306717	0.423087	0.070101	0	119	74	153	278	241	113	167	167	210	156
ENSMUSG00000028937	chr4	Acot7	1.52E+08	1.52E+08	2124	-0.22835	4.278996	0.306711	0.423087	0.055553	0	212	154	359	538	444	286	369	282	403	283
ENSMUSG00000033454	chr12	Zbtb1	76370266	76370730	12190	-0.18787	3.427577	0.306641	0.423087	0.034228	0	151	136	258	156	221	116	248	160	180	207
ENSMUSG00000037031	chr10	Tspan15	62185396	62188162	3605	0.186011	3.315495	0.306717	0.423087	0.031423	0	157	108	175	118	177	166	241	152	248	157
ENSMUSG00000028443	chr4	Nudt2	41465151	41465180	845	-0.17429	3.784719	0.306819	0.42314	0.030776	0	199	208	278	235	222	183	242	259	272	211
ENSMUSG00000034509	chr17	Mad2l1bp	46147390	46148284	1269	0.184766	3.977225	0.306801	0.42314	0.034455	0	171	152	255	312	288	225	362	250	445	262
ENSMUSG00000046822	chr10	Slc39a3	81028538	81031700	4016	-0.15024	4.726165	0.306935	0.423256	0.023105	0	348	273	611	507	530	358	541	435	539	414
ENSMUSG00000037514	chr2	Pank2	1.31E+08	1.31E+08	4912	0.166797	4.603261	0.30705	0.42337	0.028552	0	324	317	537	277	374	341	577	517	582	348
ENSMUSG00000040428	chr7	Plekha4	45526330	45526441	4187	0.272137	1.68071	0.307143	0.423455	0.062205	0	31	29	52	66	47	33	89	69	58	62
ENSMUSG00000097320	chr7	C630016N16Rik	30729579	30729854	1416	0.242142	1.350307	0.307186	0.42347	0.033809	0	31	29	46	34	39	39	60	49	62	33
ENSMUSG00000021891	chr14	Mettl6	31478320	31479810	2436	0.203678	2.804834	0.307356	0.423661	0.034707	0	92	94	134	86	101	95	185	119	177	108
ENSMUSG00000015053	chr6	Gata2	88193891	88194000	3351	0.236075	2.083488	0.307475	0.423781	0.047956	0	42	32	79	82	75	52	107	69	122	67
ENSMUSG00000097121	chr12	D130020L05Rik	1.01E+08	1.01E+08	2431	0.392589	-0.06424	0.307616	0.423931	0.082319	0	13	5	11	17	12	11	13	24	24	15
ENSMUSG00000038605	chr2	Samd10	1.82E+08	1.82E+08	2448	0.20976	2.584277	0.307652	0.423936	0.04045	0	87	50	144	69	100	105	123	106	168	79
ENSMUSG00000020828	chr11	Pld2	70540064	70540208	6252	0.16465	3.838994	0.307708	0.423969	0.027549	0	199	133	351	177	244	239	306	303	300	216
ENSMUSG00000057147	chr2	Dph6	1.15E+08	1.15E+08	7407	-0.22795	2.077153	0.308293	0.424732	0.042068	0	54	47	115	53	99	46	90	53	98	65
ENSMUSG00000021453	chr13	Gadd45g	51846678	51846832	1173	0.332836	5.423908	0.308338	0.424749	0.124859	0	516	628	353	439	964	647	1996	573	545	726
ENSMUSG00000076012	chr6	Mir705	85336292	85336373	82	0.274443	1.068691	0.308439	0.424845	0.04274	0	25	21	36	32	30	31	62	32	51	26
ENSMUSG00000004127	chr3	Trmt10a	1.38E+08	1.38E+08	7976	-0.30732	0.890058	0.308598	0.425013	0.059854	0	29	15	42	40	31	23	25	35	27	30
ENSMUSG00000079677	chr9	Fdx1l	21067520	21067925	782	0.163506	5.133699	0.308625	0.425013	0.02843	0	526	401	532	554	581	561	793	595	874	572
ENSMUSG00000025902	chr1	Sox17	4490931	4492668	4772	0.200454	2.273093	0.308846	0.425228	0.031783	0	57	54	102	71	71	80	112	84	123	66
ENSMUSG00000031370	chrX	Zrsr2	1.64E+08	1.64E+08	7194	0.178645	3.942455	0.308815	0.425228	0.031069	0	218	208	299	172	237	240	352	246	420	240
ENSMUSG00000005625	chr3	Psmd4	95032694	95032984	2808	0.175029	7.325397	0.308906	0.425267	0.034899	0	2086	2252	3136	2048	2348	2558	3294	2844	4478	2486
ENSMUSG00000002504	chr17	Slc9a3r2	24639282	24640389	2257	0.197814	4.931817	0.30904	0.425406	0.043242	0	254	295	511	620	627	454	649	491	804	582
ENSMUSG00000021621	chr13	Zcchc9	91796533	91797254	3422	0.163649	3.414669	0.309113	0.425463	0.0248	0	137	122	224	132	191	177	257	187	221	175
ENSMUSG00000031843	chr8	Mphosph6	1.18E+08	1.18E+08	1054	0.266472	1.825882	0.309324	0.425709	0.051821	0	49	46	52	52	44	41	106	68	83	52
ENSMUSG00000031767	chr8	Nudt7	1.14E+08	1.14E+08	5618	-0.26517	4.060446	0.309491	0.425896	0.077243	0	174	160	199	494	421	196	341	295	325	230
ENSMUSG00000029407	chr5	Uso1	92137938	92138163	3897	-0.14976	6.679765	0.309868	0.42637	0.025419	0	1507	1246	2757	1473	1824	1393	2206	1636	2125	1559
ENSMUSG00000039254	chr2	Pomt1	32236590	32236741	6442	0.166095	3.671513	0.309947	0.426434	0.0268	0	161	128	240	215	216	201	265	281	281	189
ENSMUSG00000002910	chr8	Arrdc2	70835155	70835994	2329	0.415487	4.753874	0.310187	0.426708	0.196096	0	288	305	456	396	390	1056	511	650	137	222
ENSMUSG00000010051	chr9	Hyal1	1.08E+08	1.08E+08	3777	-0.20251	2.295688	0.31021	0.426708	0.033973	0	72	53	101	98	90	63	90	88	105	64
ENSMUSG00000053641	chr9	Dennd4a	64811340	64811586	8645	0.221611	2.154001	0.310328	0.426826	0.043342	0	39	48	119	46	82	68	100	85	104	71
ENSMUSG00000034037	chr6	Fgd5	91978878	91979042	6292	-0.23632	3.281789	0.310432	0.426925	0.05635	0	80	89	249	204	254	105	193	196	170	144
ENSMUSG00000028463	chr4	Car9	43506966	43507395	2304	0.317206	0.771501	0.310478	0.426943	0.068166	0	24	17	40	15	19	29	46	36	37	15
ENSMUSG00000002957	chr7	Ap2a2	1.42E+08	1.42E+08	4639	0.149963	6.382749	0.310944	0.42754	0.025578	0	1049	767	1839	1388	1438	1298	1854	1540	2010	1340
ENSMUSG00000016833	chr5	Mrps18c	1.01E+08	1.01E+08	1076	0.198412	4.682561	0.311001	0.427558	0.041962	0	398	364	408	344	319	440	686	383	620	394
ENSMUSG00000028582	chr4	Cc2d1b	1.09E+08	1.09E+08	4771	-0.1466	4.702517	0.311021	0.427558	0.022244	0	389	272	689	397	497	369	524	404	580	384
ENSMUSG00000013495	chr5	Tmem175	1.09E+08	1.09E+08	3875	-0.18173	3.100239	0.311269	0.427775	0.031594	0	125	116	164	139	173	105	197	126	149	149
ENSMUSG00000020883	chr11	Fbxl20	98082556	98089698	12106	-0.16044	4.323814	0.311276	0.427775	0.026271	0	265	195	576	324	396	268	460	353	416	246
ENSMUSG00000050069	chr1	Grem2	1.75E+08	1.75E+08	3745	-0.47366	3.286399	0.311223	0.427775	0.252876	0	307	218	190	26	83	189	133	161	171	74
ENSMUSG00000047146	chr10	Tet1	62804570	62813412	14710	0.261902	1.268682	0.311486	0.428019	0.054361	0	21	24	64	29	35	29	66	49	40	45
ENSMUSG00000035637	chr4	Grhpr	44981395	44981534	1603	0.146213	4.942939	0.311559	0.428075	0.022552	0	432	340	557	449	550	481	642	556	786	489
ENSMUSG00000022241	chr15	Tars	11383663	11384159	2636	-0.14411	5.536684	0.311646	0.428103	0.023072	0	677	616	1146	680	805	592	962	767	1013	716
ENSMUSG00000036103	chr18	Colec12	9707648	9707759	3322	0.191055	3.705523	0.311638	0.428103	0.039648	0	116	104	302	206	288	202	299	275	241	232
ENSMUSG00000079049	chr13	Serpinb1c	32881833	32882225	1353	0.321514	0.532666	0.311676	0.428103	0.075315	0	20	10	17	21	27	34	31	24	20	23
ENSMUSG00000047910	chr18	Pcdhb16	37477814	37483038	5225	-0.48437	-0.28338	0.311713	0.428109	0.118096	0	3	7	31	10	20	7	11	16	9	10
ENSMUSG00000044533	chr17	Rps2	24718116	24718158	1830	0.16313	8.698018	0.311958	0.428402	0.030987	0	6126	5007	6781	6087	6793	6775	10231	7404	9774	6207
ENSMUSG00000023027	chr15	Atf1	1E+08	1E+08	3060	-0.15761	5.346774	0.312088	0.428536	0.02766	0	629	491	1039	524	812	436	884	654	932	658
ENSMUSG00000022130	chr14	Tgds	1.18E+08	1.18E+08	2265	-0.22507	2.35245	0.312336	0.428773	0.049627	0	97	74	89	75	86	50	110	88	91	85
ENSMUSG00000027679	chr3	Dnajc19	34057758	34058114	1015	0.180275	5.445629	0.312313	0.428773	0.035935	0	689	573	760	533	629	728	1230	677	1026	623
ENSMUSG00000028187	chr3	Rpf1	1.47E+08	1.47E+08	1263	0.175401	3.590767	0.312358	0.428773	0.029354	0	167	148	252	149	182	195	337	187	262	187
ENSMUSG00000026820	chr2	Ptges2	32395896	32396550	5058	-0.20246	5.236145	0.312398	0.428784	0.046399	0	494	337	619	931	871	427	830	565	887	551
ENSMUSG00000028104	chr3	Polr3gl	96577872	96578588	1597	0.164865	5.871358	0.312472	0.428797	0.030399	0	843	773	1010	727	980	967	1291	989	1532	902
ENSMUSG00000057716	chr6	Tmem178b	39873271	39873452	9729	-0.44492	0.121479	0.312451	0.428797	0.14007	0	9	2	28	22	35	12	23	7	21	13
ENSMUSG00000027811	chr3	4930579G24Rik	79629079	79629356	1970	0.306855	1.086408	0.312645	0.428989	0.069179	0	39	22	33	16	32	31	38	36	67	33
ENSMUSG00000002103	chr2	Acp2	91202885	91203048	5186	-0.14411	4.804485	0.312764	0.429108	0.021767	0	413	309	685	415	570	402	573	504	538	397
ENSMUSG00000023232	chr4	Serinc2	1.3E+08	1.3E+08	2319	0.171364	6.581888	0.312822	0.429143	0.033837	0	1409	1051	2074	1122	1626	1606	1683	1613	2676	1662
ENSMUSG00000026447	chr1	Pik3c2b	1.33E+08	1.33E+08	9237	0.154153	4.613836	0.312952	0.429261	0.025428	0	311	232	567	347	444	328	530	400	719	411
ENSMUSG00000027173	chr2	Depdc7	1.05E+08	1.05E+08	2096	0.284429	1.663839	0.312973	0.429261	0.065915	0	43	33	62	45	37	38	122	53	69	36
ENSMUSG00000019920	chr10	Lims1	58323466	58323687	4891	-0.2116	5.144998	0.313067	0.429347	0.050577	0	405	302	733	817	872	378	659	457	936	610
ENSMUSG00000029454	chr5	Mapkapk5	1.22E+08	1.22E+08	6209	-0.15015	6.090419	0.313108	0.429358	0.025714	0	1067	856	1495	1147	1155	1007	1472	1052	1418	969
ENSMUSG00000031565	chr8	Fgfr1	25513654	25513714	8120	0.171175	6.445369	0.313226	0.429475	0.033848	0	1084	1030	2066	1052	1440	1579	1575	1867	1813	1430
ENSMUSG00000006732	chr10	Mettl1	1.27E+08	1.27E+08	2907	-0.18453	4.119948	0.313283	0.42951	0.037063	0	359	227	322	230	302	240	397	255	321	269
ENSMUSG00000079427	chr9	Mthfsl	88688602	88688985	4728	0.244265	2.137375	0.313438	0.429638	0.049194	0	74	55	70	54	53	70	122	72	99	66
ENSMUSG00000093571	chr7	Gm24757	30311525	30311895	371	-0.21314	2.333821	0.313442	0.429638	0.042517	0	84	66	108	60	108	67	124	61	111	63

ENSMUSG00000024446	chr17	Rpp21	36255645	36255798	1218	0.187314	3.484146	0.313542	0.429732	0.033118	0	154	127	161	191	182	155	306	198	256	178
ENSMUSG00000057561	chr18	Eif1a	46597704	46597800	2879	0.185239	4.005729	0.313584	0.429744	0.034967	0	223	213	307	184	257	221	481	323	297	247
ENSMUSG00000031834	chr8	Pik3r2	70768176	70768897	4176	0.152121	4.442128	0.31369	0.429801	0.024357	0	286	224	481	336	337	316	411	440	546	367
ENSMUSG00000051224	chrX	Tceanc	1.66E+08	1.67E+08	4201	-0.28681	0.987766	0.313683	0.429801	0.051326	0	20	25	52	32	40	28	46	21	28	31
ENSMUSG00000045007	chr11	Tubg2	1.01E+08	1.01E+08	1754	-0.24245	1.07942	0.313873	0.430007	0.037762	0	28	32	45	31	38	30	41	33	39	25
ENSMUSG00000031059	chrX	Ndufb11	20615326	20615542	908	0.17453	8.050094	0.314022	0.430166	0.035697	0	3514	2732	3895	4840	4757	4168	6568	4182	7046	4102
ENSMUSG00000019868	chr10	Vta1	14654755	14655845	2263	0.15653	4.302316	0.31417	0.430275	0.024593	0	284	253	363	261	306	300	453	357	451	332
ENSMUSG00000038845	chr11	Phb	95666957	95667042	2805	-0.18677	7.01743	0.314199	0.430275	0.040749	0	1620	1341	2209	3034	2895	1721	2964	1864	2727	1916
ENSMUSG00000060671	chr3	Atp8b2	89939481	89941431	8561	0.198861	3.117227	0.314173	0.430275	0.040356	0	78	92	210	113	169	110	182	150	196	195
ENSMUSG00000062038	chr5	Gm10108	13121449	13121766	318	-0.28034	1.256808	0.314334	0.430417	0.060396	0	35	25	44	44	54	41	57	20	46	26
ENSMUSG00000037103	chr8	Dcaf15	84097075	84097508	2320	0.181554	2.935386	0.314472	0.43056	0.029251	0	104	71	153	107	140	102	178	145	213	108
ENSMUSG00000021684	chr13	Pde8b	95024454	95026229	5879	0.311264	0.589321	0.314543	0.430613	0.061978	0	11	12	24	16	39	21	37	22	38	24
ENSMUSG00000039483	chr2	Asb6	30823097	30824504	5439	0.167786	3.211427	0.314602	0.43065	0.026304	0	127	88	190	120	178	126	195	170	228	169
ENSMUSG00000024583	chr18	Txnl1	63662801	63664332	2558	0.149783	5.892329	0.314661	0.430687	0.025235	0	789	689	1226	876	934	843	1570	944	1468	971
ENSMUSG00000070493	chr5	Chchd2	1.3E+08	1.3E+08	2269	0.184137	8.460216	0.314793	0.430822	0.039922	0	5576	4437	5136	4919	5487	6054	8986	5789	9045	4827
ENSMUSG00000019471	chr9	Cdc37	21138541	21139963	2456	0.154575	6.676265	0.314899	0.430924	0.027611	0	1291	1139	1796	1743	1750	1606	2114	1856	2666	1637
ENSMUSG00000028909	chr4	Ptpru	1.32E+08	1.32E+08	7113	-0.46588	0.165005	0.315219	0.431317	0.151329	0	16	11	20	12	38	21	13	24	5	11
ENSMUSG00000045629	chr18	Sh3tc2	61953075	61953167	4536	-0.35017	0.384389	0.315389	0.431505	0.08121	0	13	9	23	38	26	16	24	19	26	12
ENSMUSG00000026924	chr2	Sec16a	26409431	26410953	9189	-0.18908	5.128338	0.315686	0.431867	0.040204	0	366	319	1023	654	783	352	712	536	816	606
ENSMUSG00000052609	chr12	Plekhg3	76533560	76533818	4955	0.188127	2.999511	0.315724	0.431874	0.033963	0	74	87	179	115	151	104	173	179	196	122
ENSMUSG00000001445	chr11	Mrpl10	97041560	97041652	1708	-0.1464	5.239999	0.315852	0.432004	0.024086	0	556	457	721	682	747	546	845	566	828	517
ENSMUSG00000022370	chr15	Mrpl13	55534094	55534337	7936	0.176029	5.634491	0.316152	0.43237	0.034989	0	742	638	724	735	775	836	1365	830	1134	698
ENSMUSG00000063015	chr5	Ccni	93181933	93183420	3303	0.159719	5.783112	0.316416	0.432686	0.02922	0	612	615	1136	906	937	730	1054	1255	1364	909
ENSMUSG00000037013	chr18	Ss18	14624198	14627311	4523	0.161401	3.852699	0.316555	0.432832	0.025734	0	172	175	284	211	245	197	350	322	304	218
ENSMUSG00000042099	chr17	Kank3	33810520	33810565	3118	0.172352	3.930141	0.316871	0.433219	0.031167	0	163	178	303	259	242	276	276	323	347	226
ENSMUSG00000031953	chr8	Tmem170	1.12E+08	1.12E+08	1943	-0.29717	0.483898	0.317041	0.433408	0.04812	0	18	15	39	19	26	15	33	17	30	13
ENSMUSG00000020255	chr10	D10Wsu102e	83360221	83360373	3509	0.190918	2.941282	0.317225	0.433493	0.0353	0	105	73	151	120	122	115	185	154	126	149
ENSMUSG00000025795	chr10	Rassf3	1.21E+08	1.21E+08	3425	0.203572	5.720585	0.317235	0.433493	0.048537	0	466	396	892	1137	1144	768	1235	914	1393	897
ENSMUSG00000027082	chr2	Tfpi	84432855	84433184	5463	0.232865	2.046644	0.317146	0.433493	0.046002	0	44	59	84	48	60	74	94	75	73	75
ENSMUSG00000040289	chr3	Hey1	8663359	8665064	3265	0.267333	1.659916	0.317192	0.433493	0.060873	0	20	35	64	44	64	53	69	72	79	33
ENSMUSG00000063821	chr14	Dupd1	21676582	21677160	1093	0.261355	5.929964	0.317303	0.433541	0.080451	0	1243	566	1020	535	1018	1504	870	1274	1357	846
ENSMUSG00000041263	chr3	Rusc1	89083981	89084650	3840	0.189445	3.896844	0.317338	0.433545	0.03827	0	159	128	255	318	259	187	360	269	394	254
ENSMUSG00000039959	chr5	Hip1	1.35E+08	1.35E+08	7850	0.165082	4.91815	0.317419	0.433611	0.031127	0	303	269	859	477	486	438	711	539	760	494
ENSMUSG00000040794	chr2	C1qtnf4	90885860	90886003	1290	0.263509	3.010166	0.317586	0.433771	0.070824	0	109	139	141	81	83	172	159	129	197	126
ENSMUSG00000050295	chr13	Foxc1	31806691	31810643	3953	-0.36584	0.002428	0.317602	0.433771	0.076044	0	18	12	16	16	18	8	15	9	17	22
ENSMUSG00000027628	chr2	Aar2	1.57E+08	1.57E+08	3615	0.140199	4.993818	0.317764	0.433948	0.021675	0	393	348	675	496	536	526	675	559	701	561
ENSMUSG00000101104	chr1	Gm29247	44091463	44091591	676	0.289119	1.360217	0.317868	0.434046	0.064055	0	31	32	44	35	33	51	68	59	40	27
ENSMUSG00000029432	chr5	Gbas	1.3E+08	1.3E+08	2750	-0.17957	9.046484	0.318016	0.434203	0.03862	0	6876	4983	10778	11718	11501	6431	12826	7327	11739	7904
ENSMUSG00000002741	chr11	Ykt6	5955693	5956004	2984	-0.15391	6.275653	0.318191	0.434352	0.027748	0	1150	920	1458	1460	1514	1106	1546	1187	1776	1120
ENSMUSG00000051671	chr8	Coa6	1.26E+08	1.26E+08	762	-0.16838	3.589884	0.318168	0.434352	0.030233	0	194	164	217	199	222	171	282	168	267	154
ENSMUSG00000025607	chr6	Copg2	30747554	30748987	4477	-0.14522	4.338592	0.318294	0.434448	0.022036	0	290	250	535	275	378	278	420	325	434	299
ENSMUSG00000009630	chr8	Ppp2cb	33599621	33600018	1826	-0.15921	5.040236	0.318405	0.434556	0.029103	0	512	506	735	438	546	405	694	529	733	501
ENSMUSG00000048616	chr11	Nog	89300638	89302332	1695	-0.21977	1.898097	0.318605	0.434784	0.04329	0	40	49	74	72	79	39	91	51	75	55
ENSMUSG00000045409	chr17	Trim39	36258873	36260921	7223	-0.15507	3.539828	0.31873	0.434909	0.023973	0	174	152	248	194	202	161	224	182	254	177
ENSMUSG00000085498	chr2	Gm14023	1.29E+08	1.29E+08	1781	-0.30582	0.228206	0.319072	0.435331	0.056675	0	10	19	24	23	18	13	23	15	19	17
ENSMUSG00000024069	chr17	Slc30a6	74395608	74395668	2171	0.179717	2.622891	0.319168	0.435417	0.0298	0	72	54	138	97	105	91	154	105	130	109
ENSMUSG00000031577	chr8	Tti2	31150316	31151499	5039	0.161436	3.337286	0.319461	0.435772	0.024014	0	135	111	204	132	181	140	255	193	228	158
ENSMUSG00000030222	chr6	Rerg	1.37E+08	1.37E+08	2563	-0.3925	0.108835	0.319761	0.436137	0.111512	0	8	5	27	25	27	6	22	9	25	16
ENSMUSG00000026971	chr2	Itgb6	60598292	60600583	7111	0.208639	5.296706	0.320092	0.436543	0.051181	0	428	291	644	735	893	608	1100	458	1026	716
ENSMUSG00000024248	chr17	Cox7a2l	83501919	83502737	1147	0.164359	6.92159	0.320229	0.436685	0.032026	0	1548	1540	1907	1995	1972	2008	2991	1998	2954	1848
ENSMUSG00000028521	chr4	Slc35d1	1.03E+08	1.03E+08	8528	0.202306	3.329327	0.320468	0.436966	0.039125	0	131	142	192	119	146	123	291	176	265	145
ENSMUSG00000001632	chr6	Brpf1	1.13E+08	1.13E+08	6714	-0.157	3.733091	0.320707	0.437247	0.023937	0	186	135	346	221	258	186	284	237	239	193
ENSMUSG00000062563	chr12	Cys1	24665838	24666252	2646	-0.2765	2.236364	0.320743	0.437251	0.07422	0	40	58	114	85	120	51	82	114	56	71
ENSMUSG00000050428	chr7	Fbxo46	19119859	19119936	3025	0.225248	1.598583	0.320793	0.437254	0.037049	0	38	27	60	46	47	38	58	58	74	59
ENSMUSG00000056962	chr11	Jmjd6	1.17E+08	1.17E+08	4698	0.163144	4.541634	0.320811	0.437254	0.02935	0	288	226	384	429	430	406	512	437	572	318
ENSMUSG00000098597	chr5	Mir6418	1.38E+08	1.38E+08	115	0.155141	3.854129	0.321022	0.437496	0.024515	0	187	137	262	249	262	230	326	248	367	221
ENSMUSG00000009569	chr16	Mkl2	13256481	13256554	8990	-0.18694	4.938667	0.321298	0.437828	0.040063	0	432	279	1080	429	551	360	674	460	784	403
ENSMUSG00000066607	chr9	6030419C18Rik	58488603	58489239	2139	-0.14508	4.519798	0.321363	0.437871	0.022611	0	323	241	514	428	445	295	443	367	510	374
ENSMUSG00000003039	chr8	Fam32a	72219730	72219860	1910	0.16079	4.0508	0.321722	0.438316	0.026627	0	206	216	294	236	281	283	388	330	341	241
ENSMUSG00000025579	chr11	Gaa	1.19E+08	1.19E+08	4783	-0.15585	8.256289	0.32183	0.438418	0.029411	0	4338	3333	8178	4900	5799	4042	5108	5400	6902	4903
ENSMUSG00000028116	chr3	Myoz2	1.23E+08	1.23E+08	3399	-0.89063	4.206783	0.321864	0.438419	0.909327	0	7	2	54	1331	554	60	420	144	416	220
ENSMUSG00000024169	chr17	Ift140	25016091	25016136	7572	-0.23562	1.884102	0.322052	0.438629	0.048032	0	64	29	106	57	65	49	61	61	88	44
ENSMUSG00000034083	chr6	Ccdc174	91878053	91878186	9188	-0.1819	3.2179	0.322271	0.438883	0.034989	0	167	122	191	122	176	110	243	136	178	134
ENSMUSG00000033596	chr8	Rfwd3	1.11E+08	1.11E+08	4443	0.192313	2.873503	0.322392	0.439002	0.03475	0	103	64	122	116	138	93	186	153	152	124
ENSMUSG00000029507	chr5	Pus1	1.11E+08	1.11E+08	2180	0.169864	3.395322	0.322505	0.439067	0.028669	0	136	100	170	167	217	157	230	209	247	167

ENSMUSG00000031616	chr8	Ednra	77663031	77665116	5476	0.265544	1.917364	0.322485	0.439067	0.067945	0	45	37	66	38	85	32	96	91	70	78
ENSMUSG00000020591	chr12	Ntsr2	16653470	16654123	1547	0.372736	0.537277	0.322678	0.439257	0.113877	0	29	10	31	8	16	22	22	18	52	25
ENSMUSG00000028107	chr3	Tars2	95739976	95740319	4438	0.136609	4.829988	0.322789	0.439362	0.02056	0	372	294	577	412	538	422	623	505	715	465
ENSMUSG00000059669	chr12	Taf1b	24498581	24498649	2019	-0.18706	2.594085	0.322825	0.439367	0.03307	0	84	83	138	103	98	87	138	102	108	74
ENSMUSG00000021318	chr13	Gli3	15463235	15463408	9589	0.291146	1.394191	0.323143	0.439755	0.082655	0	21	20	68	24	59	39	34	47	76	54
ENSMUSG00000021047	chr12	Nova1	46694517	46700973	7000	-0.26999	2.146255	0.323279	0.439894	0.070289	0	58	61	143	53	75	47	56	108	93	53
ENSMUSG00000028648	chr4	Ndufs5	1.24E+08	1.24E+08	860	0.169681	6.556248	0.323545	0.440211	0.034452	0	1340	1072	1415	1532	1602	1555	2573	1431	2306	1373
ENSMUSG00000097006	chr17	9530082P21Rik	23743234	23743421	4842	-0.19549	2.155998	0.323616	0.440263	0.032116	0	77	46	93	69	90	57	86	71	93	65
ENSMUSG00000059343	chr4	Aldoart1	72850583	72852632	2052	0.235702	2.305822	0.323657	0.440273	0.048933	0	66	63	104	59	62	62	151	74	137	69
ENSMUSG00000051041	chr7	Olfml1	1.08E+08	1.08E+08	1685	-0.2509	1.469448	0.323775	0.440388	0.051289	0	29	43	79	30	56	30	54	48	51	40
ENSMUSG00000041440	chr9	Gk5	96119362	96119612	8493	-0.30743	0.520455	0.323849	0.440444	0.065222	0	15	17	47	16	27	10	25	25	33	17
ENSMUSG00000003923	chr10	Tfam	71225464	71228699	4438	-0.14244	5.43563	0.324217	0.440825	0.023792	0	609	521	898	749	871	562	1067	626	948	616
ENSMUSG00000056131	chr9	Pgm3	86554377	86555403	4487	-0.2341	1.880836	0.324203	0.440825	0.050763	0	48	65	85	54	54	52	70	68	58	50
ENSMUSG00000057788	chr8	Ddx49	70292866	70293687	2928	0.139892	4.356946	0.324229	0.440825	0.020784	0	283	219	439	300	327	314	443	357	496	347
ENSMUSG00000018417	chr1	Myo1b	51749765	51751296	10792	-0.17886	3.295196	0.324401	0.440982	0.03223	0	102	107	225	191	223	130	217	142	198	151
ENSMUSG00000021431	chr13	Snrnp48	38204939	38205128	1799	-0.18941	2.64946	0.324411	0.440982	0.035556	0	92	96	123	92	117	78	118	119	116	94
ENSMUSG00000044080	chr3	S100a1	90511034	90511364	694	0.188738	6.859193	0.324494	0.44105	0.043207	0	1582	1235	1606	2066	2053	2098	2697	1874	3383	1425
ENSMUSG00000033917	chr7	Gde1	1.19E+08	1.19E+08	1692	-0.13997	5.905114	0.32458	0.441122	0.023241	0	884	762	1293	1019	1061	844	1262	994	1243	876
ENSMUSG00000002625	chr17	Akap8l	32321425	32321785	2075	-0.14983	4.620374	0.324744	0.4413	0.024839	0	334	327	579	398	437	406	434	379	501	377
ENSMUSG00000000149	chr5	Gna12	1.41E+08	1.41E+08	3416	0.18317	5.085802	0.324931	0.441429	0.039819	0	369	263	564	664	738	523	666	695	890	526
ENSMUSG00000029198	chr5	Grpel1	36464998	36465255	3528	-0.15381	6.143833	0.324877	0.441429	0.028419	0	967	831	1424	1378	1375	937	1645	990	1495	1107
ENSMUSG00000050621	chr9	Rps27rt	1.15E+08	1.15E+08	370	0.242153	3.537053	0.324939	0.441429	0.063752	0	215	156	182	138	114	225	319	205	238	154
ENSMUSG00000030037	chr6	Mrpl53	83109095	83109203	735	0.164339	5.725717	0.32505	0.441533	0.031621	0	827	669	819	740	825	843	1280	845	1297	873
ENSMUSG00000046070	chr17	Igfals	24878770	24878824	2111	-0.35787	1.929285	0.325084	0.441535	0.140236	0	67	52	89	50	76	26	50	138	53	29
ENSMUSG00000001472	chr8	Tcf25	1.23E+08	1.23E+08	3765	-0.14876	7.269015	0.325214	0.441666	0.027017	0	2568	1857	3627	2343	2643	2075	3085	2584	3333	2334
ENSMUSG00000038690	chr5	Atp5j2	1.45E+08	1.45E+08	1231	0.178596	8.306556	0.325276	0.441705	0.039216	0	4182	3442	4612	5825	5348	5156	9004	4704	7736	4675
ENSMUSG00000019883	chr10	Echdc1	29313166	29313297	3317	-0.17523	4.369245	0.325558	0.441998	0.03485	0	299	264	462	322	411	238	377	500	361	282
ENSMUSG00000032558	chr9	Nphp3	1.04E+08	1.04E+08	6639	-0.35594	0.432591	0.325546	0.441998	0.080413	0	14	10	43	14	37	9	28	21	22	20
ENSMUSG00000020289	chr11	Nprl3	32225628	32226835	7572	-0.15193	4.028273	0.325971	0.442513	0.024764	0	290	169	361	259	298	228	321	259	372	232
ENSMUSG00000028756	chr4	Pink1	1.38E+08	1.38E+08	2673	-0.14998	10.06569	0.326031	0.442549	0.027902	0	14371	13789	23873	19164	19410	15036	22569	15351	23811	16653
ENSMUSG00000050271	chr8	D8Ertd82e	36094828	36094988	9606	-0.24902	1.784217	0.326079	0.442569	0.05472	0	36	29	72	81	80	35	69	58	68	51
ENSMUSG00000041737	chr9	Tmem45b	31426199	31426956	1572	0.608129	3.283179	0.3267	0.443367	0.43585	0	255	147	61	27	39	117	79	567	110	144
ENSMUSG00000007656	chr9	Arpp19	75037614	75037719	4957	0.163979	6.101988	0.326762	0.443406	0.032252	0	846	822	1192	1089	1198	1109	1766	978	1911	995
ENSMUSG00000038150	chr11	Ormdl3	98581256	98582847	2184	0.162352	5.75325	0.32685	0.443435	0.031407	0	773	671	1031	718	836	861	1070	1265	1106	840
ENSMUSG00000053897	chr3	Slc39a8	1.36E+08	1.36E+08	7664	0.330961	0.172948	0.326834	0.443435	0.086477	0	7	6	25	14	23	8	28	24	19	24
ENSMUSG00000040356	chr17	Skiv2l	34839228	34839831	4977	0.142332	5.14202	0.327062	0.443677	0.02313	0	501	410	740	449	593	540	756	643	909	550
ENSMUSG00000053553	chr5	3110082I17Rik	1.39E+08	1.39E+08	1429	0.190527	2.806287	0.327252	0.443889	0.034798	0	99	57	118	113	133	94	185	131	170	102
ENSMUSG00000016427	chrX	Ndufa1	37187588	37187741	419	0.17146	6.629644	0.327755	0.444321	0.035898	0	1418	1067	1400	1695	1744	1648	2644	1653	2379	1383
ENSMUSG00000025139	chr7	Tollip	1.42E+08	1.42E+08	4333	-0.14235	5.786181	0.327702	0.444321	0.023982	0	746	548	1409	957	1119	732	1088	902	1282	820
ENSMUSG00000029629	chr6	Phf14	11907809	11908017	4547	-0.13663	4.321307	0.327772	0.444321	0.020103	0	269	241	479	343	358	284	415	320	430	290
ENSMUSG00000049285	chr5	Mblac1	1.38E+08	1.38E+08	1308	0.396298	-0.02862	0.327706	0.444321	0.088461	0	20	11	11	6	10	15	18	19	24	14
ENSMUSG00000085227	chr5	6330418K02Rik	1.38E+08	1.38E+08	1339	0.390477	0.091909	0.327669	0.444321	0.095755	0	17	12	9	11	15	19	32	13	13	21
ENSMUSG00000086003	chr11	B230206L02Rik	94133485	94133555	1042	0.319388	0.317811	0.327631	0.444321	0.062052	0	9	17	24	14	17	27	25	21	27	14
ENSMUSG00000026048	chr1	Ercc5	44147744	44149522	5864	-0.16398	3.753679	0.327869	0.444385	0.02745	0	164	141	335	222	308	208	299	232	232	180
ENSMUSG00000032299	chr9	Commd4	57155041	57155280	824	0.183013	4.209309	0.327939	0.444385	0.036638	0	307	247	325	215	248	309	440	304	477	273
ENSMUSG00000041479	chr14	Syt15	34219595	34220180	5165	0.312708	1.01699	0.32802	0.444385	0.079892	0	26	16	46	19	33	35	50	42	58	12
ENSMUSG00000042579	chr3	4632404H12Rik	89767511	89769562	2791	-0.28011	1.113825	0.327997	0.444385	0.066158	0	29	26	41	28	59	15	50	45	38	25
ENSMUSG00000068580	chr2	Zfyve19	1.19E+08	1.19E+08	3255	0.179302	3.253163	0.327931	0.444385	0.030923	0	131	123	177	132	136	160	190	190	224	146
ENSMUSG00000095588	chr4	Gm12350	34485832	34486293	462	0.200603	3.678856	0.327955	0.444385	0.042189	0	197	164	167	205	177	201	338	219	322	180
ENSMUSG00000039069	chr2	Mtg2	1.8E+08	1.8E+08	5949	-0.14572	4.213086	0.328166	0.444538	0.023536	0	283	236	365	322	335	259	405	272	364	301
ENSMUSG00000024841	chr19	Eif1ad	5366813	5367210	2469	-0.13637	4.836875	0.328224	0.44457	0.021093	0	430	310	626	478	575	403	631	433	630	406
ENSMUSG00000000826	chr2	Dnajc5	1.82E+08	1.82E+08	6953	-0.13785	5.749824	0.328292	0.444617	0.02259	0	734	577	1327	939	1037	684	1116	916	1243	771
ENSMUSG00000038871	chr6	Bpgm	34476207	34476422	3588	-0.16151	6.805199	0.328541	0.444909	0.032327	0	1935	1565	2348	1558	1906	1647	2601	1712	2422	1386
ENSMUSG00000064105	chr19	Cnnm2	46761596	46763393	3558	-0.30348	1.333673	0.328647	0.445007	0.087991	0	38	22	64	34	63	22	36	70	48	22
ENSMUSG00000029599	chr5	Ddx54	1.21E+08	1.21E+08	3929	0.140953	4.849803	0.328971	0.445399	0.022672	0	362	291	561	489	508	427	597	552	721	467
ENSMUSG00000034574	chr12	Daam1	71831078	71831331	6004	-0.16395	3.962352	0.329004	0.445399	0.029365	0	153	197	403	267	328	200	307	257	376	212
ENSMUSG00000057841	chr6	Rpl32	1.16E+08	1.16E+08	517	0.171544	7.234644	0.329145	0.445545	0.036395	0	2171	2105	2644	1982	2126	2581	3871	2711	3313	2171
ENSMUSG00000024997	chr19	Prdx3	60864051	60864719	1478	-0.154	7.622053	0.32935	0.445687	0.029604	0	2827	2280	4000	3840	3695	2610	4692	2829	4510	2721
ENSMUSG00000027882	chr3	Stxbp3a	1.09E+08	1.09E+08	5340	-0.17782	5.360914	0.329343	0.445687	0.03848	0	696	619	1044	447	665	619	881	559	932	557
ENSMUSG00000030839	chr7	Sergef	46443168	46443535	2368	0.240441	1.361013	0.329313	0.445687	0.046431	0	35	19	41	39	48	44	61	37	49	50
ENSMUSG00000025940	chr1	Tmem70	16665207	16665505	1820	-0.15135	5.814545	0.329435	0.44571	0.027883	0	812	598	1104	1060	1204	659	1382	890	1258	786
ENSMUSG00000059049	chr4	Frem1	82897920	82900598	13978	-0.40889	-0.10689	0.329411	0.44571	0.126758	0	13	14	33	5	12	5	18	17	9	15
ENSMUSG00000027349	chr2	Fam98b	1.17E+08	1.17E+08	3390	0.141534	4.633603	0.329535	0.4458	0.022296	0	319	303	559	315	404	369	558	451	596	407
ENSMUSG00000031642	chr8	Sh3rf1	61224171	61224346	5181	0.250202	1.349643	0.329577	0.445811	0.052263	0	27	16	40	50	48	36	59	51	63	35
ENSMUSG00000020376	chr11	Rnf130	50025346	50025647	1558	0.145749	5.426084	0.329617	0.44582	0.024849	0	555	559	764	612	734	712	979	787	962	674

ENSMUSG00000029307	chr5	Dmp1	1.04E+08	1.04E+08	2760	0.389345	-0.10175	0.329703	0.445891	0.131839	0	4	2	18	13	23	8	16	18	17	24
ENSMUSG00000098955	chr11	Mir6935	1.2E+08	1.2E+08	64	0.260253	1.017521	0.329775	0.445942	0.054332	0	24	13	37	25	44	38	44	44	39	24
ENSMUSG00000039167	chr3	Eltd1	1.51E+08	1.51E+08	4343	-0.15574	3.992305	0.329831	0.445973	0.026302	0	185	183	334	285	372	192	355	272	312	246
ENSMUSG00000037351	chr1	Actr1b	36698114	36700178	4274	-0.145	7.272067	0.329934	0.446066	0.026148	0	2056	1819	3415	2871	2965	2088	3331	2332	3387	2376
ENSMUSG00000032782	chr11	Cntrob	69299487	69299990	6660	0.255223	1.552753	0.330251	0.446405	0.05321	0	40	38	39	27	59	41	60	51	75	54
ENSMUSG00000083836	chr4	Ldha-ps2	1.19E+08	1.19E+08	1057	-0.2408	2.384584	0.330242	0.446405	0.05627	0	82	33	169	96	87	65	103	96	103	64
ENSMUSG00000056174	chr4	Col8a2	1.26E+08	1.26E+08	4489	-0.41419	1.912291	0.330447	0.446623	0.184713	0	16	32	96	80	135	45	55	68	23	80
ENSMUSG00000010755	chr7	Cars	1.44E+08	1.44E+08	4639	-0.1408	5.392363	0.330581	0.446759	0.023464	0	587	462	1016	732	790	612	790	633	1035	598
ENSMUSG00000024594	chr18	Prrc1	57354733	57354891	4801	-0.15643	4.748882	0.330696	0.446823	0.028173	0	337	255	704	484	570	296	570	429	615	438
ENSMUSG00000080059	chr4	Rps19-ps3	1.48E+08	1.48E+08	426	0.403497	-0.11887	0.330689	0.446823	0.09156	0	15	6	7	7	20	10	25	12	22	16
ENSMUSG00000027474	chr2	Ccm2l	1.53E+08	1.53E+08	2407	0.226841	1.901465	0.33073	0.446824	0.04354	0	40	32	57	66	75	53	84	79	92	52
ENSMUSG00000020646	chr12	Mboat2	24831599	24831774	2802	0.412559	-0.14546	0.330837	0.446923	0.143259	0	10	1	9	18	17	15	12	9	29	17
ENSMUSG00000049728	chr7	Zfp668	1.28E+08	1.28E+08	4655	-0.19521	2.050757	0.331369	0.447596	0.031704	0	55	51	103	57	86	52	78	63	96	58
ENSMUSG00000006599	chr7	Gtf2h1	46796103	46796288	2984	-0.15722	4.229257	0.331542	0.447785	0.028487	0	281	284	445	232	328	278	407	279	392	263
ENSMUSG00000022476	chr15	Polr3h	81915030	81916665	2514	0.174646	3.385796	0.331797	0.448082	0.030466	0	175	114	189	129	165	155	228	196	253	173
ENSMUSG00000000282	chr11	Mnt	74830920	74831401	4627	0.169557	3.52091	0.331932	0.44822	0.032165	0	142	110	320	127	195	160	260	228	253	201
ENSMUSG00000062526	chr18	Mppe1	67225530	67225884	2007	0.311315	1.635588	0.332104	0.448407	0.101717	0	22	19	33	73	70	53	85	60	56	48
ENSMUSG00000000223	chrX	Drp2	1.34E+08	1.34E+08	8553	-0.24039	2.33496	0.332183	0.448467	0.056931	0	49	49	122	114	108	55	112	68	81	97
ENSMUSG00000015656	chr9	Hspa8	40800984	40801348	4156	0.150961	9.769564	0.332309	0.448571	0.028992	0	11306	9200	16507	14010	15629	15402	18903	17417	19203	12607
ENSMUSG00000034893	chr14	Cog3	75702351	75704060	4222	-0.14618	4.064463	0.332361	0.448571	0.022788	0	237	174	451	267	312	240	371	245	357	241
ENSMUSG00000095325	chr17	Zfp870	32879228	32884165	5126	-0.16355	3.101385	0.332349	0.448571	0.027951	0	117	111	182	140	171	108	220	132	178	107
ENSMUSG00000021024	chr12	Psma6	55384222	55384327	1234	0.173653	7.081405	0.332473	0.448676	0.037723	0	1867	1990	2459	1756	1822	2123	3407	2241	3505	2032
ENSMUSG00000026283	chr1	Ing5	93803965	93804039	4729	0.212916	2.587925	0.332616	0.448808	0.042669	0	67	65	115	89	106	64	198	113	129	91
ENSMUSG00000030470	chr7	Csrp3	48830398	48830706	973	-0.77947	4.078931	0.332672	0.448808	0.735619	0	8	4	108	1033	619	78	360	261	296	182
ENSMUSG00000048429	chr9	1810026J23Rik	21592722	21593070	3170	-0.14026	6.650678	0.332639	0.448808	0.024539	0	1509	1117	2292	1653	1977	1302	2245	1563	2352	1411
ENSMUSG00000017734	chr2	Dbndd2	1.64E+08	1.64E+08	4389	0.149219	4.538465	0.33326	0.449555	0.025081	0	266	269	394	388	438	366	556	392	584	348
ENSMUSG00000027479	chr2	Mapre1	1.54E+08	1.54E+08	7811	0.144495	5.756385	0.333848	0.450302	0.025426	0	747	654	1150	637	939	897	1323	920	1209	845
ENSMUSG00000045095	chr6	Magi1	93675455	93679002	7701	0.24628	1.615444	0.334043	0.45052	0.060935	0	28	16	70	49	64	37	87	45	76	53
ENSMUSG00000028454	chr4	Pigo	43017635	43018038	4283	-0.22848	3.122151	0.334206	0.450694	0.056987	0	108	67	146	211	227	99	175	143	164	144
ENSMUSG00000007817	chr14	Zmiz1	25459185	25459556	12523	-0.2018	5.067219	0.334383	0.450887	0.049513	0	404	247	1124	563	743	333	635	644	664	573
ENSMUSG00000021840	chr14	Mapk1ip1l	47298314	47298405	4608	0.139831	4.411718	0.334464	0.450951	0.021986	0	264	244	480	269	385	301	525	383	474	360
ENSMUSG00000021546	chr13	Hnrnpk	58391142	58392476	5634	0.143649	7.258831	0.334854	0.451384	0.026078	0	1982	1809	3096	2256	2528	2186	3894	2548	3681	2562
ENSMUSG00000057134	chr10	Ado	67544512	67548955	4444	-0.13218	5.250214	0.334853	0.451384	0.021	0	519	477	847	616	747	484	783	647	866	562
ENSMUSG00000048495	chr1	Tyw5	57388237	57388752	2672	0.289208	1.303789	0.335313	0.451956	0.067152	0	38	34	37	27	29	53	56	48	50	28
ENSMUSG00000062421	chr11	Arf2	1.04E+08	1.04E+08	2998	-0.139	4.520341	0.335645	0.452359	0.022361	0	296	305	466	390	462	312	492	366	453	366
ENSMUSG00000026678	chr1	Rgs5	1.7E+08	1.7E+08	4546	-0.18123	7.895647	0.335807	0.452531	0.042216	0	2759	2558	4873	4374	6215	2724	6555	3171	5581	3098
ENSMUSG00000026670	chr1	Uap1	1.7E+08	1.7E+08	4011	-0.13713	5.656162	0.335936	0.452658	0.023176	0	710	595	1171	876	917	706	1248	813	1009	661
ENSMUSG00000020780	chr11	Srp68	1.16E+08	1.16E+08	2737	-0.14032	6.515233	0.336105	0.452794	0.024789	0	1186	1123	2169	1568	1736	1243	1769	1433	2085	1444
ENSMUSG00000030761	chr7	Myo7a	98051060	98051716	8524	0.233246	2.010316	0.336081	0.452794	0.056982	0	40	32	89	65	72	70	65	104	71	67
ENSMUSG00000033819	chr15	Ppp1r16a	76671615	76671762	4119	0.139638	4.969621	0.336509	0.453292	0.022871	0	467	345	608	449	508	476	646	558	782	534
ENSMUSG00000051339	chr5	2900026A02Rik	1.13E+08	1.13E+08	5876	0.164026	5.416604	0.336864	0.453725	0.033906	0	468	330	1121	589	903	555	1082	726	1145	696
ENSMUSG00000006289	chr14	Osgep	50906478	50907357	4933	0.157485	5.465356	0.33693	0.453768	0.030049	0	644	604	752	572	685	687	1095	718	1060	723
ENSMUSG00000041769	chr7	Ppp2r2d	1.39E+08	1.39E+08	5903	-0.14849	5.142341	0.336994	0.453808	0.026972	0	570	414	803	631	550	547	692	565	811	452
ENSMUSG00000052135	chr4	Foxo6	1.2E+08	1.2E+08	2615	0.270385	3.04627	0.337256	0.454115	0.088415	0	66	49	107	176	212	100	217	179	150	167
ENSMUSG00000042406	chr15	Atf4	80255184	80255685	1724	0.15518	7.583363	0.337518	0.454329	0.030952	0	2825	2130	3542	3020	2891	3319	4420	3516	4757	2573
ENSMUSG00000051316	chr18	Taf7	37640491	37643532	3302	-0.17798	3.046121	0.337461	0.454329	0.034202	0	86	117	199	137	164	94	198	120	186	116
ENSMUSG00000068267	chr2	Cenpb	1.31E+08	1.31E+08	4886	-0.14888	7.780257	0.337495	0.454329	0.028594	0	3149	2468	4307	4138	4533	3048	4014	3602	5200	3259
ENSMUSG00000004394	chr11	Tmed4	6270369	6271800	2178	0.131103	5.795019	0.337677	0.454496	0.021184	0	725	587	1154	859	961	850	1253	982	1369	877
ENSMUSG00000018848	chr11	Rars	35808381	35808591	3228	0.144171	5.852843	0.337852	0.454687	0.025726	0	786	719	1194	749	938	952	1460	937	1345	884
ENSMUSG00000022637	chr16	Cblb	52031549	52031685	6323	-0.14565	4.095474	0.338263	0.455193	0.023854	0	242	189	444	257	335	202	368	331	371	223
ENSMUSG00000030876	chr7	Mettl9	1.21E+08	1.21E+08	1822	0.142185	4.15094	0.338484	0.455444	0.022268	0	218	196	334	281	323	243	422	296	421	323
ENSMUSG00000100370	chr7	Gm4790	39566946	39570556	3611	-0.19466	2.758518	0.338626	0.455588	0.03851	0	79	77	198	113	122	69	142	111	127	121
ENSMUSG00000028329	chr4	Xpa	46155347	46155826	1894	-0.21787	2.3	0.338679	0.455589	0.052845	0	76	88	99	74	66	71	106	66	112	58
ENSMUSG00000031494	chr8	Cd209a	3743395	3744234	1484	0.274663	1.852297	0.338695	0.455589	0.078544	0	62	30	88	29	50	68	100	68	88	31
ENSMUSG00000052395	chr14	Rft1	30654360	30654475	4355	-0.1771	2.692042	0.338739	0.455603	0.032015	0	110	79	141	88	124	84	150	100	114	99
ENSMUSG00000022913	chr16	Psmg1	95979933	95980111	1344	0.19405	3.223718	0.33908	0.455994	0.039448	0	146	121	171	123	114	138	224	196	231	122
ENSMUSG00000026617	chr1	Bpnt1	1.85E+08	1.85E+08	2263	-0.1499	3.98741	0.339099	0.455994	0.025788	0	262	198	323	263	272	212	300	306	315	229
ENSMUSG00000027472	chr2	Pdrg1	1.53E+08	1.53E+08	2443	0.162657	6.815221	0.339228	0.456122	0.033862	0	1601	1565	1914	1473	1731	1876	2811	1765	2712	1780
ENSMUSG00000070697	chr5	Utp3	88554483	88556083	1601	0.166555	5.009572	0.339369	0.456264	0.033506	0	431	476	551	397	505	567	716	517	772	526
ENSMUSG00000034826	chr5	Nup54	92415540	92416338	2867	-0.16335	2.835805	0.339483	0.456372	0.025457	0	100	85	167	110	142	86	150	121	152	103
ENSMUSG00000026626	chr1	Ppp2r5a	1.91E+08	1.91E+08	9607	0.159036	6.631886	0.339883	0.456863	0.032512	0	1467	1113	1921	1404	1567	1437	2122	2418	2000	1533
ENSMUSG00000021514	chr13	Zfp369	65278814	65278987	5896	-0.24913	1.584094	0.340079	0.456941	0.050162	0	32	33	89	41	67	32	44	52	60	52
ENSMUSG00000039128	chr2	Cdc123	5794294	5794880	3463	0.147551	5.45256	0.340067	0.456941	0.026642	0	623	563	824	623	638	714	1070	721	1005	704
ENSMUSG00000041741	chr6	Pde3a	1.41E+08	1.41E+08	10794	-0.22446	2.21236	0.34002	0.456941	0.048328	0	61	35	128	74	112	54	85	61	118	69
ENSMUSG00000097368	chr5	Gm10390	1.2E+08	1.2E+08	8066	-0.30525	0.941416	0.340024	0.456941	0.081291	0	19	17	33	40	55	28	45	15	39	23

ENSMUSG00000034640	chr3	Tiparp	65528410	65528632	4358	-0.17325	4.186935	0.340261	0.457139	0.036109	0	295	258	448	242	292	282	381	371	309	206
ENSMUSG00000021910	chr14	Nisch	31170930	31172178	13198	0.158645	6.08016	0.340439	0.457333	0.032586	0	772	532	1680	1063	1317	989	1358	1363	1651	1153
ENSMUSG00000046312	chr4	AI464131	41495604	41499690	4701	-0.1482	6.953485	0.340611	0.457516	0.028296	0	1712	1209	3416	1991	2520	1701	2338	2160	2508	1983
ENSMUSG00000020718	chr11	Polg2	1.07E+08	1.07E+08	4356	0.222395	1.887936	0.340761	0.457673	0.041739	0	60	39	63	41	61	54	89	70	97	48
ENSMUSG00000028795	chr4	Ccdc28b	1.3E+08	1.3E+08	2026	-0.16659	4.206461	0.340951	0.457881	0.033702	0	244	240	320	384	349	260	415	224	403	292
ENSMUSG00000041548	chr5	Hspb8	1.16E+08	1.16E+08	1950	0.202827	9.391764	0.341024	0.457933	0.054182	0	12184	8394	12699	6219	9433	13055	14280	10513	17917	9933
ENSMUSG00000048546	chr15	Tob2	81848270	81851872	3994	-0.19113	5.560541	0.341069	0.457947	0.04697	0	617	672	1221	670	891	502	1425	607	702	847
ENSMUSG00000038240	chr10	Pdss2	43221486	43222060	5963	-0.15806	4.503936	0.341199	0.458074	0.029853	0	322	198	484	484	459	309	493	336	503	330
ENSMUSG00000024079	chr17	Eif2ak2	78852564	78855261	5113	-0.20043	2.317321	0.3415	0.458337	0.039011	0	87	56	108	73	96	80	98	92	88	55
ENSMUSG00000028868	chr4	Wasf2	1.33E+08	1.33E+08	6258	0.151359	4.861953	0.341481	0.458337	0.028831	0	329	238	656	453	613	405	617	610	655	500
ENSMUSG00000030768	chr1	Disp1	1.83E+08	1.83E+08	5224	-0.20838	2.06618	0.341533	0.458337	0.039124	0	55	45	98	81	77	49	66	82	81	66
ENSMUSG00000050860	chr11	Phospho1	95824499	95824709	2029	-0.15173	7.572017	0.34153	0.458337	0.030161	0	2969	1993	4214	3389	3666	2420	3516	2846	4826	3027
ENSMUSG00000030930	chr7	Chst15	1.32E+08	1.32E+08	5388	0.18502	2.822619	0.341579	0.458354	0.035333	0	81	70	152	87	146	106	149	150	191	89
ENSMUSG00000091896	chr18	Ube2d2a	35771559	35772012	2483	0.151485	5.213547	0.341673	0.458433	0.028086	0	570	463	756	456	538	586	841	704	903	546
ENSMUSG00000097906	chr13	Gm9625	67810246	67811200	955	0.215079	1.966149	0.341739	0.458475	0.041362	0	62	32	77	60	52	61	99	71	75	66
ENSMUSG00000002228	chr3	Ppm1j	1.05E+08	1.05E+08	1721	-0.1537	5.515043	0.341882	0.458621	0.030083	0	858	564	981	643	772	727	935	691	986	615
ENSMUSG00000027575	chr2	Arfgap1	1.81E+08	1.81E+08	5367	0.13891	5.11173	0.341931	0.45864	0.02406	0	444	324	824	528	582	563	813	529	805	599
ENSMUSG00000014791	chr8	Elmo3	1.05E+08	1.05E+08	3060	0.239455	1.501506	0.342188	0.458846	0.046379	0	45	30	61	25	40	40	70	51	57	51
ENSMUSG00000029131	chr5	Dnajb6	29735688	29736116	5721	-0.14232	6.006736	0.342139	0.458846	0.026059	0	903	890	1390	988	1213	903	1299	952	1500	964
ENSMUSG00000044937	chr10	BC030307	86705811	86706017	4646	-0.25689	0.788735	0.342187	0.458846	0.055748	0	18	31	33	26	32	24	32	20	39	21
ENSMUSG00000024050	chr17	Wiz	32354055	32355183	9204	0.153732	4.180998	0.342321	0.458977	0.028552	0	199	181	465	282	285	247	357	379	408	337
ENSMUSG00000041115	chrX	Iqsec2	1.52E+08	1.52E+08	6980	0.284021	4.048158	0.342742	0.459496	0.10326	0	102	94	206	421	402	201	401	309	482	290
ENSMUSG00000039458	chr15	Mtmr12	12205028	12205279	4785	-0.22108	2.169918	0.342871	0.459621	0.047873	0	50	55	142	67	79	40	89	85	93	68
ENSMUSG00000045822	chr2	Zswim3	1.65E+08	1.65E+08	2708	-0.25565	0.882517	0.343224	0.460049	0.046455	0	31	22	32	35	30	28	31	24	36	25
ENSMUSG00000035456	chr5	Prdm8	98180869	98181112	3119	-0.35492	0.002512	0.343319	0.460129	0.076304	0	10	12	25	15	20	7	8	17	21	18
ENSMUSG00000047669	chr10	Msl3l2	56106917	56107029	2140	0.354593	0.051313	0.343418	0.460215	0.065627	0	13	15	11	12	12	19	25	17	18	15
ENSMUSG00000046675	chr12	Tmem251	1.03E+08	1.03E+08	3369	0.233579	2.513032	0.343524	0.460312	0.053848	0	76	89	95	66	73	85	139	100	169	72
ENSMUSG00000069379	chr18	Gm4950	51865264	51865881	618	0.298453	0.455759	0.343605	0.460373	0.051319	0	20	16	20	17	16	21	24	30	31	20
ENSMUSG00000025878	chr13	Uimc1	55027880	55028718	5085	0.160467	3.79047	0.343789	0.460573	0.028495	0	191	172	254	196	215	262	320	233	309	196
ENSMUSG00000029179	chr5	Zcchc4	52775409	52775594	10890	-0.18178	2.694602	0.343978	0.46078	0.034137	0	91	64	128	126	140	94	151	90	129	86
ENSMUSG00000024947	chr19	Men1	6334979	6335070	3458	0.175949	2.945131	0.344075	0.460816	0.033603	0	101	68	164	114	136	114	148	184	160	124
ENSMUSG00000028854	chr4	Slc9a1	1.33E+08	1.33E+08	5324	-0.15136	3.768023	0.344057	0.460816	0.025097	0	188	124	350	242	274	181	296	219	306	184
ENSMUSG00000048003	chr4	Catsper4	1.34E+08	1.34E+08	2101	0.328276	0.16482	0.344441	0.46126	0.080861	0	12	12	21	11	16	26	19	21	29	7
ENSMUSG00000073415	chr17	Gm10501	34976899	34978751	2200	-0.21229	1.628386	0.344535	0.46134	0.040464	0	45	45	77	46	44	45	58	41	61	47
ENSMUSG00000057069	chr13	Ero1lb	12565883	12566178	4237	0.215888	1.590284	0.344707	0.461523	0.040239	0	31	28	70	45	46	46	63	68	55	50
ENSMUSG00000006014	chr1	Prg4	1.5E+08	1.5E+08	4280	-0.41888	4.315333	0.345085	0.461983	0.228071	0	52	94	413	495	939	252	408	157	412	329
ENSMUSG00000097462	chr6	9530026P05Rik	92940369	92940809	5463	-0.38753	0.304535	0.345323	0.462254	0.141623	0	18	21	38	5	22	15	35	20	10	10
ENSMUSG00000029345	chr5	Tfip11	1.12E+08	1.12E+08	4086	-0.14594	4.196202	0.345636	0.462627	0.024453	0	223	183	457	342	377	229	406	318	360	279
ENSMUSG00000026856	chr2	Dolpp1	30392254	30392512	3233	0.176003	2.745872	0.345843	0.462763	0.030453	0	90	77	138	96	96	92	138	131	157	121
ENSMUSG00000030560	chr7	Ctsc	88278085	88278374	5801	-0.13659	5.893435	0.345857	0.462763	0.023949	0	805	721	1501	844	1219	813	1274	950	1174	959
ENSMUSG00000031808	chr8	Slc27a1	71568927	71569023	2795	-0.31018	6.181359	0.345794	0.462763	0.127873	0	618	544	1045	2489	1852	705	1365	1924	1216	745
ENSMUSG00000034758	chr10	Tle6	81590904	81591139	3088	-0.20881	1.902873	0.345878	0.462763	0.041658	0	47	53	88	59	67	56	84	66	68	36
ENSMUSG00000013593	chr1	Ndufs2	1.71E+08	1.71E+08	2313	-0.17743	9.585592	0.345919	0.462772	0.042368	0	11337	7488	14528	16320	16200	11183	17203	9841	20108	9165
ENSMUSG00000055523	chr19	Gucy2g	55198297	55198788	3690	-0.44972	0.31909	0.345993	0.462824	0.193968	0	7	8	20	33	41	8	36	11	9	24
ENSMUSG00000006542	chr1	Prkag3	74738922	74740060	3682	-0.287	7.916054	0.346159	0.462969	0.110418	0	4794	5083	5782	1576	2989	4589	3629	3514	4840	2912
ENSMUSG00000046191	chr18	Pcdhb20	37504264	37507822	3559	0.391496	0.580226	0.34617	0.462969	0.157914	0	7	20	48	3	23	22	28	34	31	26
ENSMUSG00000097656	chr6	Gm26712	57689433	57689649	217	0.170066	4.41284	0.346346	0.463157	0.034918	0	292	224	334	394	334	347	577	306	558	302
ENSMUSG00000025982	chr1	Sf3b1	54985169	54987492	11370	-0.14308	6.783709	0.346443	0.46324	0.027064	0	1540	1437	2750	1591	2055	1646	2510	1683	1990	1711
ENSMUSG00000028896	chr4	Rcc1	1.32E+08	1.32E+08	3848	0.161834	3.691761	0.346497	0.463265	0.028815	0	192	151	248	176	196	212	277	248	340	169
ENSMUSG00000022472	chr15	Desi1	81992523	81994845	3635	0.155937	3.809053	0.346551	0.46329	0.028234	0	174	132	257	240	263	212	311	318	302	198
ENSMUSG00000002058	chr11	Unc119	78343482	78343786	2448	0.227817	2.75819	0.347036	0.463826	0.057176	0	111	81	136	66	93	119	123	157	182	76
ENSMUSG00000022433	chr15	Csnk1e	79417856	79419187	6406	-0.13759	5.726391	0.347056	0.463826	0.02456	0	799	590	1230	880	995	635	1081	800	1342	818
ENSMUSG00000071632	chr16	2510002D24Rik	18836578	18836619	1486	-0.15303	3.934855	0.347026	0.463826	0.027815	0	215	181	276	273	337	230	355	204	321	215
ENSMUSG00000029145	chr5	Eif2b4	31187558	31187800	2594	0.142567	5.693471	0.347246	0.464032	0.026248	0	641	494	978	914	956	714	1131	897	1421	857
ENSMUSG00000032554	chr9	Trf	1.03E+08	1.03E+08	3320	0.412373	6.773917	0.347373	0.464156	0.22703	0	2397	1577	1747	478	798	2103	1177	4712	1598	1287
ENSMUSG00000024002	chr17	Brd4	32196274	32197820	8402	0.154897	5.017122	0.347507	0.464241	0.031372	0	360	253	857	477	635	442	687	591	817	588
ENSMUSG00000041439	chr1	Mfsd6	52656286	52658545	8231	0.197269	3.017541	0.347478	0.464241	0.045413	0	87	62	134	144	183	92	213	148	192	147
ENSMUSG00000022159	chr14	Rab2b	52261759	52263817	4163	0.21473	1.763409	0.3476	0.464271	0.040847	0	39	39	77	46	45	52	64	77	78	50
ENSMUSG00000028834	chr4	Trim63	1.34E+08	1.34E+08	2842	-0.19011	7.927785	0.347593	0.464271	0.048867	0	3936	4073	5669	3036	3622	3733	5825	3033	5837	2803
ENSMUSG00000038991	chr13	Txndc5	38500273	38501708	4298	0.165898	5.645687	0.347881	0.464601	0.036442	0	580	374	1008	937	996	661	1123	1134	1030	875
ENSMUSG00000032355	chr9	Mlip	77102081	77102393	8916	0.138423	6.478691	0.348107	0.464855	0.025343	0	1152	961	2132	1214	1482	1346	2286	1472	2145	1394
ENSMUSG00000026942	chr2	Traf2	25517982	25519628	5101	-0.18388	4.27913	0.348522	0.465363	0.043118	0	362	276	479	228	287	325	376	318	432	207
ENSMUSG00000038208	chr11	Pgap3	98388677	98390101	3248	0.228103	1.582364	0.348727	0.465589	0.045413	0	47	20	49	48	50	37	74	55	75	47
ENSMUSG00000003099	chr7	Ppp5c	17004640	17005171	3136	-0.14692	5.979846	0.348923	0.465804	0.028403	0	905	623	1327	1218	1317	913	1372	922	1435	880
ENSMUSG00000079511	chr6	Ccdc142	83101617	83102638	3763	0.154157	5.76575	0.349034	0.465905	0.030722	0	846	686	863	762	856	863	1307	873	1330	892

ENSMUSG00000024969	chr19	Mark2	7275396	7277450	7942	-0.13605	5.090242	0.349364	0.466252	0.023126	0	503	324	802	604	685	476	683	561	762	492
ENSMUSG00000038279	chr6	Nop2	1.25E+08	1.25E+08	2623	0.138827	4.3747	0.349363	0.466252	0.023244	0	269	211	421	344	344	300	449	431	439	352
ENSMUSG00000019518	chr5	Ap4m1	1.38E+08	1.38E+08	3640	-0.22033	1.96309	0.349674	0.466619	0.043583	0	51	30	94	69	95	59	75	64	75	47
ENSMUSG00000000441	chr6	Raf1	1.16E+08	1.16E+08	6363	-0.13805	7.344696	0.349776	0.466661	0.025742	0	2343	1777	3891	2774	3103	2237	3612	2484	3761	2243
ENSMUSG00000001380	chr18	Hars	36766530	36766953	1987	0.135344	5.188337	0.349774	0.466661	0.022851	0	442	446	678	565	638	543	835	645	918	570
ENSMUSG00000037149	chr12	Ddx1	13219308	13219628	2507	-0.14439	7.215283	0.350117	0.467069	0.028268	0	2129	2120	3404	2230	2563	2176	3247	2185	3241	2136
ENSMUSG00000022808	chr16	Snx4	33251456	33251601	2442	0.137333	4.20098	0.350468	0.467349	0.022635	0	199	186	406	299	339	249	458	324	418	318
ENSMUSG00000023153	chr4	Tmem52	1.55E+08	1.55E+08	1157	0.165927	6.107833	0.350436	0.467349	0.037173	0	684	578	1437	1278	1407	1011	1583	1305	1356	1350
ENSMUSG00000040459	chr8	Arglu1	8666577	8667416	1711	0.14431	5.37345	0.350412	0.467349	0.026551	0	570	554	832	482	687	634	954	736	998	668
ENSMUSG00000078153	chr11	Psme2b	48945354	48946190	837	0.206904	1.456082	0.350383	0.467349	0.033364	0	37	27	60	36	38	43	65	50	63	38
ENSMUSG00000073176	chrX	Zfp449	56346400	56346439	3738	-0.21712	1.900756	0.350538	0.467395	0.045678	0	50	47	85	52	83	31	79	74	66	59
ENSMUSG00000028849	chr4	Map7d1	1.26E+08	1.26E+08	3652	0.148294	8.13836	0.35099	0.467952	0.030099	0	4107	2503	6023	4171	5049	4068	5543	4924	7258	5288
ENSMUSG00000034263	chr9	Vwa9	64960832	64960938	3208	-0.13061	4.253707	0.351344	0.468377	0.020106	0	272	222	436	311	367	270	433	312	374	274
ENSMUSG00000005125	chr15	Ndrg1	66929321	66931108	6593	0.146533	4.851982	0.351412	0.46842	0.027298	0	322	292	531	538	526	447	719	571	611	428
ENSMUSG00000019590	chr11	Cyb561	1.06E+08	1.06E+08	3653	0.209508	2.823221	0.351623	0.468654	0.051692	0	61	87	159	100	120	132	176	162	141	72
ENSMUSG00000028029	chr3	Aimp1	1.33E+08	1.33E+08	1122	0.165047	6.535201	0.351697	0.468706	0.036551	0	1353	1327	1539	1164	1398	1562	2326	1566	2235	1343
ENSMUSG00000024604	chr18	Rbm22	60560736	60560879	5338	0.137798	4.005766	0.351829	0.468835	0.021399	0	210	175	327	243	272	211	411	294	376	257
ENSMUSG00000028322	chr4	Exosc3	45316613	45317028	1324	0.175215	3.186141	0.352099	0.469147	0.032169	0	118	125	146	127	147	152	227	153	192	147
ENSMUSG00000054408	chr8	Spcs3	54520433	54523395	3466	0.135189	5.677568	0.35224	0.469287	0.023939	0	681	563	1171	684	865	778	1410	822	1142	799
ENSMUSG00000099112	chr15	Gm27406	1.02E+08	1.02E+08	182	-0.16132	3.951691	0.352845	0.470046	0.030754	0	214	125	411	265	343	197	379	255	297	215
ENSMUSG00000030588	chr7	Yif1b	29238329	29238436	1378	0.152768	4.614975	0.353113	0.470356	0.029697	0	320	215	439	463	431	346	538	390	636	454
ENSMUSG00000024383	chr18	Map3k2	32163089	32163550	10791	-0.17979	3.140261	0.353265	0.470417	0.035726	0	109	105	256	121	176	115	164	187	149	126
ENSMUSG00000026694	chr1	Mettl13	1.63E+08	1.63E+08	9740	0.153054	3.623851	0.353228	0.470417	0.026026	0	150	152	273	162	198	153	290	239	310	200
ENSMUSG00000034126	chr12	Pomt2	87106866	87109293	5059	-0.15675	3.217276	0.353241	0.470417	0.025159	0	126	109	247	132	182	128	183	167	181	135
ENSMUSG00000004748	chr11	Mtfp1	4091480	4092299	1738	-0.22488	5.877346	0.353387	0.470485	0.069013	0	643	478	924	1606	1510	709	1328	701	1442	880
ENSMUSG00000009076	chr11	Zmat5	4704678	4704721	1248	0.157291	4.298732	0.353372	0.470485	0.029662	0	308	237	320	289	297	323	464	301	497	314
ENSMUSG00000026918	chr2	Brd3	27445579	27448580	7336	-0.14261	4.904912	0.35364	0.470772	0.025727	0	385	299	728	501	680	349	614	557	621	469
ENSMUSG00000044145	chr2	1810024B03Rik	1.27E+08	1.27E+08	3550	0.35229	0.524816	0.353673	0.470772	0.087735	0	18	24	20	12	16	30	33	19	40	15
ENSMUSG00000009035	chr15	Tmem184b	79360684	79362885	3434	0.138489	4.800983	0.353912	0.471043	0.024646	0	345	289	631	406	492	384	531	597	659	483
ENSMUSG00000031523	chr8	Dlc1	36567751	36570403	14694	-0.16065	4.593622	0.354041	0.471166	0.032947	0	351	292	570	362	486	303	428	576	413	336
ENSMUSG00000058444	chr9	Map2k5	63163769	63164190	2309	-0.13496	4.281504	0.354191	0.471318	0.02181	0	291	214	463	313	367	263	356	304	453	313
ENSMUSG00000033016	chr18	Nfatc1	80606205	80608025	7433	-0.13836	5.374664	0.354498	0.471633	0.025001	0	586	408	1058	679	855	502	951	606	912	678
ENSMUSG00000044037	chr9	Als2cl	1.11E+08	1.11E+08	5848	-0.2329	2.274238	0.354467	0.471633	0.058328	0	66	32	119	87	124	55	118	95	75	58
ENSMUSG00000021819	chr14	Zswim8	20707552	20708056	6072	-0.14886	4.840687	0.354754	0.471856	0.028076	0	373	267	809	481	582	328	590	518	587	466
ENSMUSG00000035235	chr14	Trim13	61598226	61598346	1699	-0.19466	3.157272	0.354714	0.471856	0.04906	0	131	152	176	121	157	90	189	105	230	154
ENSMUSG00000048040	chrX	Arxes2	1.36E+08	1.36E+08	1532	0.734817	1.114608	0.354772	0.471856	0.666712	0	48	37	10	8	3	20	6	152	28	23
ENSMUSG00000020263	chr10	Appl2	83600033	83601041	5949	-0.14031	4.131669	0.355064	0.472196	0.023804	0	258	198	436	257	345	218	444	267	329	274
ENSMUSG00000020088	chr10	Sar1a	61680310	61680413	2611	-0.13459	7.224866	0.35529	0.472449	0.025026	0	2267	1775	3463	2448	2680	2087	3271	2394	3348	2066
ENSMUSG00000024785	chr19	Rcl1	29101375	29101640	1803	0.179283	2.946519	0.355502	0.472623	0.037735	0	102	67	151	111	151	105	191	184	133	123
ENSMUSG00000038717	chr9	Atp5l	44913250	44913466	511	0.1867	8.279785	0.355508	0.472623	0.048597	0	4344	3250	4277	5835	5119	5267	9066	4046	8274	4316
ENSMUSG00000049044	chr2	Rapgef4	71981240	71981351	6677	-0.45746	0.249243	0.355528	0.472623	0.224654	0	2	14	18	32	36	8	35	10	10	21
ENSMUSG00000031134	chrX	Rbmx	57383530	57384561	4330	-0.14448	3.906577	0.355677	0.472645	0.025431	0	176	213	335	266	264	205	334	235	297	227
ENSMUSG00000038902	chr3	Pogz	94837567	94837740	9218	-0.13714	4.234611	0.355687	0.472645	0.022252	0	267	192	482	289	388	233	387	329	382	304
ENSMUSG00000048439	chr5	Nupl2	24164963	24165203	3768	-0.17206	2.644925	0.35566	0.472645	0.032245	0	91	82	140	90	122	77	122	82	153	100
ENSMUSG00000051396	chr2	Hspa14	3488850	3489069	8083	0.148378	3.801274	0.355606	0.472645	0.025219	0	183	163	306	202	203	198	379	232	302	232
ENSMUSG00000020218	chr10	Wif1	1.21E+08	1.21E+08	2427	-0.37565	1.099958	0.355961	0.472914	0.156076	0	11	25	70	44	44	24	47	48	10	29
ENSMUSG00000029782	chr6	Tmem209	30479053	30481137	8130	-0.15005	3.717171	0.35595	0.472914	0.026818	0	194	168	340	196	214	151	268	230	265	220
ENSMUSG00000003531	chr16	Dgcr6	18052860	18053121	2985	0.163996	5.00607	0.356038	0.47297	0.034917	0	439	429	491	484	512	575	617	563	878	463
ENSMUSG00000042082	chr13	Arsb	93771679	93772092	3989	0.193858	3.120275	0.356114	0.472976	0.047968	0	94	59	217	124	183	124	173	197	155	174
ENSMUSG00000071001	chr4	Hrct1	43727188	43728639	1452	0.301903	1.162634	0.35608	0.472976	0.084224	0	37	22	32	31	27	23	42	38	90	29
ENSMUSG00000074272	chr7	Ceacam1	25461702	25463900	3736	-0.24249	1.874528	0.356292	0.473165	0.062145	0	40	34	76	64	105	39	104	48	58	54
ENSMUSG00000091971	chr17	Hspa1a	34969190	34972156	2967	0.362815	1.834762	0.35633	0.473169	0.163085	0	16	25	28	52	130	50	66	65	90	80
ENSMUSG00000057982	chr9	Zfp809	22225714	22225832	1325	-0.24266	1.10931	0.35639	0.4732	0.053654	0	19	35	47	33	45	26	51	33	31	31
ENSMUSG00000030888	chr7	Rrp8	1.06E+08	1.06E+08	3072	0.134443	3.996163	0.356835	0.473743	0.022269	0	189	159	377	226	294	268	338	288	375	246
ENSMUSG00000020952	chr12	Scfd1	51377580	51377636	2091	-0.16642	3.989088	0.357471	0.474482	0.035458	0	243	229	320	226	305	220	410	254	223	249
ENSMUSG00000046275	chr11	Tusc5	76679808	76680537	3302	-0.5088	2.98728	0.357491	0.474482	0.351299	0	252	196	101	50	54	89	46	299	68	66
ENSMUSG00000049969	chr4	Plekhf2	10988662	10991354	3039	0.138083	3.735597	0.357498	0.474482	0.022522	0	154	140	281	195	257	217	314	213	296	226
ENSMUSG00000068039	chr17	Tcp1	12915701	12915871	5030	0.143266	7.510552	0.357578	0.47454	0.028589	0	2406	2362	3642	2594	2753	2675	4335	3149	4509	2992
ENSMUSG00000001741	chr7	Il16	83642848	83644076	7842	0.217348	2.128706	0.357774	0.474753	0.057791	0	48	36	94	49	101	73	70	106	79	80
ENSMUSG00000027544	chr2	Nfatc2	1.68E+08	1.68E+08	10578	0.215371	3.55739	0.357848	0.474756	0.061524	0	116	79	287	202	227	136	258	145	332	284
ENSMUSG00000031871	chr8	Cdh5	1.04E+08	1.04E+08	3986	-0.17792	5.676113	0.357825	0.474756	0.043335	0	569	416	1087	1142	1290	564	1104	882	1167	738
ENSMUSG00000086596	chr9	Susd5	1.14E+08	1.14E+08	3874	0.33138	0.519344	0.357984	0.474889	0.107244	0	10	9	31	22	25	8	34	18	35	40
ENSMUSG00000030598	chr7	Fbxo17	28716804	28717038	2497	-0.2013	2.610702	0.358062	0.474946	0.048159	0	94	88	148	69	118	85	106	88	174	67
ENSMUSG00000022664	chr16	Slc35a5	45139573	45142212	8105	0.193116	2.279654	0.358264	0.475118	0.041588	0	44	41	126	63	98	69	123	96	100	77
ENSMUSG00000033047	chr15	Eif3l	79075223	79075292	1893	0.129442	5.741128	0.358263	0.475118	0.022415	0	707	593	1091	844	869	799	1138	1012	1332	843

ENSMUSG00000003813	chr8	Rad23a	84834019	84834324	2577	0.139333	7.103154	0.358404	0.475256	0.026978	0	1782	1658	2622	2213	2132	1964	3274	2434	3308	2302
ENSMUSG00000070044	chr8	Fam149a	45336717	45339372	5954	0.23531	1.387069	0.358502	0.475338	0.062928	0	25	14	48	44	60	41	59	50	44	50
ENSMUSG00000072915	chr11	Gm12258	58847158	58847259	4429	-0.29667	0.148248	0.358542	0.475344	0.061874	0	18	11	23	17	20	6	18	18	19	21
ENSMUSG00000028248	chr4	Pnisr	21847583	21848139	10187	0.143664	5.036457	0.358773	0.475603	0.027162	0	450	398	754	349	569	478	810	609	708	548
ENSMUSG00000033170	chr15	Card10	78775138	78776830	4952	-0.18093	3.246672	0.358957	0.47571	0.036417	0	140	74	274	151	198	123	182	171	172	152
ENSMUSG00000057842	chr13	Zfp595	67312998	67314909	5430	-0.25811	0.767751	0.358893	0.47571	0.050146	0	22	24	44	21	30	13	32	30	34	25
ENSMUSG00000071567	chr14	A830039N20Rik	23292291	23293643	1353	-0.19604	2.463914	0.358962	0.47571	0.041971	0	100	61	115	87	100	88	95	66	136	77
ENSMUSG00000034648	chr6	Lrrn1	1.08E+08	1.08E+08	3756	-0.47425	2.806975	0.359038	0.475763	0.299621	0	25	26	75	320	218	59	117	51	150	151
ENSMUSG00000097882	chr8	0610038B21Rik	77517056	77518579	3071	-0.2905	0.355337	0.359691	0.476582	0.060925	0	14	11	29	21	31	8	19	21	29	20
ENSMUSG00000022529	chr16	Zfp263	3744093	3744767	4521	0.146793	3.303136	0.359885	0.476791	0.024184	0	133	102	214	134	170	162	234	178	201	160
ENSMUSG00000040767	chr11	Snrnp25	32205415	32205663	1041	0.206401	2.885324	0.359949	0.476829	0.047415	0	104	102	99	95	125	141	186	113	177	99
ENSMUSG00000071343	chr10	Gm10327	33808497	33809498	1002	0.355879	-0.13968	0.360043	0.476905	0.097413	0	15	4	16	12	9	13	13	21	28	7
ENSMUSG00000025439	chr7	Clns1a	97696634	97696869	1515	0.141325	5.084313	0.360301	0.477199	0.025912	0	464	462	627	438	547	524	808	610	770	543
ENSMUSG00000034321	chr19	Exosc1	41922980	41924088	1622	-0.1564	3.320032	0.360648	0.477611	0.029614	0	163	127	246	152	149	143	212	165	216	125
ENSMUSG00000063383	chr17	Zfp947	22144359	22146534	2872	-0.38015	0.144202	0.360925	0.47793	0.143612	0	17	20	23	4	26	4	20	23	16	17
ENSMUSG00000022148	chr15	Fyb	6579871	6581046	5186	0.195437	2.929382	0.361146	0.478175	0.047335	0	73	69	120	135	173	146	192	116	177	104
ENSMUSG00000019179	chr5	Mdh2	1.36E+08	1.36E+08	2089	-0.19615	9.633467	0.361375	0.478405	0.055189	0	9921	6420	14220	19695	19162	10153	17474	10601	19961	10989
ENSMUSG00000026999	chr2	Nup35	80617236	80617284	3366	-0.16159	3.171039	0.361392	0.478405	0.030832	0	147	120	197	126	161	120	223	127	160	142
ENSMUSG00000021904	chr14	Sema3g	31217860	31218025	4538	0.146417	3.953367	0.361449	0.478433	0.026684	0	143	178	331	261	277	229	341	277	371	264
ENSMUSG00000011148	chr12	Adssl1	1.13E+08	1.13E+08	1861	-0.144	9.861127	0.361889	0.478968	0.029828	0	13053	9666	20912	17929	17947	12117	18870	13497	21851	15113
ENSMUSG00000032285	chr9	Dnaja4	54698873	54699413	3589	-0.22876	6.309081	0.361978	0.479038	0.074312	0	855	606	1268	2244	2020	859	1731	1070	1669	1409
ENSMUSG00000005514	chr5	Por	1.36E+08	1.36E+08	4021	0.187042	4.920406	0.362143	0.479209	0.047855	0	435	353	547	437	465	396	499	898	606	495
ENSMUSG00000041840	chr18	Haus1	77757567	77757753	1004	0.168487	3.32222	0.362384	0.47948	0.032922	0	151	119	194	139	136	181	237	150	223	163
ENSMUSG00000027478	chr2	Dnmt3b	1.54E+08	1.54E+08	5106	0.286866	0.09628	0.362465	0.479539	0.073525	0	7	5	26	15	19	19	28	16	15	17
ENSMUSG00000003421	chr7	Nosip	45062429	45062531	2920	0.133615	4.91118	0.362683	0.479684	0.023181	0	421	339	542	461	518	466	657	491	750	513
ENSMUSG00000029128	chr5	Rab28	41624976	41625862	1636	-0.13251	6.453691	0.362665	0.479684	0.02471	0	1350	953	1870	1524	1700	1138	1982	1431	1855	1306
ENSMUSG00000029547	chr5	Ints1	1.4E+08	1.4E+08	7113	-0.15509	5.323748	0.362615	0.479684	0.032602	0	473	369	1074	685	934	462	710	705	929	665
ENSMUSG00000021831	chr14	Ero1l	45283092	45286088	4413	-0.1844	2.388663	0.363147	0.480201	0.03555	0	69	52	121	90	116	52	109	95	105	82
ENSMUSG00000031917	chr8	Nip7	1.07E+08	1.07E+08	3031	0.155143	3.64034	0.363134	0.480201	0.027893	0	183	154	225	163	202	208	323	206	265	192
ENSMUSG00000023330	chr2	Dtwd1	1.26E+08	1.26E+08	1350	0.189548	2.147627	0.363257	0.480299	0.034436	0	60	47	86	54	79	67	108	64	122	66
ENSMUSG00000025035	chr19	Arl3	46531109	46531386	822	0.143084	5.91527	0.363707	0.480845	0.028316	0	852	763	1122	826	971	1008	1526	939	1343	984
ENSMUSG00000002279	chr17	Lmf1	25579174	25579379	13471	0.193936	3.335373	0.364154	0.481344	0.049623	0	92	78	174	214	206	155	188	210	260	160
ENSMUSG00000006057	chr11	Atp5g1	96068852	96073218	4912	-0.22484	8.482794	0.36419	0.481344	0.073206	0	4019	2745	5855	10085	8809	4467	7827	4446	9469	4776
ENSMUSG00000020610	chr11	Amz2	1.09E+08	1.09E+08	5584	-0.13866	6.52125	0.364193	0.481344	0.027436	0	1374	1290	1909	1487	1551	1367	1977	1430	1945	1298
ENSMUSG00000031111	chrX	Igsf1	49782536	49782952	5768	0.309975	0.564661	0.36452	0.481729	0.100077	0	12	9	22	33	23	28	41	31	15	21
ENSMUSG00000078440	chr10	Dohh	81384428	81384578	3202	0.135238	5.415465	0.364579	0.481758	0.024756	0	584	507	775	619	748	632	859	723	1131	745
ENSMUSG00000019779	chr10	Frk	34483400	34484369	4799	0.27348	0.123346	0.364701	0.481872	0.055849	0	9	6	24	15	19	17	27	17	17	19
ENSMUSG00000028857	chr4	Tmem222	1.33E+08	1.33E+08	2003	0.152621	4.726151	0.364772	0.481895	0.030542	0	427	319	462	369	384	462	586	445	663	388
ENSMUSG00000052783	chr5	Grk4	34660379	34661004	4830	0.335965	0.466876	0.364791	0.481895	0.109969	0	8	9	29	28	18	8	48	27	25	24
ENSMUSG00000036977	chr8	Anapc10	79711820	79711844	2802	-0.19855	1.942462	0.365141	0.482309	0.040908	0	60	50	90	58	63	47	101	52	63	58
ENSMUSG00000039164	chr2	Naif1	32450457	32452949	4650	0.18413	2.207382	0.365232	0.482382	0.037529	0	47	39	118	76	70	68	104	82	109	77
ENSMUSG00000004268	chr6	Emg1	1.25E+08	1.25E+08	1404	0.143584	5.746317	0.365274	0.482389	0.028375	0	775	695	918	751	860	873	1368	915	1256	778
ENSMUSG00000029062	chr4	Cdk11b	1.56E+08	1.56E+08	3752	0.127565	5.886734	0.365659	0.48285	0.022604	0	719	673	1205	886	1084	840	1347	1046	1483	975
ENSMUSG00000025133	chr7	Ints4	97480956	97481150	3243	-0.13198	4.789416	0.366058	0.483254	0.022929	0	356	332	752	448	475	398	557	443	604	408
ENSMUSG00000030583	chr7	Sipa1l3	29320372	29322287	16555	-0.20895	2.301588	0.366075	0.483254	0.045752	0	50	51	132	94	102	63	79	93	84	84
ENSMUSG00000040811	chr7	Eml2	19176421	19176761	3540	0.143238	4.125397	0.366012	0.483254	0.025487	0	260	209	372	202	280	265	381	302	445	281
ENSMUSG00000024480	chr18	Ap3s1	46741917	46742081	1479	0.198421	3.53121	0.366123	0.483269	0.050541	0	158	160	231	123	173	185	180	304	270	166
ENSMUSG00000037788	chr6	Vopp1	57727807	57730230	9661	0.280516	2.766568	0.366252	0.483391	0.103516	0	41	46	81	172	153	93	198	149	150	92
ENSMUSG00000004070	chr16	Hmox2	4726361	4726471	2217	0.1389	5.341979	0.3664	0.483538	0.026069	0	503	539	755	629	619	632	985	706	991	601
ENSMUSG00000024082	chr17	Ndufaf7	78937135	78937201	2303	-0.13477	4.291865	0.366638	0.483788	0.024052	0	300	255	363	316	385	290	408	292	441	276
ENSMUSG00000046573	chr13	Lyrm4	35978797	35979907	1515	-0.17674	2.577621	0.366662	0.483788	0.037922	0	90	88	103	100	108	84	128	81	138	78
ENSMUSG00000054728	chr13	Phactr1	42680623	42680926	9611	0.206945	1.236603	0.366721	0.483818	0.036143	0	25	22	50	34	39	28	56	39	53	45
ENSMUSG00000028167	chr3	Bdh2	1.35E+08	1.35E+08	1202	0.243577	0.769631	0.366807	0.483883	0.044912	0	19	18	41	17	24	24	32	33	38	30
ENSMUSG00000062081	chr14	Gm6055	48079375	48079752	378	-0.19615	2.284607	0.366846	0.483887	0.044751	0	69	74	110	76	76	72	129	63	80	65
ENSMUSG00000019861	chr10	Gopc	52337024	52339853	4317	-0.14335	3.958782	0.366897	0.483906	0.025426	0	236	174	392	199	329	201	348	262	285	248
ENSMUSG00000024871	chr19	Doc2g	4003321	4003401	3027	0.37613	-0.20799	0.367235	0.484264	0.116257	0	5	6	9	23	9	16	14	19	19	9
ENSMUSG00000071451	chr13	Psmg4	34162964	34163249	554	0.184894	2.64317	0.367242	0.484264	0.035819	0	77	80	93	94	109	97	159	96	151	99
ENSMUSG00000005682	chr10	Pan2	1.28E+08	1.28E+08	4450	0.170038	2.977763	0.367602	0.484691	0.037152	0	109	60	202	90	150	108	186	146	168	145
ENSMUSG00000020818	chr11	Mfsd11	1.17E+08	1.17E+08	7076	0.130183	4.543097	0.36806	0.485246	0.021851	0	333	252	463	316	423	350	497	434	606	348
ENSMUSG00000035495	chr4	Tstd2	46114746	46117083	5570	-0.15064	3.721633	0.368538	0.485829	0.028021	0	162	151	371	233	217	161	247	229	298	205
ENSMUSG00000090622	chr10	A930033H14Rik	69209762	69212384	2969	-0.31756	0.422987	0.368888	0.486241	0.112666	0	17	29	18	22	19	15	27	32	20	8
ENSMUSG00000028445	chr4	Enho	41638144	41639001	1269	-0.20089	4.523117	0.369065	0.486426	0.057059	0	437	366	470	232	407	415	318	327	524	330
ENSMUSG00000050608	chr4	Minos1	1.39E+08	1.39E+08	2766	0.155042	6.74197	0.369371	0.486781	0.03485	0	1508	1265	1660	1812	1693	1627	3029	1617	2611	1619
ENSMUSG00000034278	chr2	Dnajc17	1.19E+08	1.19E+08	1308	0.185012	2.43979	0.369495	0.486897	0.035426	0	73	69	107	65	83	99	121	94	126	76
ENSMUSG00000074884	chr2	Serf2	1.21E+08	1.21E+08	5455	0.154267	7.978987	0.369605	0.486993	0.035055	0	3921	3194	3993	3460	4063	4308	6103	3865	6122	4016

ENSMUSG00000039536	chr2	Stau1	1.67E+08	1.67E+08	6065	0.124607	5.400508	0.369795	0.487195	0.021657	0	515	435	920	644	782	623	918	722	1099	690
ENSMUSG00000071856	chr18	Mcc	44425061	44430067	8426	-0.2223	1.717854	0.369977	0.487387	0.047181	0	40	33	72	57	79	35	58	54	55	64
ENSMUSG00000024747	chr19	Aldh1a7	20692953	20693535	2066	0.523801	1.409674	0.370104	0.487505	0.360632	0	73	29	32	13	8	60	29	122	28	24
ENSMUSG00000058447	chr7	Gm26920	30056034	30057519	2374	-0.20901	1.267548	0.370422	0.487875	0.043829	0	36	31	57	42	32	25	45	36	60	32
ENSMUSG00000093071	chr4	Gm25951	1.41E+08	1.41E+08	64	0.300512	0.001449	0.370589	0.488047	0.079615	0	12	4	20	6	24	13	20	16	27	14
ENSMUSG00000058454	chr7	Dhcr7	1.44E+08	1.44E+08	3784	0.160572	3.089988	0.371006	0.488548	0.032656	0	104	78	164	123	180	116	156	173	198	163
ENSMUSG00000039929	chr16	Urb1	90751527	90752178	8190	-0.17514	2.445934	0.371124	0.488654	0.033792	0	90	59	143	80	90	71	122	90	117	65
ENSMUSG00000071291	chr13	Zfp58	67490167	67492150	2435	-0.21589	1.789357	0.371202	0.488708	0.047921	0	67	41	82	44	55	48	67	66	53	47
ENSMUSG00000054715	chr7	Zscan22	12897815	12897943	3501	0.19245	1.71735	0.371637	0.489232	0.038013	0	41	23	66	53	60	53	69	63	69	54
ENSMUSG00000040855	chrX	Reps2	1.62E+08	1.62E+08	8296	-0.22524	1.92152	0.371705	0.489273	0.052622	0	48	45	118	51	67	44	49	73	78	63
ENSMUSG00000100954	chr1	Gm10138	1.51E+08	1.51E+08	2843	-0.33315	-0.02872	0.371757	0.489294	0.063715	0	15	7	26	13	19	7	14	18	15	16
ENSMUSG00000024498	chr18	Tcerg1	42511510	42511585	4246	-0.12915	4.701797	0.371953	0.489477	0.022875	0	368	326	649	366	495	341	630	403	570	357
ENSMUSG00000071645	chr19	Tut1	8953850	8954021	2747	0.147756	3.395421	0.37197	0.489477	0.025707	0	160	109	205	148	171	170	227	185	230	183
ENSMUSG00000042502	chr7	Cd2bp2	1.27E+08	1.27E+08	3379	0.128053	5.330886	0.372176	0.489699	0.022801	0	595	424	762	609	685	636	869	744	988	610
ENSMUSG00000029030	chr4	Tprgl	1.54E+08	1.54E+08	2242	0.137274	6.847398	0.372289	0.489799	0.027649	0	1692	1354	2400	1589	1723	1822	2735	1986	2921	1678
ENSMUSG00000023912	chr17	Slc25a27	43641900	43643676	2687	0.164247	2.858061	0.372443	0.489841	0.03172	0	86	66	169	106	128	120	186	139	161	90
ENSMUSG00000026087	chr1	Mrpl30	37890477	37890584	3226	-0.15005	6.401635	0.372394	0.489841	0.033377	0	1334	1099	1568	1592	1397	1208	2113	1197	1799	1118
ENSMUSG00000028675	chr4	Pnrc2	1.36E+08	1.36E+08	2213	-0.13126	5.004435	0.372468	0.489841	0.024095	0	416	408	705	544	626	379	738	518	629	546
ENSMUSG00000043510	chr5	Hscb	1.11E+08	1.11E+08	905	-0.16563	2.631295	0.372386	0.489841	0.031656	0	88	82	110	113	118	84	134	97	128	85
ENSMUSG00000041966	chr2	Dcaf17	71055328	71055496	9806	-0.19121	2.203953	0.372781	0.490204	0.039391	0	52	52	120	74	98	59	120	74	87	51
ENSMUSG00000004771	chr9	Rab11a	64715299	64716988	2992	0.13188	5.753561	0.37295	0.490288	0.024771	0	712	668	1195	694	870	718	1243	994	1332	913
ENSMUSG00000015290	chrX	Ubl4	74365718	74367586	3142	-0.12961	6.401928	0.37296	0.490288	0.02466	0	1237	1003	1909	1403	1577	1228	1859	1232	1920	1206
ENSMUSG00000018405	chr11	Mrm1	84813061	84814511	2868	-0.19883	2.885876	0.372993	0.490288	0.049214	0	109	64	112	143	203	107	151	117	146	100
ENSMUSG00000097994	chr6	Gm26982	1.14E+08	1.14E+08	1151	0.276953	0.701064	0.372901	0.490288	0.054474	0	18	18	31	20	23	20	27	36	50	20
ENSMUSG00000024352	chr18	Spata24	35656690	35656844	967	-0.29239	1.026732	0.373072	0.490343	0.104067	0	41	37	34	21	31	33	32	18	59	20
ENSMUSG00000024740	chr19	Ddb1	10605625	10605766	4155	0.131262	7.870066	0.373318	0.490618	0.025807	0	3269	2218	5268	3473	4045	3508	5153	3977	5908	3942
ENSMUSG00000045999	chr17	AY036118	39847526	39848829	1304	0.936201	2.81249	0.373446	0.490738	1.219341	0	1	0	223	191	17	5	5	69	449	312
ENSMUSG00000034751	chr13	Mast4	1.03E+08	1.03E+08	32204	-0.19234	5.839541	0.373674	0.490988	0.054442	0	916	488	2151	603	1084	706	1096	857	1457	836
ENSMUSG00000061589	chr10	Dot1l	80755206	80755524	8705	0.162581	4.585141	0.37383	0.491145	0.038478	0	227	174	574	397	537	328	615	420	508	448
ENSMUSG00000043673	chr12	Kcns3	11090202	11092755	3059	-0.50863	-0.34149	0.37411	0.491465	0.272531	0	20	17	11	4	9	1	10	23	6	12
ENSMUSG00000024146	chr17	Cript	87025550	87025675	1712	-0.14887	5.264585	0.374154	0.491474	0.032431	0	624	605	756	540	620	552	880	590	718	587
ENSMUSG00000005373	chr5	Mlxipl	1.35E+08	1.35E+08	5367	-0.1582	5.51737	0.37442	0.491774	0.0362	0	615	371	1184	813	1059	470	1067	847	882	731
ENSMUSG00000062960	chr5	Kdr	75932827	75934618	7278	-0.21798	4.961965	0.374888	0.49234	0.069706	0	350	215	612	762	843	248	728	605	637	468
ENSMUSG00000006418	chr2	Rnf114	1.67E+08	1.67E+08	3356	-0.16718	5.805698	0.375007	0.492447	0.041191	0	745	431	1130	1279	1278	747	1232	833	1323	754
ENSMUSG00000045886	chr10	Gm9803	43524102	43524617	516	0.24428	2.055099	0.375176	0.49262	0.064367	0	68	51	57	63	47	81	119	61	91	52
ENSMUSG00000038214	chr10	Bend3	43479140	43479372	6028	-0.16992	2.688938	0.375215	0.492623	0.034725	0	93	76	163	106	108	60	140	109	149	98
ENSMUSG00000010057	chr9	Nprl2	1.08E+08	1.08E+08	2013	0.157017	3.520567	0.375333	0.492729	0.029036	0	150	149	216	164	174	148	283	217	305	164
ENSMUSG00000040048	chr17	Ndufb10	24722060	24722520	1217	0.183701	7.937579	0.375675	0.49313	0.05119	0	2806	1955	3423	5426	4891	3653	6073	3885	6709	3924
ENSMUSG00000012114	chr16	Med15	17651221	17652263	3383	0.130905	4.154413	0.375904	0.493381	0.02348	0	220	148	409	285	337	273	405	325	418	279
ENSMUSG00000005262	chr16	Ufd1l	18811779	18811883	4336	0.140529	5.71197	0.376088	0.493572	0.028446	0	781	674	1041	644	805	825	1287	896	1326	747
ENSMUSG00000018666	chr11	Cbx1	96789127	96789353	4273	-0.12934	5.075605	0.376124	0.493572	0.023902	0	485	457	763	451	671	472	786	505	687	506
ENSMUSG00000038141	chr17	Tmem181a	6270475	6270590	1869	0.214561	1.480959	0.376551	0.494083	0.046009	0	35	19	49	47	52	42	57	60	51	50
ENSMUSG00000042165	chr3	Gm9774	92428032	92429423	1392	0.193012	2.897947	0.376618	0.494122	0.043834	0	102	94	161	96	94	98	149	131	243	110
ENSMUSG00000003135	chr1	Cnot11	39534992	39535047	3508	-0.12585	4.962469	0.376773	0.494276	0.022552	0	464	417	733	440	553	407	712	510	638	471
ENSMUSG00000060475	chr17	Wtap	12966796	12968051	5651	-0.13098	4.469223	0.376888	0.494379	0.023649	0	365	244	508	344	403	305	552	352	439	299
ENSMUSG00000032333	chr9	Stoml1	58253164	58253399	1987	0.144563	3.624717	0.377002	0.49448	0.025963	0	173	132	210	188	225	205	246	217	306	197
ENSMUSG00000039205	chr2	Ciz1	32352327	32352527	8604	0.129211	4.616592	0.37709	0.494547	0.022806	0	373	241	521	357	396	394	542	420	620	371
ENSMUSG00000038388	chr6	Mpp6	50110241	50110464	2843	-0.13077	5.959305	0.377206	0.49465	0.025345	0	929	805	1394	962	1118	908	1405	892	1274	962
ENSMUSG00000014748	chr6	Tex261	83768885	83771303	4088	0.129313	6.440838	0.377272	0.494687	0.024956	0	1154	867	1846	1349	1532	1323	1841	1595	2299	1303
ENSMUSG00000028164	chr3	Manba	1.35E+08	1.35E+08	6971	0.162562	2.977585	0.377389	0.494791	0.032095	0	90	90	170	121	122	124	154	179	178	112
ENSMUSG00000062591	chr17	Tubb4a	57080066	57081747	2228	0.279093	0.352065	0.377525	0.494921	0.083665	0	10	8	22	15	32	14	28	32	17	24
ENSMUSG00000034189	chr8	Hsdl1	1.2E+08	1.2E+08	3168	-0.12955	4.335675	0.37775	0.495167	0.022612	0	307	227	459	337	368	296	415	378	417	253
ENSMUSG00000021671	chr13	Poc5	96388294	96388531	3033	-0.18136	2.447352	0.377807	0.495193	0.036694	0	64	67	128	92	112	67	118	80	90	101
ENSMUSG00000027637	chr2	1110008F13Rik	1.57E+08	1.57E+08	2871	0.13393	5.53147	0.37813	0.495567	0.025696	0	655	603	815	653	738	727	1052	838	1068	738
ENSMUSG00000061477	chr12	Rps7	28630847	28631193	961	0.155572	7.23311	0.378196	0.495604	0.036702	0	2338	1993	2594	2022	2138	2567	3988	2580	3191	2229
ENSMUSG00000026687	chr1	Aldh9a1	1.67E+08	1.67E+08	3383	0.20265	2.873882	0.378382	0.495799	0.054323	0	75	74	131	120	145	125	136	207	131	95
ENSMUSG00000020056	chr10	Ccdc53	88201093	88201292	4536	0.153654	4.336338	0.378487	0.495888	0.031393	0	311	265	315	299	288	317	479	349	489	313
ENSMUSG00000043061	chr12	Tmem18	30584443	30584562	2952	-0.14982	3.432644	0.378532	0.495898	0.028647	0	149	137	246	157	222	132	257	156	195	190
ENSMUSG00000056598	chr11	Lrrc48	60353329	60353432	4519	0.26249	1.282212	0.3787	0.496069	0.078199	0	16	19	43	54	40	43	52	34	75	30
ENSMUSG00000101628	chr1	Gm28177	52077261	52077300	3532	-0.18976	3.546329	0.379007	0.496422	0.048637	0	164	128	256	193	265	147	291	204	125	210
ENSMUSG00000045639	chr7	Zfp629	1.28E+08	1.28E+08	6723	-0.18145	3.554159	0.379232	0.496668	0.044868	0	120	108	265	271	258	129	287	161	266	177
ENSMUSG00000022018	chr14	Rgcc	79288756	79289119	918	0.14353	4.718164	0.379497	0.496965	0.028606	0	400	319	453	361	433	475	626	424	621	376
ENSMUSG00000039286	chr3	Fndc3b	27416162	27419602	11485	-0.17736	3.870421	0.379599	0.49705	0.042527	0	165	156	440	215	320	150	263	304	251	267
ENSMUSG00000033128	chr15	Gga1	78877190	78877617	3034	-0.12713	5.845994	0.37982	0.49729	0.023972	0	803	658	1258	1044	1083	815	1074	936	1346	861
ENSMUSG00000093485	chr11	Gm20708	1.18E+08	1.18E+08	1780	-0.1307	4.076595	0.380107	0.497617	0.022808	0	243	213	412	222	335	233	357	249	383	253

ENSMUSG00000031391	chrX	L1cam	73853778	73855266	7347	-0.27526	1.315084	0.380194	0.497633	0.080551	0	26	12	56	60	64	29	57	36	47	30
ENSMUSG00000040029	chr6	Ipo8	1.49E+08	1.49E+08	10623	-0.14005	4.514943	0.380163	0.497633	0.026681	0	357	212	581	363	455	308	417	433	434	371
ENSMUSG00000004945	chr17	Tmem242	5410870	5411467	1837	-0.14544	5.998615	0.38027	0.497683	0.032192	0	1035	782	1117	1156	1207	854	1619	892	1336	929
ENSMUSG00000006932	chr9	Ctnnb1	1.21E+08	1.21E+08	5099	-0.12727	7.883883	0.380343	0.49771	0.024969	0	3501	2757	5769	3624	4406	2951	5271	4022	4876	3678
ENSMUSG00000038895	chr9	Zfp653	22055460	22055893	2132	0.180083	2.082955	0.380403	0.49771	0.035221	0	53	44	88	61	67	65	81	79	85	85
ENSMUSG00000058440	chr6	Nrf1	30047988	30048113	10282	0.141515	3.555649	0.380396	0.49771	0.024949	0	126	141	252	171	209	182	271	196	302	177
ENSMUSG00000014444	chr8	Piezo1	1.22E+08	1.22E+08	9933	0.213499	4.810663	0.380804	0.498185	0.068837	0	423	281	912	205	353	493	511	506	831	412
ENSMUSG00000044534	chr9	Ackr2	1.22E+08	1.22E+08	2784	-0.26266	0.770093	0.381307	0.498794	0.058706	0	27	15	47	19	36	16	26	36	34	21
ENSMUSG00000009863	chr4	Sdhb	1.41E+08	1.41E+08	2239	-0.21937	8.535947	0.381403	0.498822	0.074906	0	3978	3111	5474	10629	9207	4130	9208	4955	8166	5640
ENSMUSG00000094568	chr8	Gm1815	41657593	41658669	1077	-0.26217	0.467564	0.381374	0.498822	0.066321	0	22	16	25	24	24	24	32	10	28	13
ENSMUSG00000000184	chr6	Ccnd2	1.27E+08	1.27E+08	5701	0.201545	3.659919	0.381604	0.499035	0.058082	0	130	153	293	169	205	156	235	407	228	186
ENSMUSG00000021222	chr12	Dcaf4	83520466	83520617	2081	-0.13212	4.632578	0.381944	0.499346	0.024561	0	339	284	601	431	448	394	588	337	498	348
ENSMUSG00000027999	chr3	Pla2g12a	1.3E+08	1.3E+08	1654	-0.21027	5.370307	0.381929	0.499346	0.067569	0	476	335	667	1223	882	534	937	608	1046	469
ENSMUSG00000056228	chr8	Cars2	11514021	11514191	1846	-0.13771	4.204875	0.381954	0.499346	0.026568	0	255	205	348	318	427	230	422	256	434	281
ENSMUSG00000028988	chr4	Ctnnbip1	1.5E+08	1.5E+08	2792	0.198257	4.561594	0.382258	0.499651	0.057467	0	410	331	511	191	274	354	506	481	645	336
ENSMUSG00000038332	chr10	Sesn1	41810574	41811300	3327	0.166365	4.637111	0.382263	0.499651	0.040469	0	317	250	565	371	405	250	815	441	462	478
ENSMUSG00000028180	chr3	Zranb2	1.58E+08	1.58E+08	4301	-0.13553	5.687921	0.382631	0.500082	0.0279	0	715	775	1166	700	939	612	1041	879	1135	844
ENSMUSG00000067931	chr17	Zfp948	21567046	21567245	2612	-0.22442	1.081032	0.382835	0.5003	0.047693	0	26	24	42	46	36	20	45	38	35	32
ENSMUSG00000068854	chr3	Hist2h2be	96221119	96223738	2620	-0.18011	3.384086	0.383127	0.500632	0.045371	0	196	163	230	112	161	155	193	176	207	150
ENSMUSG00000023806	chr17	Rsph3b	6904716	6905120	1614	0.169488	3.189264	0.383854	0.501433	0.037547	0	108	80	147	179	170	151	190	142	243	149
ENSMUSG00000078185	chr1	Chml	1.76E+08	1.76E+08	6117	0.236758	1.278624	0.383822	0.501433	0.06267	0	32	27	53	24	36	34	36	67	48	40
ENSMUSG00000090266	chr11	Mettl23	1.17E+08	1.17E+08	2697	-0.14494	5.317605	0.383786	0.501433	0.032219	0	599	618	746	667	624	537	982	593	802	580
ENSMUSG00000030823	chr7	9130019O22Rik	1.27E+08	1.27E+08	3878	-0.24322	1.190227	0.384249	0.501874	0.055547	0	25	24	53	50	40	36	52	24	34	35
ENSMUSG00000055897	chr2	Ppp4r1l-ps	1.74E+08	1.74E+08	12025	0.161537	2.950159	0.384267	0.501874	0.033673	0	113	73	175	81	148	134	174	138	179	111
ENSMUSG00000056486	chr2	Chn1	73610660	73613196	5146	-0.22047	1.194968	0.384311	0.501883	0.043909	0	33	23	47	35	53	27	45	48	36	28
ENSMUSG00000027160	chr2	Ccdc34	1.1E+08	1.1E+08	6558	0.229259	1.558988	0.384421	0.501977	0.057652	0	47	31	44	34	51	65	54	55	67	35
ENSMUSG00000035105	chr12	Egln3	54178981	54180655	2662	0.43879	4.786409	0.384678	0.502263	0.29809	0	69	54	230	935	666	280	832	469	926	504
ENSMUSG00000018340	chr11	Anxa6	54979108	54979521	2930	0.125693	8.059367	0.384945	0.502562	0.024857	0	3340	2847	6113	3937	4608	4099	6018	4488	6730	4297
ENSMUSG00000081895	chr7	Rpl17-ps10	72648757	72649311	555	0.257873	2.340563	0.385091	0.502703	0.080264	0	83	76	57	62	63	96	141	76	136	54
ENSMUSG00000026814	chr2	Eng	32646595	32647024	4048	0.146756	5.05357	0.38518	0.50277	0.032848	0	352	262	731	541	743	439	728	703	819	521
ENSMUSG00000031161	chrX	Hdac6	7930120	7930537	5817	0.162772	2.940033	0.385428	0.503043	0.032041	0	91	97	159	106	120	123	163	167	177	101
ENSMUSG00000028427	chr4	Aqp7	41033074	41034459	2828	0.213387	3.129201	0.385773	0.503444	0.060468	0	164	110	109	99	132	131	201	207	214	104
ENSMUSG00000030534	chr7	Vps33b	80269649	80270079	3343	-0.20779	1.995379	0.385812	0.503446	0.050269	0	64	46	93	45	91	55	107	50	60	59
ENSMUSG00000040648	chr1	Ppip5k2	97706048	97707830	14381	0.24686	1.560892	0.386198	0.5039	0.072601	0	26	26	59	40	63	26	58	86	76	39
ENSMUSG00000047749	chr6	Zc3hav1l	38287396	38293137	6536	0.364582	-0.0099	0.386291	0.503972	0.13598	0	5	6	24	7	23	4	23	19	19	25
ENSMUSG00000021694	chr13	Ercc8	1.08E+08	1.08E+08	7657	-0.18626	2.171875	0.386499	0.504178	0.039747	0	60	67	97	68	82	69	94	78	66	65
ENSMUSG00000021707	chr13	Dhfr	92354783	92355344	5290	-0.20887	1.744176	0.386525	0.504178	0.042514	0	38	40	81	63	61	56	56	53	54	51
ENSMUSG00000048402	chr1	Gli2	1.19E+08	1.19E+08	6869	-0.29964	0.502942	0.386771	0.504449	0.065577	0	19	11	38	18	34	10	24	30	22	21
ENSMUSG00000018909	chr7	Arrb1	99535466	99535798	11175	0.14031	4.396226	0.387046	0.504675	0.029631	0	254	176	577	299	368	342	440	433	486	306
ENSMUSG00000037820	chr2	Tgm2	1.58E+08	1.58E+08	4608	0.128836	6.640869	0.387097	0.504675	0.025939	0	1320	1012	2230	1380	1858	1568	2551	1752	2440	1353
ENSMUSG00000038876	chr10	Rnf146	29344178	29347883	4454	-0.11813	5.489001	0.387068	0.504675	0.021132	0	636	566	1028	732	795	594	997	737	977	661
ENSMUSG00000059824	chr7	Dbp	45705088	45705762	2945	0.141422	7.094762	0.386992	0.504675	0.031375	0	1838	1813	2784	1879	1986	1816	2934	2489	3476	2474
ENSMUSG00000069899	chr11	Gm12166	46051354	46052311	968	0.326161	0.277656	0.3873	0.504891	0.07248	0	22	12	21	11	11	16	32	16	35	15
ENSMUSG00000002395	chr8	Use1	71366848	71367078	2203	0.143844	5.695388	0.387372	0.504909	0.031481	0	660	592	773	954	898	730	1188	853	1308	925
ENSMUSG00000027956	chr3	Tmem144	79812564	79814146	3487	0.308747	0.261314	0.38739	0.504909	0.074715	0	17	10	25	15	11	11	40	22	18	20
ENSMUSG00000025036	chr19	Sfxn2	46573365	46573459	3210	0.205433	2.013523	0.387648	0.505155	0.052389	0	41	43	111	37	72	63	91	91	72	64
ENSMUSG00000072494	chr14	Ppp1r3e	54872669	54873312	2508	-0.19617	1.678526	0.387655	0.505155	0.041051	0	61	38	64	41	60	38	75	48	64	42
ENSMUSG00000006127	chr11	Inpp5k	75630988	75631197	5728	0.12489	5.255707	0.388028	0.505492	0.022917	0	481	442	780	619	607	562	954	647	959	567
ENSMUSG00000057963	chr12	Itpk1	1.03E+08	1.03E+08	3320	0.15452	3.220677	0.387976	0.505492	0.032707	0	116	91	208	128	172	113	197	218	186	170
ENSMUSG00000081603	chrX	Gm14681	66778442	66778852	411	0.255167	0.868639	0.387992	0.505492	0.049864	0	19	26	28	27	23	26	49	31	36	29
ENSMUSG00000026639	chr1	Lamb3	1.93E+08	1.93E+08	6612	-0.31034	1.177315	0.388168	0.505625	0.113867	0	22	11	52	67	46	22	65	24	36	32
ENSMUSG00000044502	chr11	Bod1	31665181	31665867	1644	0.137617	7.445659	0.388544	0.506065	0.03002	0	2604	2126	3196	2444	2747	2797	4083	2770	4405	2769
ENSMUSG00000032437	chr9	Stt3b	1.15E+08	1.15E+08	4195	-0.12856	6.682766	0.38861	0.506102	0.026096	0	1619	1290	2501	1401	1851	1423	2159	1643	2379	1450
ENSMUSG00000030105	chr6	Arl8b	1.09E+08	1.09E+08	2928	-0.13341	7.078813	0.388711	0.506183	0.02831	0	2141	1682	3326	2057	2182	1738	3168	2029	2898	2090
ENSMUSG00000036751	chr7	Cox6b1	30616974	30617162	505	0.162149	8.484087	0.388829	0.506238	0.042183	0	4478	3478	5236	7378	6301	5566	9497	5411	9302	5427
ENSMUSG00000058239	chr7	Usf2	30945252	30946669	2647	0.149503	5.694357	0.388823	0.506238	0.034309	0	697	595	699	939	910	849	1217	976	1210	741
ENSMUSG00000039018	chr7	Mtg1	1.4E+08	1.4E+08	4019	0.142651	4.721719	0.388926	0.506314	0.029154	0	399	306	402	417	438	401	658	449	667	382
ENSMUSG00000083022	chr11	Rps15a-ps6	6172644	6173036	393	0.333459	0.340432	0.388979	0.506333	0.090288	0	15	17	17	13	18	24	47	14	20	14
ENSMUSG00000021532	chr13	Fastkd3	68582248	68582350	2362	-0.14287	3.386634	0.389313	0.506668	0.026175	0	166	104	211	181	217	151	221	168	210	151
ENSMUSG00000033852	chr2	Gm28042	1.2E+08	1.2E+08	5188	0.187265	2.022514	0.389287	0.506668	0.043687	0	55	34	77	62	72	84	76	70	77	69
ENSMUSG00000035851	chr5	Ythdc1	86804221	86804591	10352	0.118591	4.810538	0.389682	0.507098	0.020566	0	348	316	624	389	505	439	615	515	623	464
ENSMUSG00000040272	chr2	Accs	93833467	93835828	8364	0.218017	1.797427	0.389857	0.507277	0.056059	0	63	32	67	32	56	64	70	75	66	51
ENSMUSG00000003345	chr10	Csnk1g2	80622780	80622950	2511	-0.12864	6.772867	0.390248	0.507736	0.026377	0	1680	1433	2247	1805	1901	1588	2145	1721	2450	1654
ENSMUSG00000034437	chr3	Gm9761	1.17E+08	1.17E+08	342	0.312423	0.28857	0.390492	0.508004	0.085152	0	17	16	18	10	17	25	36	19	13	18
ENSMUSG00000076441	chr2	Ass1	31470207	31470339	2414	0.21922	1.403878	0.390753	0.508293	0.052771	0	21	27	46	45	51	31	61	49	50	57

ENSMUSG00000034832	chr6	Tet3	83362373	83369825	11999	-0.14455	4.243945	0.390874	0.5084	0.029835	0	190	217	527	309	407	221	392	299	433	309
ENSMUSG00000081476	chr2	Itpa-ps1	94384502	94385098	597	-0.27356	0.17787	0.391132	0.508686	0.0584	0	15	17	20	18	19	18	27	13	17	10
ENSMUSG00000022864	chr16	D16Ertd472e	78544012	78545284	2453	-0.38715	-0.19878	0.391279	0.508777	0.113149	0	4	7	22	17	22	12	22	13	7	6
ENSMUSG00000028031	chr3	Dkk2	1.32E+08	1.32E+08	3694	-0.39274	3.074493	0.391276	0.508777	0.237503	0	136	187	316	39	78	187	78	207	82	65
ENSMUSG00000023068	chr10	Nus1	52417547	52418168	4876	-0.12221	5.112874	0.39134	0.508807	0.022768	0	495	449	771	526	651	451	811	630	667	485
ENSMUSG00000021754	chr13	Map3k1	1.12E+08	1.12E+08	7447	0.196747	2.926015	0.391399	0.508826	0.055153	0	59	67	162	139	152	84	184	191	147	128
ENSMUSG00000028645	chr4	Slc2a1	1.19E+08	1.19E+08	2853	0.184163	3.129523	0.391431	0.508826	0.049769	0	84	53	180	171	189	115	192	169	218	152
ENSMUSG00000061306	chr11	Slc38a10	1.2E+08	1.2E+08	6421	-0.14683	5.724286	0.391558	0.50894	0.033709	0	611	512	1059	1154	1202	680	1036	908	1117	844
ENSMUSG00000004096	chr9	Cwc15	14500617	14500781	1111	0.151028	6.143309	0.391781	0.509181	0.035844	0	998	1037	1303	883	995	1143	1627	1156	1777	1129
ENSMUSG00000020801	chr11	Med31	72211724	72212077	1730	0.175637	2.621192	0.391869	0.509246	0.035811	0	93	72	96	73	116	83	154	110	146	99
ENSMUSG00000020019	chr10	Ntn4	93640681	93640775	3741	0.212628	3.582259	0.392009	0.509328	0.069171	0	80	83	225	266	264	144	327	190	304	222
ENSMUSG00000031605	chr8	Klhl2	64739863	64740974	3025	0.253172	3.02413	0.391979	0.509328	0.093806	0	147	97	122	86	117	118	110	284	161	109
ENSMUSG00000030706	chr7	Mrpl48	1.01E+08	1.01E+08	6119	0.134	5.865137	0.392063	0.509348	0.027776	0	841	725	1009	867	929	935	1413	929	1437	902
ENSMUSG00000049281	chr9	Scn3b	40269216	40270047	5546	0.305815	0.548882	0.392373	0.5097	0.084185	0	17	18	34	14	14	22	52	14	30	21
ENSMUSG00000034216	chr2	Vps18	1.19E+08	1.19E+08	4786	0.131951	4.111352	0.392728	0.510112	0.025172	0	202	177	379	286	293	251	320	318	428	319
ENSMUSG00000020922	chr11	Lsm12	1.02E+08	1.02E+08	2388	-0.13053	5.424308	0.392911	0.510299	0.02682	0	723	557	958	601	734	618	889	705	1025	545
ENSMUSG00000003234	chr16	Abcf3	20548577	20548745	3557	0.125913	6.073561	0.393203	0.510546	0.024937	0	950	752	1336	976	1150	1118	1579	1147	1598	1005
ENSMUSG00000037316	chr8	Bag4	25764538	25768409	4798	-0.1924	2.752051	0.393214	0.510546	0.050815	0	89	97	160	106	116	79	105	166	106	101
ENSMUSG00000089889	chr5	0610040B10Rik	1.43E+08	1.43E+08	683	0.336626	0.198068	0.393216	0.510546	0.102817	0	12	9	9	24	18	21	23	9	29	23
ENSMUSG00000017801	chr11	Mlx	1.01E+08	1.01E+08	1999	-0.13215	3.696149	0.393277	0.510574	0.024126	0	189	159	279	224	228	181	266	244	266	168
ENSMUSG00000063785	chrX	Utp14a	48256862	48256968	4130	-0.14412	3.569919	0.393402	0.510688	0.029304	0	182	160	259	167	221	185	289	193	216	144
ENSMUSG00000039485	chr10	Tspyl4	34297442	34301320	3879	-0.19823	1.476149	0.393579	0.510867	0.034808	0	37	28	59	46	63	39	57	36	54	42
ENSMUSG00000025077	chr19	Dclre1a	56529167	56529662	6384	-0.2216	1.776758	0.393701	0.510926	0.055769	0	65	29	73	47	77	42	89	50	47	53
ENSMUSG00000040247	chr19	Tbc1d10c	4184358	4185073	1758	0.259456	2.028919	0.39368	0.510926	0.08767	0	87	46	72	23	55	64	109	74	99	55
ENSMUSG00000079555	chr5	Haus3	34153921	34154106	1950	-0.1987	1.954562	0.39408	0.511367	0.049946	0	58	60	76	59	65	59	80	73	77	34
ENSMUSG00000028851	chr4	Nudc	1.34E+08	1.34E+08	1425	0.127203	5.711985	0.394184	0.511452	0.024993	0	699	675	903	779	892	809	1208	950	1199	841
ENSMUSG00000087408	chr8	Cers1	70315775	70316108	3171	0.156916	4.937577	0.394254	0.511493	0.03898	0	464	278	746	321	580	482	494	539	824	581
ENSMUSG00000098234	chr1	Snhg6	9941959	9942155	1146	-0.17588	3.185248	0.394388	0.511616	0.046047	0	154	151	150	126	156	143	197	121	209	110
ENSMUSG00000003778	chr18	Brd8	34598615	34600241	10633	-0.129	4.078919	0.394446	0.511642	0.023362	0	228	201	416	239	352	215	400	252	331	279
ENSMUSG00000025290	chr14	Rps24	24490681	24490758	840	0.170276	8.168269	0.394614	0.51181	0.04755	0	4477	4229	4600	3639	3829	5428	7546	4793	6206	3937
ENSMUSG00000033857	chr11	Engase	1.18E+08	1.18E+08	5184	0.185055	2.76315	0.394711	0.511885	0.045793	0	94	79	141	73	117	80	121	172	155	119
ENSMUSG00000083097	chr2	Gm14494	1.54E+08	1.54E+08	435	-0.21775	1.137351	0.394878	0.512052	0.0577	0	38	38	38	31	30	31	39	31	50	27
ENSMUSG00000038181	chr5	Chpf2	24586741	24588300	5371	0.147384	4.011121	0.394946	0.51209	0.031302	0	233	190	385	184	238	246	305	322	433	239
ENSMUSG00000021592	chr13	Arsk	76060422	76062602	5681	-0.19326	2.355408	0.395193	0.51236	0.044623	0	65	47	144	93	95	64	101	90	75	92
ENSMUSG00000020021	chr10	Fgd6	94036001	94036310	8241	-0.19675	2.320064	0.395468	0.512667	0.045123	0	75	42	155	67	99	57	92	87	94	85
ENSMUSG00000022438	chr15	Parvb	84232043	84232186	4416	0.189672	6.05763	0.395751	0.512983	0.059015	0	690	397	1259	1320	1539	939	1330	1015	1909	1325
ENSMUSG00000007570	chr17	Fance	28313530	28313882	3183	0.163642	3.043781	0.396109	0.513397	0.03293	0	117	102	153	119	117	120	206	119	199	148
ENSMUSG00000054381	chr7	Zfp747	1.27E+08	1.27E+08	2657	-0.22889	1.230083	0.396282	0.513514	0.050075	0	27	28	65	32	47	34	56	22	41	36
ENSMUSG00000078768	chr7	Zfp566	30077337	30078618	1728	-0.23214	1.240142	0.3963	0.513514	0.059846	0	23	45	56	26	45	30	46	32	46	36
ENSMUSG00000100594	chr1	2810414N06Rik	1.52E+08	1.52E+08	1381	-0.19635	1.460661	0.396315	0.513514	0.040659	0	34	32	56	53	53	29	51	56	57	34
ENSMUSG00000029780	chr6	Nt5c3	56882400	56883058	4250	-0.14414	5.402397	0.396642	0.513888	0.03355	0	722	558	976	623	647	620	979	529	1058	551
ENSMUSG00000035245	chr6	Eogt	97110024	97112206	4900	-0.17356	2.481714	0.396927	0.514206	0.035002	0	70	55	154	92	111	63	132	94	101	85
ENSMUSG00000035293	chr12	G2e3	51348061	51348444	7886	-0.26015	1.292266	0.397125	0.514398	0.073224	0	26	25	89	31	45	19	44	43	42	46
ENSMUSG00000038349	chr1	Plcl1	55405921	55406630	6687	-0.25972	3.270174	0.39718	0.514398	0.102807	0	92	46	186	243	313	90	213	133	206	164
ENSMUSG00000043384	chrX	Gprasp1	1.36E+08	1.36E+08	8119	-0.12789	4.530298	0.397192	0.514398	0.024407	0	300	317	581	313	439	313	489	367	452	386
ENSMUSG00000016128	chr5	Stard13	1.51E+08	1.51E+08	8044	0.165973	2.913371	0.397505	0.514739	0.039477	0	76	67	155	105	177	94	165	143	164	151
ENSMUSG00000037890	chr5	Wdr19	65199696	65199760	4403	0.23584	0.932118	0.397532	0.514739	0.054575	0	20	21	36	18	39	37	33	26	44	35
ENSMUSG00000030216	chr6	Wbp11	1.37E+08	1.37E+08	5029	-0.13327	5.141359	0.397933	0.515207	0.027632	0	506	321	803	676	715	460	687	527	852	567
ENSMUSG00000000093	chr11	Tbx2	85832551	85833501	3626	0.228694	1.793093	0.398085	0.515353	0.067146	0	33	37	55	40	86	32	69	62	97	74
ENSMUSG00000007877	chr11	Tcap	98383811	98383956	948	-0.16742	11.68937	0.398246	0.515413	0.047026	0	47928	45836	53868	64071	61551	47859	61725	36629	88855	52384
ENSMUSG00000037216	chr1	Lipt1	37871738	37872031	2051	0.177084	2.231825	0.398269	0.515413	0.034428	0	57	60	89	63	75	70	114	90	116	60
ENSMUSG00000037935	chr11	Smarce1	99209047	99210277	6650	0.127006	5.261833	0.398286	0.515413	0.024813	0	521	496	724	524	638	640	887	623	921	594
ENSMUSG00000066361	chr12	Serpina3c	1.04E+08	1.04E+08	2213	0.440303	2.383537	0.398194	0.515413	0.299335	0	116	79	82	13	34	103	56	234	77	48
ENSMUSG00000073062	chrX	Zxdb	94724569	94730187	5619	0.287655	0.34749	0.398516	0.51566	0.068127	0	13	14	24	15	18	13	22	37	31	14
ENSMUSG00000043065	chr16	Spice1	44347121	44347506	5416	-0.17077	2.174994	0.398853	0.516047	0.031413	0	53	51	109	72	98	59	83	73	93	71
ENSMUSG00000036862	chr7	Dchs1	1.06E+08	1.06E+08	11070	0.221166	2.13301	0.398965	0.516077	0.071707	0	34	28	104	77	90	40	99	74	119	94
ENSMUSG00000044952	chr7	Kctd21	97332327	97332371	2966	-0.17419	2.800752	0.398994	0.516077	0.038397	0	112	60	165	118	142	98	135	142	112	97
ENSMUSG00000084235	chr5	Gm15421	22528321	22528719	399	0.309755	0.223903	0.398944	0.516077	0.056321	0	19	14	17	12	12	16	30	18	24	19
ENSMUSG00000022701	chr16	2610015P09Rik	43889800	43890038	4230	-0.19284	1.637344	0.399175	0.51611	0.036289	0	34	40	74	56	56	44	68	46	53	45
ENSMUSG00000039230	chr11	Tbcd	1.21E+08	1.21E+08	8096	-0.13039	4.089766	0.399169	0.51611	0.024176	0	207	190	430	298	328	240	312	257	415	260
ENSMUSG00000049411	chr18	Tmem241	11981303	11983593	3336	0.225549	1.348186	0.399144	0.51611	0.051172	0	32	21	48	46	34	28	72	35	62	47
ENSMUSG00000059810	chr4	Rgs3	62559847	62559882	10801	0.153563	3.003144	0.399062	0.51611	0.033391	0	86	72	179	116	167	112	158	173	172	142
ENSMUSG00000022878	chr16	Adipoq	23146536	23146641	1381	0.530076	5.918254	0.399246	0.516152	0.45955	0	1590	1005	444	144	211	872	617	3515	501	684
ENSMUSG00000040269	chr3	Mrps28	8802146	8802414	783	0.131334	5.70993	0.399364	0.516254	0.027329	0	784	632	949	756	821	811	1344	785	1275	838
ENSMUSG00000018166	chr10	Erbb3	1.29E+08	1.29E+08	6016	-0.33366	2.307192	0.399799	0.516715	0.167898	0	24	30	92	161	146	43	97	47	95	109

ENSMUSG00000020898	chr11	Ctc1	69015911	69016165	6797	0.123326	3.984236	0.399773	0.516715	0.022124	0	207	156	351	241	273	255	311	290	377	260
ENSMUSG00000027552	chr3	E2f5	14578641	14579023	1782	-0.22658	0.9422	0.399922	0.516823	0.061433	0	37	24	46	28	21	20	49	30	32	24
ENSMUSG00000036764	chr10	Dnajc12	63382443	63382518	2740	-0.13669	3.698685	0.400112	0.51702	0.028203	0	162	190	286	214	226	163	304	201	307	169
ENSMUSG00000025224	chr19	Gbf1	46152509	46152792	9062	-0.14947	6.091414	0.400254	0.517152	0.036486	0	913	546	2027	1139	1442	849	1287	1088	1644	1083
ENSMUSG00000049265	chr5	Kcnk3	30588170	30588599	3810	0.418514	0.345119	0.400393	0.517282	0.216491	0	36	5	18	6	13	15	15	46	24	19
ENSMUSG00000019124	chr6	Scrn1	54505890	54509362	8371	0.199501	1.531947	0.400703	0.517581	0.036582	0	32	32	53	38	54	47	57	51	79	39
ENSMUSG00000028452	chr4	Vcp	42979963	42980634	4851	0.1297	9.065401	0.400703	0.517581	0.028417	0	7622	6193	11861	7114	8453	8345	11319	9335	14033	8464
ENSMUSG00000060935	chr10	Tmem263	85102627	85102997	3778	0.151614	3.722505	0.400835	0.517701	0.031908	0	160	189	262	153	223	165	293	253	342	221
ENSMUSG00000038570	chr7	Fam154b	82632960	82635407	4767	0.352187	-0.14078	0.401005	0.517871	0.078201	0	7	13	13	12	10	18	18	19	19	7
ENSMUSG00000020770	chr11	Unk	1.16E+08	1.16E+08	4438	0.141267	2.984573	0.401069	0.517903	0.026892	0	100	81	177	114	133	120	168	152	161	142
ENSMUSG00000033335	chr9	Dnm2	21424908	21425256	5330	0.131118	5.339679	0.401184	0.518	0.027914	0	504	332	804	689	845	556	873	747	1023	690
ENSMUSG00000024097	chr17	Srsf7	80200089	80201602	2279	0.12577	4.589312	0.401316	0.518121	0.0234	0	338	285	430	369	398	371	564	481	502	368
ENSMUSG00000002870	chr6	Mcm2	88883475	88884110	3370	-0.14753	3.436971	0.401453	0.518247	0.029546	0	177	107	287	159	196	169	239	148	222	155
ENSMUSG00000024974	chr19	Smc3	53600398	53600554	5541	-0.12163	4.715214	0.401566	0.518343	0.022663	0	332	348	601	437	480	364	518	462	518	419
ENSMUSG00000097915	chr15	A330009N23Rik	1.01E+08	1.01E+08	1392	0.307975	0.011547	0.401605	0.518343	0.055839	0	9	9	14	17	15	17	22	13	27	12
ENSMUSG00000026566	chr1	Mpzl1	1.66E+08	1.66E+08	3550	0.182297	2.210889	0.401676	0.518384	0.040936	0	44	43	89	80	90	65	132	74	93	79
ENSMUSG00000004263	chr6	Atn1	1.25E+08	1.25E+08	5085	0.124939	6.761435	0.401869	0.518582	0.025899	0	1612	1199	2133	1496	1878	1686	2376	2006	2772	1583
ENSMUSG00000020525	chr11	Ppm1d	85311244	85311923	3173	0.15967	2.495875	0.401946	0.518631	0.033477	0	70	51	113	92	99	99	105	108	126	90
ENSMUSG00000027465	chr2	Tbc1d20	1.52E+08	1.52E+08	4171	0.124304	5.391528	0.402239	0.518959	0.024847	0	560	425	870	663	733	665	797	855	1075	606
ENSMUSG00000020994	chr12	Pnn	59066919	59067115	3469	0.127835	4.540305	0.402416	0.519037	0.025298	0	262	253	492	327	477	294	548	458	484	432
ENSMUSG00000021072	chr12	Tmx1	70453095	70453320	3299	-0.1299	4.052765	0.402417	0.519037	0.024834	0	216	213	403	261	305	192	313	312	348	276
ENSMUSG00000028677	chr4	Rnf220	1.17E+08	1.17E+08	7229	0.116361	5.775194	0.402385	0.519037	0.02173	0	737	612	1067	840	959	844	1276	980	1311	826
ENSMUSG00000078994	chr13	Zfp429	67389309	67391064	2134	0.275125	0.374247	0.402519	0.519119	0.053004	0	20	12	15	14	24	19	29	19	27	24
ENSMUSG00000000088	chr9	Cox5a	57521232	57521415	690	0.156456	8.865126	0.402694	0.519294	0.041716	0	5724	4133	7506	9326	8869	6936	11704	6790	13364	7157
ENSMUSG00000056167	chr9	Cnot10	1.15E+08	1.15E+08	2979	0.133107	4.558346	0.40283	0.519418	0.026695	0	357	294	472	295	360	390	493	395	593	374
ENSMUSG00000033712	chr14	Ccar2	70138177	70138947	3716	-0.12113	4.403437	0.402938	0.519507	0.021628	0	313	223	473	343	435	316	410	336	473	311
ENSMUSG00000041229	chrX	Phf8	1.52E+08	1.52E+08	9318	0.150205	3.327796	0.403474	0.520101	0.032621	0	132	89	236	132	189	112	237	222	229	166
ENSMUSG00000050821	chr16	Fam131a	20693282	20693472	2853	-0.17145	6.960012	0.403478	0.520101	0.049891	0	2370	1305	2740	1800	2403	2246	2113	1634	3479	1314
ENSMUSG00000030271	chr6	Ogg1	1.13E+08	1.13E+08	2034	-0.16133	2.351465	0.40363	0.520186	0.030807	0	69	65	123	76	95	63	108	70	113	81
ENSMUSG00000030541	chr7	Idh2	80094846	80095203	2588	-0.33113	7.215585	0.403661	0.520186	0.186145	0	783	796	1936	6285	3832	1536	3820	1777	3128	2128
ENSMUSG00000062691	chr17	Cebpzos	78916500	78916525	1131	0.14357	4.250313	0.403635	0.520186	0.030327	0	306	233	335	244	299	305	497	285	460	290
ENSMUSG00000018322	chr2	Tomm34	1.64E+08	1.64E+08	3040	0.137076	3.778794	0.403822	0.520312	0.026373	0	177	178	273	189	217	216	269	231	339	244
ENSMUSG00000046727	chr18	Cystm1	36345619	36345840	2840	0.150761	7.148778	0.403837	0.520312	0.038373	0	2263	1819	2718	1832	1922	2192	3516	2068	3981	2151
ENSMUSG00000022951	chr16	Rcan1	92391953	92393628	2506	-0.20137	6.306477	0.404001	0.520422	0.068736	0	865	656	1449	1639	2421	1114	1959	945	2154	799
ENSMUSG00000104117	chr1	RP23-152I6.3	1.65E+08	1.65E+08	4171	0.328785	0.393424	0.40397	0.520422	0.105414	0	11	13	12	31	16	9	34	28	29	24
ENSMUSG00000047694	chrX	Yipf6	98936316	98936345	7149	-0.13042	3.791523	0.404083	0.520478	0.025622	0	206	193	317	183	253	175	316	208	306	209
ENSMUSG00000067995	chr14	Gtf2f2	75896937	75897653	1467	0.148495	3.426843	0.404419	0.52086	0.03127	0	151	124	206	147	180	203	278	154	232	157
ENSMUSG00000057967	chr11	Fgf18	33117430	33118031	1187	0.294112	0.113227	0.404481	0.520888	0.077112	0	14	8	23	10	16	12	31	25	11	18
ENSMUSG00000027878	chr3	Notch2	98013538	98013771	10506	0.151656	3.86716	0.404589	0.520927	0.037339	0	176	125	404	164	289	231	309	301	264	268
ENSMUSG00000038910	chr17	Plcl2	50509547	50509937	4050	-0.12226	6.336569	0.404573	0.520927	0.025003	0	1270	938	1828	1247	1511	1183	1632	1223	1837	1217
ENSMUSG00000041147	chr5	Brca2	1.51E+08	1.51E+08	10724	-0.27587	0.069382	0.404646	0.52095	0.050694	0	14	8	29	14	20	12	20	11	20	15
ENSMUSG00000035772	chr2	Mrps2	28468066	28468142	2919	-0.12925	4.296007	0.405032	0.521345	0.025722	0	283	202	390	330	455	269	457	315	452	243
ENSMUSG00000039826	chr2	Trub2	29761224	29761688	6316	-0.13731	4.840969	0.405006	0.521345	0.030566	0	378	298	575	579	596	392	689	412	708	346
ENSMUSG00000089698	chr16	Gm2541	85553233	85553943	711	-0.21161	1.0508	0.405256	0.521582	0.05167	0	28	32	30	34	42	26	50	25	38	29
ENSMUSG00000031546	chr8	Gins4	23226610	23227175	1364	0.146922	3.676305	0.405383	0.521695	0.029949	0	172	160	230	208	180	160	298	249	292	226
ENSMUSG00000019952	chr10	Poc1b	99107036	99107223	3748	0.17784	2.082229	0.406024	0.522429	0.035865	0	45	52	92	64	59	57	93	88	95	68
ENSMUSG00000075040	chr2	Zfp408	91643669	91646473	4008	-0.2186	1.70681	0.406063	0.522429	0.058982	0	41	37	85	63	51	35	57	33	74	68
ENSMUSG00000084830	chrX	Gm14539	20581141	20581314	174	-0.15809	4.489011	0.406071	0.522429	0.041804	0	332	347	362	428	353	321	594	305	476	275
ENSMUSG00000046756	chr11	Mrps7	1.16E+08	1.16E+08	2072	-0.1329	6.261858	0.406865	0.523399	0.030146	0	1177	946	1359	1422	1439	1102	1752	1119	1743	1053
ENSMUSG00000021495	chr13	Fam193b	55539319	55539712	4338	0.136119	3.549389	0.406996	0.523517	0.02752	0	165	118	277	151	192	197	233	239	244	186
ENSMUSG00000027498	chr2	Cstf1	1.72E+08	1.72E+08	3504	0.120579	4.24289	0.40715	0.523665	0.020962	0	259	228	391	257	313	270	449	338	446	304
ENSMUSG00000026895	chr2	Ndufa8	36036326	36036641	861	-0.17065	7.435711	0.407576	0.524161	0.050461	0	2120	1593	2956	4263	3918	2240	3736	2351	4485	2399
ENSMUSG00000003746	chr10	Man1a	53904788	53907563	9058	-0.16649	4.026824	0.407681	0.524246	0.043481	0	201	227	500	170	320	190	311	328	285	272
ENSMUSG00000033486	chr2	Catsper2	1.21E+08	1.21E+08	3695	-0.22809	1.106963	0.407757	0.524293	0.053812	0	25	23	34	50	45	31	39	27	48	28
ENSMUSG00000029134	chr5	Plb1	32232708	32232791	8859	-0.26608	0.211241	0.408702	0.525457	0.063079	0	25	14	21	12	19	15	24	19	16	13
ENSMUSG00000018287	chr11	Spag7	70663771	70664220	1480	0.137561	6.760591	0.408968	0.525726	0.032375	0	1587	1399	1854	1499	1763	1824	2524	1650	2873	1611
ENSMUSG00000021615	chr13	Xrcc4	89774027	89776408	4213	-0.16881	2.688738	0.408991	0.525726	0.041471	0	92	98	159	83	106	91	170	85	118	88
ENSMUSG00000073591	chr18	Pcdhb22	37517871	37524479	6609	0.254565	0.598024	0.409696	0.526582	0.073975	0	13	12	30	14	37	23	21	34	28	30
ENSMUSG00000024170	chr17	Telo2	25099570	25100120	8006	0.168582	2.828048	0.40991	0.526805	0.041844	0	74	55	132	138	141	100	163	117	157	139
ENSMUSG00000058581	chr14	Gm5801	56010536	56011315	780	-0.34208	-0.12693	0.410156	0.527071	0.105467	0	17	9	25	14	8	5	9	12	21	18
ENSMUSG00000026516	chr1	Nvl	1.81E+08	1.81E+08	13488	0.146275	3.678341	0.410281	0.52718	0.032929	0	140	114	266	222	249	187	389	225	256	182
ENSMUSG00000058325	chr7	Dock1	1.35E+08	1.35E+08	6807	0.154379	3.035106	0.41041	0.527295	0.036021	0	96	69	183	119	167	96	179	180	171	153
ENSMUSG00000016495	chr19	Plgrkt	29348599	29349005	3799	0.160542	3.577112	0.410718	0.52761	0.037473	0	170	176	223	130	177	210	283	207	267	174
ENSMUSG00000026280	chr1	Atg4b	93751500	93751581	8278	0.115614	4.65101	0.410735	0.52761	0.020927	0	358	265	502	353	462	402	569	434	576	401
ENSMUSG00000024960	chr19	Plcb3	6953714	6954299	4201	0.116876	4.305482	0.411028	0.527935	0.021432	0	262	182	429	289	387	309	444	372	461	293

ENSMUSG00000021737	chr14	Psmd6	14112184	14112386	2326	-0.14317	7.040835	0.411215	0.528074	0.036075	0	2009	2152	2814	1791	2037	1767	2934	1992	2987	1899
ENSMUSG00000046027	chr7	Stard5	83631959	83632139	5450	0.220584	1.934777	0.411188	0.528074	0.074636	0	37	32	71	49	95	72	54	103	76	51
ENSMUSG00000074063	chr8	Osgin1	1.19E+08	1.19E+08	2674	0.147687	4.483966	0.411371	0.528223	0.036302	0	255	180	534	354	443	310	664	475	463	272
ENSMUSG00000023885	chr17	Thbs2	14665500	14667520	5922	-0.2193	4.910331	0.411487	0.528321	0.081388	0	221	319	1002	440	802	477	454	651	353	493
ENSMUSG00000041278	chr11	Ttc1	43729512	43730607	2032	-0.13146	5.362189	0.411558	0.528361	0.029617	0	679	582	822	626	663	638	958	600	852	555
ENSMUSG00000029086	chr5	Prom1	43993625	43994496	4517	-0.2358	1.33152	0.411621	0.528391	0.061764	0	30	29	77	48	30	41	44	27	56	34
ENSMUSG00000030711	chr7	Sult1a1	1.27E+08	1.27E+08	1507	0.219597	4.135636	0.411706	0.528448	0.081573	0	240	224	386	207	233	392	272	525	226	224
ENSMUSG00000101892	chr15	9130401M01Rik	58022259	58022563	2666	0.131149	3.774077	0.411981	0.528751	0.024308	0	202	151	251	209	220	204	307	266	332	197
ENSMUSG00000004934	chr10	Pias4	81153266	81154372	4582	-0.12508	4.215964	0.41235	0.529173	0.024558	0	280	204	450	269	373	225	367	287	494	272
ENSMUSG00000030008	chr6	Pradc1	85446810	85447297	1594	0.140578	3.452254	0.412599	0.52944	0.028188	0	163	109	209	149	202	147	222	199	308	175
ENSMUSG00000021951	chr14	N6amt2	57549598	57549879	836	-0.17027	4.394209	0.412642	0.529445	0.049737	0	355	386	441	226	303	288	446	384	424	269
ENSMUSG00000070729	chr4	Gm12966	1.3E+08	1.3E+08	810	0.233903	0.829734	0.412852	0.529662	0.048096	0	28	16	32	19	28	25	46	22	43	30
ENSMUSG00000057342	chr7	Sphk2	45709467	45711811	4159	0.136831	3.983815	0.412981	0.529777	0.030061	0	166	142	312	306	299	243	320	312	364	261
ENSMUSG00000022367	chr15	Has2	56665627	56668588	4237	0.269038	0.334368	0.413082	0.529843	0.080028	0	11	7	38	12	20	13	32	26	19	24
ENSMUSG00000064037	chr5	Gpn1	31494741	31494883	7845	0.12128	4.580674	0.413112	0.529843	0.022808	0	313	294	432	352	427	399	530	407	580	359
ENSMUSG00000040856	chr12	Dlk1	1.09E+08	1.09E+08	5657	-0.29202	0.496826	0.413165	0.529859	0.090391	0	30	15	41	11	20	15	19	24	20	27
ENSMUSG00000016253	chr2	Nelfcd	1.74E+08	1.74E+08	2883	0.122007	4.846872	0.413622	0.530386	0.024462	0	404	262	540	473	547	427	619	479	715	502
ENSMUSG00000018604	chr5	Tbx3	1.2E+08	1.2E+08	5365	0.224642	2.577166	0.413656	0.530386	0.076329	0	55	56	75	112	136	67	168	79	206	83
ENSMUSG00000042606	chr7	Hirip3	1.27E+08	1.27E+08	3023	-0.15955	2.586864	0.413696	0.530386	0.032316	0	97	58	142	84	129	92	122	87	120	88
ENSMUSG00000023078	chr5	Cxcl13	95956928	95957031	1172	-0.46721	-0.1225	0.413758	0.530416	0.255612	0	19	21	24	5	5	26	9	10	9	6
ENSMUSG00000009406	chrX	Elk1	20933395	20935548	5381	-0.13624	3.755524	0.41382	0.530443	0.02677	0	194	120	350	206	297	200	292	196	287	198
ENSMUSG00000022685	chr16	Parn	13537964	13538902	2902	0.141748	3.262686	0.414228	0.530915	0.027465	0	124	120	199	132	148	144	236	144	231	162
ENSMUSG00000025162	chr11	Csnk1d	1.21E+08	1.21E+08	5022	0.120213	6.194039	0.414511	0.531226	0.025172	0	930	721	1521	1191	1349	1083	1503	1374	1852	1180
ENSMUSG00000026174	chr1	Rqcd1	74506058	74506461	3826	0.121265	4.42562	0.41467	0.531276	0.023142	0	268	222	443	375	350	338	492	392	529	303
ENSMUSG00000029387	chr5	Gtf2h3	1.25E+08	1.25E+08	3840	-0.14886	3.359742	0.414604	0.531276	0.032855	0	178	87	208	184	210	148	228	161	216	135
ENSMUSG00000029438	chr5	Bcl7a	1.23E+08	1.23E+08	8580	0.135907	4.071223	0.414656	0.531276	0.029045	0	222	154	313	269	336	204	477	326	339	276
ENSMUSG00000031754	chr8	Nudt21	94017770	94019704	2726	0.135399	3.038359	0.415086	0.531661	0.025586	0	108	78	183	113	151	114	203	138	190	138
ENSMUSG00000070315	chr9	4930581F22Rik	35116728	35116840	3462	0.334943	-0.19697	0.415091	0.531661	0.076944	0	7	12	19	6	10	13	23	17	18	7
ENSMUSG00000084384	chr11	Gm12251	58392769	58393560	792	0.159419	3.314855	0.415062	0.531661	0.036116	0	117	127	147	185	153	146	241	177	237	156
ENSMUSG00000045377	chr11	Tmem88	69396519	69397881	1582	0.201981	2.478994	0.415326	0.53191	0.059451	0	59	47	73	111	119	85	131	70	150	103
ENSMUSG00000036356	chr8	Csgalnact1	68356781	68358713	4774	0.2445	1.415685	0.415815	0.532486	0.082894	0	28	24	79	26	39	33	97	33	44	50
ENSMUSG00000052033	chr2	Pfdn4	1.7E+08	1.7E+08	2520	0.197106	2.842982	0.415958	0.532618	0.055956	0	84	113	132	94	91	134	204	88	168	103
ENSMUSG00000025825	chr5	Iscu	1.14E+08	1.14E+08	2176	0.137887	6.520278	0.416047	0.532628	0.033466	0	1128	1037	1522	1703	1545	1436	2380	1455	2417	1268
ENSMUSG00000031221	chrX	Igbp1	1E+08	1E+08	5717	-0.12463	5.13765	0.416021	0.532628	0.026698	0	491	509	707	543	653	559	755	588	741	437
ENSMUSG00000029022	chr4	Miip	1.48E+08	1.48E+08	3354	0.155713	3.006976	0.416287	0.532884	0.033868	0	95	97	167	138	103	127	182	127	184	143
ENSMUSG00000002205	chr7	Vrk3	44748413	44748651	3098	0.118241	4.594742	0.416667	0.533299	0.022272	0	337	280	449	343	436	407	501	419	564	389
ENSMUSG00000033845	chr1	Mrpl15	4773206	4774516	8487	0.12787	5.999746	0.416691	0.533299	0.028489	0	835	647	1099	1138	1181	966	1585	1046	1588	992
ENSMUSG00000032051	chr9	Fdx1	51943307	51943649	861	-0.15348	4.430774	0.416808	0.533397	0.040183	0	325	230	318	447	476	331	505	292	489	267
ENSMUSG00000024422	chr17	Dhx16	35879819	35880118	4094	0.119339	4.231397	0.417245	0.533756	0.022697	0	211	200	413	322	312	276	414	340	411	334
ENSMUSG00000026930	chr2	Gpsm1	26315515	26315720	5383	-0.1836	1.663658	0.417234	0.533756	0.03543	0	36	33	75	49	75	43	63	55	58	43
ENSMUSG00000084289	chrX	Gm6977	90744546	90744992	512	0.188777	2.023106	0.417249	0.533756	0.0449	0	46	56	91	52	51	70	86	60	91	75
ENSMUSG00000098661	chr7	Mir7052	44470347	44470411	65	0.24369	0.31055	0.417169	0.533756	0.05584	0	12	9	26	13	25	25	24	15	29	18
ENSMUSG00000052512	chr7	Nav2	48908716	48908745	32073	-0.16211	3.575406	0.417568	0.534112	0.04134	0	120	111	312	214	291	129	267	165	309	176
ENSMUSG00000028293	chr4	Slc35a1	34663257	34664230	2293	0.128613	4.062108	0.417727	0.534263	0.02488	0	204	221	293	228	315	245	397	299	375	275
ENSMUSG00000030990	chr7	Pgap2	1.02E+08	1.02E+08	4531	-0.12176	4.746056	0.418153	0.534757	0.024512	0	412	270	627	463	499	409	560	389	642	362
ENSMUSG00000015850	chr3	Adamtsl4	95676201	95676969	4198	-0.25606	4.329509	0.418297	0.53489	0.114681	0	144	103	375	636	576	222	458	314	362	322
ENSMUSG00000048696	chr10	Mex3d	80380355	80382621	3266	0.195043	1.884795	0.418399	0.534969	0.054575	0	38	24	97	54	68	38	88	68	108	56
ENSMUSG00000048109	chr3	Rbm15	1.07E+08	1.07E+08	3270	0.155029	3.082445	0.418571	0.535137	0.034923	0	113	98	215	99	120	115	182	180	218	119
ENSMUSG00000033021	chr1	Gmppa	75435930	75436011	2395	0.123699	5.156078	0.4189	0.535506	0.025561	0	532	445	730	450	553	556	809	630	891	530
ENSMUSG00000001134	chrX	Uxt	20941722	20941797	1639	0.149043	4.208033	0.4194	0.535992	0.035255	0	226	269	337	255	283	318	501	266	466	244
ENSMUSG00000021765	chr13	Fst	1.14E+08	1.14E+08	2337	0.162123	2.427317	0.419546	0.535992	0.035255	0	62	63	122	64	94	78	145	103	98	86
ENSMUSG00000036438	chr17	Calm2	87433412	87434055	1467	0.15081	8.045111	0.419467	0.535992	0.041412	0	4064	3796	4576	2951	4070	4023	6480	3826	6640	4675
ENSMUSG00000040606	chr4	Kazn	1.42E+08	1.42E+08	10721	0.25442	1.462883	0.419511	0.535992	0.09664	0	25	18	62	43	53	44	114	43	45	24
ENSMUSG00000041445	chr14	Mmrn2	34375504	34375778	3935	-0.13764	3.830305	0.419373	0.535992	0.028999	0	152	138	363	260	320	184	321	238	307	195
ENSMUSG00000044060	chr5	A830010M20Rik	1.07E+08	1.07E+08	9127	-0.18082	3.016949	0.419433	0.535992	0.047922	0	95	74	176	161	194	100	148	118	138	170
ENSMUSG00000050248	chr5	Evc2	37338499	37338727	5837	-0.27407	3.476179	0.419563	0.535992	0.129068	0	65	59	205	370	316	143	204	180	210	170
ENSMUSG00000038244	chr7	Mical2	1.12E+08	1.12E+08	11510	-0.22381	6.366417	0.419665	0.53607	0.091106	0	1683	1343	2428	594	991	1069	1435	1891	1572	967
ENSMUSG00000020857	chr11	Nme2	93949814	93950046	1171	-0.13947	8.151963	0.420497	0.537029	0.035762	0	4444	3677	4703	5220	5360	4291	6346	3848	6793	3798
ENSMUSG00000038351	chr11	Sgsm2	74849261	74850895	6884	0.191153	2.281019	0.420487	0.537029	0.052106	0	45	63	114	67	71	87	73	106	101	85
ENSMUSG00000022964	chr16	Tmem50b	91574503	91576158	2446	0.134515	3.899721	0.420724	0.537236	0.029629	0	191	120	310	252	289	181	365	312	317	254
ENSMUSG00000048486	chr2	Fitm2	1.63E+08	1.63E+08	3967	-0.17123	6.794777	0.42074	0.537236	0.053415	0	1276	832	2078	2742	2777	1331	2467	1817	2365	1676
ENSMUSG00000004187	chr15	Kifc2	76660641	76660765	3143	0.178095	1.97471	0.421454	0.53803	0.044281	0	40	38	109	39	74	57	87	67	94	67
ENSMUSG00000030737	chr7	Slco2b1	99657804	99660176	5612	0.152657	4.153906	0.42145	0.53803	0.040084	0	216	203	462	212	285	337	337	427	345	228
ENSMUSG00000034563	chr9	Ccpg1	72985429	72985673	7497	0.129651	6.836113	0.421483	0.53803	0.030643	0	1164	1148	2300	2157	2136	1642	2734	1972	2633	1989
ENSMUSG00000045757	chr7	Zfp764	1.27E+08	1.27E+08	2508	0.233848	0.978305	0.421977	0.538557	0.058183	0	27	22	31	24	32	33	40	35	27	44

ENSMUSG00000047921	chr15	Trappc9	72589621	72590162	6363	0.122469	5.659085	0.421957	0.538557	0.026763	0	652	462	1139	811	906	730	975	846	1415	873
ENSMUSG00000002007	chrX	Srpk3	73774405	73774506	2784	0.135566	5.450686	0.422457	0.539118	0.03234	0	651	532	957	537	653	650	1051	588	1059	849
ENSMUSG00000034345	chr17	Gtf2h5	6079786	6079911	3855	0.141289	5.536574	0.422554	0.539189	0.034965	0	702	660	837	587	644	804	1157	794	1053	655
ENSMUSG00000001248	chr7	Gramd1a	31130127	31130584	5103	0.142224	4.6045	0.422635	0.539241	0.035321	0	289	199	410	493	480	355	552	490	488	428
ENSMUSG00000029518	chr5	Rab35	1.16E+08	1.16E+08	2799	-0.11307	5.147252	0.423062	0.539733	0.021904	0	480	370	829	608	722	452	738	575	837	537
ENSMUSG00000045598	chr7	Zfp553	1.27E+08	1.27E+08	3373	-0.1389	3.011356	0.423104	0.539735	0.026785	0	114	97	182	114	170	124	155	120	176	117
ENSMUSG00000043257	chr4	Pigv	1.34E+08	1.34E+08	4180	-0.13097	3.955294	0.423454	0.54013	0.028524	0	276	190	362	210	253	200	295	279	365	216
ENSMUSG00000021607	chr13	Mrpl36	73331009	73331091	899	-0.1259	4.790084	0.423813	0.540536	0.027849	0	468	355	529	456	461	412	634	396	546	426
ENSMUSG00000042472	chr12	Zfp410	84316859	84317174	2697	-0.11989	3.968094	0.423948	0.540655	0.022532	0	217	168	332	283	313	228	356	266	306	212
ENSMUSG00000038168	chr16	Leprel1	25959288	25960450	3721	-0.23853	1.551716	0.424004	0.540675	0.074101	0	24	20	67	61	85	34	51	52	52	46
ENSMUSG00000085965	chr1	2310016D23Rik	60778843	60778916	388	0.25454	1.675067	0.424361	0.541079	0.08248	0	59	44	45	28	40	51	80	64	88	30
ENSMUSG00000024163	chr17	Mapk8ip3	24892153	24892683	14558	-0.12011	4.357601	0.424849	0.541649	0.023584	0	257	246	502	333	397	258	469	326	381	356
ENSMUSG00000060950	chr12	Trmt61a	1.12E+08	1.12E+08	2433	0.204759	2.016892	0.424997	0.541734	0.056641	0	66	45	66	44	69	51	71	107	85	68
ENSMUSG00000089798	chr5	1700028K03Rik	1.08E+08	1.08E+08	8149	0.259862	0.282751	0.42498	0.541734	0.061394	0	10	11	17	19	24	15	29	19	19	27
ENSMUSG00000021120	chr12	Pigh	79080673	79082496	2349	0.179908	1.576684	0.425119	0.541837	0.035737	0	30	33	67	37	53	43	73	60	57	46
ENSMUSG00000025161	chr11	Slc16a3	1.21E+08	1.21E+08	5318	-0.15278	7.993168	0.425239	0.541937	0.043676	0	4486	1985	6412	4008	5348	3588	4611	3768	7261	3228
ENSMUSG00000022503	chr16	Nubp1	10411948	10411995	3637	0.142201	3.307169	0.425383	0.542069	0.030792	0	150	110	209	115	166	166	248	159	192	170
ENSMUSG00000003068	chr10	Stk11	80115803	80116907	4580	0.116755	6.867845	0.426103	0.542883	0.025127	0	1585	1288	2273	1843	2003	1693	2599	1962	2988	1955
ENSMUSG00000022840	chr16	Adcy5	35154877	35157235	7007	0.328228	2.411579	0.426081	0.542883	0.182481	0	93	61	98	51	60	55	63	265	71	62
ENSMUSG00000000325	chr16	Arvcf	18348182	18348456	6425	0.120054	3.813406	0.426311	0.543095	0.022883	0	169	138	335	216	242	201	326	234	365	220
ENSMUSG00000022332	chr15	Khdrbs3	68928420	68928833	1887	-0.31424	3.275745	0.42663	0.543449	0.177341	0	45	56	125	355	299	101	207	109	230	150
ENSMUSG00000065124	chr2	Snora65	32963291	32963420	130	0.309728	0.471227	0.426809	0.543624	0.090278	0	13	19	20	21	16	24	49	19	30	10
ENSMUSG00000043987	chr9	Cep164	45766946	45768363	5980	0.18293	2.12748	0.426851	0.543627	0.045356	0	54	46	78	58	86	43	87	101	105	80
ENSMUSG00000037005	chrX	Xpnpep2	48108725	48109194	4878	-0.3245	0.887994	0.427203	0.54397	0.141883	0	30	23	69	14	26	26	21	50	17	22
ENSMUSG00000090639	chr9	Gm20425	1.03E+08	1.03E+08	3028	0.309275	6.883481	0.427165	0.54397	0.179403	0	2554	1665	2024	692	1024	2167	1401	4670	1762	1428
ENSMUSG00000049670	chr19	Morn4	42074939	42076255	1816	-0.27936	2.713063	0.427299	0.54404	0.136678	0	157	107	174	46	69	130	120	77	166	46
ENSMUSG00000002280	chr17	Narfl	25773776	25773887	3826	-0.14229	4.901653	0.427751	0.544511	0.036067	0	398	269	540	617	724	407	630	408	695	472
ENSMUSG00000034575	chr13	Papd7	69497959	69500110	3972	0.150343	2.941704	0.427725	0.544511	0.034489	0	80	83	162	110	152	93	191	147	147	151
ENSMUSG00000028898	chr4	Trnau1ap	1.32E+08	1.32E+08	2710	0.168108	3.409411	0.427845	0.544578	0.042713	0	156	151	170	142	150	118	278	210	280	157
ENSMUSG00000028736	chr4	Pax7	1.4E+08	1.4E+08	5860	0.197513	1.550678	0.4292	0.546148	0.047277	0	42	31	65	28	47	37	79	42	83	41
ENSMUSG00000035547	chr7	Capn5	98121559	98124055	5485	0.166689	1.752727	0.429201	0.546148	0.039375	0	40	29	83	48	53	53	68	54	70	67
ENSMUSG00000067713	chr15	Prkag1	98812798	98813480	1638	0.129065	5.955301	0.429149	0.546148	0.030711	0	822	608	1007	1175	1120	967	1470	1050	1454	1006
ENSMUSG00000057649	chr13	Brd9	73937838	73937945	2406	0.128796	3.568387	0.429252	0.546159	0.02628	0	143	118	218	186	247	185	291	231	246	173
ENSMUSG00000029048	chr4	Rer1	1.55E+08	1.55E+08	1814	0.121088	6.469262	0.429337	0.546215	0.027107	0	1281	1112	1654	1272	1386	1304	2121	1602	1966	1473
ENSMUSG00000015671	chr13	Psma2	14613242	14613315	944	0.13298	6.633809	0.429629	0.546535	0.032952	0	1401	1383	1800	1284	1555	1587	2629	1574	2313	1496
ENSMUSG00000019802	chr10	Sec63	42761496	42761888	8787	0.109731	5.434973	0.430381	0.547386	0.021635	0	536	500	960	592	788	674	1042	808	946	644
ENSMUSG00000074227	chr7	Spint2	29256331	29256837	1459	-0.2343	1.82922	0.430361	0.547386	0.086861	0	84	52	82	32	42	48	52	57	87	47
ENSMUSG00000002769	chr17	Gnmt	46725664	46725971	1206	-0.316	0.166006	0.431115	0.548267	0.123403	0	9	7	15	26	35	5	20	21	20	17
ENSMUSG00000025934	chr1	Gsta3	21240589	21240659	4344	0.470356	0.386448	0.431249	0.548285	0.328286	0	26	17	14	9	11	46	4	42	15	12
ENSMUSG00000028033	chr1	Kcnq5	21398403	21403125	7689	0.2497	4.413157	0.43118	0.548285	0.117664	0	126	108	374	480	557	208	677	303	449	504
ENSMUSG00000066235	chr9	Pomgnt2	1.22E+08	1.22E+08	2369	-0.13358	3.869355	0.431253	0.548285	0.028288	0	202	129	351	278	291	197	296	242	271	252
ENSMUSG00000031429	chrX	Psmd10	1.41E+08	1.41E+08	1469	0.152999	3.433846	0.432304	0.549569	0.035524	0	128	162	181	163	157	165	277	186	238	170
ENSMUSG00000055116	chr7	Arntl	1.13E+08	1.13E+08	2904	-0.16956	2.978303	0.432358	0.549584	0.04401	0	103	83	271	97	140	113	163	141	130	117
ENSMUSG00000046897	chr15	Zfp740	1.02E+08	1.02E+08	4822	0.108783	5.180462	0.432458	0.549659	0.021379	0	495	370	845	497	642	561	863	662	792	564
ENSMUSG00000030591	chr7	Psmd8	29174188	29174747	1540	-0.16158	7.841176	0.432614	0.549805	0.050555	0	3897	3514	5006	2947	3644	3785	4302	2535	6388	3016
ENSMUSG00000079588	chr1	Tmem182	40805601	40805887	2716	-0.1282	8.224985	0.432813	0.550005	0.031772	0	3897	2871	7156	5774	6061	3609	6922	4314	6683	4967
ENSMUSG00000027714	chr3	Exosc9	36552606	36552751	4711	0.146975	4.415005	0.432865	0.550018	0.037234	0	339	289	382	252	314	372	547	306	531	305
ENSMUSG00000042229	chr1	Rabif	1.34E+08	1.34E+08	2861	0.122745	3.522587	0.43293	0.550047	0.023788	0	143	118	244	177	205	183	293	212	226	173
ENSMUSG00000020528	chr11	Prpsap2	61729650	61730302	1962	0.170537	2.644252	0.433073	0.550177	0.042892	0	93	79	119	71	97	82	176	118	107	113
ENSMUSG00000085881	chr13	Gm15912	74008152	74008464	578	0.267627	0.874872	0.433334	0.550455	0.08496	0	21	24	34	24	21	42	25	24	58	22
ENSMUSG00000029158	chr5	Yipf7	69516675	69517198	1214	0.14908	6.23009	0.433443	0.550541	0.042256	0	881	784	1296	1392	1355	1026	2331	916	1860	1274
ENSMUSG00000033423	chr4	Eri3	1.18E+08	1.18E+08	3007	0.117104	6.507383	0.433622	0.550716	0.025871	0	1298	1071	1751	1378	1444	1423	2009	1574	2269	1420
ENSMUSG00000066151	chr4	Fkbp15	62300342	62300990	7515	-0.12822	4.019331	0.433704	0.550767	0.026327	0	220	151	414	268	342	235	356	282	275	252
ENSMUSG00000002820	chr9	Atg4d	21265299	21265717	2541	-0.1268	5.731334	0.433842	0.55089	0.030267	0	725	533	1019	1092	1111	675	1098	795	1329	806
ENSMUSG00000020288	chr11	Ahsa2	23487882	23490570	4532	-0.12228	5.205612	0.434376	0.551515	0.027866	0	625	503	707	533	653	568	733	626	729	546
ENSMUSG00000003868	chr7	Ruvbl2	45421852	45422005	2573	-0.11191	4.610311	0.43454	0.55167	0.02153	0	304	266	536	426	533	333	508	400	531	375
ENSMUSG00000025474	chr7	Tubgcp2	1.4E+08	1.4E+08	3085	-0.11308	4.516006	0.434604	0.5517	0.022113	0	289	265	543	388	447	307	441	357	566	347
ENSMUSG00000032187	chr9	Smarca4	21616169	21616400	6475	-0.11672	5.740552	0.435036	0.552195	0.025177	0	689	510	1348	945	1113	720	1038	919	1190	827
ENSMUSG00000097062	chr11	Gm17586	1.21E+08	1.21E+08	908	0.187087	2.337601	0.435152	0.552289	0.053961	0	83	54	109	52	74	94	80	75	141	87
ENSMUSG00000032834	chr10	Pwp2	78170910	78172134	3871	-0.11589	4.239988	0.435272	0.552389	0.022134	0	265	185	445	306	407	271	371	297	435	282
ENSMUSG00000025027	chr19	Xpnpep1	52943417	52943656	7120	0.125607	4.877171	0.435534	0.552621	0.028977	0	337	270	571	547	561	400	653	473	753	538
ENSMUSG00000036781	chr9	Rps27l	66946086	66946180	816	-0.15752	5.840657	0.435539	0.552621	0.0482	0	960	1026	1173	729	749	866	1317	808	1197	793
ENSMUSG00000055301	chr3	Adh7	1.38E+08	1.38E+08	3369	-0.36041	-0.09384	0.435729	0.55281	0.140424	0	6	14	16	19	20	21	20	13	6	5
ENSMUSG00000049957	chr11	Ccdc137	1.2E+08	1.2E+08	3803	-0.14345	2.82562	0.436313	0.553498	0.031431	0	97	82	144	109	162	96	146	141	132	92
ENSMUSG00000079605	chr17	Zbtb9	26973167	26973314	2798	-0.16633	2.081709	0.436372	0.553519	0.034683	0	60	47	108	61	81	65	89	54	78	68

ENSMUSG00000091471	chr19	Gm20538	44543722	44543812	225	0.143413	7.723658	0.436493	0.55362	0.040325	0	2664	1971	3091	4069	4301	3211	5228	3150	5783	3273
ENSMUSG00000021835	chr14	Bmp4	46383520	46384712	2224	0.172253	2.260311	0.436689	0.553815	0.043463	0	41	53	93	79	92	55	123	93	96	89
ENSMUSG00000049097	chr3	Ankrd34a	96596636	96596808	2583	-0.2238	0.651688	0.436826	0.553936	0.057891	0	27	17	37	16	31	20	35	18	39	14
ENSMUSG00000063765	chr15	Chadl	81678296	81678756	4965	0.273907	0.412072	0.436949	0.553987	0.076617	0	13	18	27	17	13	19	17	35	33	17
ENSMUSG00000078566	chr7	Bnip3	1.39E+08	1.39E+08	2265	-0.12448	7.658773	0.436947	0.553987	0.030543	0	3083	2786	4534	3142	3206	2628	4591	3191	4993	2645
ENSMUSG00000024287	chr18	Thoc1	9958180	9958246	3855	-0.14315	3.448861	0.437212	0.554217	0.036506	0	171	165	233	159	167	150	272	174	175	169
ENSMUSG00000032420	chr9	Nt5e	88327197	88328030	8411	-0.23134	1.204111	0.437223	0.554217	0.061089	0	25	24	72	33	44	29	55	33	26	40
ENSMUSG00000035601	chr4	Trmt10b	45297127	45297195	2641	-0.16437	2.09674	0.437256	0.554217	0.036611	0	62	52	91	62	89	60	107	62	67	64
ENSMUSG00000027510	chr2	Rbm38	1.73E+08	1.73E+08	2869	0.14715	7.047926	0.437395	0.554267	0.042607	0	1484	983	2502	2756	2611	1795	2853	2258	3402	2477
ENSMUSG00000029389	chr5	Ddx55	1.25E+08	1.25E+08	5121	-0.17011	2.401865	0.437421	0.554267	0.046842	0	78	88	106	77	81	79	122	78	82	82
ENSMUSG00000073437	chr17	D330041H03Rik	24404649	24405338	3749	-0.28666	-0.16413	0.437368	0.554267	0.084736	0	7	16	14	17	14	7	21	10	12	15
ENSMUSG00000058979	chr6	Cecr5	1.21E+08	1.21E+08	3355	-0.16198	4.30372	0.437487	0.554297	0.048438	0	235	163	358	487	452	250	467	253	467	292
ENSMUSG00000017999	chr2	Ddx27	1.67E+08	1.67E+08	4817	0.151647	3.663997	0.437837	0.554688	0.039337	0	206	148	241	140	213	231	255	280	279	156
ENSMUSG00000067586	chr13	S1pr3	51408618	51408945	4484	-0.16054	3.109317	0.438003	0.554846	0.041982	0	97	92	235	122	206	107	221	99	214	116
ENSMUSG00000053333	chr1	Dis3l2	86703808	86703871	8901	-0.12384	4.069626	0.438248	0.555103	0.027131	0	219	202	398	325	262	202	344	259	407	266
ENSMUSG00000054863	chr15	Fam19a5	87625230	87625486	2575	0.170376	2.998026	0.438299	0.555114	0.048223	0	79	108	207	109	99	88	190	149	181	160
ENSMUSG00000080772	chr4	Gm12543	59833677	59834219	543	0.253729	0.144542	0.43869	0.555557	0.057149	0	7	13	20	16	17	17	29	12	23	18
ENSMUSG00000044847	chr11	Lsm11	45928269	45934023	6453	0.181727	1.686307	0.438977	0.555867	0.047503	0	41	26	74	34	66	37	61	71	84	51
ENSMUSG00000074793	chr2	Hspa12b	1.31E+08	1.31E+08	3685	0.137118	3.360167	0.439044	0.555898	0.032324	0	128	88	203	180	191	150	181	190	264	185
ENSMUSG00000042616	chr4	Oscp1	1.26E+08	1.26E+08	5254	-0.22714	1.299982	0.439223	0.556073	0.069289	0	50	32	56	24	41	48	45	28	44	31
ENSMUSG00000035152	chr11	Ap2b1	83299024	83299053	8755	-0.11793	5.549397	0.439279	0.55609	0.026057	0	611	473	1315	760	890	574	903	848	1044	747
ENSMUSG00000054405	chr4	Dnajc8	1.33E+08	1.33E+08	2555	0.120625	5.306876	0.439351	0.556128	0.026725	0	560	514	717	565	628	631	1023	629	882	622
ENSMUSG00000048661	chr10	Lemd3	1.21E+08	1.21E+08	4809	-0.12983	3.769549	0.439603	0.556395	0.028616	0	154	171	340	233	257	153	270	218	300	246
ENSMUSG00000000732	chr10	Icosl	78069360	78069535	2756	0.198069	1.602686	0.439942	0.55677	0.064411	0	24	28	72	28	77	49	59	66	59	49
ENSMUSG00000060166	chr16	Zdhhc8	18220754	18223377	4867	0.125751	5.120024	0.440189	0.55703	0.030268	0	471	287	807	565	608	503	672	558	1000	603
ENSMUSG00000023988	chr17	Bysl	47599331	47601898	3854	-0.12032	4.794237	0.440303	0.557121	0.026365	0	423	258	599	473	602	359	513	454	664	444
ENSMUSG00000001018	chr3	Snapin	90488026	90489593	2290	-0.12283	6.431775	0.440706	0.557549	0.029878	0	1428	1176	1887	1271	1360	1281	1961	1303	1884	1186
ENSMUSG00000035834	chr13	Polr3g	81673843	81676122	3936	-0.17729	1.802249	0.440726	0.557549	0.042084	0	64	38	76	59	50	52	66	55	76	42
ENSMUSG00000033233	chr3	Trim45	1.01E+08	1.01E+08	6005	-0.1745	1.443902	0.440906	0.557724	0.035803	0	31	32	52	49	60	34	51	46	56	38
ENSMUSG00000064326	chr12	Siva1	1.13E+08	1.13E+08	782	0.162702	3.374929	0.441429	0.558332	0.042629	0	134	153	148	164	149	164	219	159	272	180
ENSMUSG00000047656	chr19	Trpt1	6996131	6996524	1142	-0.12831	3.939628	0.441475	0.558338	0.029828	0	221	172	274	308	296	183	307	236	383	240
ENSMUSG00000043795	chr7	Prr33	1.42E+08	1.42E+08	2348	0.111534	7.687056	0.441518	0.558339	0.024901	0	2689	1975	4495	3087	4011	3064	4751	3795	4916	3183
ENSMUSG00000058835	chr2	Abi1	22940073	22942047	4032	-0.10953	4.158317	0.441585	0.55837	0.020308	0	234	205	442	282	345	229	398	304	367	274
ENSMUSG00000033585	chr7	Ndn	62348277	62349928	1652	0.141373	3.239211	0.441698	0.558433	0.034963	0	126	103	216	131	144	178	153	168	209	168
ENSMUSG00000040268	chr7	Plekha1	1.31E+08	1.31E+08	8527	-0.11117	4.989343	0.441719	0.558433	0.02302	0	420	343	676	572	664	396	656	535	764	468
ENSMUSG00000034109	chr3	Golim4	75875084	75878177	11072	0.152906	3.582434	0.441772	0.558447	0.0425	0	101	139	263	155	270	142	258	239	252	248
ENSMUSG00000001017	chr3	Chtop	90498956	90500107	3637	0.111659	6.862435	0.441819	0.558452	0.024584	0	1613	1383	2410	1588	1981	1765	2595	2071	2803	1861
ENSMUSG00000070572	chr4	Trmt112-ps2	1.49E+08	1.49E+08	378	0.320457	0.094829	0.442527	0.559294	0.086247	0	22	6	15	13	11	10	27	15	31	16
ENSMUSG00000022498	chr16	Txndc11	11074911	11075642	8835	0.131995	3.261659	0.442598	0.559331	0.029039	0	123	94	204	142	175	133	211	223	191	147
ENSMUSG00000037958	chr11	Ccdc55	77044292	77046754	3628	-0.11526	3.949348	0.443082	0.559878	0.023717	0	228	213	317	225	288	215	353	234	311	239
ENSMUSG00000059119	chr7	Nap1l4	1.44E+08	1.44E+08	2283	-0.11181	7.811344	0.443116	0.559878	0.02523	0	3269	2722	4856	3790	4107	3295	4932	3340	5045	3272
ENSMUSG00000020283	chr11	Pex13	23646479	23649590	4644	-0.11785	4.389487	0.443368	0.560144	0.025892	0	303	292	443	320	370	285	441	418	419	272
ENSMUSG00000038069	chr8	Cdkn2aip	47709344	47712294	3494	-0.15753	2.506824	0.443436	0.560176	0.041317	0	76	74	113	98	110	51	107	115	126	88
ENSMUSG00000053600	chr17	Zfp472	32965814	32965929	2376	0.198594	0.904319	0.443727	0.560491	0.043554	0	29	16	32	21	34	28	39	29	40	35
ENSMUSG00000020682	chr11	Mmp28	83440768	83442945	3874	-0.24051	1.454039	0.443854	0.560598	0.082435	0	40	32	46	45	66	28	38	74	34	42
ENSMUSG00000097868	chr2	A330069E16Rik	91237146	91237401	887	-0.25838	1.049468	0.444062	0.560807	0.105316	0	43	40	30	29	20	38	36	23	39	27
ENSMUSG00000021890	chr14	Eaf1	31495079	31495371	4238	0.109935	4.432473	0.444278	0.561027	0.02131	0	295	221	457	317	390	277	511	399	536	345
ENSMUSG00000026857	chr2	Ntmt1	30807826	30808083	2798	-0.1467	3.620465	0.444689	0.561492	0.038631	0	226	121	199	219	254	193	217	178	284	183
ENSMUSG00000031209	chrX	Heph	96455359	96455713	7662	-0.37665	1.09351	0.444914	0.561723	0.250211	0	64	41	29	14	24	37	23	61	14	21
ENSMUSG00000023249	chr9	Parp3	1.06E+08	1.06E+08	3699	0.128472	6.721751	0.445201	0.561978	0.033367	0	1299	906	1959	2005	2048	1627	2632	1559	2487	1838
ENSMUSG00000061723	chr7	Tnnt3	1.42E+08	1.42E+08	1391	-0.13763	14.55632	0.445167	0.561978	0.038939	0	412155	360843	488751	304515	412528	369415	466885	361759	596300	319888
ENSMUSG00000034601	chr12	2700049A03Rik	71136848	71138038	5879	-0.15498	2.254531	0.445501	0.562303	0.031644	0	65	52	119	70	97	58	109	82	83	73
ENSMUSG00000024764	chr19	Naa40	7225668	7228091	3275	-0.12885	3.824604	0.44561	0.562387	0.028863	0	194	131	366	249	276	175	299	193	364	219
ENSMUSG00000056220	chr1	Pla2g4a	1.5E+08	1.5E+08	6391	-0.26266	0.709066	0.445844	0.562629	0.076522	0	13	12	42	34	38	17	36	30	19	24
ENSMUSG00000034807	chr8	Colgalt1	71611024	71611444	3179	0.107808	5.863078	0.445964	0.562726	0.02281	0	723	616	1259	940	1012	790	1328	1024	1410	1004
ENSMUSG00000030738	chr7	Eif3c	1.27E+08	1.27E+08	3383	-0.1112	7.246879	0.446156	0.562915	0.025147	0	2043	1823	3501	2516	2906	2057	3141	2426	3666	2204
ENSMUSG00000032551	chr9	1110059G10Rik	1.23E+08	1.23E+08	3361	0.166686	2.735278	0.446283	0.563022	0.041565	0	89	98	125	76	98	111	172	116	154	86
ENSMUSG00000005102	chr2	Eif2ak4	1.18E+08	1.18E+08	7457	-0.15182	2.391688	0.4464	0.563116	0.032857	0	67	59	143	70	108	71	110	95	98	72
ENSMUSG00000022484	chr15	Hoxc10	1.03E+08	1.03E+08	1909	-0.12017	6.418425	0.446779	0.563352	0.029186	0	1385	1029	1930	1252	1564	1368	1621	1274	2126	1135
ENSMUSG00000022553	chr15	Maf1	76351294	76351659	2412	0.116107	6.711929	0.446799	0.563352	0.027052	0	1497	1281	2129	1454	1658	1546	2384	1767	2810	1593
ENSMUSG00000024271	chr18	Elp2	24603961	24604132	2789	0.114516	4.73749	0.446777	0.563352	0.023942	0	386	329	562	345	419	407	630	437	623	441
ENSMUSG00000041654	chr11	Slc39a11	1.13E+08	1.13E+08	3359	0.162633	2.042544	0.446637	0.563352	0.039859	0	52	36	97	58	68	52	101	96	88	54
ENSMUSG00000050211	chr2	Pla2g4e	1.2E+08	1.2E+08	6960	0.125643	4.830965	0.44677	0.563352	0.030823	0	382	237	756	376	520	401	680	444	810	429
ENSMUSG00000039116	chr10	Gpr126	14402585	14405438	6505	-0.21614	0.759649	0.446877	0.563396	0.050487	0	30	15	40	28	25	17	32	33	28	24
ENSMUSG00000022557	chr15	Bop1	76452996	76453378	2476	-0.11131	4.899738	0.447684	0.564361	0.02393	0	423	416	651	446	530	450	583	467	684	435

ENSMUSG00000019433	chr8	Gipc1	83652678	83652737	1615	0.119819	4.064323	0.447828	0.564488	0.025176	0	224	166	289	286	316	232	361	300	436	269
ENSMUSG00000035297	chr5	Cops4	1.01E+08	1.01E+08	5006	-0.11338	6.334523	0.447967	0.56461	0.02609	0	1158	1012	1810	1385	1357	1141	1813	1176	1821	1199
ENSMUSG00000041846	chr12	Smek1	1.01E+08	1.01E+08	4594	-0.11363	4.220317	0.448251	0.564913	0.023422	0	271	247	441	245	351	261	360	348	385	271
ENSMUSG00000002661	chr17	Alkbh7	56997339	56997567	1029	0.152446	3.777968	0.448322	0.564932	0.043127	0	159	118	203	296	260	183	283	241	354	255
ENSMUSG00000032902	chr3	Slc16a1	1.05E+08	1.05E+08	4426	-0.26429	5.305226	0.448351	0.564932	0.142796	0	353	213	476	1360	1133	390	1019	424	1035	549
ENSMUSG00000020514	chr11	Mrpl22	58171661	58171713	981	0.132063	4.305828	0.448428	0.564976	0.030816	0	289	280	331	269	293	308	474	325	484	305
ENSMUSG00000021661	chr13	Ankra2	98263158	98263476	3510	-0.12754	3.848676	0.448565	0.565071	0.029752	0	158	223	353	220	247	196	306	227	295	228
ENSMUSG00000053286	chr1	Trmt1l	1.51E+08	1.51E+08	8211	0.111561	4.199262	0.448588	0.565071	0.022555	0	240	185	371	309	316	285	432	315	368	327
ENSMUSG00000008450	chr8	Nutf2	1.06E+08	1.06E+08	1966	0.111536	5.428469	0.448727	0.565151	0.023928	0	599	518	877	636	670	668	1079	676	1033	667
ENSMUSG00000059534	chr11	Uqcr10	4701973	4702220	584	0.138001	8.064855	0.448737	0.565151	0.039422	0	3830	2708	3904	4879	4861	4062	7565	3944	6747	3905
ENSMUSG00000037148	chr8	Arhgap10	77250366	77251007	3038	-0.12376	5.394442	0.449013	0.565444	0.030049	0	587	377	908	800	921	601	799	587	1010	686
ENSMUSG00000040723	chr1	Rcsd1	1.66E+08	1.66E+08	10131	-0.12723	7.222176	0.449177	0.565598	0.033449	0	1967	1612	3408	2635	3122	1814	3241	1867	3970	2426
ENSMUSG00000032604	chr9	Qars	1.09E+08	1.09E+08	7267	0.111653	6.535748	0.449373	0.565757	0.025232	0	1200	1140	1994	1380	1436	1418	2140	1603	2218	1476
ENSMUSG00000064302	chr1	Clasp1	1.18E+08	1.18E+08	19275	-0.12435	5.719484	0.449389	0.565757	0.030671	0	656	463	1474	890	1134	635	1060	838	1266	853
ENSMUSG00000032547	chr9	Ryk	1.03E+08	1.03E+08	4534	-0.11937	6.413882	0.449532	0.565883	0.029264	0	1335	1198	2001	1128	1416	1239	1769	1330	1941	1230
ENSMUSG00000064373	chr15	Sepp1	3268547	3268768	2845	0.126275	7.959452	0.449692	0.566031	0.033192	0	3082	3069	5713	3338	4056	4084	4585	5537	4971	4156
ENSMUSG00000015994	chr8	Fnta	25998729	25999564	1874	0.122302	6.296551	0.450329	0.566779	0.030257	0	1113	1060	1510	1068	1174	1318	1835	1393	1777	1171
ENSMUSG00000079043	chr2	Fastkd5	1.31E+08	1.31E+08	3015	-0.12688	3.190517	0.450407	0.566823	0.026383	0	127	100	212	154	174	137	216	152	184	107
ENSMUSG00000022848	chr16	Dirc2	35694062	35698020	5395	0.111344	6.408942	0.450535	0.56693	0.025303	0	1185	828	1764	1375	1471	1296	1939	1362	2158	1375
ENSMUSG00000029600	chr5	Rita1	1.21E+08	1.21E+08	2836	-0.15925	2.00695	0.450658	0.567031	0.040033	0	73	40	81	63	75	52	84	52	100	55
ENSMUSG00000001056	chr11	Nhp2	51619735	51619977	1146	0.134317	4.169297	0.450882	0.56726	0.032333	0	298	233	286	236	275	299	417	333	390	270
ENSMUSG00000040818	chr14	Dennd6a	26579578	26579862	5710	-0.13614	3.094	0.450974	0.567267	0.030807	0	94	105	235	122	174	105	180	162	171	121
ENSMUSG00000070426	chr7	Rnf121	1.02E+08	1.02E+08	4427	0.10826	5.034678	0.450934	0.567267	0.022439	0	487	342	664	468	576	535	785	565	766	469
ENSMUSG00000070972	chr4	Dnajc25	58995062	58995105	4542	-0.13318	3.525465	0.451085	0.567354	0.031619	0	162	139	250	200	210	200	207	167	286	137
ENSMUSG00000021066	chr12	Atl1	69893105	69893344	2818	0.244771	0.616754	0.451173	0.56741	0.08301	0	17	12	40	20	18	18	60	23	24	19
ENSMUSG00000035934	chr9	Pknox2	36890982	36893057	6942	-0.11834	5.397938	0.451489	0.567754	0.027985	0	508	540	1138	642	762	534	1054	772	748	610
ENSMUSG00000061118	chr5	Dnajc30	1.35E+08	1.35E+08	1661	0.127258	4.382808	0.451748	0.568026	0.030932	0	277	185	348	380	412	326	452	319	556	343
ENSMUSG00000020380	chr11	Rad50	53649519	53650655	5375	-0.15468	2.716112	0.451969	0.56825	0.038964	0	70	90	137	115	137	96	148	114	98	99
ENSMUSG00000070327	chr11	Rnf213	1.19E+08	1.19E+08	16888	-0.14831	4.008883	0.452087	0.568344	0.040149	0	196	148	526	213	350	209	378	287	253	257
ENSMUSG00000032010	chr9	Usp2	44067021	44067220	4807	-0.12208	7.715477	0.452137	0.568353	0.031202	0	2743	2353	5191	3566	4102	3683	3710	3040	4857	2973
ENSMUSG00000025142	chr11	Aspscr1	1.21E+08	1.21E+08	4770	0.121123	4.900044	0.452265	0.568406	0.028413	0	370	401	673	369	478	467	572	527	787	485
ENSMUSG00000047819	chr3	Tigd4	84593574	84597032	3459	-0.20865	3.7585	0.452264	0.568406	0.084879	0	92	132	317	316	348	157	351	201	154	266
ENSMUSG00000030615	chr7	Tmem126a	90450700	90450935	1018	-0.12589	5.964178	0.452402	0.568525	0.032968	0	1059	845	1280	967	974	908	1503	840	1408	870
ENSMUSG00000018651	chr11	Tada2a	84078920	84079777	2974	-0.14989	4.247748	0.452738	0.568893	0.045254	0	313	307	455	195	302	281	388	249	490	253
ENSMUSG00000029084	chr5	Cd38	43868809	43869120	3014	-0.1492	2.722832	0.45297	0.569131	0.034016	0	76	66	146	107	169	83	142	108	139	96
ENSMUSG00000022771	chr16	Ppil2	17086555	17087115	6171	0.108466	4.851354	0.453276	0.569461	0.02244	0	403	330	582	436	468	477	688	499	596	462
ENSMUSG00000039461	chr9	Tcta	1.08E+08	1.08E+08	1838	-0.1113	4.985024	0.453843	0.570083	0.024816	0	447	384	589	593	600	466	680	530	710	411
ENSMUSG00000069920	chr8	B3gnt9	1.05E+08	1.05E+08	2516	0.177857	1.720753	0.453857	0.570083	0.053214	0	38	20	78	40	75	46	82	58	60	62
ENSMUSG00000017664	chr2	Slc35c2	1.65E+08	1.65E+08	3914	0.120631	4.518313	0.454026	0.570242	0.027412	0	335	268	448	316	379	361	417	422	646	337
ENSMUSG00000070709	chr7	1700049G17Rik	27907392	27912261	7518	-0.17788	1.093685	0.454188	0.57039	0.038004	0	27	30	53	29	35	29	45	28	45	28
ENSMUSG00000042487	chr9	Leo1	75441524	75441635	2192	-0.12351	4.419842	0.454346	0.570535	0.029531	0	338	284	541	252	380	304	449	306	438	364
ENSMUSG00000016382	chrX	Pls3	75785654	75786899	4238	-0.12489	4.355515	0.454613	0.570817	0.030016	0	227	235	429	388	452	234	486	378	375	322
ENSMUSG00000039834	chr2	Zfp335	1.65E+08	1.65E+08	4743	-0.14059	3.569498	0.454904	0.571112	0.033661	0	146	99	326	215	248	184	215	214	240	164
ENSMUSG00000049086	chr2	Bmyc	25706739	25707721	983	-0.15787	2.282805	0.454935	0.571112	0.041037	0	84	69	113	59	75	74	96	77	103	62
ENSMUSG00000024817	chr19	Uhrf2	30030513	30030931	8590	0.110356	3.853333	0.455209	0.571402	0.021414	0	176	164	312	214	253	217	326	289	311	220
ENSMUSG00000053329	chr10	D10Jhu81e	78162067	78162718	1363	0.12624	7.808233	0.455396	0.571583	0.033936	0	2773	2183	3668	4295	4298	3426	5687	3514	5625	3443
ENSMUSG00000029346	chr5	Srrd	1.12E+08	1.12E+08	1638	0.171803	2.127492	0.455488	0.571644	0.044274	0	59	46	68	63	84	83	115	56	94	65
ENSMUSG00000002688	chr12	Prkd1	50341231	50342220	3778	-0.17292	1.718599	0.455641	0.571714	0.037404	0	43	38	75	53	65	51	57	52	53	56
ENSMUSG00000026500	chr1	Cox20	1.78E+08	1.78E+08	883	0.119753	4.003917	0.455673	0.571714	0.025865	0	213	178	268	280	276	261	367	265	345	274
ENSMUSG00000085793	chr12	Lin52	84451508	84451543	2144	0.115813	3.827569	0.455616	0.571714	0.025013	0	169	127	301	258	252	214	328	245	310	244
ENSMUSG00000087644	chrX	Gm14703	7651106	7652711	1820	-0.37972	-0.20466	0.455781	0.571796	0.205275	0	3	5	10	29	23	8	17	4	14	17
ENSMUSG00000021144	chr12	Mta1	1.13E+08	1.13E+08	3104	-0.11063	4.791357	0.456931	0.573184	0.023735	0	389	287	715	453	513	370	512	466	683	412
ENSMUSG00000020089	chr10	Ppa1	61648552	61648791	2902	0.126783	5.497403	0.457013	0.573233	0.032938	0	689	508	788	688	741	694	924	1099	958	611
ENSMUSG00000024350	chr18	Dnajc18	35671103	35675243	5169	-0.11091	5.054778	0.457361	0.573615	0.024214	0	424	350	844	539	686	465	625	502	814	522
ENSMUSG00000080746	chr4	Rpsa-ps12	1.49E+08	1.49E+08	892	0.264725	0.36801	0.457597	0.573857	0.080688	0	8	23	18	15	20	26	29	17	27	18
ENSMUSG00000030433	chr7	Sbk2	4956134	4957713	2426	0.193628	6.835204	0.45768	0.573907	0.080776	0	1532	774	1831	2035	2550	2313	1285	1655	3840	1912
ENSMUSG00000009640	chr4	Dmap1	1.18E+08	1.18E+08	2636	0.129223	3.859314	0.458082	0.574357	0.031287	0	208	155	221	226	284	254	271	263	317	251
ENSMUSG00000029535	chr5	Triap1	1.15E+08	1.15E+08	1088	0.127258	4.292106	0.45815	0.574388	0.030094	0	287	265	328	272	305	325	486	369	394	285
ENSMUSG00000045466	chr6	Zfp956	47953390	47953582	2968	-0.12151	3.465571	0.458426	0.57468	0.027008	0	166	129	275	159	199	130	233	160	264	183
ENSMUSG00000041695	chr11	Kcnj2	1.11E+08	1.11E+08	5444	-0.19911	5.865494	0.458626	0.574875	0.084986	0	514	469	1558	1186	1580	399	1453	690	1756	920
ENSMUSG00000021903	chr14	Galnt15	32028989	32030031	6326	0.134055	4.678774	0.45868	0.574888	0.03807	0	218	238	704	412	482	434	500	490	521	457
ENSMUSG00000031708	chr8	Tecr	83571700	83571935	1334	0.146474	8.291075	0.458943	0.575164	0.046513	0	5183	4457	6085	3497	3889	5052	6534	5380	8720	4670
ENSMUSG00000053226	chr8	Dand5	84815405	84816533	1584	0.123626	3.532663	0.459009	0.575192	0.027348	0	155	102	210	204	218	169	287	189	270	188
ENSMUSG00000036686	chr8	Cc2d1a	84132828	84133257	3710	-0.11403	3.990095	0.459116	0.575273	0.024371	0	230	170	343	270	319	200	291	268	408	234
ENSMUSG00000041215	chr16	Yeats2	20141063	20141235	6116	-0.17806	2.275767	0.459286	0.575431	0.048214	0	64	37	133	87	99	50	112	93	78	75

ENSMUSG00000027984	chr3	Hadh	1.31E+08	1.31E+08	4977	-0.17066	7.425748	0.459581	0.575583	0.063303	0	2007	1412	2676	4805	3834	2264	3654	2683	4137	2289
ENSMUSG00000033373	chr12	Fntb	76765589	76765638	3987	-0.11011	5.257604	0.459571	0.575583	0.025451	0	618	488	747	612	675	523	911	552	849	564
ENSMUSG00000091780	chr15	Sco2	89371639	89372465	1143	0.147353	3.139633	0.45953	0.575583	0.038239	0	102	90	126	175	165	124	197	147	218	155
ENSMUSG00000092241	chr17	Gm20522	35122738	35123238	784	0.207197	1.3366	0.459555	0.575583	0.056117	0	24	21	40	51	45	36	59	32	73	40
ENSMUSG00000024014	chr17	Pim1	29490812	29491225	2638	0.232765	3.945039	0.459642	0.575605	0.109896	0	220	324	254	106	138	295	460	232	329	210
ENSMUSG00000030533	chr7	Unc45a	80325292	80325877	3991	0.130253	3.327029	0.460126	0.576156	0.031736	0	124	77	198	182	197	151	222	189	216	169
ENSMUSG00000001062	chr8	Vps9d1	1.23E+08	1.23E+08	5153	-0.11559	4.445458	0.460214	0.57621	0.02649	0	344	223	442	395	414	320	418	358	546	279
ENSMUSG00000028920	chr4	Fbxo42	1.41E+08	1.41E+08	5934	-0.12187	3.946102	0.460275	0.57621	0.027712	0	220	136	391	257	319	169	337	269	364	226
ENSMUSG00000034175	chr11	Rhbdd3	5098926	5099566	2790	-0.13168	5.142938	0.460299	0.57621	0.037037	0	580	550	694	491	558	486	617	613	933	458
ENSMUSG00000019437	chr11	Tlcd1	78176711	78176887	5009	0.300396	1.868696	0.460983	0.576957	0.180879	0	34	26	83	87	30	37	26	132	96	60
ENSMUSG00000028759	chr4	Hp1bp3	1.38E+08	1.38E+08	8433	-0.10571	6.441523	0.460972	0.576957	0.023881	0	1179	1064	2056	1410	1586	1155	1762	1523	1828	1386
ENSMUSG00000098954	chr4	Mir7658	1.56E+08	1.56E+08	57	0.227141	0.075201	0.461106	0.577057	0.061128	0	11	8	22	11	19	17	25	24	14	12
ENSMUSG00000003809	chr8	Gcdh	84886393	84887053	2754	-0.12049	5.538313	0.461237	0.577167	0.030801	0	560	506	929	981	935	556	1182	723	1012	674
ENSMUSG00000049907	chr5	Rasl11b	74195288	74195590	1941	0.238204	1.34167	0.461436	0.577361	0.094783	0	25	23	29	47	54	37	40	79	43	36
ENSMUSG00000053647	chr5	Gper1	1.39E+08	1.39E+08	2537	-0.21753	0.693275	0.461514	0.577404	0.053701	0	17	16	41	31	28	21	29	16	42	21
ENSMUSG00000032553	chr9	Srprb	1.03E+08	1.03E+08	4287	0.099515	5.273901	0.461585	0.577438	0.020325	0	518	402	856	560	702	571	860	708	868	647
ENSMUSG00000000378	chr11	Ccm2	6546887	6547029	3666	0.124789	3.618979	0.461667	0.577462	0.027629	0	167	134	236	210	185	184	258	258	295	171
ENSMUSG00000092356	chr2	Gm20532	26586639	26586681	780	0.143147	3.460728	0.461691	0.577462	0.036705	0	144	113	157	213	194	173	269	184	279	154
ENSMUSG00000032407	chr9	U2surp	95456898	95461543	14642	-0.1073	4.66088	0.461787	0.577528	0.022565	0	339	284	639	398	483	307	567	432	505	419
ENSMUSG00000020238	chr10	Ncln	81486249	81487605	3465	0.104627	5.656679	0.461918	0.577637	0.023155	0	675	495	1085	778	927	769	985	1018	1150	825
ENSMUSG00000023868	chr17	Pde10a	8525372	8525815	12598	-0.20713	1.047483	0.462071	0.577774	0.052996	0	21	17	51	31	55	23	48	33	43	22
ENSMUSG00000043487	chr12	Acot6	84100654	84101428	3388	-0.14677	2.498515	0.462224	0.577911	0.035926	0	80	67	107	89	126	70	99	82	137	95
ENSMUSG00000048076	chr11	Arf1	59211412	59212695	2089	0.110023	7.919066	0.462313	0.577968	0.02651	0	3535	2853	5080	3388	3773	3659	5672	4143	5911	3785
ENSMUSG00000027677	chr3	Ttc14	33800195	33800436	11072	-0.14694	3.397341	0.462543	0.578201	0.039453	0	130	132	273	150	214	143	224	232	145	151
ENSMUSG00000046318	chr18	Ccbe1	66045302	66047469	9511	-0.22008	1.684264	0.463091	0.578777	0.079427	0	22	36	65	47	108	32	63	53	74	44
ENSMUSG00000092118	chr7	Fancf	51860577	51862267	1691	0.251369	0.283702	0.463072	0.578777	0.06681	0	11	15	30	12	14	15	23	32	22	17
ENSMUSG00000045193	chr10	Cirbp	80165985	80166076	2604	0.15612	5.089982	0.463198	0.578856	0.050866	0	533	531	573	343	494	579	712	506	1019	496
ENSMUSG00000026142	chr1	Rhbdd1	82316452	82316648	6966	-0.12686	3.388935	0.463335	0.578972	0.029293	0	135	122	266	158	207	107	215	198	222	172
ENSMUSG00000005803	chr2	Sqrdl	1.23E+08	1.23E+08	4084	-0.10995	5.706861	0.463506	0.579132	0.026033	0	801	722	1082	777	909	714	1165	987	993	737
ENSMUSG00000022892	chr16	App	84954440	84955432	3128	0.143189	6.88835	0.463638	0.579205	0.045386	0	1097	1002	2461	2127	2697	1549	2487	2306	2344	2547
ENSMUSG00000031533	chr8	Mrps31	22411340	22411584	1536	-0.10718	4.724409	0.463652	0.579205	0.02371	0	359	316	520	470	529	342	629	391	603	390
ENSMUSG00000002109	chr2	Ddb2	91211572	91212012	2736	0.18264	1.934601	0.464016	0.579605	0.04874	0	58	55	69	39	52	66	83	69	79	61
ENSMUSG00000024052	chr17	Lpin2	71182560	71183257	12233	0.167424	1.895201	0.464077	0.579626	0.045306	0	47	30	81	49	73	57	61	82	99	50
ENSMUSG00000015971	chr14	Actr8	29978337	29978588	2121	-0.10492	4.927262	0.464304	0.579856	0.022772	0	453	387	707	484	492	434	640	459	679	471
ENSMUSG00000018167	chr11	Stard3	98358368	98358508	3557	-0.11401	4.312315	0.464472	0.580011	0.026158	0	279	251	421	331	366	316	382	268	504	276
ENSMUSG00000032194	chr9	Kank2	21766773	21769004	4853	0.112925	5.122648	0.464627	0.58015	0.027065	0	340	381	788	560	676	515	687	701	806	581
ENSMUSG00000097392	chr5	D930016D06Rik	1.05E+08	1.05E+08	4509	-0.14433	2.76796	0.465253	0.580876	0.0354	0	96	86	156	90	143	71	126	120	143	123
ENSMUSG00000053730	chr4	Tmem39b	1.3E+08	1.3E+08	2286	-0.17083	1.440347	0.465593	0.581246	0.03785	0	34	34	66	50	39	36	47	43	58	40
ENSMUSG00000001855	chr2	Nup214	31974436	31974608	9659	-0.13317	3.804976	0.465998	0.581698	0.032824	0	183	126	429	198	289	174	255	261	302	219
ENSMUSG00000028788	chr4	Ptp4a2	1.3E+08	1.3E+08	4377	-0.11633	10.00834	0.466356	0.582089	0.030534	0	15928	14496	23628	13860	17486	13989	23629	16480	22667	14688
ENSMUSG00000025417	chr10	Pip4k2c	1.27E+08	1.27E+08	3374	0.10466	4.192423	0.466524	0.582244	0.021062	0	248	177	364	302	329	270	426	345	407	282
ENSMUSG00000039157	chr2	Fam102a	32535332	32536232	6066	0.151852	2.615005	0.466756	0.582479	0.043724	0	67	46	138	105	117	89	148	137	142	70
ENSMUSG00000038816	chr4	Ctnnal1	56810935	56812388	7661	-0.17291	2.562598	0.467014	0.582746	0.056042	0	57	82	142	108	110	65	158	120	78	81
ENSMUSG00000072847	chr11	A530017D24Rik	61864568	61866225	2614	0.131763	2.549545	0.467615	0.583441	0.028732	0	72	53	122	86	116	89	138	104	124	95
ENSMUSG00000030298	chr6	Sec13	1.14E+08	1.14E+08	1663	-0.1024	5.854816	0.467708	0.583484	0.022636	0	841	643	1277	1003	1077	820	1229	910	1203	935
ENSMUSG00000039016	chr9	Timm8b	50603901	50604039	527	-0.13068	6.107703	0.467737	0.583484	0.038228	0	1175	998	1180	1066	1173	1092	1726	1023	1358	865
ENSMUSG00000084067	chr2	Gm14269	1.7E+08	1.7E+08	306	-0.23354	0.120136	0.467829	0.583543	0.075703	0	23	11	22	17	11	12	29	13	15	14
ENSMUSG00000023830	chr17	Igf2r	12682406	12684126	9438	-0.12484	6.46973	0.468	0.583702	0.034452	0	1033	814	2510	1487	1946	1038	1983	1301	2027	1500
ENSMUSG00000058922	chr9	Gm10052	1.24E+08	1.24E+08	960	0.170511	1.861008	0.468186	0.583879	0.038105	0	43	46	55	52	67	56	89	55	86	57
ENSMUSG00000057130	chr18	Txnl4a	80206795	80206901	2185	0.10331	4.197568	0.468737	0.584511	0.020866	0	254	193	396	264	320	276	391	370	394	292
ENSMUSG00000029060	chr4	Mib2	1.56E+08	1.56E+08	4724	0.103091	4.425442	0.469032	0.584824	0.021838	0	269	213	524	323	368	352	492	379	484	322
ENSMUSG00000025574	chr11	Tk1	1.18E+08	1.18E+08	5198	0.178083	1.978276	0.469149	0.584859	0.050297	0	55	47	81	59	44	67	75	54	114	63
ENSMUSG00000046861	chr4	Hectd3	1.17E+08	1.17E+08	4901	-0.10202	4.817061	0.469124	0.584859	0.021395	0	407	300	620	504	527	381	579	491	619	419
ENSMUSG00000085315	chr2	A430018G15Rik	52425012	52425155	1713	0.310783	-0.01946	0.469407	0.585126	0.097602	0	19	13	8	8	12	18	16	19	17	17
ENSMUSG00000033285	chr3	Wdr3	1E+08	1E+08	5218	-0.12873	3.520745	0.469474	0.585155	0.032624	0	205	145	245	154	197	181	272	180	197	161
ENSMUSG00000044709	chr7	Gemin7	19564946	19565676	1519	0.120655	5.482356	0.469612	0.585272	0.031064	0	712	595	828	567	647	732	1031	767	1073	666
ENSMUSG00000047420	chr6	Fam180a	35312746	35313869	1528	0.224773	0.323451	0.469846	0.585508	0.050356	0	13	9	18	19	26	21	29	23	24	15
ENSMUSG00000050315	chr3	Synpo2	1.23E+08	1.23E+08	9403	-0.13121	9.38037	0.470028	0.58568	0.03943	0	8258	6385	14517	13554	14541	7498	16651	8823	16055	10634
ENSMUSG00000064284	chr15	Cdpf1	85806972	85807538	1215	-0.11224	4.079786	0.470181	0.585816	0.026601	0	284	205	313	278	304	223	391	273	400	216
ENSMUSG00000040990	chrX	Sh3kbp1	1.6E+08	1.6E+08	10100	-0.18125	5.188096	0.470339	0.585958	0.072534	0	340	208	812	928	987	471	750	539	761	602
ENSMUSG00000044950	chr11	Pwwp2a	43681998	43682616	5508	-0.14717	2.294138	0.470478	0.586076	0.034535	0	70	57	138	72	76	59	107	74	108	73
ENSMUSG00000004994	chr8	Ccdc130	84257795	84258926	2694	0.145285	2.42153	0.470531	0.586087	0.035939	0	65	59	99	69	111	79	111	97	104	107
ENSMUSG00000040521	chr10	Tsfm	1.27E+08	1.27E+08	2904	0.133266	4.012572	0.4708	0.586366	0.035898	0	224	145	232	299	323	214	366	262	416	291
ENSMUSG00000066894	chr5	Vsig10	1.17E+08	1.17E+08	5122	-0.13261	2.777607	0.47098	0.586536	0.028276	0	93	70	160	115	140	93	161	98	136	105
ENSMUSG00000003662	chr2	Ciao1	1.27E+08	1.27E+08	3197	0.10234	5.507559	0.471158	0.586647	0.022257	0	577	563	926	670	775	649	1118	765	1073	737

ENSMUSG00000020067	chr10	Mypn	63115795	63117026	5246	-0.11452	8.516144	0.47115	0.586647	0.030056	0	4959	3805	10284	5593	7010	4754	7095	5649	9041	5878
ENSMUSG00000032000	chr9	Birc3	7848699	7849456	5009	0.145462	2.763124	0.471641	0.587193	0.040528	0	68	65	153	114	122	118	194	102	155	82
ENSMUSG00000058620	chr2	Adra2b	1.27E+08	1.27E+08	4014	-0.2089	0.487995	0.472036	0.58763	0.045549	0	21	15	29	21	26	16	24	17	25	27
ENSMUSG00000034911	chr8	Ushbp1	71384274	71385793	3549	0.129712	3.617362	0.472561	0.588229	0.032768	0	142	121	213	242	217	181	274	258	293	165
ENSMUSG00000034203	chr6	Chchd4	91464276	91465313	1245	-0.10978	4.31752	0.472666	0.588305	0.025957	0	314	260	370	323	362	284	420	323	488	252
ENSMUSG00000020072	chr10	Pbld1	63024315	63024465	4889	0.230844	0.788797	0.473058	0.588737	0.067439	0	27	15	21	31	23	26	44	39	27	23
ENSMUSG00000017715	chr11	Pgs1	1.18E+08	1.18E+08	5333	0.108548	4.80521	0.473162	0.588811	0.024457	0	406	307	499	434	493	450	581	462	725	435
ENSMUSG00000039117	chr2	Taf4a	1.8E+08	1.8E+08	4627	-0.12885	3.204945	0.47322	0.588828	0.03036	0	152	93	207	154	165	112	188	178	163	152
ENSMUSG00000020271	chr11	Fbxw11	32642724	32642935	4327	-0.11168	6.170431	0.473655	0.589314	0.028063	0	1057	815	2004	953	1334	1022	1414	1209	1699	1018
ENSMUSG00000030714	chr7	Ccdc101	1.27E+08	1.27E+08	1802	0.12233	4.172751	0.473716	0.589334	0.029761	0	290	225	374	228	244	282	369	333	448	279
ENSMUSG00000021368	chr13	Tbc1d7	43151744	43151980	1259	0.10651	4.119643	0.473997	0.589629	0.022319	0	208	198	335	288	310	267	357	300	416	296
ENSMUSG00000024084	chr17	Qpct	79051906	79052388	1924	-0.22549	1.621322	0.474403	0.590064	0.086019	0	44	45	97	25	52	49	45	71	50	31
ENSMUSG00000026309	chr1	Ilkap	91373861	91375538	5556	0.10611	5.323545	0.474525	0.590064	0.024176	0	549	493	721	606	684	658	878	650	962	642
ENSMUSG00000032497	chr9	Lrrfip2	1.11E+08	1.11E+08	3260	0.108422	6.123042	0.474508	0.590064	0.026393	0	973	787	1396	1011	1217	1078	1500	1082	1877	1124
ENSMUSG00000037904	chr12	Ankrd9	1.11E+08	1.11E+08	3160	0.125501	6.611689	0.474505	0.590064	0.036398	0	1465	973	2448	1196	1593	1905	1801	1940	2055	1445
ENSMUSG00000032667	chr6	Pon2	5264147	5265479	4655	0.111015	5.666846	0.474757	0.590298	0.027084	0	666	625	829	809	928	831	1211	944	1155	699
ENSMUSG00000085241	chr4	Snhg3	1.32E+08	1.32E+08	986	0.197086	2.591484	0.474877	0.590391	0.069931	0	107	89	99	68	59	95	162	103	161	70
ENSMUSG00000020042	chr10	Btbd11	85386814	85388478	10033	0.218499	0.460515	0.47497	0.590451	0.050776	0	15	13	36	13	19	15	27	26	35	22
ENSMUSG00000001120	chr10	Pcbp3	76761857	76762526	2933	0.169011	1.347078	0.475159	0.590631	0.037259	0	31	28	60	33	34	37	64	38	62	37
ENSMUSG00000037827	chr6	Gm5884	1.29E+08	1.29E+08	2259	0.135215	2.691425	0.475605	0.591131	0.033453	0	80	58	140	107	110	79	157	98	171	113
ENSMUSG00000038827	chr4	Fam206a	56802345	56803647	5574	0.204254	1.254213	0.475654	0.591135	0.064314	0	29	19	35	28	61	23	56	40	55	50
ENSMUSG00000019689	chr6	1110001J03Rik	38533502	38533711	689	0.114053	5.201443	0.475947	0.591444	0.028276	0	535	367	607	637	667	549	942	590	927	538
ENSMUSG00000035086	chr11	Becn1	1.01E+08	1.01E+08	7065	-0.10576	6.012792	0.476052	0.591464	0.025566	0	982	853	1376	932	1195	948	1341	1014	1446	952
ENSMUSG00000072115	chr14	Ang	51091077	51091253	1273	0.15572	2.645882	0.476041	0.591464	0.047502	0	75	71	149	83	96	129	129	120	91	106
ENSMUSG00000070953	chr2	Rabepk	34777556	34779529	3814	-0.13662	3.022782	0.476332	0.591757	0.037882	0	111	132	146	119	151	126	156	115	185	117
ENSMUSG00000033174	chr6	Mgll	88724412	88724571	4868	0.173082	5.633438	0.476446	0.591787	0.069022	0	698	532	805	809	852	609	855	1748	899	635
ENSMUSG00000071661	chr19	Zbtb3	8802530	8802685	2037	-0.23834	0.308147	0.476442	0.591787	0.070067	0	17	13	24	26	18	9	35	17	16	19
ENSMUSG00000037750	chr11	Fam222b	78094660	78094791	3490	-0.12489	3.29058	0.476531	0.591837	0.02904	0	161	102	246	130	187	132	193	142	227	157
ENSMUSG00000029406	chr5	Pitpnm2	1.24E+08	1.24E+08	12843	-0.12143	4.901738	0.476734	0.592034	0.032172	0	425	237	675	601	624	373	617	541	694	416
ENSMUSG00000025216	chr19	Lbx1	45232684	45234257	2484	-0.11956	5.891767	0.477069	0.592394	0.033132	0	1018	748	1329	863	965	795	1133	975	1653	741
ENSMUSG00000024072	chr17	Yipf4	74489493	74489794	2133	0.122012	4.14442	0.4773	0.592592	0.029312	0	258	248	319	208	291	246	402	322	432	286
ENSMUSG00000045573	chr4	Penk	4133531	4134507	1634	-0.20703	3.633591	0.477317	0.592592	0.092266	0	117	157	411	160	270	307	134	196	243	121
ENSMUSG00000004843	chr16	Chmp2b	65539133	65540250	1838	0.111244	5.163846	0.478391	0.593869	0.026733	0	479	460	682	548	555	454	795	617	935	633
ENSMUSG00000042569	chr11	Dhrs7b	60830631	60830731	3325	0.113383	4.787544	0.47845	0.593887	0.02704	0	410	350	511	392	424	396	644	577	618	396
ENSMUSG00000024661	chr19	Fth1	9982703	9982983	866	0.133757	10.65094	0.478645	0.594073	0.04264	0	24598	22674	30685	19770	22024	28945	34051	27852	42976	20918
ENSMUSG00000004462	chr16	Tbccd1	22813215	22813956	2702	0.12522	3.159731	0.479321	0.594801	0.027823	0	119	93	159	163	141	133	217	155	202	140
ENSMUSG00000030020	chr6	Prickle2	92370892	92376820	8637	-0.26025	1.225682	0.479305	0.594801	0.111494	0	15	17	76	39	62	15	52	45	32	41
ENSMUSG00000026834	chr2	Acvr1c	58267453	58275043	9292	0.465808	0.990467	0.479366	0.594801	0.437289	0	43	31	28	6	10	28	10	112	14	26
ENSMUSG00000031214	chrX	Ophn1	98554277	98558405	13100	0.147373	2.442109	0.47951	0.594924	0.036742	0	81	63	116	63	83	78	110	118	111	91
ENSMUSG00000021807	chr14	2700060E02Rik	19811402	19812237	1510	0.127943	6.867282	0.479769	0.595189	0.038315	0	1744	1735	2050	1454	1656	1920	2905	1943	2731	1726
ENSMUSG00000037366	chr4	Pafah2	1.34E+08	1.34E+08	3616	0.153705	1.718858	0.479932	0.595336	0.035808	0	36	30	65	56	58	53	79	56	62	55
ENSMUSG00000029093	chr5	Sorcs2	36017180	36019392	8803	0.174086	1.672839	0.480215	0.595632	0.057415	0	33	19	65	56	67	33	71	69	67	59
ENSMUSG00000019933	chr10	2310015B20Rik	70204664	70204759	1180	-0.19194	5.826182	0.480396	0.595801	0.087645	0	1106	1146	1087	551	643	1014	1398	653	1053	725
ENSMUSG00000038074	chr6	Fkbp14	54577604	54579686	4185	0.113959	3.2176	0.480543	0.595928	0.023538	0	112	106	193	135	169	139	190	176	213	154
ENSMUSG00000018433	chr11	Nol11	1.07E+08	1.07E+08	5357	-0.10584	3.986948	0.481405	0.59694	0.022586	0	227	169	401	242	301	216	393	242	325	228
ENSMUSG00000046618	chr2	Olfml2a	38931978	38932181	5579	-0.17938	3.005673	0.481724	0.59728	0.065148	0	57	72	256	140	198	83	194	131	146	132
ENSMUSG00000020063	chr10	Sirt1	63319005	63320964	5331	-0.12667	3.045089	0.482225	0.59779	0.029934	0	108	102	221	119	146	100	192	143	148	132
ENSMUSG00000045980	chr11	Tmem104	1.15E+08	1.15E+08	4610	0.113331	3.502474	0.482193	0.59779	0.027279	0	135	99	290	171	202	160	232	221	265	190
ENSMUSG00000010054	chr9	Tusc2	1.08E+08	1.08E+08	1785	0.109992	5.678861	0.482834	0.598488	0.027527	0	777	651	891	710	840	859	1184	902	1181	740
ENSMUSG00000061411	chr2	Nol4l	1.53E+08	1.53E+08	9083	-0.19781	0.63985	0.483026	0.59867	0.046842	0	22	14	45	19	28	18	34	19	34	20
ENSMUSG00000025190	chr19	Got1	43499752	43500557	2539	-0.25023	8.475908	0.483136	0.598738	0.151341	0	2416	1750	5185	11896	11172	3265	8827	4796	8384	5445
ENSMUSG00000031310	chrX	Zmym3	1.01E+08	1.01E+08	8021	-0.10606	3.859027	0.483221	0.598738	0.022322	0	184	179	378	210	272	210	309	237	310	208
ENSMUSG00000036854	chr7	Hspb6	30552178	30553062	2299	-0.23504	9.221754	0.483261	0.598738	0.133804	0	4403	3077	10718	19685	16345	5833	12846	6945	13855	11475
ENSMUSG00000044906	chr18	4930503L19Rik	70453140	70453388	2291	-0.2337	0.659498	0.483177	0.598738	0.067326	0	24	14	39	25	28	23	46	16	18	21
ENSMUSG00000020372	chr11	Gnb2l1	48800332	48803968	5119	0.113719	8.403747	0.484011	0.599577	0.031349	0	4709	4638	6268	4862	5056	5356	8277	5856	7711	5181
ENSMUSG00000026578	chr1	Ccdc181	1.64E+08	1.64E+08	1909	-0.11691	3.6039	0.484029	0.599577	0.029724	0	188	174	257	171	205	179	245	178	304	162
ENSMUSG00000047370	chr7	Gm7367	60155538	60156170	633	0.221297	0.120914	0.484108	0.599619	0.069533	0	8	8	29	11	19	15	23	26	22	10
ENSMUSG00000055652	chr7	Klhl25	75848338	75848484	3385	0.136388	2.359567	0.484225	0.599708	0.03373	0	54	51	97	80	108	87	117	91	109	76
ENSMUSG00000025025	chr19	Mxi1	53310506	53310973	5619	-0.10972	5.561888	0.484398	0.599838	0.028203	0	524	551	1054	914	944	531	1084	784	1077	740
ENSMUSG00000090110	chrX	Mtcp1	75404846	75405218	1310	-0.16865	2.014847	0.48442	0.599838	0.055024	0	62	71	89	55	49	57	73	69	90	51
ENSMUSG00000004567	chr8	Mcoln1	3500457	3500627	3260	0.09896	4.673791	0.484532	0.59992	0.021538	0	344	263	544	385	459	427	554	465	591	368
ENSMUSG00000026255	chr1	Efhd1	87264363	87264754	2125	-0.20024	2.073916	0.484677	0.600044	0.075623	0	75	44	112	41	89	55	49	101	69	66
ENSMUSG00000032193	chr9	Ldlr	21723576	21723844	4531	-0.19179	3.963727	0.484759	0.600089	0.082867	0	120	87	469	281	493	214	371	259	319	178
ENSMUSG00000023990	chr17	Tfeb	47737030	47737316	5669	-0.11835	6.472009	0.485021	0.600358	0.033909	0	1453	1298	2036	1144	1377	1093	1790	1491	1975	1467
ENSMUSG00000104496	chr1	RP23-13N24.1	1.4E+08	1.4E+08	1369	-0.22699	0.142595	0.485142	0.600452	0.045925	0	15	13	27	15	17	15	17	15	25	12

ENSMUSG00000022621	chr15	Rabl2	89582533	89583430	2960	0.18267	1.045317	0.4858	0.60121	0.04632	0	20	19	51	33	27	25	58	33	43	33
ENSMUSG00000015711	chr3	Prune	95253674	95255427	3618	0.110194	6.853317	0.486178	0.601335	0.029303	0	1599	1296	2696	1526	1918	1656	3109	1710	3011	1734
ENSMUSG00000022095	chr14	Fam160b2	70583296	70585183	4033	-0.10516	6.123984	0.486102	0.601335	0.026426	0	969	825	1444	1089	1511	983	1347	1096	1749	1014
ENSMUSG00000046808	chr5	Atp10d	72203329	72203563	7848	-0.19498	1.082988	0.486164	0.601335	0.057202	0	32	23	52	35	32	35	46	42	27	20
ENSMUSG00000051586	chr6	Mical3	1.21E+08	1.21E+08	7398	-0.12284	4.669967	0.486219	0.601335	0.033455	0	354	184	649	472	555	351	577	424	519	364
ENSMUSG00000055137	chr13	Sugct	16857855	16858018	1311	0.294904	0.018767	0.48607	0.601335	0.103137	0	9	14	6	15	19	14	15	24	16	20
ENSMUSG00000058709	chr7	Egln2	27158658	27159211	2800	-0.10831	6.925138	0.486073	0.601335	0.028543	0	1862	1679	2677	1662	2163	1715	2295	1992	2824	1879
ENSMUSG00000059713	chr4	Rcan3	1.35E+08	1.35E+08	5111	-0.16902	2.540645	0.486099	0.601335	0.051848	0	52	63	123	105	156	96	93	87	116	92
ENSMUSG00000040350	chr11	Trim7	48826140	48826279	7149	0.115013	5.379583	0.486564	0.601706	0.030969	0	550	417	648	751	823	591	968	834	814	728
ENSMUSG00000091050	chr15	9330020H09Rik	98567324	98567525	2147	0.281823	-0.08689	0.48705	0.602251	0.078678	0	9	12	16	17	5	16	17	15	23	12
ENSMUSG00000017550	chr11	Atad5	80089400	80089836	7532	-0.22435	0.479215	0.487314	0.602369	0.053505	0	14	16	35	25	23	23	30	13	23	19
ENSMUSG00000054226	chr6	Tprkb	85915738	85915790	3491	-0.10984	4.549116	0.487327	0.602369	0.02785	0	369	343	485	313	401	367	490	396	473	320
ENSMUSG00000058240	chr16	Cryzl1	91689322	91689915	4353	-0.11668	3.70718	0.487326	0.602369	0.0309	0	199	196	251	196	217	154	308	212	263	210
ENSMUSG00000091625	chr6	Lsm5	56701063	56701289	774	0.207491	1.90027	0.487234	0.602369	0.075919	0	66	54	65	25	52	64	102	55	75	60
ENSMUSG00000034781	chr10	Gna11	81528724	81530985	4097	-0.10406	5.433234	0.487638	0.602697	0.025062	0	585	401	1045	793	861	576	887	772	991	607
ENSMUSG00000022885	chr16	St6gal1	23224740	23225229	4916	-0.14204	2.618258	0.487883	0.602944	0.036416	0	66	74	159	91	132	67	128	117	115	99
ENSMUSG00000074733	chr19	5830428H23Rik	61053840	61054421	6503	0.178462	2.149533	0.488294	0.603395	0.058077	0	66	62	102	42	51	61	95	101	84	76
ENSMUSG00000028479	chr4	Gne	44034075	44037353	6358	-0.12933	3.084203	0.48855	0.603656	0.030479	0	109	74	229	129	191	118	172	145	178	121
ENSMUSG00000047821	chr11	Trim16	62820231	62820999	4568	-0.12769	5.493571	0.488653	0.603727	0.038818	0	614	329	937	979	1019	613	1036	758	948	615
ENSMUSG00000042305	chr1	Tmem183a	1.34E+08	1.34E+08	3564	0.106529	3.973246	0.488741	0.603779	0.023544	0	227	179	346	208	252	235	324	318	363	239
ENSMUSG00000000916	chr5	Nsun5	1.35E+08	1.35E+08	3142	0.131531	2.478984	0.488868	0.603879	0.030402	0	68	53	119	85	101	84	118	116	129	77
ENSMUSG00000028525	chr4	Pde4b	1.02E+08	1.02E+08	10560	-0.20635	6.032961	0.488915	0.603881	0.10562	0	1319	952	1512	720	1006	592	2798	625	1280	674
ENSMUSG00000024045	chr17	Akap8	32303676	32305706	3695	0.101035	4.833057	0.488992	0.60392	0.023857	0	321	283	683	444	534	412	700	539	564	476
ENSMUSG00000033628	chr18	Pik3c3	30272747	30273018	4466	-0.10116	4.510132	0.489252	0.604185	0.022593	0	335	273	566	330	404	308	529	374	424	369
ENSMUSG00000024260	chr18	Sap130	31634371	31634489	4050	-0.12251	3.300295	0.489311	0.604202	0.029639	0	124	95	228	193	193	125	209	179	183	157
ENSMUSG00000001604	chr4	Tcea3	1.36E+08	1.36E+08	1400	-0.10575	7.61165	0.489639	0.604495	0.027872	0	2906	2645	4027	3139	3363	2699	4370	2985	4560	2824
ENSMUSG00000027739	chr3	Rab33b	51483920	51484112	3538	0.126347	3.057319	0.489622	0.604495	0.029394	0	96	108	176	119	132	111	200	163	168	143
ENSMUSG00000001661	chr15	Hoxc6	1.03E+08	1.03E+08	2408	0.15524	3.158995	0.489689	0.604499	0.053689	0	91	74	164	159	199	107	136	185	216	196
ENSMUSG00000014077	chr2	Chp1	1.2E+08	1.2E+08	3499	-0.10391	6.576277	0.489764	0.604536	0.026516	0	1296	1241	2152	1526	1730	1210	1816	1837	2115	1449
ENSMUSG00000031608	chr8	Galnt7	57523828	57526251	5253	-0.17622	2.136053	0.490112	0.60491	0.056915	0	56	43	94	76	104	59	84	110	68	45
ENSMUSG00000043770	chr4	Gm12481	43664043	43664339	297	0.122963	5.191227	0.490365	0.605109	0.035132	0	586	455	543	525	609	621	940	538	878	531
ENSMUSG00000050148	chrX	Ubqln2	1.53E+08	1.54E+08	3344	-0.12606	4.204778	0.490335	0.605109	0.035771	0	226	212	521	290	334	176	318	348	438	333
ENSMUSG00000054426	chr3	A930005H10Rik	1.16E+08	1.16E+08	2385	0.12911	3.040534	0.490436	0.605138	0.030309	0	124	93	147	125	127	134	195	128	203	121
ENSMUSG00000063253	chr8	Scoc	83434493	83436040	2062	0.109039	4.887929	0.49048	0.605138	0.026697	0	468	371	563	364	482	435	708	531	661	478
ENSMUSG00000028957	chr4	Per3	1.51E+08	1.51E+08	9608	-0.1115	4.790392	0.490538	0.605153	0.028066	0	299	323	755	454	541	368	506	536	562	439
ENSMUSG00000032735	chr18	Ablim3	61799395	61801408	4560	-0.13231	4.001423	0.490708	0.605194	0.038893	0	157	169	338	368	327	246	294	292	345	208
ENSMUSG00000041096	chrX	Tspyl2	1.52E+08	1.52E+08	2820	0.111974	3.848245	0.490658	0.605194	0.026638	0	229	148	272	193	261	249	286	244	341	230
ENSMUSG00000045464	chr2	2810002D19Rik	94406151	94406966	2040	0.152539	1.759689	0.490666	0.605194	0.035828	0	49	39	65	44	51	60	75	54	74	51
ENSMUSG00000001930	chr6	Vwf	1.26E+08	1.26E+08	16064	-0.13011	4.602565	0.490833	0.605292	0.040026	0	305	274	653	405	447	202	451	516	620	366
ENSMUSG00000027823	chr3	Gmps	63976106	63976310	8105	-0.09368	5.092467	0.490975	0.605355	0.020293	0	483	389	778	561	638	442	735	592	736	524
ENSMUSG00000054237	chr19	Fra10ac1	38188481	38188800	1402	0.118609	3.772982	0.490943	0.605355	0.028307	0	178	185	246	210	206	234	311	230	314	202
ENSMUSG00000020492	chr11	Ska2	87109234	87109304	3272	-0.16143	2.110005	0.491134	0.605494	0.046118	0	54	57	101	47	104	64	76	66	76	76
ENSMUSG00000022941	chr16	Ripply3	94328420	94328597	1531	0.25381	0.28141	0.491189	0.605506	0.064565	0	22	14	18	12	13	21	20	20	30	18
ENSMUSG00000033540	chr5	Idua	1.09E+08	1.09E+08	4204	-0.14348	3.366962	0.491539	0.605881	0.043237	0	126	72	256	216	227	121	226	169	208	169
ENSMUSG00000040283	chr11	Btnl9	49165585	49169691	6054	0.250376	1.483244	0.491767	0.60605	0.126304	0	24	26	25	61	58	26	52	93	62	35
ENSMUSG00000086877	chrX	A230072C01Rik	20961684	20961712	1581	-0.23364	0.723892	0.491765	0.60605	0.097392	0	36	14	16	30	35	14	25	27	34	30
ENSMUSG00000021629	chr13	Slc30a5	1.01E+08	1.01E+08	3178	-0.10436	3.691009	0.49226	0.606601	0.022806	0	173	157	272	207	263	176	306	218	247	188
ENSMUSG00000028013	chr3	Ppa2	1.33E+08	1.33E+08	2535	0.111851	5.209316	0.492459	0.60679	0.029608	0	486	386	582	654	724	593	914	549	871	601
ENSMUSG00000023092	chrX	Fhl1	56731787	56731868	3714	-0.42699	8.905174	0.492555	0.606796	0.452771	0	934	898	4659	22806	17112	2400	12762	3244	10285	10185
ENSMUSG00000031667	chr8	Aktip	91112041	91112611	2992	-0.10908	6.071212	0.492512	0.606796	0.029586	0	1142	831	1312	1052	1185	1015	1558	985	1505	907
ENSMUSG00000030929	chr7	Eri2	1.2E+08	1.2E+08	7170	-0.25923	0.682012	0.492602	0.606797	0.092859	0	20	18	52	24	21	21	31	29	11	29
ENSMUSG00000052369	chr15	Tmem106c	97964229	97964503	1635	0.123877	3.055623	0.49265	0.606799	0.030004	0	108	93	163	124	144	143	155	161	210	112
ENSMUSG00000038982	chr13	Bloc1s5	38602709	38604028	1766	0.12	3.689135	0.49273	0.606842	0.030035	0	161	142	208	221	247	222	312	220	303	169
ENSMUSG00000019989	chr10	Enpp3	24773814	24774072	2815	0.169756	1.323809	0.492913	0.60701	0.057253	0	33	13	58	31	53	39	56	38	46	50
ENSMUSG00000056459	chr12	Zbtb25	76347782	76350273	3131	-0.15344	2.187539	0.492982	0.607039	0.050163	0	56	60	96	71	95	53	113	43	120	67
ENSMUSG00000028277	chr4	Ube2j1	33031416	33031616	3530	0.106739	4.995964	0.493075	0.607098	0.026476	0	453	405	700	416	476	560	713	562	702	469
ENSMUSG00000021178	chr12	Psmc1	1E+08	1E+08	1518	0.119096	7.244594	0.493243	0.607245	0.035497	0	2167	2183	2857	1926	2240	2436	3456	2519	3962	2208
ENSMUSG00000039005	chr4	Tlr4	66827584	66827921	5556	0.153594	1.917755	0.493286	0.607245	0.044496	0	33	42	80	55	74	48	94	73	65	72
ENSMUSG00000030286	chr6	Emc3	1.14E+08	1.14E+08	2422	0.1027	6.205971	0.493782	0.607752	0.02592	0	1127	834	1516	1031	1186	1123	1644	1400	1610	1198
ENSMUSG00000038828	chr5	Tmem214	30869579	30869818	6024	-0.10125	4.829148	0.49379	0.607752	0.023371	0	386	279	699	525	519	404	583	498	621	403
ENSMUSG00000008892	chr8	Vdac3	22577075	22577602	1423	-0.10688	8.54638	0.49393	0.607868	0.029119	0	5339	4459	7237	7024	6884	5513	8754	5556	7936	5415
ENSMUSG00000000563	chr3	Atp5f1	1.06E+08	1.06E+08	4105	-0.12508	9.262583	0.494105	0.608028	0.040004	0	8312	6523	10867	13067	12655	8262	16668	8347	13346	8349
ENSMUSG00000019808	chr10	Adat2	13552894	13553361	1466	-0.17839	1.177837	0.494183	0.608067	0.050923	0	37	25	55	34	34	32	55	20	48	32
ENSMUSG00000073609	chr1	D2hgdh	93824909	93825051	4281	0.098372	4.413069	0.494282	0.608132	0.021402	0	292	215	439	317	401	301	510	411	500	305
ENSMUSG00000032058	chr9	Ppp2r1b	50845301	50845406	6449	0.233189	2.726218	0.494628	0.608501	0.123182	0	124	94	76	73	85	111	92	233	99	88

ENSMUSG00000039239	chr1	Tgfb2	1.87E+08	1.87E+08	5791	-0.10899	4.379963	0.494738	0.60858	0.027928	0	260	281	496	314	389	250	505	274	473	350
ENSMUSG00000027858	chr3	Tspan2	1.03E+08	1.03E+08	4585	0.158189	2.627609	0.494803	0.608604	0.056856	0	46	53	147	94	143	74	137	109	125	137
ENSMUSG00000030291	chr6	Med21	1.47E+08	1.47E+08	2102	-0.1193	4.384925	0.494851	0.608606	0.035238	0	354	318	383	311	315	283	521	335	442	270
ENSMUSG00000015536	chr13	Mocs2	1.15E+08	1.15E+08	9054	0.100982	5.398354	0.495236	0.60891	0.024084	0	584	511	748	640	741	686	998	731	981	608
ENSMUSG00000039470	chr8	Zdhhc2	40423815	40424169	5528	0.273042	0.122	0.495208	0.60891	0.114712	0	10	11	15	23	11	12	20	35	12	17
ENSMUSG00000044155	chr6	Lsm8	18848579	18848763	4108	0.134408	3.311012	0.495182	0.60891	0.035596	0	129	141	160	152	149	140	257	155	220	174
ENSMUSG00000024754	chr19	Tmem2	21778342	21778786	6667	-0.11038	4.384829	0.495543	0.609231	0.027657	0	310	200	554	295	432	300	531	309	448	270
ENSMUSG00000010607	chr9	Pigyl	22156846	22156913	777	0.119293	3.854653	0.495868	0.609574	0.02947	0	231	172	249	224	206	215	339	235	360	230
ENSMUSG00000063281	chr18	Zfp35	23989632	23989731	3040	-0.11431	3.214655	0.496033	0.60972	0.028089	0	158	113	198	144	148	119	212	156	182	141
ENSMUSG00000032816	chr9	Igdcc4	65101486	65101598	6366	0.122633	5.386714	0.496101	0.609748	0.03805	0	509	272	971	753	849	629	1038	627	959	748
ENSMUSG00000025373	chr10	Rnf41	1.28E+08	1.28E+08	4374	0.101434	3.992934	0.496405	0.610047	0.022591	0	190	188	379	202	288	231	348	289	366	266
ENSMUSG00000029385	chr5	Ccng2	93267257	93267797	5458	-0.0973	4.248367	0.496483	0.610047	0.021108	0	253	248	414	285	374	277	390	317	391	292
ENSMUSG00000097960	chr8	A330074K22Rik	1.2E+08	1.2E+08	2489	-0.24828	1.838592	0.496463	0.610047	0.12891	0	31	20	67	115	78	34	59	38	80	78
ENSMUSG00000046062	chr1	Ppp1r15b	1.33E+08	1.33E+08	5594	0.110636	4.703107	0.496682	0.610236	0.029748	0	323	248	647	369	481	332	600	621	521	397
ENSMUSG00000029394	chr5	Cdk2ap1	1.24E+08	1.24E+08	1945	0.100793	5.42018	0.496785	0.610259	0.0242	0	615	538	884	584	665	673	1000	705	1037	656
ENSMUSG00000038888	chr7	Ctu1	43672016	43672075	2475	0.177541	1.625038	0.496793	0.610259	0.051752	0	55	29	39	42	55	50	58	56	69	53
ENSMUSG00000027132	chr2	Katnbl1	1.12E+08	1.12E+08	4051	0.167257	1.746296	0.497034	0.610499	0.05103	0	39	43	78	33	55	51	56	73	65	63
ENSMUSG00000026843	chr2	Fubp3	31572651	31572953	5914	-0.12396	3.122248	0.497143	0.610536	0.030166	0	126	83	230	120	185	112	176	124	209	139
ENSMUSG00000038797	chr7	Zscan2	80860920	80861077	2712	0.235441	0.263612	0.497157	0.610536	0.072037	0	8	11	18	19	25	10	24	23	23	27
ENSMUSG00000027656	chr2	Wisp2	1.64E+08	1.64E+08	1924	0.187364	2.313494	0.497343	0.610708	0.078311	0	50	63	136	48	78	101	70	125	114	54
ENSMUSG00000028295	chr4	Smim8	34768664	34769147	1510	0.120177	3.960548	0.497442	0.610753	0.030418	0	220	198	236	242	266	216	413	243	370	252
ENSMUSG00000040732	chr16	Erg	95359169	95361326	3466	-0.15973	2.439754	0.497472	0.610753	0.050971	0	60	52	91	101	155	70	108	86	130	71
ENSMUSG00000066175	chr7	2510046G10Rik	1.27E+08	1.27E+08	1052	0.307698	0.046273	0.497696	0.610972	0.131977	0	23	12	12	10	6	12	14	27	19	20
ENSMUSG00000045776	chr14	Lrtm1	29018208	29018609	7318	-0.12532	5.950874	0.497774	0.611012	0.039464	0	601	817	1779	1037	1087	890	1260	1186	984	1005
ENSMUSG00000040717	chr14	Il17rd	27039001	27039229	8220	-0.17793	2.260362	0.498026	0.611264	0.061233	0	45	51	126	82	110	38	85	107	90	82
ENSMUSG00000003154	chr6	Foxj2	1.23E+08	1.23E+08	5283	-0.10064	5.221236	0.498404	0.611672	0.02457	0	543	408	998	547	670	488	771	558	923	582
ENSMUSG00000007739	chr11	Cct4	22990519	22990880	4201	0.107461	6.720714	0.498543	0.61178	0.029238	0	1541	1403	2059	1427	1574	1554	2595	1883	2465	1601
ENSMUSG00000038848	chr2	Ythdf1	1.81E+08	1.81E+08	3316	-0.09144	5.482259	0.498585	0.61178	0.020361	0	605	512	1068	730	835	611	979	745	972	669
ENSMUSG00000024810	chr19	Il33	29925114	29925161	2886	-0.22338	2.575684	0.498741	0.611915	0.10975	0	45	42	142	137	168	76	167	130	65	58
ENSMUSG00000035770	chr8	Dync1li2	1.04E+08	1.04E+08	4633	-0.09968	6.40468	0.498974	0.612145	0.025213	0	1161	880	1877	1490	1740	1092	1758	1364	1975	1346
ENSMUSG00000002319	chr14	Ipo4	55625400	55626041	5362	0.097133	5.87114	0.499339	0.612536	0.023627	0	733	650	1369	868	986	837	1200	1083	1499	938
ENSMUSG00000007279	chr7	Scube2	1.1E+08	1.1E+08	4153	-0.37669	0.039457	0.499534	0.612718	0.206997	0	2	4	32	22	30	10	17	8	11	24
ENSMUSG00000038685	chr2	Rtel1	1.81E+08	1.81E+08	6616	0.123251	2.875035	0.500114	0.613316	0.030204	0	84	86	171	92	132	106	186	145	149	107
ENSMUSG00000063849	chr9	Ppcdc	57412668	57414726	2747	0.119147	2.971947	0.500103	0.613316	0.028532	0	114	76	162	98	154	117	197	145	173	111
ENSMUSG00000027131	chr2	Emc4	1.12E+08	1.12E+08	1052	-0.11719	5.54257	0.500332	0.613527	0.03521	0	770	693	971	606	766	721	1110	592	924	741
ENSMUSG00000057606	chr14	Colq	31523082	31524479	3803	0.12431	3.587705	0.500673	0.613888	0.034847	0	189	111	259	182	182	208	239	167	341	187
ENSMUSG00000005611	chr7	Mrvi1	1.11E+08	1.11E+08	6827	-0.15061	2.700135	0.500896	0.614104	0.046135	0	57	63	157	122	162	74	129	104	156	98
ENSMUSG00000100621	chr19	Gm28374	6076945	6077478	728	0.140722	2.2789	0.501158	0.614369	0.037203	0	66	50	91	60	98	90	90	78	117	76
ENSMUSG00000097353	chr10	A430046D13Rik	1.28E+08	1.28E+08	1997	-0.11131	4.776931	0.50137	0.614572	0.031397	0	403	380	574	432	463	327	728	354	583	454
ENSMUSG00000000085	chr4	Scmh1	1.2E+08	1.2E+08	7731	-0.10224	5.217958	0.501989	0.615217	0.025835	0	489	376	842	677	765	487	708	599	971	549
ENSMUSG00000029623	chr5	Pdap1	1.45E+08	1.45E+08	3201	0.110064	6.217841	0.501952	0.615217	0.030836	0	1103	949	1274	1093	1196	1243	1835	1181	1738	1106
ENSMUSG00000034164	chr11	Emid1	5106265	5106969	2890	0.201057	2.134235	0.502365	0.615621	0.084406	0	94	36	102	35	54	58	93	98	126	51
ENSMUSG00000056537	chrX	Rlim	1.04E+08	1.04E+08	8917	0.10033	4.618666	0.50268	0.61595	0.023615	0	336	276	540	347	412	397	668	389	541	346
ENSMUSG00000028691	chr4	Prdx1	1.17E+08	1.17E+08	3043	0.124274	8.002556	0.502948	0.616221	0.040804	0	4000	3616	4446	3399	3561	4424	6559	4719	5645	3278
ENSMUSG00000026478	chr1	Lamc1	1.53E+08	1.53E+08	8272	0.134593	6.582867	0.503024	0.616225	0.048184	0	1124	581	2645	1418	2077	1380	1863	1834	2182	1836
ENSMUSG00000031668	chr6	Eif2ak3	70844515	70845021	5428	0.135377	2.593412	0.503043	0.616225	0.041403	0	68	49	156	75	126	84	150	131	115	89
ENSMUSG00000022887	chr16	Masp1	23451785	23452572	2752	-0.40679	0.222349	0.503439	0.616653	0.321298	0	3	4	8	50	33	8	31	10	15	20
ENSMUSG00000071359	chr10	Tbpl1	22703879	22705895	3271	0.120765	3.744975	0.503619	0.616816	0.032848	0	146	178	315	177	216	150	323	245	299	260
ENSMUSG00000027286	chr2	Lrrc57	1.21E+08	1.21E+08	2227	-0.0965	4.012904	0.503669	0.61682	0.021199	0	216	193	377	259	301	216	393	247	340	238
ENSMUSG00000018999	chr6	Slc35b4	34153380	34158626	9177	0.117377	3.360021	0.503728	0.616836	0.030307	0	129	115	219	134	195	157	218	236	190	157
ENSMUSG00000069255	chr13	Dusp22	30659999	30660146	1743	0.109885	4.974904	0.504096	0.617229	0.029791	0	344	332	566	618	569	438	801	496	796	496
ENSMUSG00000030255	chr6	Sspn	1.46E+08	1.46E+08	4996	-0.10252	6.63632	0.504427	0.617577	0.027432	0	1204	1042	2398	1792	2044	1464	2066	1440	2262	1563
ENSMUSG00000024855	chr19	Pacs1	5133688	5135025	4339	-0.18192	3.408206	0.504635	0.617718	0.080819	0	79	77	208	298	268	116	222	172	253	153
ENSMUSG00000038619	chr3	Ensa	95624980	95625176	2947	-0.09766	7.730505	0.504619	0.617718	0.025433	0	3153	2603	4598	3474	3778	3042	4614	3176	4903	3178
ENSMUSG00000062116	chr7	Zfp954	7114690	7116200	1999	0.15299	2.315051	0.504711	0.617754	0.046295	0	56	63	85	70	94	92	115	93	73	86
ENSMUSG00000020790	chr11	Ankfy1	72690006	72690034	11332	0.101126	4.262053	0.504801	0.617779	0.025364	0	221	179	468	291	369	275	421	407	390	309
ENSMUSG00000029203	chr5	Ube2k	65537233	65537546	5173	0.111892	5.816389	0.504825	0.617779	0.031793	0	833	783	1049	713	865	909	1315	991	1429	758
ENSMUSG00000033720	chr6	Sfxn5	85213051	85215746	5743	-0.17789	2.234412	0.504972	0.617845	0.066212	0	53	44	94	102	106	49	109	116	74	50
ENSMUSG00000078202	chr2	Nrarp	25180758	25183339	2582	0.175688	2.200619	0.504936	0.617845	0.059078	0	54	55	51	76	95	63	140	70	111	62
ENSMUSG00000020235	chr10	Fzr1	81366222	81367550	4488	0.096852	4.505029	0.505029	0.617858	0.022641	0	279	232	471	391	401	365	452	394	545	374
ENSMUSG00000022983	chr16	Scaf4	90228957	90230244	4364	0.107314	3.504909	0.505175	0.617866	0.02678	0	132	111	285	158	211	175	230	232	268	163
ENSMUSG00000026917	chr2	Wdr5	27515157	27515280	3596	0.092874	4.879845	0.505148	0.617866	0.020899	0	381	307	616	454	551	401	711	559	654	467
ENSMUSG00000097617	chr9	Gm10687	44123768	44125293	1651	0.266722	0.56147	0.505173	0.617866	0.107471	0	23	27	23	7	15	18	30	34	33	22
ENSMUSG00000042684	chr1	Npl	1.54E+08	1.54E+08	2961	-0.18039	1.436322	0.505255	0.617906	0.068689	0	41	32	41	49	56	29	85	46	35	32
ENSMUSG00000030431	chr7	Tmem238	4784595	4785279	1337	0.176838	1.098556	0.505371	0.617991	0.040245	0	28	23	47	27	29	25	41	44	50	37

ENSMUSG00000034656	chr8	Cacna1a	84388440	84388522	11418	-0.25761	1.207066	0.505473	0.618047	0.1307	0	12	19	51	61	57	25	30	58	29	36
ENSMUSG00000089083	chr6	Rnu7	1.25E+08	1.25E+08	62	0.262243	0.494036	0.50551	0.618047	0.103929	0	30	15	21	12	14	30	34	13	26	25
ENSMUSG00000028437	chr4	Ubap1	41348996	41349231	3583	-0.0974	5.689103	0.505662	0.618176	0.024328	0	795	632	1187	747	929	859	1019	835	1097	718
ENSMUSG00000036298	chr15	Slc2a13	91267696	91272380	8367	-0.28302	0.375561	0.506071	0.618506	0.130931	0	27	11	40	10	20	23	26	24	7	15
ENSMUSG00000071648	chr19	Rom1	8927382	8927887	1526	0.147607	3.340334	0.506023	0.618506	0.053912	0	113	67	164	212	224	152	196	162	288	171
ENSMUSG00000091228	chr11	Gm20390	93949819	93950046	991	-0.11562	8.2821	0.506032	0.618506	0.036089	0	4733	3958	5055	5782	5910	4772	6986	4271	7466	4171
ENSMUSG00000021179	chr12	Nrde2	1E+08	1E+08	3723	-0.11714	3.567256	0.506161	0.618508	0.031389	0	149	151	280	192	219	159	224	146	294	212
ENSMUSG00000025049	chr19	Taf5	47067748	47068326	3258	0.165008	1.676513	0.506167	0.618508	0.056207	0	33	36	91	27	55	49	67	72	61	47
ENSMUSG00000026740	chr2	Dnajc1	18195654	18195921	11651	-0.11483	3.948751	0.506217	0.618513	0.028956	0	161	159	413	255	344	239	323	250	290	237
ENSMUSG00000098488	chr2	Pla2g4b	1.2E+08	1.2E+08	5831	0.183056	1.101847	0.506322	0.618584	0.071936	0	30	12	46	34	35	41	29	46	35	40
ENSMUSG00000035206	chr10	Sppl2b	80855275	80855388	2866	-0.13068	3.601274	0.506959	0.619306	0.038619	0	154	95	266	257	267	148	251	192	241	218
ENSMUSG00000006315	chr7	Tmem147	30727701	30727903	868	0.100522	6.553247	0.507185	0.619468	0.026518	0	1314	1103	1783	1506	1501	1345	2207	1600	2406	1442
ENSMUSG00000021771	chr14	Vdac2	21831269	21831667	4658	0.104016	8.106762	0.50714	0.619468	0.029167	0	3800	2947	5177	4670	4695	4215	6553	4289	7447	4040
ENSMUSG00000052632	chr12	Asap2	21111748	21112169	5687	0.18209	2.634846	0.507269	0.619513	0.08397	0	44	37	128	118	157	81	157	94	109	146
ENSMUSG00000001014	chr9	Icam4	21029373	21029823	907	0.25202	0.255557	0.507412	0.619624	0.075973	0	19	14	14	17	13	23	17	15	29	22
ENSMUSG00000025173	chr11	Wdr45b	1.21E+08	1.21E+08	4562	-0.09947	4.368586	0.507454	0.619624	0.023703	0	299	228	490	367	340	321	440	324	463	276
ENSMUSG00000050714	chr2	Zbtb26	37432168	37436999	5267	-0.13776	2.05984	0.508501	0.620845	0.035271	0	68	40	90	68	79	51	90	79	73	61
ENSMUSG00000014601	chr3	Strip1	1.08E+08	1.08E+08	3231	0.095325	4.777769	0.508777	0.621052	0.022689	0	323	281	596	414	554	385	606	455	712	451
ENSMUSG00000020092	chr10	Pald1	61319657	61321242	4274	0.106705	3.555863	0.508857	0.621052	0.026773	0	136	107	277	181	228	171	246	196	317	186
ENSMUSG00000022009	chr14	Nufip1	76110891	76111326	3974	-0.13625	2.844722	0.508815	0.621052	0.045364	0	99	127	124	99	127	108	157	97	152	105
ENSMUSG00000029486	chr5	Mrpl1	96209493	96209565	4295	-0.10264	4.98613	0.508772	0.621052	0.027126	0	432	380	595	565	649	478	800	428	644	461
ENSMUSG00000039047	chr3	Pigk	1.53E+08	1.53E+08	9367	0.091426	5.206052	0.509333	0.621575	0.02125	0	469	403	760	549	712	565	876	625	780	627
ENSMUSG00000032477	chr9	Cdc25a	1.1E+08	1.1E+08	3625	0.124162	2.916761	0.509736	0.621953	0.036114	0	87	76	212	88	131	114	142	150	177	124
ENSMUSG00000034484	chr18	Snx2	53176365	53176487	2013	0.109729	4.70216	0.509707	0.621953	0.029808	0	346	366	542	304	426	429	599	504	508	405
ENSMUSG00000041837	chr9	Pdcd7	65346068	65347008	2454	0.11097	3.861953	0.509824	0.622003	0.02907	0	186	136	319	257	234	189	331	215	394	261
ENSMUSG00000063445	chr16	Nmral1	4710059	4711603	3891	0.170919	1.937526	0.509931	0.622077	0.059414	0	69	34	65	44	68	77	88	75	80	39
ENSMUSG00000056313	chr8	1810011O10Rik	24437180	24438984	1805	0.125099	3.536168	0.510299	0.622468	0.035255	0	151	134	173	183	232	139	293	238	225	206
ENSMUSG00000015944	chr5	Gatsl2	1.34E+08	1.34E+08	7560	0.119268	6.852639	0.510985	0.623196	0.039088	0	1100	1002	2725	2100	2334	1557	2294	1903	3065	2222
ENSMUSG00000032469	chr9	Dbr1	99575799	99576125	2488	0.135134	2.379916	0.51099	0.623196	0.035923	0	56	62	122	63	94	75	145	93	106	74
ENSMUSG00000031465	chr8	Angpt2	18690263	18692208	3690	0.200088	1.257842	0.511212	0.623409	0.079453	0	23	24	44	40	41	48	43	67	37	23
ENSMUSG00000025156	chr11	Gps1	1.21E+08	1.21E+08	2879	-0.09245	5.625495	0.511568	0.623787	0.022518	0	789	578	1063	731	928	726	1030	773	1080	759
ENSMUSG00000027593	chr2	Raly	1.55E+08	1.55E+08	3292	0.09525	5.654894	0.511647	0.623817	0.023468	0	685	597	911	826	846	761	1150	953	1114	782
ENSMUSG00000042246	chr7	Tmc7	1.19E+08	1.19E+08	5761	-0.15344	4.120166	0.511687	0.623817	0.059608	0	199	99	390	378	472	223	381	234	418	263
ENSMUSG00000022234	chr15	Cct5	31590800	31591055	2809	0.108069	7.32913	0.51179	0.623885	0.031899	0	2261	2249	3019	2122	2505	2595	3817	2812	3481	2550
ENSMUSG00000029632	chr6	Ndufa4	11900373	11900591	492	-0.12083	8.79545	0.51191	0.623974	0.040576	0	7057	5269	7571	8666	7927	6747	11579	5776	10171	5471
ENSMUSG00000018677	chr11	Slc25a39	1.02E+08	1.02E+08	2756	0.118908	5.963361	0.512116	0.624054	0.03832	0	732	578	996	1274	1234	924	1195	1267	1561	987
ENSMUSG00000022960	chr16	Donson	91677268	91677619	2834	0.205968	0.213077	0.512023	0.624054	0.052031	0	11	8	29	17	15	16	31	20	21	15
ENSMUSG00000025466	chr7	Fuom	1.4E+08	1.4E+08	3272	0.145004	3.91584	0.512116	0.624054	0.052411	0	182	136	205	338	272	209	472	213	356	227
ENSMUSG00000028019	chr3	Pdgfc	81036416	81037554	5089	0.227511	1.325087	0.512208	0.624108	0.110661	0	40	28	53	30	25	43	38	85	36	28
ENSMUSG00000002833	chr17	Hdgfrp2	56079657	56079826	2251	0.096479	4.956195	0.512344	0.624207	0.023532	0	450	358	633	415	547	486	635	492	755	550
ENSMUSG00000024797	chr19	Vps51	6067842	6068375	4748	-0.09976	3.988649	0.512525	0.624207	0.023332	0	204	187	392	246	305	212	291	279	396	225
ENSMUSG00000031661	chr8	Nkd1	88521344	88521531	4459	-0.22648	0.808432	0.512493	0.624207	0.108644	0	29	30	29	23	27	9	21	42	36	31
ENSMUSG00000038241	chr2	Cep250	1.56E+08	1.56E+08	10373	-0.11811	3.109103	0.512475	0.624207	0.028323	0	107	95	212	133	182	123	161	161	153	141
ENSMUSG00000051390	chr17	Zbtb22	33915904	33915964	2672	-0.09542	4.301124	0.512403	0.624207	0.022789	0	297	240	404	285	403	272	489	306	412	276
ENSMUSG00000036285	chr5	Noa1	77294182	77294556	4029	0.096141	4.108412	0.512984	0.624651	0.021391	0	253	188	368	228	303	251	423	313	376	267
ENSMUSG00000066838	chr7	Zfp772	7202122	7204359	2772	-0.13787	1.607856	0.51297	0.624651	0.039125	0	42	43	62	46	53	33	64	40	72	50
ENSMUSG00000031505	chr8	Carkd	11497506	11497626	3694	0.092208	4.906531	0.513122	0.624763	0.021271	0	437	317	603	457	516	453	724	526	650	478
ENSMUSG00000001767	chr2	Crnkl1	1.46E+08	1.46E+08	3844	0.101162	4.360386	0.513314	0.624863	0.02452	0	268	254	448	289	327	295	549	331	425	348
ENSMUSG00000036966	chr15	Spryd3	1.02E+08	1.02E+08	2927	0.108642	3.490639	0.513324	0.624863	0.026975	0	150	126	211	168	205	176	211	198	244	214
ENSMUSG00000089781	chr6	Gm15756	90596685	90597034	682	-0.15262	2.101499	0.513346	0.624863	0.046764	0	76	37	91	55	101	55	111	57	86	59
ENSMUSG00000041313	chr5	Slc7a1	1.48E+08	1.48E+08	7527	0.17242	1.634487	0.513564	0.625071	0.069249	0	21	19	65	65	65	41	68	53	83	48
ENSMUSG00000039810	chr10	Zc3h10	1.29E+08	1.29E+08	4384	0.124849	2.998472	0.514377	0.626003	0.031167	0	98	93	148	136	128	117	210	123	202	113
ENSMUSG00000017286	chr11	Glod4	76120987	76121596	6005	-0.09359	4.820159	0.514779	0.626435	0.022862	0	392	379	598	440	514	435	636	432	598	399
ENSMUSG00000014195	chr11	Dnajc7	1.01E+08	1.01E+08	4863	0.113269	6.621758	0.514913	0.626541	0.035218	0	1383	1281	1705	1441	1627	1789	2300	1451	2604	1298
ENSMUSG00000057614	chr5	Gnai1	18265135	18267209	3193	-0.27571	2.414216	0.51552	0.627221	0.202294	0	103	110	85	52	83	51	52	208	44	63
ENSMUSG00000032398	chr9	Snapc5	64179297	64179420	757	0.127691	4.637452	0.515846	0.627452	0.041444	0	371	376	368	298	414	412	691	414	509	358
ENSMUSG00000079671	chr1	2610203C22Rik	9560832	9561778	4910	0.222379	0.301604	0.515851	0.627452	0.058043	0	18	13	17	15	19	20	24	12	31	23
ENSMUSG00000093677	chr15	Gm20712	58780461	58781951	1491	0.217021	1.82927	0.515778	0.627452	0.114164	0	21	18	51	84	90	46	99	52	101	49
ENSMUSG00000078773	chr4	Rad54b	11558922	11559013	5782	-0.31347	-0.01019	0.516339	0.627988	0.146363	0	6	15	40	4	18	18	15	11	14	12
ENSMUSG00000070056	chr8	Mfhas1	35587798	35591358	6666	0.135669	2.848398	0.5166	0.628247	0.043608	0	89	57	141	125	142	76	171	157	141	136
ENSMUSG00000101188	chr1	Eif4a-ps4	60703932	60705149	1218	0.12078	3.342578	0.516682	0.62829	0.032338	0	143	129	198	151	141	167	265	181	189	153
ENSMUSG00000033543	chr9	Gtf2a2	70012550	70012661	4047	0.132874	4.915791	0.517038	0.628664	0.046199	0	456	495	515	308	432	466	800	523	684	438
ENSMUSG00000051351	chr4	Zfp46	1.36E+08	1.36E+08	5212	0.155026	3.778706	0.517542	0.629219	0.065205	0	111	87	240	293	346	180	290	231	377	247
ENSMUSG00000022710	chr16	Usp7	8689595	8690886	7766	-0.09993	6.34031	0.517674	0.629322	0.027803	0	1162	1028	2118	1085	1425	1190	1840	1192	1787	1191
ENSMUSG00000031495	chr8	Cd209d	3871827	3872110	916	-0.23292	2.145626	0.517764	0.629374	0.135433	0	71	72	134	40	60	81	53	127	57	33

ENSMUSG00000007950	chr8	Abhd8	71456700	71457377	1985	-0.1055	4.219019	0.517947	0.629539	0.028246	0	273	205	345	328	391	245	324	282	451	329
ENSMUSG00000033429	chr7	Mcee	64392645	64392843	824	-0.11056	5.134776	0.518124	0.629697	0.033931	0	514	431	567	689	668	489	931	493	753	473
ENSMUSG00000091478	chr11	Gm10039	1E+08	1E+08	411	-0.15074	5.170429	0.518263	0.629807	0.063088	0	407	290	569	946	864	464	759	451	985	523
ENSMUSG00000022615	chr15	Tymp	89371931	89372465	2037	0.132335	2.931317	0.518359	0.629866	0.040357	0	91	72	113	155	143	112	163	126	188	132
ENSMUSG00000014907	chr8	Naf1	66860217	66861046	2990	-0.13346	2.317056	0.518893	0.630268	0.039026	0	68	67	135	71	73	56	103	87	120	66
ENSMUSG00000025047	chr19	Pdcd11	47090766	47090867	6041	-0.10202	3.944853	0.518896	0.630268	0.024654	0	189	157	403	246	319	219	340	254	362	193
ENSMUSG00000027566	chr2	Psma7	1.8E+08	1.8E+08	3072	0.119498	6.60523	0.518927	0.630268	0.03989	0	1323	1522	1643	1312	1399	1619	2372	1519	2414	1427
ENSMUSG00000028089	chr3	Chd1l	97560742	97561087	3008	-0.09675	4.266429	0.518892	0.630268	0.023934	0	258	219	427	348	350	264	447	261	460	285
ENSMUSG00000031994	chr9	Adamts8	30942562	30943601	4613	-0.42718	0.366457	0.518915	0.630268	0.438064	0	1	1	13	59	38	7	30	28	17	11
ENSMUSG00000031158	chrX	Timm17b	7899357	7899469	2557	0.096191	4.974424	0.519552	0.630969	0.023919	0	475	381	633	423	502	496	706	507	725	528
ENSMUSG00000018770	chr2	Atp5g3	73908447	73908707	2181	0.139793	9.085652	0.519748	0.631149	0.056313	0	6153	4420	7588	12109	11468	7218	14485	8298	15235	8323
ENSMUSG00000025150	chr11	Cbr2	1.21E+08	1.21E+08	1327	-0.1785	5.391265	0.520507	0.632013	0.089733	0	781	405	1201	490	803	939	370	612	1119	457
ENSMUSG00000000884	chr16	Gnb1l	18498768	18498851	4164	0.151753	1.226069	0.520723	0.632218	0.048916	0	29	19	45	35	44	45	56	40	33	37
ENSMUSG00000027217	chr2	Tspan18	93201760	93204422	8175	0.213555	1.283196	0.521079	0.632592	0.109458	0	40	8	40	26	64	21	55	57	61	37
ENSMUSG00000022556	chr15	Hsf1	76477445	76477717	2018	-0.0929	5.344216	0.521193	0.632673	0.023163	0	587	412	974	691	759	578	756	717	950	593
ENSMUSG00000062234	chr5	Gak	1.09E+08	1.09E+08	5938	0.099717	4.055217	0.521249	0.632683	0.025908	0	211	176	430	214	284	240	335	348	355	277
ENSMUSG00000019478	chr8	Rab4a	1.24E+08	1.24E+08	1757	0.09187	4.274422	0.521379	0.632783	0.021186	0	257	197	406	313	339	323	430	328	455	284
ENSMUSG00000022661	chr16	Cd200	45382135	45383457	3321	-0.14745	4.259741	0.521619	0.632901	0.060023	0	184	192	368	423	476	145	468	386	448	261
ENSMUSG00000029312	chr5	Klhl8	1.04E+08	1.04E+08	3489	0.104374	5.453275	0.521592	0.632901	0.030245	0	646	488	1148	504	661	720	1010	680	1052	696
ENSMUSG00000035351	chr10	Nup37	88146992	88147072	1362	0.137476	2.09609	0.521581	0.632901	0.039488	0	48	35	88	64	92	62	112	59	106	66
ENSMUSG00000036452	chr18	Arhgap26	38601534	38601697	17331	-0.16945	2.594933	0.521725	0.632914	0.076685	0	106	118	136	55	70	73	121	112	132	79
ENSMUSG00000096401	chr8	Gm21811	20136502	20136663	930	-0.26461	-0.06436	0.521704	0.632914	0.075377	0	12	7	27	9	22	12	14	20	11	12
ENSMUSG00000030759	chr7	Far1	1.14E+08	1.14E+08	8055	0.099801	3.5045	0.521791	0.632935	0.023972	0	143	119	273	151	205	154	252	214	247	198
ENSMUSG00000032114	chr9	Slc37a4	44398176	44398621	2083	-0.12691	7.208319	0.522105	0.633258	0.046637	0	2753	1950	3593	1633	2393	2652	2555	2385	3431	1815
ENSMUSG00000021149	chr13	Gtpbp4	8972071	8973274	2977	-0.09304	5.442174	0.522288	0.633331	0.024357	0	643	604	928	644	740	625	987	678	955	625
ENSMUSG00000032519	chr9	Slc25a38	1.2E+08	1.2E+08	2747	0.095323	3.867071	0.522309	0.633331	0.021805	0	195	141	295	238	269	198	338	268	339	236
ENSMUSG00000038732	chr13	Mboat1	30136498	30136762	3474	0.166337	1.142803	0.522279	0.633331	0.058372	0	36	10	52	32	33	32	52	33	48	38
ENSMUSG00000070733	chr5	Fryl	73020322	73022297	14668	-0.13538	3.865387	0.522645	0.633681	0.045953	0	157	115	480	194	363	180	299	235	338	222
ENSMUSG00000027091	chr2	Zc3h15	83644435	83644727	2789	-0.10048	5.911185	0.522877	0.633905	0.028985	0	855	897	1302	888	978	891	1342	929	1376	817
ENSMUSG00000008348	chr5	Ubc	1.25E+08	1.25E+08	2893	0.114784	7.44242	0.522987	0.633955	0.03835	0	2784	1718	3718	2506	2753	3444	3048	2636	4208	2916
ENSMUSG00000089865	chr9	Dyx1c1Ccpg1	72958852	72958997	4383	0.103251	6.782827	0.52302	0.633955	0.030775	0	1142	1095	2244	2106	2087	1571	2628	1851	2526	1908
ENSMUSG00000100410	chr13	2310020H05Rik	99076526	99076800	720	0.230544	1.442287	0.523062	0.633955	0.124985	0	17	15	29	77	56	36	63	43	77	42
ENSMUSG00000027394	chr2	Ttl	1.29E+08	1.29E+08	5945	-0.11335	3.795264	0.523171	0.634029	0.030933	0	169	125	286	272	325	213	279	221	286	208
ENSMUSG00000029376	chr5	Mthfd2l	90931196	90931433	2235	-0.14564	1.447619	0.523281	0.634104	0.043745	0	30	36	47	52	55	35	65	46	53	31
ENSMUSG00000034007	chr9	Scaper	55549883	55550871	5158	-0.10954	3.269759	0.523711	0.634568	0.029065	0	129	116	267	135	166	116	190	167	235	141
ENSMUSG00000052446	chr8	Zfp961	71951038	71951103	3950	0.154203	1.49868	0.523855	0.634684	0.051384	0	26	25	54	57	47	50	68	37	56	49
ENSMUSG00000043644	chr11	0610009L18Rik	1.2E+08	1.2E+08	619	0.126449	3.498253	0.523964	0.634758	0.038074	0	195	131	208	167	140	164	236	178	288	205
ENSMUSG00000026553	chr1	Copa	1.72E+08	1.72E+08	9427	-0.09523	7.177082	0.524179	0.634949	0.026264	0	1958	1576	3815	2312	2643	1880	3208	2308	3091	2380
ENSMUSG00000038213	chr6	Tapbpl	1.25E+08	1.25E+08	2352	-0.13952	2.503977	0.524217	0.634949	0.045572	0	96	81	101	71	111	96	94	97	105	84
ENSMUSG00000001924	chrX	Uba1	20658326	20658526	4819	0.098068	7.253731	0.52457	0.635318	0.028098	0	1880	1465	3494	2511	2771	2122	3090	2782	4054	2493
ENSMUSG00000027424	chr2	Mgme1	1.44E+08	1.44E+08	3348	-0.09906	3.925576	0.524718	0.635439	0.025624	0	221	186	325	252	269	186	353	310	296	200
ENSMUSG00000032243	chr9	Itga11	62677826	62677996	5131	0.158719	2.795181	0.524775	0.635451	0.07269	0	60	40	209	99	152	87	164	142	113	145
ENSMUSG00000013997	chr1	Nit1	1.71E+08	1.71E+08	4932	-0.09053	4.714006	0.524973	0.635632	0.02228	0	394	309	523	424	513	358	625	397	556	401
ENSMUSG00000040943	chr3	Tet2	1.33E+08	1.33E+08	9179	-0.1279	3.14843	0.525701	0.636456	0.038301	0	79	98	247	137	206	116	205	130	179	141
ENSMUSG00000004558	chr14	Ndrg2	51905271	51906306	2157	0.098937	11.22628	0.526094	0.636873	0.029169	0	29739	25450	45921	40479	45452	34749	58795	37105	63686	36479
ENSMUSG00000032309	chr9	Fbxo22	55208925	55209188	2394	0.088027	4.639108	0.526862	0.637744	0.020687	0	336	272	537	363	442	410	533	454	531	397
ENSMUSG00000071984	chr17	Fndc1	7738569	7739330	9903	0.136539	5.522647	0.527243	0.638148	0.055435	0	431	367	1438	569	979	580	812	1052	952	934
ENSMUSG00000065529	chr11	Mir22	75463716	75463810	95	-0.16714	1.50034	0.527493	0.638393	0.065045	0	29	40	58	51	53	25	79	28	58	50
ENSMUSG00000029364	chr5	Wsb2	1.17E+08	1.17E+08	5857	-0.09834	7.173709	0.527574	0.638432	0.028525	0	2114	1546	3246	2455	2765	2223	2663	2078	3527	2257
ENSMUSG00000038013	chr11	Wipf2	98863638	98863902	7819	-0.10581	3.419702	0.527878	0.638741	0.027545	0	142	120	258	177	200	114	238	199	255	146
ENSMUSG00000079164	chr1	Tlr5	1.83E+08	1.83E+08	4790	-0.27757	0.373301	0.527974	0.6388	0.114264	0	15	8	41	10	37	21	12	14	31	18
ENSMUSG00000027309	chr2	4930402H24Rik	1.31E+08	1.31E+08	10659	0.151502	2.714207	0.52827	0.639099	0.054737	0	103	67	122	86	112	73	143	189	114	100
ENSMUSG00000075704	chr16	Txnrd2	18426417	18426559	3359	0.093817	4.422569	0.529027	0.639956	0.022688	0	320	230	425	316	368	341	484	369	535	302
ENSMUSG00000025701	chr6	Alox5	1.16E+08	1.16E+08	4106	0.183558	0.8315	0.529344	0.640048	0.066695	0	16	18	31	25	37	34	38	36	20	30
ENSMUSG00000028102	chr3	Pex11b	96635376	96635500	5615	-0.08916	4.618121	0.529317	0.640048	0.022064	0	352	334	505	368	450	362	545	388	517	362
ENSMUSG00000032125	chr9	Robo4	37401897	37402151	4107	0.115596	3.423498	0.529318	0.640048	0.032903	0	139	108	173	180	219	127	253	229	237	173
ENSMUSG00000035960	chr14	Apex1	50924968	50925029	1422	0.112669	4.850394	0.529221	0.640048	0.034374	0	429	421	515	364	423	482	657	507	719	386
ENSMUSG00000055653	chrX	Gpc3	52272426	52272954	2690	0.144511	3.681124	0.529336	0.640048	0.05813	0	155	149	308	145	233	161	271	389	185	198
ENSMUSG00000021494	chr13	Ddx41	55530410	55530731	2205	-0.09948	3.51175	0.529532	0.640218	0.024509	0	173	136	261	180	192	172	257	197	227	148
ENSMUSG00000031972	chr8	Acta1	1.24E+08	1.24E+08	1433	-0.10037	14.89102	0.529605	0.640248	0.030567	0	467486	296881	729362	488768	597462	389136	565850	487427	775689	487534
ENSMUSG00000034300	chr18	Fam53c	34758906	34759144	4517	0.089171	5.043338	0.529727	0.640337	0.022736	0	417	301	778	490	652	498	710	586	813	510
ENSMUSG00000031586	chr8	Rbpms	33782643	33784186	4022	-0.12339	3.165233	0.529828	0.6404	0.039569	0	148	128	206	94	163	118	172	180	197	113
ENSMUSG00000060548	chr14	Tnfrsf19	60963834	60966465	4777	0.242677	4.339302	0.530192	0.640781	0.175072	0	75	106	353	510	526	208	575	173	533	539
ENSMUSG00000024392	chr17	Bag6	35135178	35135471	6215	-0.10009	7.246536	0.530647	0.6411	0.030049	0	1956	1607	3746	2728	2862	1897	2794	2504	3935	2403
ENSMUSG00000038132	chr13	Rbm24	46418300	46419198	3215	-0.09733	7.260446	0.530625	0.6411	0.028472	0	2295	1766	3843	2367	2615	1976	3112	2285	3815	2497

ENSMUSG00000045867	chr10	Cradd	95174746	95175978	1650	0.143864	2.975532	0.530535	0.6411	0.047408	0	107	107	150	106	112	84	247	165	154	112
ENSMUSG00000048138	chr19	Dmrt2	25672420	25672758	2347	-0.18181	2.1264	0.530649	0.6411	0.084703	0	82	63	93	48	72	53	79	125	60	45
ENSMUSG00000001948	chr9	Spa17	37603295	37603486	689	0.180115	1.734051	0.531233	0.641747	0.058801	0	55	48	47	45	37	52	78	65	67	50
ENSMUSG00000020115	chr10	Tbk1	1.22E+08	1.22E+08	3031	-0.10506	3.659813	0.531288	0.641755	0.027886	0	180	156	288	171	258	209	303	200	224	167
ENSMUSG00000057969	chr9	Sema3b	1.08E+08	1.08E+08	4777	-0.12492	3.628315	0.531455	0.641899	0.039468	0	130	103	276	257	298	173	255	181	260	204
ENSMUSG00000042997	chr3	Nhlrc3	53448588	53452649	5601	-0.12776	2.536113	0.531614	0.642032	0.036144	0	84	54	113	99	134	71	104	107	130	87
ENSMUSG00000050471	chr9	Fam118b	35216965	35217747	5981	-0.10207	4.646475	0.531771	0.642163	0.030118	0	371	354	619	347	377	369	615	392	544	311
ENSMUSG00000020357	chr11	Flt4	49609263	49609827	8232	0.132778	2.682898	0.531979	0.642356	0.046957	0	69	50	123	98	159	106	128	143	140	84
ENSMUSG00000029439	chr5	Sfswap	1.3E+08	1.3E+08	3302	0.093349	3.896121	0.53204	0.642371	0.022082	0	186	174	313	221	261	252	345	251	304	237
ENSMUSG00000043411	chr4	Usp48	1.38E+08	1.38E+08	9686	-0.09465	4.423241	0.532543	0.64292	0.023798	0	255	262	534	315	443	293	491	381	395	330
ENSMUSG00000087366	chr4	Junos	95051534	95051765	4117	-0.12536	2.384102	0.532643	0.642982	0.03306	0	72	58	132	80	94	65	116	77	95	94
ENSMUSG00000058392	chr17	Rrp1b	32036100	32036604	7702	0.117206	2.797497	0.532822	0.643086	0.032076	0	87	67	166	103	116	97	195	109	138	118
ENSMUSG00000071528	chr19	Usmg5	47083471	47083569	341	-0.1191	7.358338	0.532826	0.643086	0.04347	0	2605	2156	2635	3154	2758	2423	4504	2116	3489	2138
ENSMUSG00000029913	chr6	Prdm5	65778988	65779193	3711	0.164446	1.055779	0.532908	0.643127	0.045726	0	19	21	51	32	29	25	50	36	39	40
ENSMUSG00000028470	chr4	Hint2	43654227	43654411	1540	-0.11293	4.045512	0.533083	0.643187	0.036175	0	231	185	252	357	326	207	321	282	402	244
ENSMUSG00000028999	chr5	Rint1	23787711	23787882	6972	0.103519	3.168536	0.533071	0.643187	0.024278	0	114	106	191	114	169	127	218	165	198	139
ENSMUSG00000037363	chr8	Letm2	25578492	25578804	2098	-0.12952	2.252004	0.533104	0.643187	0.032606	0	61	48	104	84	100	77	93	74	91	69
ENSMUSG00000028917	chr4	Plekhm2	1.42E+08	1.42E+08	5186	-0.10512	4.849696	0.533634	0.643768	0.030958	0	393	234	656	555	626	355	564	537	637	450
ENSMUSG00000032127	chr9	Vps11	44348106	44348584	3179	-0.09008	4.881475	0.533758	0.6438	0.022569	0	354	352	714	483	573	400	565	531	676	439
ENSMUSG00000070942	chr1	Il1rl2	40324610	40327606	6812	0.154973	2.374574	0.533715	0.6438	0.062574	0	70	58	145	36	89	95	100	107	101	78
ENSMUSG00000029683	chr6	Lmod2	24597771	24598155	1967	-0.39133	6.166956	0.534183	0.644254	0.462247	0	150	151	432	3776	2216	437	1613	535	1550	1661
ENSMUSG00000026289	chr1	Atg16l1	87755870	87756085	9628	-0.08589	4.675156	0.534402	0.644461	0.020355	0	375	298	559	380	508	361	549	436	544	376
ENSMUSG00000025821	chr6	Zfp282	47877204	47877836	7663	0.099269	3.388831	0.534538	0.644565	0.024704	0	150	107	226	143	187	173	213	178	251	164
ENSMUSG00000085411	chr2	Gm14319	1.68E+08	1.68E+08	703	-0.32972	-0.1783	0.535301	0.645426	0.181767	0	15	11	36	3	7	12	14	19	7	9
ENSMUSG00000044197	chr5	Gpr146	1.39E+08	1.39E+08	6786	0.10212	5.527166	0.535549	0.645667	0.031308	0	609	436	1109	668	842	801	1364	706	925	610
ENSMUSG00000027673	chr3	Ndufb5	32736990	32737205	4995	-0.11525	7.978758	0.535884	0.645895	0.041345	0	3615	2770	4066	5501	4852	3534	6150	3402	6237	3321
ENSMUSG00000078762	chr7	Haus5	30653711	30654055	3455	0.139446	1.857757	0.535874	0.645895	0.041235	0	43	40	74	61	51	64	82	59	62	65
ENSMUSG00000083854	chr7	Dnajc19-ps	1.04E+08	1.04E+08	351	0.185439	1.027713	0.535863	0.645895	0.049135	0	24	25	38	29	28	22	63	33	38	34
ENSMUSG00000022216	chr14	Psme1	55578123	55578248	2209	0.101335	5.237318	0.536106	0.646045	0.02997	0	426	437	651	688	701	638	874	737	825	493
ENSMUSG00000028430	chr4	Nol6	41114427	41115506	5242	-0.0936	4.931336	0.536106	0.646045	0.0249	0	433	353	778	435	570	399	527	550	733	485
ENSMUSG00000041375	chr7	Ccdc9	16274042	16274416	5507	0.088011	4.418864	0.536212	0.646114	0.020866	0	300	240	437	298	389	329	471	400	457	344
ENSMUSG00000068270	chrX	Shroom4	6399854	6400261	8880	-0.15007	2.780476	0.53635	0.646222	0.056713	0	73	46	164	149	165	83	157	135	135	83
ENSMUSG00000001627	chr12	Ifrd1	40201567	40203451	5858	0.104992	5.024867	0.536492	0.646276	0.032403	0	442	275	619	603	605	499	731	638	861	393
ENSMUSG00000104394	chr1	RP23-306B14.3	1.87E+08	1.87E+08	2262	0.210272	0.481556	0.536457	0.646276	0.079568	0	18	15	32	9	23	28	41	14	25	18
ENSMUSG00000071180	chr13	Smim15	1.08E+08	1.08E+08	1852	-0.09731	3.880935	0.536812	0.646603	0.025564	0	214	205	311	210	265	209	301	245	275	252
ENSMUSG00000022340	chr15	Sybu	44671859	44673648	3599	0.249864	0.478258	0.537011	0.646732	0.11823	0	6	13	12	32	30	13	37	24	36	20
ENSMUSG00000032534	chr9	Cep63	1.03E+08	1.03E+08	9588	-0.09024	4.140634	0.537017	0.646732	0.0227	0	270	220	341	289	319	249	361	274	396	277
ENSMUSG00000033032	chr18	Afap1l1	61730261	61731310	3680	0.091316	5.711499	0.537238	0.646929	0.024749	0	702	557	1205	779	885	798	1365	845	1328	696
ENSMUSG00000035640	chr10	Dos	80130451	80132251	4996	0.228972	0.21154	0.537279	0.646929	0.088751	0	16	8	30	12	13	9	16	19	38	22
ENSMUSG00000031021	chr7	Tmem9b	1.1E+08	1.1E+08	2002	0.092625	5.540917	0.537339	0.646943	0.024928	0	687	581	917	666	717	750	1070	775	1109	702
ENSMUSG00000025103	chr7	Btbd1	81792075	81793726	3000	-0.11292	7.538463	0.537811	0.647394	0.039867	0	2139	1819	3629	4238	3900	2616	4577	2671	4129	2592
ENSMUSG00000026755	chr2	Arpc5l	39008076	39008346	4438	-0.11133	6.94409	0.537763	0.647394	0.038896	0	2082	1881	2306	1752	1895	1785	2839	1734	2999	1644
ENSMUSG00000046280	chr3	She	89831370	89832103	5733	-0.12334	2.683296	0.537894	0.647435	0.035542	0	67	62	150	124	141	80	132	111	136	97
ENSMUSG00000042828	chr7	Trim72	1.28E+08	1.28E+08	2553	0.100091	7.578696	0.538037	0.647548	0.031379	0	2296	1678	4407	3181	3736	2511	4890	2935	4856	3229
ENSMUSG00000022722	chr16	Arl6	59612949	59613844	2098	-0.12936	1.512808	0.538637	0.648212	0.038045	0	46	34	59	43	48	36	63	51	63	30
ENSMUSG00000008690	chr15	Ncaph2	89355719	89355850	4198	0.091133	6.075401	0.538974	0.6485	0.025117	0	922	778	1329	1071	1120	1065	1474	1135	1655	1050
ENSMUSG00000031072	chr7	Oraov1	1.45E+08	1.45E+08	4400	0.100042	3.816787	0.538945	0.6485	0.025262	0	208	159	235	213	258	223	342	253	295	212
ENSMUSG00000048731	chr17	Ggnbp1	26973217	26973314	6943	-0.09758	4.479552	0.5393	0.648834	0.02717	0	357	239	415	334	504	335	486	310	478	356
ENSMUSG00000036850	chr2	Mrpl41	24974117	24974681	888	0.112824	4.334834	0.54052	0.650242	0.035532	0	248	229	290	386	372	297	514	297	536	300
ENSMUSG00000066043	chr4	Phactr4	1.32E+08	1.32E+08	4960	-0.11084	3.70607	0.540647	0.650335	0.032761	0	159	111	308	233	308	146	309	225	289	190
ENSMUSG00000036983	chr17	Tfb1m	3519263	3519795	1327	-0.11033	2.970166	0.540712	0.650355	0.031525	0	123	103	173	121	120	111	176	110	154	129
ENSMUSG00000024253	chr17	Dync2li1	84626496	84626576	1324	0.158472	2.168916	0.540832	0.650391	0.052896	0	67	65	81	44	69	72	132	65	98	62
ENSMUSG00000075528	chr11	Aarsd1	1.01E+08	1.01E+08	3052	0.090168	5.383888	0.54084	0.650391	0.023707	0	581	505	744	674	694	624	938	711	1004	672
ENSMUSG00000029729	chr5	Zkscan1	1.38E+08	1.38E+08	8541	-0.09605	3.623424	0.541139	0.650691	0.024577	0	172	150	298	174	233	152	288	179	273	201
ENSMUSG00000074405	chr7	Zfp865	5020376	5020655	3873	-0.10473	3.465229	0.541479	0.651042	0.026765	0	134	125	304	150	227	146	225	182	241	174
ENSMUSG00000022956	chr16	Atp5o	91684398	91684480	2259	0.114348	8.835224	0.541611	0.651141	0.04186	0	5467	4477	7223	9572	8366	6716	11822	6705	12328	6810
ENSMUSG00000046949	chr13	Nqo2	33964659	33964800	3974	-0.10347	4.953623	0.541666	0.651148	0.031284	0	385	261	730	563	727	449	779	472	591	452
ENSMUSG00000038712	chr3	Fam63a	95281345	95281611	6458	0.08559	5.039092	0.541829	0.651226	0.021432	0	462	344	749	476	558	500	733	571	823	486
ENSMUSG00000043518	chrX	Rai2	1.62E+08	1.62E+08	2403	-0.0987	4.249275	0.541818	0.651226	0.028897	0	274	254	476	264	311	199	421	313	458	309
ENSMUSG00000007029	chr17	Vars	35000987	35001232	5608	-0.09311	5.264658	0.54189	0.651241	0.025915	0	521	427	980	613	705	494	654	694	972	595
ENSMUSG00000026721	chr1	Rabgap1l	1.6E+08	1.6E+08	23232	0.107829	2.881107	0.542016	0.651332	0.029725	0	86	67	164	122	135	101	173	152	163	105
ENSMUSG00000068739	chr3	Sars	1.08E+08	1.08E+08	3653	-0.09425	6.395962	0.542066	0.651334	0.027895	0	1168	948	1727	1516	1649	1242	1621	1288	2154	1198
ENSMUSG00000024829	chr19	Mrpl21	3282901	3283171	2011	0.108162	5.012245	0.542634	0.651957	0.034223	0	455	416	476	514	558	513	862	456	791	477
ENSMUSG00000047583	chr3	Tyw3	1.55E+08	1.55E+08	4499	-0.14138	1.604005	0.542688	0.651963	0.038178	0	38	36	80	48	49	45	69	51	47	42
ENSMUSG00000028578	chr4	Caap1	94500081	94501416	3591	0.162259	1.027367	0.542738	0.651963	0.05188	0	21	25	40	23	38	23	40	31	44	47

ENSMUSG00000022635	chr15	Zcrb1	93386097	93386283	3074	-0.1041	6.471944	0.542832	0.652018	0.034788	0	1441	1347	1534	1271	1541	1184	2064	1379	2031	1273
ENSMUSG00000021732	chr13	Fgf10	1.19E+08	1.19E+08	4601	-0.31366	0.565744	0.543027	0.65216	0.263246	0	35	23	44	3	17	14	18	51	14	13
ENSMUSG00000028799	chr4	Zfp362	1.29E+08	1.29E+08	3052	-0.10884	3.487156	0.543049	0.65216	0.029581	0	159	100	288	176	233	157	191	201	265	164
ENSMUSG00000030942	chr7	Thumpd1	1.2E+08	1.2E+08	2653	0.091844	5.035745	0.543188	0.652268	0.024383	0	443	434	625	456	554	526	768	532	743	523
ENSMUSG00000038079	chr1	Tmem237	59100590	59101198	2389	0.144093	1.546855	0.543749	0.652882	0.042683	0	44	27	75	30	43	39	61	54	66	50
ENSMUSG00000021376	chr13	Tpmt	47025170	47025477	1914	-0.1562	0.653176	0.543925	0.652975	0.046594	0	27	21	26	23	25	21	34	20	30	22
ENSMUSG00000027546	chr2	Atp9a	1.69E+08	1.69E+08	5917	0.114635	5.26833	0.54389	0.652975	0.041001	0	358	382	729	789	753	487	798	593	1054	756
ENSMUSG00000032786	chr9	Alas1	1.06E+08	1.06E+08	4310	-0.14556	6.874377	0.544137	0.653116	0.068158	0	1335	750	2091	3120	2889	1385	2584	2081	2767	1561
ENSMUSG00000094530	chr8	Gm21399	1.29E+08	1.29E+08	600	0.223661	0.340186	0.544141	0.653116	0.090765	0	16	9	23	20	18	18	23	37	29	7
ENSMUSG00000025509	chr7	Pnpla2	1.41E+08	1.41E+08	3020	0.153105	7.780488	0.544468	0.653332	0.075988	0	2453	1601	3257	5369	4175	2603	4374	6228	5476	2732
ENSMUSG00000032531	chr9	Amotl2	1.03E+08	1.03E+08	6289	0.122887	4.206457	0.544424	0.653332	0.043736	0	242	257	351	248	290	182	410	443	348	364
ENSMUSG00000032913	chr3	Lrig2	1.04E+08	1.04E+08	7111	0.11255	3.003366	0.544375	0.653332	0.035408	0	97	74	208	89	167	126	161	131	200	134
ENSMUSG00000002455	chr2	Prpf6	1.82E+08	1.82E+08	3859	0.088397	5.452428	0.544873	0.653759	0.023737	0	503	564	980	617	759	650	921	776	1079	707
ENSMUSG00000023944	chr17	Hsp90ab1	45567775	45568124	2999	-0.09433	10.31685	0.545574	0.65454	0.029165	0	19880	16767	27228	18066	23125	18973	24100	22469	29579	17881
ENSMUSG00000054737	chrX	Zfp182	21028939	21031652	5733	-0.22868	0.466642	0.54567	0.654597	0.069336	0	20	14	40	18	21	24	19	27	15	19
ENSMUSG00000030042	chr6	Pole4	82618992	82619138	2509	-0.09209	4.571858	0.545738	0.654619	0.025803	0	362	343	490	326	413	331	467	393	509	391
ENSMUSG00000016308	chrX	Ube2a	36874358	36874529	1662	0.090359	4.807185	0.545926	0.654785	0.023504	0	394	346	514	383	515	435	670	452	629	454
ENSMUSG00000022043	chr14	Trim35	66297031	66297549	4045	0.111265	7.18708	0.546036	0.654858	0.04045	0	1722	1013	3127	2627	3223	2084	3435	2269	3418	2693
ENSMUSG00000036120	chr8	Rfxank	70130812	70133463	3676	-0.11355	3.140944	0.54618	0.654972	0.034332	0	103	104	160	181	179	134	201	121	177	134
ENSMUSG00000090136	chr9	Gm10177	37252922	37253365	444	0.174404	2.55319	0.546723	0.655564	0.076969	0	101	91	69	70	78	101	185	83	126	74
ENSMUSG00000043155	chr4	Hpdl	1.17E+08	1.17E+08	1804	-0.33025	0.212671	0.546802	0.655599	0.268125	0	8	2	8	42	35	5	26	16	24	16
ENSMUSG00000083692	chr16	Gm9575	50665008	50666346	1339	-0.27712	-0.25585	0.547528	0.65641	0.173279	0	17	14	12	13	5	3	7	18	24	10
ENSMUSG00000018102	chr13	Hist1h2bc	23684199	23684621	736	-0.09209	5.394099	0.5477	0.656505	0.02704	0	708	560	840	627	679	624	822	715	939	614
ENSMUSG00000022965	chr16	Ifngr2	91547072	91547232	3313	0.08835	6.287663	0.547706	0.656505	0.024779	0	1118	871	1549	1246	1273	1146	1787	1437	1822	1208
ENSMUSG00000019578	chr17	Ubxn6	56067045	56068683	5685	-0.10162	6.052385	0.54805	0.656858	0.033625	0	1049	952	1304	1044	1029	1062	1223	1030	1585	943
ENSMUSG00000000976	chr11	Heatr6	83753696	83753941	6419	-0.10106	3.588613	0.548283	0.656893	0.026943	0	159	140	329	168	220	146	242	206	249	210
ENSMUSG00000018372	chr11	Cep95	1.07E+08	1.07E+08	4199	-0.12971	2.203996	0.548317	0.656893	0.036095	0	51	55	114	74	91	70	105	73	74	69
ENSMUSG00000022663	chr16	Atg3	45158785	45159171	3154	-0.09094	4.666487	0.548224	0.656893	0.0257	0	374	360	529	392	410	381	575	405	509	373
ENSMUSG00000032583	chr9	Mon1a	1.08E+08	1.08E+08	2826	-0.09815	3.646222	0.548327	0.656893	0.026562	0	177	149	259	237	205	178	235	214	255	207
ENSMUSG00000049532	chr14	Sall2	52311172	52315663	5433	0.153577	0.956761	0.548327	0.656893	0.042695	0	21	15	45	25	37	21	42	37	48	30
ENSMUSG00000019917	chr10	Sept10	59164113	59164944	2539	0.121697	2.744482	0.549039	0.657686	0.034494	0	81	80	141	99	108	84	164	152	149	87
ENSMUSG00000019978	chr10	Epb4.1l2	25359798	25359981	4464	-0.09737	4.854872	0.549119	0.6577	0.028559	0	419	327	712	383	602	393	598	595	481	457
ENSMUSG00000045374	chr11	Wdr81	75440944	75442089	7038	0.104616	3.42099	0.549149	0.6577	0.033414	0	135	89	278	166	182	150	201	220	225	199
ENSMUSG00000016756	chr13	Cmah	24327420	24327488	9972	-0.24152	0.937622	0.54935	0.657881	0.128013	0	19	16	63	23	46	15	28	56	18	30
ENSMUSG00000032306	chr9	Mpi	57544256	57544938	3142	-0.09635	5.690454	0.549446	0.657936	0.029893	0	657	557	1010	1046	1033	705	1186	693	1278	771
ENSMUSG00000023008	chr15	Fmnl3	99317225	99318372	5021	0.126344	3.176869	0.549547	0.657998	0.0453	0	83	72	189	180	184	116	202	186	247	118
ENSMUSG00000021969	chr14	Zdhhc20	57832702	57836646	5173	0.136504	2.398226	0.549901	0.658362	0.05372	0	48	48	150	61	109	55	108	102	133	100
ENSMUSG00000039768	chr4	Dnajc11	1.52E+08	1.52E+08	10678	0.096122	5.422623	0.550029	0.658456	0.029713	0	544	356	804	779	904	634	903	719	1103	709
ENSMUSG00000031820	chr8	Babam1	71396855	71397020	1592	0.087658	6.06113	0.550263	0.658624	0.024569	0	831	813	1308	1028	1205	1026	1482	1135	1563	1091
ENSMUSG00000036955	chr10	2510003E04Rik	62538626	62540056	6547	-0.08461	4.932755	0.550268	0.658624	0.021933	0	391	376	727	492	559	422	672	443	698	488
ENSMUSG00000031770	chr8	Herpud1	94386438	94386738	2333	-0.08852	7.069391	0.551088	0.659485	0.025953	0	1994	1417	3169	2232	2463	1815	2855	2185	3321	1889
ENSMUSG00000032740	chr11	Ccdc88a	29373658	29374410	10891	0.144704	1.5059	0.551045	0.659485	0.05442	0	28	34	70	29	52	47	44	59	53	53
ENSMUSG00000043872	chr4	Zmym1	1.27E+08	1.27E+08	4164	-0.13371	1.789254	0.551306	0.659687	0.041872	0	52	42	88	49	53	44	80	68	66	37
ENSMUSG00000073627	chr1	C130036L24Rik	86359574	86360007	6437	-0.17051	1.023755	0.551564	0.659937	0.064928	0	35	27	32	35	31	34	32	26	55	20
ENSMUSG00000021103	chr12	Mnat1	73123717	73123926	5385	-0.09334	3.799408	0.55245	0.660937	0.025661	0	196	192	298	202	252	216	304	191	306	209
ENSMUSG00000025575	chr11	Cant1	1.18E+08	1.18E+08	4358	0.089058	4.244068	0.552863	0.661371	0.023922	0	266	202	419	253	345	280	401	382	365	332
ENSMUSG00000028487	chr4	Bnc2	84275095	84276447	8174	0.187584	0.600603	0.552959	0.661426	0.073689	0	22	5	34	19	29	13	35	30	35	25
ENSMUSG00000030314	chr6	Atg7	1.15E+08	1.15E+08	5273	0.100205	3.331611	0.553147	0.661591	0.027868	0	148	91	209	168	163	153	199	194	226	166
ENSMUSG00000028932	chr5	Psmc2	21785283	21785517	5031	0.101933	7.10351	0.553459	0.661905	0.03463	0	1970	2004	2722	1761	1932	2093	3327	2349	3245	2112
ENSMUSG00000054414	chr3	Slc30a7	1.16E+08	1.16E+08	9020	0.111994	2.682234	0.553661	0.662087	0.037103	0	89	51	159	85	119	89	142	125	119	120
ENSMUSG00000037722	chr14	Gnpnat1	45376334	45378486	2629	-0.12035	2.637876	0.554031	0.66247	0.039655	0	86	93	117	99	108	81	155	101	98	101
ENSMUSG00000082127	chr2	Gm13577	64474745	64474957	213	0.224653	1.545653	0.554318	0.662753	0.123761	0	41	54	46	20	37	68	83	29	70	30
ENSMUSG00000037152	chr3	Ndufc1	51404677	51405619	1495	0.102277	7.104043	0.55442	0.662815	0.035056	0	2042	1772	2270	2182	2090	2315	3524	2157	3231	1924
ENSMUSG00000021967	chr14	Mrpl57	57826239	57826322	2321	0.104003	4.54215	0.554548	0.662904	0.031908	0	387	305	377	318	353	348	568	375	556	370
ENSMUSG00000069633	chr8	Pex11g	3457105	3459434	3397	0.13867	2.334163	0.554595	0.662904	0.041415	0	80	61	76	75	76	66	110	102	126	73
ENSMUSG00000019845	chr10	Tube1	39134023	39134107	2929	0.19071	0.213447	0.555026	0.663331	0.055068	0	18	12	27	9	13	17	25	20	24	16
ENSMUSG00000044167	chr3	Foxo1	52268336	52269422	8665	0.125761	4.442113	0.555051	0.663331	0.05229	0	224	267	565	275	373	509	356	446	393	287
ENSMUSG00000042814	chr2	Mcts2	1.53E+08	1.53E+08	917	0.12475	2.682338	0.555187	0.663433	0.037304	0	99	78	108	86	106	114	119	116	156	93
ENSMUSG00000048170	chr7	Mcmbp	1.29E+08	1.29E+08	5107	-0.09164	4.152393	0.555334	0.663549	0.023925	0	222	168	451	303	370	225	408	295	385	270
ENSMUSG00000006526	chr14	Tmem110	30825590	30825890	4058	-0.09489	3.448753	0.555616	0.663785	0.024555	0	143	130	222	184	222	147	243	171	214	182
ENSMUSG00000040040	chr14	Ift88	57424062	57424187	4628	-0.12312	2.369651	0.555632	0.663785	0.042259	0	63	77	112	79	91	63	146	84	97	62
ENSMUSG00000059820	chr9	AU019823	50605240	50607936	5321	-0.09645	3.369448	0.555743	0.663858	0.026673	0	153	130	245	159	164	161	232	168	204	140
ENSMUSG00000068040	chr2	Tm9sf4	1.53E+08	1.53E+08	7281	0.100525	4.799264	0.555881	0.663963	0.033427	0	324	216	593	520	565	360	570	566	625	502
ENSMUSG00000045482	chr5	Trrap	1.45E+08	1.45E+08	15185	-0.10725	4.546783	0.556227	0.664317	0.035027	0	254	195	713	405	486	285	478	423	514	363
ENSMUSG00000031990	chr9	Jam3	27097385	27098401	2539	0.126593	2.878867	0.556484	0.664564	0.046128	0	67	70	118	144	164	95	187	122	171	125

ENSMUSG00000032656	chr18	March3	56761716	56762568	6006	0.211476	0.512393	0.556606	0.66459	0.08864	0	18	16	36	11	18	15	38	38	29	11
ENSMUSG00000059423	chr4	Zfp933	1.48E+08	1.48E+08	4270	-0.10497	3.001983	0.556593	0.66459	0.028384	0	110	78	183	119	184	105	182	135	156	122
ENSMUSG00000020198	chr10	Ap3d1	80706978	80707983	4730	-0.0839	5.319204	0.556773	0.664729	0.022296	0	583	423	1020	598	741	591	790	711	870	574
ENSMUSG00000001802	chr7	Lrp3	35200027	35200415	4571	0.09349	3.562978	0.557069	0.664844	0.025277	0	144	117	235	190	237	169	235	237	270	193
ENSMUSG00000025265	chrX	Fgd1	1.51E+08	1.51E+08	4931	-0.14256	1.472985	0.557062	0.664844	0.035198	0	36	25	73	44	53	40	60	40	51	41
ENSMUSG00000042992	chr6	Loh12cr1	1.35E+08	1.35E+08	1822	0.087337	4.23313	0.556938	0.664844	0.022044	0	260	198	389	305	312	248	437	307	466	323
ENSMUSG00000103515	chr8	AL591003.1	1.22E+08	1.22E+08	1990	0.259057	0.06012	0.557013	0.664844	0.136301	0	11	5	12	22	18	22	37	7	15	12
ENSMUSG00000061315	chr10	Naca	1.28E+08	1.28E+08	7034	-0.10299	8.531009	0.557221	0.664966	0.036653	0	4868	3460	11471	5489	7069	4438	7616	5640	9638	5844
ENSMUSG00000037703	chr2	Lzts3	1.31E+08	1.31E+08	4252	0.120917	2.261888	0.55756	0.665309	0.034885	0	46	56	103	75	85	81	112	78	94	79
ENSMUSG00000059327	chrX	Eda	99975606	99976176	6825	0.131783	1.733865	0.55771	0.665429	0.05409	0	28	22	94	53	63	55	76	52	72	52
ENSMUSG00000039801	chr15	2410089E03Rik	8169106	8169489	13017	-0.14294	2.260242	0.557954	0.66566	0.047878	0	51	45	134	86	94	47	106	78	86	91
ENSMUSG00000025184	chr19	R3hcc1l	42518759	42518857	7397	0.093741	3.71181	0.558285	0.665841	0.02486	0	196	135	276	199	208	225	303	216	301	185
ENSMUSG00000030967	chr7	Zranb1	1.33E+08	1.33E+08	5431	-0.09449	6.855293	0.558245	0.665841	0.030738	0	1626	1466	2795	1866	1885	1636	2151	1678	3153	1730
ENSMUSG00000039450	chr11	Dcxr	1.21E+08	1.21E+08	1144	0.105131	3.17091	0.558306	0.665841	0.029645	0	107	109	177	133	164	122	167	188	238	133
ENSMUSG00000099226	chrX	Mir7091	74274027	74274105	79	0.164402	1.908538	0.55824	0.665841	0.062106	0	55	59	70	28	58	67	85	62	81	56
ENSMUSG00000025076	chr19	Casp7	56397129	56397317	2350	-0.12998	1.975982	0.55839	0.665881	0.043274	0	45	53	75	66	82	52	109	57	75	47
ENSMUSG00000027695	chr3	Pld1	27938695	27938750	12961	-0.14605	2.145232	0.558632	0.666109	0.054045	0	34	51	116	70	107	53	101	89	82	53
ENSMUSG00000045996	chr15	Polr2k	36174010	36174081	624	-0.14461	3.991671	0.558984	0.666409	0.071827	0	283	311	250	185	218	216	474	204	282	224
ENSMUSG00000085151	chr2	1110018N20Rik	1.67E+08	1.67E+08	1579	-0.1888	1.031744	0.558966	0.666409	0.09872	0	36	46	31	20	23	28	37	31	43	28
ENSMUSG00000027170	chr2	Eif3m	1.05E+08	1.05E+08	2590	-0.10168	6.180224	0.559227	0.666639	0.035884	0	1057	1151	1460	1076	1114	1113	1783	1080	1516	961
ENSMUSG00000044715	chr12	Gskip	1.06E+08	1.06E+08	2776	0.103674	3.514923	0.559409	0.666797	0.028712	0	168	146	197	148	205	169	282	179	252	195
ENSMUSG00000013787	chr17	Ehmt2	34898469	34898540	5489	0.081656	5.343182	0.559953	0.667385	0.02185	0	541	426	866	612	755	560	825	788	995	656
ENSMUSG00000048706	chr4	Lurap1l	80910646	80911645	3066	0.169198	1.186608	0.560281	0.667715	0.051978	0	32	27	24	32	45	34	56	38	47	35
ENSMUSG00000080896	chrX	Gm14567	38969817	38969990	174	-0.19251	0.544516	0.560637	0.66808	0.100007	0	15	32	21	19	24	10	33	16	37	23
ENSMUSG00000102827	chr18	RP23-56B11.5	37652433	37652907	1740	-0.17232	0.590544	0.560757	0.668162	0.062092	0	17	22	30	27	22	21	41	13	29	18
ENSMUSG00000027166	chr2	Dnajc24	1.06E+08	1.06E+08	1369	-0.13428	1.513626	0.560962	0.668227	0.045087	0	47	33	53	42	55	44	65	33	69	32
ENSMUSG00000030980	chr7	Knop1	1.19E+08	1.19E+08	5871	-0.08146	4.656437	0.560888	0.668227	0.02056	0	354	282	561	391	512	354	526	459	525	371
ENSMUSG00000059278	chr11	Naa38	69395487	69395681	890	0.102678	4.597648	0.560913	0.668227	0.032414	0	333	352	393	374	352	368	590	452	488	385
ENSMUSG00000067722	chr17	BC003965	25184561	25184640	3022	0.095241	4.828851	0.561361	0.668642	0.029081	0	393	292	447	485	571	422	765	458	616	443
ENSMUSG00000008333	chr2	Snrpb2	1.43E+08	1.43E+08	2857	0.107664	4.090423	0.561524	0.668716	0.034059	0	245	256	327	198	251	240	444	317	367	254
ENSMUSG00000027875	chr3	Hmgcs2	98280435	98280587	3290	-0.21968	0.75787	0.561509	0.668716	0.123994	0	26	33	37	22	15	37	17	30	32	15
ENSMUSG00000022369	chr15	Mtbp	55557408	55557737	5481	0.199359	0.35523	0.561618	0.668751	0.081346	0	7	9	27	29	17	19	37	18	25	16
ENSMUSG00000095159	chr5	Tubb4b-ps1	7179365	7180699	1335	-0.22976	0.041403	0.561654	0.668751	0.11271	0	8	18	21	7	26	7	31	13	14	14
ENSMUSG00000022554	chr15	Hgh1	76368898	76369569	1959	0.166778	1.447043	0.561822	0.668891	0.064442	0	50	27	38	29	51	46	62	63	46	34
ENSMUSG00000039199	chr8	Zdhhc1	1.05E+08	1.05E+08	1737	0.100068	3.843236	0.562197	0.669278	0.030023	0	211	157	265	244	217	207	262	266	323	276
ENSMUSG00000001729	chr12	Akt1	1.13E+08	1.13E+08	4098	0.094481	5.814896	0.562359	0.669411	0.030471	0	643	576	1032	1111	1025	706	1315	1116	1309	917
ENSMUSG00000062590	chr1	Armc9	86154780	86154843	13006	0.146427	1.081363	0.562891	0.669983	0.045864	0	22	22	43	27	41	34	37	27	51	42
ENSMUSG00000042197	chr1	Zfp451	33761545	33762209	15839	0.095595	3.370636	0.563059	0.670122	0.026719	0	131	104	244	137	198	143	247	194	199	183
ENSMUSG00000015697	chr3	Setdb1	95323525	95324190	6853	0.085423	4.031418	0.563425	0.670499	0.022846	0	203	172	376	256	280	251	346	335	328	260
ENSMUSG00000033542	chr6	Arhgef5	43265582	43265743	9977	-0.10547	3.366813	0.563572	0.670564	0.031693	0	146	122	250	156	186	169	167	164	267	133
ENSMUSG00000036270	chr8	Edc4	1.06E+08	1.06E+08	5497	-0.09815	4.549646	0.563617	0.670564	0.030133	0	272	213	621	394	521	288	496	354	506	424
ENSMUSG00000047129	chr10	1700113H08Rik	87058045	87058159	1550	-0.27241	0.063788	0.563632	0.670564	0.110811	0	8	5	16	30	25	17	14	15	17	13
ENSMUSG00000002808	chr13	Epdr1	19591709	19593348	2386	-0.09534	7.289238	0.563694	0.670578	0.032189	0	1976	1477	3510	3084	3235	1950	3878	2389	3349	2463
ENSMUSG00000021884	chr14	Hacl1	31552905	31552990	5123	-0.11127	3.095943	0.563824	0.670673	0.037587	0	147	106	177	120	149	108	172	194	150	116
ENSMUSG00000000532	chr15	Acvr1b	1.01E+08	1.01E+08	4413	-0.09474	6.448958	0.564089	0.670927	0.031236	0	1088	1022	2395	1302	1638	1283	1547	1281	1927	1606
ENSMUSG00000036402	chr6	Gng12	66896397	66896527	4694	-0.09179	4.520075	0.564395	0.671226	0.026915	0	289	266	624	363	397	308	484	484	458	296
ENSMUSG00000060450	chr18	Rnf14	38296635	38296798	3515	-0.08208	6.641731	0.564441	0.671226	0.023692	0	1470	1162	2300	1574	1796	1334	2222	1666	2113	1577
ENSMUSG00000051510	chr11	Mafg	1.21E+08	1.21E+08	5613	0.086455	6.301737	0.564498	0.671233	0.026113	0	1143	847	1794	1035	1401	1261	1677	1449	1934	1131
ENSMUSG00000021983	chr14	Atp8a2	59647531	59647924	6419	0.158777	1.659863	0.564836	0.671575	0.05734	0	30	47	61	39	53	53	86	34	66	56
ENSMUSG00000038042	chr13	Ptpdc1	48577873	48579843	4310	-0.12901	2.064123	0.565065	0.671787	0.035566	0	59	40	111	62	79	54	71	67	92	71
ENSMUSG00000063235	chr2	Ptpmt1	90908716	90911319	3684	-0.08704	5.164349	0.565504	0.672248	0.025877	0	626	385	737	568	635	551	803	538	798	502
ENSMUSG00000097343	chr7	9030407P20Rik	1.21E+08	1.21E+08	2347	0.174059	0.538001	0.565618	0.672324	0.057182	0	15	10	33	27	18	22	39	17	32	21
ENSMUSG00000034235	chr14	Usp54	20548912	20550460	8921	-0.13403	2.678313	0.565674	0.67233	0.047448	0	76	56	171	110	137	118	141	111	108	67
ENSMUSG00000002500	chr17	Rpl3l	24727820	24727886	1643	-0.09324	8.869893	0.565804	0.672366	0.031475	0	6750	4726	9039	8985	9514	6561	10992	6737	10984	6747
ENSMUSG00000025537	chr5	Phkg1	1.3E+08	1.3E+08	3232	-0.1011	9.252577	0.565856	0.672366	0.037077	0	10564	8228	14981	6907	9829	8887	13097	10314	13505	8372
ENSMUSG00000060376	chr7	Bckdha	25629852	25630433	1773	-0.1099	7.433902	0.565815	0.672366	0.043473	0	2118	1558	3005	3947	3960	2246	3963	2759	4122	2388
ENSMUSG00000049871	chr16	Nlrc3	3945007	3947539	7068	0.180836	0.260195	0.565912	0.672373	0.055653	0	11	12	25	13	22	14	30	26	16	19
ENSMUSG00000100863	chr4	Gm12669	91805547	91806555	1009	-0.11316	3.078512	0.56672	0.673272	0.042629	0	119	142	168	104	148	124	192	104	198	123
ENSMUSG00000024972	chr19	Lgals12	7596660	7598171	2773	0.372639	2.300925	0.567006	0.673455	0.471017	0	140	87	30	11	24	79	50	261	37	50
ENSMUSG00000035572	chr4	Dcaf10	45342101	45342727	7305	-0.09733	3.625303	0.566955	0.673455	0.028012	0	167	151	322	189	201	208	226	204	274	164
ENSMUSG00000049804	chrX	Armcx4	1.35E+08	1.35E+08	7996	-0.1642	4.300987	0.567026	0.673455	0.092973	0	165	100	422	572	491	203	480	319	410	309
ENSMUSG00000027993	chr3	Trim2	84160439	84165249	18113	-0.15313	1.456407	0.56724	0.673582	0.04571	0	26	26	70	50	58	31	59	48	45	45
ENSMUSG00000029016	chr4	Clcn6	1.48E+08	1.48E+08	5933	0.100574	3.013743	0.567286	0.673582	0.031443	0	93	69	171	148	150	128	162	139	189	134
ENSMUSG00000102717	chr1	RP23-211F21.1	1.36E+08	1.36E+08	3246	0.493896	0.645402	0.5672	0.673582	0.805159	0	3	1	41	52	5	1	2	44	84	27
ENSMUSG00000048120	chr19	Entpd1	40612366	40612523	5580	0.099335	3.446522	0.567423	0.673685	0.032163	0	108	112	251	156	236	180	250	219	201	164

ENSMUSG00000022142	chr15	Nup155	8109313	8109602	6402	-0.09156	3.625773	0.567605	0.67384	0.023339	0	169	123	304	207	234	184	271	191	247	191
ENSMUSG00000100680	chr6	1810044D09Rik	91440987	91441158	486	0.177651	1.463058	0.567825	0.674042	0.072121	0	42	39	42	36	34	51	57	68	52	27
ENSMUSG00000061731	chr15	Ext1	53064038	53068849	8077	0.097913	3.383056	0.567966	0.674148	0.026993	0	141	123	206	157	172	142	274	181	202	181
ENSMUSG00000041126	chr11	H2afv	6427229	6428432	1633	0.087674	5.841806	0.568138	0.674292	0.026496	0	755	772	1077	839	949	906	1409	944	1240	913
ENSMUSG00000039683	chr5	Sdk1	1.41E+08	1.41E+08	11087	0.179056	2.138357	0.568339	0.674471	0.105702	0	39	39	178	37	58	46	111	86	75	96
ENSMUSG00000029613	chr5	Eif2ak1	1.44E+08	1.44E+08	5675	-0.08341	6.221134	0.568589	0.674646	0.024804	0	959	917	1772	1179	1405	1013	1751	1120	1620	1175
ENSMUSG00000064181	chr10	Rab3ip	1.17E+08	1.17E+08	2690	-0.10165	4.192192	0.568565	0.674646	0.034451	0	207	185	342	403	390	245	440	309	408	229
ENSMUSG00000051557	chr4	Pusl1	1.56E+08	1.56E+08	2329	0.107503	2.621555	0.568721	0.674743	0.028442	0	77	74	124	83	111	98	146	97	146	90
ENSMUSG00000031921	chr8	Terf2	1.07E+08	1.07E+08	4597	0.09044	3.875093	0.568943	0.674945	0.024202	0	188	171	335	207	244	201	351	291	360	192
ENSMUSG00000030546	chr7	Plin1	79721164	79721759	1916	0.354178	4.379378	0.569133	0.675111	0.446543	0	557	378	182	59	86	286	155	1150	161	255
ENSMUSG00000034566	chr11	Atp5h	1.15E+08	1.15E+08	1465	0.107518	8.042699	0.569364	0.675324	0.042408	0	3270	2725	3807	5450	4892	3822	6621	4048	7247	3832
ENSMUSG00000037003	chr15	Tenc1	1.02E+08	1.02E+08	4728	0.083041	5.453424	0.56956	0.675496	0.024672	0	557	405	980	684	873	723	878	861	946	674
ENSMUSG00000020715	chr11	Ern1	1.06E+08	1.06E+08	8173	-0.11192	3.496712	0.569851	0.675781	0.038316	0	112	106	303	200	254	118	257	214	249	162
ENSMUSG00000092659	chr7	Mir3100	19086828	19086892	65	-0.18972	0.951151	0.570302	0.676256	0.086623	0	19	13	41	48	39	21	56	31	23	26
ENSMUSG00000026240	chr1	Cops7b	86582904	86583096	5515	0.094411	3.560215	0.57052	0.676332	0.026757	0	153	111	230	215	207	168	267	229	283	167
ENSMUSG00000029840	chr6	Mtpn	35508906	35512317	3960	0.082637	4.793594	0.570476	0.676332	0.023234	0	343	296	654	407	500	374	623	593	587	430
ENSMUSG00000030611	chr7	Mrps11	78783119	78783423	2172	-0.09672	4.120911	0.570447	0.676332	0.031326	0	280	181	298	322	345	280	361	239	417	240
ENSMUSG00000055760	chr17	Gemin6	80224441	80224670	1428	0.107132	2.751229	0.571091	0.676949	0.030845	0	90	84	137	95	104	115	157	122	132	99
ENSMUSG00000060380	chr9	C030014I23Rik	44479924	44479733	2446	-0.18967	0.546029	0.571233	0.677057	0.057317	0	23	12	30	23	29	22	18	16	32	26
ENSMUSG00000021578	chr13	Ccdc127	74350309	74350408	9559	-0.07802	5.538155	0.571572	0.677217	0.021482	0	656	534	1052	776	837	623	1106	741	969	722
ENSMUSG00000029500	chr5	Pgam5	1.1E+08	1.1E+08	2373	0.085048	5.038988	0.571479	0.677217	0.024778	0	443	313	659	583	582	426	802	548	785	563
ENSMUSG00000041936	chr4	Agrn	1.56E+08	1.56E+08	9285	0.110734	3.482103	0.571545	0.677217	0.042383	0	103	94	287	176	237	134	262	243	209	202
ENSMUSG00000055720	chr9	Ubl7	57910986	57911059	1364	0.08354	5.886597	0.571531	0.677217	0.024789	0	841	609	1237	942	1010	848	1273	963	1588	949
ENSMUSG00000037058	chr18	Paip2	35598617	35598759	2789	-0.0891	7.026028	0.571804	0.67737	0.029451	0	1895	1810	2730	2060	2146	1863	3216	1928	2657	1976
ENSMUSG00000057409	chr17	Zfp53	21491256	21491316	2058	-0.14425	0.817478	0.571762	0.67737	0.042778	0	22	24	43	27	24	21	37	30	32	24
ENSMUSG00000030110	chr6	Ret	1.18E+08	1.18E+08	7341	0.107128	3.082809	0.572014	0.677558	0.040366	0	96	75	215	118	168	152	132	141	192	160
ENSMUSG00000029334	chr5	Prkg2	98929773	98932105	5369	-0.18659	0.526063	0.572103	0.677603	0.060642	0	16	21	40	11	28	21	29	21	27	16
ENSMUSG00000006906	chr6	Stambp	83543206	83544036	2157	0.107091	3.103759	0.572399	0.67766	0.032672	0	121	115	152	117	140	152	194	154	161	135
ENSMUSG00000019849	chr10	Prep	45067206	45067375	2729	-0.08703	4.527078	0.572333	0.67766	0.024886	0	316	217	525	434	445	305	502	342	518	383
ENSMUSG00000021040	chr12	Slirp	87443896	87444026	3104	0.111738	5.023975	0.572401	0.67766	0.043055	0	476	490	510	484	435	590	833	458	713	493
ENSMUSG00000026434	chr1	Nucks1	1.32E+08	1.32E+08	6779	0.08788	6.486659	0.572426	0.67766	0.027925	0	1410	1065	1745	1237	1444	1306	2113	1442	2211	1456
ENSMUSG00000029066	chr4	Mrpl20	1.56E+08	1.56E+08	1664	0.096002	4.959718	0.572284	0.67766	0.030773	0	480	416	488	446	505	508	751	520	719	450
ENSMUSG00000030956	chr7	Fam53b	1.33E+08	1.33E+08	6911	-0.08828	5.073389	0.572457	0.67766	0.026382	0	457	312	762	612	701	521	598	569	767	507
ENSMUSG00000069237	chr13	C78339	46669522	46670255	3827	-0.08848	5.132951	0.572654	0.677833	0.02796	0	564	466	879	439	551	482	743	593	785	518
ENSMUSG00000027076	chr2	Timm10	84826997	84827147	815	-0.10232	3.984247	0.573068	0.678262	0.036987	0	255	181	248	308	291	237	358	233	400	184
ENSMUSG00000028955	chr4	Vamp3	1.51E+08	1.51E+08	2889	0.084548	6.022272	0.573288	0.678461	0.025579	0	918	808	1320	888	1099	968	1414	1098	1596	1063
ENSMUSG00000031232	chrX	Magt1	1.06E+08	1.06E+08	4672	-0.08461	5.157687	0.573375	0.678504	0.024538	0	505	346	945	533	711	443	774	674	751	540
ENSMUSG00000084838	chr16	Gm10241	20176727	20177012	286	-0.16016	0.373049	0.573475	0.678562	0.045278	0	19	16	26	13	27	15	25	17	28	18
ENSMUSG00000053192	chr3	Mllt11	95219135	95220463	1923	0.114666	6.695145	0.573685	0.678749	0.048804	0	1880	1204	2383	1097	1370	1774	2138	1842	2958	1250
ENSMUSG00000023826	chr17	Park2	10840384	10840489	10101	-0.11078	2.669179	0.573887	0.678906	0.033613	0	89	69	173	103	98	79	121	100	138	112
ENSMUSG00000042535	chr15	Gtpbp1	79690895	79691098	3398	0.085904	5.215042	0.573919	0.678906	0.026692	0	447	327	812	632	749	552	748	622	984	604
ENSMUSG00000027522	chr2	Stx16	1.74E+08	1.74E+08	3962	0.080138	4.543905	0.573995	0.678935	0.022005	0	307	238	524	304	481	346	512	453	522	355
ENSMUSG00000040675	chr10	Mthfd1l	3973118	3973478	4435	0.158365	0.444859	0.574047	0.678936	0.056263	0	14	7	29	26	21	19	24	21	32	24
ENSMUSG00000040666	chr16	Sh3bgr	96200470	96200748	1542	0.102496	9.602635	0.574151	0.678998	0.039738	0	13432	9793	14566	8909	12276	13973	18140	12379	17900	11288
ENSMUSG00000047417	chr10	Rexo1	80540922	80542824	7155	-0.10083	3.926685	0.57481	0.679717	0.03207	0	200	121	381	302	294	201	281	260	363	234
ENSMUSG00000004610	chr7	Etfb	43444108	43444204	1139	-0.11878	7.522972	0.574942	0.679813	0.053449	0	2061	2134	2572	4560	3825	2350	4390	3027	4212	2455
ENSMUSG00000095567	chr4	Noc2l	1.56E+08	1.56E+08	2867	0.081249	5.332868	0.57518	0.680033	0.023001	0	598	473	836	547	679	644	912	726	937	577
ENSMUSG00000066705	chr9	Fxyd6	45370185	45370488	1791	0.300982	5.764504	0.57543	0.680268	0.339182	0	97	128	418	2132	1262	712	1415	692	1524	1212
ENSMUSG00000028771	chr5	Ptpn12	20986645	20987494	3509	0.091248	3.636793	0.575663	0.680483	0.027408	0	129	123	270	195	268	174	288	251	278	181
ENSMUSG00000002129	chr11	Sf3a1	4160350	4160550	6147	0.079421	4.33544	0.575757	0.68052	0.021133	0	248	200	434	340	373	285	445	382	461	322
ENSMUSG00000073643	chr1	Wdfy1	79702262	79705570	6488	-0.0873	4.246856	0.575797	0.68052	0.024988	0	230	204	471	300	401	214	448	325	398	310
ENSMUSG00000028433	chr4	Ubap2	41194313	41195246	4802	-0.10086	6.426145	0.576145	0.680871	0.037778	0	1094	682	2329	1550	1832	1099	1574	1324	2235	1414
ENSMUSG00000022338	chr15	Eny2	44428111	44428242	2429	-0.08466	4.645055	0.576445	0.681015	0.025977	0	352	343	496	411	432	337	639	387	493	378
ENSMUSG00000022672	chr16	Prkdc	15637866	15638042	13187	0.092608	3.36058	0.576473	0.681015	0.028312	0	119	103	282	140	174	153	232	198	231	150
ENSMUSG00000028841	chr4	Cnksr1	1.34E+08	1.34E+08	2804	0.105832	5.979569	0.576432	0.681015	0.041769	0	958	648	1548	840	957	1130	1371	809	1928	832
ENSMUSG00000029447	chr5	Cct6a	1.3E+08	1.3E+08	1599	-0.0843	6.608485	0.576411	0.681015	0.026841	0	1481	1318	2142	1343	1725	1317	2290	1641	2036	1446
ENSMUSG00000043024	chr6	Gm16433	1.09E+08	1.09E+08	2248	-0.17546	0.623275	0.576641	0.681153	0.052275	0	18	15	42	15	36	22	32	25	27	17
ENSMUSG00000025137	chr11	Pcyt2	1.21E+08	1.21E+08	4346	0.09523	4.828914	0.57689	0.681387	0.032812	0	322	250	514	600	540	435	641	525	622	453
ENSMUSG00000017765	chr8	Slc12a4	1.06E+08	1.06E+08	4297	0.152471	4.021325	0.577212	0.681706	0.086624	0	110	97	265	427	372	222	316	315	385	308
ENSMUSG00000031171	chrX	Ftsj1	8238668	8240830	4760	-0.08664	3.839868	0.577349	0.681808	0.024596	0	188	191	339	231	229	225	310	230	296	200
ENSMUSG00000029388	chr5	Eif2b1	1.25E+08	1.25E+08	2577	0.079438	5.232497	0.577822	0.682245	0.022248	0	513	387	747	634	663	557	930	644	878	554
ENSMUSG00000072774	chr5	Zfp951	1.05E+08	1.05E+08	4730	-0.1721	0.309245	0.577788	0.682245	0.055313	0	23	15	29	14	15	15	28	19	23	13
ENSMUSG00000060260	chr7	Pwwp2b	1.39E+08	1.39E+08	2640	0.129213	1.990846	0.577979	0.682369	0.048471	0	50	29	73	86	61	56	82	70	96	66
ENSMUSG00000041429	chr17	Nthl1	24632682	24632854	1080	0.149008	1.359754	0.578044	0.682385	0.05083	0	33	34	54	25	41	34	51	34	64	53
ENSMUSG00000003308	chr9	Keap1	21229730	21230868	4664	-0.08125	6.305024	0.578143	0.682442	0.024828	0	1090	979	1721	1274	1474	1191	1603	1381	1806	1066

ENSMUSG00000039958	chr6	Mettl20	1.49E+08	1.49E+08	2496	0.106598	3.548253	0.578361	0.682638	0.035135	0	181	152	235	152	163	202	303	166	250	181
ENSMUSG00000038623	chr7	Tm6sf1	81859001	81859540	5921	-0.22166	3.104056	0.57857	0.682824	0.173381	0	46	39	105	283	292	101	168	161	144	137
ENSMUSG00000030247	chr6	Kcnj8	1.43E+08	1.43E+08	2188	-0.1085	3.964941	0.579118	0.68341	0.040843	0	185	128	329	298	396	171	408	236	376	215
ENSMUSG00000055313	chr13	Pgbd1	21421275	21423624	3585	-0.18655	0.589221	0.57926	0.683517	0.07258	0	20	11	25	35	29	16	35	18	21	29
ENSMUSG00000031563	chr8	Wwc2	47826083	47828784	6546	-0.08886	3.544051	0.579342	0.683553	0.024832	0	151	139	240	191	242	146	259	197	226	198
ENSMUSG00000024376	chr18	Epb4.1l4a	33796327	33797470	3853	-0.16314	1.119249	0.580146	0.68444	0.068439	0	29	25	36	43	41	18	40	26	44	50
ENSMUSG00000055932	chr8	Fto	91313532	91313620	13026	0.082406	6.891043	0.580791	0.68514	0.02621	0	1567	1167	2857	1709	2200	1622	2683	1929	2993	2043
ENSMUSG00000028444	chr4	Cntfr	41657498	41658152	2782	-0.19063	4.283564	0.581483	0.685896	0.135252	0	145	169	515	356	584	346	226	581	165	241
ENSMUSG00000024664	chr19	Fads3	10041548	10041956	3269	0.195199	3.179862	0.581616	0.68593	0.135485	0	225	107	132	66	106	149	133	296	131	136
ENSMUSG00000032579	chr9	Hemk1	1.07E+08	1.07E+08	3646	-0.09272	3.491295	0.581568	0.68593	0.030316	0	162	148	200	210	187	139	229	185	261	179
ENSMUSG00000023064	chr14	Sncg	34370274	34370565	852	-0.21921	4.153684	0.581705	0.685975	0.185702	0	465	410	177	139	151	185	279	469	257	283
ENSMUSG00000013629	chr5	Cad	31054780	31055036	8164	-0.10562	3.314793	0.581792	0.686016	0.034127	0	124	84	245	171	226	133	216	200	181	138
ENSMUSG00000055334	chr9	Snupn	56950878	56950953	1391	-0.08651	3.577657	0.582072	0.686285	0.02543	0	191	148	258	179	199	169	289	185	244	171
ENSMUSG00000003848	chr8	Nob1	1.07E+08	1.07E+08	3486	0.083017	4.170365	0.582301	0.686494	0.022577	0	242	216	335	275	320	297	358	313	425	284
ENSMUSG00000010064	chr9	Slc38a3	1.08E+08	1.08E+08	5277	-0.19275	4.830829	0.582414	0.686566	0.142505	0	252	96	472	894	837	300	691	370	587	507
ENSMUSG00000092558	chr17	Med20	47611582	47611692	7324	-0.08523	4.340549	0.582478	0.68658	0.025066	0	308	203	397	330	444	324	446	318	436	271
ENSMUSG00000066632	chr12	Pgk1-rs7	10898566	10900296	1731	0.131531	1.875543	0.582658	0.686732	0.045598	0	61	26	73	54	62	44	93	76	78	53
ENSMUSG00000012428	chr5	Steap4	7960472	7960541	3140	0.101784	5.551567	0.583	0.686991	0.039602	0	567	546	1089	530	975	688	1413	996	830	566
ENSMUSG00000024135	chr17	Srbd1	85984665	85985483	3530	-0.12905	1.966892	0.583034	0.686991	0.043025	0	57	39	87	59	82	43	72	81	64	69
ENSMUSG00000032336	chr9	Nptn	58582240	58582526	6168	0.094101	6.884209	0.583002	0.686991	0.034456	0	1669	1581	2809	1224	1907	1683	2536	2294	2754	1912
ENSMUSG00000039671	chr2	Zmynd8	1.66E+08	1.66E+08	11031	0.0817	3.996721	0.583763	0.687789	0.023844	0	219	133	360	246	313	243	372	274	351	256
ENSMUSG00000029557	chr5	Ftsj2	1.4E+08	1.4E+08	1443	-0.10953	2.837226	0.584214	0.68826	0.039427	0	101	66	122	137	165	85	168	108	146	118
ENSMUSG00000024451	chr18	Arap3	37972624	37973651	5224	0.104233	3.595692	0.584294	0.688293	0.037736	0	157	108	221	247	198	169	252	280	238	190
ENSMUSG00000091243	chr16	Vgll3	65815633	65815758	3322	0.123629	2.089738	0.584445	0.68841	0.043008	0	49	52	107	43	74	78	98	72	84	61
ENSMUSG00000029627	chr5	Zkscan14	1.45E+08	1.45E+08	1967	0.099637	3.410314	0.584516	0.688432	0.029965	0	155	116	217	146	185	155	240	148	308	162
ENSMUSG00000086583	chr7	Gm15500	1.15E+08	1.15E+08	1019	-0.09242	4.458165	0.584718	0.688609	0.033133	0	349	330	445	296	354	303	581	355	461	272
ENSMUSG00000029578	chr5	Wipi2	1.43E+08	1.43E+08	8041	-0.07492	5.48585	0.584881	0.688679	0.021284	0	662	556	975	676	816	659	979	720	970	669
ENSMUSG00000074622	chr2	Mafb	1.6E+08	1.6E+08	3363	-0.19469	5.088744	0.584877	0.688679	0.148506	0	186	304	524	453	1634	393	1101	442	672	399
ENSMUSG00000024091	chr17	Vapa	65580056	65580847	1640	-0.08733	6.983721	0.585634	0.689382	0.030399	0	2066	1612	2926	1761	2065	1753	2913	1766	3026	1916
ENSMUSG00000032657	chr3	Fam189b	89183143	89183494	3649	0.088347	4.318492	0.585536	0.689382	0.027904	0	317	186	489	259	326	267	425	363	540	302
ENSMUSG00000034163	chr10	Zfc3h1	1.15E+08	1.15E+08	7848	-0.09498	3.529321	0.585597	0.689382	0.029035	0	148	152	274	140	248	162	225	200	222	195
ENSMUSG00000027077	chr2	Smtnl1	84811176	84811539	1761	-0.30516	5.443406	0.585866	0.689594	0.366721	0	133	99	318	2040	1397	307	1050	452	936	892
ENSMUSG00000018427	chr11	Ypel2	86936425	86940688	4847	0.101505	3.273127	0.585978	0.689664	0.030113	0	131	125	197	121	164	119	202	200	235	155
ENSMUSG00000024393	chr17	Prrc2a	35149076	35149401	7631	-0.0881	7.348556	0.586038	0.689673	0.03076	0	2212	1494	4142	2649	3473	2127	2969	2939	3798	2627
ENSMUSG00000030595	chr7	Nfkbib	28758251	28759008	2169	-0.08349	4.952555	0.586148	0.689742	0.026804	0	418	457	607	505	516	469	605	493	704	468
ENSMUSG00000022510	chr16	Trp63	25683763	25684351	8391	0.103905	3.38177	0.586201	0.689743	0.034289	0	135	126	203	146	188	112	265	231	201	176
ENSMUSG00000027087	chr2	Itgav	83724397	83724919	10744	-0.08427	4.844437	0.586543	0.690025	0.025543	0	400	301	743	391	602	361	554	475	652	504
ENSMUSG00000058297	chr10	Spock2	60106219	60106656	5533	-0.14998	3.271214	0.586545	0.690025	0.076941	0	56	114	268	152	260	148	123	165	212	163
ENSMUSG00000038822	chr10	Hace1	45577829	45578150	12851	-0.11429	1.869404	0.586969	0.690462	0.033343	0	52	41	85	51	71	44	82	70	67	50
ENSMUSG00000033323	chr18	Ctdp1	80407959	80408781	3910	-0.10015	3.113925	0.587047	0.690493	0.03054	0	96	97	230	134	175	143	163	142	194	112
ENSMUSG00000028967	chr4	Errfi1	1.51E+08	1.51E+08	3582	0.132795	4.600269	0.587636	0.691002	0.066521	0	277	405	449	229	448	341	919	340	470	320
ENSMUSG00000032425	chr9	Zfp949	88548020	88548508	4110	-0.10417	3.263399	0.587625	0.691002	0.03822	0	157	111	193	147	180	158	269	125	169	123
ENSMUSG00000061740	chr15	Cyp2d22	82370528	82371725	2771	0.100449	3.279455	0.587571	0.691002	0.034354	0	124	83	160	173	212	127	228	175	220	165
ENSMUSG00000042895	chr15	Abra	41865293	41866352	1762	-0.13129	6.786326	0.587718	0.691038	0.069963	0	1160	1645	1957	2393	1906	1168	3500	1754	2820	943
ENSMUSG00000040177	chr7	2310057M21Rik	1.31E+08	1.31E+08	2214	-0.09724	3.571323	0.587873	0.691159	0.031597	0	182	111	239	234	218	181	247	162	249	199
ENSMUSG00000031105	chrX	Slc25a14	48623413	48623508	2364	-0.13959	1.224157	0.588065	0.691323	0.042968	0	27	32	39	35	54	30	41	39	46	37
ENSMUSG00000014075	chr16	Tctex1d2	32419702	32419927	2385	0.13425	2.565367	0.588797	0.69203	0.055056	0	102	84	111	69	65	105	141	93	119	95
ENSMUSG00000019998	chr10	Stx7	24149317	24149726	2500	0.075036	5.016284	0.588871	0.69203	0.020994	0	396	354	686	503	617	462	688	558	791	542
ENSMUSG00000029427	chr5	Zcchc8	1.24E+08	1.24E+08	4286	-0.08776	3.434784	0.588875	0.69203	0.025011	0	154	122	255	179	185	150	248	200	199	154
ENSMUSG00000039109	chr13	F13a1	36867178	36868918	3927	-0.11372	4.988838	0.588728	0.69203	0.049357	0	481	370	956	321	604	582	521	639	508	448
ENSMUSG00000029838	chr6	Ptn	36715663	36715762	2021	-0.19326	0.584641	0.58939	0.692574	0.080645	0	14	16	33	21	38	9	37	23	20	30
ENSMUSG00000057337	chr10	Chst3	60181532	60186883	6497	-0.23151	-0.16929	0.589644	0.692811	0.123036	0	11	3	12	27	15	7	15	16	12	15
ENSMUSG00000100801	chr5	Gm15459	5781615	5783555	1941	-0.08271	5.139484	0.589915	0.693067	0.025863	0	466	377	756	619	725	572	745	664	700	435
ENSMUSG00000015937	chr13	H2afy	56073619	56074392	6809	0.078718	5.933824	0.59	0.693106	0.024412	0	841	664	1275	989	1018	990	1323	985	1392	1029
ENSMUSG00000028549	chr4	Itgb3bp	99765402	99767576	4632	-0.11266	2.266944	0.590179	0.693255	0.04659	0	80	73	79	76	72	56	110	76	94	80
ENSMUSG00000006651	chr7	Aplp1	30434981	30435391	2391	0.223011	0.087304	0.590493	0.693562	0.100097	0	8	8	10	24	20	11	26	16	16	24
ENSMUSG00000017210	chr11	Med24	98704591	98705016	6528	-0.08051	5.651471	0.590903	0.693983	0.025396	0	686	494	1186	908	956	628	1057	771	1264	802
ENSMUSG00000072381	chr3	Gm10355	1.01E+08	1.01E+08	519	-0.15598	0.423864	0.590986	0.694018	0.067745	0	17	14	20	24	29	9	30	18	38	15
ENSMUSG00000042292	chr15	Mkl1	81012281	81013802	6114	-0.08597	4.951494	0.591171	0.694175	0.028077	0	431	299	829	461	620	407	766	405	750	465
ENSMUSG00000032666	chr1	1700025G04Rik	1.52E+08	1.52E+08	11788	0.08764	6.541083	0.591229	0.694181	0.031164	0	1148	901	2208	1430	1765	1227	2549	1312	2469	1449
ENSMUSG00000068394	chr2	Cep152	1.26E+08	1.26E+08	5768	-0.13233	0.774397	0.591446	0.694375	0.043292	0	25	21	30	25	33	20	39	20	36	26
ENSMUSG00000024899	chr19	Papss2	32620005	32620186	3635	-0.11638	3.070997	0.591936	0.694888	0.044484	0	112	103	214	112	165	155	145	178	131	102
ENSMUSG00000029097	chr5	Trmt44	35557206	35558055	4151	-0.14989	0.785767	0.592122	0.695045	0.042678	0	25	17	43	22	32	20	36	33	33	19
ENSMUSG00000034724	chr5	Cnot6l	96070333	96077392	10313	-0.08968	4.146635	0.592555	0.695459	0.028699	0	219	195	460	276	348	193	317	330	411	314
ENSMUSG00000058267	chr1	Mrps14	1.6E+08	1.6E+08	3258	0.085562	5.543885	0.592579	0.695459	0.028169	0	674	619	800	717	729	723	1033	742	1139	764

ENSMUSG00000041849	chr15	Card6	5095981	5101095	6101	-0.13669	1.775982	0.592658	0.69549	0.052078	0	40	29	81	64	73	28	83	55	67	60
ENSMUSG00000002107	chr2	Celf2	6539694	6545675	25884	-0.11503	6.203922	0.593404	0.696304	0.05469	0	1118	1051	2321	727	1039	802	1327	1381	1813	1200
ENSMUSG00000026333	chr1	Gin1	97770172	97770255	6048	-0.12483	1.76987	0.593843	0.696756	0.052527	0	65	44	62	49	51	47	92	49	55	48
ENSMUSG00000046679	chr6	C87436	86438374	86438487	4092	0.095847	3.116926	0.594041	0.696866	0.028627	0	110	111	202	115	130	135	205	146	174	147
ENSMUSG00000101257	chr1	2310015K22Rik	80225044	80225171	1461	-0.12965	2.70419	0.59403	0.696866	0.057038	0	139	58	177	78	94	104	157	95	130	78
ENSMUSG00000049396	chr11	Gemin4	76210571	76213923	3734	0.104808	2.554637	0.594369	0.697189	0.03273	0	74	58	112	102	103	71	149	108	123	100
ENSMUSG00000030084	chr6	Plxna1	89316316	89319471	9025	-0.09566	4.759729	0.594825	0.697662	0.034197	0	336	214	778	435	601	358	530	535	553	408
ENSMUSG00000043635	chr5	Adamts3	89673841	89677926	7663	0.202858	0.581985	0.59516	0.697994	0.125832	0	11	12	47	17	22	21	49	33	10	21
ENSMUSG00000039531	chr10	Zufsp	33926936	33927621	2364	0.119505	2.420411	0.595298	0.698093	0.040934	0	66	69	107	87	71	82	153	77	113	80
ENSMUSG00000034371	chr19	Dak	10592200	10592789	2253	0.13896	1.686927	0.5955	0.698269	0.054464	0	50	36	52	48	48	42	48	62	70	71
ENSMUSG00000060679	chr1	Mrps9	42851233	42851426	5524	-0.10786	4.808013	0.595571	0.69829	0.046898	0	327	255	448	643	676	389	677	378	676	385
ENSMUSG00000028399	chr4	Ptprd	75941238	75945026	22702	-0.14936	2.550911	0.595855	0.698486	0.069902	0	46	41	181	107	146	92	108	113	113	69
ENSMUSG00000028797	chr4	Tmem234	1.3E+08	1.3E+08	4273	0.082605	5.265569	0.59586	0.698486	0.027034	0	533	391	689	714	656	657	838	684	871	554
ENSMUSG00000092085	chr1	Gm17224	1.72E+08	1.72E+08	500	0.453957	2.064722	0.595896	0.698486	0.823462	0	3	1	170	111	31	6	6	135	175	105
ENSMUSG00000021481	chr13	Zfp346	55105311	55105518	4176	0.07704	4.37059	0.59626	0.698789	0.021119	0	275	249	442	307	338	310	447	376	489	317
ENSMUSG00000036964	chr11	Trim17	58954685	58955392	3736	-0.11262	3.304118	0.596244	0.698789	0.049002	0	196	137	191	118	152	147	150	185	233	139
ENSMUSG00000019804	chr10	Snx3	42502030	42502426	1413	0.082069	6.851334	0.596433	0.69893	0.027927	0	1763	1442	2188	1614	1862	1866	2591	2048	2577	1770
ENSMUSG00000020807	chr11	4933427D14Rik	72153929	72155438	5697	0.163571	1.177445	0.596517	0.698967	0.059981	0	30	25	38	31	38	33	51	61	42	21
ENSMUSG00000030816	chr7	Rnf40	1.28E+08	1.28E+08	4154	-0.07728	5.40975	0.596652	0.699002	0.023645	0	546	445	888	784	882	621	840	701	973	646
ENSMUSG00000036398	chr17	Ppp1r11	36948356	36949554	1975	0.089787	4.513441	0.596651	0.699002	0.02979	0	306	283	336	400	404	330	484	435	511	381
ENSMUSG00000028975	chr4	Pex14	1.49E+08	1.49E+08	6272	0.076748	4.741092	0.596897	0.699227	0.02305	0	337	290	539	406	532	425	502	491	615	449
ENSMUSG00000025602	chr9	Zfp202	40192316	40192437	3877	-0.14482	1.294322	0.597465	0.699827	0.057838	0	35	27	63	27	50	37	67	30	53	21
ENSMUSG00000035382	chr9	Pcsk7	45906569	45907039	3784	-0.09048	3.677282	0.597515	0.699827	0.026786	0	166	119	288	228	275	193	244	218	254	206
ENSMUSG00000038563	chr7	Eftud1	82648614	82648649	4398	0.089089	3.157362	0.597732	0.700019	0.026096	0	122	95	219	112	151	142	197	142	203	147
ENSMUSG00000068240	chr4	Gm11808	3973092	3973595	504	0.098028	4.514025	0.5981	0.700326	0.036793	0	325	267	334	400	400	421	601	324	497	317
ENSMUSG00000103480	chr3	Bdh2	1.35E+08	1.35E+08	768	0.152214	0.668745	0.59807	0.700326	0.043259	0	19	17	38	17	23	21	32	25	35	29
ENSMUSG00000026110	chr1	Mgat4a	37439340	37444685	12881	0.103106	2.434091	0.598353	0.700541	0.035018	0	53	53	114	90	109	72	139	92	111	91
ENSMUSG00000059486	chr6	Kbtbd2	56777524	56780413	4083	-0.0778	4.411276	0.598389	0.700541	0.023621	0	319	271	512	275	381	275	481	356	474	318
ENSMUSG00000097445	chr9	Gm26631	57531287	57533585	2505	-0.51167	0.70303	0.598518	0.700631	0.952129	0	1	0	70	74	12	0	2	39	39	31
ENSMUSG00000036580	chr3	Spg20	55112108	55112217	5362	0.078021	5.011352	0.598905	0.701022	0.024456	0	411	299	763	506	604	396	819	563	771	524
ENSMUSG00000020430	chr11	Pes1	3963975	3964060	3024	0.074535	4.953767	0.599107	0.701196	0.02137	0	467	333	608	440	573	455	687	568	732	472
ENSMUSG00000021972	chr14	Hmbox1	64811600	64813419	9681	0.089803	3.70249	0.599219	0.701258	0.032281	0	136	103	325	218	268	189	289	247	318	186
ENSMUSG00000038861	chr3	Pi4kb	94974731	94975085	3880	0.080647	4.628234	0.599265	0.701258	0.026787	0	294	201	566	441	484	370	557	466	535	390
ENSMUSG00000031950	chr8	Gabarapl2	1.12E+08	1.12E+08	2325	0.092122	6.137889	0.59945	0.701412	0.035103	0	1100	1009	1288	864	1047	1028	1669	1175	1658	1156
ENSMUSG00000006392	chr4	Med8	1.18E+08	1.18E+08	3001	0.085809	4.75312	0.59961	0.701414	0.027634	0	366	379	536	352	430	370	610	443	702	436
ENSMUSG00000024963	chr19	Dnajc4	6987911	6988108	1074	0.097177	4.012975	0.59956	0.701414	0.033026	0	245	209	294	261	205	236	408	277	398	221
ENSMUSG00000026939	chr2	Tmem141	25620067	25620530	1122	0.106975	3.523392	0.59957	0.701414	0.038355	0	193	159	183	145	171	174	276	223	252	161
ENSMUSG00000078580	chr7	E430018J23Rik	1.27E+08	1.27E+08	3334	-0.12226	1.157504	0.599795	0.701568	0.035743	0	34	28	49	29	38	28	43	32	47	36
ENSMUSG00000056267	chr9	Cep70	99243367	99243490	4806	0.125957	1.474813	0.599861	0.701583	0.035627	0	36	34	51	37	46	47	58	52	52	43
ENSMUSG00000032590	chr9	Apeh	1.08E+08	1.08E+08	5651	0.073459	5.113968	0.599985	0.701629	0.021041	0	462	389	701	537	624	476	839	583	790	578
ENSMUSG00000038383	chr2	Pigu	1.55E+08	1.55E+08	9326	0.081685	4.515925	0.600006	0.701629	0.026459	0	273	229	481	397	425	418	539	351	524	314
ENSMUSG00000021938	chr14	Pspc1	56722441	56723280	4003	-0.10009	3.246021	0.600068	0.70164	0.039036	0	111	139	182	158	182	119	222	110	219	168
ENSMUSG00000034928	chr13	Rnf44	54679399	54681811	5202	-0.09654	4.65433	0.600133	0.701654	0.036016	0	281	206	675	419	613	301	499	486	553	390
ENSMUSG00000024926	chr19	Kat5	5603017	5603552	2008	0.08338	4.120657	0.600571	0.702042	0.025775	0	273	171	323	280	299	279	340	304	437	267
ENSMUSG00000048445	chr11	Ccdc57	1.21E+08	1.21E+08	3743	-0.123	2.141175	0.600541	0.702042	0.044325	0	71	40	107	57	94	59	70	61	112	75
ENSMUSG00000005951	chr11	Shpk	73199460	73199680	2985	0.190947	0.43154	0.601541	0.703106	0.072704	0	20	13	21	18	20	10	23	36	26	25
ENSMUSG00000047712	chr10	Ust	8204753	8207670	4284	-0.17097	1.742165	0.601587	0.703106	0.098715	0	18	59	96	51	56	42	60	77	45	50
ENSMUSG00000028936	chr4	Rpl22	1.52E+08	1.52E+08	2911	0.0986	6.976502	0.601657	0.703126	0.041688	0	1848	1978	2130	1665	1726	2085	3083	2178	2803	1810
ENSMUSG00000031504	chr8	Rab20	11453392	11454526	1446	-0.16199	1.353829	0.602009	0.703475	0.099494	0	41	30	40	47	46	44	88	26	41	18
ENSMUSG00000050017	chr5	Pitpnb	1.11E+08	1.11E+08	2761	-0.07528	4.695453	0.602063	0.703477	0.021878	0	344	298	621	365	541	354	536	488	553	375
ENSMUSG00000028207	chr4	Asph	9448069	9448275	16102	-0.0825	7.907445	0.602257	0.703537	0.029825	0	3737	3135	5731	3043	4221	3583	5587	3597	5345	3411
ENSMUSG00000031996	chr9	Aplp2	31149557	31150972	3694	-0.08595	7.923458	0.602274	0.703537	0.032246	0	3754	2636	5577	3370	5045	3830	3904	4597	5632	3405
ENSMUSG00000061666	chr11	Gdpd1	87033867	87035295	2336	-0.13608	2.49918	0.602185	0.703537	0.063394	0	45	55	103	133	140	77	101	84	122	97
ENSMUSG00000019923	chr10	Zwint	72654845	72654977	4434	-0.0852	5.511337	0.602774	0.704011	0.031491	0	646	730	954	619	731	659	1024	792	998	601
ENSMUSG00000024168	chr17	Tmem204	25057702	25058473	2022	0.109146	3.510942	0.602786	0.704011	0.048191	0	103	93	199	221	281	150	281	226	222	195
ENSMUSG00000045671	chr11	Spred2	19924375	19924956	4619	0.118347	2.902079	0.602891	0.704072	0.056873	0	63	48	172	145	168	89	199	142	169	114
ENSMUSG00000020458	chr11	Rtn4	29692947	29693693	6991	-0.08438	10.05775	0.603472	0.704689	0.031595	0	17008	14233	25109	13876	17556	15345	23983	15849	23257	16721
ENSMUSG00000071497	chr19	Nutf2-ps1	53588204	53589067	864	-0.14679	0.854608	0.60365	0.704834	0.065668	0	29	28	27	23	33	28	38	24	45	15
ENSMUSG00000005078	chr12	Jkamp	72085589	72085673	2692	-0.0814	3.518395	0.603847	0.704939	0.024264	0	165	153	251	170	195	168	245	190	225	178
ENSMUSG00000073079	chr12	Srp54a	55089202	55089279	1515	-0.1579	1.311589	0.603831	0.704939	0.058609	0	35	25	62	31	53	44	33	29	47	47
ENSMUSG00000007476	chr2	Lrrc8a	30237715	30237805	4308	-0.09547	3.616915	0.603907	0.704948	0.033656	0	125	143	235	235	282	190	278	198	227	180
ENSMUSG00000006435	chr19	Neurl1a	47178820	47179551	4411	0.083564	7.856686	0.604193	0.70522	0.030893	0	3381	2207	5041	3598	4113	3861	4234	3819	6346	3569
ENSMUSG00000025377	chr11	Enthd2	1.2E+08	1.2E+08	3329	0.104345	2.70501	0.604798	0.705863	0.036826	0	90	54	135	112	113	70	169	120	147	111
ENSMUSG00000023106	chr5	Denr	1.24E+08	1.24E+08	2844	-0.0824	5.770174	0.605114	0.706149	0.029908	0	828	791	976	803	995	831	1299	849	1183	724
ENSMUSG00000034902	chr10	Pip5k1c	81292963	81293152	5730	-0.08246	4.926079	0.605149	0.706149	0.027393	0	407	265	745	589	569	412	607	538	714	440

ENSMUSG00000027208	chr2	Fgf7	1.26E+08	1.26E+08	3248	-0.14598	1.858375	0.605271	0.70623	0.072158	0	32	54	92	66	55	38	94	76	44	54
ENSMUSG00000046862	chr4	Pramef8	1.43E+08	1.43E+08	4176	-0.0828	3.154877	0.605624	0.706579	0.026164	0	128	122	184	131	157	118	210	139	187	134
ENSMUSG00000027776	chr3	Il12a	68690644	68690741	1701	-0.14798	2.443996	0.606268	0.707268	0.08671	0	88	93	168	39	62	74	112	73	133	77
ENSMUSG00000053004	chr6	Hrh1	1.14E+08	1.14E+08	4450	-0.19171	0.041662	0.606419	0.707382	0.088607	0	17	16	20	8	17	14	26	12	9	17
ENSMUSG00000032860	chr7	P2ry2	1.01E+08	1.01E+08	3000	-0.14405	5.266769	0.6065	0.707386	0.091358	0	393	241	667	1035	1009	341	1163	471	924	586
ENSMUSG00000044600	chr8	Smim7	72565188	72567808	3266	0.079888	6.281688	0.606529	0.707386	0.027857	0	1224	792	1635	1097	1357	1315	1743	1265	1915	1104
ENSMUSG00000050619	chr2	Zscan29	1.21E+08	1.21E+08	7169	-0.10849	2.396748	0.607098	0.707987	0.036456	0	61	54	122	95	107	71	91	102	125	67
ENSMUSG00000031948	chr8	Kars	1.12E+08	1.12E+08	2249	0.07482	6.747659	0.607336	0.708203	0.024622	0	1359	1289	2318	1698	1759	1606	2404	1778	2594	1749
ENSMUSG00000070385	chr3	Ampd1	1.03E+08	1.03E+08	2921	-0.11382	10.21015	0.607687	0.708549	0.058816	0	19365	20372	30742	10809	15633	17208	25919	19060	24936	17343
ENSMUSG00000025939	chr1	Ube2w	16540790	16541789	4930	0.089546	3.283479	0.607859	0.708688	0.03117	0	122	104	220	157	155	170	173	202	212	140
ENSMUSG00000027305	chr2	Ndufaf1	1.2E+08	1.2E+08	1501	-0.0818	5.399785	0.608067	0.708868	0.029599	0	540	524	751	832	798	546	1081	656	933	597
ENSMUSG00000021772	chr14	Nkiras1	18271136	18271323	5430	-0.08012	5.253167	0.608122	0.708869	0.027836	0	551	432	711	712	719	542	968	526	777	600
ENSMUSG00000020232	chr10	Hmg20b	81346048	81346477	3149	0.094499	3.362924	0.608614	0.709337	0.034606	0	112	104	186	199	195	176	207	161	219	187
ENSMUSG00000030685	chr7	Kctd13	1.27E+08	1.27E+08	2487	0.128154	1.303961	0.60863	0.709337	0.036182	0	29	31	42	34	44	37	46	48	55	38
ENSMUSG00000020152	chr11	Actr2	20062304	20064859	5204	-0.07459	5.499838	0.609254	0.709878	0.023897	0	564	514	1059	767	879	562	1092	826	864	707
ENSMUSG00000029012	chr5	Orc5	22486485	22487217	2825	-0.08193	3.670157	0.609205	0.709878	0.027196	0	202	168	250	202	205	195	290	198	256	184
ENSMUSG00000039145	chr2	Camk1d	5293457	5299101	7427	0.111299	2.19853	0.609233	0.709878	0.051	0	43	38	110	76	92	87	91	78	75	84
ENSMUSG00000030806	chr7	Stx1b	1.28E+08	1.28E+08	4802	-0.18033	0.826678	0.609354	0.709932	0.072588	0	28	22	48	19	27	34	21	34	29	21
ENSMUSG00000073758	chr4	Sh3d21	1.26E+08	1.26E+08	2717	-0.17122	0.297123	0.60959	0.710145	0.075509	0	13	16	17	27	21	13	14	24	22	22
ENSMUSG00000026819	chr2	Slc25a25	32414487	32416322	7862	0.213333	4.858739	0.610166	0.710752	0.202063	0	349	726	356	245	226	384	1444	459	285	384
ENSMUSG00000019487	chr17	Trip10	57249451	57249571	2290	-0.07712	7.124384	0.610303	0.710788	0.026987	0	2048	1572	3131	2294	2540	2053	2786	2034	3516	2116
ENSMUSG00000050490	chr10	Gm8394	85313488	85314439	952	-0.1601	0.622976	0.610254	0.710788	0.069444	0	14	26	43	21	18	23	25	21	37	18
ENSMUSG00000035354	chr7	Uvrag	98886743	98888592	3438	-0.08426	3.664327	0.61091	0.711432	0.025732	0	170	142	347	192	213	192	256	187	284	198
ENSMUSG00000029279	chr5	Brdt	1.07E+08	1.07E+08	5115	0.144004	1.13057	0.611215	0.711725	0.042385	0	32	22	51	27	28	25	53	34	54	36
ENSMUSG00000030862	chr7	Cpxm2	1.32E+08	1.32E+08	4450	0.139567	4.442741	0.611445	0.71193	0.088794	0	101	232	524	367	514	388	390	527	309	386
ENSMUSG00000021943	chr14	Gdf10	33923587	33924202	2507	-0.11132	3.190246	0.611692	0.712155	0.047755	0	108	100	233	110	229	95	141	161	219	176
ENSMUSG00000057363	chr1	Uxs1	43746966	43750362	5097	-0.0802	3.83812	0.611833	0.712224	0.025209	0	216	185	300	197	270	218	256	236	314	229
ENSMUSG00000062906	chr15	Hdac10	89123307	89123479	3379	-0.08224	3.373787	0.611858	0.712224	0.027866	0	163	140	220	150	166	137	217	188	229	146
ENSMUSG00000018858	chr11	Ict1	1.15E+08	1.15E+08	3332	0.074817	4.725176	0.61236	0.712745	0.022825	0	350	304	492	443	463	422	612	427	584	428
ENSMUSG00000022434	chr15	Fam118a	85037062	85037244	2543	0.107354	2.314076	0.612578	0.712936	0.036511	0	68	54	119	59	82	72	134	81	121	62
ENSMUSG00000015961	chr1	Adss	1.78E+08	1.78E+08	4531	0.088602	3.250084	0.612927	0.713217	0.027894	0	128	101	191	134	185	111	243	180	197	164
ENSMUSG00000047875	chr4	Gpr157	1.5E+08	1.5E+08	4900	0.085296	5.970303	0.612876	0.713217	0.032829	0	966	586	1385	856	1172	982	1687	860	1624	869
ENSMUSG00000078570	chr4	1110065P20Rik	1.25E+08	1.25E+08	2069	-0.10007	3.603945	0.613573	0.713907	0.042406	0	224	123	204	238	195	196	224	188	307	154
ENSMUSG00000020658	chr12	Efr3b	3962554	3966547	6547	-0.16587	2.418111	0.613726	0.714022	0.109829	0	68	29	74	145	135	39	139	78	136	77
ENSMUSG00000037740	chr2	Mrps26	1.31E+08	1.31E+08	4358	0.083135	4.83856	0.613891	0.714151	0.028466	0	381	361	444	479	514	431	634	470	736	436
ENSMUSG00000026878	chr2	Rab14	35180205	35182447	5431	0.071942	6.422905	0.614041	0.714263	0.023451	0	1160	939	1853	1296	1527	1192	2061	1430	2049	1392
ENSMUSG00000011158	chr12	Brf1	1.13E+08	1.13E+08	2755	-0.08045	3.974647	0.614323	0.71434	0.024013	0	195	158	416	244	320	219	341	234	341	259
ENSMUSG00000022360	chr15	Atad2	58094047	58095571	5683	0.140539	0.860244	0.614305	0.71434	0.058636	0	22	14	28	31	36	24	40	44	27	27
ENSMUSG00000027865	chr3	Gdap2	1E+08	1E+08	3507	-0.10196	2.673399	0.614298	0.71434	0.035998	0	74	93	149	93	114	85	135	124	107	99
ENSMUSG00000074797	chr2	Itpa	1.31E+08	1.31E+08	1963	-0.08351	4.542158	0.614302	0.71434	0.030934	0	370	304	426	367	417	377	590	302	452	346
ENSMUSG00000002984	chr7	Tomm40	19701313	19701857	4239	0.085409	4.879999	0.614451	0.714426	0.032042	0	366	260	547	621	512	436	634	520	744	450
ENSMUSG00000082456	chr11	Gm11598	1E+08	1E+08	357	0.211592	-0.03714	0.614574	0.714507	0.084062	0	16	7	25	9	8	8	18	22	23	14
ENSMUSG00000029073	chr4	Cptp	1.56E+08	1.56E+08	2709	0.077962	3.580552	0.614795	0.714639	0.022326	0	167	123	261	169	219	168	270	219	293	175
ENSMUSG00000058254	chrX	Tspan7	10485158	10485238	7067	0.078804	6.684185	0.61475	0.714639	0.028843	0	1168	1066	2196	1649	2119	1319	2340	1763	2242	2003
ENSMUSG00000027395	chr2	Polr1b	1.29E+08	1.29E+08	5805	-0.07746	3.84114	0.614865	0.714657	0.022773	0	193	162	371	208	265	181	315	265	293	219
ENSMUSG00000003865	chr7	Gys1	45434844	45435170	4789	-0.11501	8.885108	0.615131	0.714903	0.062435	0	5736	3014	9908	11330	11003	5137	10493	6759	12425	7694
ENSMUSG00000029504	chr5	Ddx51	1.11E+08	1.11E+08	5248	-0.08617	3.300771	0.615784	0.7156	0.026268	0	142	100	266	144	176	139	229	156	207	141
ENSMUSG00000027905	chr3	Ddx20	1.06E+08	1.06E+08	4142	0.084857	3.502779	0.61619	0.716009	0.0259	0	134	141	232	192	174	161	268	212	243	177
ENSMUSG00000054517	chr11	Trim65	1.16E+08	1.16E+08	5883	-0.09929	2.676027	0.61628	0.716051	0.031417	0	67	71	149	108	139	95	125	111	132	91
ENSMUSG00000019792	chr10	Trmt11	30534225	30535244	2359	0.116784	2.096458	0.616485	0.716115	0.040221	0	67	46	87	49	73	56	121	65	104	59
ENSMUSG00000020212	chr10	Mdm1	1.18E+08	1.18E+08	3149	-0.15059	0.861853	0.6164	0.716115	0.058687	0	18	27	46	31	23	25	34	29	26	32
ENSMUSG00000028669	chr4	Pithd1	1.36E+08	1.36E+08	2477	0.077271	5.093533	0.616552	0.716115	0.025353	0	509	435	673	476	534	543	776	550	829	517
ENSMUSG00000097383	chr10	1500026H17Rik	89686371	89686519	3027	-0.16267	0.518691	0.616527	0.716115	0.068663	0	27	18	26	25	14	23	23	16	32	20
ENSMUSG00000086096	chr4	Gm12688	99653607	99654239	701	-0.26233	-0.28998	0.616739	0.71627	0.188037	0	14	12	11	6	18	14	4	17	22	2
ENSMUSG00000074218	chr7	Cox7a1	30184171	30184245	364	0.108538	7.86004	0.616886	0.716379	0.05598	0	2809	1933	3262	5317	4631	3402	5810	3279	6788	3338
ENSMUSG00000072889	chr5	Nfxl1	72513301	72514331	4919	0.101139	2.296315	0.616947	0.716387	0.03525	0	69	54	116	63	74	81	109	93	88	79
ENSMUSG00000026659	chr1	Dusp12	1.71E+08	1.71E+08	2743	0.12223	2.416474	0.617092	0.716493	0.047637	0	96	70	96	59	71	80	109	102	120	86
ENSMUSG00000022801	chr16	Lrch3	32914100	32914403	6610	-0.08604	4.195207	0.61723	0.716522	0.028532	0	217	170	521	290	377	288	354	337	360	265
ENSMUSG00000061474	chr13	Mrps36	1.01E+08	1.01E+08	1274	-0.08731	4.787743	0.617279	0.716522	0.034349	0	386	293	499	582	508	418	733	375	531	405
ENSMUSG00000085492	chr17	Trmt61b	71557027	71558343	2897	-0.15885	0.585396	0.617173	0.716522	0.061542	0	27	15	21	21	33	15	29	32	23	21
ENSMUSG00000036661	chr15	Dennd3	73512560	73512847	5703	0.123134	1.415385	0.617714	0.716906	0.047233	0	41	15	57	41	47	34	64	47	65	37
ENSMUSG00000046404	chr1	Yod1	1.31E+08	1.31E+08	6128	0.116646	2.129231	0.617719	0.716906	0.051114	0	32	61	100	55	86	64	101	82	79	77
ENSMUSG00000003464	chr1	Pex19	1.72E+08	1.72E+08	3815	-0.07928	6.898514	0.618025	0.716947	0.029847	0	1559	1308	2273	2373	2346	1535	2614	2016	2915	1692
ENSMUSG00000004508	chr7	Gab2	97081751	97081906	5997	0.109931	3.025932	0.618078	0.716947	0.051751	0	66	65	161	169	180	115	173	146	169	155
ENSMUSG00000023495	chr9	Pcbp4	1.06E+08	1.06E+08	4242	-0.08067	5.714422	0.618015	0.716947	0.02983	0	722	540	1053	1015	1029	829	909	804	1333	782

ENSMUSG00000023967	chr17	Mrps18a	46110986	46111129	3690	-0.07875	5.707204	0.61781	0.716947	0.029154	0	761	655	952	950	923	782	1086	853	1338	643
ENSMUSG00000029310	chr5	Nudt9	1.04E+08	1.04E+08	2392	0.07742	5.888179	0.617919	0.716947	0.027117	0	842	741	1111	889	980	976	1242	980	1520	861
ENSMUSG00000050088	chr17	1600012H06Rik	14943184	14943319	3294	-0.07575	3.530588	0.617989	0.716947	0.022993	0	160	143	261	187	196	150	250	183	268	178
ENSMUSG00000001105	chr11	Ift20	78536361	78536576	1525	0.08579	3.709374	0.618485	0.717147	0.027943	0	211	153	236	180	218	224	284	230	294	187
ENSMUSG00000004815	chr5	Dgkq	1.09E+08	1.09E+08	7189	-0.11332	1.858169	0.618503	0.717147	0.038557	0	41	40	83	66	68	55	73	68	75	39
ENSMUSG00000005897	chr10	Nr2c1	94148023	94148102	4607	0.094883	2.811559	0.618539	0.717147	0.02977	0	85	82	153	110	110	89	178	128	143	119
ENSMUSG00000015748	chr3	Prpf3	95830124	95830965	5661	-0.07831	4.006462	0.618368	0.717147	0.026028	0	247	215	319	229	293	270	321	261	335	225
ENSMUSG00000019558	chrX	Slc6a8	73673150	73674050	5210	-0.0887	6.833766	0.618351	0.717147	0.037198	0	1393	968	2556	2378	2425	1552	2776	1536	2627	1767
ENSMUSG00000087177	chr10	E130307A14Rik	39621412	39622727	7141	-0.0867	3.261814	0.618575	0.717147	0.029976	0	153	111	242	137	149	146	222	137	214	130
ENSMUSG00000029798	chr6	Herc6	57580992	57581232	5279	0.128508	1.02451	0.618991	0.717566	0.055616	0	24	22	50	17	38	34	44	42	30	31
ENSMUSG00000025544	chr14	Tm9sf2	1.22E+08	1.22E+08	3107	0.071524	6.608619	0.619371	0.717881	0.024056	0	1339	1081	2152	1419	1720	1363	2069	1761	2439	1572
ENSMUSG00000075394	chr15	Hoxc4	1.03E+08	1.03E+08	2568	0.105075	2.518463	0.619345	0.717881	0.041392	0	63	68	139	62	113	82	102	94	157	99
ENSMUSG00000031673	chr8	Cdh11	1.03E+08	1.03E+08	4216	0.187048	0.959811	0.619625	0.718114	0.138764	0	13	11	33	29	58	13	47	44	25	47
ENSMUSG00000029328	chr5	Hnrnpdl	1E+08	1E+08	4818	-0.07688	6.503914	0.619857	0.718319	0.028379	0	1408	1246	1916	1314	1492	1295	2191	1463	1868	1319
ENSMUSG00000020547	chr12	Bzw2	36091846	36092309	1860	0.080288	6.785099	0.62062	0.71914	0.030588	0	1556	1283	2302	1691	1757	1693	2884	1545	2925	1540
ENSMUSG00000091931	chr12	AK010878	1.03E+08	1.03E+08	1417	0.110555	2.539047	0.620912	0.719416	0.040501	0	98	62	94	84	96	66	151	99	140	95
ENSMUSG00000026427	chr1	Eif2d	1.31E+08	1.31E+08	7374	0.074402	4.877665	0.621046	0.719508	0.023501	0	389	345	541	495	507	410	717	517	706	435
ENSMUSG00000024935	chr19	Slc1a1	28835049	28835332	6170	-0.15901	0.99549	0.621646	0.720141	0.07275	0	19	18	35	36	55	23	53	34	24	29
ENSMUSG00000019082	chr7	Slc25a22	1.41E+08	1.41E+08	4041	0.117297	3.543091	0.621788	0.720179	0.062631	0	122	86	179	276	238	166	239	290	213	180
ENSMUSG00000033439	chr3	Trmt13	1.17E+08	1.17E+08	5035	-0.1178	1.119086	0.621763	0.720179	0.047449	0	38	24	42	37	30	24	56	36	38	29
ENSMUSG00000069631	chr11	Strada	1.06E+08	1.06E+08	5569	-0.07156	4.990546	0.622241	0.720642	0.023641	0	456	437	664	433	602	460	644	517	699	505
ENSMUSG00000024213	chr17	Nudt3	27579382	27580954	2985	-0.07936	7.376855	0.622514	0.720895	0.030885	0	2554	2109	3282	2693	2915	2626	3399	2426	4195	2256
ENSMUSG00000086938	chr19	4930481A15Rik	5406740	5407083	2240	-0.15067	1.56123	0.622921	0.721303	0.074562	0	53	24	97	30	46	56	57	40	61	31
ENSMUSG00000020131	chr10	Pcsk4	80321283	80321951	2958	0.190164	0.367589	0.623149	0.721315	0.099739	0	15	13	22	20	18	11	22	45	25	12
ENSMUSG00000022508	chr16	Bcl6	23965052	23966268	6700	-0.13575	6.388614	0.623131	0.721315	0.090321	0	1598	1298	1332	907	1619	1561	1926	1759	733	1089
ENSMUSG00000030733	chr7	Sh2b1	1.26E+08	1.26E+08	3422	-0.07401	6.406083	0.623042	0.721315	0.025931	0	1197	855	2205	1285	1640	1266	1662	1444	1745	1381
ENSMUSG00000068184	chr13	Ndufaf2	1.08E+08	1.08E+08	679	0.111732	3.257588	0.623056	0.721315	0.049926	0	133	156	143	107	163	183	199	163	205	139
ENSMUSG00000014243	chr11	Zswim7	62267224	62267606	732	-0.0786	4.638728	0.623608	0.72174	0.029681	0	375	329	441	414	451	370	614	361	596	307
ENSMUSG00000078681	chr7	Tm2d3	65691169	65691290	1489	-0.08165	4.429742	0.623625	0.72174	0.031698	0	370	309	393	305	344	329	427	366	491	296
ENSMUSG00000018362	chr11	Kpna2	1.07E+08	1.07E+08	2873	0.083127	3.926768	0.623978	0.721985	0.028435	0	190	202	337	184	269	259	369	272	336	192
ENSMUSG00000022822	chr16	Abcc5	20331303	20332705	10592	0.075283	5.78566	0.623895	0.721985	0.027789	0	671	458	1429	823	1125	784	1225	973	1289	921
ENSMUSG00000066643	chr12	Wdr35	8973892	8974179	7273	-0.07942	3.658065	0.624	0.721985	0.02502	0	160	156	306	169	260	166	284	205	247	213
ENSMUSG00000022428	chr15	Cby1	79659227	79659293	1119	-0.08142	3.475052	0.624284	0.722188	0.027631	0	145	135	216	185	230	141	262	158	230	194
ENSMUSG00000029089	chr5	Pacrgl	48372392	48372495	1464	0.180267	0.648796	0.624273	0.722188	0.07697	0	19	13	39	27	13	16	48	19	34	27
ENSMUSG00000018209	chr2	Stk4	1.64E+08	1.64E+08	5860	0.072147	3.881049	0.624381	0.722237	0.022916	0	198	136	345	207	290	221	351	269	302	231
ENSMUSG00000003644	chr4	Rps6ka1	1.34E+08	1.34E+08	4258	0.092852	3.284043	0.624547	0.722365	0.039878	0	134	63	238	140	207	156	184	186	213	162
ENSMUSG00000098905	chr13	Zfp953	67339307	67343657	4676	-0.14317	0.407605	0.624664	0.722438	0.050408	0	13	17	28	24	21	14	35	17	23	18
ENSMUSG00000037049	chr7	Smpd1	1.06E+08	1.06E+08	2411	-0.08404	6.339995	0.624744	0.722467	0.034203	0	1084	691	1665	1644	1750	1092	1702	1246	1789	1376
ENSMUSG00000034343	chr1	Ube2f	91250304	91250437	8842	0.069946	5.808577	0.624928	0.722617	0.023035	0	800	594	1106	881	1018	858	1426	933	1227	841
ENSMUSG00000073633	chr1	Fbxo36	84839841	84839968	2148	-0.12925	1.020423	0.625335	0.723025	0.058813	0	36	22	30	39	31	21	54	34	34	27
ENSMUSG00000027167	chr2	Elp4	1.06E+08	1.06E+08	3318	-0.10858	2.283819	0.625504	0.723129	0.038512	0	67	41	112	95	90	58	90	92	113	69
ENSMUSG00000034674	chr10	Tdg	82629828	82629939	5374	0.080102	3.409142	0.625574	0.723129	0.026371	0	141	96	262	159	186	135	266	187	248	167
ENSMUSG00000037458	chr15	Azin1	38487430	38490472	6231	0.081622	5.531164	0.625588	0.723129	0.03145	0	605	535	1061	581	874	568	1327	637	1199	739
ENSMUSG00000034040	chr5	Wbscr17	1.31E+08	1.31E+08	8989	-0.14327	3.59188	0.625697	0.723192	0.093895	0	126	116	360	195	264	234	143	112	431	129
ENSMUSG00000019899	chr10	Lama2	26980036	26984513	16338	-0.10374	5.655861	0.625812	0.723198	0.051236	0	496	382	1714	790	1152	751	1035	700	995	917
ENSMUSG00000027936	chr3	Crtc2	90254163	90254558	4094	0.070359	4.449312	0.625798	0.723198	0.021249	0	297	247	467	332	369	352	461	380	533	317
ENSMUSG00000058558	chr5	Rpl5	1.08E+08	1.08E+08	3920	-0.08944	7.847635	0.626188	0.723569	0.040276	0	3439	3819	4628	3022	3562	3541	5750	3564	4334	3298
ENSMUSG00000081058	chr3	Hist2h3c2	96238108	96239127	1020	0.147748	1.128061	0.626609	0.723993	0.059093	0	35	28	47	20	27	36	35	38	59	31
ENSMUSG00000032244	chr9	Fem1b	62791832	62797728	6488	-0.07117	4.595635	0.62743	0.724816	0.02276	0	322	298	612	329	454	317	573	426	469	374
ENSMUSG00000098004	chr2	Gm27027	93956817	93957105	547	0.084824	3.442802	0.627419	0.724816	0.027869	0	170	113	220	154	184	179	277	171	249	147
ENSMUSG00000015120	chr17	Ube2i	25261916	25262491	5474	0.06987	4.107836	0.627789	0.724859	0.020422	0	242	192	366	237	316	249	380	293	396	291
ENSMUSG00000025050	chr19	Pcgf6	47033619	47034685	2098	-0.1004	2.074113	0.627845	0.724859	0.036535	0	72	44	81	63	81	55	88	77	96	50
ENSMUSG00000026245	chr1	Farsb	78417975	78418222	2620	0.069416	5.782212	0.627646	0.724859	0.02293	0	827	602	1156	843	880	801	1228	965	1313	870
ENSMUSG00000031065	chrX	Cdk16	20687954	20688361	4378	-0.07684	7.3131	0.627626	0.724859	0.029639	0	2100	1635	3217	3214	3047	2164	3519	2560	3568	2453
ENSMUSG00000051890	chr12	Klhdc1	69241176	69241381	3137	-0.07433	4.887659	0.627847	0.724859	0.026896	0	457	366	686	476	440	368	739	454	671	444
ENSMUSG00000052921	chr11	Arhgef15	68943155	68944829	6483	-0.09795	3.614776	0.627652	0.724859	0.041566	0	127	110	240	284	268	154	249	213	286	181
ENSMUSG00000055923	chr5	Aasdh	76873659	76874313	6287	-0.09323	3.008371	0.62785	0.724859	0.034232	0	139	86	189	113	136	101	187	149	135	130
ENSMUSG00000022623	chr15	Shank3	89499623	89499919	8896	0.082458	3.400346	0.628289	0.72513	0.031399	0	117	87	230	167	243	161	235	201	227	160
ENSMUSG00000035696	chr4	Rnf38	44126210	44129656	8336	0.091904	3.366581	0.628227	0.72513	0.039278	0	109	77	249	186	206	121	222	202	272	161
ENSMUSG00000039725	chr2	2810408M09Rik	1.65E+08	1.65E+08	2118	0.084841	3.352569	0.628304	0.72513	0.027843	0	157	99	175	159	197	150	242	169	233	163
ENSMUSG00000073405	chr17	C920025E04Rik	36109234	36109270	1067	0.406608	1.12841	0.628302	0.72513	0.732796	0	34	48	33	15	0	40	13	136	8	10
ENSMUSG00000001911	chr8	Nfix	84699876	84700219	7351	-0.07691	7.993382	0.628739	0.725564	0.030002	0	3345	2577	6400	4044	5286	2894	5271	4180	6238	4375
ENSMUSG00000027016	chr2	Zfp385b	77410634	77412140	8223	-0.37471	2.485667	0.628789	0.725564	0.661163	0	4	4	47	199	284	26	82	46	44	212
ENSMUSG00000097616	chr6	1110019D14Rik	13871526	13871627	1722	0.114927	1.596179	0.62885	0.725571	0.037073	0	37	36	64	38	51	49	76	57	60	36
ENSMUSG00000035109	chr2	Shc4	1.26E+08	1.26E+08	8263	0.195638	0.069947	0.629072	0.725764	0.113052	0	2	7	25	19	20	8	28	21	19	16

ENSMUSG00000089838	chr1	Gm2962	1.71E+08	1.71E+08	336	0.094705	2.760198	0.629462	0.72615	0.035039	0	93	62	117	117	131	90	180	103	146	117
ENSMUSG00000051730	chr2	Mettl5	69871198	69871316	2437	-0.09463	3.223704	0.629968	0.726672	0.045063	0	148	157	173	120	142	115	251	142	191	133
ENSMUSG00000049922	chr2	Slc35c1	92452764	92454774	3275	-0.08778	3.126199	0.630165	0.726835	0.029027	0	115	81	222	146	171	103	172	166	203	128
ENSMUSG00000022151	chr15	Ttc33	5185525	5185572	2163	-0.06996	5.398652	0.630383	0.727023	0.02425	0	567	544	904	682	761	550	995	599	957	698
ENSMUSG00000052656	chr6	Rnf103	71493894	71494888	4348	-0.0702	4.649796	0.630696	0.727321	0.022709	0	348	296	585	397	450	310	493	453	545	431
ENSMUSG00000034488	chr13	Edil3	88821472	88822048	13677	-0.2295	-0.24148	0.631146	0.727777	0.101415	0	7	8	17	13	20	4	22	9	9	18
ENSMUSG00000015149	chr7	Sirt2	28766735	28766867	3568	-0.06862	6.538017	0.631233	0.727814	0.023804	0	1282	1053	2057	1592	1712	1308	1954	1526	2177	1384
ENSMUSG00000024137	chr17	E4f1	24443792	24444337	2561	-0.07573	3.489121	0.631677	0.728263	0.02375	0	171	124	259	158	216	160	268	177	235	159
ENSMUSG00000058975	chr7	Kcnc1	46396497	46398247	9128	-0.1636	6.475645	0.631774	0.728311	0.137663	0	640	391	1702	2584	2689	799	2150	1053	2273	1622
ENSMUSG00000004929	chr10	Thop1	81070035	81070278	5059	-0.07409	4.863945	0.63225	0.728621	0.026495	0	376	339	588	561	528	379	532	513	690	476
ENSMUSG00000020334	chr11	Slc22a4	53983123	53983685	2553	-0.14882	2.631782	0.632262	0.728621	0.097345	0	49	45	90	174	168	93	104	122	112	89
ENSMUSG00000037138	chr1	Aff3	38177326	38179570	6579	-0.17705	1.778847	0.632258	0.728621	0.131996	0	30	60	105	33	61	23	52	105	48	54
ENSMUSG00000045106	chr2	Ccdc73	1.05E+08	1.05E+08	4351	0.229324	-0.05058	0.632125	0.728621	0.100271	0	18	12	12	8	11	12	12	21	30	10
ENSMUSG00000033653	chr16	Vps8	21423118	21423225	8670	0.07942	3.374992	0.632449	0.728772	0.024999	0	130	109	225	172	175	136	234	208	240	155
ENSMUSG00000086158	chr9	Ccpg1os	72979722	72980196	2404	-0.09708	2.64274	0.632668	0.728961	0.045882	0	91	108	116	87	91	83	140	89	134	100
ENSMUSG00000037376	chr2	Trmt6	1.33E+08	1.33E+08	5384	0.078779	3.537536	0.632856	0.729115	0.02482	0	160	138	236	157	209	176	303	193	230	183
ENSMUSG00000097350	chr17	4732491K20Rik	12318885	12319172	3142	-0.16438	1.483203	0.633165	0.729408	0.100663	0	28	21	36	80	64	38	74	33	45	43
ENSMUSG00000097354	chr6	2310001H17Rik	1.29E+08	1.29E+08	5694	-0.11868	4.274316	0.633839	0.730121	0.073416	0	330	410	278	211	257	308	405	276	432	273
ENSMUSG00000034445	chr19	Cyb561a3	10577454	10578083	1474	-0.10537	2.469701	0.633897	0.730124	0.042905	0	88	50	132	75	118	53	128	103	102	96
ENSMUSG00000035011	chr10	Zbtb7a	81135220	81135591	6808	-0.07134	5.042133	0.634055	0.730242	0.023886	0	426	344	826	529	650	424	622	585	717	575
ENSMUSG00000024846	chr19	Cst6	5344705	5348049	3951	0.098508	4.359569	0.63422	0.730369	0.043911	0	311	328	355	276	244	313	489	326	525	303
ENSMUSG00000027102	chr2	Hoxd8	74704615	74704724	2744	0.198988	4.15276	0.63449	0.730616	0.199544	0	392	312	368	48	116	266	439	393	508	171
ENSMUSG00000032641	chr6	Gpr19	1.35E+08	1.35E+08	2637	0.114423	1.779381	0.634847	0.730964	0.038438	0	53	39	66	44	53	49	76	73	75	44
ENSMUSG00000003166	chr16	Dgcr2	17839482	17842777	6638	0.068502	5.316679	0.635316	0.731441	0.023924	0	453	382	911	668	791	590	879	772	884	606
ENSMUSG00000028364	chr4	Tnc	63959785	63960543	7772	-0.18407	3.810562	0.635384	0.731455	0.168803	0	57	123	407	282	415	143	302	283	92	329
ENSMUSG00000038365	chr8	Fbxo25	13907806	13907863	2008	0.080713	3.588332	0.635866	0.731947	0.026754	0	173	151	248	159	195	159	270	222	249	219
ENSMUSG00000036985	chrX	Zdhhc9	48171969	48173641	6733	-0.08347	3.547315	0.636176	0.73224	0.02953	0	165	127	258	195	222	171	180	234	262	173
ENSMUSG00000025495	chr7	Ptdss2	1.41E+08	1.41E+08	4875	-0.07871	4.124556	0.63676	0.732849	0.027637	0	209	164	387	337	368	233	367	261	384	302
ENSMUSG00000030649	chr7	Anapc15	1.02E+08	1.02E+08	4737	0.078525	3.583424	0.637203	0.733294	0.026625	0	175	121	209	193	229	200	247	197	281	188
ENSMUSG00000005667	chr6	Mthfd2	83305691	83306809	2722	0.115889	2.460107	0.637588	0.733635	0.063324	0	71	35	104	103	113	121	102	69	134	80
ENSMUSG00000022323	chr15	Hrsp12	34484021	34484535	3192	-0.0907	3.316323	0.637664	0.733635	0.041339	0	172	143	212	119	157	141	251	179	205	110
ENSMUSG00000023051	chr15	Tarbp2	1.03E+08	1.03E+08	4549	-0.07131	4.479177	0.637624	0.733635	0.024566	0	339	252	426	373	432	364	448	331	515	322
ENSMUSG00000061100	chr16	Retnla	48842552	48842628	598	-0.19538	5.082008	0.637919	0.733864	0.202215	0	637	723	911	200	290	764	428	919	431	208
ENSMUSG00000025964	chr1	Adam23	63445891	63446412	17907	0.132361	1.581878	0.638257	0.734189	0.063682	0	39	35	88	23	42	57	65	50	63	39
ENSMUSG00000005397	chr13	Nid1	13437602	13437926	6046	0.081703	6.539266	0.638463	0.734362	0.036049	0	1050	851	2675	1167	1915	1411	1780	1928	2108	1466
ENSMUSG00000029397	chr5	Rchy1	91948904	91949864	2894	-0.06948	5.282125	0.638715	0.734589	0.025026	0	641	470	881	538	661	562	919	585	879	558
ENSMUSG00000056851	chr15	Pcbp2	1.02E+08	1.02E+08	2868	0.070476	7.359884	0.638915	0.734755	0.026765	0	2104	1515	3979	2626	3031	2339	3840	2875	3755	2676
ENSMUSG00000032649	chr1	Colgalt2	1.52E+08	1.52E+08	4245	0.114453	2.038973	0.639211	0.735031	0.063703	0	34	35	95	64	93	39	78	85	86	90
ENSMUSG00000020027	chr10	Socs2	95385362	95388395	9531	0.125299	3.736996	0.639758	0.735585	0.081246	0	124	98	289	200	359	117	392	380	251	154
ENSMUSG00000066892	chr9	Fbxl12	20618118	20618410	5090	0.101174	2.012104	0.639803	0.735585	0.035123	0	46	45	68	60	86	62	92	75	82	60
ENSMUSG00000098917	chr8	Mir7654	8690093	8690162	70	-0.13049	0.657357	0.639863	0.73559	0.049348	0	24	21	31	17	30	16	36	20	30	27
ENSMUSG00000020381	chr11	3010026O09Rik	50174444	50174547	2039	0.141821	1.403125	0.639936	0.73561	0.056955	0	36	40	51	36	26	36	50	56	57	43
ENSMUSG00000000194	chr2	Gpr107	31152316	31152481	12766	-0.06508	5.501061	0.640085	0.735655	0.021202	0	618	479	1078	720	892	653	935	733	987	732
ENSMUSG00000031365	chrX	Zfp275	73342621	73342751	6745	-0.09811	3.315729	0.640068	0.735655	0.040418	0	132	103	310	111	200	119	192	194	196	167
ENSMUSG00000043122	chr12	A530016L24Rik	1.12E+08	1.12E+08	2636	0.306007	2.037327	0.640144	0.735658	0.46676	0	130	58	40	13	15	56	34	230	41	30
ENSMUSG00000006221	chr4	Hspb7	1.41E+08	1.41E+08	2769	0.264743	7.651727	0.640514	0.736019	0.377904	0	443	338	1350	8152	4892	2148	5326	2505	7198	3749
ENSMUSG00000026674	chr1	Ddr2	1.7E+08	1.7E+08	9264	0.089723	5.070984	0.641055	0.736578	0.043799	0	337	335	957	398	724	463	704	759	557	627
ENSMUSG00000081534	chr15	Slc48a1	97784355	97784616	2690	0.071136	5.893509	0.64117	0.736645	0.026488	0	842	624	1220	965	1020	891	1229	1181	1522	788
ENSMUSG00000028614	chr4	Ndc1	1.07E+08	1.07E+08	4924	-0.09352	3.578835	0.641572	0.737043	0.039922	0	132	98	262	268	250	149	277	219	235	176
ENSMUSG00000026946	chr2	Nmi	51948487	51948776	2001	-0.11283	2.519297	0.641685	0.737109	0.062748	0	96	92	85	75	104	94	142	109	94	57
ENSMUSG00000078919	chr2	Dpm1	1.68E+08	1.68E+08	7489	0.094684	5.708108	0.641855	0.737241	0.046898	0	763	874	1035	560	671	837	1255	811	1319	763
ENSMUSG00000024160	chr17	Spsb3	24886643	24886760	2719	0.067848	5.435434	0.642074	0.737428	0.023455	0	657	442	870	684	742	657	1039	727	1050	616
ENSMUSG00000052752	chr17	Traf7	24508562	24509358	5872	-0.06544	4.564653	0.642325	0.737653	0.020784	0	309	262	540	416	433	309	496	429	531	355
ENSMUSG00000049811	chr11	Fam161a	23007531	23007608	4396	-0.12698	1.459402	0.642643	0.737954	0.061014	0	38	48	62	33	37	45	38	45	59	41
ENSMUSG00000039678	chr2	Tbc1d13	30133746	30133912	4719	0.068039	4.297484	0.64284	0.738053	0.021865	0	232	228	416	313	358	264	465	376	403	328
ENSMUSG00000046351	chr13	Zfp322a	23353103	23357713	5197	-0.07136	3.672808	0.64283	0.738053	0.023136	0	152	161	274	198	265	169	277	218	274	196
ENSMUSG00000024191	chr17	Bnip1	26781079	26781176	5097	-0.07009	4.256455	0.643135	0.738328	0.025177	0	267	242	358	293	397	282	417	318	463	237
ENSMUSG00000083396	chr7	Gm15542	1.41E+08	1.41E+08	1194	0.133939	0.854374	0.643307	0.738461	0.061135	0	32	12	26	24	36	32	37	33	30	28
ENSMUSG00000017802	chr11	Fam134c	1.01E+08	1.01E+08	3589	-0.06766	5.975451	0.64371	0.738731	0.024202	0	881	660	1516	1037	1168	981	1335	1033	1323	932
ENSMUSG00000021139	chr12	Gm20498	81358860	81359344	3241	-0.07423	5.664354	0.643634	0.738731	0.030121	0	785	706	1044	724	848	835	1254	744	1059	652
ENSMUSG00000031024	chr7	St5	1.1E+08	1.1E+08	4526	0.086609	2.970724	0.643695	0.738731	0.031919	0	96	86	164	132	128	102	149	127	211	143
ENSMUSG00000015243	chr4	Abca1	53030787	53034083	10363	-0.10678	4.564965	0.643836	0.738812	0.059604	0	336	322	785	252	321	341	335	550	460	350
ENSMUSG00000027506	chr3	Tpd52	8925593	8931174	7487	-0.08621	4.875748	0.643923	0.738848	0.040376	0	479	440	753	316	413	408	651	473	711	391
ENSMUSG00000072407	chr10	Gm6419	74862988	74863419	432	-0.14761	0.17258	0.643978	0.738848	0.06966	0	19	14	22	17	13	9	23	24	14	18
ENSMUSG00000016181	chr1	Diexf	1.93E+08	1.93E+08	6530	-0.0863	2.958399	0.644154	0.738986	0.030547	0	101	86	192	122	145	107	140	162	146	119

ENSMUSG00000027405	chr2	Nop56	1.3E+08	1.3E+08	4099	0.069879	4.702464	0.644824	0.73969	0.023603	0	340	326	549	384	431	375	665	500	545	366
ENSMUSG00000022678	chr16	Nde1	14163275	14163368	3205	0.063087	5.005536	0.645347	0.740226	0.020388	0	428	350	686	499	575	514	710	576	702	488
ENSMUSG00000092260	chr8	Zfp963	69741639	69743610	2299	0.114679	2.178316	0.645455	0.740286	0.048358	0	57	68	105	52	56	76	100	85	100	59
ENSMUSG00000028907	chr4	Utp11l	1.25E+08	1.25E+08	4711	-0.07349	4.250006	0.645881	0.740711	0.027381	0	299	228	462	263	317	303	415	254	460	268
ENSMUSG00000055538	chr14	Zcchc24	25711642	25715402	4557	0.083331	6.940279	0.645964	0.740742	0.03888	0	1644	1428	3506	1262	2028	1837	2482	2070	3429	1855
ENSMUSG00000029777	chr6	Gars	55038001	55038233	2390	0.066968	6.178805	0.646727	0.741488	0.024482	0	957	822	1533	1150	1241	1118	1551	1164	1777	1183
ENSMUSG00000038299	chr18	Wdr36	32837225	32837558	3281	-0.06639	4.50217	0.646683	0.741488	0.022451	0	346	253	548	334	395	302	548	405	477	308
ENSMUSG00000029326	chr5	Enoph1	1E+08	1E+08	1826	0.083733	2.961155	0.64702	0.741761	0.02899	0	102	104	165	99	127	124	169	139	170	119
ENSMUSG00000085172	chr18	Gm6542	36609958	36610729	772	-0.10669	0.794878	0.647449	0.742188	0.054472	0	25	28	28	27	24	18	35	30	40	22
ENSMUSG00000049882	chr12	Vcpkmt	69577628	69577940	1027	0.127155	1.379959	0.647576	0.74227	0.045234	0	39	37	47	28	37	38	61	48	57	35
ENSMUSG00000049800	chr11	Sertad2	20543253	20543760	6352	-0.0703	4.107074	0.648009	0.742702	0.023519	0	223	169	414	271	373	213	423	280	380	257
ENSMUSG00000086298	chr11	Gm11716	1.07E+08	1.07E+08	470	-0.13259	3.966012	0.648383	0.743066	0.095699	0	133	127	279	485	299	175	522	180	276	242
ENSMUSG00000036306	chr8	Lzts1	69132669	69136159	6993	-0.26013	1.269933	0.648596	0.743182	0.328539	0	7	3	25	93	82	19	57	45	44	29
ENSMUSG00000042428	chr15	Mgat3	80173721	80173838	4665	-0.16917	0.634246	0.648565	0.743182	0.09514	0	12	17	24	30	41	12	32	27	19	33
ENSMUSG00000020806	chr11	Rhbdf2	1.17E+08	1.17E+08	5293	-0.0751	4.017407	0.649685	0.744301	0.029526	0	283	197	390	222	231	220	330	290	368	233
ENSMUSG00000055835	chr8	Zfp1	1.12E+08	1.12E+08	1871	-0.08766	2.92063	0.649681	0.744301	0.038566	0	113	76	167	118	153	70	205	126	182	101
ENSMUSG00000075467	chr2	Dnlz	26348121	26350558	2916	-0.0665	5.040883	0.649919	0.744504	0.023832	0	450	374	661	622	589	501	710	502	740	490
ENSMUSG00000079225	chr9	Gm9531	81677598	81677859	1080	-0.11657	2.058117	0.650434	0.74503	0.049966	0	66	47	89	56	83	67	81	48	68	85
ENSMUSG00000025958	chr1	Creb1	64532645	64532904	13742	-0.07564	4.096123	0.650871	0.745467	0.027343	0	195	178	437	286	349	204	346	346	339	279
ENSMUSG00000021411	chr13	Pxdc1	34627840	34628888	2103	0.118673	1.618474	0.651026	0.74558	0.043439	0	32	39	57	44	56	29	76	60	71	50
ENSMUSG00000034729	chr17	Mrps10	47368887	47368954	8079	0.075507	4.754144	0.651545	0.746109	0.02872	0	392	375	476	378	431	430	618	417	652	419
ENSMUSG00000020305	chr11	Asb3	30954395	30954569	5275	-0.08568	2.944313	0.651639	0.746152	0.035302	0	86	112	176	107	150	86	184	114	174	126
ENSMUSG00000020776	chr11	Fbf1	1.16E+08	1.16E+08	7751	-0.07883	3.362189	0.651958	0.746408	0.026353	0	140	112	250	146	209	148	202	194	187	166
ENSMUSG00000022297	chr15	Fzd6	39006280	39006432	4134	-0.11101	1.96288	0.651974	0.746408	0.048089	0	37	41	74	71	99	44	81	71	75	63
ENSMUSG00000009995	chrX	Taz	74281912	74282040	5364	-0.06382	5.613507	0.652095	0.746481	0.023019	0	699	608	1007	777	910	715	1163	717	1063	746
ENSMUSG00000034190	chr14	Chmp7	69716979	69718300	2706	-0.06517	5.924975	0.652369	0.74673	0.024301	0	896	784	1244	926	1097	898	1338	974	1313	917
ENSMUSG00000032744	chr4	Heyl	1.23E+08	1.23E+08	5113	0.105575	3.057904	0.652699	0.747044	0.059667	0	74	73	195	127	195	82	233	103	204	174
ENSMUSG00000001674	chr1	Ddx18	1.22E+08	1.22E+08	2483	0.070881	3.994362	0.652886	0.74713	0.024489	0	201	204	366	198	281	243	394	284	322	244
ENSMUSG00000038855	chr1	Itpkb	1.8E+08	1.8E+08	10463	-0.09495	4.564474	0.652885	0.74713	0.049107	0	285	182	500	492	560	246	382	445	652	384
ENSMUSG00000014313	chr15	Cox6c	35925886	35926368	3567	0.087307	8.601701	0.653238	0.747274	0.044942	0	5441	4176	5452	7756	6797	6010	11058	5676	9352	5305
ENSMUSG00000038611	chr7	Phrf1	1.41E+08	1.41E+08	6765	0.068785	4.019836	0.653195	0.747274	0.026197	0	181	146	398	266	317	239	336	329	352	251
ENSMUSG00000057176	chr7	Gm166	1.28E+08	1.28E+08	2535	0.15814	0.728129	0.653224	0.747274	0.084948	0	17	10	25	39	27	16	29	26	42	36
ENSMUSG00000091803	chr12	Cox16	81359026	81359344	3751	0.076902	5.496681	0.653166	0.747274	0.032318	0	675	620	861	602	690	778	1169	690	1018	611
ENSMUSG00000055799	chr6	Tcf7l1	72626378	72627793	3924	0.109067	2.810428	0.65341	0.747407	0.065341	0	67	76	208	68	142	121	108	175	145	94
ENSMUSG00000028964	chr4	Park7	1.51E+08	1.51E+08	2479	0.109883	9.198842	0.653553	0.747505	0.071459	0	10266	9928	10517	5469	6720	10652	13945	9440	14997	7298
ENSMUSG00000020676	chr11	Ccl11	82057823	82058042	1082	0.06753	4.287524	0.653702	0.747611	0.025136	0	242	196	427	290	401	308	455	341	346	350
ENSMUSG00000027079	chr2	Clp1	84722104	84722752	2672	0.110821	2.20909	0.653787	0.747644	0.044513	0	64	59	72	64	84	51	110	104	92	74
ENSMUSG00000078247	chr17	Airn	12741311	12741424	3583	0.096278	2.491379	0.653852	0.747654	0.040812	0	84	58	112	75	101	99	145	72	103	99
ENSMUSG00000020949	chr12	Fkbp3	65062436	65062740	947	-0.07811	7.171856	0.653932	0.747681	0.036261	0	2295	2070	2492	2373	2268	2087	3621	2103	3114	2064
ENSMUSG00000001657	chr15	Hoxc8	1.03E+08	1.03E+08	2832	-0.14862	2.111387	0.654386	0.748136	0.098397	0	57	54	82	69	95	75	32	109	64	68
ENSMUSG00000019132	chr13	BC005537	24801657	24803509	3665	0.069619	6.336232	0.654599	0.748315	0.027799	0	1191	988	1850	1032	1276	1083	1854	1463	1922	1309
ENSMUSG00000032180	chr9	Tmed1	21507380	21508391	1487	0.065091	5.179971	0.654722	0.748391	0.023274	0	504	356	687	626	681	534	799	618	872	577
ENSMUSG00000100691	chr8	2010320M18Rik	70776815	70777823	1009	-0.09812	3.392077	0.654832	0.748452	0.054421	0	209	166	163	128	155	159	219	165	251	133
ENSMUSG00000030727	chr7	Rabep2	1.26E+08	1.26E+08	5322	0.374933	5.612406	0.655114	0.748709	0.809214	0	38	31	2118	1418	365	68	96	1588	1978	1329
ENSMUSG00000004698	chr12	Hdac9	34371503	34374138	4422	-0.14068	2.413787	0.655511	0.748716	0.103358	0	54	59	139	95	105	39	119	35	173	106
ENSMUSG00000016984	chr11	Etaa1	17938756	17940350	4185	-0.12115	1.269635	0.655482	0.748716	0.059072	0	32	41	55	25	38	29	65	31	42	37
ENSMUSG00000031380	chrX	Figf	1.64E+08	1.64E+08	2408	0.139515	2.62132	0.655507	0.748716	0.095677	0	93	114	129	49	57	94	121	146	154	69
ENSMUSG00000035969	chr4	Rusc2	43381979	43382199	7923	0.093194	4.784494	0.655433	0.748716	0.050767	0	257	215	561	531	654	297	533	517	685	568
ENSMUSG00000044149	chrX	Nkrf	36887540	36890512	3268	-0.09574	1.601759	0.655514	0.748716	0.039163	0	48	41	60	46	45	34	60	54	70	43
ENSMUSG00000067787	chr2	Blcap	1.58E+08	1.58E+08	3043	-0.06525	5.222731	0.655349	0.748716	0.024117	0	583	439	716	575	731	531	782	725	771	523
ENSMUSG00000082241	chr16	Gm15776	22295027	22295231	205	0.106683	1.24796	0.655198	0.748716	0.040778	0	31	25	49	34	37	39	53	34	40	46
ENSMUSG00000032316	chr9	Clk3	57750711	57751121	2494	-0.06321	5.275161	0.655837	0.748955	0.022605	0	625	428	803	570	753	556	856	611	886	573
ENSMUSG00000043311	chr17	D17H6S53E	35126373	35126450	2280	-0.08805	3.421586	0.655782	0.748955	0.038469	0	119	98	242	228	213	124	252	148	259	175
ENSMUSG00000032301	chr9	Psma4	54950790	54950903	2370	0.082804	6.785374	0.65612	0.749151	0.040159	0	1602	1695	2015	1407	1590	1870	2787	1778	2598	1447
ENSMUSG00000063870	chr6	Chd4	1.25E+08	1.25E+08	8019	-0.07082	6.735222	0.656121	0.749151	0.029337	0	1405	998	2990	1651	2086	1363	2143	1792	2593	1691
ENSMUSG00000012076	chr12	Brms1l	55836366	55836645	2566	0.066933	4.119831	0.656774	0.749832	0.022362	0	247	181	362	277	297	225	426	308	367	301
ENSMUSG00000040653	chr10	Ppp1r14c	3366150	3366969	2524	-0.08042	7.025091	0.656838	0.74984	0.038814	0	1997	1815	3477	1470	2038	1813	2944	1754	2937	2204
ENSMUSG00000037210	chr5	Fam193a	34369933	34370427	7418	-0.0829	3.560163	0.657046	0.750013	0.031315	0	132	106	298	218	247	173	267	190	217	189
ENSMUSG00000020936	chr11	Nmt1	1.03E+08	1.03E+08	5017	-0.06337	6.204716	0.657215	0.750141	0.023515	0	1019	895	1701	1133	1345	1108	1604	1260	1557	1071
ENSMUSG00000073775	chr4	Kti12	1.09E+08	1.09E+08	1629	0.071762	4.558838	0.657327	0.750204	0.026168	0	372	299	421	321	391	332	517	460	538	361
ENSMUSG00000021365	chr13	Nedd9	41309916	41312170	4712	0.102213	2.242169	0.657522	0.750234	0.043738	0	53	46	85	85	92	50	136	82	97	80
ENSMUSG00000030795	chr7	Fus	1.28E+08	1.28E+08	5690	0.068193	6.622645	0.657468	0.750234	0.027342	0	1265	1169	1912	1532	1840	1398	2539	1432	2336	1639
ENSMUSG00000031982	chr8	Arv1	1.25E+08	1.25E+08	1165	0.12805	0.920925	0.657523	0.750234	0.061953	0	20	20	44	25	30	38	53	28	36	16
ENSMUSG00000028910	chr4	Mecr	1.32E+08	1.32E+08	3041	-0.07033	4.053863	0.657747	0.750425	0.026846	0	262	193	320	253	325	232	316	339	379	212
ENSMUSG00000046574	chr7	Prr12	45027707	45028624	6879	0.078686	4.034279	0.658172	0.750846	0.035017	0	194	154	447	218	313	170	341	331	401	301

ENSMUSG00000025650	chr9	Col7a1	1.09E+08	1.09E+08	10267	0.111942	3.758151	0.65831	0.750918	0.072954	0	227	139	356	96	246	291	201	182	319	246
ENSMUSG00000048537	chr9	Phldb1	44686304	44687698	7179	0.068138	5.320533	0.658349	0.750918	0.027468	0	474	383	926	645	786	539	729	840	925	684
ENSMUSG00000036073	chr4	Galt	41755228	41755652	2471	-0.09187	4.646117	0.658512	0.75104	0.048652	0	254	248	417	606	558	311	619	349	535	422
ENSMUSG00000022329	chr15	Stk3	34875496	34876820	3237	-0.09488	2.156358	0.659225	0.75166	0.041391	0	52	59	103	61	90	53	109	92	86	50
ENSMUSG00000025085	chr19	Ablim1	57032733	57037337	11949	-0.10248	5.09029	0.65921	0.75166	0.061097	0	294	298	722	764	853	407	591	840	628	504
ENSMUSG00000029028	chr4	Lrrc47	1.54E+08	1.54E+08	3510	-0.06731	4.963762	0.659209	0.75166	0.025281	0	397	345	658	461	743	428	609	496	777	488
ENSMUSG00000060301	chr10	2610008E11Rik	79064374	79068051	4229	0.070244	4.207542	0.659944	0.752414	0.025184	0	256	212	364	269	340	294	461	247	460	280
ENSMUSG00000058301	chr8	Upf1	70331522	70332479	4616	0.065814	5.448138	0.66003	0.752448	0.025984	0	567	406	1018	658	867	590	829	856	997	786
ENSMUSG00000037172	chr6	E330009J07Rik	40401375	40406934	7511	0.137902	0.951484	0.6601	0.752463	0.089712	0	17	22	44	20	40	25	35	55	21	34
ENSMUSG00000033544	chr1	Angptl1	1.57E+08	1.57E+08	2841	0.117342	3.778528	0.660171	0.752479	0.082128	0	80	157	371	202	291	141	286	262	221	360
ENSMUSG00000039163	chr9	Cmc1	1.18E+08	1.18E+08	1181	0.08455	3.72221	0.660366	0.752573	0.033764	0	187	180	196	220	205	208	299	234	310	187
ENSMUSG00000047613	chr4	A430005L14Rik	1.54E+08	1.54E+08	1552	0.077064	4.057083	0.660349	0.752573	0.028944	0	247	226	324	232	240	257	387	304	399	220
ENSMUSG00000028676	chr4	Srsf10	1.36E+08	1.36E+08	7003	0.065489	4.472371	0.660627	0.752797	0.022214	0	277	293	458	310	392	322	485	412	499	352
ENSMUSG00000030619	chr7	Eed	89954656	89955063	2218	0.065514	4.276438	0.660676	0.752797	0.022083	0	254	242	443	258	325	298	466	313	433	302
ENSMUSG00000024665	chr19	Fads2	10064164	10064314	1508	-0.16871	0.961838	0.660846	0.75286	0.073944	0	18	12	54	37	43	36	28	31	31	28
ENSMUSG00000027828	chr3	Ssr3	65379655	65382034	4172	-0.07631	7.820386	0.660903	0.75286	0.036107	0	3548	3328	5386	2677	3496	3325	5234	3874	4951	2939
ENSMUSG00000030979	chr7	Uros	1.34E+08	1.34E+08	3576	-0.0686	4.393716	0.660819	0.75286	0.028331	0	308	309	384	335	341	292	469	373	460	288
ENSMUSG00000056763	chr1	Cspp1	10037987	10039342	17553	-0.10388	1.877261	0.660995	0.7529	0.040845	0	45	44	95	47	72	51	77	74	57	53
ENSMUSG00000073563	chr18	Csnk1g3	53862113	53862600	4394	0.071785	3.187937	0.661317	0.753203	0.024263	0	111	105	194	138	163	123	187	170	203	160
ENSMUSG00000021990	chr14	Spata13	60634001	60634183	9102	0.093164	1.744796	0.661538	0.753363	0.044748	0	47	22	83	43	66	45	72	64	66	58
ENSMUSG00000025880	chr18	Smad7	75367529	75369568	4521	-0.09622	2.730739	0.661571	0.753363	0.049636	0	103	74	110	107	145	60	154	95	138	136
ENSMUSG00000031174	chrX	Rpgr	10073621	10073828	7247	-0.11168	1.239741	0.663063	0.754997	0.05486	0	41	34	40	30	39	26	44	53	43	32
ENSMUSG00000068391	chr15	Chrac1	73090392	73090583	2353	-0.07222	5.429224	0.663189	0.755076	0.032425	0	677	639	889	559	705	629	1121	633	911	593
ENSMUSG00000041143	chr4	Tmco4	1.39E+08	1.39E+08	3596	-0.07928	3.887103	0.663418	0.755272	0.03632	0	226	217	320	207	223	239	261	193	371	239
ENSMUSG00000015605	chr17	Srf	46546839	46549178	4093	-0.06788	6.544912	0.663567	0.755376	0.02835	0	1445	880	2098	1605	1763	1318	1874	1464	2390	1372
ENSMUSG00000039354	chr1	Smarcal1	72583251	72583438	5728	-0.06324	4.478031	0.663733	0.755435	0.021126	0	306	222	553	344	444	296	492	376	486	348
ENSMUSG00000058886	chr7	Deaf1	1.41E+08	1.41E+08	2192	0.071751	3.51209	0.663682	0.755435	0.02496	0	163	131	227	182	178	181	238	214	237	182
ENSMUSG00000033717	chr19	Adra2a	54045182	54048982	3801	0.155081	0.034576	0.663833	0.755484	0.07885	0	12	6	27	17	9	20	17	18	22	10
ENSMUSG00000019826	chr10	Zbtb24	41450396	41450530	2828	-0.08696	2.125628	0.664575	0.756261	0.031511	0	52	56	107	61	81	58	99	75	84	63
ENSMUSG00000022973	chr16	Synj1	90936092	90939034	8085	-0.10357	2.902144	0.664686	0.756261	0.049832	0	84	49	209	146	158	117	166	126	130	107
ENSMUSG00000052712	chr17	BC004004	29268788	29269002	6017	-0.06547	6.523418	0.66468	0.756261	0.026901	0	1302	1145	1778	1588	1674	1306	1966	1392	2270	1369
ENSMUSG00000083327	chrX	Vcp-rs	1.04E+08	1.04E+08	2406	-0.06284	5.035116	0.664812	0.756339	0.022636	0	450	362	856	513	558	483	665	535	776	480
ENSMUSG00000048856	chr12	Slc25a47	1.09E+08	1.09E+08	1579	-0.11133	1.964488	0.664969	0.756388	0.053469	0	50	26	76	71	103	46	79	73	84	54
ENSMUSG00000074771	chr2	Ankef1	1.37E+08	1.37E+08	7185	-0.27505	0.625614	0.664968	0.756388	0.397388	0	39	36	19	6	17	21	9	67	10	9
ENSMUSG00000063060	chr14	Sox7	63943674	63943993	3298	-0.11418	2.511223	0.665235	0.756625	0.067331	0	63	37	119	135	128	65	101	93	166	76
ENSMUSG00000062270	chr9	Morf4l1	90091665	90092402	9754	0.068944	7.298113	0.665303	0.756638	0.029747	0	2190	2052	3226	2156	2606	2471	3891	2306	3746	2459
ENSMUSG00000000346	chr15	Dazap2	1.01E+08	1.01E+08	1826	0.06508	6.313358	0.665436	0.756725	0.02596	0	976	939	1598	1360	1364	1133	1786	1308	1962	1303
ENSMUSG00000038175	chr13	Mylip	45389742	45390043	3062	-0.06676	4.236438	0.665517	0.756752	0.024944	0	270	234	438	258	352	222	382	376	381	314
ENSMUSG00000031639	chr8	Tlr3	45395665	45397141	4396	0.131008	1.280309	0.665578	0.756756	0.087454	0	17	25	50	40	50	24	42	66	35	50
ENSMUSG00000055067	chr1	Smyd3	1.79E+08	1.79E+08	9184	-0.08212	2.955024	0.666003	0.757175	0.031707	0	113	87	198	90	158	95	155	130	179	125
ENSMUSG00000102976	chr1	Zc3h11a	1.34E+08	1.34E+08	6031	-0.06882	6.946613	0.666215	0.757351	0.02995	0	1944	1504	3199	1468	2154	1753	2674	2044	2719	1868
ENSMUSG00000044006	chr8	Cilp2	69880369	69883208	4314	0.186063	2.8161	0.666444	0.757481	0.2177	0	19	31	144	142	232	98	115	127	81	216
ENSMUSG00000059981	chr7	Taok2	1.27E+08	1.27E+08	9247	0.061778	4.80713	0.666434	0.757481	0.022763	0	338	275	648	461	523	377	588	540	656	456
ENSMUSG00000031231	chrX	Cox7b	1.06E+08	1.06E+08	1214	-0.08534	8.298244	0.666756	0.75777	0.046923	0	4220	3573	5097	6836	5976	4467	9308	3980	6669	4213
ENSMUSG00000061759	chr10	1700052N19Rik	4432467	4432711	8243	-0.0691	4.608715	0.667338	0.758368	0.028932	0	347	321	595	339	405	343	687	383	449	336
ENSMUSG00000042225	chrX	Ammecr1	1.43E+08	1.43E+08	5437	0.090366	2.138805	0.667419	0.758395	0.045735	0	43	40	126	55	86	67	86	68	121	66
ENSMUSG00000019878	chr10	Hsf2	57486385	57486601	2613	0.067723	4.629474	0.667637	0.758512	0.025952	0	328	271	559	393	402	285	587	395	641	440
ENSMUSG00000044424	chr19	Gm9493	23619742	23620320	579	0.145384	0.853711	0.667615	0.758512	0.059713	0	22	25	26	24	30	20	43	29	30	40
ENSMUSG00000002997	chr12	Prkar2b	31958476	31960522	3652	0.256177	3.44158	0.668161	0.759042	0.407929	0	275	202	103	43	71	143	69	607	85	112
ENSMUSG00000030551	chr7	Nr2f2	70351946	70354931	4863	0.076252	4.110496	0.668244	0.759072	0.03403	0	195	210	435	213	320	205	300	351	443	315
ENSMUSG00000025218	chr19	Poll	45552275	45553170	2324	-0.06433	4.428255	0.668452	0.759243	0.023265	0	326	218	429	364	434	304	412	372	480	345
ENSMUSG00000040688	chr17	Tbl3	24697949	24700785	5686	-0.06317	4.368027	0.668758	0.759525	0.022848	0	289	215	445	363	393	278	436	315	514	316
ENSMUSG00000032384	chr9	Csnk1g1	65908974	65909168	11973	0.07824	2.877039	0.668995	0.759665	0.031663	0	94	76	149	121	130	99	154	167	146	112
ENSMUSG00000075324	chr2	Fign	63971507	63980899	9969	-0.11229	1.525052	0.668964	0.759665	0.051179	0	30	38	78	31	60	34	47	58	66	39
ENSMUSG00000028995	chr5	Fam126a	23915276	23915537	7107	0.090109	2.9054	0.66975	0.760457	0.045893	0	75	54	159	145	162	90	178	155	160	119
ENSMUSG00000028088	chr3	Fmo5	97628804	97628901	5675	0.086485	3.450074	0.66984	0.760489	0.040694	0	133	141	220	157	190	125	283	229	168	211
ENSMUSG00000066877	chr1	Nck2	43444579	43444706	4321	-0.06578	4.18796	0.669893	0.760489	0.025406	0	296	228	437	233	298	251	420	304	369	282
ENSMUSG00000019842	chr10	Traf3ip2	39612934	39613346	3687	0.093166	1.988305	0.669963	0.760503	0.041976	0	54	38	94	50	70	67	70	80	100	47
ENSMUSG00000008859	chr13	Rala	17880575	17882501	2684	-0.06796	5.179659	0.670111	0.760541	0.029442	0	529	536	725	520	604	599	836	581	714	495
ENSMUSG00000038637	chr7	Lrrc56	1.41E+08	1.41E+08	6068	0.122753	1.212758	0.670089	0.760541	0.050638	0	34	23	37	40	34	36	36	51	55	31
ENSMUSG00000031913	chr8	Vps4a	1.07E+08	1.07E+08	2522	0.063273	6.373151	0.670419	0.76063	0.025237	0	1147	1011	1721	1229	1377	1265	1945	1406	1995	1203
ENSMUSG00000040720	chr4	1110037F02Rik	11485958	11486105	7138	-0.07032	4.015251	0.670395	0.76063	0.025802	0	192	185	441	240	302	236	359	281	285	264
ENSMUSG00000047632	chr19	Fgfbp3	36917550	36919277	1772	-0.15294	0.27993	0.670403	0.76063	0.072916	0	21	18	21	12	20	16	15	13	28	23
ENSMUSG00000061013	chr18	Mkx	6910459	6910633	3925	-0.2057	0.248055	0.670311	0.76063	0.149206	0	6	11	27	15	38	8	29	21	8	24
ENSMUSG00000024953	chr19	Prdx5	6906697	6907127	2139	0.078485	7.30399	0.670553	0.760717	0.040161	0	1787	1697	2469	3329	2975	2341	3548	2484	4261	2412

ENSMUSG00000022120	chr14	Rnf219	1.04E+08	1.04E+08	3456	0.119061	1.915918	0.670612	0.760719	0.059761	0	50	56	69	43	59	41	111	63	61	75
ENSMUSG00000084819	chr11	Gm11967	5915315	5915396	480	-0.15693	0.522419	0.670703	0.760757	0.114556	0	23	18	29	21	20	23	28	11	50	7
ENSMUSG00000031788	chr8	Kifc3	95099832	95100452	3758	0.077761	3.506487	0.671046	0.761081	0.032101	0	145	108	201	184	252	134	277	183	303	183
ENSMUSG00000020167	chr10	Tcf3	80409514	80410274	4039	0.065294	3.761938	0.671198	0.761188	0.022302	0	161	150	294	228	235	185	297	255	326	206
ENSMUSG00000042524	chr15	Sun2	79724070	79725560	4969	0.068422	7.42946	0.671592	0.76157	0.030973	0	2420	1454	4124	2763	3160	2582	3535	2762	4498	2847
ENSMUSG00000090996	chr2	Gm20458	1.64E+08	1.64E+08	1369	0.066488	4.862552	0.671698	0.761625	0.025573	0	375	362	488	494	524	442	681	483	665	455
ENSMUSG00000030722	chr7	Nfatc2ip	1.26E+08	1.26E+08	3388	-0.0988	1.830499	0.672126	0.762045	0.042209	0	41	46	80	60	61	44	72	43	78	68
ENSMUSG00000020153	chr10	Ndufs7	80249121	80249204	1718	0.080336	8.007162	0.672311	0.76216	0.042897	0	3197	2240	3977	5409	5355	3597	5926	4084	7024	3976
ENSMUSG00000024900	chr19	Cpt1a	3323301	3323374	4300	0.077885	3.527919	0.672342	0.76216	0.029883	0	159	155	215	164	187	160	278	245	233	162
ENSMUSG00000046032	chrX	Snx12	1.01E+08	1.01E+08	2953	-0.0671	4.721695	0.672497	0.76227	0.026284	0	337	242	580	512	537	373	514	461	595	407
ENSMUSG00000011306	chr8	Sugp1	70042813	70043080	2287	-0.06301	4.411673	0.672948	0.762717	0.023905	0	281	264	462	371	361	287	440	319	486	368
ENSMUSG00000021391	chr13	Cenpp	49464027	49464337	1101	-0.16819	0.153132	0.67323	0.762971	0.095162	0	27	14	18	12	12	21	16	18	17	13
ENSMUSG00000099843	chr1	Gm7160	1.06E+08	1.06E+08	1417	0.169882	0.344137	0.673334	0.763024	0.067252	0	20	18	18	15	14	19	18	22	35	18
ENSMUSG00000020720	chr11	Psmd12	1.07E+08	1.07E+08	2649	0.069456	6.797538	0.673461	0.763101	0.031369	0	1494	1604	2176	1617	1633	1710	2659	1831	2657	1653
ENSMUSG00000033739	chr17	Fkbpl	34644764	34644953	1336	0.103107	2.191	0.673518	0.763101	0.043841	0	65	63	85	68	57	66	87	93	113	64
ENSMUSG00000019889	chr10	Ptprk	28074820	28075177	6177	-0.1413	2.469025	0.673868	0.763406	0.113964	0	39	34	83	150	167	66	132	65	126	90
ENSMUSG00000041199	chr17	Rpusd1	25727751	25727847	1703	0.091041	2.324538	0.673902	0.763406	0.039321	0	86	47	92	65	91	83	97	88	100	88
ENSMUSG00000028550	chr4	Atg4c	99193934	99194452	3351	-0.0807	2.956994	0.674059	0.763519	0.031304	0	110	86	190	127	127	115	180	129	125	127
ENSMUSG00000022544	chr16	Fam86	5244152	5245385	2649	-0.06961	3.469648	0.674416	0.763811	0.028553	0	191	122	250	164	177	147	273	178	245	151
ENSMUSG00000052713	chr18	Zfp608	54888045	54889081	6112	-0.12317	1.763968	0.674432	0.763811	0.071922	0	31	26	71	61	97	36	97	42	76	45
ENSMUSG00000027523	chr2	Gnas	1.74E+08	1.74E+08	11186	0.062401	10.02045	0.674996	0.764385	0.026489	0	13912	10706	22092	17323	18496	14226	24057	17446	25057	17239
ENSMUSG00000002660	chr17	Clpp	56990264	56990513	1207	0.064718	4.918289	0.675339	0.764707	0.025718	0	371	313	529	555	606	429	706	515	725	471
ENSMUSG00000023723	chr11	Mrps23	88204388	88204485	1560	0.071441	6.337039	0.675444	0.764725	0.033387	0	1127	952	1307	1437	1390	1244	1876	1184	2162	1211
ENSMUSG00000064208	chr10	Gm10145	27936364	27936828	465	-0.13523	0.200887	0.67547	0.764725	0.06174	0	9	19	24	19	16	17	25	17	21	11
ENSMUSG00000041438	chr8	Cirh1a	1.07E+08	1.07E+08	2248	-0.06174	4.48984	0.675607	0.764816	0.023687	0	365	256	471	359	378	352	484	367	508	300
ENSMUSG00000019961	chr10	Tmpo	91147571	91149758	6478	-0.06714	5.496389	0.675785	0.764951	0.028889	0	729	519	1172	586	746	767	865	744	966	650
ENSMUSG00000074811	chr19	Hps6	46003478	46006173	2696	0.086107	2.145591	0.675842	0.764951	0.033786	0	56	51	93	69	68	64	89	72	92	86
ENSMUSG00000028385	chr4	Snx30	59805840	59806225	7795	-0.09979	2.683973	0.676232	0.765327	0.048932	0	69	66	185	96	131	75	141	93	106	138
ENSMUSG00000022793	chr16	B4galt4	38742264	38742368	3032	0.10976	1.975344	0.676392	0.765377	0.063756	0	31	39	64	82	82	60	110	77	65	52
ENSMUSG00000051232	chr11	Tmem199	78507055	78507805	1902	0.072284	3.710294	0.676359	0.765377	0.027396	0	189	161	267	165	233	209	329	196	321	178
ENSMUSG00000038759	chr6	Nup205	35177430	35177659	6406	-0.07724	3.500376	0.676615	0.765565	0.031319	0	136	133	291	181	202	200	223	214	202	146
ENSMUSG00000000435	chr10	Myf5	1.07E+08	1.07E+08	2083	-0.16653	0.33968	0.676684	0.765577	0.099305	0	7	20	33	23	16	13	19	31	26	11
ENSMUSG00000103041	chr3	RP24-372I24.4	65957758	65962036	4279	-0.13537	0.449605	0.676808	0.765652	0.056289	0	26	14	29	13	24	22	29	16	23	19
ENSMUSG00000025059	chrX	Gyk	85701937	85704396	7743	-0.18964	0.330423	0.67696	0.765759	0.173402	0	7	5	16	35	38	8	20	15	29	26
ENSMUSG00000062861	chr7	Zfp28	6383318	6383601	4142	-0.10734	1.609635	0.67702	0.765762	0.055303	0	25	49	73	49	50	48	50	43	71	46
ENSMUSG00000005312	chr13	Ubqln1	58176156	58178028	3686	0.060845	5.927579	0.677215	0.765851	0.024327	0	795	691	1451	893	1016	835	1282	1103	1519	979
ENSMUSG00000026277	chr1	Stk25	93619751	93622526	5812	-0.05995	6.318902	0.677222	0.765851	0.024005	0	1164	934	1796	1209	1480	1161	1630	1283	1832	1252
ENSMUSG00000044986	chr15	Tst	78399556	78400030	1096	-0.10679	4.558546	0.677272	0.765851	0.075283	0	386	293	501	384	371	381	283	679	491	199
ENSMUSG00000079036	chr12	Alkbh1	87425840	87429437	6574	0.077384	2.600756	0.677405	0.765936	0.031627	0	82	64	145	76	107	104	144	101	116	92
ENSMUSG00000040875	chr9	Osbpl10	1.15E+08	1.15E+08	5139	-0.10677	1.623288	0.677578	0.766066	0.046289	0	50	35	61	33	70	46	49	54	71	41
ENSMUSG00000020178	chr10	Adora2a	75316943	75317147	2534	-0.12187	0.50996	0.677708	0.766147	0.049887	0	22	15	20	25	27	15	24	27	28	21
ENSMUSG00000066554	chr5	Gm10167	1.48E+08	1.48E+08	1479	-0.1479	0.248032	0.678212	0.766652	0.059835	0	13	7	29	18	27	14	30	14	25	12
ENSMUSG00000063145	chr2	Bbs5	69647171	69647342	2445	-0.09695	1.607511	0.67833	0.76672	0.04043	0	52	31	71	49	42	46	66	42	66	41
ENSMUSG00000070699	chr7	Sars2	28741968	28742282	1910	-0.06759	3.888133	0.678519	0.766869	0.026219	0	212	142	314	270	286	209	348	203	316	245
ENSMUSG00000090035	chr10	Galnt4	99108159	99113247	5089	0.094783	2.019603	0.678708	0.767017	0.037593	0	47	43	68	68	81	54	100	82	78	60
ENSMUSG00000008307	chr5	1700109H08Rik	3571566	3571810	880	0.170464	-0.1224	0.678866	0.767065	0.083948	0	11	5	27	10	10	12	13	20	24	9
ENSMUSG00000100017	chr14	2410022M11Rik	56811953	56815597	3645	0.132221	0.620773	0.678836	0.767065	0.059997	0	19	14	25	19	33	25	31	27	43	12
ENSMUSG00000075327	chr10	Zbtb2	4367074	4369851	3338	0.082748	2.415477	0.679124	0.76729	0.03196	0	72	54	129	74	86	69	136	99	106	85
ENSMUSG00000047496	chr1	Rnf152	1.05E+08	1.05E+08	8532	-0.13804	0.106581	0.679466	0.767612	0.047364	0	14	12	21	12	23	11	19	16	20	18
ENSMUSG00000052906	chr8	Ubxn8	33619586	33621700	2817	-0.08664	2.360594	0.679661	0.767766	0.043124	0	75	80	110	54	93	67	105	97	105	73
ENSMUSG00000032198	chr9	Dock6	21800184	21800399	6556	-0.08829	3.557466	0.679837	0.767774	0.04254	0	135	81	290	207	303	165	252	210	230	177
ENSMUSG00000042272	chr2	Sestd1	77180340	77187260	9857	0.064691	3.666678	0.679841	0.767774	0.023927	0	146	147	313	179	224	182	299	239	281	185
ENSMUSG00000055254	chr13	Ntrk2	58806596	58806852	13806	-0.12839	3.51601	0.679815	0.767774	0.10769	0	204	180	321	67	178	164	167	322	183	134
ENSMUSG00000053080	chr19	2700081O15Rik	7417625	7417917	7032	-0.08472	3.023391	0.680322	0.768251	0.036534	0	95	85	186	144	167	115	122	160	164	140
ENSMUSG00000017264	chr4	Exosc10	1.49E+08	1.49E+08	3594	-0.0604	4.34746	0.680474	0.768358	0.022575	0	250	252	449	346	374	313	476	299	436	299
ENSMUSG00000006763	chr7	Saal1	46686108	46689455	8108	0.099814	2.331062	0.680594	0.768427	0.041169	0	69	73	93	62	78	64	123	105	108	70
ENSMUSG00000061535	chr5	C1qtnf7	43515569	43515986	4136	0.185665	0.801844	0.681015	0.768837	0.189498	0	4	19	25	38	38	14	50	33	16	44
ENSMUSG00000026229	chr1	Psmd1	86064387	86064805	7265	-0.06532	7.721299	0.681257	0.769046	0.03012	0	3010	2982	5032	2823	3419	3172	4601	3448	4893	2894
ENSMUSG00000031097	chr7	Tnni2	1.42E+08	1.42E+08	1497	-0.08048	13.42728	0.681436	0.769182	0.046058	0	192942	165794	212134	134316	176089	184788	234099	155007	279667	136191
ENSMUSG00000020022	chr10	Ndufa12	94198955	94199130	1334	-0.07078	7.409689	0.681663	0.769341	0.035506	0	2620	2075	2870	3089	3067	2618	4185	2390	4007	2208
ENSMUSG00000068706	chr15	Gm10250	5120602	5121172	571	-0.07229	4.538549	0.681693	0.769341	0.035584	0	297	273	374	507	428	324	534	337	583	321
ENSMUSG00000054855	chr15	Rnd1	98663421	98663890	2967	0.158192	1.145696	0.68199	0.76961	0.10848	0	30	35	51	16	25	29	82	37	44	18
ENSMUSG00000029647	chr5	Pan3	1.47E+08	1.47E+08	7316	0.078197	3.290618	0.682243	0.769765	0.033198	0	155	113	196	125	164	150	208	220	190	136
ENSMUSG00000036352	chr2	Ubac1	25998543	25999067	2632	0.062651	7.879964	0.682235	0.769765	0.02766	0	3600	2657	4979	3423	3830	3569	5203	3656	6088	3700
ENSMUSG00000026155	chr1	Smap1	23844846	23845357	3575	-0.05874	4.119086	0.682437	0.769918	0.019884	0	236	199	387	278	329	260	360	291	359	273

ENSMUSG00000020648	chr12	Dus4l	31640055	31640944	1768	-0.10525	1.865786	0.682603	0.770037	0.057288	0	60	32	69	69	65	34	103	53	61	65
ENSMUSG00000024096	chr17	Ralbp1	65848433	65850195	4335	-0.06143	5.038772	0.682658	0.770037	0.024463	0	384	377	745	573	652	483	607	549	814	489
ENSMUSG00000079481	chrX	Nhsl2	1.02E+08	1.02E+08	16952	0.09138	1.849089	0.683153	0.77053	0.045544	0	31	38	88	50	73	46	64	77	88	55
ENSMUSG00000025728	chr17	Pigq	25926427	25926515	5769	0.063183	4.66476	0.683532	0.770891	0.026592	0	330	225	550	450	471	354	510	518	620	372
ENSMUSG00000059482	chr4	2610301B20Rik	10874498	10874772	2391	-0.08671	2.297858	0.683902	0.771243	0.044759	0	71	78	116	58	71	70	108	68	112	72
ENSMUSG00000033722	chr1	BC034090	1.55E+08	1.55E+08	8222	0.12829	0.541636	0.684044	0.771338	0.072747	0	17	16	26	15	30	31	16	30	29	19
ENSMUSG00000024866	chr19	Acy3	3986661	3987305	1505	0.142563	0.87554	0.684146	0.771387	0.068079	0	26	22	35	27	20	17	29	46	46	28
ENSMUSG00000028179	chr3	Cth	1.58E+08	1.58E+08	2263	0.122382	1.24337	0.684257	0.771447	0.06763	0	25	17	41	55	37	26	53	48	41	46
ENSMUSG00000020228	chr10	Helb	1.2E+08	1.2E+08	5011	0.084132	2.4377	0.684398	0.771474	0.043919	0	63	45	116	71	133	82	150	97	103	72
ENSMUSG00000055436	chr3	Srsf11	1.58E+08	1.58E+08	7135	-0.06208	5.010705	0.684371	0.771474	0.02546	0	453	377	768	432	649	381	665	638	658	538
ENSMUSG00000020023	chr10	Tmcc3	94311949	94312202	7153	-0.06359	4.93755	0.684793	0.771855	0.02671	0	399	330	720	480	632	324	685	550	641	553
ENSMUSG00000030254	chr6	Rad18	1.13E+08	1.13E+08	5796	0.12785	0.354298	0.685035	0.772061	0.049237	0	18	11	22	15	24	22	28	23	18	19
ENSMUSG00000101841	chr11	Gm11993	9149778	9150597	820	-0.14444	0.319962	0.685195	0.772176	0.078947	0	16	23	22	15	18	26	23	12	22	15
ENSMUSG00000027460	chr2	Angpt4	1.52E+08	1.52E+08	2335	-0.21985	-0.32066	0.685438	0.772384	0.189155	0	4	15	21	8	13	19	5	17	5	9
ENSMUSG00000033191	chr4	Tie1	1.18E+08	1.18E+08	4917	0.081378	4.699815	0.685573	0.772471	0.0462	0	267	195	447	548	617	345	650	410	638	429
ENSMUSG00000006920	chr11	Ezh1	1.01E+08	1.01E+08	7440	0.055316	5.490047	0.686206	0.7728	0.02135	0	600	450	1066	685	809	697	981	756	1040	714
ENSMUSG00000018678	chr11	Sp2	96953340	96954570	3415	-0.06727	3.585515	0.686234	0.7728	0.026328	0	140	157	300	165	232	157	261	200	243	203
ENSMUSG00000029480	chr5	Dhx37	1.25E+08	1.25E+08	4139	-0.08277	2.875463	0.686168	0.7728	0.03382	0	104	66	178	128	135	103	123	146	155	111
ENSMUSG00000032121	chr9	Tmem218	37208333	37208405	1019	0.102112	2.296933	0.685954	0.7728	0.05515	0	63	54	60	101	86	71	118	71	99	95
ENSMUSG00000038233	chr9	Fam198a	1.22E+08	1.22E+08	3622	0.132784	0.255571	0.686205	0.7728	0.094237	0	9	13	33	9	22	14	17	32	17	21
ENSMUSG00000048482	chr2	Bdnf	1.1E+08	1.1E+08	6217	-0.24631	-0.31743	0.685987	0.7728	0.288882	0	1	4	6	25	25	4	25	6	11	13
ENSMUSG00000061062	chr17	Gm10093	78491565	78493541	1977	0.157397	0.194901	0.686273	0.7728	0.070524	0	12	17	13	12	23	23	24	15	23	14
ENSMUSG00000047635	chr5	2810006K23Rik	1.24E+08	1.24E+08	2873	-0.0717	3.06515	0.687615	0.774245	0.029527	0	118	101	167	154	136	122	189	123	164	138
ENSMUSG00000048997	chr3	Atxn7l2	1.08E+08	1.08E+08	4817	-0.0795	2.883533	0.68805	0.77467	0.033981	0	125	68	188	101	131	103	140	128	179	101
ENSMUSG00000015839	chr2	Nfe2l2	75675513	75677184	3796	-0.05952	5.263122	0.688138	0.774703	0.02464	0	500	463	980	546	711	490	1000	673	767	550
ENSMUSG00000005198	chr11	Polr2a	69733997	69735566	7067	-0.07232	5.929599	0.688292	0.774714	0.036801	0	757	541	1797	793	1415	753	1171	1092	1463	983
ENSMUSG00000026189	chr1	Pecr	72259167	72259433	1516	0.084947	4.090968	0.688334	0.774714	0.044064	0	262	280	304	209	208	263	387	306	406	243
ENSMUSG00000026970	chr2	Rbms1	60750193	60752982	5473	0.063618	4.776194	0.688428	0.774714	0.027901	0	271	306	605	434	578	341	621	548	603	455
ENSMUSG00000049659	chr11	Aftph	20685084	20686198	6979	0.059379	4.634124	0.68844	0.774714	0.023103	0	358	284	527	376	401	385	496	492	520	397
ENSMUSG00000071256	chr17	Zfp213	23556769	23558312	2672	0.088351	2.137695	0.688258	0.774714	0.043302	0	68	47	81	60	77	59	72	90	89	88
ENSMUSG00000004056	chr7	Akt2	27591552	27591879	7131	-0.05939	8.195814	0.688777	0.775028	0.02616	0	4664	3215	6558	4535	5195	4165	6382	4625	6877	4432
ENSMUSG00000022231	chr15	Sema5a	32244813	32245299	10809	0.079971	2.182167	0.689033	0.77525	0.040683	0	57	47	121	50	81	73	86	68	103	83
ENSMUSG00000021756	chr13	Il6st	1.12E+08	1.12E+08	11099	-0.06092	7.330721	0.689309	0.775494	0.027286	0	2023	1685	4215	2554	3136	2080	3874	2779	3496	2367
ENSMUSG00000028982	chr4	Slc25a33	1.5E+08	1.5E+08	1887	-0.07236	4.023531	0.689367	0.775494	0.036049	0	207	212	282	330	277	254	295	220	412	260
ENSMUSG00000073755	chr4	5730409E04Rik	1.27E+08	1.27E+08	2891	0.063905	5.243674	0.689504	0.775582	0.02736	0	577	496	771	494	592	591	831	642	962	537
ENSMUSG00000018378	chr11	Cuedc1	88098058	88098128	5779	-0.06235	7.466354	0.689713	0.775751	0.028735	0	2550	1697	3933	3084	3507	2299	3473	3431	3968	2698
ENSMUSG00000018931	chr11	Natd1	60902246	60906121	4247	-0.06563	3.823589	0.690356	0.776409	0.026866	0	242	141	302	226	248	199	290	280	275	208
ENSMUSG00000053716	chr9	Dusp7	1.06E+08	1.06E+08	3356	-0.10482	4.391006	0.690486	0.776489	0.076858	0	173	135	459	503	560	234	497	477	396	259
ENSMUSG00000060073	chr12	Psma3	70974621	70974767	3894	-0.07131	7.071654	0.690802	0.776779	0.038384	0	2095	2104	2847	1771	1960	2000	3320	1973	2976	1874
ENSMUSG00000006998	chr16	Psmd2	20651652	20651851	4038	-0.06283	8.262231	0.691368	0.777349	0.029885	0	4134	4203	7251	4554	5034	4297	6080	5022	7948	4422
ENSMUSG00000027661	chr2	Slc2a10	1.66E+08	1.66E+08	3570	0.117943	0.816515	0.691717	0.777675	0.064499	0	13	14	34	24	46	19	37	27	48	28
ENSMUSG00000090946	chr12	Ccdc71l	32378704	32382943	4240	-0.07352	3.174159	0.69191	0.777827	0.036002	0	148	116	213	115	142	109	222	181	188	108
ENSMUSG00000025037	chrX	Maoa	16619698	16619913	4167	0.079387	3.975324	0.692057	0.777926	0.040077	0	251	218	368	149	225	219	393	295	356	223
ENSMUSG00000039253	chr11	Fn3krp	1.21E+08	1.21E+08	2520	0.086614	2.445949	0.692143	0.777957	0.037833	0	63	71	113	72	98	67	111	91	119	113
ENSMUSG00000030629	chr7	Zfand6	84615054	84615968	1668	0.060827	6.483132	0.692399	0.778178	0.02706	0	1257	1180	1868	1203	1461	1258	1972	1537	2137	1490
ENSMUSG00000035184	chr14	Fam124a	62555737	62555914	4406	0.083235	2.156616	0.692532	0.778262	0.049346	0	41	38	125	63	89	64	84	82	84	89
ENSMUSG00000024142	chr17	Mlst8	24473550	24475951	3366	-0.06241	4.07455	0.692593	0.778265	0.023936	0	243	158	370	300	325	252	363	312	329	240
ENSMUSG00000031534	chr8	Smim19	22462615	22463375	1458	0.062322	5.251186	0.6928	0.778432	0.026961	0	553	439	687	660	608	613	838	569	924	615
ENSMUSG00000024066	chr17	Xdh	73883908	73884483	4587	0.072961	4.822158	0.692926	0.778508	0.040106	0	298	241	705	498	557	488	671	628	485	352
ENSMUSG00000013973	chr1	Dedd	1.71E+08	1.71E+08	5861	0.060193	5.160524	0.693021	0.778548	0.025654	0	517	373	763	561	611	622	743	601	911	467
ENSMUSG00000014551	chr6	Mrps25	92169525	92175208	6576	0.069985	4.80467	0.69326	0.77875	0.032581	0	413	374	468	452	413	472	680	444	661	373
ENSMUSG00000048186	chr2	Bend7	4717831	4718292	4194	-0.16482	0.409147	0.693396	0.778837	0.108727	0	9	6	40	28	26	18	40	16	20	12
ENSMUSG00000021244	chr12	Ylpm1	84996321	84997356	9914	-0.06403	4.012344	0.693533	0.778926	0.024553	0	176	175	423	258	327	226	331	296	339	243
ENSMUSG00000080893	chr5	Gm15920	1.3E+08	1.3E+08	402	-0.07336	3.15403	0.693724	0.779074	0.035425	0	116	103	163	167	174	136	206	128	230	99
ENSMUSG00000097908	chr5	4933404O12Rik	1.37E+08	1.37E+08	4101	0.128665	1.10232	0.694624	0.780018	0.063331	0	31	29	36	22	36	21	48	53	35	37
ENSMUSG00000063320	chr10	1190007I07Rik	82619851	82620217	1197	-0.06729	3.603424	0.694742	0.780085	0.030533	0	201	129	226	227	198	179	284	177	247	192
ENSMUSG00000041716	chr12	Gm20604	1.03E+08	1.03E+08	2795	-0.07074	3.362753	0.694899	0.780195	0.036706	0	129	135	179	196	188	113	281	168	208	156
ENSMUSG00000018239	chr11	Zcchc10	53324679	53324741	1391	0.098236	2.668005	0.695249	0.780456	0.050343	0	97	90	96	70	119	85	170	103	172	77
ENSMUSG00000037813	chr2	D630003M21Rik	1.58E+08	1.58E+08	5104	-0.16375	0.956223	0.695193	0.780456	0.121222	0	17	10	40	51	43	18	27	27	33	49
ENSMUSG00000045795	chr7	Whamm	81571292	81571909	3069	-0.06715	3.577356	0.695355	0.780509	0.030401	0	191	159	292	151	178	179	250	187	262	180
ENSMUSG00000009894	chr11	Snap47	59407134	59407810	2651	-0.07174	4.632244	0.695695	0.780762	0.036808	0	303	212	464	531	561	296	615	407	531	387
ENSMUSG00000026798	chr2	Coq4	29787493	29788357	3399	0.080291	3.013208	0.695757	0.780762	0.039334	0	114	75	125	164	139	131	160	140	192	124
ENSMUSG00000037773	chr2	Pced1a	1.3E+08	1.3E+08	5072	-0.08253	2.628186	0.695716	0.780762	0.035457	0	106	56	157	85	108	89	121	105	119	102
ENSMUSG00000026923	chr2	Notch1	26457903	26460976	14232	-0.08321	3.459265	0.695843	0.780792	0.042942	0	128	76	257	196	286	147	232	201	219	169
ENSMUSG00000000538	chr11	Tom1l2	60226714	60230241	8764	0.070407	7.101547	0.696146	0.781066	0.038638	0	1713	996	2996	2595	2839	1942	3026	2209	3782	2105

ENSMUSG00000006641	chr5	Slc5a6	31036036	31036953	3991	0.079997	3.319418	0.696569	0.781409	0.046115	0	150	77	188	175	191	146	164	227	182	188
ENSMUSG00000020331	chr10	Hcn2	79716634	79717219	3195	0.118405	0.74425	0.696538	0.781409	0.05678	0	23	9	30	31	29	23	33	22	41	30
ENSMUSG00000028672	chr4	Hmgcl	1.36E+08	1.36E+08	2434	0.064659	5.347579	0.696828	0.781634	0.030263	0	517	467	628	771	764	618	972	642	944	648
ENSMUSG00000022023	chr14	Wbp4	79459937	79462129	3452	-0.05289	4.825275	0.696922	0.781673	0.020223	0	402	337	626	432	527	382	644	491	633	411
ENSMUSG00000091586	chr17	Cyp4f17	32506462	32506578	1693	-0.12739	0.980774	0.697108	0.781815	0.048976	0	33	15	46	30	35	29	40	35	27	30
ENSMUSG00000024603	chr18	Dctn4	60526221	60526365	3714	-0.05517	5.092825	0.697533	0.782225	0.021689	0	459	390	723	583	647	534	687	562	717	536
ENSMUSG00000043432	chr7	Leng9	4147915	4150374	2460	-0.07351	1.852724	0.697906	0.782577	0.031658	0	53	39	70	61	66	45	76	60	83	51
ENSMUSG00000025521	chr8	Tmem192	64947185	64947333	1123	0.068112	3.969232	0.698415	0.783082	0.028119	0	246	191	294	227	245	220	347	288	418	206
ENSMUSG00000031093	chrX	Dock11	35888832	35889032	9240	0.090939	2.631128	0.698688	0.783296	0.054672	0	63	79	134	87	115	103	141	146	76	96
ENSMUSG00000097729	chr12	2310015A10Rik	80120548	80125126	4843	0.075431	3.968459	0.698724	0.783296	0.039013	0	218	150	262	292	292	266	364	194	446	213
ENSMUSG00000021266	chr12	Wars	1.09E+08	1.09E+08	3447	-0.05643	5.241106	0.698806	0.783322	0.022746	0	504	370	834	636	812	539	833	648	770	595
ENSMUSG00000019809	chr10	Pex3	13523842	13523943	4740	-0.06644	3.396955	0.69888	0.783338	0.030461	0	171	142	202	133	198	153	225	193	203	155
ENSMUSG00000098789	chr2	Jmjd7	1.2E+08	1.2E+08	1960	0.112116	1.108104	0.699135	0.783558	0.051818	0	26	23	36	31	42	45	49	24	45	30
ENSMUSG00000030327	chr6	Necap1	1.23E+08	1.23E+08	2386	0.061578	3.848581	0.699252	0.783624	0.024751	0	220	148	339	201	230	200	366	264	296	220
ENSMUSG00000069206	chr13	Zfp874a	67424549	67426365	5263	-0.07849	2.654615	0.699602	0.783949	0.03195	0	83	69	158	99	111	98	152	94	107	98
ENSMUSG00000036158	chr15	Prickle1	93499114	93501303	4345	-0.08036	2.559221	0.699672	0.783962	0.033779	0	75	59	140	93	122	79	107	84	153	95
ENSMUSG00000059013	chr2	Sh2d3c	32721055	32721195	5233	0.083245	2.492876	0.699865	0.784112	0.045851	0	69	39	102	95	137	85	125	90	142	82
ENSMUSG00000031250	chrX	Tnmd	1.34E+08	1.34E+08	1353	0.133325	3.438114	0.699936	0.784125	0.138157	0	42	121	214	220	251	183	286	179	90	253
ENSMUSG00000085095	chr7	Gm15635	99661439	99661661	1056	0.167946	0.829924	0.700147	0.784294	0.130823	0	30	27	34	12	19	14	70	20	31	32
ENSMUSG00000050627	chr9	Gpd1l	1.15E+08	1.15E+08	5077	-0.05507	5.261163	0.700212	0.784302	0.021832	0	477	407	969	602	764	516	809	677	836	606
ENSMUSG00000020781	chr11	Tsen54	1.16E+08	1.16E+08	2458	-0.07002	2.972637	0.700601	0.78467	0.032836	0	115	94	160	121	147	101	138	147	212	101
ENSMUSG00000015363	chr15	Trabd	89075124	89075214	5591	0.059573	5.320365	0.700712	0.784728	0.026619	0	545	377	731	727	776	572	903	700	1027	570
ENSMUSG00000032485	chr9	Scap	1.1E+08	1.1E+08	4275	-0.06643	4.293536	0.701567	0.78562	0.029897	0	225	164	458	371	444	262	421	327	450	298
ENSMUSG00000030880	chr7	Polr3e	1.21E+08	1.21E+08	4234	-0.06367	3.631267	0.702135	0.78619	0.028349	0	175	174	250	177	222	174	234	242	237	201
ENSMUSG00000052676	chrX	Zmat1	1.35E+08	1.35E+08	5391	0.132827	0.288219	0.702214	0.786212	0.071304	0	18	6	19	18	25	14	26	17	20	28
ENSMUSG00000053581	chr5	Zfand2a	1.39E+08	1.39E+08	3407	-0.06941	3.665961	0.702335	0.78628	0.030689	0	173	112	290	215	273	201	263	245	269	148
ENSMUSG00000047719	chr4	Ubiad1	1.48E+08	1.48E+08	2992	-0.07301	3.655762	0.702401	0.786289	0.033369	0	175	100	298	237	249	187	265	178	252	226
ENSMUSG00000034432	chr1	Cops8	90602981	90603627	4448	-0.0574	6.720516	0.702514	0.786348	0.026753	0	1586	1385	2199	1636	1732	1570	2371	1629	2416	1534
ENSMUSG00000022111	chr14	Uchl3	1.02E+08	1.02E+08	929	-0.0646	4.214255	0.702696	0.786464	0.033732	0	289	287	334	276	280	279	439	327	380	236
ENSMUSG00000048406	chr4	B330016D10Rik	1.42E+08	1.42E+08	1701	-0.07344	2.903465	0.702736	0.786464	0.037123	0	117	100	156	115	112	119	135	102	190	112
ENSMUSG00000042699	chr1	Dhx9	1.53E+08	1.53E+08	9603	0.055296	5.49321	0.702816	0.786487	0.023067	0	564	579	1014	625	774	633	1057	850	952	713
ENSMUSG00000029655	chr5	N4bp2l2	1.51E+08	1.51E+08	12262	-0.06731	3.61445	0.702968	0.786524	0.02785	0	161	121	316	187	243	153	282	206	222	221
ENSMUSG00000039781	chr11	Cep131	1.2E+08	1.2E+08	3833	0.077743	2.612786	0.702935	0.786524	0.038806	0	72	67	142	97	98	98	109	84	144	123
ENSMUSG00000058793	chr2	Cds2	1.32E+08	1.32E+08	9125	-0.05547	5.536118	0.703122	0.786631	0.023794	0	559	504	1054	788	963	581	1037	854	1090	653
ENSMUSG00000034908	chr9	Sidt2	45937857	45939316	5135	-0.06198	5.859592	0.703192	0.786643	0.029776	0	658	544	1485	1058	1192	714	1246	1127	1265	877
ENSMUSG00000015112	chr6	Slc25a13	6041218	6042332	3122	-0.24244	-0.22788	0.703778	0.787216	0.28973	0	7	0	9	27	23	2	15	20	17	9
ENSMUSG00000027803	chr3	Wwtr1	57455649	57459110	4779	-0.05814	4.741421	0.703823	0.787216	0.024764	0	340	266	586	484	550	332	536	465	648	428
ENSMUSG00000026889	chr2	Rbm18	36116079	36117974	5740	0.053786	5.407146	0.703907	0.787244	0.021707	0	586	494	939	654	675	608	985	701	995	685
ENSMUSG00000039089	chr10	L3mbtl3	26274468	26276263	4651	0.071965	3.014708	0.703994	0.787274	0.036763	0	92	65	173	142	171	109	165	152	221	111
ENSMUSG00000034810	chr2	Scn7a	66673425	66676561	7338	-0.09421	3.41185	0.704255	0.787478	0.062965	0	111	148	347	114	187	150	184	266	212	116
ENSMUSG00000039065	chr15	Fam173b	31601852	31602149	5248	-0.06596	3.082449	0.704295	0.787478	0.026342	0	107	98	216	120	161	113	166	135	208	131
ENSMUSG00000027111	chr2	Itga6	71745616	71745650	9025	0.066764	4.089627	0.704384	0.787511	0.034484	0	185	132	351	310	396	220	433	296	391	267
ENSMUSG00000017670	chr2	Elmo2	1.65E+08	1.65E+08	6652	-0.06184	4.316109	0.704472	0.787543	0.025638	0	287	169	504	310	412	288	412	370	428	280
ENSMUSG00000069939	chr11	Gm12070	26786633	26787634	1002	-0.10675	1.390494	0.704878	0.78793	0.064131	0	46	20	60	50	35	28	68	31	68	33
ENSMUSG00000028789	chr4	Azin2	1.29E+08	1.29E+08	4024	0.084296	2.260221	0.705184	0.788206	0.036629	0	81	45	85	69	84	66	107	96	107	67
ENSMUSG00000024335	chr17	Brd2	34112023	34112708	7285	0.054699	6.510469	0.705284	0.788251	0.024049	0	1273	1045	2007	1350	1541	1375	2216	1554	2079	1341
ENSMUSG00000022335	chr15	Zfat	68083766	68084561	7321	-0.10987	1.657092	0.705617	0.788558	0.057533	0	49	20	89	48	58	33	60	56	56	61
ENSMUSG00000034880	chr8	Mrpl34	71464926	71465067	645	-0.07536	4.489404	0.705917	0.788826	0.045029	0	330	207	325	517	447	334	502	307	555	319
ENSMUSG00000030048	chr6	Gkn3	87383268	87383530	844	-0.15069	-0.10103	0.706014	0.788868	0.107452	0	8	14	25	12	11	6	21	25	13	7
ENSMUSG00000003948	chr11	Mmd	90187684	90188235	5386	0.146552	4.770343	0.706283	0.789051	0.173859	0	635	482	453	141	190	369	386	863	573	384
ENSMUSG00000021548	chr13	Ccnh	85189408	85189652	3105	0.058438	4.254857	0.706304	0.789051	0.022953	0	274	228	422	258	317	270	481	304	456	286
ENSMUSG00000022814	chr16	Umps	33954782	33956935	3484	-0.06589	2.965255	0.706357	0.789051	0.029725	0	120	96	153	124	135	96	165	150	151	126
ENSMUSG00000031107	chrX	Rbmx2	48695004	48695120	1872	0.144697	1.022791	0.706485	0.789128	0.082244	0	38	22	27	21	35	23	73	29	35	29
ENSMUSG00000038550	chr3	Ciart	95878503	95879149	2261	0.080187	2.467283	0.706806	0.78942	0.046249	0	61	50	156	66	110	82	105	85	165	79
ENSMUSG00000035958	chr13	Tdp2	24831679	24831929	2095	-0.06511	3.004962	0.707156	0.789745	0.03051	0	116	111	147	134	131	114	177	132	176	113
ENSMUSG00000025723	chr7	Nmb	80902227	80902503	793	0.141204	1.989382	0.707916	0.79039	0.142872	0	49	62	72	45	61	125	42	56	107	29
ENSMUSG00000034709	chr17	Ppp1r21	88530118	88530318	4255	0.067959	2.865129	0.708032	0.79039	0.032512	0	92	84	167	97	130	135	132	132	157	107
ENSMUSG00000040151	chr3	Hs2st1	1.44E+08	1.44E+08	4916	0.058719	4.328471	0.707838	0.79039	0.026981	0	271	203	536	240	375	274	419	330	512	344
ENSMUSG00000061533	chr12	Cep128	90998492	90999659	11591	0.144447	0.088943	0.707931	0.79039	0.073388	0	14	5	17	21	16	11	22	25	23	11
ENSMUSG00000086866	chr8	4930512H18Rik	61849006	61849092	1493	-0.17596	0.913729	0.70799	0.79039	0.171661	0	11	24	94	11	25	36	28	27	31	25
ENSMUSG00000039623	chr5	Ap5z1	1.42E+08	1.42E+08	3817	0.075603	2.45093	0.708623	0.790984	0.035217	0	91	47	110	69	107	76	118	100	122	88
ENSMUSG00000031543	chr8	Ank1	22974844	22975261	13527	-0.0643	9.156245	0.709726	0.792098	0.035671	0	9644	7645	12965	6788	9412	9352	11917	9961	11685	7891
ENSMUSG00000031816	chr8	Mthfsd	1.21E+08	1.21E+08	4894	0.069229	3.580589	0.709741	0.792098	0.031983	0	166	132	191	208	223	153	307	196	240	220
ENSMUSG00000019302	chr11	Atp6v0a1	1.01E+08	1.01E+08	6556	-0.05971	6.506745	0.709971	0.792279	0.029781	0	1312	981	2563	1185	1639	1209	1728	1608	2135	1475
ENSMUSG00000020319	chr11	Wdpcp	21572235	21572370	5934	0.104481	1.246806	0.710082	0.792279	0.045386	0	30	27	41	32	45	23	60	48	59	29

ENSMUSG00000044751	chr11	Gm12231	55118101	55118795	695	-0.08386	3.667577	0.710061	0.792279	0.05504	0	161	115	186	316	260	160	320	166	263	222
ENSMUSG00000020706	chr11	Ftsj3	1.06E+08	1.06E+08	4358	-0.0539	5.070014	0.710311	0.792467	0.023961	0	464	452	707	457	654	502	764	583	739	441
ENSMUSG00000102805	chr3	RP24-559D1.1	84496426	84497891	2913	-0.05647	4.15865	0.710502	0.792614	0.022776	0	241	207	462	263	308	231	354	311	396	302
ENSMUSG00000026888	chr2	Grb14	64912476	64912853	7185	-0.13998	4.487339	0.710697	0.792765	0.163924	0	166	89	249	785	648	288	604	304	442	336
ENSMUSG00000003134	chr1	Tbc1d8	39371492	39372786	5239	-0.06075	3.906513	0.710896	0.79292	0.027681	0	234	163	385	202	259	181	392	228	313	240
ENSMUSG00000021484	chr13	Lman2	55343833	55347037	4315	0.056452	6.502755	0.711137	0.793108	0.027413	0	1272	786	2113	1506	1641	1415	1950	1704	2040	1344
ENSMUSG00000038777	chr3	Sema6c	95160457	95160702	5935	0.078739	6.96467	0.711184	0.793108	0.053987	0	1363	794	2946	2460	2695	1496	2677	1904	3123	2596
ENSMUSG00000021958	chr14	Pinx1	63860312	63860447	1351	0.110341	1.847054	0.711418	0.793254	0.051105	0	43	52	60	60	48	52	96	58	91	41
ENSMUSG00000029918	chr6	Mrps33	39801804	39802544	1236	-0.07075	3.891925	0.711435	0.793254	0.041468	0	256	185	225	237	279	248	400	190	290	198
ENSMUSG00000032422	chr9	Snx14	88376750	88376939	6107	0.056192	3.920965	0.711577	0.793347	0.02221	0	212	155	343	241	248	214	385	250	330	237
ENSMUSG00000024942	chr19	Capn1	5988546	5989387	3190	0.05501	6.769075	0.711758	0.793415	0.026014	0	1476	1192	2648	1523	1908	1592	2158	1832	2680	1898
ENSMUSG00000033282	chr8	Rpgrip1l	91217030	91220289	9855	-0.10356	1.44861	0.711707	0.793415	0.051512	0	31	23	78	40	55	22	63	50	59	41
ENSMUSG00000024395	chr18	Lims2	31931507	31931550	1688	-0.0678	4.249652	0.711907	0.793513	0.034467	0	218	177	361	417	405	286	371	314	393	314
ENSMUSG00000002475	chr18	Abhd3	10644411	10645235	1962	0.128606	-0.2061	0.712554	0.793969	0.084997	0	10	3	11	12	23	14	13	16	16	12
ENSMUSG00000019948	chr10	Actr6	89711973	89712560	1703	-0.07011	2.775396	0.712451	0.793969	0.035638	0	117	88	127	84	132	105	139	121	137	97
ENSMUSG00000029869	chr6	Ephb6	41605482	41605820	3773	0.105842	0.675228	0.712424	0.793969	0.055136	0	12	14	30	28	33	17	33	25	35	31
ENSMUSG00000031790	chr8	Mmp15	95352268	95353018	4348	-0.05286	4.725813	0.712555	0.793969	0.022544	0	373	326	621	377	476	324	554	463	619	427
ENSMUSG00000028869	chr4	Gnl2	1.25E+08	1.25E+08	3683	-0.0554	5.077494	0.712665	0.793991	0.026299	0	468	482	708	510	553	505	838	540	692	469
ENSMUSG00000070713	chr8	Gm10282	72304118	72305276	1159	-0.11544	1.375519	0.712694	0.793991	0.083274	0	39	27	36	44	60	42	64	18	68	31
ENSMUSG00000015377	chr15	Dennd6b	89182217	89185109	4607	-0.05828	3.75713	0.712869	0.794119	0.023173	0	170	139	297	240	272	180	288	215	298	226
ENSMUSG00000053774	chr16	Ubxn7	32332252	32332360	10318	0.053963	4.042122	0.713148	0.794363	0.022085	0	217	175	397	247	277	224	369	305	345	283
ENSMUSG00000016933	chr2	Plcg1	1.61E+08	1.61E+08	7857	-0.05152	4.794572	0.713227	0.794385	0.02024	0	376	300	677	433	519	392	581	470	619	430
ENSMUSG00000025854	chr5	Fam20c	1.39E+08	1.39E+08	4223	0.057811	4.040447	0.713353	0.794458	0.028709	0	201	140	415	251	330	229	376	295	312	306
ENSMUSG00000056305	chr6	Usp39	72318678	72319239	2425	0.055592	4.400446	0.713493	0.794547	0.022804	0	312	240	454	319	331	335	458	353	510	311
ENSMUSG00000014402	chr7	Tsg101	46888949	46889704	2730	0.054381	5.612926	0.713781	0.794801	0.023976	0	651	626	989	748	808	786	1135	819	1150	691
ENSMUSG00000027968	chr3	Larp7	1.28E+08	1.28E+08	1880	-0.06206	3.189209	0.714552	0.795526	0.028528	0	126	107	159	153	192	117	221	155	178	141
ENSMUSG00000047710	chr8	Champ1	13869641	13869811	4040	0.064107	3.502451	0.714524	0.795526	0.029529	0	142	139	271	139	203	165	295	162	234	199
ENSMUSG00000022564	chr15	Grina	76246807	76246900	1693	0.058431	7.129114	0.714794	0.795729	0.030024	0	1922	1687	3133	2005	2301	2230	2586	2856	3436	1931
ENSMUSG00000071644	chr19	Eef1g	8967041	8967225	2600	-0.05864	8.786117	0.714949	0.795834	0.030832	0	6633	5967	8386	6859	7693	6921	8914	6738	10704	6430
ENSMUSG00000027430	chr2	Dtd1	1.45E+08	1.45E+08	2353	0.066192	3.547962	0.71518	0.796025	0.028774	0	160	152	221	179	186	160	288	180	244	215
ENSMUSG00000014592	chr4	Camta1	1.51E+08	1.51E+08	14570	-0.08499	3.971592	0.715573	0.796395	0.06068	0	163	140	236	426	327	181	378	241	391	226
ENSMUSG00000014504	chr18	Srp19	34330847	34331111	3630	0.053528	4.956531	0.715781	0.796509	0.022201	0	457	385	604	427	548	444	703	560	687	498
ENSMUSG00000063576	chr17	Klhdc3	46674550	46675152	2126	0.070041	6.672441	0.715795	0.796509	0.043565	0	1145	851	1895	2159	2095	1226	2720	1497	2674	1684
ENSMUSG00000063902	chr7	Gm7964	83755904	83756233	1392	-0.05986	3.454777	0.71592	0.796514	0.026958	0	139	141	239	180	193	126	266	197	219	174
ENSMUSG00000096768	chrY	Erdr1	90784738	90784822	1124	0.217723	2.00146	0.715887	0.796514	0.376522	0	73	60	63	31	48	0	64	81	106	135
ENSMUSG00000085890	chr11	Tnfsf13os	69682138	69682147	1109	-0.14033	0.443466	0.71643	0.797015	0.121915	0	35	14	27	14	13	23	40	13	24	11
ENSMUSG00000002845	chr16	Tmem39a	38558698	38558762	4094	0.072332	3.066766	0.717082	0.797648	0.037997	0	127	89	225	86	136	110	226	143	182	126
ENSMUSG00000018196	chr1	Glrx2	1.44E+08	1.44E+08	8772	0.056376	5.148869	0.71718	0.797648	0.025552	0	512	446	751	470	598	547	882	543	881	495
ENSMUSG00000023923	chr17	Tbc1d5	50733127	50736244	5613	-0.06893	3.429568	0.717158	0.797648	0.031983	0	155	104	314	147	189	130	213	207	231	174
ENSMUSG00000033594	chr8	Spata2l	1.23E+08	1.23E+08	2683	-0.15602	0.370819	0.717467	0.797901	0.106528	0	11	6	24	32	30	16	13	22	35	16
ENSMUSG00000049516	chr7	Spty2d1	46990396	46993386	5223	0.068189	2.630902	0.717539	0.797914	0.035552	0	75	62	171	69	118	92	144	105	127	102
ENSMUSG00000020122	chr11	Egfr	16752203	16752570	11326	-0.0736	4.072118	0.718867	0.799323	0.041997	0	210	202	504	181	332	319	325	219	344	261
ENSMUSG00000028684	chr4	Urod	1.17E+08	1.17E+08	2591	0.052475	5.765338	0.719381	0.799828	0.0241	0	698	562	1094	1002	954	812	1185	965	1292	828
ENSMUSG00000000142	chr11	Axin2	1.09E+08	1.09E+08	5506	-0.106	2.566448	0.719474	0.799864	0.083306	0	51	37	127	129	164	48	134	108	125	104
ENSMUSG00000013150	chr8	Gfod2	1.06E+08	1.06E+08	4608	-0.05975	3.149462	0.719557	0.799889	0.027234	0	131	105	179	150	151	133	196	167	179	112
ENSMUSG00000032413	chr9	Rasa2	96539300	96542475	15856	-0.08396	1.95809	0.719622	0.799895	0.046141	0	45	55	108	48	61	47	82	78	69	59
ENSMUSG00000073600	chr18	Prob1	35650351	35655240	4890	-0.06031	6.425615	0.720066	0.800321	0.032608	0	1169	746	2151	1473	1750	1141	1624	1280	2256	1450
ENSMUSG00000026482	chr1	Rgl1	1.53E+08	1.53E+08	6907	0.068443	3.906789	0.720216	0.800421	0.040884	0	148	143	357	241	322	167	360	360	263	247
ENSMUSG00000015468	chr17	Notch4	34564268	34564509	8061	-0.08362	3.224859	0.720456	0.80062	0.052784	0	98	91	201	188	204	134	128	220	218	115
ENSMUSG00000022013	chr14	Dnajc15	77826217	77826470	648	-0.06036	5.599826	0.720517	0.800622	0.033978	0	809	706	882	695	753	752	1151	782	1086	610
ENSMUSG00000022843	chr16	Clcn2	20702964	20703437	6022	-0.11303	1.08566	0.720936	0.800964	0.053215	0	25	13	50	44	41	27	44	36	35	34
ENSMUSG00000024427	chr18	Spry4	38586268	38590755	4587	0.09813	2.264409	0.720946	0.800964	0.079007	0	55	30	96	56	145	63	157	64	92	76
ENSMUSG00000037894	chr3	H2afz	1.38E+08	1.38E+08	1776	0.055003	5.283077	0.721184	0.801161	0.025277	0	636	455	738	541	656	578	934	629	904	605
ENSMUSG00000021947	chr14	Cryl1	57275034	57275562	1410	0.07514	2.486884	0.721333	0.801239	0.037428	0	65	79	127	67	93	81	135	109	107	84
ENSMUSG00000032606	chr9	Nicn1	1.08E+08	1.08E+08	2835	0.053573	3.959833	0.721375	0.801239	0.022176	0	201	161	298	267	299	235	328	273	359	246
ENSMUSG00000102781	chr2	Pla2r1	60420013	60420302	4464	0.089132	1.397415	0.721658	0.801487	0.061736	0	22	26	70	28	59	48	49	34	54	49
ENSMUSG00000018446	chr11	C1qbp	70977836	70978244	2826	0.055075	5.994661	0.721856	0.801639	0.027253	0	818	669	1212	1197	1131	953	1478	1157	1472	920
ENSMUSG00000066042	chr4	Med18	1.32E+08	1.32E+08	1998	0.115585	0.658905	0.72215	0.801899	0.042302	0	23	15	31	17	28	18	35	29	38	21
ENSMUSG00000027573	chr2	Gid8	1.81E+08	1.81E+08	2464	-0.04938	5.023572	0.722619	0.802271	0.020912	0	449	358	706	520	646	481	769	507	697	481
ENSMUSG00000043557	chr17	Mdga1	29827956	29832399	9395	-0.10719	4.56048	0.722653	0.802271	0.101242	0	203	125	490	529	734	307	324	369	459	549
ENSMUSG00000066640	chr5	Fbxl18	1.43E+08	1.43E+08	12563	0.061764	3.566381	0.722667	0.802271	0.033872	0	140	86	273	216	242	166	251	201	289	196
ENSMUSG00000057897	chr11	Camk2b	5969644	5971826	9125	-0.05327	7.766281	0.72307	0.802651	0.026723	0	2931	2338	5154	3682	4007	2845	4558	3312	5211	3751
ENSMUSG00000024999	chr19	Noc3l	38788128	38789697	3977	-0.06217	3.061016	0.723331	0.802874	0.027496	0	133	93	187	107	162	115	182	149	162	129
ENSMUSG00000092074	chr17	Dynlt1a	6310547	6310943	742	0.140259	0.513791	0.723745	0.803266	0.084068	0	18	15	12	30	23	30	25	22	26	21
ENSMUSG00000026109	chr1	Tmeff2	50900647	50900782	6707	0.09897	2.023369	0.723904	0.803375	0.079701	0	54	49	104	29	78	62	73	113	64	55

ENSMUSG00000029148	chr5	Nrbp1	31240864	31241002	3559	-0.05341	5.989342	0.724213	0.803583	0.026541	0	843	750	1290	1140	1168	980	1426	926	1467	934
ENSMUSG00000040187	chr6	Arntl2	1.47E+08	1.47E+08	3032	0.130281	0.380821	0.724192	0.803583	0.046707	0	20	15	19	17	19	17	27	24	23	22
ENSMUSG00000038671	chr2	Arfrp1	1.81E+08	1.81E+08	4320	0.057335	4.809834	0.724297	0.80361	0.02816	0	426	265	492	491	525	417	681	537	628	370
ENSMUSG00000020963	chr12	Tshr	91400994	91401254	4873	0.22195	0.292151	0.724467	0.803719	0.357098	0	29	18	14	8	9	20	7	57	6	15
ENSMUSG00000042453	chr5	Reln	21884454	21885569	19834	0.085927	2.448332	0.724516	0.803719	0.066747	0	49	41	171	53	135	90	108	99	128	77
ENSMUSG00000034457	chrX	Eda2r	97333840	97337450	5891	-0.0708	4.688881	0.725171	0.804377	0.047122	0	413	359	728	280	345	363	647	361	672	311
ENSMUSG00000022010	chr14	Tsc22d1	76414961	76415717	8994	0.060667	7.083867	0.725264	0.804414	0.03541	0	1627	1133	3415	2279	2651	2096	3678	1897	3290	1939
ENSMUSG00000020962	chr12	Gtf2a1	91555916	91559851	5587	0.063331	4.168842	0.725783	0.804855	0.031103	0	264	257	385	220	258	241	387	296	456	305
ENSMUSG00000027423	chr2	Snx5	1.44E+08	1.44E+08	4177	-0.05647	6.41528	0.725776	0.804855	0.030532	0	1242	1217	1959	1167	1335	1374	1942	1329	1760	1242
ENSMUSG00000018583	chr11	G3bp1	55469685	55469801	7064	-0.0525	6.950845	0.725869	0.804883	0.0263	0	1946	1408	3014	1653	2211	1700	2702	2114	2738	1911
ENSMUSG00000032064	chr9	Dixdc1	50662752	50666275	9971	0.087875	1.544105	0.726005	0.804966	0.050029	0	31	23	58	60	50	37	70	64	57	38
ENSMUSG00000041747	chr13	Utp15	98246845	98249376	4071	0.065071	2.82558	0.726115	0.80502	0.028169	0	92	85	150	101	122	99	161	144	138	110
ENSMUSG00000083610	chr3	Oaz2-ps	1.36E+08	1.36E+08	537	-0.07713	1.739837	0.726511	0.805393	0.035501	0	44	36	71	61	56	49	58	61	74	45
ENSMUSG00000026374	chr1	Tsn	1.18E+08	1.18E+08	9046	0.049535	5.721784	0.726734	0.805505	0.022325	0	646	654	1180	755	958	781	1239	848	1237	834
ENSMUSG00000036636	chr17	Clcn7	25133391	25133614	5292	0.051613	4.686159	0.726734	0.805505	0.025532	0	318	222	636	413	507	377	535	485	554	429
ENSMUSG00000022404	chr15	Slc25a17	81318921	81319776	1667	0.068141	3.210707	0.726798	0.805508	0.033047	0	128	131	180	119	149	145	188	192	180	143
ENSMUSG00000024077	chr17	Strn	78649913	78655659	8858	-0.06723	3.289442	0.726923	0.80558	0.033667	0	92	121	266	170	166	130	206	165	211	155
ENSMUSG00000026750	chr2	Psmb7	38588036	38588288	1214	0.067468	8.039288	0.7274	0.805974	0.044251	0	3890	4236	4717	3298	3654	4392	6422	4004	6259	3753
ENSMUSG00000080904	chr11	Gm11966	5818497	5818583	87	0.095281	1.886871	0.727375	0.805974	0.048482	0	53	32	69	64	62	42	97	57	109	45
ENSMUSG00000044433	chr8	Camsap3	3587450	3587959	4295	0.153146	-0.04141	0.727687	0.806224	0.068891	0	15	10	9	14	16	12	16	22	17	15
ENSMUSG00000068959	chr7	Zfp619	39517766	39517864	5964	-0.13855	0.317213	0.727773	0.806252	0.059059	0	18	8	29	17	26	15	25	14	19	25
ENSMUSG00000020061	chr10	Mybpc1	88518279	88518569	4527	-0.20974	10.33068	0.727914	0.806341	0.426818	0	1724	3187	18199	49959	45779	7808	34471	9639	20020	37638
ENSMUSG00000066551	chr5	Hmgb1	1.49E+08	1.49E+08	4944	-0.05764	7.030107	0.727986	0.806354	0.032843	0	1927	1989	2497	1821	2194	1880	3123	2027	2877	1919
ENSMUSG00000015176	chr19	Nolc1	46075863	46076149	3634	-0.04833	4.936353	0.728201	0.806525	0.020798	0	444	352	704	441	578	419	635	573	673	454
ENSMUSG00000023952	chr17	Gtpbp2	46161032	46161326	5305	-0.05012	5.589177	0.728415	0.806694	0.023101	0	627	474	1116	845	954	627	1122	796	1077	745
ENSMUSG00000041012	chr9	Cmtm8	1.15E+08	1.15E+08	1064	-0.09295	1.036604	0.728561	0.806789	0.079666	0	30	37	38	18	34	16	38	38	56	28
ENSMUSG00000071064	chr8	Zfp827	79028437	79028729	8944	-0.16165	1.595998	0.72867	0.806842	0.195729	0	14	14	36	103	87	25	60	39	72	58
ENSMUSG00000035877	chr2	Zhx3	1.61E+08	1.61E+08	13259	0.051221	4.486737	0.728799	0.806917	0.02435	0	283	234	581	316	396	348	422	427	539	338
ENSMUSG00000040435	chr7	Ppp1r15a	45522916	45523273	2937	0.056527	4.862408	0.729093	0.807175	0.027483	0	427	382	609	363	485	457	741	448	671	416
ENSMUSG00000015806	chr5	Qdpr	45434032	45434678	1914	-0.05067	5.614637	0.729294	0.807269	0.02477	0	684	682	1016	730	841	758	990	802	1072	759
ENSMUSG00000041153	chr4	Osgin2	15997121	15999000	5571	0.072684	2.319164	0.729299	0.807269	0.03708	0	56	44	106	84	101	63	123	103	95	76
ENSMUSG00000030417	chr7	Pdcd5	35641982	35642185	2486	0.063506	5.955569	0.729643	0.807582	0.03784	0	898	944	1083	883	884	1014	1569	942	1369	934
ENSMUSG00000034187	chr11	Nsf	1.04E+08	1.04E+08	8346	-0.05513	4.103899	0.730001	0.807843	0.024131	0	230	153	412	298	346	222	359	290	403	272
ENSMUSG00000036371	chr6	Serbp1	67266979	67267409	6685	-0.05198	7.964334	0.729949	0.807843	0.027052	0	3637	3336	5460	3568	4299	3290	5820	4144	5441	3938
ENSMUSG00000035671	chr8	Zswim4	84210942	84212805	4348	0.056849	3.515752	0.731244	0.809152	0.029228	0	131	100	248	217	217	175	230	195	269	187
ENSMUSG00000022354	chr15	Ndufb9	58933810	58933938	651	0.06147	8.557274	0.731815	0.809715	0.038253	0	4986	3925	5889	7465	7077	5744	9503	5448	9582	5513
ENSMUSG00000028455	chr4	Stoml2	43027690	43028293	3022	0.049939	5.777095	0.731986	0.809837	0.023897	0	768	571	1009	918	1062	848	1240	895	1269	861
ENSMUSG00000097787	chr19	2700046G09Rik	32389216	32389376	1641	0.114399	0.917069	0.732134	0.809934	0.060716	0	30	24	43	22	17	28	48	25	40	29
ENSMUSG00000014074	chr16	Rnf168	32277459	32278415	4462	-0.05576	3.712102	0.732517	0.810011	0.027027	0	178	172	314	169	240	198	335	205	254	182
ENSMUSG00000024423	chr18	Impact	12972252	12972372	3432	-0.05802	3.700182	0.732621	0.810011	0.02759	0	187	157	320	193	208	180	242	264	251	208
ENSMUSG00000030653	chr7	Pde2a	1.01E+08	1.01E+08	4220	0.055484	5.181297	0.732632	0.810011	0.029916	0	556	344	837	479	694	625	852	682	808	424
ENSMUSG00000034024	chr10	Cct2	1.17E+08	1.17E+08	1962	-0.05497	6.766889	0.732566	0.810011	0.030854	0	1547	1651	2292	1528	1718	1567	2519	1803	2365	1583
ENSMUSG00000039372	chr1	March4	72427112	72429009	4553	0.150724	0.199986	0.73249	0.810011	0.124167	0	23	10	30	7	9	9	39	17	25	13
ENSMUSG00000053684	chr10	BC048403	1.22E+08	1.22E+08	3136	0.110687	0.916992	0.732276	0.810011	0.061855	0	36	17	41	15	29	20	41	36	43	30
ENSMUSG00000087165	chr11	2010001A14Rik	57795499	57795794	714	0.121376	0.174083	0.732609	0.810011	0.046722	0	16	11	19	15	17	19	23	14	27	14
ENSMUSG00000030678	chr7	Maz	1.27E+08	1.27E+08	2365	0.050659	6.418197	0.732762	0.81005	0.025553	0	1238	902	1828	1261	1577	1337	1642	1480	2148	1345
ENSMUSG00000073436	chr17	Eme2	24888486	24892944	6000	-0.08491	2.634142	0.732789	0.81005	0.05365	0	53	65	131	133	133	70	134	91	121	125
ENSMUSG00000052488	chr8	Cherp	72460489	72461355	3794	0.052005	4.3312	0.732863	0.810064	0.026546	0	275	167	496	308	387	276	399	405	459	326
ENSMUSG00000022711	chr16	Pmm2	8637674	8637828	4519	-0.05078	3.962768	0.733008	0.810106	0.023248	0	224	178	292	270	298	221	348	287	330	213
ENSMUSG00000090258	chr12	Churc1	76765538	76765638	5693	0.059614	5.083922	0.733023	0.810106	0.032017	0	520	423	524	549	575	520	880	490	808	503
ENSMUSG00000040667	chr11	Nup88	70943058	70943322	8144	-0.05028	5.127198	0.733681	0.810766	0.024407	0	486	390	812	555	642	479	925	487	759	532
ENSMUSG00000040586	chrX	Ofd1	1.66E+08	1.66E+08	4453	-0.061	3.010119	0.734433	0.811529	0.027679	0	92	97	196	134	143	116	186	142	157	113
ENSMUSG00000021033	chr12	Gstz1	87147707	87147844	1665	0.078314	5.776037	0.73469	0.811746	0.06161	0	1024	696	931	723	751	847	1016	1551	897	731
ENSMUSG00000020149	chr11	Rab1	20201432	20201652	3799	-0.04908	6.914064	0.73498	0.811999	0.024663	0	1691	1366	2752	1826	2334	1520	2827	1968	2686	1957
ENSMUSG00000025280	chr14	Polr3a	24448694	24449222	4683	-0.06068	2.99692	0.735351	0.812226	0.025935	0	109	85	192	115	158	109	194	126	166	117
ENSMUSG00000034501	chr12	Pcnxl4	72536357	72536539	4420	0.07154	2.897901	0.735252	0.812226	0.03639	0	104	89	116	119	139	113	142	112	176	141
ENSMUSG00000078429	chr10	Ctdsp2	1.27E+08	1.27E+08	5065	0.052793	7.346008	0.73537	0.812226	0.028851	0	2192	1504	3917	2727	2807	2152	3711	2717	4209	2589
ENSMUSG00000003518	chr11	Dusp3	1.02E+08	1.02E+08	4682	-0.05408	7.549231	0.736062	0.812923	0.030546	0	3118	2297	4474	2350	3111	2771	4124	3002	4141	2836
ENSMUSG00000038644	chr7	Pold1	44532746	44532894	4860	-0.07685	2.61498	0.736218	0.813027	0.03933	0	71	53	132	128	123	92	117	95	125	103
ENSMUSG00000053414	chr16	Hunk	90386397	90386716	5009	-0.17599	0.112572	0.737041	0.813869	0.150822	0	8	19	35	4	19	17	30	15	10	11
ENSMUSG00000022787	chr16	Wdr53	32247227	32247267	1523	0.086512	2.731967	0.737194	0.81397	0.047847	0	112	95	101	93	88	100	156	103	169	95
ENSMUSG00000004937	chr10	Sgta	81044075	81045003	1969	0.052137	6.817217	0.737669	0.814281	0.027988	0	1675	1338	2072	1781	1915	1839	2400	1883	2814	1609
ENSMUSG00000018697	chr11	Aatf	84422855	84423019	2869	-0.05853	3.287798	0.737617	0.814281	0.030254	0	134	134	231	125	170	127	177	182	230	151
ENSMUSG00000032377	chr9	Plscr4	92457373	92457925	3590	0.078403	2.601243	0.737691	0.814281	0.049586	0	58	67	122	99	127	62	151	131	101	115
ENSMUSG00000096210	chr15	H1f0	79028212	79030498	2287	-0.0563	7.148127	0.737721	0.814281	0.033629	0	2344	1874	3124	1784	2382	2074	3125	1940	3510	2199

ENSMUSG00000031145	chrX	Prickle3	7657260	7657500	4902	-0.06285	3.724049	0.737872	0.814379	0.030915	0	158	123	320	247	258	213	229	253	259	202
ENSMUSG00000028527	chr4	Ak4	1.01E+08	1.01E+08	4646	-0.12919	3.248905	0.738136	0.814602	0.162652	0	50	78	153	211	332	56	250	248	115	158
ENSMUSG00000043290	chr7	Zfp784	5034439	5036479	2153	0.092611	1.458392	0.738516	0.814955	0.042653	0	27	31	47	51	49	39	51	51	71	38
ENSMUSG00000102252	chr7	Snrpn	59982495	59983277	2159	0.059475	5.943871	0.73936	0.815818	0.03699	0	725	606	1182	1160	1222	854	1298	799	1748	1112
ENSMUSG00000030785	chr7	Cox6a2	1.28E+08	1.28E+08	658	0.063421	9.524552	0.739838	0.816278	0.043621	0	8378	6169	13234	15667	15456	10078	16796	10951	19399	12571
ENSMUSG00000046721	chr7	Rpl14-ps1	45324941	45325456	710	0.057543	4.700601	0.740302	0.816721	0.030304	0	392	369	497	353	379	413	640	430	547	393
ENSMUSG00000022091	chr14	Sorbs3	70180468	70181231	2914	-0.05719	6.106873	0.740574	0.816954	0.03413	0	969	791	1760	989	1234	1131	1047	1055	1731	1142
ENSMUSG00000024312	chr17	Wdr46	33940660	33940806	2442	0.056399	3.136874	0.741206	0.817515	0.029009	0	112	78	201	145	165	110	219	177	191	124
ENSMUSG00000024847	chr19	Aip	4114446	4114796	1937	0.052224	6.214403	0.741169	0.817515	0.028426	0	1192	910	1481	951	1258	1100	1557	1320	1696	1229
ENSMUSG00000063800	chr4	Prpf38a	1.09E+08	1.09E+08	5298	0.062076	3.485619	0.741327	0.817581	0.029688	0	141	150	208	153	214	160	247	182	309	155
ENSMUSG00000017288	chr11	Vps53	76046226	76046582	5203	0.050471	4.539568	0.741492	0.817673	0.022969	0	310	301	508	315	393	339	494	401	593	346
ENSMUSG00000024130	chr17	Abca3	24351950	24352251	8797	-0.06361	3.713848	0.741535	0.817673	0.034006	0	153	122	343	240	247	178	232	291	269	188
ENSMUSG00000031828	chr8	Klhl36	1.2E+08	1.2E+08	2141	-0.11299	0.522585	0.741803	0.817902	0.046329	0	16	12	34	26	25	16	34	25	28	15
ENSMUSG00000017969	chr2	Ptgis	1.67E+08	1.67E+08	2567	-0.13283	1.727769	0.742088	0.817963	0.134353	0	26	28	87	51	93	46	33	108	45	37
ENSMUSG00000032594	chr9	Ip6k1	1.08E+08	1.08E+08	6487	0.04612	5.129244	0.742106	0.817963	0.022133	0	475	342	819	579	595	530	737	619	787	567
ENSMUSG00000041801	chr1	Phlda3	1.36E+08	1.36E+08	1559	0.059524	7.78723	0.742037	0.817963	0.038611	0	3476	2366	3596	3893	3757	3183	4140	3522	6670	3389
ENSMUSG00000075225	chr10	Ccdc162	41538846	41539304	5572	-0.15799	0.610203	0.741932	0.817963	0.185242	0	29	18	33	23	16	46	34	8	26	7
ENSMUSG00000030562	chr7	Nox4	87246096	87246219	8471	0.096667	1.682251	0.742226	0.818027	0.090693	0	24	23	82	56	68	30	54	89	54	61
ENSMUSG00000042709	chr11	Atpaf2	60400626	60401538	2137	-0.05025	4.598754	0.742381	0.81813	0.026629	0	395	251	453	403	466	290	552	410	616	345
ENSMUSG00000015016	chr8	Acsf3	1.23E+08	1.23E+08	2206	-0.06654	3.842543	0.742547	0.818177	0.042219	0	147	147	240	335	307	211	304	255	276	221
ENSMUSG00000030664	chr7	Sox6os	1.16E+08	1.16E+08	420	-0.09889	1.203972	0.742501	0.818177	0.085815	0	56	26	49	17	32	38	43	38	45	29
ENSMUSG00000032479	chr9	Map4	1.1E+08	1.1E+08	10576	0.052883	9.134755	0.742808	0.818397	0.031033	0	7182	5653	13486	8769	10347	8015	11685	8111	15622	9530
ENSMUSG00000040025	chr4	Ythdf2	1.32E+08	1.32E+08	4572	-0.04896	4.296448	0.74298	0.818518	0.02457	0	260	256	440	297	347	218	445	369	423	320
ENSMUSG00000019761	chr11	Krt10	99385254	99385636	2094	-0.08068	0.882995	0.743054	0.818532	0.052968	0	28	29	32	26	25	26	32	30	45	22
ENSMUSG00000031516	chr8	Dctn6	34090420	34090842	2853	0.056635	5.208333	0.743338	0.818709	0.03155	0	559	534	729	466	549	574	858	597	907	535
ENSMUSG00000063873	chr2	Slc24a3	1.45E+08	1.45E+08	4564	0.094044	1.450288	0.743314	0.818709	0.070262	0	51	26	52	25	50	32	49	68	45	50
ENSMUSG00000040147	chrX	Maob	16709282	16710191	2789	-0.05016	5.614045	0.744112	0.819494	0.027535	0	789	596	1079	711	805	657	1095	1001	1063	621
ENSMUSG00000003382	chr3	Etv3	87525407	87525659	10274	-0.05529	3.800909	0.744316	0.81965	0.025503	0	161	138	350	235	284	201	312	262	278	192
ENSMUSG00000031627	chr8	Irf2	46739745	46739936	2484	-0.05616	4.082015	0.745022	0.820359	0.028241	0	235	139	463	270	328	211	366	313	390	247
ENSMUSG00000075268	chr19	Gm10819	16267061	16267621	561	0.089359	1.476537	0.745211	0.820499	0.044728	0	51	28	46	33	48	40	59	54	55	43
ENSMUSG00000020359	chr11	Phykpl	51584757	51584879	9699	-0.05833	4.266321	0.745734	0.821007	0.034182	0	222	180	388	404	403	260	451	255	477	300
ENSMUSG00000024218	chr17	Taf11	27901122	27901789	2290	0.05355	4.180948	0.745874	0.821076	0.025199	0	286	227	364	234	297	257	388	323	452	273
ENSMUSG00000024560	chr18	Cxxc1	74216131	74216482	2618	-0.04894	4.100063	0.745921	0.821076	0.021985	0	218	204	374	266	344	233	331	324	353	284
ENSMUSG00000000827	chr2	Tpd52l2	1.81E+08	1.81E+08	4982	0.049911	5.647374	0.746084	0.821188	0.025855	0	751	650	975	693	825	803	1212	878	1058	718
ENSMUSG00000063480	chr15	Nhp2l1	82041319	82042368	2130	0.055676	5.752995	0.746444	0.821516	0.032712	0	784	764	889	790	886	910	1345	859	1102	806
ENSMUSG00000028194	chr3	Ddah1	1.46E+08	1.46E+08	3983	0.090691	3.646611	0.746586	0.821536	0.092364	0	87	80	259	302	284	204	210	139	332	272
ENSMUSG00000032386	chr9	Trip4	65828930	65833448	8394	-0.04882	4.132907	0.746541	0.821536	0.024232	0	236	240	405	259	282	241	395	295	344	292
ENSMUSG00000024759	chr19	Atl3	7494040	7494361	6698	-0.06405	3.905723	0.747077	0.822008	0.038384	0	179	176	420	177	313	192	306	336	244	240
ENSMUSG00000032060	chr9	Cryab	50752758	50753477	1185	0.084591	9.232519	0.747727	0.822655	0.082628	0	6231	4016	7386	14771	15243	9263	13384	8098	14014	11757
ENSMUSG00000062110	chr5	Scfd2	74204816	74206395	8127	0.057161	3.193829	0.74787	0.822743	0.028353	0	105	93	216	140	176	104	217	167	233	139
ENSMUSG00000032582	chr9	Rbm6	1.08E+08	1.08E+08	13944	0.049622	4.606153	0.748245	0.823088	0.024151	0	341	307	549	309	414	358	529	482	565	335
ENSMUSG00000021913	chr14	Ogdhl	32322019	32322116	3449	0.149044	0.740592	0.748365	0.823152	0.198922	0	6	10	17	57	29	34	28	19	50	19
ENSMUSG00000020537	chr11	Drg2	60454591	60454743	2716	0.047899	4.63706	0.748584	0.823175	0.023156	0	364	264	464	418	442	408	542	415	546	387
ENSMUSG00000022052	chr14	Ppp2r2a	67014057	67016653	4036	0.047562	5.978794	0.748574	0.823175	0.02493	0	905	706	1391	879	1136	1001	1502	1028	1484	891
ENSMUSG00000028556	chr4	Dock7	98936665	98937300	8115	0.055003	3.4066	0.748635	0.823175	0.032295	0	116	112	285	145	198	147	285	172	196	183
ENSMUSG00000038152	chr13	5033430I15Rik	45965253	45965383	952	0.103766	0.991104	0.748539	0.823175	0.085803	0	31	8	30	39	39	40	45	29	41	22
ENSMUSG00000038393	chr3	Txnip	96557957	96558485	3031	-0.08083	9.154126	0.749311	0.823851	0.076548	0	9227	9188	8965	7194	10518	5637	19841	6220	10102	10485
ENSMUSG00000026778	chr2	Prkcq	11172108	11172460	7081	-0.04971	6.694597	0.749408	0.823889	0.028281	0	1343	1116	2335	1882	1894	1444	2697	1487	2100	1668
ENSMUSG00000053841	chr4	Txlna	1.3E+08	1.3E+08	5348	0.049359	4.423928	0.749971	0.824439	0.025151	0	251	236	432	350	437	299	442	459	489	305
ENSMUSG00000018765	chr11	Fxr2	69632990	69633398	3766	-0.04736	7.098213	0.750996	0.825498	0.026391	0	2001	1677	3025	2164	2305	1874	2798	2277	3431	2061
ENSMUSG00000028188	chr3	Spata1	1.46E+08	1.46E+08	4114	0.083199	1.137185	0.751439	0.825916	0.052212	0	24	15	50	42	36	39	54	37	39	27
ENSMUSG00000022706	chr16	Mrpl40	18872018	18872662	1214	0.059073	4.332352	0.752056	0.826526	0.033553	0	334	259	314	309	311	296	520	305	432	331
ENSMUSG00000017309	chr11	Cd300lg	1.02E+08	1.02E+08	2737	-0.05694	4.92236	0.752226	0.826645	0.036517	0	325	310	555	581	747	358	760	568	676	404
ENSMUSG00000029462	chr5	Vps29	1.22E+08	1.22E+08	3089	-0.04876	4.257926	0.752866	0.827143	0.026805	0	293	268	433	252	294	278	422	330	400	284
ENSMUSG00000029861	chr6	Fam131b	42315312	42318631	4104	0.134668	-0.25307	0.752856	0.827143	0.156906	0	8	5	29	10	7	19	4	13	15	15
ENSMUSG00000056832	chr6	Ttc26	38381469	38381593	4673	-0.11717	0.504778	0.752752	0.827143	0.056277	0	23	10	34	16	29	12	26	27	27	23
ENSMUSG00000099481	chr7	Xndc1	1.02E+08	1.02E+08	5278	-0.07477	2.149061	0.753104	0.827336	0.03489	0	47	42	111	80	87	65	92	76	91	62
ENSMUSG00000030399	chr7	Ckm	19411094	19411146	1415	-0.0571	14.61919	0.753489	0.82769	0.039633	0	463777	311942	553985	317894	390940	376522	469319	428388	668802	334282
ENSMUSG00000050270	chr11	Tmem220	67025154	67025271	1669	-0.09122	0.717831	0.753583	0.827724	0.057931	0	24	26	32	14	30	20	37	24	38	19
ENSMUSG00000057156	chr14	Homez	54852736	54858281	5907	-0.07377	1.792328	0.754386	0.828537	0.036135	0	57	36	79	52	54	45	72	49	76	58
ENSMUSG00000027804	chr3	Ppid	79591342	79591557	4638	0.055579	5.708884	0.754621	0.828727	0.034918	0	831	761	1008	592	817	731	1288	929	1052	881
ENSMUSG00000025185	chr19	Loxl4	42593982	42595404	4213	0.08555	0.781082	0.754821	0.828879	0.077898	0	13	14	54	19	32	27	52	23	28	22
ENSMUSG00000000399	chr6	Ndufa9	1.27E+08	1.27E+08	1322	-0.06132	7.882288	0.755177	0.8292	0.045997	0	2870	2037	4060	5336	5306	3092	5455	3449	6230	3368
ENSMUSG00000083567	chr2	Gm11451	1.63E+08	1.63E+08	630	0.087412	1.980206	0.755741	0.829751	0.0559	0	61	44	99	36	63	36	102	79	88	63
ENSMUSG00000037017	chr5	Zscan21	1.38E+08	1.38E+08	3198	0.047126	4.227594	0.756094	0.83007	0.022066	0	244	226	420	295	292	293	455	314	404	274

ENSMUSG00000024440	chr18	Pcdh12	38267092	38269211	6055	0.084045	1.972269	0.756654	0.830537	0.075323	0	36	22	77	93	79	43	80	72	88	76
ENSMUSG00000029344	chr5	Tpst2	1.12E+08	1.12E+08	2789	0.05592	3.848529	0.756718	0.830537	0.035882	0	189	116	254	293	287	247	283	256	308	226
ENSMUSG00000030869	chr7	Ndufab1	1.22E+08	1.22E+08	6883	0.056084	7.363874	0.756625	0.830537	0.038536	0	2335	1583	2590	3293	3078	2433	4365	2506	3951	2375
ENSMUSG00000038705	chr2	Gmeb2	1.81E+08	1.81E+08	4988	-0.05659	3.176928	0.75677	0.830537	0.026745	0	123	85	224	150	168	141	211	138	176	136
ENSMUSG00000028899	chr4	Taf12	1.32E+08	1.32E+08	4038	0.0545	4.949469	0.756891	0.830601	0.032342	0	461	439	620	392	468	509	748	424	711	491
ENSMUSG00000022889	chr16	Mrpl39	84717576	84718384	2533	0.047772	4.668927	0.757144	0.830713	0.024667	0	358	255	460	439	494	367	645	429	555	383
ENSMUSG00000040842	chr4	Szrd1	1.41E+08	1.41E+08	3327	-0.04477	7.223192	0.757195	0.830713	0.024717	0	2198	1647	3078	2417	2898	2089	3287	2513	3357	2287
ENSMUSG00000053470	chr6	Kdm3a	71588974	71589715	4921	-0.05545	3.623891	0.757092	0.830713	0.030067	0	140	157	329	170	227	187	306	184	225	195
ENSMUSG00000096458	chr12	Moap1	1.03E+08	1.03E+08	1328	-0.06403	2.696376	0.757244	0.830713	0.042588	0	73	87	106	124	127	83	174	102	119	98
ENSMUSG00000089979	chr16	Gm15954	18069214	18069335	466	0.062562	3.574928	0.757325	0.830733	0.03652	0	178	159	192	166	212	206	227	201	319	154
ENSMUSG00000019080	chr15	Mfsd3	76701542	76702350	2169	-0.05358	3.332224	0.757581	0.830946	0.025221	0	132	107	216	166	205	159	192	158	221	160
ENSMUSG00000047514	chr10	Tspyl1	34282190	34285275	3086	-0.04493	6.36595	0.757676	0.830981	0.02481	0	1151	1047	1884	1176	1490	1119	1903	1329	1835	1297
ENSMUSG00000057738	chr2	Sptan1	29965560	29965785	11428	-0.05287	5.688512	0.757993	0.83126	0.032719	0	551	517	1244	1002	1020	705	956	1115	1048	771
ENSMUSG00000007415	chr5	Gatad1	3632932	3634030	4125	-0.04497	6.02733	0.758515	0.831711	0.024905	0	931	769	1307	1111	1180	941	1527	1017	1426	996
ENSMUSG00000028772	chr4	Zcchc17	1.3E+08	1.3E+08	4560	0.047563	5.45569	0.75862	0.831711	0.02549	0	595	592	796	650	770	699	1003	712	1017	657
ENSMUSG00000030982	chr7	9030624J02Rik	1.19E+08	1.19E+08	8969	0.046275	4.508483	0.758717	0.831711	0.024346	0	363	208	474	332	436	320	474	441	512	361
ENSMUSG00000062169	chr1	Cnih4	1.81E+08	1.81E+08	3783	-0.04359	5.401033	0.758659	0.831711	0.022208	0	555	458	906	755	798	617	980	662	898	658
ENSMUSG00000067276	chrX	Capn6	1.44E+08	1.44E+08	7795	-0.08631	1.823292	0.758538	0.831711	0.054225	0	44	23	106	52	74	46	69	46	82	62
ENSMUSG00000015766	chr6	Eps8	1.37E+08	1.37E+08	5731	-0.07923	2.806431	0.758998	0.83188	0.057607	0	74	66	241	96	126	79	163	158	111	102
ENSMUSG00000026975	chr2	Dph7	24962400	24962625	2365	-0.06527	2.113817	0.758983	0.83188	0.03937	0	64	58	88	56	79	59	116	60	78	67
ENSMUSG00000048349	chr14	Pou4f1	1.04E+08	1.04E+08	4672	-0.11926	1.834915	0.759243	0.83208	0.173937	0	73	72	86	20	24	51	78	60	102	24
ENSMUSG00000038587	chr10	Akap12	4266329	4266668	6244	-0.06137	3.625041	0.759331	0.832109	0.036728	0	135	106	294	213	296	147	302	190	243	221
ENSMUSG00000001524	chr17	Gtf2h4	35667730	35668002	3313	0.053578	3.814919	0.759794	0.832546	0.026792	0	193	177	241	238	234	218	305	218	340	224
ENSMUSG00000032869	chr2	Psmf1	1.52E+08	1.52E+08	6441	0.046157	4.058701	0.759887	0.83258	0.024855	0	241	138	371	257	335	234	358	313	383	258
ENSMUSG00000015083	chr2	C8g	25498651	25498823	1493	0.096722	0.864581	0.760242	0.8329	0.047487	0	20	23	32	28	29	29	45	22	33	32
ENSMUSG00000021476	chr13	Habp4	64161866	64162334	2566	-0.04992	5.165444	0.760487	0.833006	0.028993	0	436	378	719	696	726	535	678	544	771	659
ENSMUSG00000049184	chr8	Purg	33386325	33387531	2119	-0.09985	0.836515	0.760527	0.833006	0.05047	0	17	23	38	24	39	26	34	34	25	27
ENSMUSG00000075514	chr2	Gm13375	20969054	20969383	854	0.098114	0.750713	0.760434	0.833006	0.060002	0	15	16	24	34	33	17	33	34	37	28
ENSMUSG00000032763	chr10	Ilvbl	78574500	78574665	2325	0.069843	3.431964	0.760838	0.833278	0.052883	0	116	101	155	258	204	129	231	184	274	193
ENSMUSG00000037035	chr1	Inhbb	1.19E+08	1.19E+08	4255	0.122909	1.277617	0.761086	0.833481	0.129031	0	33	51	42	19	24	38	45	63	29	41
ENSMUSG00000036339	chr14	Tmem260	48446128	48446335	8165	-0.07003	2.027342	0.761232	0.833572	0.032409	0	58	38	97	63	77	59	82	76	86	52
ENSMUSG00000026806	chr2	Ddx31	28840406	28840860	3534	0.053207	2.882709	0.761763	0.834084	0.030082	0	96	61	178	123	131	109	175	129	163	106
ENSMUSG00000022314	chr15	Rad21	51962605	51964247	3604	0.050042	5.944324	0.761864	0.834126	0.031769	0	744	578	1362	1020	1280	673	1394	1136	1412	1158
ENSMUSG00000039115	chr9	Itga9	1.19E+08	1.19E+08	7691	0.077273	3.129636	0.76217	0.834392	0.07515	0	64	80	245	163	158	123	186	254	134	106
ENSMUSG00000048772	chr4	Tmem53	1.17E+08	1.17E+08	1713	0.129152	0.935591	0.76234	0.83451	0.107916	0	32	19	21	36	26	27	32	60	34	18
ENSMUSG00000032330	chr9	Cox7a2	79755241	79755605	754	0.056202	7.196768	0.762406	0.834512	0.040525	0	1943	1527	2262	3043	2638	2201	3842	2094	3687	2116
ENSMUSG00000074918	chr2	Inafm2	1.19E+08	1.19E+08	3053	0.073571	2.575047	0.762699	0.834765	0.04897	0	78	97	115	70	87	89	114	133	123	86
ENSMUSG00000075600	chr15	Zc3h3	75754432	75754950	3360	0.074087	1.930566	0.763041	0.83507	0.047406	0	62	29	79	67	55	47	80	76	99	50
ENSMUSG00000030966	chr7	Trim21	1.03E+08	1.03E+08	2775	0.094613	1.585996	0.763715	0.835739	0.07062	0	48	37	61	25	53	35	86	72	51	33
ENSMUSG00000005267	chr11	Zfp287	62700356	62700626	7632	0.108906	0.275842	0.763981	0.835961	0.062244	0	13	17	23	9	23	12	31	24	21	17
ENSMUSG00000026154	chr1	1110058L19Rik	23995939	23996360	874	0.059268	4.231211	0.764213	0.836145	0.039438	0	230	206	282	414	314	244	469	283	441	328
ENSMUSG00000058492	chr9	Scp2-ps2	1.23E+08	1.23E+08	432	-0.06042	2.155836	0.764503	0.836394	0.039101	0	69	63	85	68	65	59	105	81	84	62
ENSMUSG00000016503	chr5	Gtf3a	1.47E+08	1.47E+08	2548	-0.0463	4.812593	0.765009	0.836865	0.028075	0	385	409	536	457	450	429	622	414	623	438
ENSMUSG00000020681	chr11	Ace	1.06E+08	1.06E+08	5287	-0.06257	6.110604	0.765249	0.836865	0.049998	0	880	618	2353	875	1310	1291	1138	1156	1654	874
ENSMUSG00000030663	chr7	1110004F10Rik	1.16E+08	1.16E+08	1495	0.042357	5.377667	0.765112	0.836865	0.021378	0	617	468	830	603	766	581	958	725	970	648
ENSMUSG00000031068	chr7	Glrx3	1.37E+08	1.37E+08	1651	-0.05132	6.949848	0.765212	0.836865	0.03538	0	1953	1810	2374	1842	1832	1928	2883	1829	2875	1697
ENSMUSG00000063760	chr10	Rnf217	31493193	31502731	11013	-0.0491	4.415871	0.765148	0.836865	0.026351	0	291	184	549	345	429	275	455	338	513	348
ENSMUSG00000033697	chr15	Arhgap39	76723985	76725176	7367	-0.07249	2.058116	0.765825	0.837425	0.039492	0	40	44	113	68	80	54	81	63	92	72
ENSMUSG00000002635	chr7	Pdcd2l	34184499	34184811	1315	0.052811	3.710655	0.765897	0.837436	0.029436	0	197	152	254	203	210	185	326	226	225	241
ENSMUSG00000086610	chr5	Gm15408	1.49E+08	1.49E+08	1379	-0.05828	1.716386	0.766118	0.837572	0.037713	0	46	43	60	58	50	47	64	60	67	46
ENSMUSG00000089902	chr2	Gm13625	69871412	69871842	480	0.110657	1.122181	0.766148	0.837572	0.063879	0	34	33	39	26	23	25	61	35	53	27
ENSMUSG00000097885	chr3	5031434O11Rik	51560035	51560208	3731	0.125486	0.738762	0.76666	0.838063	0.120946	0	21	33	29	11	22	38	20	33	28	25
ENSMUSG00000029199	chr5	Lias	65391497	65391673	4570	-0.04584	5.590395	0.766803	0.838149	0.027699	0	649	555	904	902	899	738	1206	678	1081	678
ENSMUSG00000036309	chr11	Skp1a	52231995	52232118	2211	0.052768	7.714087	0.766878	0.838162	0.037119	0	2975	3252	4105	2741	2993	3056	5065	3375	5104	3199
ENSMUSG00000000738	chr8	Spg7	1.23E+08	1.23E+08	4188	-0.04598	7.04415	0.767034	0.838212	0.02863	0	1826	1593	2679	2251	2387	1939	2960	2012	3447	1725
ENSMUSG00000097388	chr7	Gm3200	1.01E+08	1.01E+08	1002	0.112365	-0.022	0.76705	0.838212	0.120699	0	5	9	18	23	13	7	10	23	22	20
ENSMUSG00000020190	chr10	Mknk2	80665332	80667332	3065	-0.04956	7.910191	0.767351	0.838472	0.033239	0	3097	2220	5521	4879	4360	3103	4978	4752	5721	3304
ENSMUSG00000062397	chr15	Zfp706	36997031	37000923	4413	0.046785	5.85367	0.767596	0.838671	0.027809	0	888	752	1284	716	892	852	1326	1009	1298	905
ENSMUSG00000082516	chr2	Gm13342	22410525	22410731	207	-0.14205	0.275541	0.767738	0.838757	0.066132	0	11	9	34	21	21	15	23	19	14	23
ENSMUSG00000074698	chr2	Csnk2a1	1.52E+08	1.52E+08	7089	-0.04366	7.104816	0.768184	0.839175	0.025907	0	2037	1685	2972	2056	2461	2106	2906	2124	3231	2075
ENSMUSG00000073485	chr1	H3f3aos	1.81E+08	1.81E+08	3044	0.092861	1.11487	0.768397	0.839338	0.066652	0	36	17	29	46	29	30	44	29	55	37
ENSMUSG00000037185	chr15	Krt80	1.01E+08	1.01E+08	1774	0.1003	0.510263	0.768561	0.839449	0.069384	0	16	18	39	17	13	21	30	32	21	19
ENSMUSG00000042670	chr2	Immp1l	1.06E+08	1.06E+08	955	0.064137	5.640887	0.768944	0.839798	0.052891	0	809	837	814	590	653	815	1398	781	1063	661
ENSMUSG00000023963	chr17	Cyp39a1	43667425	43667794	3053	-0.06464	3.09293	0.769398	0.840157	0.041269	0	85	89	173	171	186	112	200	132	146	160
ENSMUSG00000039067	chr8	Psmd7	1.08E+08	1.08E+08	1599	-0.04746	7.362552	0.769526	0.840157	0.031402	0	2417	2402	3326	2238	2806	2351	3702	2570	3950	2398

ENSMUSG00000040705	chr7	A930016O22Rik	19418812	19419553	1214	0.246858	5.246796	0.769424	0.840157	0.814422	0	34	45	1695	1158	279	34	60	1048	2019	757
ENSMUSG00000059022	chr6	Kcp	29473162	29473780	7806	-0.09607	1.660343	0.769465	0.840157	0.066353	0	39	23	73	61	65	38	42	65	53	65
ENSMUSG00000027611	chr2	Procr	1.56E+08	1.56E+08	2031	0.071359	3.208108	0.769843	0.840433	0.064162	0	131	109	248	95	147	188	152	228	175	94
ENSMUSG00000038518	chr13	Jarid2	44729474	44729777	9715	0.046942	4.916456	0.769958	0.84049	0.028129	0	488	306	719	376	526	414	811	524	594	480
ENSMUSG00000029699	chr5	Ssc4d	1.36E+08	1.36E+08	2976	0.134351	0.027901	0.770089	0.840495	0.058086	0	15	13	18	8	15	15	20	14	18	19
ENSMUSG00000038400	chr2	Pmepa1	1.73E+08	1.73E+08	4913	0.068006	4.760794	0.77003	0.840495	0.060207	0	555	336	537	238	405	408	419	605	608	451
ENSMUSG00000028568	chr4	Btf3l4	1.09E+08	1.09E+08	4546	-0.0446	4.332564	0.770168	0.840512	0.027579	0	325	265	428	282	317	263	525	320	445	284
ENSMUSG00000018820	chr19	Zfyve27	42163951	42164050	8623	0.043782	3.872545	0.770378	0.840565	0.021815	0	178	167	315	230	272	230	300	236	352	233
ENSMUSG00000021265	chr12	Slc25a29	1.09E+08	1.09E+08	2606	0.081319	3.118743	0.770325	0.840565	0.087281	0	65	51	146	223	208	92	210	175	196	144
ENSMUSG00000032567	chr9	Aste1	1.05E+08	1.05E+08	6367	0.115633	0.798918	0.770407	0.840565	0.062693	0	16	29	34	21	24	23	41	38	35	19
ENSMUSG00000026914	chr2	Psmd14	61711694	61711873	2820	-0.04775	5.853372	0.770493	0.84059	0.031935	0	815	911	1165	768	944	874	1332	900	1251	860
ENSMUSG00000011958	chr9	Bnip2	69989466	69989689	3455	-0.04188	6.541089	0.770585	0.840621	0.024185	0	1283	1180	2035	1436	1647	1348	2103	1487	2047	1444
ENSMUSG00000038930	chr7	Rccd1	80316596	80317050	3630	0.073415	2.283839	0.770648	0.840621	0.052818	0	89	61	99	52	66	76	99	102	83	80
ENSMUSG00000034248	chr14	Slc25a37	69241848	69245354	6021	0.043095	4.670934	0.770742	0.840654	0.024588	0	364	244	618	339	496	399	532	486	588	355
ENSMUSG00000027314	chr2	Dll4	1.19E+08	1.19E+08	3852	0.061659	2.710732	0.771328	0.841224	0.048577	0	65	49	140	124	146	85	139	150	130	97
ENSMUSG00000022179	chr14	4931414P19Rik	54583663	54584706	2585	0.07242	1.872059	0.771497	0.841339	0.038889	0	55	37	59	60	65	53	75	62	72	68
ENSMUSG00000032615	chr11	Nt5m	59839447	59839756	3361	-0.05223	4.050141	0.77216	0.841993	0.034342	0	255	137	296	335	332	210	351	284	413	241
ENSMUSG00000020085	chr10	Aifm2	61715263	61715352	4121	-0.06102	4.236641	0.772228	0.841997	0.049376	0	259	229	316	382	326	265	318	501	338	235
ENSMUSG00000021748	chr14	Pdhb	8165991	8166481	1485	-0.05105	8.163805	0.772428	0.842078	0.037208	0	3774	3160	4841	5854	5669	4117	7265	3966	6978	3964
ENSMUSG00000059173	chr2	Pde1a	79834453	79836924	6012	-0.08569	1.639559	0.772428	0.842078	0.084154	0	35	49	71	28	67	31	56	87	60	34
ENSMUSG00000019326	chr11	Aoc3	1.01E+08	1.01E+08	4621	0.119811	4.373968	0.772723	0.842329	0.196267	0	553	296	325	113	189	213	276	789	284	346
ENSMUSG00000036160	chr2	Surf6	26888628	26889378	4071	-0.05057	3.338508	0.772855	0.842404	0.024684	0	122	118	219	160	209	154	214	170	197	160
ENSMUSG00000020482	chr11	Ccdc117	5528887	5531533	3372	-0.04136	4.890025	0.773063	0.842461	0.021974	0	380	317	661	502	587	381	677	556	650	428
ENSMUSG00000063787	chr14	Chchd1	20703027	20703197	587	0.057032	5.994177	0.773052	0.842461	0.043704	0	1033	941	974	937	896	989	1711	942	1424	946
ENSMUSG00000072955	chrX	Tmsb15l	1.37E+08	1.37E+08	816	-0.0994	1.191229	0.773098	0.842461	0.119211	0	35	52	37	21	25	42	47	35	53	18
ENSMUSG00000011960	chr15	Ccnt1	98538689	98544608	9157	0.044115	4.056002	0.773549	0.842884	0.025309	0	211	175	438	206	319	215	378	291	375	286
ENSMUSG00000024970	chr19	AI846148	7356464	7358487	3183	0.054551	2.848736	0.77376	0.843044	0.028788	0	92	70	139	128	135	96	168	135	158	109
ENSMUSG00000024593	chr18	Megf10	57133090	57133730	7718	0.087489	0.102589	0.774278	0.843539	0.053751	0	9	10	24	18	15	18	24	13	18	17
ENSMUSG00000042873	chr6	Lhfpl4	1.13E+08	1.13E+08	4762	0.09051	0.873381	0.775162	0.844433	0.083104	0	13	19	27	34	42	27	40	20	31	42
ENSMUSG00000007655	chr6	Cav1	17306335	17306479	3444	-0.05229	6.985461	0.775249	0.844459	0.039723	0	1866	1551	2267	2206	2328	1602	2052	3029	2719	1894
ENSMUSG00000026712	chr2	Mrc1	14229392	14229573	6371	0.053753	4.736504	0.77548	0.84464	0.04063	0	385	301	787	255	433	445	627	514	502	375
ENSMUSG00000047166	chr15	Tigd5	75909760	75910466	2387	0.093511	0.822639	0.775629	0.844733	0.065045	0	20	13	28	33	36	23	24	30	53	27
ENSMUSG00000037072	chr3	Sep15	1.45E+08	1.45E+08	2104	0.048223	6.588655	0.775927	0.84491	0.032901	0	1487	1336	2018	1148	1486	1474	2335	1608	2023	1527
ENSMUSG00000041995	chr13	Zbed3	95325237	95325344	1894	0.074278	1.995179	0.775918	0.84491	0.049485	0	38	42	73	81	71	47	85	92	87	55
ENSMUSG00000057137	chr6	Tmem140	34863146	34863340	5687	0.049825	5.30057	0.775982	0.84491	0.032606	0	672	500	741	522	603	626	1055	645	834	536
ENSMUSG00000032526	chr9	Deb1	1.22E+08	1.22E+08	517	-0.04949	5.458921	0.776805	0.845737	0.03682	0	765	611	774	674	641	659	1077	617	1061	596
ENSMUSG00000073131	chrX	Vma21	71815924	71816334	7303	-0.0475	5.02456	0.776923	0.845795	0.031974	0	429	449	782	443	554	369	624	518	789	631
ENSMUSG00000042831	chr7	Alkbh6	30308717	30308834	3123	-0.04172	3.966197	0.777126	0.845947	0.024826	0	229	210	302	236	272	237	357	241	361	215
ENSMUSG00000085287	chr17	4833418N02Rik	87274886	87275370	2762	-0.06359	1.973289	0.777681	0.846482	0.043474	0	49	57	73	54	78	59	78	47	97	62
ENSMUSG00000010122	chr11	Slc47a1	61343401	61344528	3383	-0.09278	4.086699	0.777963	0.846719	0.123183	0	204	72	270	451	450	167	592	236	429	162
ENSMUSG00000047414	chr12	Flrt2	95692226	95692615	7721	0.054318	3.005016	0.778237	0.846948	0.040115	0	76	81	196	133	158	112	177	180	135	128
ENSMUSG00000026269	chr1	Rnpepl1	92910783	92911483	9467	-0.04467	5.960216	0.778368	0.846961	0.028184	0	857	563	1442	1117	1217	869	1194	1027	1489	1028
ENSMUSG00000087578	chr6	Ccdc142os	83106608	83107190	1083	0.107422	0.433253	0.778376	0.846961	0.092033	0	16	12	10	29	27	20	35	20	19	23
ENSMUSG00000048307	chr15	Ankrd46	36477668	36479473	2480	0.042291	4.668385	0.778443	0.846964	0.022843	0	382	275	491	382	475	330	569	467	564	431
ENSMUSG00000021518	chr13	Ptdss1	66932830	66933686	3424	0.043433	4.950339	0.778529	0.846988	0.026196	0	392	301	558	573	633	430	645	576	708	507
ENSMUSG00000020224	chr10	Llph	1.2E+08	1.2E+08	1517	0.063381	3.459623	0.779389	0.847854	0.043153	0	178	172	190	128	156	173	258	175	258	161
ENSMUSG00000020447	chr11	Npc1l1	6211013	6211660	4467	0.090205	0.542111	0.779743	0.848169	0.077951	0	21	10	38	14	25	20	33	36	16	20
ENSMUSG00000015305	chr10	Sash1	8722219	8725760	7183	0.042473	4.052191	0.779937	0.848311	0.027256	0	191	169	424	225	341	252	306	295	363	299
ENSMUSG00000037434	chr1	Slc30a1	1.92E+08	1.92E+08	5244	0.050676	3.441676	0.780272	0.848606	0.029478	0	115	132	211	172	225	128	262	193	247	183
ENSMUSG00000090394	chr1	4930523C07Rik	1.6E+08	1.6E+08	10195	-0.05658	2.167658	0.780702	0.849004	0.039399	0	55	57	95	67	87	55	101	99	91	51
ENSMUSG00000025324	chr7	Atp10a	58658202	58658915	5469	-0.08387	1.552526	0.78137	0.849659	0.048164	0	35	25	62	49	68	44	55	39	51	58
ENSMUSG00000042203	chr17	Tbc1d22b	29549788	29549994	4139	-0.04409	3.891776	0.781432	0.849659	0.023404	0	217	138	314	254	297	196	321	257	320	239
ENSMUSG00000028465	chr4	Tln1	43531519	43532085	9801	-0.06166	6.793795	0.781628	0.849695	0.057842	0	1077	764	2471	2506	2719	1362	2044	1929	2943	1755
ENSMUSG00000034639	chr6	Setmar	1.08E+08	1.08E+08	1765	0.068394	2.358126	0.781658	0.849695	0.047106	0	79	42	129	79	73	59	136	84	140	65
ENSMUSG00000045854	chr4	Lyrm2	32800253	32800335	1140	-0.0503	3.654794	0.781561	0.849695	0.037675	0	225	174	208	169	214	214	275	191	268	173
ENSMUSG00000022791	chr16	Tnk2	32643874	32643942	5496	-0.04521	6.004906	0.782074	0.850077	0.030562	0	845	577	1400	1210	1321	778	1558	1027	1508	1006
ENSMUSG00000101013	chr5	A630072M18Rik	20950989	20956398	5410	-0.08192	1.042783	0.78264	0.850623	0.047108	0	16	29	44	29	45	27	42	31	44	30
ENSMUSG00000040631	chr8	Dok4	94863828	94865247	2604	-0.05633	2.674732	0.78281	0.850738	0.037412	0	86	62	112	131	124	78	140	100	157	96
ENSMUSG00000020389	chr11	Cdkl3	52004221	52004417	5360	-0.08614	0.916723	0.783088	0.85089	0.06073	0	21	15	34	47	31	22	45	31	35	26
ENSMUSG00000039166	chr10	Akap7	25169090	25171248	4375	0.056989	3.079292	0.783049	0.85089	0.037735	0	127	84	122	161	154	122	172	156	208	124
ENSMUSG00000045201	chr14	Lrrc3b	15357519	15358761	1835	0.127658	0.010937	0.78327	0.85089	0.076656	0	13	10	8	11	26	12	24	15	20	15
ENSMUSG00000061104	chr8	Gm10094	95825354	95826133	780	0.073425	2.392333	0.783256	0.85089	0.051386	0	77	86	87	69	68	81	134	81	110	79
ENSMUSG00000087404	chr11	Gm11752	1.19E+08	1.19E+08	510	0.157731	1.344496	0.783185	0.85089	0.278705	0	36	66	48	8	10	30	76	68	52	18
ENSMUSG00000021038	chr12	Vipas39	87238875	87239836	2701	0.052165	3.235182	0.783481	0.851049	0.032648	0	105	105	172	170	185	137	253	176	180	128
ENSMUSG00000021892	chr14	Sh3bp5	31359880	31359966	3194	-0.04212	4.621406	0.783591	0.851098	0.023201	0	346	235	626	354	499	352	556	450	536	333

ENSMUSG00000046711	chr17	Hmga1	27556620	27556711	1990	0.040017	4.579814	0.783764	0.851217	0.021503	0	346	249	472	383	444	373	512	397	587	351
ENSMUSG00000027357	chr2	Crls1	1.33E+08	1.33E+08	2082	-0.04219	3.930819	0.784053	0.851231	0.026571	0	250	193	309	227	240	227	363	270	305	206
ENSMUSG00000027722	chr3	Spata5	37419896	37420500	3788	-0.04888	2.897554	0.78407	0.851231	0.030079	0	104	93	158	130	112	112	152	117	176	106
ENSMUSG00000029446	chr5	Psph	1.3E+08	1.3E+08	4010	0.048554	3.335177	0.784116	0.851231	0.028193	0	164	96	225	132	182	148	251	179	207	149
ENSMUSG00000036863	chr3	Syde2	1.46E+08	1.46E+08	5495	-0.1262	0.511093	0.784162	0.851231	0.12568	0	15	23	43	7	25	24	22	35	16	15
ENSMUSG00000046658	chr5	Zfp316	1.43E+08	1.43E+08	6891	-0.05427	3.029396	0.784115	0.851231	0.030699	0	94	76	187	131	192	116	164	137	187	122
ENSMUSG00000057522	chr11	Spop	95414080	95414131	3159	-0.04079	8.242489	0.784044	0.851231	0.026404	0	4089	3764	6210	4382	6298	4171	7129	4792	6817	4681
ENSMUSG00000002679	chr12	Med6	81573557	81573960	1447	0.059393	2.979505	0.784431	0.851281	0.03327	0	111	110	139	101	141	117	200	122	170	122
ENSMUSG00000030098	chr6	Grip2	91761509	91763606	5849	-0.08419	2.631378	0.784358	0.851281	0.083064	0	63	33	148	123	165	87	155	59	165	87
ENSMUSG00000031634	chr8	Ufsp2	45975528	45975588	2566	-0.04469	5.20163	0.78447	0.851281	0.031699	0	560	549	685	527	591	612	834	554	785	522
ENSMUSG00000033985	chr4	Tesk2	1.17E+08	1.17E+08	4272	-0.0968	0.804156	0.784451	0.851281	0.050517	0	22	11	46	32	29	20	40	28	35	23
ENSMUSG00000056820	chr8	Tsnax	1.25E+08	1.25E+08	2391	-0.04056	6.936986	0.784529	0.851281	0.02601	0	1719	1464	2615	2038	2141	1813	2858	1800	2884	1809
ENSMUSG00000022521	chr16	Crebbp	4081328	4086198	12920	-0.04383	4.604009	0.784697	0.851393	0.025239	0	320	230	669	361	471	328	522	474	538	336
ENSMUSG00000049076	chr16	Acap2	31092413	31096446	6493	0.046621	3.532513	0.78489	0.851533	0.02871	0	135	146	277	159	200	157	254	207	219	221
ENSMUSG00000038648	chr6	Creb3l2	37327255	37332500	7283	0.046792	4.653555	0.785027	0.851612	0.034462	0	286	224	745	356	476	284	620	458	551	445
ENSMUSG00000028954	chr5	Nub1	24685815	24686022	3455	-0.03735	5.641163	0.785218	0.851749	0.021117	0	696	583	1114	809	873	737	1138	804	1046	782
ENSMUSG00000062963	chr1	Ufc1	1.71E+08	1.71E+08	2070	-0.04554	6.054769	0.785908	0.852429	0.033475	0	1102	940	1277	883	1084	1065	1439	1020	1526	947
ENSMUSG00000078851	chr11	Hist3h2a	58954685	58956830	2146	-0.05625	3.790964	0.78609	0.852556	0.049446	0	256	209	267	159	197	225	222	253	343	184
ENSMUSG00000021124	chr12	Vti1b	79156017	79156571	1612	0.04333	6.070918	0.786184	0.852588	0.028263	0	965	887	1259	1031	1074	989	1611	1075	1500	1094
ENSMUSG00000019984	chr10	Med23	24869986	24870146	6692	-0.05891	2.942432	0.786349	0.852698	0.036185	0	87	67	190	121	181	97	164	154	148	117
ENSMUSG00000027660	chr3	Skil	31095058	31095157	9694	-0.07227	3.480086	0.786741	0.853053	0.072053	0	106	100	260	239	236	99	227	143	224	287
ENSMUSG00000032435	chr9	Dync1li1	1.15E+08	1.15E+08	2601	-0.03965	5.25332	0.787909	0.85425	0.024704	0	611	454	807	498	729	569	809	590	924	564
ENSMUSG00000045576	chr3	St7l	1.05E+08	1.05E+08	7583	-0.04411	3.618163	0.787988	0.854265	0.026947	0	177	134	291	199	203	156	332	191	241	191
ENSMUSG00000020527	chr11	Myo19	84880148	84880511	7113	-0.09122	1.013286	0.788279	0.854441	0.076869	0	24	17	41	44	34	21	48	51	25	24
ENSMUSG00000051864	chr15	Tbc1d22a	86214459	86214636	3229	0.037805	4.64797	0.788261	0.854441	0.020584	0	339	269	550	409	431	372	528	443	581	394
ENSMUSG00000024240	chr18	Epc1	6435951	6437307	4475	0.039316	4.166033	0.788461	0.854568	0.022323	0	234	184	425	299	296	253	393	358	376	276
ENSMUSG00000050555	chr9	Hyls1	35560820	35562104	5970	0.097522	0.17986	0.788542	0.854587	0.058962	0	18	8	24	15	15	17	14	22	23	19
ENSMUSG00000086432	chr12	B430119L08Rik	1.04E+08	1.04E+08	1994	0.24513	-0.57686	0.788815	0.854813	0.565171	0	17	11	9	1	1	21	4	23	2	3
ENSMUSG00000027937	chr3	Jtb	90231597	90232040	1531	0.046281	5.979967	0.788944	0.854882	0.032936	0	903	934	1164	848	1000	974	1442	1008	1551	934
ENSMUSG00000020181	chr10	Nav3	1.1E+08	1.1E+08	13806	0.077643	0.525586	0.789087	0.854968	0.093271	0	10	12	45	19	23	15	36	20	18	34
ENSMUSG00000028833	chr4	Ncdn	1.27E+08	1.27E+08	3710	-0.04105	4.402937	0.78932	0.85515	0.023696	0	304	246	489	307	385	299	371	399	474	344
ENSMUSG00000009633	chr1	G0s2	1.93E+08	1.93E+08	871	0.087763	4.185143	0.790086	0.855841	0.122274	0	174	154	201	543	316	168	540	521	264	238
ENSMUSG00000028252	chr4	Ccnc	21727701	21727915	5115	0.048355	3.014709	0.790046	0.855841	0.026864	0	121	91	156	114	147	114	185	125	185	136
ENSMUSG00000024526	chr18	Cidea	67343564	67343840	1164	-0.15738	0.401844	0.79068	0.856414	0.278651	0	10	11	4	49	26	20	8	25	35	16
ENSMUSG00000074182	chr3	Znhit6	1.46E+08	1.46E+08	2813	0.043548	3.595057	0.7908	0.856474	0.023774	0	151	145	259	188	209	199	268	189	286	174
ENSMUSG00000005510	chr2	Ndufs3	90894634	90894877	2178	-0.04656	8.015879	0.791122	0.856753	0.036957	0	3327	3286	4255	5076	4814	4019	6176	3620	6305	3507
ENSMUSG00000040213	chr3	Ccbl2	1.43E+08	1.43E+08	2619	0.051905	3.689173	0.791467	0.857057	0.038327	0	127	147	217	225	300	151	317	226	270	236
ENSMUSG00000037347	chrX	Chst7	20059560	20061208	2206	-0.07316	0.907715	0.791585	0.857114	0.045277	0	21	22	30	35	37	28	38	34	34	23
ENSMUSG00000020677	chr11	Ddx52	83942062	83942264	3332	-0.03771	4.329526	0.791947	0.857436	0.02295	0	302	258	438	279	346	283	490	317	432	300
ENSMUSG00000051177	chr2	Plcb1	1.35E+08	1.35E+08	8685	-0.0892	1.251582	0.792173	0.857611	0.072633	0	24	23	52	31	64	24	38	63	43	32
ENSMUSG00000074476	chr9	Spc24	21755442	21756295	1349	-0.08747	1.233591	0.792797	0.858216	0.114064	0	31	57	40	22	25	44	39	34	45	35
ENSMUSG00000023919	chr17	Cenpq	40923051	40923616	2604	-0.06696	1.833604	0.793017	0.858385	0.055093	0	39	42	86	74	45	46	102	50	64	51
ENSMUSG00000073838	chr7	Tufm	1.26E+08	1.26E+08	1776	0.049842	6.691202	0.793487	0.858823	0.042485	0	1279	893	1647	2225	2159	1445	2335	1638	2838	1528
ENSMUSG00000032175	chr9	Tyk2	21104069	21105183	4619	0.043085	3.726135	0.793581	0.858854	0.029495	0	188	131	312	202	223	220	224	278	286	195
ENSMUSG00000031750	chr8	Il34	1.11E+08	1.11E+08	1959	-0.0508	3.080349	0.793713	0.858927	0.031763	0	118	109	185	108	165	125	144	161	164	145
ENSMUSG00000037640	chr7	Zfp60	27731389	27731470	8390	-0.05074	2.932989	0.793821	0.858974	0.031982	0	91	102	190	107	132	129	143	129	153	115
ENSMUSG00000001576	chr17	Ergic1	26561489	26561632	6456	0.038126	5.414466	0.794492	0.859489	0.024361	0	604	429	1057	626	731	583	825	830	1039	678
ENSMUSG00000021039	chr12	Snw1	87449936	87450716	2231	-0.0418	6.1588	0.794461	0.859489	0.03074	0	980	1078	1468	1050	1124	1081	1627	1161	1572	1027
ENSMUSG00000026688	chr1	Mgst3	1.67E+08	1.67E+08	1097	-0.0547	7.367942	0.794473	0.859489	0.052452	0	2419	1661	3097	3271	3068	2747	4083	1625	4659	2076
ENSMUSG00000001143	chr1	Lman2l	36419871	36420035	7359	0.038974	4.965145	0.795176	0.860089	0.02583	0	400	310	621	506	668	445	642	602	601	567
ENSMUSG00000052798	chr10	Nup107	1.18E+08	1.18E+08	3111	-0.0466	2.948077	0.79513	0.860089	0.0281	0	107	85	170	135	128	103	190	138	150	109
ENSMUSG00000002881	chr1	Nab1	52457294	52459306	4100	-0.04867	3.56562	0.795309	0.860094	0.031706	0	129	117	237	211	286	160	276	190	241	193
ENSMUSG00000028617	chr4	Lrrc42	1.07E+08	1.07E+08	2139	-0.0463	3.173833	0.79531	0.860094	0.034241	0	146	121	199	104	154	111	174	176	215	132
ENSMUSG00000090625	chr2	Gm20721	1.74E+08	1.74E+08	1484	-0.21319	2.549416	0.795982	0.860751	0.739378	0	7	7	267	221	55	6	9	149	200	122
ENSMUSG00000039943	chr2	Plcb4	1.36E+08	1.36E+08	8970	-0.04627	4.195209	0.796525	0.861267	0.031427	0	189	171	426	334	419	215	445	320	387	293
ENSMUSG00000028633	chr4	Ctps	1.21E+08	1.21E+08	3316	-0.03922	4.377223	0.796639	0.861277	0.025124	0	324	237	475	286	374	276	553	352	404	303
ENSMUSG00000032598	chr9	Nckipsd	1.09E+08	1.09E+08	4656	0.042065	3.142071	0.796663	0.861277	0.029927	0	110	78	201	145	174	132	188	187	167	131
ENSMUSG00000025236	chr9	Adpgk	59291572	59291866	2470	-0.04938	3.10107	0.796816	0.86132	0.028618	0	121	93	226	120	147	124	152	162	184	135
ENSMUSG00000027890	chr3	Gstm4	1.08E+08	1.08E+08	1707	0.047377	4.141665	0.796833	0.86132	0.033192	0	298	225	367	213	265	299	326	285	430	281
ENSMUSG00000040848	chr1	Sft2d2	1.65E+08	1.65E+08	5702	0.037979	5.126753	0.797015	0.861447	0.024675	0	494	355	915	461	613	469	798	675	748	554
ENSMUSG00000029598	chr5	Plbd2	1.2E+08	1.2E+08	6620	0.063647	5.391425	0.797435	0.86183	0.073039	0	358	259	728	1039	1031	567	758	772	1042	766
ENSMUSG00000022364	chr15	Tbc1d31	57912199	57912391	6366	-0.07063	1.510496	0.797742	0.862092	0.049261	0	36	39	69	29	55	34	55	53	47	53
ENSMUSG00000072837	chr10	Mir546	1.27E+08	1.27E+08	121	-0.03978	3.945446	0.798059	0.862364	0.024929	0	225	168	385	216	275	193	378	226	379	232
ENSMUSG00000057594	chr11	Arl16	1.2E+08	1.2E+08	2742	0.066277	1.817951	0.798674	0.862958	0.038592	0	50	37	53	58	68	43	76	66	79	57
ENSMUSG00000026604	chr1	Ptpn14	1.9E+08	1.9E+08	13413	-0.04483	4.437846	0.799304	0.863499	0.031884	0	261	200	567	376	420	218	480	378	529	371

ENSMUSG00000037669	chr12	1110057K04Rik	8208107	8208192	2748	0.049694	3.396941	0.799302	0.863499	0.036158	0	142	129	197	160	190	138	217	257	182	167
ENSMUSG00000027582	chr2	Zgpat	1.81E+08	1.81E+08	5624	0.038083	4.01774	0.799569	0.863705	0.025201	0	232	146	371	271	279	253	320	306	329	269
ENSMUSG00000035845	chr15	Alg12	88805244	88806054	2356	-0.061	1.836717	0.799626	0.863705	0.037839	0	41	41	73	63	68	47	60	66	71	63
ENSMUSG00000023186	chr9	Vwa5a	38718268	38718387	4899	0.037782	5.159339	0.799873	0.863723	0.024026	0	477	429	894	464	604	489	886	632	747	572
ENSMUSG00000036537	chrX	Rnf113a1	37191245	37192467	1223	0.07314	0.911935	0.799899	0.863723	0.051183	0	28	20	36	21	34	26	30	45	35	28
ENSMUSG00000059842	chr2	Zfp341	1.55E+08	1.55E+08	3299	0.068258	1.714313	0.799968	0.863723	0.046791	0	46	33	51	64	52	52	70	59	55	57
ENSMUSG00000090523	chr18	Gypc	32528322	32530201	2331	0.046726	5.207975	0.799961	0.863723	0.037584	0	645	447	839	424	541	695	813	556	832	517
ENSMUSG00000103715	chr9	RP23-58N8.6	85749078	85750429	1352	0.096049	1.205777	0.799826	0.863723	0.063867	0	29	39	39	25	34	25	44	36	69	37
ENSMUSG00000041530	chr4	Ago1	1.26E+08	1.26E+08	8120	-0.05019	3.907063	0.800062	0.863754	0.033671	0	165	123	426	259	307	230	285	278	331	212
ENSMUSG00000021606	chr13	Ndufs6	73319874	73320060	629	0.045886	7.209243	0.800176	0.863766	0.038129	0	2186	1862	2203	2547	2565	2320	3939	2259	3499	1964
ENSMUSG00000048707	chr2	Tprn	25262618	25264553	2932	0.07829	1.41334	0.800203	0.863766	0.060597	0	47	28	59	26	40	34	44	51	81	33
ENSMUSG00000025917	chr1	Cops5	10024601	10025063	3766	-0.04386	7.061112	0.800856	0.8644	0.03629	0	2125	1971	2714	1830	1967	2053	3276	1987	3017	1831
ENSMUSG00000003299	chr9	Mrpl4	21002737	21002997	1285	0.044592	5.396148	0.800925	0.864404	0.035728	0	521	373	698	843	920	632	844	681	1105	664
ENSMUSG00000025089	chr19	Gfra1	58235604	58238546	5476	-0.06846	2.729314	0.801	0.864415	0.059764	0	61	65	215	93	134	80	189	128	96	94
ENSMUSG00000021054	chr12	Sgpp1	75714248	75716664	3324	0.037896	4.687336	0.801067	0.864417	0.02502	0	309	261	532	430	538	369	484	489	631	407
ENSMUSG00000023147	chr16	Wrb	96145407	96145578	4261	0.043882	3.465933	0.801377	0.864681	0.024279	0	155	140	222	161	182	160	240	190	244	182
ENSMUSG00000020053	chr10	Igf1	87858265	87859013	9904	-0.05652	4.506524	0.801583	0.864833	0.054505	0	351	240	548	272	483	240	398	624	348	386
ENSMUSG00000087381	chr4	Gm16008	1.56E+08	1.56E+08	1324	-0.08688	0.38165	0.80271	0.865979	0.049854	0	15	12	29	23	21	10	32	21	24	20
ENSMUSG00000004264	chr6	Phb2	1.25E+08	1.25E+08	3718	0.041284	6.641945	0.803394	0.866646	0.031757	0	1242	1052	1742	2026	1817	1423	2294	1732	2442	1475
ENSMUSG00000022820	chr16	Ndufb4	37647170	37647719	1170	0.041502	6.36617	0.803721	0.866858	0.03159	0	1300	913	1512	1423	1290	1290	2084	1239	1946	1183
ENSMUSG00000059363	chr19	Fxn	24261453	24262053	2053	-0.03637	4.045739	0.803677	0.866858	0.024886	0	261	213	319	249	274	241	381	256	372	243
ENSMUSG00000044864	chr3	Ankrd50	38449261	38452505	8488	-0.05267	2.999711	0.803885	0.866926	0.036715	0	94	66	194	151	162	96	150	149	188	129
ENSMUSG00000045538	chr8	Ddx28	1.06E+08	1.06E+08	2262	-0.04253	3.762508	0.803914	0.866926	0.030541	0	156	190	247	236	256	216	281	199	277	231
ENSMUSG00000045287	chr11	Rtn4rl1	75193783	75194294	3525	0.076212	1.329399	0.804023	0.866972	0.054958	0	39	30	58	22	40	33	40	54	52	44
ENSMUSG00000013858	chr10	Tmem259	79974948	79977853	4663	-0.04016	6.277444	0.804156	0.867045	0.030317	0	1079	753	1536	1537	1452	1073	1501	1364	1920	1172
ENSMUSG00000000148	chr5	Brat1	1.41E+08	1.41E+08	6179	-0.05203	2.945161	0.804504	0.867208	0.040106	0	111	90	154	126	139	86	154	139	131	164
ENSMUSG00000028343	chr4	Erp44	48193323	48194709	3418	0.038327	5.160967	0.804414	0.867208	0.024655	0	572	443	716	476	591	521	809	623	788	574
ENSMUSG00000048921	chr7	Zfp689	1.27E+08	1.27E+08	2005	-0.08617	0.286139	0.804453	0.867208	0.063721	0	18	9	24	17	25	8	30	23	18	20
ENSMUSG00000020841	chr11	Cpd	76778424	76782410	8332	0.04204	6.493839	0.804729	0.867381	0.033888	0	1262	1051	2501	1017	1474	1419	1777	1499	2314	1373
ENSMUSG00000020538	chr11	Srebf1	60199089	60200151	5634	0.052818	5.696583	0.804875	0.867397	0.053875	0	840	518	1427	605	798	785	628	1172	1300	856
ENSMUSG00000028551	chr4	Cdkn2c	1.1E+08	1.1E+08	2686	0.078894	3.541537	0.80484	0.867397	0.11	0	244	149	250	94	144	176	145	380	212	144
ENSMUSG00000026701	chr1	Prdx6	1.61E+08	1.61E+08	4804	0.042222	6.490053	0.805224	0.867703	0.033849	0	1053	969	1518	1853	1691	1342	1990	1627	2169	1275
ENSMUSG00000028798	chr4	Eif3i	1.3E+08	1.3E+08	3702	0.037983	6.657371	0.80534	0.867758	0.026931	0	1447	1294	1909	1516	1722	1567	2411	1594	2342	1507
ENSMUSG00000057143	chr7	Trim12c	1.04E+08	1.04E+08	3740	-0.05151	3.104108	0.805579	0.867944	0.05125	0	117	149	194	97	123	125	187	186	150	112
ENSMUSG00000034462	chr5	Pkd2	1.04E+08	1.04E+08	10169	-0.05358	4.105793	0.806006	0.868263	0.046	0	159	142	444	317	412	185	343	347	347	313
ENSMUSG00000042548	chr2	Asxl1	1.53E+08	1.53E+08	7428	-0.0469	3.914838	0.805946	0.868263	0.032405	0	175	124	414	261	306	182	348	238	329	263
ENSMUSG00000030894	chr7	Tpp1	1.06E+08	1.06E+08	3494	0.036653	6.006406	0.807384	0.869677	0.026609	0	782	633	1609	1017	1208	843	1437	1183	1371	1124
ENSMUSG00000058586	chr15	Serhl	83089506	83089765	7393	-0.04089	4.42925	0.807671	0.869916	0.032834	0	249	283	360	406	428	312	520	295	524	312
ENSMUSG00000044231	chr13	Nhlrc1	47012558	47014850	2293	-0.04394	3.216138	0.80784	0.870027	0.027521	0	131	114	200	135	171	124	159	169	211	160
ENSMUSG00000011254	chr11	Thg1l	45946843	45948328	3015	-0.05363	2.018834	0.808167	0.870308	0.049127	0	53	68	60	62	69	60	90	62	80	62
ENSMUSG00000020705	chr11	Ddx42	1.06E+08	1.06E+08	4228	0.035013	5.333474	0.808684	0.870653	0.022079	0	534	495	929	556	703	539	974	713	911	627
ENSMUSG00000028687	chr4	Mutyh	1.17E+08	1.17E+08	2612	-0.06086	1.212963	0.808644	0.870653	0.033386	0	33	25	46	35	43	33	55	33	47	31
ENSMUSG00000031478	chr8	Nek3	22128283	22128790	2153	0.069358	1.820272	0.808662	0.870653	0.044332	0	55	45	68	46	51	56	99	53	68	47
ENSMUSG00000020716	chr11	Nf1	79339693	79340059	15820	-0.04293	4.090459	0.808909	0.870748	0.02925	0	223	141	455	271	349	199	376	320	404	250
ENSMUSG00000026021	chr1	Sumo1	59586558	59586694	2076	-0.04115	5.506975	0.808969	0.870748	0.035316	0	648	729	853	681	662	673	1134	682	1002	648
ENSMUSG00000029094	chr5	Afap1	35893319	35893540	8543	0.051646	2.726318	0.808865	0.870748	0.036667	0	98	74	138	96	108	93	123	148	164	81
ENSMUSG00000039376	chr14	Synpo2l	20658946	20662465	4629	0.039654	7.694373	0.809162	0.870885	0.032036	0	2514	1941	5069	3264	4189	2483	4747	3226	5645	3494
ENSMUSG00000021716	chr13	Srek1ip1	1.05E+08	1.05E+08	3254	-0.03655	3.893981	0.809898	0.871606	0.02222	0	213	153	301	247	297	214	342	226	330	230
ENSMUSG00000050103	chr12	Agmo	37241641	37242167	6285	0.070316	1.886845	0.810081	0.871733	0.075302	0	60	48	78	32	62	44	70	101	54	62
ENSMUSG00000032376	chr9	Usp3	66514637	66518578	6848	-0.03917	3.432693	0.810189	0.871779	0.02507	0	159	108	262	169	188	146	251	201	227	148
ENSMUSG00000028893	chr4	Sesn2	1.32E+08	1.32E+08	3475	-0.05961	1.798863	0.810329	0.871858	0.035952	0	44	37	83	54	63	41	79	68	59	55
ENSMUSG00000018347	chr11	Zkscan6	65807175	65807261	2371	0.066838	1.661309	0.810736	0.872225	0.045748	0	46	41	50	34	66	47	61	49	70	57
ENSMUSG00000028345	chr4	Tex10	48430858	48431083	4382	-0.03728	3.753787	0.811003	0.872442	0.025547	0	178	186	312	194	218	213	305	218	290	186
ENSMUSG00000078786	chr7	BC024978	27195781	27196107	2756	0.045622	2.743167	0.811128	0.872505	0.03187	0	86	68	150	87	141	92	172	99	137	116
ENSMUSG00000020260	chr10	Pofut2	77259300	77259453	2219	0.033995	4.457088	0.811719	0.87307	0.022762	0	269	216	492	371	424	321	479	351	480	390
ENSMUSG00000026051	chr1	1500015O10Rik	43730602	43730963	902	-0.13755	1.05935	0.812126	0.873437	0.275296	0	4	26	43	37	64	26	25	40	9	60
ENSMUSG00000033703	chr8	Fuk	1.11E+08	1.11E+08	3838	-0.04838	2.454918	0.812314	0.873569	0.03117	0	84	50	121	83	108	78	115	103	108	79
ENSMUSG00000021097	chr12	Clmn	1.05E+08	1.05E+08	11962	0.090371	1.736715	0.812529	0.873658	0.152792	0	51	43	68	24	65	39	34	133	55	36
ENSMUSG00000066306	chr7	Numa1	1.02E+08	1.02E+08	7195	0.034627	5.814912	0.812483	0.873658	0.025302	0	705	515	1464	888	1053	817	1178	1026	1333	869
ENSMUSG00000037296	chr8	Lsm1	25785591	25785717	2360	0.051744	3.080092	0.812777	0.873853	0.036175	0	140	99	145	133	129	138	178	170	186	105
ENSMUSG00000006362	chr8	Cbfa2t3	1.23E+08	1.23E+08	4775	0.051181	3.788334	0.813292	0.874268	0.055382	0	124	108	289	278	325	169	300	208	274	315
ENSMUSG00000028763	chr4	Hspg2	1.37E+08	1.37E+08	14307	0.058057	7.326899	0.813294	0.874268	0.072604	0	1357	915	4383	2780	4263	2051	2931	2988	3676	3220
ENSMUSG00000032035	chr9	Ets1	32636221	32636314	8476	0.041062	3.87172	0.813791	0.874731	0.03225	0	169	124	294	265	329	171	333	269	359	236
ENSMUSG00000075703	chr5	Ept1	30232581	30232815	10855	0.036689	3.698762	0.813866	0.874741	0.026661	0	176	112	310	191	264	166	285	256	283	209
ENSMUSG00000045730	chr18	Adrb2	62177817	62179959	2143	-0.04935	4.044531	0.814124	0.874948	0.052272	0	251	227	261	167	417	216	467	231	401	205

ENSMUSG00000039043	chr7	2610034B18Rik	79925361	79926850	2277	0.060397	2.352076	0.814529	0.875312	0.045423	0	56	65	84	91	93	55	123	101	96	93
ENSMUSG00000046572	chr5	Zfp518b	38668484	38674853	6882	-0.05642	2.012481	0.814807	0.875539	0.035132	0	44	45	101	68	70	49	95	72	76	62
ENSMUSG00000029059	chr4	Fam213b	1.55E+08	1.55E+08	1027	0.046207	6.916069	0.815044	0.875724	0.045133	0	2391	1547	2138	1442	1692	1886	2570	2124	3029	1688
ENSMUSG00000032480	chr9	Dhx30	1.1E+08	1.1E+08	3726	-0.03877	4.784127	0.815161	0.875778	0.026731	0	339	241	671	480	583	403	614	515	547	400
ENSMUSG00000024948	chr19	Map4k2	6341135	6341345	6646	-0.0483	2.881668	0.815244	0.875796	0.031321	0	86	74	171	125	151	113	154	146	140	98
ENSMUSG00000059288	chr13	Cdyl	35659862	35659993	4018	-0.05109	2.243788	0.81547	0.875968	0.046333	0	62	50	117	77	79	38	116	97	105	69
ENSMUSG00000048175	chr15	Asb8	98134637	98136438	2410	0.040768	7.023321	0.815954	0.876417	0.03607	0	1573	1312	2627	2363	2564	1806	2729	1689	3758	2259
ENSMUSG00000028960	chr4	Ube4b	1.49E+08	1.49E+08	7078	-0.0353	5.103114	0.816152	0.876488	0.024478	0	423	368	905	537	635	430	712	585	868	540
ENSMUSG00000038793	chr1	Lefty1	1.81E+08	1.81E+08	1758	-0.08536	0.549724	0.816093	0.876488	0.044831	0	21	14	32	22	24	26	29	19	30	16
ENSMUSG00000030530	chr7	Furin	80388585	80391296	9178	0.032937	5.67263	0.816542	0.876836	0.023287	0	711	507	1246	747	928	735	997	906	1262	822
ENSMUSG00000053819	chr3	Camk2d	1.27E+08	1.27E+08	15928	0.035721	5.924867	0.816984	0.877239	0.026398	0	900	745	1338	791	1041	831	1243	1136	1504	941
ENSMUSG00000037362	chr15	Nov	54745702	54746037	2869	-0.08239	2.393378	0.817138	0.877333	0.119061	0	44	52	126	95	125	39	103	84	58	159
ENSMUSG00000029228	chr5	Lnx1	74592446	74592973	3988	-0.08969	1.19756	0.81723	0.877362	0.08542	0	19	13	45	55	55	32	41	48	47	25
ENSMUSG00000060227	chr2	Casc4	1.22E+08	1.22E+08	5858	-0.0471	2.851077	0.81732	0.877387	0.029227	0	87	72	166	116	153	95	139	123	158	124
ENSMUSG00000005378	chr5	Wbscr22	1.35E+08	1.35E+08	3386	-0.03348	4.295597	0.817395	0.877396	0.024499	0	307	257	384	300	315	270	406	330	450	315
ENSMUSG00000097820	chr9	E530011L22Rik	1.22E+08	1.22E+08	3304	-0.0788	0.487036	0.819213	0.879277	0.055972	0	14	15	30	22	27	13	39	15	34	17
ENSMUSG00000021497	chr13	Txndc15	55714650	55714844	1521	0.036395	5.15402	0.819411	0.879418	0.0254	0	485	497	679	534	570	535	792	600	822	552
ENSMUSG00000026766	chr2	Mmadhc	50279881	50280402	2012	-0.03467	6.797965	0.819593	0.879542	0.027535	0	1571	1390	2213	1799	2008	1633	2777	1583	2595	1610
ENSMUSG00000003208	chr17	Ccdc94	55959187	55959261	1311	0.054134	2.373717	0.81995	0.879854	0.039745	0	73	59	82	82	100	94	113	96	99	67
ENSMUSG00000056310	chr5	Tyw1	1.3E+08	1.3E+08	7388	-0.0366	3.66736	0.820744	0.880635	0.023565	0	171	143	279	196	247	182	237	247	291	181
ENSMUSG00000041775	chr7	Mapk1ip1	1.39E+08	1.39E+08	1883	-0.03389	4.248046	0.821374	0.88124	0.025074	0	284	228	415	328	273	271	408	338	428	272
ENSMUSG00000038781	chr17	Stap2	55997081	55997361	1491	0.058162	2.526786	0.821509	0.881314	0.058862	0	88	70	121	81	82	125	84	101	146	64
ENSMUSG00000021948	chr14	Prkcd	30595356	30596025	4983	0.045732	3.716266	0.821637	0.881379	0.050896	0	191	100	338	144	307	260	221	260	276	171
ENSMUSG00000096917	chr8	2500002B13Rik	57488054	57488193	2618	0.059053	2.24784	0.821731	0.881408	0.041294	0	77	63	83	66	68	78	114	76	104	63
ENSMUSG00000040441	chr10	Slc26a10	1.27E+08	1.27E+08	2215	0.078468	1.687887	0.821857	0.881472	0.084304	0	36	21	38	75	74	35	75	49	91	49
ENSMUSG00000026632	chr1	Tatdn3	1.91E+08	1.91E+08	2786	0.044992	3.237193	0.821984	0.881538	0.032134	0	124	132	192	118	166	145	244	137	190	153
ENSMUSG00000001774	chr9	Chordc1	18292267	18292460	2205	0.036199	5.380769	0.8222	0.881637	0.02721	0	578	584	839	524	734	553	877	805	933	689
ENSMUSG00000021798	chr14	Ldb3	34526699	34529549	6016	-0.03563	10.88323	0.82221	0.881637	0.030096	0	27610	17275	42788	32231	37035	24258	47028	28960	44513	29042
ENSMUSG00000032925	chr14	Itgbl1	1.24E+08	1.24E+08	4229	0.060338	3.805493	0.822565	0.881947	0.085228	0	64	136	270	276	392	210	278	247	268	272
ENSMUSG00000032481	chr9	Smarcc1	1.1E+08	1.1E+08	5672	0.031556	4.828287	0.822749	0.882072	0.021916	0	396	294	657	411	531	424	626	563	581	421
ENSMUSG00000002767	chr17	Mrpl2	46646229	46646398	1170	-0.03702	5.901414	0.822848	0.882107	0.032297	0	785	656	1042	1198	1153	801	1475	882	1492	853
ENSMUSG00000040771	chr17	Oard1	48410014	48410372	1336	-0.03347	4.308791	0.823264	0.882482	0.027224	0	274	274	390	302	342	290	525	290	439	267
ENSMUSG00000066553	chr12	Gm6969	24638669	24639010	342	-0.07328	0.591888	0.823503	0.882667	0.047623	0	19	17	30	28	21	19	36	17	28	25
ENSMUSG00000005983	chr16	1700037C18Rik	3895179	3895414	3227	-0.05247	1.085468	0.823632	0.882733	0.055681	0	22	35	40	34	31	19	52	34	47	32
ENSMUSG00000021087	chr12	Rtn1	72211752	72212577	4003	0.079298	0.374365	0.823698	0.882733	0.077455	0	11	8	19	26	30	15	18	27	32	19
ENSMUSG00000026585	chr1	Kifap3	1.64E+08	1.64E+08	4012	0.031954	5.408036	0.823768	0.882737	0.021725	0	562	543	916	604	740	615	966	734	920	691
ENSMUSG00000052915	chr11	Msl1	98795516	98796604	5433	-0.0328	6.186519	0.823858	0.882763	0.02505	0	980	785	1566	1237	1408	977	1519	1287	1822	1051
ENSMUSG00000024862	chr19	Klc2	5107746	5108688	4134	-0.03377	6.396228	0.824358	0.883155	0.027018	0	1268	950	1910	1276	1481	1150	1618	1403	2219	1288
ENSMUSG00000033157	chr16	Abhd10	45729725	45731959	3710	-0.03407	3.645116	0.824342	0.883155	0.025136	0	197	139	274	188	214	160	321	195	273	189
ENSMUSG00000022750	chr16	Klhl22	17759618	17759694	5745	-0.03344	4.953216	0.824455	0.883188	0.022562	0	426	295	742	510	598	413	659	544	648	528
ENSMUSG00000032239	chr9	Rp9	22448311	22448854	1142	0.037649	4.940677	0.824646	0.883235	0.028519	0	472	420	515	415	545	481	655	544	695	461
ENSMUSG00000046916	chr10	Myct1	5593728	5593901	2775	0.053242	2.747803	0.824699	0.883235	0.050169	0	72	59	126	133	140	66	171	100	188	109
ENSMUSG00000068523	chr3	Gng5	1.46E+08	1.47E+08	2738	0.035225	7.028052	0.824573	0.883235	0.029496	0	1819	1270	2577	2458	2283	1854	3155	2001	3050	2139
ENSMUSG00000020180	chr10	Snrpd3	75517551	75518125	3434	-0.0355	6.030655	0.82504	0.88352	0.030925	0	882	851	1203	1170	1123	956	1702	998	1467	874
ENSMUSG00000029390	chr5	Tmed2	1.25E+08	1.25E+08	2199	-0.03286	6.675482	0.825099	0.88352	0.0263	0	1538	1289	2143	1533	1739	1518	2516	1607	2234	1456
ENSMUSG00000021108	chr12	Prkch	73584797	73585525	4519	-0.04572	2.856611	0.826069	0.884488	0.037966	0	85	68	146	153	138	103	178	131	144	92
ENSMUSG00000049536	chrX	Tceal1	1.37E+08	1.37E+08	2803	-0.04969	2.15278	0.826503	0.884881	0.061687	0	50	80	67	62	84	48	99	69	87	88
ENSMUSG00000030802	chr7	Bckdk	1.28E+08	1.28E+08	3063	0.038696	7.62832	0.826742	0.884923	0.036912	0	2433	1886	3470	4100	3873	2941	5073	2968	4786	2871
ENSMUSG00000060121	chr12	Gemin2	59013393	59013613	2415	-0.04097	2.597286	0.82673	0.884923	0.036541	0	92	88	126	75	97	93	132	90	125	95
ENSMUSG00000074466	chr3	Gm15417	89391850	89392506	1669	-0.04752	4.333957	0.826613	0.884923	0.057297	0	424	304	366	231	235	316	436	331	478	259
ENSMUSG00000002409	chr7	Dyrk1b	28179469	28179640	2695	-0.03667	5.723249	0.827314	0.885392	0.031338	0	733	481	1294	901	1001	560	1155	956	1113	1002
ENSMUSG00000064090	chr11	Vrk2	26471322	26471786	6591	0.044076	2.731957	0.827311	0.885392	0.029676	0	101	78	134	81	123	101	141	113	142	108
ENSMUSG00000026885	chr2	Ttll11	35751241	35752492	4024	0.075875	1.241303	0.82757	0.885595	0.045042	0	31	29	45	30	41	28	46	46	68	27
ENSMUSG00000001763	chr6	Tspan33	29694222	29694544	5195	-0.06666	1.460637	0.827909	0.885746	0.045763	0	26	27	71	38	63	40	47	39	62	47
ENSMUSG00000017817	chr2	Jph2	1.63E+08	1.63E+08	4255	0.03444	10.17605	0.828029	0.885746	0.030117	0	16178	11942	29343	15822	20922	17905	21206	19978	27540	19784
ENSMUSG00000020261	chr11	Slc36a1	55204350	55204488	5626	0.04216	2.615231	0.827973	0.885746	0.049307	0	68	48	132	106	138	100	92	116	121	116
ENSMUSG00000026000	chr1	Lancl1	67000517	67003557	6863	-0.03578	5.537362	0.82792	0.885746	0.031713	0	807	596	992	565	768	745	907	744	1146	655
ENSMUSG00000029343	chr5	Crybb1	1.12E+08	1.12E+08	985	0.081679	0.987486	0.828179	0.885746	0.106018	0	18	11	28	36	57	26	38	18	57	38
ENSMUSG00000039850	chr11	Endov	1.19E+08	1.19E+08	6138	-0.04511	2.405585	0.828166	0.885746	0.03525	0	82	62	119	72	90	68	112	101	91	92
ENSMUSG00000099200	chr4	Mir7019	1.38E+08	1.38E+08	69	-0.04138	3.773556	0.828092	0.885746	0.032624	0	156	123	327	265	268	176	277	197	342	241
ENSMUSG00000022718	chr16	Dgcr8	18253948	18255605	7286	-0.04066	3.659733	0.828252	0.885753	0.028124	0	176	131	338	188	213	210	263	223	223	197
ENSMUSG00000036526	chr5	Card11	1.41E+08	1.41E+08	4112	0.10874	0.127418	0.828411	0.885851	0.131619	0	22	8	26	7	14	30	16	11	24	10
ENSMUSG00000019977	chr10	Hbs1l	21295979	21296176	4893	-0.03126	6.321208	0.829251	0.886671	0.024326	0	1122	943	1692	1311	1425	1241	1720	1295	1766	1210
ENSMUSG00000029033	chr4	Acap3	1.56E+08	1.56E+08	5367	0.03442	3.533163	0.829312	0.886671	0.029142	0	133	104	261	184	257	163	216	213	280	190
ENSMUSG00000025949	chr1	Pikfyve	65186683	65186778	18504	-0.04456	3.171741	0.829442	0.886739	0.031446	0	110	103	246	119	169	114	168	173	182	160

ENSMUSG00000029735	chr6	Tpk1	43345001	43346900	4329	-0.08694	0.109453	0.830106	0.887377	0.071443	0	19	7	19	11	25	9	27	20	19	12
ENSMUSG00000030652	chr7	Coq7	1.19E+08	1.19E+08	4003	-0.0402	5.512042	0.830443	0.887666	0.041198	0	648	466	670	945	942	715	1089	593	1137	634
ENSMUSG00000026307	chr1	Scly	91298338	91298448	4549	0.041743	3.398722	0.83052	0.887677	0.038188	0	133	82	193	221	210	149	244	201	237	146
ENSMUSG00000020453	chr11	Patz1	3288874	3289347	5904	-0.03389	3.515742	0.830725	0.887825	0.022683	0	149	135	275	168	207	150	242	188	266	185
ENSMUSG00000032126	chr9	Hmbs	44336350	44336845	1755	-0.03343	4.393935	0.831562	0.888648	0.028854	0	325	271	399	347	328	346	515	324	428	285
ENSMUSG00000002578	chr10	Ikzf4	1.29E+08	1.29E+08	5995	0.12184	-0.14861	0.831741	0.888767	0.255678	0	3	8	25	3	25	15	31	5	23	3
ENSMUSG00000022687	chr16	Boc	44485045	44485799	4456	0.045898	3.024014	0.832039	0.888871	0.056589	0	53	88	206	136	178	131	165	140	139	156
ENSMUSG00000078484	chr4	Klhl17	1.56E+08	1.56E+08	3014	0.031953	3.282995	0.832023	0.888871	0.027471	0	120	88	224	142	214	146	214	180	201	149
ENSMUSG00000078789	chr11	Dph1	75177643	75178387	2690	-0.04799	2.685627	0.831947	0.888871	0.034369	0	81	55	137	119	136	104	127	103	142	92
ENSMUSG00000075254	chr16	Heg1	33684466	33684855	12632	-0.04006	4.838804	0.832439	0.889226	0.035581	0	300	281	782	386	693	367	577	584	554	478
ENSMUSG00000005936	chr17	Kctd20	28951950	28952023	4379	-0.0312	5.644534	0.832527	0.889226	0.02533	0	657	662	1145	725	874	781	1070	832	1241	638
ENSMUSG00000025735	chr17	Rhbdl1	25834465	25835056	1723	0.041664	4.632657	0.832573	0.889226	0.041225	0	408	202	431	454	465	337	745	461	494	305
ENSMUSG00000037643	chr3	Prkci	30995747	30996085	5551	-0.05389	2.229182	0.832851	0.889452	0.041061	0	54	50	105	80	92	73	93	95	69	74
ENSMUSG00000024319	chr17	Vps52	33955812	33956182	3876	0.0302	5.406438	0.83335	0.889913	0.023697	0	605	405	943	651	824	599	880	680	982	769
ENSMUSG00000026594	chr1	Ralgps2	1.57E+08	1.57E+08	12085	0.06859	0.569606	0.833469	0.889969	0.061626	0	16	21	37	19	15	27	32	24	23	21
ENSMUSG00000032044	chr9	Rpusd4	35267865	35268078	2647	0.037284	3.44811	0.833683	0.890125	0.030526	0	132	97	226	201	218	185	236	175	261	148
ENSMUSG00000045008	chr10	9030612E09Rik	43174704	43176562	1859	0.086086	0.992353	0.833945	0.890323	0.078374	0	21	27	29	33	34	37	43	14	49	34
ENSMUSG00000048007	chrX	Timm8a1	1.35E+08	1.35E+08	1421	0.067392	1.550299	0.834002	0.890323	0.060743	0	33	29	44	54	61	41	87	30	71	41
ENSMUSG00000074754	chr2	Gm561	1.45E+08	1.45E+08	471	-0.03633	4.523646	0.834336	0.890607	0.037016	0	390	314	392	353	356	368	581	292	525	326
ENSMUSG00000027663	chr3	Zmat3	32334792	32341695	11435	0.035925	3.697255	0.834837	0.891071	0.027598	0	182	135	252	191	269	148	278	252	288	231
ENSMUSG00000094724	chr17	Rnaset2b	6978860	6979098	2555	-0.05639	2.020826	0.834935	0.891103	0.084943	0	79	65	70	61	32	58	77	69	105	50
ENSMUSG00000089768	chrX	Tmsb15b1	1.37E+08	1.37E+08	439	0.10988	0.737475	0.835029	0.891132	0.121135	0	22	36	27	13	16	34	36	27	38	14
ENSMUSG00000016257	chr2	Slmo2	1.74E+08	1.74E+08	1860	0.031601	5.650294	0.835458	0.891518	0.026045	0	613	506	986	954	964	753	1074	818	1260	765
ENSMUSG00000035900	chr15	Gramd4	86057695	86057831	5567	-0.03128	3.993664	0.836123	0.892156	0.023295	0	208	206	386	207	292	234	358	263	364	224
ENSMUSG00000090083	chr17	Rnf8	29614790	29615078	3178	0.031521	4.512065	0.836278	0.892249	0.02246	0	308	288	476	355	369	370	469	399	500	352
ENSMUSG00000028024	chr3	Enpep	1.29E+08	1.29E+08	4706	-0.04726	3.157402	0.83645	0.892298	0.0444	0	118	111	222	95	188	123	147	209	160	141
ENSMUSG00000103235	chr9	DHX30	1.1E+08	1.1E+08	3585	-0.03472	4.776221	0.836457	0.892298	0.027041	0	337	238	668	477	579	403	613	513	544	396
ENSMUSG00000026890	chr2	Lhx6	36081953	36084075	4805	0.097542	0.636173	0.836572	0.892348	0.103422	0	22	14	28	21	27	6	45	17	37	35
ENSMUSG00000052751	chr6	Repin1	48593883	48594052	3975	0.029844	4.781511	0.836944	0.892673	0.02424	0	324	275	660	452	526	397	544	445	672	477
ENSMUSG00000026429	chr1	Ube2t	1.35E+08	1.35E+08	4832	0.058742	1.649753	0.837111	0.892681	0.053379	0	42	31	51	53	61	53	68	73	55	32
ENSMUSG00000029227	chr5	Fip1l1	74535449	74535761	10442	0.028876	4.355874	0.837127	0.892681	0.020347	0	281	206	460	314	387	293	490	368	432	310
ENSMUSG00000037808	chr9	Fam76b	13827716	13828061	4325	-0.04524	2.521475	0.837154	0.892681	0.040684	0	70	78	158	76	84	77	137	101	100	92
ENSMUSG00000033364	chr1	Usp37	74435511	74439478	11081	-0.03876	3.336674	0.837527	0.893008	0.027453	0	154	100	268	136	176	146	213	162	223	160
ENSMUSG00000024222	chr17	Fkbp5	28399095	28401151	6363	-0.05865	4.954467	0.837687	0.893051	0.089599	0	450	227	984	455	569	855	463	459	617	270
ENSMUSG00000029714	chr5	Gigyf1	1.38E+08	1.38E+08	5437	0.028807	4.792653	0.837703	0.893051	0.02192	0	347	303	669	429	490	397	549	489	639	473
ENSMUSG00000024580	chr18	Grpel2	61712440	61716127	4030	0.031188	4.435388	0.837865	0.893119	0.022701	0	331	221	501	308	373	291	534	357	507	330
ENSMUSG00000037738	chr8	Nek5	22073616	22074094	2404	0.085645	0.660024	0.837901	0.893119	0.099804	0	34	15	38	7	21	22	42	24	28	23
ENSMUSG00000027931	chr3	Npr1	90450591	90451182	4783	0.035681	3.784874	0.838056	0.893212	0.030253	0	158	152	290	216	286	195	272	311	324	171
ENSMUSG00000045005	chr1	Fzd5	64730558	64736853	6915	0.063206	1.294886	0.838998	0.894037	0.050888	0	21	22	45	48	51	29	61	42	60	31
ENSMUSG00000066270	chr9	Gm10157	1.19E+08	1.19E+08	343	0.063942	1.74757	0.839015	0.894037	0.046954	0	42	39	65	66	41	47	75	53	89	44
ENSMUSG00000104011	chr1	RP24-272N10.3	1.64E+08	1.64E+08	540	-0.11862	0.763891	0.839031	0.894037	0.307206	0	3	6	15	59	53	23	33	15	57	15
ENSMUSG00000030922	chr7	Lyrm1	1.2E+08	1.2E+08	1513	0.045671	2.621599	0.839733	0.894713	0.036097	0	101	66	127	88	95	102	150	83	144	87
ENSMUSG00000022837	chr16	Iqcb1	36828385	36828492	5387	0.052358	2.111858	0.839852	0.894768	0.044276	0	65	57	87	48	73	81	103	66	81	59
ENSMUSG00000054499	chr7	Dedd2	25202840	25203931	1828	0.040966	2.611931	0.840077	0.894866	0.043762	0	73	56	135	109	112	79	98	107	133	132
ENSMUSG00000083364	chrX	Llph-ps2	13218210	13218602	393	-0.06502	0.231976	0.84008	0.894866	0.066326	0	17	13	22	18	17	17	36	13	22	9
ENSMUSG00000030505	chr7	Prmt3	49778346	49778501	3361	-0.02961	4.236711	0.8408	0.895562	0.023127	0	247	247	466	257	318	243	413	329	427	298
ENSMUSG00000028840	chr4	Zfp593	1.34E+08	1.34E+08	2088	-0.04447	2.982521	0.840989	0.895683	0.055136	0	140	129	149	85	110	135	176	131	139	115
ENSMUSG00000059689	chr6	Zfp637	1.18E+08	1.18E+08	2565	0.034956	4.725793	0.841049	0.895683	0.029109	0	426	332	483	427	376	421	597	433	589	403
ENSMUSG00000084319	chr6	Tpt1-ps3	99877816	99878334	519	-0.03485	7.397294	0.841343	0.895924	0.036345	0	2866	2294	3278	2389	2533	2589	4331	2612	3261	2510
ENSMUSG00000029050	chr4	Ski	1.55E+08	1.55E+08	5562	-0.0313	5.841562	0.841893	0.896438	0.026564	0	740	584	1429	880	1150	741	1084	1065	1224	1038
ENSMUSG00000026643	chr2	Nmt2	3284212	3284406	6556	-0.03377	4.165994	0.842064	0.896476	0.033704	0	281	259	441	212	246	235	398	314	407	273
ENSMUSG00000038160	chr10	Atg5	44268358	44268584	2352	-0.02863	3.894228	0.842048	0.896476	0.022689	0	206	189	302	215	284	202	302	261	367	216
ENSMUSG00000025200	chr19	Cwf19l1	44108644	44110660	3574	0.052071	2.087959	0.842207	0.896484	0.037243	0	67	45	85	64	65	71	94	76	96	50
ENSMUSG00000035367	chr13	Rmi1	58402597	58402789	3522	0.047651	2.504658	0.842198	0.896484	0.03753	0	100	61	110	74	92	77	141	108	118	78
ENSMUSG00000044072	chr11	Eml6	29743048	29744610	9279	-0.06794	0.661952	0.842275	0.896484	0.062005	0	10	24	38	18	33	20	30	23	36	23
ENSMUSG00000024566	chr18	Atp9b	80734143	80736149	5397	-0.03022	4.273449	0.842718	0.896783	0.022109	0	253	223	513	284	321	268	414	334	433	300
ENSMUSG00000036395	chr9	Glb1l2	26763044	26764823	5031	0.104637	3.448037	0.842758	0.896783	0.307732	0	301	183	145	48	82	175	103	488	96	112
ENSMUSG00000098974	chr19	Gm27505	5844638	5844747	110	0.041928	5.417333	0.842705	0.896783	0.050941	0	686	500	882	413	911	644	1114	465	848	881
ENSMUSG00000078784	chr3	1810022K09Rik	14606284	14606408	1753	0.046669	3.677913	0.843061	0.897033	0.047149	0	191	209	254	134	186	199	352	216	266	162
ENSMUSG00000004865	chr17	Srpk1	28587648	28590241	9647	0.032477	4.195415	0.843539	0.897368	0.027105	0	222	225	435	315	257	300	361	319	417	280
ENSMUSG00000021687	chr13	Scamp1	94201310	94204163	4582	0.029333	5.099704	0.843579	0.897368	0.022669	0	428	435	750	474	648	459	810	567	776	573
ENSMUSG00000025545	chr14	Clybl	1.22E+08	1.22E+08	1239	0.034457	5.872271	0.843571	0.897368	0.032841	0	899	731	950	947	1006	930	1457	867	1461	783
ENSMUSG00000028133	chr3	Rwdd3	1.21E+08	1.21E+08	5063	0.098044	0.561643	0.844287	0.897618	0.076822	0	21	23	21	16	22	28	41	24	21	15
ENSMUSG00000029276	chr5	Glmn	1.08E+08	1.08E+08	2688	-0.04072	2.549245	0.844257	0.897618	0.043452	0	94	80	134	70	87	74	152	99	99	96
ENSMUSG00000030735	chr8	Gm9755	67514000	67515606	1607	0.044999	2.97679	0.844089	0.897618	0.05881	0	97	44	164	163	168	104	142	134	231	119

ENSMUSG00000039684	chr10	Gm5422	31248140	31251045	2906	-0.05738	1.428705	0.843954	0.897618	0.064028	0	40	35	66	28	44	20	53	57	51	51
ENSMUSG00000042348	chr13	Arl15	1.14E+08	1.14E+08	3364	-0.04387	2.450391	0.844111	0.897618	0.03452	0	69	56	124	75	123	70	130	100	95	88
ENSMUSG00000057177	chr7	Gsk3a	25228258	25228918	2260	0.029295	6.805994	0.84398	0.897618	0.025647	0	1530	1127	2371	1921	2045	1506	2450	1918	2859	1731
ENSMUSG00000079560	chr6	Hoxa3	52169062	52170742	6014	0.069448	1.278959	0.844167	0.897618	0.083307	0	13	28	51	51	41	23	64	55	46	32
ENSMUSG00000021248	chr12	Tmed10	85340614	85343549	3526	0.029326	6.887204	0.84467	0.897952	0.025673	0	1728	1434	2706	1649	1911	1678	2719	2058	2749	1818
ENSMUSG00000045410	chr13	Akr1e1	4590757	4593298	3514	-0.032	4.417873	0.844846	0.898068	0.032135	0	328	313	373	323	339	319	488	327	414	368
ENSMUSG00000019428	chr8	Fkbp8	70527724	70527836	4529	0.031334	7.059824	0.845072	0.898236	0.029434	0	1985	1792	2540	1909	2172	2007	2742	2266	3239	2108
ENSMUSG00000083899	chr11	Gm12346	77293444	77294873	2255	0.072366	0.82184	0.845301	0.898407	0.083666	0	17	24	30	19	40	31	52	27	18	26
ENSMUSG00000033430	chr8	Terf2ip	1.12E+08	1.12E+08	3599	0.029262	4.31801	0.845467	0.898512	0.020257	0	270	236	440	279	365	280	474	338	468	294
ENSMUSG00000024570	chr18	Rbfa	80192265	80192882	1377	0.031249	4.933259	0.846089	0.899046	0.024996	0	413	391	523	488	570	471	671	526	729	435
ENSMUSG00000071141	chr6	Rpl36a-ps3	1.36E+08	1.36E+08	321	0.067989	1.976934	0.846105	0.899046	0.074509	0	67	69	51	46	50	70	85	70	79	53
ENSMUSG00000000948	chr7	Snrpn	59974149	59974175	5216	0.034817	5.349397	0.846303	0.899185	0.036289	0	457	411	818	775	816	552	866	514	1176	717
ENSMUSG00000081967	chr2	Gm14017	1.21E+08	1.21E+08	386	-0.06511	0.392085	0.846662	0.899494	0.108138	0	21	24	9	12	28	17	23	18	33	18
ENSMUSG00000021866	chr14	Anxa11	25842156	25842295	4135	-0.0336	6.113007	0.846887	0.899601	0.034619	0	871	650	1734	1179	1369	810	1537	950	1933	1162
ENSMUSG00000032311	chr9	Nrg4	55220222	55221408	6075	0.147557	0.790849	0.846899	0.899601	0.520503	0	45	32	21	4	11	16	7	102	18	10
ENSMUSG00000030170	chr6	Wnt5b	1.19E+08	1.19E+08	2654	-0.09715	1.208303	0.847136	0.899709	0.210819	0	8	11	28	81	59	17	57	42	40	40
ENSMUSG00000035505	chr5	Cox18	90214724	90215175	2009	-0.04384	2.442942	0.847102	0.899709	0.036714	0	69	51	107	103	110	62	109	107	125	81
ENSMUSG00000028114	chr3	Mettl14	1.23E+08	1.23E+08	5119	0.033072	4.004769	0.847459	0.89995	0.026144	0	203	218	333	214	295	249	413	264	309	244
ENSMUSG00000061313	chr8	Ddhd2	25725324	25727363	4267	0.029239	3.835934	0.847499	0.89995	0.022793	0	219	136	304	212	270	206	317	267	300	221
ENSMUSG00000030602	chr7	Pak4	28399549	28401617	7845	0.028743	4.108916	0.84758	0.899952	0.026363	0	206	168	426	251	358	228	321	342	398	293
ENSMUSG00000052428	chr1	Tmco1	1.67E+08	1.67E+08	4764	-0.02885	5.199666	0.847637	0.899952	0.027001	0	543	519	729	503	632	502	876	601	740	611
ENSMUSG00000029403	chr5	Cdkl2	92006074	92008134	4967	0.04115	3.515059	0.848386	0.900594	0.036695	0	209	146	197	145	176	167	225	201	275	183
ENSMUSG00000031906	chr8	Smpd3	1.06E+08	1.06E+08	5148	0.071267	1.753098	0.848444	0.900594	0.157284	0	52	36	107	30	39	45	31	127	51	41
ENSMUSG00000034687	chr5	Fras1	96373955	96374885	15848	0.07255	1.747208	0.848409	0.900594	0.162097	0	7	23	118	54	78	53	69	48	53	72
ENSMUSG00000008540	chr6	Mgst1	1.38E+08	1.38E+08	2013	0.074887	5.40746	0.848698	0.90079	0.179452	0	769	448	469	852	627	588	392	1900	548	388
ENSMUSG00000069682	chr10	Gm10275	29698746	29699380	635	0.041329	4.488203	0.848829	0.900857	0.045059	0	380	333	411	274	309	371	645	320	455	306
ENSMUSG00000026510	chr1	Trp53bp2	1.82E+08	1.82E+08	4418	-0.0358	3.581555	0.849339	0.901038	0.030342	0	152	143	332	156	206	207	260	199	249	155
ENSMUSG00000032512	chr9	Wdr48	1.2E+08	1.2E+08	3821	-0.03413	3.824172	0.849275	0.901038	0.028256	0	134	165	345	250	276	201	313	253	287	218
ENSMUSG00000033623	chr5	Pcgf3	1.08E+08	1.08E+08	9544	-0.03185	5.593171	0.849332	0.901038	0.033238	0	726	628	1243	554	795	655	1127	828	1260	588
ENSMUSG00000041734	chr3	Kirrel	87078593	87083620	7463	-0.04827	3.269854	0.849288	0.901038	0.0503	0	96	91	292	146	196	106	168	200	180	193
ENSMUSG00000100215	chr1	Gm8292	55335401	55335796	396	0.112937	0.335055	0.849334	0.901038	0.199202	0	24	23	3	10	22	27	32	15	20	16
ENSMUSG00000049300	chr3	Prmt6	1.1E+08	1.1E+08	4197	0.047957	2.0403	0.849685	0.901333	0.03447	0	59	50	86	48	74	63	95	61	85	68
ENSMUSG00000032264	chr9	Zw10	49055581	49055787	2895	0.033078	3.387012	0.850054	0.901581	0.027293	0	123	123	191	186	198	149	218	191	222	175
ENSMUSG00000032399	chr9	Rpl4	64173387	64173433	1422	-0.03277	9.244662	0.850025	0.901581	0.036061	0	8920	9386	12267	8164	9264	9114	14489	9787	13301	8635
ENSMUSG00000032212	chr9	Sltm	70542920	70543081	3646	-0.028	5.050555	0.850892	0.902397	0.024695	0	457	443	684	470	611	562	670	569	700	472
ENSMUSG00000050394	chrX	Armcx6	1.35E+08	1.35E+08	2486	0.064745	0.991393	0.850986	0.902425	0.039145	0	26	20	38	31	33	27	46	24	48	32
ENSMUSG00000014767	chr17	Tbp	15499888	15500024	13399	0.037316	2.551394	0.851791	0.902625	0.033383	0	60	65	140	87	115	75	143	102	114	101
ENSMUSG00000018387	chr11	Shroom1	53457205	53457341	4600	-0.08203	-0.11563	0.851726	0.902625	0.06231	0	8	13	18	15	13	15	12	17	15	12
ENSMUSG00000022244	chr15	Amacr	10981756	10982053	2575	-0.03478	4.3927	0.851808	0.902625	0.037832	0	232	212	367	457	443	261	546	312	462	339
ENSMUSG00000025354	chr10	Dnajc14	1.29E+08	1.29E+08	4229	0.026189	4.996424	0.851855	0.902625	0.021062	0	404	369	680	511	587	495	668	591	676	495
ENSMUSG00000025971	chr1	9430016H08Rik	57406328	57407222	7878	0.031514	4.166877	0.851708	0.902625	0.022897	0	277	219	343	268	296	255	424	305	411	270
ENSMUSG00000030865	chr7	Chp2	1.22E+08	1.22E+08	1603	-0.05196	2.177923	0.851816	0.902625	0.072885	0	76	72	111	35	63	64	99	99	77	57
ENSMUSG00000035048	chr9	Anapc13	1.03E+08	1.03E+08	2377	0.037944	5.430222	0.851422	0.902625	0.042886	0	696	703	753	518	587	682	1014	740	952	617
ENSMUSG00000036327	chr2	Qsox2	26208637	26211459	4644	0.039847	2.628322	0.851279	0.902625	0.043204	0	102	59	131	67	129	88	161	94	109	111
ENSMUSG00000045414	chr9	1190002N15Rik	94517864	94520646	3950	0.044484	2.605685	0.851417	0.902625	0.061807	0	58	50	132	107	143	53	105	124	163	115
ENSMUSG00000048970	chrX	C1galt1c1	38630785	38632123	1449	0.037232	3.593144	0.851762	0.902625	0.032162	0	191	164	222	158	194	189	285	203	222	202
ENSMUSG00000013089	chr16	Etv5	22381309	22383691	4103	-0.04524	3.863387	0.851964	0.902668	0.056952	0	164	100	328	266	377	149	374	187	317	293
ENSMUSG00000061898	chr5	Rbak	1.43E+08	1.43E+08	3623	-0.04264	1.922875	0.852226	0.902874	0.044127	0	55	46	77	60	61	62	92	44	66	66
ENSMUSG00000020530	chr11	Ggnbp2	84832361	84833213	4726	-0.02875	5.475147	0.852523	0.903105	0.027989	0	653	600	930	662	713	726	1100	679	846	666
ENSMUSG00000074649	chr2	BC029722	1.56E+08	1.56E+08	1615	0.035678	5.219324	0.85258	0.903105	0.03713	0	601	538	653	555	492	584	803	598	961	526
ENSMUSG00000023882	chr17	Zfp54	21423227	21423561	2832	-0.08169	-0.06683	0.852762	0.903131	0.058707	0	9	11	26	12	13	14	18	17	18	8
ENSMUSG00000028309	chr4	Rnf20	49632006	49632033	7288	-0.02611	4.86176	0.85281	0.903131	0.020446	0	398	309	675	448	560	397	671	475	665	445
ENSMUSG00000056870	chr1	Gulp1	44551511	44551872	3758	-0.06126	1.50642	0.852708	0.903131	0.08797	0	40	32	45	44	62	20	38	80	64	43
ENSMUSG00000039046	chr2	Usp6nl	6322667	6322954	8059	0.036943	2.561657	0.853001	0.903261	0.041324	0	65	44	126	116	122	91	136	99	132	82
ENSMUSG00000024158	chr17	Hagh	24840143	24840281	1908	-0.02765	5.626084	0.853242	0.903445	0.026173	0	714	570	888	897	890	767	1146	750	1115	717
ENSMUSG00000027475	chr2	Kif3b	1.53E+08	1.53E+08	5635	-0.03921	3.016899	0.853516	0.903594	0.028853	0	99	81	206	113	172	120	180	139	153	127
ENSMUSG00000052852	chr6	Reep1	71707561	71708001	3924	-0.03211	6.86914	0.85352	0.903594	0.035829	0	1723	1678	2953	1374	1735	1644	2556	1877	2434	2041
ENSMUSG00000027242	chr2	Wdr76	1.22E+08	1.22E+08	6305	0.070569	0.664941	0.853733	0.903748	0.077224	0	22	18	34	19	23	16	35	37	16	32
ENSMUSG00000004270	chr6	Lpcat3	1.25E+08	1.25E+08	3268	-0.03045	4.109071	0.853898	0.90385	0.025841	0	267	188	358	260	324	266	297	346	367	260
ENSMUSG00000035285	chr7	Nat14	4922251	4922639	1612	0.067474	1.04837	0.854238	0.904041	0.067811	0	23	21	27	28	55	19	49	29	51	38
ENSMUSG00000049904	chr11	Tmem17	22512088	22512583	1568	0.059059	2.003299	0.854264	0.904041	0.052534	0	53	69	71	50	54	59	99	63	80	64
ENSMUSG00000054387	chr1	Mdm4	1.33E+08	1.33E+08	14798	-0.02854	4.743102	0.854282	0.904041	0.025839	0	409	326	665	349	432	382	575	521	536	399
ENSMUSG00000047187	chr4	Rab2a	8535644	8535908	2133	-0.03349	7.988531	0.854513	0.904213	0.040077	0	3863	3883	5850	3204	3439	3531	5832	3695	6367	3877
ENSMUSG00000038046	chr11	Rnmtl1	76243715	76244086	1935	-0.03809	3.41663	0.854625	0.904259	0.043802	0	132	96	166	235	235	130	235	191	261	152
ENSMUSG00000034858	chr9	Fam214a	74953053	74953278	4521	-0.03171	4.586822	0.854786	0.904357	0.029151	0	245	240	545	454	514	312	531	385	525	421

ENSMUSG00000020882	chr11	Cacnb1	98001508	98003362	4529	0.027774	7.584035	0.855517	0.905059	0.027241	0	2614	2003	3981	3203	3603	2407	4599	3748	4435	2794
ENSMUSG00000022031	chr14	Elp3	65530446	65531600	2891	-0.02625	6.219498	0.855904	0.905324	0.023918	0	1018	914	1657	1096	1380	1103	1598	1248	1567	1216
ENSMUSG00000029673	chr5	Auts2	1.31E+08	1.31E+08	16200	-0.03898	3.221736	0.855865	0.905324	0.03868	0	133	95	265	98	188	107	220	142	216	159
ENSMUSG00000057286	chr11	St6galnac2	1.17E+08	1.17E+08	7090	0.037892	1.903472	0.856075	0.905432	0.049241	0	35	36	92	60	74	56	88	82	56	52
ENSMUSG00000019088	chrX	Dnase1l1	74273217	74273691	2121	0.034586	6.943758	0.856242	0.905537	0.042036	0	1969	1776	2897	1283	1711	1927	2921	2110	2858	1677
ENSMUSG00000021076	chr12	Actr10	70937857	70938031	4022	0.028679	5.784794	0.85681	0.906065	0.026395	0	763	761	1164	777	862	771	1284	907	1347	838
ENSMUSG00000026435	chr1	Slc45a3	1.32E+08	1.32E+08	3563	0.064569	1.184394	0.857156	0.906151	0.122968	0	26	7	34	43	66	26	41	61	45	28
ENSMUSG00000031167	chrX	Rbm3	8138975	8141208	4698	-0.03869	5.471688	0.857165	0.906151	0.055701	0	633	726	944	523	693	788	947	605	1311	429
ENSMUSG00000032712	chr6	2810474O19Rik	1.49E+08	1.49E+08	6802	0.041096	3.338692	0.856972	0.906151	0.061708	0	71	77	303	176	222	118	246	165	276	147
ENSMUSG00000089996	chrX	Tmsb15b2	1.37E+08	1.37E+08	450	-0.06325	0.550779	0.857162	0.906151	0.099552	0	22	31	23	15	15	27	28	21	32	14
ENSMUSG00000047227	chr12	Gm527	64917911	64918191	1463	-0.05411	0.023058	0.857388	0.906315	0.054452	0	12	15	21	10	16	10	24	17	19	12
ENSMUSG00000092243	chr17	Gm7030	36109719	36109732	927	0.193398	0.909185	0.857487	0.906348	1.073891	0	33	44	30	12	2	29	5	130	0	1
ENSMUSG00000022426	chr15	Josd1	79674250	79676179	3394	0.025227	4.664717	0.857723	0.906525	0.020746	0	328	267	556	424	463	373	550	463	570	382
ENSMUSG00000031889	chr8	D230025D16Rik	1.05E+08	1.05E+08	4704	-0.02583	4.564103	0.858796	0.907586	0.021047	0	339	262	563	374	392	365	502	413	521	337
ENSMUSG00000035878	chr9	Hykk	54917283	54917858	8936	0.051716	0.016403	0.859068	0.907802	0.059765	0	10	9	27	9	18	10	16	18	25	15
ENSMUSG00000030322	chr6	Mbd4	1.16E+08	1.16E+08	5059	-0.07872	0.625122	0.859169	0.907803	0.045786	0	18	16	42	19	26	24	32	18	29	24
ENSMUSG00000054079	chr11	Utp18	93859243	93860068	3597	0.038407	2.803707	0.859206	0.907803	0.037514	0	96	88	146	84	132	122	156	133	150	77
ENSMUSG00000001707	chr13	Eef1e1	38645698	38646310	1032	0.03754	3.486784	0.85943	0.907958	0.031982	0	172	157	225	145	166	140	260	194	258	186
ENSMUSG00000032067	chr9	Pts	50521618	50522336	1035	0.03433	3.462295	0.85949	0.907958	0.031925	0	167	139	229	155	169	171	262	214	183	172
ENSMUSG00000028028	chr3	Alpk1	1.28E+08	1.28E+08	6709	-0.07208	0.416733	0.859635	0.907966	0.072499	0	23	12	36	9	23	13	37	19	25	17
ENSMUSG00000038604	chr8	Fam65a	1.06E+08	1.06E+08	4109	-0.03507	4.488163	0.85958	0.907966	0.038595	0	258	173	527	451	477	261	417	414	579	367
ENSMUSG00000022106	chr14	Rcbtb2	73123037	73123132	9489	0.028678	4.579252	0.859975	0.908254	0.024859	0	367	297	485	334	394	315	509	473	491	406
ENSMUSG00000050565	chr1	Tor1aip2	1.56E+08	1.56E+08	9218	-0.02615	6.285803	0.860136	0.908351	0.025654	0	1090	959	1925	1091	1317	1092	1851	1356	1712	1123
ENSMUSG00000036225	chr18	Kctd1	14968685	14969695	3587	-0.09376	0.425454	0.860498	0.908662	0.225531	0	6	5	12	47	33	7	32	18	34	21
ENSMUSG00000015980	chr7	Lrrc27	1.39E+08	1.39E+08	3637	-0.0795	1.052233	0.860771	0.908877	0.115134	0	27	10	28	51	48	25	35	56	38	20
ENSMUSG00000049792	chr12	Bag5	1.12E+08	1.12E+08	2508	-0.02554	3.95119	0.861569	0.909575	0.023489	0	229	184	295	250	279	195	342	279	320	260
ENSMUSG00000068697	chr14	Myoz1	20649102	20649609	1294	0.030675	11.19259	0.861564	0.909575	0.037035	0	40199	25724	53275	30171	37011	38682	49721	35048	64143	31377
ENSMUSG00000024966	chr19	Stip1	7020696	7021171	2173	-0.02638	6.809948	0.861683	0.909623	0.026793	0	1771	1199	2147	1775	2190	1688	2521	2061	2242	1645
ENSMUSG00000060279	chr7	Ap2a1	44900373	44900815	4301	-0.02859	6.494975	0.861777	0.909649	0.030696	0	1298	897	2146	1408	1717	1286	1536	1405	2409	1536
ENSMUSG00000030353	chr6	Tead4	1.28E+08	1.28E+08	3596	0.04064	2.857556	0.861896	0.909703	0.057388	0	133	51	214	83	106	116	183	126	133	104
ENSMUSG00000025413	chr4	Ttc4	1.07E+08	1.07E+08	3568	0.025056	5.356785	0.862135	0.909882	0.022502	0	608	418	798	653	794	621	957	682	883	640
ENSMUSG00000068921	chr3	Dap3	88920803	88923913	6483	0.026791	5.90168	0.8623	0.909984	0.025445	0	792	729	1139	973	1092	867	1539	966	1372	849
ENSMUSG00000041396	chr1	Mettl18	1.64E+08	1.64E+08	1513	-0.04052	2.003547	0.862673	0.910306	0.033996	0	58	42	81	66	72	68	85	69	76	52
ENSMUSG00000051223	chr1	Bzw1	58392898	58393216	4033	-0.02582	6.165077	0.863088	0.910671	0.026339	0	1006	928	1686	1003	1201	962	1721	1288	1486	1090
ENSMUSG00000002814	chr11	Top3a	60740058	60740701	4599	-0.04767	2.387757	0.863331	0.910855	0.043013	0	57	47	113	86	128	62	97	98	107	95
ENSMUSG00000021540	chr13	Smad5	56703010	56703131	7420	-0.0256	5.186877	0.863679	0.911004	0.022836	0	440	370	898	593	729	486	840	641	832	533
ENSMUSG00000037119	chr15	D15Ertd621e	58415468	58415777	5621	-0.0315	3.447993	0.86357	0.911004	0.027541	0	134	126	270	170	193	152	262	206	186	170
ENSMUSG00000093962	chr4	Gm11756	73916728	73917145	1312	-0.08617	-0.36643	0.86367	0.911004	0.317002	0	15	20	11	1	3	7	22	15	17	2
ENSMUSG00000044894	chr11	Uqcrq	53427922	53429150	1831	-0.03678	8.013386	0.864002	0.911273	0.05499	0	3208	2470	3494	6274	5396	3557	6323	3676	6483	3760
ENSMUSG00000027011	chr2	Ube2e3	78868124	78868597	4390	-0.02354	4.707652	0.86428	0.911494	0.02198	0	368	325	537	407	464	342	540	471	625	401
ENSMUSG00000026836	chr2	Acvr1	58388644	58389178	4829	-0.03562	4.073779	0.86462	0.91178	0.042444	0	211	156	420	277	342	166	355	224	404	374
ENSMUSG00000029790	chr6	Cep41	30653457	30655850	4979	0.047974	0.003701	0.864885	0.911914	0.070934	0	12	4	20	18	18	18	15	18	15	15
ENSMUSG00000062352	chr12	Itgb1bp1	21240825	21241109	3321	-0.02516	4.396738	0.864832	0.911914	0.026372	0	324	285	407	286	372	313	428	338	521	311
ENSMUSG00000021963	chr14	Sap18	57798180	57798354	3781	0.027023	5.611509	0.865165	0.912065	0.025923	0	741	649	941	715	766	721	1127	805	1088	782
ENSMUSG00000028894	chr4	Inpp5b	1.25E+08	1.25E+08	4657	0.026468	3.357958	0.865118	0.912065	0.028285	0	132	85	254	158	207	157	239	180	215	149
ENSMUSG00000031849	chr8	Comp	70373548	70373647	2425	0.07551	4.071352	0.865332	0.912168	0.236763	0	45	66	276	360	678	206	227	332	264	467
ENSMUSG00000029569	chr6	Tmem168	13580687	13583334	5825	-0.02704	3.666143	0.865449	0.912219	0.023653	0	180	151	275	181	239	163	263	232	262	219
ENSMUSG00000004814	chr5	Ccl24	1.36E+08	1.36E+08	1289	-0.05019	1.89507	0.865691	0.912401	0.077475	0	43	54	100	39	63	61	124	51	61	34
ENSMUSG00000041528	chr9	Rnf123	1.08E+08	1.08E+08	6754	0.027196	7.038871	0.866481	0.913089	0.031227	0	1909	1251	3627	1784	2248	1795	2620	2290	3132	2309
ENSMUSG00000069171	chr13	Nr2f1	78188973	78190013	4752	0.042823	-0.10265	0.866451	0.913089	0.093796	0	11	5	26	15	10	13	15	22	9	15
ENSMUSG00000043542	chr3	Zc2hc1a	7503483	7503527	3508	-0.03619	2.763992	0.866601	0.913143	0.038119	0	77	91	153	96	131	74	142	125	129	132
ENSMUSG00000036197	chr15	Gxylt1	93239742	93245129	6704	-0.03463	3.238973	0.866734	0.913211	0.030245	0	98	104	208	162	202	133	199	173	174	159
ENSMUSG00000062981	chr10	Mrpl42	95480806	95480977	666	-0.02726	7.650806	0.867461	0.913904	0.031843	0	2984	2231	3453	3554	3933	3114	5067	2985	4501	2761
ENSMUSG00000022437	chr15	Samm50	84192233	84192384	1673	0.028707	7.461572	0.86782	0.914205	0.034987	0	2186	1708	3163	3644	3384	2513	3927	2813	4547	2688
ENSMUSG00000087174	chrX	5530601H04Rik	1.05E+08	1.05E+08	9005	0.05959	1.011531	0.867885	0.914205	0.055829	0	23	28	36	25	37	23	59	28	32	37
ENSMUSG00000050697	chr15	Prkaa1	5143861	5143995	4655	0.028431	3.862195	0.868137	0.91437	0.029404	0	172	159	346	205	294	151	323	278	329	265
ENSMUSG00000070461	chr2	9230112E08Rik	1.81E+08	1.81E+08	3352	-0.03525	3.035341	0.868179	0.91437	0.030804	0	110	81	223	129	133	108	158	154	198	118
ENSMUSG00000061650	chr11	Med9	59948206	59948478	1920	0.028	4.583953	0.868469	0.914602	0.026713	0	414	280	470	314	402	373	506	395	576	362
ENSMUSG00000078173	chr3	Lenep	89400988	89402793	1806	0.03695	2.951128	0.868877	0.91496	0.048806	0	80	63	138	178	155	93	173	137	177	132
ENSMUSG00000009079	chr11	Ewsr1	5069689	5070103	5907	0.024631	6.154001	0.869025	0.915043	0.024765	0	1033	862	1534	1002	1234	1091	1613	1138	1606	1132
ENSMUSG00000032078	chr9	Zpr1	46273064	46273367	3583	0.027553	4.727706	0.869411	0.915231	0.025255	0	395	326	533	406	421	397	616	438	670	351
ENSMUSG00000041482	chr18	Piezo2	63010213	63011800	14566	0.064135	0.574599	0.869386	0.915231	0.130161	0	4	16	43	18	33	11	31	30	22	33
ENSMUSG00000060038	chr8	Dhps	85071757	85072053	2324	0.028061	4.501454	0.869367	0.915231	0.02499	0	318	311	418	328	388	355	495	378	529	332
ENSMUSG00000050846	chr15	Zfp623	75940952	75941159	2463	-0.03624	2.517709	0.869569	0.915325	0.030731	0	68	60	139	92	108	73	125	110	110	90
ENSMUSG00000098986	chr19	Gm28006	5844916	5845037	122	-0.03418	5.593823	0.869914	0.915615	0.050473	0	827	601	943	465	1067	718	1242	551	931	917

ENSMUSG00000033327	chr17	Tnxb	34670535	34670904	12209	-0.03821	6.483095	0.870117	0.915684	0.061485	0	814	663	2782	1345	2273	1248	1427	1827	1736	1663
ENSMUSG00000093672	chr10	Gm20655	17790522	17791092	3118	0.084121	0.573801	0.870079	0.915684	0.066863	0	20	22	27	22	14	14	39	19	35	25
ENSMUSG00000026273	chr1	Mterf4	93299211	93301584	5271	-0.0279	3.231101	0.870331	0.915836	0.032681	0	126	118	192	156	158	151	257	133	192	118
ENSMUSG00000042328	chr5	Hps4	1.12E+08	1.12E+08	3948	0.034729	2.606394	0.870455	0.915838	0.034622	0	66	71	128	113	99	93	112	118	137	91
ENSMUSG00000052085	chr19	Dock8	24999529	24999703	7810	0.043383	2.204504	0.87053	0.915838	0.065449	0	61	58	133	51	60	78	87	110	66	67
ENSMUSG00000080002	chr5	Gm5566	1.5E+08	1.5E+08	459	-0.06015	0.108214	0.87054	0.915838	0.066904	0	8	14	19	22	16	12	20	14	30	12
ENSMUSG00000038227	chr6	Hoxa9	52223100	52224482	5580	-0.02769	3.422618	0.870742	0.915978	0.028363	0	132	127	224	159	228	122	228	212	222	181
ENSMUSG00000018012	chr11	Rac3	1.21E+08	1.21E+08	1293	0.07696	-0.09311	0.870832	0.916001	0.10528	0	17	1	14	18	15	10	22	16	18	12
ENSMUSG00000022677	chr16	Fopnl	14299244	14300209	1465	-0.02751	6.057609	0.871197	0.916311	0.035096	0	990	924	1218	1011	1133	946	1803	858	1493	1030
ENSMUSG00000058571	chr14	Gpc6	1.17E+08	1.17E+08	9428	0.041628	2.367326	0.871782	0.916854	0.091683	0	35	50	155	60	127	70	62	115	100	107
ENSMUSG00000001642	chr6	Akr1b3	34303934	34304339	3933	0.02664	7.30521	0.872109	0.917125	0.031548	0	2518	2042	3287	2138	2427	2517	3437	2737	3807	2181
ENSMUSG00000045216	chr1	Hs6st1	36068400	36069184	5542	0.022943	5.055145	0.872328	0.91721	0.023043	0	441	312	790	524	646	427	732	584	805	540
ENSMUSG00000059183	chr9	Mtfmt	65435782	65436007	3655	-0.03649	2.334097	0.872316	0.91721	0.043668	0	68	61	94	87	89	88	135	80	87	57
ENSMUSG00000038967	chr11	Pdk2	95026258	95027322	3163	-0.02783	8.946462	0.87245	0.917266	0.035784	0	6135	4422	11181	9849	9438	6398	10355	8040	13743	7063
ENSMUSG00000000959	chr14	Oxa1l	54360841	54360917	2534	0.027864	5.740434	0.872991	0.917761	0.034218	0	700	474	959	1150	988	776	1309	855	1281	777
ENSMUSG00000024542	chr18	Cep192	67800107	67800186	8091	-0.05385	1.242424	0.873085	0.917788	0.041385	0	29	25	62	30	43	31	47	51	42	31
ENSMUSG00000047735	chr6	Samd9l	3372257	3377281	5425	0.034576	2.629012	0.87333	0.917972	0.053249	0	55	76	159	90	115	94	158	131	81	93
ENSMUSG00000050567	chr11	Maml1	50255634	50258828	5528	0.026459	3.119258	0.873477	0.918046	0.029857	0	105	83	194	166	146	136	165	158	197	133
ENSMUSG00000079055	chr12	Slc8a3	81197915	81199867	5332	-0.02828	6.292555	0.873538	0.918046	0.036743	0	1038	1019	2135	955	1317	1103	1775	979	1963	1350
ENSMUSG00000022181	chr15	C6	4727175	4727317	4036	-0.09981	-0.34136	0.874037	0.918403	0.357634	0	19	14	16	0	6	20	8	20	6	4
ENSMUSG00000030161	chr6	Gabarapl1	1.3E+08	1.3E+08	1765	-0.025	5.631086	0.874086	0.918403	0.028174	0	620	622	940	921	872	803	995	948	951	739
ENSMUSG00000097573	chr1	G730003C15Rik	59119833	59122141	2309	0.097179	0.093112	0.874032	0.918403	0.076784	0	15	10	13	18	17	17	28	9	28	10
ENSMUSG00000073968	chr7	Trim68	1.03E+08	1.03E+08	2389	-0.02887	2.769278	0.874206	0.918456	0.035849	0	84	96	156	88	122	81	152	144	136	98
ENSMUSG00000028622	chr4	Mrpl37	1.07E+08	1.07E+08	4460	-0.02491	6.381117	0.874405	0.918593	0.029265	0	1109	905	1493	1571	1662	1175	1966	1324	1983	1206
ENSMUSG00000068966	chr2	Zbtb34	33406108	33412495	6604	-0.0421	2.289957	0.87449	0.91861	0.037472	0	53	55	125	64	104	63	86	88	110	83
ENSMUSG00000030411	chr7	Nova2	18925888	18926164	8372	0.049433	1.166247	0.874577	0.918628	0.050151	0	26	22	45	31	47	19	42	50	53	36
ENSMUSG00000022450	chr15	Ndufa6	82350139	82350371	560	-0.02686	7.473473	0.874684	0.918643	0.034874	0	2524	2177	2882	3320	3224	2634	4449	2659	4187	2432
ENSMUSG00000038990	chr2	Cables2	1.8E+08	1.8E+08	4597	-0.02748	3.598161	0.87473	0.918643	0.028109	0	180	117	271	206	212	157	222	221	321	177
ENSMUSG00000029701	chr6	Rbm28	29123573	29125524	5666	0.023166	4.962644	0.874986	0.918822	0.022124	0	465	344	622	462	588	470	760	525	615	498
ENSMUSG00000041890	chr5	Git2	1.15E+08	1.15E+08	7233	-0.02562	4.100813	0.875108	0.918822	0.022272	0	218	163	415	283	342	227	380	314	386	253
ENSMUSG00000067058	chr5	Rps15a-ps5	1.06E+08	1.06E+08	393	-0.03543	1.826605	0.875043	0.918822	0.041536	0	54	39	59	56	70	40	74	66	92	44
ENSMUSG00000000171	chr9	Sdhd	50596338	50597250	1287	0.030989	8.198564	0.875776	0.91945	0.046553	0	3591	2733	4446	6498	6067	4001	8090	4357	6918	4386
ENSMUSG00000017428	chr11	Psmd11	80428615	80428755	6383	-0.0241	6.784654	0.876397	0.919904	0.029013	0	1587	1561	2348	1524	1788	1618	2609	1775	2531	1569
ENSMUSG00000034748	chr10	Sirt6	81621785	81622078	2785	0.036973	2.001042	0.87633	0.919904	0.04586	0	43	39	68	83	77	68	79	70	75	64
ENSMUSG00000096173	chr15	Gm3150	72913357	72913560	204	0.041722	1.243313	0.876416	0.919904	0.045103	0	25	25	52	39	40	47	49	30	50	32
ENSMUSG00000004661	chr9	Arid3b	57790353	57790609	7976	-0.0439	1.938586	0.876488	0.919906	0.051271	0	66	32	93	49	70	40	66	62	93	75
ENSMUSG00000020444	chr11	Guk1	59183875	59184187	1835	-0.02545	5.146355	0.877078	0.920453	0.03325	0	587	474	607	564	545	559	669	565	902	515
ENSMUSG00000047330	chr1	Kcne4	78816758	78816996	2657	0.070174	1.132376	0.877525	0.920777	0.093972	0	27	33	41	22	38	18	76	47	27	31
ENSMUSG00000074971	chr2	Fibin	1.1E+08	1.1E+08	2267	0.0401	3.680153	0.877456	0.920777	0.087674	0	115	99	317	229	302	218	178	309	141	269
ENSMUSG00000020849	chr11	Ywhae	75732869	75733091	2568	-0.02737	8.795056	0.877677	0.920864	0.038015	0	7017	6754	9199	5446	6694	6477	9938	7247	10881	6198
ENSMUSG00000029467	chr5	Atp2a2	1.22E+08	1.22E+08	5293	0.046025	6.252482	0.8787	0.921718	0.107699	0	569	467	1150	2576	1355	1092	1679	1262	1738	1319
ENSMUSG00000053950	chr18	Adnp2	80126311	80130994	5012	-0.04024	2.174353	0.878642	0.921718	0.036176	0	54	44	115	80	74	74	82	76	94	68
ENSMUSG00000092564	chr17	BC051226	33908182	33908586	979	0.064938	0.996716	0.878656	0.921718	0.073101	0	37	26	38	22	22	26	26	36	50	37
ENSMUSG00000048481	chr7	Mypop	18991245	18991354	2175	0.028286	3.205802	0.878928	0.921884	0.034421	0	129	74	209	155	177	108	192	157	262	140
ENSMUSG00000017837	chr11	Nkiras2	1.01E+08	1.01E+08	3578	0.025618	4.466748	0.87906	0.921949	0.028302	0	281	209	413	448	414	291	523	400	512	330
ENSMUSG00000018379	chr11	Srsf1	88047373	88048032	5710	0.024359	5.727883	0.879363	0.922121	0.02768	0	743	700	1128	710	911	678	1072	1112	1119	889
ENSMUSG00000022223	chr14	Sdr39u1	55897286	55898012	1226	-0.02662	6.346573	0.879307	0.922121	0.035652	0	1141	723	1485	1625	1678	1138	1917	1149	2042	1240
ENSMUSG00000003038	chr4	Hmgn2	1.34E+08	1.34E+08	3060	0.031817	3.112261	0.879575	0.922125	0.028422	0	108	114	164	142	144	143	188	138	197	124
ENSMUSG00000033706	chr6	Smyd5	85431989	85432100	3169	0.02886	3.198385	0.879529	0.922125	0.029815	0	147	79	219	140	150	131	230	154	200	132
ENSMUSG00000054434	chr5	Tmem120b	1.23E+08	1.23E+08	2852	0.034036	3.347183	0.879538	0.922125	0.048373	0	128	84	162	232	196	136	202	223	207	160
ENSMUSG00000032235	chr9	Ice2	69397906	69398053	7736	0.033636	2.34876	0.879783	0.92227	0.049765	0	55	60	128	72	89	76	139	107	69	69
ENSMUSG00000026234	chr1	Ncl	86344719	86350696	10188	-0.02485	7.750184	0.880471	0.922919	0.03285	0	3087	3240	4489	2805	3489	3391	4816	3495	4904	3017
ENSMUSG00000101795	chr1	Gm5835	1.43E+08	1.43E+08	1270	-0.03393	2.077533	0.88056	0.922938	0.044166	0	55	56	98	72	52	61	81	85	76	65
ENSMUSG00000041623	chr11	D11Wsu47e	1.14E+08	1.14E+08	2382	0.042586	2.143987	0.880862	0.923182	0.040043	0	65	53	77	58	86	61	128	69	84	63
ENSMUSG00000021130	chr12	Galnt16	80518990	80519345	3920	0.031835	2.91742	0.880999	0.923253	0.047267	0	104	79	231	90	108	120	140	159	180	90
ENSMUSG00000037104	chr17	Socs5	87107679	87108047	4392	0.025738	4.052645	0.881877	0.9241	0.031145	0	173	161	351	329	326	201	384	271	396	288
ENSMUSG00000030127	chr6	Cops7a	1.25E+08	1.25E+08	2711	0.022029	6.659279	0.882163	0.924326	0.024842	0	1521	1204	2229	1423	1676	1479	2291	1738	2336	1528
ENSMUSG00000002981	chr7	Clptm1	19631581	19633962	4130	0.023503	6.031045	0.882495	0.924602	0.029486	0	829	612	1396	1230	1230	885	1260	1239	1592	1062
ENSMUSG00000020826	chr11	Nos2	78920787	78920995	4192	-0.05231	1.375728	0.882707	0.924751	0.07079	0	22	20	45	42	81	30	57	45	56	37
ENSMUSG00000037071	chr19	Scd1	44394451	44398118	4836	-0.08272	8.514589	0.882894	0.924873	0.37122	0	11392	5707	7187	1189	2471	6819	1217	13520	4161	4400
ENSMUSG00000030754	chr7	Copb1	1.14E+08	1.14E+08	3315	0.020937	4.896574	0.883046	0.92496	0.022203	0	360	330	696	463	563	395	692	532	608	514
ENSMUSG00000030447	chr7	Cyfip1	55841745	55842066	8925	0.022366	4.73688	0.883211	0.925059	0.028756	0	352	208	640	470	521	362	590	478	560	460
ENSMUSG00000097944	chr8	A130014A01Rik	1.2E+08	1.2E+08	2323	-0.05526	0.993633	0.883325	0.925106	0.042214	0	22	22	51	29	33	33	39	33	43	21
ENSMUSG00000045435	chr5	Tmem60	20882191	20882655	1147	0.026386	3.964318	0.883961	0.925693	0.024262	0	228	190	311	254	240	218	366	243	368	249
ENSMUSG00000081272	chr2	Gm13509	49308155	49309462	1308	0.028702	2.890541	0.884025	0.925693	0.029187	0	98	76	139	122	150	109	180	108	162	120

ENSMUSG00000049929	chrX	Lpar4	1.07E+08	1.07E+08	4238	0.034941	0.210973	0.884201	0.925804	0.079565	0	18	8	31	14	14	12	15	27	19	22
ENSMUSG00000034795	chr14	Ccdc122	77036772	77036971	1985	0.075719	0.840661	0.884354	0.925891	0.108714	0	28	34	35	17	12	27	46	34	26	25
ENSMUSG00000078350	chr4	Smim1	1.54E+08	1.54E+08	5761	0.03766	2.289886	0.884767	0.926185	0.046555	0	70	67	112	50	80	93	101	82	103	61
ENSMUSG00000092176	chr17	Gm20460	34614484	34614778	1572	0.023011	4.536346	0.884775	0.926185	0.026567	0	313	213	451	428	458	336	498	349	583	380
ENSMUSG00000078813	chr7	Leng1	3660098	3661360	2222	0.030513	2.988761	0.884903	0.926246	0.038623	0	81	71	167	159	159	101	184	143	202	107
ENSMUSG00000043866	chr7	Taf10	1.06E+08	1.06E+08	4584	-0.01977	5.029087	0.885037	0.926313	0.021867	0	453	413	715	495	555	456	790	531	704	501
ENSMUSG00000024187	chr17	Itfg3	26211822	26213717	3981	-0.02768	5.959069	0.885242	0.926354	0.041306	0	694	556	1220	1373	1292	797	1107	1086	1585	1070
ENSMUSG00000038526	chr3	Car14	95897768	95898212	2543	-0.03758	4.684789	0.885197	0.926354	0.07314	0	220	163	588	632	587	298	748	335	647	367
ENSMUSG00000039159	chr6	Ube2h	30211289	30215083	4780	-0.02339	6.101697	0.885285	0.926354	0.029083	0	833	700	1623	1208	1323	845	1363	1169	1596	1263
ENSMUSG00000052962	chr6	Mrpl35	71813003	71816287	3715	0.023132	5.121461	0.885851	0.926873	0.026085	0	464	373	661	638	632	524	836	525	876	488
ENSMUSG00000070425	chr7	Trpc2	1.02E+08	1.02E+08	5673	-0.03906	2.273263	0.886114	0.927075	0.03648	0	61	42	121	79	93	81	101	84	84	72
ENSMUSG00000030965	chr7	Fam175b	1.33E+08	1.33E+08	5427	-0.02128	4.722081	0.88649	0.927396	0.021557	0	345	313	654	372	479	375	571	480	540	419
ENSMUSG00000027893	chr3	Ahcyl1	1.08E+08	1.08E+08	6690	0.019975	5.076392	0.887057	0.927842	0.022277	0	409	393	813	471	651	490	720	650	701	531
ENSMUSG00000033326	chr4	Kdm4a	1.18E+08	1.18E+08	5782	-0.02131	4.710586	0.887042	0.927842	0.020909	0	340	282	592	405	529	370	532	445	583	437
ENSMUSG00000104300	chr9	DHX30	1.1E+08	1.1E+08	3672	-0.02457	4.761443	0.887347	0.928072	0.026935	0	331	237	648	475	573	402	604	512	540	393
ENSMUSG00000078154	chr11	Gm12184	48825346	48826655	1310	0.056669	1.455099	0.887509	0.928168	0.067364	0	44	44	42	30	40	51	66	47	54	28
ENSMUSG00000020888	chr11	Dvl2	70000595	70001026	6298	0.038551	2.690481	0.887666	0.928259	0.053196	0	77	75	115	145	84	100	102	110	159	112
ENSMUSG00000031783	chr8	Polr2c	94857450	94857641	1580	0.022756	5.80075	0.887763	0.928288	0.026383	0	801	752	1044	807	957	812	1378	872	1281	845
ENSMUSG00000023206	chr2	Il15ra	11705290	11705578	4446	0.026416	3.407745	0.887843	0.928298	0.035231	0	113	106	243	156	245	139	303	196	206	142
ENSMUSG00000022972	chr16	1110004E09Rik	90925809	90926082	1360	-0.02031	4.422238	0.888166	0.928562	0.023742	0	310	287	448	298	370	318	486	344	438	350
ENSMUSG00000021062	chr12	Rab15	76797960	76800401	4614	0.06507	0.773351	0.888328	0.928659	0.215932	0	6	6	14	57	45	23	35	28	33	29
ENSMUSG00000021028	chr12	Mbip	56328306	56328799	1509	-0.0309	2.095456	0.888805	0.928992	0.036277	0	56	53	82	69	77	63	100	60	76	76
ENSMUSG00000031819	chr8	Emc8	1.21E+08	1.21E+08	6295	-0.02224	3.828228	0.888762	0.928992	0.024713	0	164	183	306	221	274	197	312	287	286	200
ENSMUSG00000084803	chr4	5830444B04Rik	1.55E+08	1.55E+08	5410	0.061447	0.289148	0.888857	0.928992	0.078875	0	14	11	23	19	21	23	15	19	38	9
ENSMUSG00000026887	chr2	Mrrf	36136389	36136699	2853	-0.02033	4.081238	0.888963	0.929029	0.02238	0	225	187	328	298	327	247	405	273	379	239
ENSMUSG00000029708	chr6	Gcc1	28416091	28419300	5287	0.027731	3.463106	0.889293	0.929302	0.029691	0	146	133	223	149	222	128	302	187	223	183
ENSMUSG00000046794	chr8	Ppp1r3b	35375741	35375805	4206	0.067517	0.730839	0.889518	0.929464	0.15174	0	27	17	43	9	28	16	33	60	21	14
ENSMUSG00000007610	chr8	Gtpbp3	71488103	71488840	3984	-0.02606	3.392938	0.889675	0.929554	0.032166	0	147	114	180	192	206	149	265	147	209	177
ENSMUSG00000045659	chr7	Plekha7	1.16E+08	1.16E+08	11618	-0.05724	0.494786	0.890279	0.930112	0.053346	0	17	12	32	25	22	19	19	30	32	16
ENSMUSG00000001054	chr11	Rmnd5b	51623671	51624146	2161	0.021729	3.730382	0.89077	0.930226	0.023918	0	190	124	287	216	249	192	337	221	270	202
ENSMUSG00000021340	chr13	Gpld1	24943152	24943249	3584	0.077633	0.380641	0.890466	0.930226	0.068199	0	11	17	25	20	20	10	20	29	36	18
ENSMUSG00000021823	chr14	Vcl	20929433	20929688	5229	0.02414	6.540754	0.890685	0.930226	0.036832	0	1366	703	2347	1383	1921	1194	1982	1434	2582	1532
ENSMUSG00000031166	chrX	Wdr13	8123301	8125729	5277	-0.02053	4.18992	0.890562	0.930226	0.022794	0	274	208	337	276	369	265	366	305	408	301
ENSMUSG00000051154	chr2	Commd3	18672384	18672407	2330	0.024273	6.049513	0.890809	0.930226	0.03313	0	1014	926	1233	963	996	1038	1669	1008	1459	978
ENSMUSG00000064138	chr13	Fam172a	77708690	77708853	4019	-0.02226	3.62415	0.890758	0.930226	0.024657	0	156	150	283	188	222	159	304	229	231	192
ENSMUSG00000028163	chr3	Nfkb1	1.36E+08	1.36E+08	4779	-0.02357	4.565108	0.891165	0.930392	0.025397	0	301	208	584	385	499	304	534	404	500	406
ENSMUSG00000045078	chr5	Rnf216	1.43E+08	1.43E+08	4671	-0.02113	4.666054	0.891061	0.930392	0.021572	0	333	258	573	428	491	364	523	463	538	404
ENSMUSG00000079179	chr12	Rab10os	3235504	3235929	6144	-0.03397	2.687374	0.891179	0.930392	0.037309	0	74	72	174	99	109	87	129	137	110	104
ENSMUSG00000064179	chr7	Tnnt1	4504570	4504800	2204	0.104445	3.323878	0.89164	0.9308	0.667964	0	11	6	17	569	161	165	201	99	301	179
ENSMUSG00000023764	chr11	Sfi1	3131850	3132131	7559	-0.02892	2.68844	0.892588	0.931643	0.029399	0	89	69	153	89	123	101	116	117	135	100
ENSMUSG00000036904	chr18	Fzd8	9212856	9216201	3346	0.030179	1.732144	0.892543	0.931643	0.048752	0	32	28	70	61	71	34	70	65	70	59
ENSMUSG00000079363	chr5	Gbp4	1.05E+08	1.05E+08	4538	0.044854	1.791983	0.892662	0.931647	0.044098	0	44	40	69	45	69	39	106	60	67	46
ENSMUSG00000002307	chr17	Daxx	33909414	33909463	3058	-0.02258	3.788744	0.892813	0.931663	0.022016	0	180	143	299	239	264	208	282	230	304	219
ENSMUSG00000030512	chr7	Snrpa1	66060299	66060585	3082	0.025359	3.800805	0.892888	0.931663	0.024912	0	200	164	269	221	242	198	372	236	299	189
ENSMUSG00000103906	chr15	TIGD5	75909735	75914535	4801	0.036408	1.025418	0.892831	0.931663	0.053299	0	22	15	41	36	42	26	30	37	57	29
ENSMUSG00000023026	chr15	Dip2b	1E+08	1E+08	9553	-0.02737	3.151151	0.893366	0.931876	0.029732	0	117	75	198	155	185	110	215	148	186	144
ENSMUSG00000029189	chr5	Sel1l3	53107084	53108174	4511	-0.02648	5.636363	0.893389	0.931876	0.043342	0	499	454	1106	1006	1091	549	1430	736	988	882
ENSMUSG00000030643	chr7	Rab30	92741603	92741842	2116	-0.04983	1.439747	0.89321	0.931876	0.048748	0	39	32	66	33	45	45	39	40	53	52
ENSMUSG00000036097	chr19	Fam178a	44931119	44931450	6880	0.020589	4.081459	0.893443	0.931876	0.028717	0	204	163	476	216	343	212	408	314	357	273
ENSMUSG00000038622	chr15	Med30	52712445	52712686	871	0.0371	3.288858	0.893415	0.931876	0.053876	0	157	170	162	112	128	163	218	160	208	145
ENSMUSG00000097210	chr7	Fam160a2	1.05E+08	1.05E+08	2508	0.034791	1.552615	0.893707	0.932078	0.040239	0	45	31	54	39	55	49	46	50	65	48
ENSMUSG00000016087	chr9	Fli1	32422204	32424305	3486	-0.02121	2.584855	0.894248	0.932513	0.036249	0	78	74	106	100	116	74	131	112	156	72
ENSMUSG00000029911	chr6	Ssbp1	40471352	40471459	3319	0.025388	4.734796	0.894265	0.932513	0.031544	0	430	366	513	376	375	391	670	409	612	395
ENSMUSG00000047434	chr16	Xxylt1	30955627	30957734	3412	-0.03206	2.306658	0.89438	0.93256	0.042042	0	62	63	121	69	82	61	113	104	75	82
ENSMUSG00000024378	chr18	Stard4	33199355	33203815	5586	0.040968	1.839098	0.894935	0.933038	0.064988	0	25	42	63	69	78	36	89	73	86	45
ENSMUSG00000029416	chr5	Slc15a4	1.28E+08	1.28E+08	5312	-0.02544	4.172704	0.895049	0.933038	0.034609	0	275	216	491	196	302	295	300	320	419	276
ENSMUSG00000030051	chr6	Aplf	87628429	87630175	3278	0.030232	1.960458	0.89503	0.933038	0.034904	0	50	43	80	63	66	68	93	61	75	52
ENSMUSG00000064210	chr15	Ano6	95790843	95791056	5640	-0.02071	5.895194	0.895419	0.93335	0.026122	0	760	574	1504	911	1223	835	1274	904	1412	1001
ENSMUSG00000029864	chr6	Gstk1	42245935	42246093	930	-0.01885	5.347403	0.895665	0.93346	0.023619	0	476	494	824	736	762	570	922	698	928	604
ENSMUSG00000060739	chr13	Nsa2	97129427	97131228	2686	-0.02092	5.252153	0.895637	0.93346	0.031951	0	550	574	673	569	618	632	893	613	795	524
ENSMUSG00000024902	chr19	Mrpl11	4962306	4962515	2882	-0.02093	5.586074	0.895883	0.933613	0.032259	0	707	694	812	772	774	769	1111	713	1122	672
ENSMUSG00000045211	chr14	Nudt18	70577847	70578110	3716	0.02631	3.810554	0.896712	0.934404	0.038287	0	219	146	245	239	251	203	277	351	262	183
ENSMUSG00000029771	chr6	Irf5	29526625	29526774	2903	-0.05915	3.109284	0.89694	0.934568	0.216935	0	38	34	80	330	235	158	155	149	161	124
ENSMUSG00000033272	chr18	Slc35a4	36679215	36679623	3275	-0.02004	6.08249	0.897239	0.934806	0.027012	0	946	672	1390	1215	1309	1054	1411	1158	1613	940
ENSMUSG00000035759	chr10	Bbs10	1.11E+08	1.11E+08	2753	-0.03303	0.969432	0.897384	0.934884	0.065909	0	33	24	35	27	29	22	62	21	33	32

ENSMUSG00000038965	chr16	Ube2l3	17152013	17154282	5599	0.01971	7.2432	0.897511	0.934942	0.026739	0	2196	1870	3377	2143	2493	2145	3331	2593	3768	2260
ENSMUSG00000036023	chr14	Parp2	50807946	50807987	1788	-0.02114	3.047059	0.897585	0.934946	0.038369	0	129	120	140	103	153	103	203	125	178	139
ENSMUSG00000049488	chr4	Tmem67	12039355	12039892	7744	-0.03914	0.680529	0.897684	0.934976	0.045811	0	24	18	33	19	28	21	35	30	35	15
ENSMUSG00000020903	chr11	Stx8	67966193	67966517	7137	0.025895	4.421206	0.897786	0.935009	0.033581	0	288	323	348	330	355	360	487	370	474	281
ENSMUSG00000027371	chr2	Fahd2a	1.27E+08	1.27E+08	1463	-0.02043	4.112856	0.898343	0.935515	0.027183	0	204	202	308	329	346	259	398	260	389	265
ENSMUSG00000018841	chr11	Rad51d	82876434	82879023	3714	0.03419	2.513535	0.898714	0.935539	0.044956	0	95	72	102	75	93	87	102	128	103	90
ENSMUSG00000023055	chr15	Calcoco1	1.03E+08	1.03E+08	3963	0.019341	6.757823	0.898683	0.935539	0.026024	0	1328	1290	2289	1800	1965	1453	2435	1691	2761	1752
ENSMUSG00000035399	chr2	Oser1	1.63E+08	1.63E+08	2600	0.0253	3.552466	0.898569	0.935539	0.029624	0	200	136	243	143	200	186	277	191	259	165
ENSMUSG00000050122	chr1	Vwa3b	37026596	37026645	5386	-0.03956	1.721143	0.898719	0.935539	0.086172	0	37	25	44	88	65	33	91	44	76	51
ENSMUSG00000074305	chr9	Peak1	56201126	56207611	12351	-0.02535	4.215194	0.898601	0.935539	0.030478	0	226	162	561	262	366	248	378	310	442	306
ENSMUSG00000055531	chr10	Cpsf6	1.17E+08	1.17E+08	10510	0.020805	4.354999	0.898814	0.935566	0.028937	0	227	238	502	316	375	254	357	423	494	347
ENSMUSG00000018339	chr11	Gpx3	54902453	54902575	1813	0.027986	8.545159	0.898914	0.935595	0.057415	0	4034	6262	8448	5512	4839	5140	9441	8939	6223	4836
ENSMUSG00000002055	chr11	Spag5	78301529	78301710	5624	-0.0389	2.188045	0.899171	0.935717	0.057162	0	77	53	129	39	71	64	77	80	95	81
ENSMUSG00000026873	chr2	Phf19	34893757	34896061	5036	0.039767	0.57303	0.899119	0.935717	0.060596	0	14	9	25	31	32	19	29	24	29	26
ENSMUSG00000022471	chr15	Xrcc6	81987835	81987952	4476	-0.01902	4.870972	0.899432	0.935915	0.024604	0	480	318	585	451	517	460	675	462	594	456
ENSMUSG00000030846	chr7	Tial1	1.28E+08	1.28E+08	5861	0.019559	5.31449	0.899759	0.936181	0.024036	0	579	508	888	527	661	601	959	690	828	592
ENSMUSG00000028649	chr4	Macf1	1.23E+08	1.23E+08	26689	-0.02736	5.911367	0.899921	0.936277	0.050704	0	593	401	1783	1031	1435	766	1211	1105	1475	935
ENSMUSG00000028608	chr4	0610037L13Rik	1.08E+08	1.08E+08	5633	0.024046	5.009243	0.900331	0.93663	0.033622	0	539	461	569	428	476	487	776	547	678	485
ENSMUSG00000043943	chr9	Naalad2	18321951	18323623	4749	0.032209	2.577356	0.900446	0.936667	0.069116	0	50	51	136	109	138	61	166	78	107	133
ENSMUSG00000070720	chr4	Tmem200b	1.32E+08	1.32E+08	1370	-0.05553	0.748594	0.900508	0.936667	0.109157	0	10	17	31	27	47	13	19	30	43	35
ENSMUSG00000029456	chr5	Acad10	1.22E+08	1.22E+08	6068	-0.03434	2.006458	0.900893	0.936993	0.038173	0	45	37	93	74	76	52	73	81	87	60
ENSMUSG00000080875	chr5	Gm7332	9260945	9261388	444	0.05077	2.065349	0.901283	0.937326	0.094971	0	83	67	65	32	60	87	78	58	107	49
ENSMUSG00000030532	chr7	Hddc3	80343137	80343249	860	0.036779	2.486943	0.901552	0.937466	0.050297	0	76	82	74	87	103	85	109	83	156	81
ENSMUSG00000061904	chr10	Slc25a3	91116574	91117124	5550	-0.0264	9.502328	0.901559	0.937466	0.054384	0	8550	5645	12495	17076	16084	9418	16540	10641	20155	10571
ENSMUSG00000026035	chr1	Ppil3	58430994	58431330	4291	0.026163	3.433625	0.901652	0.937472	0.033708	0	153	149	186	150	198	191	243	163	205	175
ENSMUSG00000091905	chr12	Gm6395	64786192	64786439	1491	0.083173	0.384697	0.901706	0.937472	0.094381	0	15	23	18	14	20	11	47	18	23	17
ENSMUSG00000026275	chr1	Ppp1r7	93342854	93343711	10495	-0.01667	4.829018	0.9019	0.9376	0.022033	0	375	373	593	449	487	407	622	485	660	419
ENSMUSG00000039221	chr3	Rpl22l1	28805436	28805543	1989	-0.02407	5.606245	0.902093	0.93772	0.047425	0	961	683	855	618	660	798	1218	663	1079	690
ENSMUSG00000039616	chr18	Mocos	24653691	24654067	2884	0.022345	2.099303	0.902157	0.93772	0.033889	0	53	37	102	66	84	57	102	82	84	62
ENSMUSG00000004500	chr7	Zfp324	12965838	12966299	4776	-0.03494	1.395152	0.902815	0.93811	0.035768	0	34	24	60	47	43	37	59	36	57	40
ENSMUSG00000020328	chr11	Nudcd2	40733667	40734154	2054	0.0285	3.588696	0.902794	0.93811	0.037437	0	168	189	257	140	177	166	293	179	276	198
ENSMUSG00000037503	chr1	Fam168b	34813219	34817404	5219	-0.01818	5.271508	0.902651	0.93811	0.022539	0	469	445	922	608	726	526	817	765	797	597
ENSMUSG00000040836	chr1	Gpr161	1.65E+08	1.65E+08	6962	-0.07145	0.926696	0.902745	0.93811	0.08454	0	10	20	61	29	35	27	26	32	35	36
ENSMUSG00000073471	chr17	Rsph3a	7945653	7946303	2189	-0.02938	2.975569	0.902961	0.938189	0.04876	0	133	57	122	147	173	102	199	136	162	112
ENSMUSG00000001942	chr9	Siae	37613847	37613926	3433	0.020324	3.151959	0.903153	0.938214	0.037508	0	131	67	224	136	166	119	189	185	155	154
ENSMUSG00000027822	chr3	Slc33a1	63933507	63933904	3548	0.024001	3.079276	0.903198	0.938214	0.02691	0	128	95	175	118	150	112	200	157	161	140
ENSMUSG00000037326	chr17	Capn15	25959556	25959733	3520	-0.0365	1.73284	0.903069	0.938214	0.038814	0	48	28	72	47	72	39	77	64	63	49
ENSMUSG00000030335	chr6	Mrpl51	1.25E+08	1.25E+08	3357	0.020551	7.077974	0.90352	0.938412	0.032525	0	1871	1609	2194	2424	2503	2035	3200	2021	3385	1970
ENSMUSG00000049401	chr2	Ogfr	1.81E+08	1.81E+08	2580	-0.01786	4.911653	0.90353	0.938412	0.023417	0	426	372	591	461	563	509	622	484	638	456
ENSMUSG00000042870	chr8	Tom1	75033686	75033827	2358	0.01968	5.125887	0.903659	0.938472	0.029413	0	399	355	777	677	618	490	781	487	853	619
ENSMUSG00000027500	chr3	Stmn2	8509360	8509630	5602	0.051305	1.4952	0.903893	0.938642	0.09672	0	33	25	37	60	57	28	103	28	69	36
ENSMUSG00000005442	chr7	Cic	25267704	25267756	10294	0.020099	5.052405	0.904131	0.93876	0.036329	0	373	255	942	537	685	442	655	707	746	502
ENSMUSG00000027358	chr2	Bmp2	1.34E+08	1.34E+08	3555	0.048106	1.025433	0.904149	0.93876	0.074393	0	17	18	42	40	38	15	54	40	32	39
ENSMUSG00000007338	chr19	Mrpl49	6053630	6054982	1722	0.019803	4.881488	0.904315	0.93886	0.024429	0	423	352	523	490	529	439	716	466	636	463
ENSMUSG00000047446	chr12	Arl4a	40005447	40005711	7701	-0.01897	4.987776	0.904834	0.939325	0.032158	0	495	482	641	400	475	452	694	596	667	470
ENSMUSG00000028140	chr3	Mrpl9	94443336	94443494	1601	0.019761	5.875319	0.9052	0.939632	0.030248	0	815	569	1039	1141	1117	890	1387	920	1426	839
ENSMUSG00000024896	chr19	Minpp1	32485769	32486559	2619	0.019598	4.177759	0.905949	0.940335	0.022069	0	269	220	362	237	345	252	391	326	403	289
ENSMUSG00000025645	chr9	Ccdc51	1.09E+08	1.09E+08	1526	-0.0267	2.730485	0.906113	0.940406	0.038782	0	90	68	107	120	144	94	175	97	127	103
ENSMUSG00000031353	chrX	Rbbp7	1.63E+08	1.63E+08	2909	-0.01844	6.846141	0.906159	0.940406	0.029563	0	1651	1626	2480	1590	1832	1779	2643	1779	2613	1699
ENSMUSG00000043162	chr6	Pyurf	57686576	57689878	3573	0.021614	5.222669	0.906354	0.940535	0.03289	0	526	413	620	738	631	555	951	554	933	505
ENSMUSG00000020832	chr11	Eral1	78073376	78074174	2268	0.018973	4.58571	0.906719	0.94084	0.02586	0	332	228	466	462	432	353	582	370	548	369
ENSMUSG00000030917	chr7	Tmem159	1.2E+08	1.2E+08	1926	0.022544	3.54284	0.907106	0.941167	0.032409	0	155	139	228	194	201	202	185	212	293	164
ENSMUSG00000099881	chr8	2810013P06Rik	1.23E+08	1.23E+08	2137	0.03172	2.871897	0.907442	0.941442	0.051788	0	100	99	98	143	113	129	142	106	186	104
ENSMUSG00000020956	chr12	Dtd2	51988312	51988855	3108	0.035425	2.388274	0.907637	0.941477	0.036902	0	73	69	83	72	104	74	120	84	129	73
ENSMUSG00000037085	chr15	Trmt12	58872649	58876781	4133	0.02998	2.808976	0.907671	0.941477	0.045897	0	106	96	122	75	142	93	130	105	170	138
ENSMUSG00000079316	chrX	Rab9	1.66E+08	1.66E+08	1749	0.021883	3.903394	0.907688	0.941477	0.027212	0	264	169	307	198	238	209	335	268	327	235
ENSMUSG00000020788	chr11	Atp2a3	72961169	72961471	5281	0.025498	3.19416	0.908237	0.941973	0.056702	0	86	68	178	200	211	96	179	178	225	163
ENSMUSG00000019647	chr18	Sema6a	47235598	47235928	8778	0.02253	2.834176	0.908943	0.942336	0.045877	0	80	58	136	119	183	99	186	114	125	124
ENSMUSG00000027615	chr3	Hps3	19995945	19997029	9103	-0.02415	2.534119	0.908889	0.942336	0.030118	0	81	71	135	75	102	89	114	103	120	87
ENSMUSG00000028232	chr4	Tmem68	3549041	3550579	3462	-0.02286	2.264885	0.908774	0.942336	0.030922	0	66	54	93	71	98	67	116	78	90	76
ENSMUSG00000031818	chr8	Cox4i1	1.21E+08	1.21E+08	1550	0.023404	9.191126	0.908842	0.942336	0.049743	0	7112	5374	8577	13209	12265	8542	13629	8858	15832	8108
ENSMUSG00000036381	chr3	P2ry14	59114626	59116061	1797	0.038065	0.628792	0.90891	0.942336	0.077212	0	8	12	34	26	38	24	39	24	32	15
ENSMUSG00000092310	chr9	Gm20509	73102470	73102675	1016	-0.02032	2.803055	0.909156	0.942484	0.037385	0	111	94	132	100	109	121	156	96	149	101
ENSMUSG00000022378	chr15	Fam49b	63929097	63931679	3869	0.016798	5.18916	0.90947	0.942735	0.022066	0	468	439	855	510	671	535	898	590	820	539
ENSMUSG00000029136	chr5	Rbks	31624439	31624656	1489	0.052892	0.727214	0.909573	0.942769	0.06313	0	24	27	31	19	18	28	29	30	35	21

ENSMUSG00000040174	chr2	Alkbh3	93980550	93980977	3159	-0.01588	4.936146	0.909801	0.942931	0.024225	0	492	366	610	440	539	459	729	479	711	428
ENSMUSG00000004936	chr9	Map2k1	64185770	64186798	3391	-0.01698	6.193237	0.910564	0.943575	0.025767	0	1029	782	1751	1108	1340	919	1653	1158	1703	1275
ENSMUSG00000028862	chr4	Map3k6	1.33E+08	1.33E+08	4604	-0.04869	1.573958	0.910498	0.943575	0.099895	0	27	37	69	47	59	75	45	62	45	22
ENSMUSG00000039910	chr10	Cited2	17723228	17723459	1968	0.025653	4.909829	0.911143	0.944101	0.060319	0	304	251	619	422	905	289	726	448	923	482
ENSMUSG00000028300	chr4	3110043O21Rik	35191285	35193294	4603	0.017881	4.207265	0.911302	0.944192	0.022604	0	256	227	406	271	308	268	387	374	370	284
ENSMUSG00000033883	chr3	D3Ertd254e	36159522	36159648	6503	-0.04365	1.613787	0.911619	0.944373	0.062644	0	30	22	79	42	80	29	76	56	56	51
ENSMUSG00000055491	chr19	Pprc1	46044886	46045062	7516	-0.01949	4.121532	0.911555	0.944373	0.026237	0	233	159	460	278	316	217	453	303	374	252
ENSMUSG00000052371	chr2	Hoxd3os1	74703248	74703622	2872	0.086453	0.712175	0.911739	0.944397	0.383708	0	42	29	35	4	1	26	25	30	56	12
ENSMUSG00000058503	chr5	Fam133b	3543844	3543947	1555	-0.02023	2.716822	0.911785	0.944397	0.034566	0	100	77	117	85	143	97	153	115	147	81
ENSMUSG00000047881	chr5	Rell1	63908896	63911151	3863	0.019871	3.508675	0.91191	0.944453	0.024467	0	154	133	273	156	195	154	290	200	233	171
ENSMUSG00000035441	chr11	Myo1d	80482126	80484382	6465	-0.03591	2.518162	0.912129	0.944606	0.063518	0	56	40	134	93	158	61	100	117	121	106
ENSMUSG00000029309	chr5	Sparcl1	1.04E+08	1.04E+08	3114	-0.01847	7.113459	0.912807	0.945234	0.032645	0	1574	1314	3145	2467	3037	1606	3281	2513	2991	2326
ENSMUSG00000070576	chr5	Mn1	1.11E+08	1.11E+08	6940	0.023426	5.610914	0.912949	0.945308	0.057509	0	474	318	1183	1038	1085	657	1004	762	951	1065
ENSMUSG00000019278	chr8	Dpep1	1.23E+08	1.23E+08	2241	0.021645	4.96974	0.913906	0.94615	0.047707	0	411	384	851	324	585	647	490	608	687	385
ENSMUSG00000028407	chr4	Toporsos	40269569	40269719	1054	0.033523	3.246027	0.913842	0.94615	0.069661	0	181	158	174	96	98	155	236	144	208	132
ENSMUSG00000016349	chr2	Eef1a2	1.81E+08	1.81E+08	2084	0.017088	10.39799	0.914115	0.946271	0.030043	0	19392	12468	29391	22867	25571	18178	26831	23203	35781	21435
ENSMUSG00000028018	chr3	Gstcd	1.33E+08	1.33E+08	4731	-0.04555	0.834066	0.914295	0.946271	0.061929	0	18	18	28	35	38	36	32	24	36	21
ENSMUSG00000029436	chr5	Mmp17	1.3E+08	1.3E+08	4395	0.070535	-0.08109	0.914237	0.946271	0.101592	0	6	13	19	10	18	6	11	20	18	22
ENSMUSG00000036106	chr15	Prr5	84669620	84669705	1917	0.026999	1.866123	0.914307	0.946271	0.070174	0	50	37	71	46	81	45	46	104	76	51
ENSMUSG00000001870	chr17	Ltbp1	75005568	75006361	10480	-0.02268	4.191009	0.914452	0.946347	0.031978	0	193	180	500	278	384	315	343	352	380	243
ENSMUSG00000071659	chr19	Hnrnpul2	8819401	8820813	5726	-0.01544	6.755518	0.914782	0.946614	0.023349	0	1418	1201	2598	1605	2069	1569	2341	1866	2327	1726
ENSMUSG00000035329	chr12	Fbxo33	59200655	59202679	4466	-0.02405	1.835285	0.914947	0.946637	0.046986	0	58	37	73	50	63	35	74	84	77	47
ENSMUSG00000093752	chr2	Gm20716	1.68E+08	1.68E+08	5288	-0.01719	6.40285	0.914889	0.946637	0.031561	0	1279	1204	1874	1087	1297	1264	1941	1303	1985	1260
ENSMUSG00000049303	chr19	Syt12	4445908	4447860	5539	0.053636	1.003807	0.915207	0.946832	0.182159	0	35	10	27	44	33	49	30	45	44	6
ENSMUSG00000027963	chr3	Extl2	1.16E+08	1.16E+08	3446	0.019021	3.788183	0.91537	0.946885	0.025218	0	219	145	319	190	232	175	313	224	337	228
ENSMUSG00000028145	chr3	Them4	94310132	94310288	1730	-0.02195	3.23786	0.915457	0.946885	0.036905	0	119	89	162	209	177	136	210	152	210	143
ENSMUSG00000029781	chr6	Fkbp9	56832059	56832427	3314	0.015756	6.783926	0.915472	0.946885	0.025426	0	1492	1349	2589	1531	1910	1612	2358	1962	2259	1887
ENSMUSG00000022325	chr15	Pop1	34495304	34495415	3795	0.029277	1.896894	0.915636	0.946981	0.043346	0	64	35	65	51	72	68	78	56	74	55
ENSMUSG00000064339	chrMT	mt-Rnr2	1094	2675	1582	-0.02696	9.486571	0.915875	0.947154	0.077567	0	5117	5540	13629	18754	17292	9539	15171	14500	17432	9224
ENSMUSG00000049823	chr17	Zbtb12	34879483	34879524	2020	0.018353	2.991693	0.915974	0.947183	0.02516	0	104	88	171	118	152	114	177	123	176	134
ENSMUSG00000002812	chr11	Flii	60714123	60714447	5039	-0.01597	6.433911	0.916457	0.947545	0.026052	0	1126	867	1992	1490	1646	1130	1863	1385	2149	1416
ENSMUSG00000035325	chr5	Sec31a	1E+08	1E+08	7884	0.016483	5.875206	0.916468	0.947545	0.030949	0	752	475	1525	970	1160	795	1140	1036	1419	1010
ENSMUSG00000023345	chr9	Poc1a	1.06E+08	1.06E+08	2995	-0.04997	1.025566	0.916574	0.947581	0.047072	0	19	18	42	35	47	30	32	34	45	31
ENSMUSG00000031349	chrX	Nsdhl	72918557	72918693	2853	0.02139	2.664642	0.916668	0.947593	0.043112	0	105	70	134	76	113	108	119	141	111	86
ENSMUSG00000032946	chr19	Rasgrp2	6399340	6399517	12384	0.025755	2.689089	0.916728	0.947593	0.041596	0	100	74	124	88	117	92	122	154	144	74
ENSMUSG00000001039	chr11	B9d1	61505144	61505271	1593	0.054018	0.991006	0.91697	0.947695	0.050222	0	28	30	33	24	30	25	37	29	48	36
ENSMUSG00000036052	chr4	Dnajb5	42949814	42950004	5936	0.0174	7.712403	0.916937	0.947695	0.033756	0	2979	1631	5564	3467	3788	3352	4247	3617	4857	3190
ENSMUSG00000073676	chr1	Hspe1	55088132	55088412	1474	-0.01687	5.959049	0.91735	0.948014	0.032924	0	926	771	929	1112	1159	832	1438	1085	1425	931
ENSMUSG00000035027	chr10	Map2k2	81105915	81106238	3722	-0.01715	7.3322	0.917538	0.94806	0.032823	0	2548	2064	3404	2316	2540	2568	2975	2582	4195	2361
ENSMUSG00000086534	chr17	Gm16758	29890084	29890577	3848	0.026332	-0.08133	0.917508	0.94806	0.115476	0	9	9	17	9	24	17	16	8	9	24
ENSMUSG00000036817	chr5	Sun1	1.39E+08	1.39E+08	7596	-0.01561	5.629473	0.917623	0.948074	0.023692	0	613	534	1239	731	983	621	1110	812	1152	843
ENSMUSG00000020823	chr11	Sec14l1	1.17E+08	1.17E+08	7176	0.015423	5.879196	0.917756	0.948138	0.025888	0	831	682	1372	781	1086	913	1084	1087	1267	994
ENSMUSG00000027012	chr2	Dync1i2	71211706	71211845	8280	0.015613	5.813462	0.918053	0.948232	0.023302	0	771	720	1209	839	931	765	1289	964	1243	930
ENSMUSG00000044086	chr6	Lmod3	97238528	97238871	2242	-0.02447	7.174042	0.918133	0.948232	0.066701	0	1465	1196	2290	3597	3320	1821	3661	1701	3671	2517
ENSMUSG00000044573	chr12	Acp1	30893326	30895953	3221	0.017861	5.052854	0.918076	0.948232	0.026827	0	453	406	583	547	626	451	758	481	862	538
ENSMUSG00000047909	chr2	Ankrd16	11777876	11778227	5926	-0.01612	3.906481	0.91802	0.948232	0.030863	0	229	206	359	179	226	219	366	248	339	199
ENSMUSG00000030751	chr7	Psma1	1.14E+08	1.14E+08	2103	-0.01648	6.33398	0.918233	0.948262	0.0315	0	1093	1155	1645	1279	1222	1275	1947	1394	1651	1093
ENSMUSG00000019848	chr10	Popdc3	45178098	45178192	2083	-0.01486	5.284396	0.918674	0.948495	0.025162	0	609	471	901	502	667	553	903	601	955	573
ENSMUSG00000027513	chr2	Pck1	1.73E+08	1.73E+08	3429	-0.07536	5.036435	0.918635	0.948495	0.627794	0	1087	777	208	67	103	302	151	1740	176	374
ENSMUSG00000054823	chr8	Whsc1l1	25601601	25601993	16513	0.015195	3.797337	0.918532	0.948495	0.032811	0	172	120	394	193	276	194	256	293	309	213
ENSMUSG00000027777	chr3	Schip1	68064802	68065007	5102	-0.02015	6.839885	0.918829	0.948582	0.044877	0	1333	972	2160	2233	2804	1774	2660	1381	2941	1777
ENSMUSG00000095687	chr17	Rnaset2a	8128610	8128886	1259	0.03167	2.516924	0.918909	0.948591	0.057827	0	100	78	129	66	66	102	133	80	141	68
ENSMUSG00000026073	chr1	Il1r2	40074079	40074248	1908	0.074049	0.82971	0.919046	0.948658	0.38035	0	35	29	51	4	11	67	30	28	20	4
ENSMUSG00000024174	chr17	Pot1b	55652025	55653518	3499	-0.04351	1.035614	0.919465	0.949017	0.051937	0	30	16	45	24	47	24	47	39	30	34
ENSMUSG00000030553	chr7	Pgpep1l	68236608	68237122	955	0.046251	1.574644	0.919826	0.949274	0.128338	0	31	54	61	43	31	40	97	18	50	65
ENSMUSG00000038215	chr8	Cep44	56531522	56531732	2817	-0.01633	2.556734	0.919858	0.949274	0.040465	0	79	90	97	87	102	90	129	112	117	77
ENSMUSG00000015337	chr2	Endog	30171493	30172066	1063	-0.01872	4.957577	0.920068	0.949418	0.037926	0	428	260	508	663	661	416	680	507	797	457
ENSMUSG00000028646	chr4	Rragc	1.24E+08	1.24E+08	3341	-0.01401	4.80041	0.920754	0.950049	0.022417	0	390	343	584	395	533	390	576	543	637	393
ENSMUSG00000057421	chrX	Las1l	95935335	95935649	8143	-0.01464	5.433221	0.920823	0.950049	0.023796	0	565	527	921	606	889	676	987	625	980	672
ENSMUSG00000041268	chr9	Dmxl2	54365158	54366627	13419	0.02425	2.032968	0.921299	0.950465	0.041714	0	52	40	97	66	68	47	84	97	77	62
ENSMUSG00000034110	chr5	Kctd7	1.3E+08	1.3E+08	4368	0.02571	2.335468	0.922024	0.951094	0.042029	0	56	48	87	102	103	63	110	90	104	89
ENSMUSG00000097048	chr6	1600020E01Rik	86526271	86527974	2092	0.029148	1.990473	0.922051	0.951094	0.045615	0	66	50	86	54	48	63	78	64	78	70
ENSMUSG00000062713	chr16	Sim2	94085260	94085990	3670	-0.06679	3.597208	0.9224	0.95138	0.541282	0	335	189	262	101	30	156	344	258	390	1
ENSMUSG00000074738	chr4	B930041F14Rik	1.56E+08	1.56E+08	2140	0.029592	1.650332	0.922965	0.951888	0.045804	0	45	38	65	39	54	38	46	58	76	60
ENSMUSG00000063296	chr15	Tmem117	94629185	94629302	2781	0.016941	4.180442	0.923782	0.952656	0.029274	0	243	199	438	278	304	248	444	219	438	329

ENSMUSG00000023452	chr5	Pisd	32736301	32737454	3814	0.01776	4.282533	0.923881	0.952685	0.031974	0	250	194	338	385	381	289	463	397	408	238
ENSMUSG00000022094	chr14	Slc39a14	70303469	70306812	10550	0.016564	3.59325	0.924218	0.952884	0.040535	0	118	95	267	218	298	192	289	201	264	162
ENSMUSG00000026883	chr2	Dab2ip	35558266	35558612	8366	-0.0184	6.150884	0.924207	0.952884	0.039833	0	1005	505	2003	1107	1423	844	1467	1406	1687	1109
ENSMUSG00000037949	chr9	Ano10	1.22E+08	1.22E+08	2599	-0.01416	5.429598	0.924392	0.95299	0.023882	0	653	495	968	633	737	673	810	805	975	634
ENSMUSG00000026389	chr1	Steap3	1.2E+08	1.2E+08	5715	-0.01657	5.57797	0.925143	0.953689	0.029973	0	595	388	1190	859	972	610	1067	862	995	815
ENSMUSG00000024317	chr18	Rnf138	21001341	21001540	3110	-0.01864	2.158574	0.92536	0.953839	0.038892	0	69	58	93	51	80	60	80	87	92	74
ENSMUSG00000028344	chr4	Invs	48279760	48279975	11431	-0.02947	1.202091	0.925515	0.95388	0.048	0	25	31	52	31	40	31	47	53	36	30
ENSMUSG00000038539	chr7	Atf5	44812257	44813520	1992	0.021038	5.602554	0.925543	0.95388	0.059888	0	466	379	781	1197	1120	638	872	994	1149	807
ENSMUSG00000044408	chr12	Sptssa	54645374	54646535	1363	0.016384	4.617247	0.92568	0.953881	0.02451	0	299	334	504	370	436	303	534	476	561	391
ENSMUSG00000091898	chr14	Tnnc1	31208312	31208378	1041	0.072405	2.531547	0.925688	0.953881	0.634303	0	4	8	15	345	66	69	81	68	182	132
ENSMUSG00000021537	chr13	Cetn3	81783292	81783357	999	0.018862	3.932363	0.925904	0.953971	0.027211	0	219	201	287	230	256	231	401	236	293	240
ENSMUSG00000029524	chr5	Sirt4	1.15E+08	1.15E+08	2398	0.021406	2.630538	0.925919	0.953971	0.029684	0	85	65	112	90	136	90	136	107	135	94
ENSMUSG00000078652	chr11	Psme3	1.01E+08	1.01E+08	2949	0.013866	5.953219	0.926379	0.954371	0.023412	0	851	733	1335	965	1075	848	1398	1030	1462	997
ENSMUSG00000037692	chr4	Ahdc1	1.33E+08	1.33E+08	8444	-0.02015	4.659968	0.926721	0.954574	0.047326	0	282	199	468	557	580	273	599	442	518	472
ENSMUSG00000047539	chr1	Fbxo28	1.82E+08	1.82E+08	5318	0.01364	4.416731	0.92667	0.954574	0.02201	0	250	242	524	326	394	316	485	374	499	297
ENSMUSG00000027998	chr3	Plrg1	83055522	83055654	2816	-0.01257	4.63615	0.926794	0.954575	0.026341	0	369	349	459	354	427	350	596	401	530	392
ENSMUSG00000005204	chr11	Senp3	69673115	69673636	3632	-0.01331	4.879315	0.927393	0.955118	0.022471	0	441	328	629	452	526	479	677	461	638	422
ENSMUSG00000024099	chr17	Ndufv2	66078795	66079587	1990	0.016471	8.397917	0.927551	0.955207	0.038432	0	4437	3783	5517	6800	6074	5166	8799	4683	8227	4722
ENSMUSG00000002768	chr17	Mea1	46681137	46681205	840	0.017868	4.569577	0.928138	0.955292	0.031359	0	398	286	361	394	396	379	498	397	548	354
ENSMUSG00000013833	chr10	Med16	79894708	79895410	4663	-0.01451	4.895021	0.928051	0.955292	0.025638	0	395	293	689	462	614	369	607	496	814	458
ENSMUSG00000025264	chrX	Tsr2	1.51E+08	1.51E+08	3805	0.014762	3.539543	0.927807	0.955292	0.023474	0	165	129	266	158	214	184	245	215	250	164
ENSMUSG00000025938	chr1	Slco5a1	12866549	12872328	13137	-0.02015	5.2129	0.928083	0.955292	0.051899	0	357	279	824	771	896	400	958	526	913	644
ENSMUSG00000032458	chr9	Copb2	98563721	98563823	6351	0.014352	6.634318	0.928028	0.955292	0.027594	0	1405	1297	2299	1306	1629	1414	2447	1601	2197	1552
ENSMUSG00000033545	chr8	Znrf1	1.12E+08	1.12E+08	7018	0.015733	6.167829	0.927873	0.955292	0.035708	0	914	551	1537	1405	1504	954	1663	1252	1817	1032
ENSMUSG00000037134	chr8	Prmt10	77549397	77549736	5679	0.014513	3.294626	0.92802	0.955292	0.023059	0	125	102	218	156	187	146	218	169	207	153
ENSMUSG00000009621	chr2	Vav2	27262104	27264211	6915	0.027663	2.276362	0.928935	0.956038	0.113411	0	37	24	68	139	119	72	95	99	102	67
ENSMUSG00000039481	chr17	Nrtn	56751325	56751830	1023	-0.02587	0.471461	0.929223	0.956195	0.062794	0	20	19	27	21	15	16	32	30	27	12
ENSMUSG00000057103	chr6	Cml1	85910154	85911020	1345	0.050361	0.405934	0.929376	0.956195	0.073814	0	20	10	26	14	27	13	39	11	34	19
ENSMUSG00000069520	chr10	Tmem19	1.15E+08	1.15E+08	3010	0.01214	4.218623	0.929334	0.956195	0.021439	0	235	206	407	296	355	304	362	316	397	306
ENSMUSG00000074890	chr2	Lcmt2	1.21E+08	1.21E+08	3350	0.023807	2.27908	0.929336	0.956195	0.037077	0	55	47	107	87	89	57	129	71	113	76
ENSMUSG00000023980	chr17	Taf8	47488050	47489896	2779	0.013896	3.973818	0.929645	0.956398	0.022487	0	227	168	365	253	246	239	356	273	320	245
ENSMUSG00000021234	chr12	Fam161b	84345309	84346409	4656	0.058713	0.247315	0.929941	0.956628	0.099067	0	11	15	10	30	16	21	19	17	27	16
ENSMUSG00000029176	chr5	Anapc4	52834015	52834392	5902	0.013906	5.41769	0.930247	0.956869	0.023364	0	599	558	925	597	717	659	978	707	996	608
ENSMUSG00000086474	chr11	9130204K15Rik	79781979	79782556	1462	0.098395	0.269659	0.930489	0.957044	0.283307	0	28	22	12	11	3	4	29	18	48	13
ENSMUSG00000024761	chr19	Gm16437	7668287	7668793	507	-0.02034	0.91174	0.930953	0.957372	0.099194	0	36	18	29	41	15	27	49	33	39	16
ENSMUSG00000079484	chr2	Phyhd1	30266203	30266625	2657	-0.03105	3.577322	0.930911	0.957372	0.132524	0	175	86	164	290	244	296	192	135	379	72
ENSMUSG00000032897	chr4	Nfyc	1.21E+08	1.21E+08	2942	-0.0124	4.984315	0.931169	0.95752	0.021058	0	443	327	745	507	567	439	736	516	759	462
ENSMUSG00000073771	chr4	Btbd19	1.17E+08	1.17E+08	3883	0.040792	0.526263	0.931322	0.957604	0.06158	0	24	12	18	25	25	18	27	33	27	18
ENSMUSG00000056899	chr12	Immp2l	41024090	41024145	1832	0.030725	2.604002	0.931464	0.957675	0.0551	0	79	76	79	126	101	77	166	82	153	88
ENSMUSG00000010392	chr11	Gosr1	76726602	76730233	4289	0.013075	4.414748	0.931601	0.957699	0.023085	0	270	242	501	292	425	284	510	418	430	320
ENSMUSG00000048174	chr1	Tmem81	1.33E+08	1.33E+08	2018	0.042284	1.348706	0.93164	0.957699	0.101512	0	48	36	51	22	32	54	26	45	61	35
ENSMUSG00000055435	chr8	Maf	1.16E+08	1.16E+08	8241	-0.01926	7.63493	0.931704	0.957699	0.060388	0	2966	3093	5528	1712	2754	2455	4308	2803	5176	3562
ENSMUSG00000001419	chr3	Mef2d	88142372	88142674	5985	0.014342	7.790953	0.931861	0.957786	0.0336	0	3034	1917	5679	3618	4072	3189	4584	3299	6341	3279
ENSMUSG00000009575	chr15	Cbx5	1.03E+08	1.03E+08	9006	-0.01357	5.692867	0.931999	0.957843	0.024477	0	734	521	1376	693	973	729	1080	914	1124	852
ENSMUSG00000040852	chr17	Plekhh2	84511895	84511964	6886	0.035528	0.649821	0.932061	0.957843	0.049476	0	18	17	28	24	29	22	25	36	26	24
ENSMUSG00000021235	chr12	Coq6	84361657	84361819	3142	-0.01864	4.399215	0.932208	0.957901	0.045447	0	232	167	365	502	461	304	493	366	456	303
ENSMUSG00000028161	chr3	Ppp3ca	1.37E+08	1.37E+08	5512	-0.01676	8.107125	0.932334	0.957901	0.046873	0	3764	4556	6681	3149	3736	3331	5555	5221	6154	4859
ENSMUSG00000053411	chr15	Cbx7	79915807	79918050	6487	-0.01289	4.923172	0.932276	0.957901	0.021316	0	436	309	712	468	558	413	623	518	713	498
ENSMUSG00000015224	chr4	Cyp2j9	96568429	96568902	3337	-0.03178	0.758818	0.932444	0.957911	0.040449	0	24	22	35	23	24	23	31	28	37	24
ENSMUSG00000034430	chr6	Zxdc	90369492	90370568	8564	0.013693	4.14663	0.932625	0.957911	0.027292	0	237	182	444	288	285	260	338	257	472	299
ENSMUSG00000038058	chr6	Nod1	54923942	54925009	4415	-0.02026	3.786066	0.932573	0.957911	0.036755	0	168	95	359	249	290	187	328	255	294	192
ENSMUSG00000093242	chr2	Gm24574	75659244	75659317	74	0.05569	1.528934	0.932633	0.957911	0.277486	0	74	55	22	26	17	17	41	28	105	77
ENSMUSG00000041079	chr16	Rwdd2b	87433407	87434626	2009	0.030878	1.48833	0.93288	0.958091	0.039403	0	44	29	57	44	40	33	54	46	72	46
ENSMUSG00000027282	chr2	Mtch2	90847155	90847385	8490	-0.01227	7.061424	0.933513	0.958667	0.026178	0	1815	1614	2557	2249	2478	1885	3046	2223	3213	1939
ENSMUSG00000030064	chr6	Frmd4b	97286867	97288480	11521	-0.02171	3.349595	0.933594	0.958675	0.034329	0	121	88	277	173	190	147	228	212	199	132
ENSMUSG00000027122	chr2	Arl14ep	1.07E+08	1.07E+08	5313	0.018966	2.555598	0.934462	0.95929	0.028646	0	75	69	123	88	108	88	121	115	118	87
ENSMUSG00000036622	chr4	Atp13a2	1.41E+08	1.41E+08	6000	-0.01406	4.857222	0.934441	0.95929	0.024542	0	397	295	686	434	571	419	532	598	624	441
ENSMUSG00000038510	chr10	Rpf2	40223246	40223920	1924	-0.0131	3.711974	0.934417	0.95929	0.038683	0	230	182	252	165	194	195	353	225	254	169
ENSMUSG00000098413	chr19	Mir6990	6914196	6914286	91	0.03963	0.559481	0.934482	0.95929	0.068782	0	17	8	23	34	27	25	33	21	28	19
ENSMUSG00000024687	chr19	Osbp	11965844	11966296	4578	0.01314	6.638238	0.9348	0.959542	0.030707	0	1217	921	2491	1603	2017	1212	2383	1514	2446	1736
ENSMUSG00000039233	chr13	Tbce	13997949	13998181	4540	-0.01175	4.320381	0.934954	0.959627	0.030648	0	323	281	416	237	321	276	506	321	440	291
ENSMUSG00000024382	chr18	Ercc3	32240300	32240421	2835	0.01398	3.686997	0.935148	0.959677	0.026349	0	146	157	261	223	237	199	263	245	249	207
ENSMUSG00000024790	chr19	Sac3d1	6116004	6116587	1374	0.019861	3.215886	0.935085	0.959677	0.033589	0	146	119	191	117	154	127	195	192	228	113
ENSMUSG00000043998	chr12	Mgat2	69184157	69186770	2614	-0.01677	3.075509	0.935384	0.959845	0.030638	0	112	85	184	131	172	91	186	164	170	149
ENSMUSG00000012405	chr14	Rpl15	18267823	18269316	2397	0.014514	7.140989	0.935732	0.960128	0.035762	0	2204	2019	2637	1883	2234	2293	3629	2266	2937	1936

ENSMUSG00000032462	chr9	Pik3cb	99036654	99039850	7193	-0.01968	3.242553	0.936637	0.960982	0.034215	0	110	95	218	164	187	110	201	209	171	157
ENSMUSG00000066233	chr9	Tmem42	1.23E+08	1.23E+08	1044	0.020487	3.180164	0.936774	0.961048	0.027401	0	135	112	187	119	160	113	223	172	197	130
ENSMUSG00000012429	chr13	Mplkip	17695413	17695820	2672	0.037016	1.781691	0.936944	0.961148	0.062635	0	55	53	61	48	38	46	95	42	78	53
ENSMUSG00000038416	chr8	Cdc16	13757676	13757854	3103	0.011972	4.843628	0.937186	0.961322	0.025344	0	418	273	626	458	551	407	730	427	573	502
ENSMUSG00000022312	chr15	Eif3h	51786558	51786825	1253	-0.01273	6.912846	0.937377	0.961444	0.032569	0	1750	1811	2336	1708	1857	1837	2786	1958	2606	1820
ENSMUSG00000020843	chr11	Timm22	76406952	76407143	3183	0.012286	5.199522	0.938734	0.962762	0.025235	0	559	372	686	636	676	588	857	581	812	541
ENSMUSG00000038286	chr13	Bphl	34037641	34037769	1209	0.013904	4.297537	0.938949	0.962907	0.023881	0	276	206	376	360	346	271	479	334	460	279
ENSMUSG00000029034	chr4	Cpsf3l	1.56E+08	1.56E+08	3067	0.012698	4.224518	0.939171	0.96306	0.022367	0	240	212	379	342	315	270	422	316	394	307
ENSMUSG00000038936	chr1	Sccpdh	1.8E+08	1.8E+08	7562	0.01324	5.795789	0.939276	0.963094	0.029972	0	801	796	1177	716	881	883	1157	837	1293	918
ENSMUSG00000042429	chr1	Adora1	1.34E+08	1.34E+08	5785	0.054139	1.486266	0.939446	0.963119	0.36572	0	75	51	44	9	17	29	16	126	36	37
ENSMUSG00000059058	chr1	Tma7-ps	1.72E+08	1.72E+08	195	-0.0168	1.244767	0.939384	0.963119	0.080043	0	30	39	65	25	23	40	52	33	59	24
ENSMUSG00000063200	chr13	Nol7	43398376	43398658	1811	0.013889	5.742927	0.939795	0.963253	0.031575	0	865	740	1026	740	797	830	1344	833	1156	788
ENSMUSG00000081228	chr5	Gm16089	1.38E+08	1.38E+08	336	-0.01769	1.522003	0.939676	0.963253	0.050719	0	39	33	45	58	45	37	75	40	50	50
ENSMUSG00000089824	chr2	Rbm12	1.56E+08	1.56E+08	6689	0.019707	2.969559	0.939723	0.963253	0.042619	0	78	111	175	104	153	119	231	111	151	109
ENSMUSG00000025204	chr19	Ndufb8	44548572	44550220	3146	0.013857	8.453462	0.940164	0.963483	0.040053	0	4556	3552	5346	7173	7249	5109	8439	5100	8840	5242
ENSMUSG00000057691	chr6	Zfp746	48062395	48064952	3651	0.015728	3.304804	0.940132	0.963483	0.025806	0	114	119	221	164	170	127	235	176	230	143
ENSMUSG00000021650	chr13	Ptcd2	99319649	99320393	1675	-0.01333	4.731074	0.940254	0.9635	0.031837	0	343	246	480	552	530	397	627	386	613	407
ENSMUSG00000074217	chr8	2210011C24Rik	84010222	84010492	1413	0.030575	1.549612	0.940442	0.963618	0.049964	0	53	37	60	33	38	44	55	57	65	39
ENSMUSG00000032440	chr9	Tgfbr2	1.16E+08	1.16E+08	4785	0.011831	5.595674	0.940771	0.963882	0.033488	0	503	415	1241	893	981	670	1110	952	910	782
ENSMUSG00000019774	chr10	Mtrf1l	5811887	5813406	3261	-0.01777	2.647274	0.940974	0.963941	0.032616	0	72	61	133	107	135	85	159	111	127	84
ENSMUSG00000045534	chr6	Kcna5	1.27E+08	1.27E+08	2834	-0.02955	2.156667	0.940943	0.963941	0.071044	0	45	36	72	74	136	56	114	93	71	61
ENSMUSG00000038762	chr17	Abcf1	35956819	35957589	4410	-0.01145	6.823204	0.941114	0.96401	0.028197	0	1449	1315	2202	1941	2238	1503	2141	1935	2920	1873
ENSMUSG00000068479	chr2	Mfap1a	1.21E+08	1.21E+08	4198	0.013023	3.482195	0.941384	0.964212	0.026826	0	126	125	229	186	230	164	281	177	217	181
ENSMUSG00000058756	chr11	Thra	98740638	98740687	4614	0.01062	6.10652	0.941568	0.964326	0.024847	0	848	704	1676	1154	1262	1023	1598	1140	1519	1069
ENSMUSG00000044330	chr3	Gm9790	85915783	85916070	288	0.027111	2.672422	0.942228	0.964927	0.05152	0	95	88	94	99	108	92	158	76	185	83
ENSMUSG00000034612	chr10	Chst11	82985498	82985982	5527	0.022795	1.838302	0.942412	0.965041	0.073282	0	39	30	108	40	74	32	77	89	89	39
ENSMUSG00000020160	chr11	Meis1	18879817	18885651	10532	-0.02057	2.271508	0.942553	0.965093	0.096068	0	101	68	116	36	53	61	139	80	118	46
ENSMUSG00000038593	chr5	Tctn1	1.22E+08	1.22E+08	4856	-0.04738	0.746176	0.942608	0.965093	0.074536	0	12	15	49	21	37	13	29	30	42	28
ENSMUSG00000028990	chr4	Lzic	1.49E+08	1.49E+08	1866	0.013211	3.085672	0.942898	0.965315	0.027928	0	107	93	171	126	181	136	183	143	207	107
ENSMUSG00000024998	chr19	Plce1	38481109	38481356	15998	-0.02562	2.719302	0.943519	0.965877	0.050937	0	52	57	187	119	138	108	124	120	139	92
ENSMUSG00000031865	chr6	Dctn1	83165920	83165994	6509	-0.01166	7.15847	0.943951	0.966095	0.031724	0	1727	1476	3111	2705	2678	1969	2645	2425	3918	2178
ENSMUSG00000034848	chr2	Ttc21b	66184327	66184843	9282	-0.0324	1.764021	0.943834	0.966095	0.040904	0	35	34	91	55	60	50	75	57	56	57
ENSMUSG00000073096	chr6	Lrrc61	48554796	48554982	2913	0.011853	4.691418	0.943887	0.966095	0.02634	0	323	294	662	373	453	329	593	380	693	414
ENSMUSG00000026470	chr1	Stx6	1.55E+08	1.55E+08	10637	-0.00975	3.55441	0.944458	0.966511	0.027592	0	180	153	236	153	209	160	240	224	279	165
ENSMUSG00000028464	chr4	Tpm2	43514711	43514861	2909	0.016246	12.69183	0.944504	0.966511	0.065213	0	55002	52010	123841	155092	161289	82096	144321	98052	159935	128456
ENSMUSG00000062761	chr5	Zfp512	31452436	31452577	3293	0.010247	4.128139	0.944676	0.966613	0.022646	0	220	195	400	271	326	277	400	248	373	296
ENSMUSG00000018921	chr11	Pelp1	70392883	70393022	3561	0.011477	4.617732	0.944941	0.966683	0.025987	0	331	267	564	373	450	292	450	448	661	415
ENSMUSG00000030188	chr6	Magohb	1.31E+08	1.31E+08	1720	0.038125	1.537729	0.945036	0.966683	0.062912	0	53	44	50	32	35	49	56	43	70	41
ENSMUSG00000072258	chr1	Taf1a	1.83E+08	1.83E+08	2409	0.015558	2.735109	0.945018	0.966683	0.033856	0	106	76	123	82	135	96	152	121	123	108
ENSMUSG00000081049	chrX	Rps24-ps3	79195047	79195448	402	0.034609	2.014772	0.944853	0.966683	0.06035	0	55	65	84	53	48	66	115	50	85	53
ENSMUSG00000102422	chr3	SCHIP1	67892232	67892321	2369	0.01334	6.79555	0.945221	0.966798	0.044659	0	1296	935	2031	2133	2699	1737	2596	1363	2901	1738
ENSMUSG00000034793	chr11	G6pc3	1.02E+08	1.02E+08	2226	0.010507	5.695855	0.945343	0.966847	0.024375	0	754	583	1110	817	889	777	945	899	1323	810
ENSMUSG00000040323	chr1	Gm15429	1.62E+08	1.62E+08	798	-0.04792	0.788102	0.945574	0.967009	0.079487	0	13	10	37	36	41	18	32	29	31	34
ENSMUSG00000020955	chr12	Ap4s1	51690966	51691314	1113	0.013363	5.846675	0.945795	0.967161	0.03565	0	938	784	1032	847	861	868	1518	818	1388	788
ENSMUSG00000028647	chr4	Mycbp	1.24E+08	1.24E+08	2934	-0.01065	3.654365	0.946029	0.967326	0.024502	0	194	148	272	184	208	201	279	189	279	191
ENSMUSG00000074406	chr7	Zfp628	4915217	4915405	3524	0.016098	2.961165	0.946203	0.967429	0.039333	0	100	66	181	145	136	107	144	140	226	100
ENSMUSG00000098022	chr7	Zfp82	30054489	30057764	6041	-0.01516	1.037394	0.94678	0.967945	0.053137	0	29	23	43	39	22	23	44	32	55	26
ENSMUSG00000015970	chr14	Chdh	30009023	30009233	6156	-0.05555	0.65082	0.947928	0.969044	0.514652	0	48	26	23	7	8	28	5	74	7	11
ENSMUSG00000025024	chr19	Smndc1	53379214	53380601	2125	-0.00878	4.382689	0.948043	0.969086	0.022887	0	286	260	456	321	350	269	444	337	514	346
ENSMUSG00000000320	chr11	Alox12	70241457	70242564	4085	0.047143	0.487755	0.948152	0.969123	0.159862	0	7	9	19	34	34	8	38	22	47	11
ENSMUSG00000049047	chrX	Armcx3	1.35E+08	1.35E+08	3540	0.014618	3.860438	0.948546	0.969451	0.027451	0	223	176	305	195	251	172	382	226	327	241
ENSMUSG00000025371	chr11	Chmp6	1.2E+08	1.2E+08	2432	0.011062	4.926405	0.948707	0.969541	0.022681	0	438	350	599	505	524	443	678	484	763	446
ENSMUSG00000027428	chr2	Rbbp9	1.45E+08	1.45E+08	2362	-0.01545	2.792258	0.949353	0.970007	0.037921	0	94	85	148	95	131	94	139	141	107	129
ENSMUSG00000029592	chr5	Usp30	1.14E+08	1.14E+08	3372	-0.01444	3.294391	0.949319	0.970007	0.027024	0	129	103	212	166	182	162	182	179	195	154
ENSMUSG00000081113	chr6	Gm7308	1.27E+08	1.27E+08	447	-0.02602	-0.21805	0.949382	0.970007	0.076231	0	15	12	16	5	12	10	21	14	12	11
ENSMUSG00000070803	chr4	Cited4	1.21E+08	1.21E+08	1249	-0.01763	3.995795	0.949967	0.970529	0.064815	0	267	147	351	205	334	335	182	201	454	241
ENSMUSG00000074215	chr8	Gm10643	84063561	84065137	1577	-0.01579	0.948657	0.950146	0.970637	0.074388	0	38	22	31	33	19	31	43	26	30	34
ENSMUSG00000021895	chr14	Arhgef3	27238039	27238153	3585	0.010372	3.618262	0.950503	0.970853	0.023734	0	144	129	277	196	249	176	306	199	274	176
ENSMUSG00000022270	chr15	Fam134b	25843264	25843612	3346	0.012292	7.022318	0.9505	0.970853	0.043845	0	1710	1437	2541	2480	2209	1446	3482	1522	3359	2440
ENSMUSG00000022610	chr15	Mapk12	89130585	89131218	1889	-0.00945	7.426444	0.950625	0.970902	0.028237	0	2497	2205	3632	2566	2863	2479	3941	2533	4029	2816
ENSMUSG00000002396	chr8	Ocel1	71371298	71371985	7133	0.012502	1.930174	0.951437	0.971508	0.046144	0	35	40	77	69	80	56	80	77	61	62
ENSMUSG00000006335	chr7	Tfpt	3620324	3620474	1197	0.018761	3.350742	0.951511	0.971508	0.039578	0	176	131	171	150	156	141	188	172	288	150
ENSMUSG00000021686	chr13	Ap3b1	94358960	94359231	4020	0.009702	4.401865	0.951304	0.971508	0.023972	0	254	240	526	334	363	283	415	395	532	320
ENSMUSG00000033306	chr16	Lpp	24393350	24393604	15994	0.011006	4.29616	0.951506	0.971508	0.042151	0	206	203	545	264	417	196	421	450	372	356
ENSMUSG00000016386	chr2	Mpped2	1.07E+08	1.07E+08	3425	-0.03053	0.752685	0.952073	0.971917	0.329403	0	12	8	16	53	37	6	74	11	58	8

ENSMUSG00000032324	chr9	Tspan3	56135885	56136735	1728	-0.00896	6.891366	0.952131	0.971917	0.025122	0	1539	1289	2594	1983	2280	1554	2672	2001	2572	2063
ENSMUSG00000058587	chr9	Tmod3	75497796	75500150	3578	0.009657	3.945218	0.951994	0.971917	0.029165	0	155	153	325	292	328	205	325	279	354	248
ENSMUSG00000038425	chr18	Poli	70508680	70509744	3863	0.027574	1.014702	0.952491	0.972209	0.075498	0	30	31	45	22	22	41	28	33	47	25
ENSMUSG00000021752	chr14	Kctd6	8214148	8214342	3253	-0.00987	2.966445	0.952653	0.9723	0.034079	0	120	108	142	91	152	114	171	131	177	113
ENSMUSG00000001441	chr11	Npepps	97205842	97206091	7206	0.008983	6.308007	0.953502	0.972793	0.02631	0	1029	796	1654	1391	1559	1165	1856	1287	1926	1122
ENSMUSG00000022827	chr16	Rabl3	37539885	37539960	6369	0.016663	2.647059	0.953541	0.972793	0.058524	0	84	50	98	126	137	70	147	76	153	127
ENSMUSG00000025736	chr17	Jmjd8	25828867	25829163	2758	-0.01252	3.614397	0.95327	0.972793	0.026188	0	143	124	287	218	229	163	260	249	257	180
ENSMUSG00000026439	chr1	Rbbp5	1.32E+08	1.32E+08	3930	0.009174	4.596443	0.953573	0.972793	0.020496	0	334	276	534	351	452	313	515	459	549	386
ENSMUSG00000030207	chr6	8430419L09Rik	1.35E+08	1.35E+08	5776	0.015019	2.495334	0.953576	0.972793	0.043396	0	57	53	105	123	109	78	115	103	129	85
ENSMUSG00000097101	chr13	1810034E14Rik	64248700	64249203	1805	0.045319	-0.02652	0.953304	0.972793	0.06506	0	10	12	10	15	21	17	16	14	19	14
ENSMUSG00000032757	chr6	Bet1	4076899	4078036	3656	0.013427	4.295166	0.953674	0.972818	0.031114	0	310	286	386	232	314	289	474	334	411	295
ENSMUSG00000042659	chr7	Arrdc4	68737045	68739533	3989	0.023055	2.992256	0.953775	0.972846	0.074849	0	168	113	153	66	104	142	193	131	178	86
ENSMUSG00000024858	chr19	Adrbk1	4286001	4287264	4476	0.008692	6.278365	0.953984	0.972933	0.025767	0	976	796	1687	1323	1537	1123	1619	1297	1977	1162
ENSMUSG00000039640	chr11	Mrpl12	1.2E+08	1.2E+08	1532	0.012039	6.940159	0.954007	0.972933	0.049278	0	1565	1158	1687	2822	2507	1744	3056	1825	3038	1810
ENSMUSG00000026276	chr1	Sept2	93478964	93479068	7979	-0.00833	6.310572	0.954335	0.973043	0.025645	0	1109	1042	1663	1146	1390	1175	1816	1289	1696	1271
ENSMUSG00000029767	chr6	Calu	29348069	29348208	4733	0.008539	7.152191	0.954283	0.973043	0.025527	0	1734	1614	3098	2401	2668	2057	3393	2333	2988	2321
ENSMUSG00000058076	chr1	Sdhc	1.71E+08	1.71E+08	3250	0.011214	8.017192	0.954248	0.973043	0.04495	0	3091	2204	4366	5854	5438	3414	6282	4008	6641	3921
ENSMUSG00000097277	chr7	2900076A07Rik	81523550	81523676	1993	0.016599	1.419413	0.954456	0.973092	0.042167	0	41	24	66	39	38	33	48	55	60	40
ENSMUSG00000000295	chr10	Hddc2	31313382	31313483	3509	-0.00821	3.472059	0.955244	0.973224	0.027419	0	169	144	225	140	202	169	259	169	240	169
ENSMUSG00000017300	chr2	Tnnc2	1.65E+08	1.65E+08	800	-0.01136	13.61434	0.954861	0.973224	0.04825	0	222858	190051	232062	139553	189861	206015	258968	201296	319786	165069
ENSMUSG00000020899	chr11	Pfas	68985697	68988273	7933	-0.01182	3.618872	0.955299	0.973224	0.025079	0	149	139	333	173	215	186	275	201	277	177
ENSMUSG00000022761	chr16	Lztr1	17508688	17509218	5445	-0.00916	5.072039	0.954697	0.973224	0.023782	0	459	371	680	574	629	559	755	538	639	542
ENSMUSG00000022860	chr16	Chodl	78930948	78931447	3820	-0.01747	3.196532	0.955466	0.973224	0.042733	0	93	90	216	170	184	132	220	151	133	177
ENSMUSG00000028886	chr4	Eya3	1.33E+08	1.33E+08	5647	0.008002	4.442536	0.95537	0.973224	0.026312	0	224	216	544	387	420	311	487	383	505	316
ENSMUSG00000030035	chr6	Wbp1	83119044	83119720	2079	-0.00958	4.428011	0.954881	0.973224	0.029942	0	317	208	371	398	433	312	437	324	566	332
ENSMUSG00000034247	chr11	Plekhm1	1.03E+08	1.03E+08	5968	-0.0106	4.729535	0.955164	0.973224	0.0262	0	363	259	698	435	432	366	499	513	593	431
ENSMUSG00000034413	chr17	Neurl1b	26414829	26414995	6331	-0.0168	1.462576	0.955192	0.973224	0.040902	0	27	36	65	43	45	31	53	47	61	49
ENSMUSG00000053740	chr18	Gm6457	14570101	14570915	815	-0.01985	0.027412	0.955098	0.973224	0.070183	0	8	14	19	19	13	13	22	14	27	8
ENSMUSG00000061950	chr17	Ppp4r1	65782573	65782683	5449	-0.01202	4.289014	0.955429	0.973224	0.025646	0	273	166	469	330	375	276	378	364	421	325
ENSMUSG00000079658	chr1	Tceb1	16641725	16643478	3026	0.011325	6.47698	0.955186	0.973224	0.040358	0	1311	1462	1733	1114	1249	1315	2027	1523	2139	1254
ENSMUSG00000014470	chr8	Rnf166	1.22E+08	1.22E+08	1985	-0.00887	5.123751	0.955863	0.973381	0.026559	0	485	333	666	671	665	496	741	579	862	521
ENSMUSG00000020349	chr11	Ppp2ca	52098681	52099150	7490	-0.00851	7.106781	0.955914	0.973381	0.028863	0	1795	1694	2685	2426	2434	2093	3497	2095	3085	1949
ENSMUSG00000031295	chrX	Phka2	1.61E+08	1.61E+08	6068	0.01201	2.936815	0.955865	0.973381	0.042189	0	112	99	168	84	142	103	144	172	131	133
ENSMUSG00000038172	chr4	Ttc39b	83220300	83227224	10199	0.007923	2.377448	0.955878	0.973381	0.059592	0	54	32	118	81	144	69	114	81	104	97
ENSMUSG00000014959	chr2	Gorasp2	70661576	70661760	4145	0.008353	6.655054	0.956062	0.973457	0.025405	0	1489	1105	2435	1484	1653	1473	2225	1694	2434	1492
ENSMUSG00000041870	chr5	Ankrd13a	1.15E+08	1.15E+08	4098	0.008346	4.290876	0.956159	0.97348	0.025429	0	258	197	449	314	372	320	387	380	464	239
ENSMUSG00000029366	chr5	Dck	88764996	88765346	3078	0.009407	1.518307	0.95653	0.973784	0.040625	0	38	27	70	34	57	39	54	54	51	52
ENSMUSG00000025555	chr14	Farp1	1.21E+08	1.21E+08	5524	0.00689	2.47216	0.956875	0.974061	0.054248	0	57	35	162	96	112	85	118	76	139	84
ENSMUSG00000073198	chr12	Gm10480	18216555	18217757	1203	0.022288	0.132419	0.956998	0.97411	0.066413	0	12	9	30	10	20	10	18	14	28	21
ENSMUSG00000032103	chr9	Pus3	35558595	35558733	2972	-0.00716	3.312445	0.957498	0.974545	0.039831	0	163	141	165	133	167	155	250	130	226	145
ENSMUSG00000098794	chr2	Gm28038	30281043	30281136	378	0.024033	1.821721	0.957791	0.974769	0.151826	0	52	23	46	83	68	85	45	38	124	25
ENSMUSG00000025422	chr10	Agap2	1.27E+08	1.27E+08	5633	0.025036	1.141397	0.957963	0.974794	0.087843	0	18	19	27	40	65	34	48	31	59	24
ENSMUSG00000055319	chr7	Sec23ip	1.29E+08	1.29E+08	4578	-0.00839	4.680796	0.957911	0.974794	0.022194	0	383	287	597	360	452	358	520	450	567	432
ENSMUSG00000004768	chr1	Rab23	33719887	33720173	8285	-0.01444	2.439565	0.958954	0.975728	0.030933	0	69	57	106	83	119	83	116	82	114	88
ENSMUSG00000006586	chr4	Runx1t1	13743436	13743729	7959	0.027358	1.27982	0.959323	0.97577	0.073737	0	39	35	59	18	33	47	39	37	53	35
ENSMUSG00000021555	chr13	Naa35	59585259	59585292	5780	-0.00769	4.589294	0.959511	0.97577	0.021808	0	367	260	529	380	404	385	549	383	521	353
ENSMUSG00000030019	chr6	Fbxl14	1.19E+08	1.19E+08	2963	0.009423	3.785769	0.959183	0.97577	0.029088	0	215	149	319	168	259	199	255	288	322	192
ENSMUSG00000036091	chr9	Hyal3	1.08E+08	1.08E+08	1948	0.029254	1.598655	0.959387	0.97577	0.04304	0	41	40	47	49	51	50	57	50	75	38
ENSMUSG00000039990	chr7	Edrf1	1.34E+08	1.34E+08	5992	0.010362	3.365619	0.959268	0.97577	0.026472	0	128	124	226	156	189	156	265	185	191	143
ENSMUSG00000052684	chr4	Jun	95049034	95052222	3189	-0.00822	6.23638	0.959459	0.97577	0.032507	0	1194	916	1440	1223	1202	959	1751	1111	1640	1438
ENSMUSG00000091514	chr8	Gm17484	25754509	25754719	2293	-0.05688	0.097709	0.959387	0.97577	0.084526	0	12	7	15	25	20	20	19	18	12	15
ENSMUSG00000026388	chr1	3110009E18Rik	1.2E+08	1.2E+08	2428	0.059824	0.253035	0.960384	0.976583	0.066954	0	19	19	20	10	15	11	27	20	26	18
ENSMUSG00000026603	chr1	Smyd2	1.9E+08	1.9E+08	2717	0.012837	7.592125	0.960471	0.976597	0.074855	0	3428	3417	3555	2016	2117	2216	5630	2696	4944	2876
ENSMUSG00000001552	chr11	Jup	1E+08	1E+08	6436	-0.01032	6.057393	0.960627	0.976605	0.04099	0	785	470	1709	1285	1379	900	1341	1087	1529	1203
ENSMUSG00000049354	chr11	Dcaf7	1.06E+08	1.06E+08	6133	0.006886	5.808517	0.960555	0.976605	0.023914	0	681	558	1254	970	1121	781	1162	991	1259	940
ENSMUSG00000060126	chr14	Tpt1	75845093	75845456	2380	-0.00861	10.40702	0.960916	0.976695	0.037155	0	22373	18992	24795	18493	21670	21355	35215	20819	27536	19781
ENSMUSG00000061559	chr9	Wdr61	54714735	54717125	4669	-0.00761	3.96789	0.960935	0.976695	0.027468	0	192	217	351	201	295	227	409	257	300	234
ENSMUSG00000074211	chr7	Sdhaf1	30321406	30323895	2490	0.01033	4.089992	0.96091	0.976695	0.028572	0	243	179	314	333	278	267	366	255	425	251
ENSMUSG00000050730	chr9	Arhgap42	8994329	8997685	7113	0.008259	2.320459	0.961017	0.976702	0.043226	0	54	44	112	89	103	60	116	103	83	85
ENSMUSG00000084093	chr1	Gm16418	1.66E+08	1.66E+08	171	-0.00686	1.688128	0.961181	0.976794	0.042078	0	44	38	58	55	54	51	88	42	65	41
ENSMUSG00000020448	chr11	Rnf185	3415982	3418087	2906	0.007566	5.029105	0.961659	0.977176	0.021304	0	483	367	739	486	550	499	731	554	739	476
ENSMUSG00000030056	chr6	Isy1	87818447	87819203	1620	-0.00742	4.077397	0.961704	0.977176	0.020986	0	212	197	349	269	334	252	365	308	378	234
ENSMUSG00000014245	chr11	Pigl	62458460	62458694	2268	-0.01935	1.753638	0.961879	0.977204	0.039405	0	55	32	74	49	56	46	66	72	63	48
ENSMUSG00000028563	chr4	Tm2d1	98355370	98355680	1124	-0.00622	4.63596	0.961807	0.977204	0.027115	0	401	313	530	353	377	331	635	386	542	394
ENSMUSG00000001403	chr2	Ube2c	1.65E+08	1.65E+08	2600	0.034637	6.180379	0.962131	0.977385	0.61661	0	143	109	3540	2206	656	137	188	1985	3040	1507

ENSMUSG00000031901	chr8	Dus2	1.06E+08	1.06E+08	3367	0.00844	3.500545	0.962293	0.977439	0.032788	0	188	89	215	197	217	173	233	201	241	177
ENSMUSG00000041476	chrX	Smpx	1.58E+08	1.58E+08	2275	0.009198	8.370715	0.962332	0.977439	0.043667	0	5571	4701	6637	3955	4981	5185	6864	4222	8218	5908
ENSMUSG00000014873	chr2	Surf2	26916367	26916503	3408	-0.01103	3.230767	0.962662	0.9777	0.023316	0	129	101	211	147	169	145	215	152	195	140
ENSMUSG00000082087	chr11	Gm12138	40672906	40673856	951	-0.01921	0.436579	0.962782	0.977747	0.056192	0	26	16	24	16	17	14	29	25	29	17
ENSMUSG00000060989	chr4	Gm11847	12232833	12233951	1119	-0.09284	-0.26113	0.962864	0.977755	0.233176	0	3	3	21	16	21	16	17	20	2	6
ENSMUSG00000044636	chr15	Csrnp2	1E+08	1E+08	4126	-0.01723	1.927568	0.963289	0.978091	0.032514	0	52	40	88	54	69	43	78	68	86	63
ENSMUSG00000054455	chr2	Vapb	1.74E+08	1.74E+08	7131	0.006959	7.58899	0.963342	0.978091	0.025801	0	2489	2237	4014	3289	3446	2757	4118	3163	4707	3031
ENSMUSG00000054716	chr7	Zfp771	1.27E+08	1.27E+08	1371	0.014714	3.362756	0.963524	0.978201	0.034521	0	165	138	198	144	153	140	186	208	247	155
ENSMUSG00000020477	chr11	Mrps24	5703983	5704732	1466	0.008226	5.57114	0.963847	0.978454	0.025179	0	697	594	818	782	844	678	1088	811	1084	723
ENSMUSG00000019732	chr8	Calr3	72424176	72424755	1962	-0.00551	1.992871	0.964038	0.978573	0.030756	0	52	44	80	66	71	54	98	63	86	56
ENSMUSG00000057719	chr18	Sh3rf2	42053667	42054195	5307	0.009595	5.22648	0.964144	0.978606	0.054064	0	366	388	1191	621	573	489	1001	390	875	724
ENSMUSG00000025870	chr13	Arl10	54575015	54575277	1729	-0.01689	0.459386	0.96422	0.978608	0.063014	0	19	14	19	17	33	13	26	18	40	20
ENSMUSG00000001847	chr5	Rac1	1.44E+08	1.44E+08	2652	-0.00666	7.615331	0.964429	0.978746	0.026233	0	2698	2274	4793	2954	3264	2762	4277	3191	4877	2976
ENSMUSG00000000743	chr8	Chmp1a	1.23E+08	1.23E+08	3260	0.007826	6.195633	0.964956	0.979205	0.028296	0	1021	979	1299	1206	1242	1057	1624	1251	1721	1109
ENSMUSG00000041459	chr4	Tardbp	1.49E+08	1.49E+08	7796	0.007276	6.595958	0.965482	0.979664	0.028539	0	1468	1278	2144	1211	1599	1437	2272	1644	2080	1471
ENSMUSG00000020361	chr11	Hspa4	53259814	53261815	5528	-0.00619	6.821461	0.965666	0.979776	0.023901	0	1476	1305	2385	1800	2202	1578	2626	1803	2574	1819
ENSMUSG00000024400	chr18	Wdr33	31804057	31804254	6413	0.005702	4.84973	0.966097	0.980138	0.022568	0	350	287	704	481	544	406	603	490	704	449
ENSMUSG00000006205	chr7	Htra1	1.31E+08	1.31E+08	2879	-0.01233	5.363431	0.967071	0.980857	0.109027	0	731	838	839	259	443	661	710	988	729	580
ENSMUSG00000038412	chr9	Higd1a	1.22E+08	1.22E+08	1873	-0.00671	6.088702	0.967102	0.980857	0.034912	0	963	890	1053	1220	1203	1097	1553	978	1584	1022
ENSMUSG00000038742	chr9	Angptl6	20873809	20874072	1581	0.011596	2.577632	0.967036	0.980857	0.04355	0	81	77	115	80	114	87	149	105	82	109
ENSMUSG00000051413	chr2	Plagl2	1.53E+08	1.53E+08	5735	-0.01728	2.485877	0.967028	0.980857	0.050713	0	51	51	153	76	136	58	133	105	117	92
ENSMUSG00000029009	chr4	Mthfr	1.48E+08	1.48E+08	7315	0.010878	2.819338	0.967976	0.981669	0.03193	0	105	79	153	109	111	102	138	136	129	125
ENSMUSG00000002250	chr17	Ppard	28232754	28232864	4631	0.005453	4.717236	0.968282	0.981904	0.026206	0	331	240	548	489	534	387	543	507	543	412
ENSMUSG00000027433	chr2	Xrn2	1.47E+08	1.47E+08	3981	-0.00593	3.924494	0.968495	0.98197	0.025426	0	189	186	361	247	241	176	352	259	343	261
ENSMUSG00000032298	chr9	Neil1	57142800	57143326	1871	0.010852	2.942333	0.968476	0.98197	0.02731	0	108	89	142	129	135	119	169	126	159	121
ENSMUSG00000033788	chr6	Dysf	84008590	84009002	8333	-0.00705	6.293946	0.969134	0.982543	0.033352	0	1080	757	2091	1082	1528	1185	1494	1192	2253	1117
ENSMUSG00000067370	chr17	B3galt4	33949909	33951477	1569	0.030029	0.7719	0.969297	0.982633	0.05528	0	16	26	37	21	27	27	25	26	39	29
ENSMUSG00000025203	chr19	Scd2	44293676	44294411	5453	0.00583	5.098141	0.969646	0.982844	0.04414	0	438	244	929	496	790	519	524	665	748	618
ENSMUSG00000038156	chr7	Spon1	1.14E+08	1.14E+08	8177	-0.0194	3.376198	0.969653	0.982844	0.178716	0	105	99	372	112	207	160	129	425	79	95
ENSMUSG00000042198	chr4	Chchd7	3938888	3938962	4060	0.010674	3.949775	0.970335	0.983459	0.029856	0	204	186	267	267	294	183	430	239	352	237
ENSMUSG00000000266	chrX	Mid2	1.41E+08	1.41E+08	8114	-0.01323	2.826515	0.970597	0.983629	0.039152	0	66	82	172	109	150	89	171	108	135	134
ENSMUSG00000024800	chr19	Rpp30	36083716	36083818	1155	-0.00423	3.269833	0.97065	0.983629	0.039243	0	138	145	211	124	138	151	251	162	202	115
ENSMUSG00000021367	chr13	Edn1	42301270	42301958	2344	0.017301	0.592476	0.971153	0.983872	0.094254	0	21	15	36	22	19	36	23	33	22	11
ENSMUSG00000028879	chr4	Stx12	1.33E+08	1.33E+08	3188	-0.00482	5.495226	0.971187	0.983872	0.023352	0	666	578	968	663	722	677	960	782	1006	689
ENSMUSG00000043822	chr10	Adamtsl5	80339110	80339143	4722	0.012506	5.061256	0.971109	0.983872	0.140147	0	228	142	452	996	958	366	786	467	873	624
ENSMUSG00000049624	chr9	Slc17a5	78536488	78538299	3356	-0.00954	2.329446	0.971084	0.983872	0.03216	0	70	54	102	71	103	56	113	88	110	85
ENSMUSG00000023267	chr4	Gabrr2	33062999	33063366	2105	0.021226	0.605074	0.971423	0.984036	0.096825	0	25	16	35	7	31	24	29	19	46	14
ENSMUSG00000059586	chr15	Nsmce2	59374198	59374355	3281	0.004666	3.709283	0.971739	0.984281	0.025507	0	186	120	277	217	257	203	254	208	296	222
ENSMUSG00000086922	chr6	Gm13835	31141979	31142663	685	-0.00412	3.924363	0.971855	0.984324	0.043498	0	213	251	325	213	175	204	392	245	346	214
ENSMUSG00000054720	chr5	Lrrc8c	1.06E+08	1.06E+08	7654	0.00277	3.359974	0.97197	0.984349	0.038144	0	104	93	269	150	238	170	209	204	192	146
ENSMUSG00000071656	chr19	Lrrn4cl	8850785	8851112	2583	0.004643	3.812999	0.972029	0.984349	0.037742	0	152	143	398	184	293	196	284	332	266	194
ENSMUSG00000034127	chr10	Tspan8	1.16E+08	1.16E+08	1522	0.008211	6.580865	0.972515	0.984724	0.057531	0	1549	1643	2153	886	1171	1427	2053	1678	2158	1475
ENSMUSG00000068732	chr3	Tmem167b	1.09E+08	1.09E+08	2948	0.005056	4.579435	0.972568	0.984724	0.019911	0	318	276	525	369	436	367	486	432	509	377
ENSMUSG00000086429	chr6	Gt(ROSA)26Sor	1.13E+08	1.13E+08	1695	0.021928	2.177421	0.972622	0.984724	0.12236	0	58	75	82	52	76	30	41	106	128	101
ENSMUSG00000039852	chr4	Rere	1.5E+08	1.5E+08	8525	0.005526	6.864132	0.97281	0.984839	0.033135	0	1440	1112	3368	1573	2292	1465	2340	2036	3014	1925
ENSMUSG00000048787	chr7	Dcun1d3	1.2E+08	1.2E+08	6203	-0.0079	3.94862	0.973037	0.984994	0.024845	0	231	151	380	234	263	216	284	294	355	247
ENSMUSG00000040749	chrX	Siah1b	1.64E+08	1.64E+08	2119	0.014775	1.144542	0.974094	0.985989	0.047231	0	24	22	54	37	34	24	59	36	36	39
ENSMUSG00000039321	chr11	Uts2r	1.21E+08	1.21E+08	1703	-0.01274	0.873884	0.974631	0.986457	0.083976	0	30	15	40	19	37	20	64	20	42	17
ENSMUSG00000045252	chr7	Zfp574	25077205	25077386	4236	-0.01054	3.303433	0.974753	0.986505	0.026972	0	113	99	243	158	197	129	195	179	225	164
ENSMUSG00000028266	chr3	Lmo4	1.44E+08	1.44E+08	3295	0.005183	4.435016	0.975027	0.986708	0.020891	0	287	232	457	365	401	293	472	407	464	342
ENSMUSG00000002963	chr7	Pnkp	44857139	44857302	3133	-0.00375	4.64181	0.975265	0.986872	0.023013	0	348	320	491	379	447	370	538	380	590	402
ENSMUSG00000084514	chr18	Mir1893	6490564	6490646	83	0.002562	0.90372	0.975455	0.98699	0.08488	0	31	23	21	36	25	24	52	36	38	15
ENSMUSG00000032621	chr13	Srek1	1.04E+08	1.04E+08	3985	0.006001	4.115856	0.975909	0.987373	0.028449	0	227	231	419	196	322	233	374	322	343	302
ENSMUSG00000022704	chr16	Qtrtd1	43861407	43863301	4629	0.009304	2.329921	0.976196	0.987549	0.052853	0	69	60	121	48	103	94	112	96	75	67
ENSMUSG00000022995	chr1	Enah	1.82E+08	1.82E+08	21452	0.005954	5.113838	0.976231	0.987549	0.053533	0	327	239	696	787	831	475	726	546	900	552
ENSMUSG00000101335	chr9	Gm28229	88441500	88443652	2153	0.028425	1.22592	0.97656	0.987806	0.055102	0	34	32	34	29	45	30	58	31	65	27
ENSMUSG00000082908	chr2	Gm13736	87526145	87526397	253	-0.00628	1.342611	0.97674	0.987913	0.045418	0	41	28	48	32	46	43	63	30	55	32
ENSMUSG00000055401	chr4	Fbxo6	1.48E+08	1.48E+08	2207	-0.00467	4.941567	0.977003	0.988104	0.026413	0	424	309	561	585	590	449	682	464	734	488
ENSMUSG00000034453	chr10	Polr3b	84622437	84622538	4829	-0.00706	4.061272	0.977104	0.988131	0.021211	0	229	161	387	271	315	244	356	287	356	270
ENSMUSG00000022421	chr15	Nptxr	79786352	79789916	5169	0.000302	1.037569	0.977523	0.988479	0.087333	0	22	14	46	25	56	28	37	33	25	49
ENSMUSG00000037720	chr5	Tmem33	67260565	67260806	7098	0.005021	4.348269	0.977696	0.988579	0.026556	0	277	238	492	278	363	249	418	447	411	330
ENSMUSG00000026198	chr1	Abcb6	75171717	75171988	5315	0.003935	4.650155	0.978068	0.988879	0.03087	0	300	209	544	506	500	362	504	423	614	397
ENSMUSG00000011171	chr12	Vipr2	1.16E+08	1.16E+08	4463	-0.03673	0.927414	0.978246	0.988984	0.113496	0	11	19	61	22	42	44	24	36	29	22
ENSMUSG00000041361	chr9	Myzap	71504347	71505229	5635	-0.00645	1.505219	0.978509	0.989174	0.043235	0	28	37	54	47	54	39	71	55	49	36
ENSMUSG00000046387	chr18	Pcdhb17	37484795	37489454	4660	0.008051	1.309959	0.979029	0.989625	0.065152	0	24	31	64	24	52	28	46	54	38	48

ENSMUSG00000032366	chr9	Tpm1	67022590	67023441	6485	-0.00688	14.55125	0.979108	0.989629	0.082573	0	462617	419436	473371	190588	285924	415424	507959	399944	613251	274235
ENSMUSG00000061518	chr1	Cox5b	36691484	36691689	1552	-0.00505	8.280925	0.979294	0.989741	0.045221	0	4041	2938	4915	7025	6031	4535	7238	4453	8383	4354
ENSMUSG00000027787	chr3	Nmd3	69721985	69722122	10155	-0.00232	4.28024	0.979616	0.989991	0.031691	0	256	296	409	281	284	284	507	282	426	289
ENSMUSG00000005846	chr16	Rsl1d1	11192970	11193737	2258	-0.00302	5.732356	0.980367	0.990448	0.02489	0	779	670	1106	816	864	728	1378	898	1115	789
ENSMUSG00000042210	chr9	Abhd14a	1.06E+08	1.06E+08	2087	-0.00534	3.52308	0.980308	0.990448	0.029204	0	164	117	221	211	205	156	212	239	261	171
ENSMUSG00000043391	chr16	2510009E07Rik	21649045	21653758	5164	0.00424	5.121148	0.980311	0.990448	0.030757	0	406	335	925	537	692	418	807	562	993	489
ENSMUSG00000047789	chr13	Slc38a9	1.13E+08	1.13E+08	8904	-0.00848	3.031154	0.980215	0.990448	0.027714	0	104	83	212	124	144	115	200	146	160	119
ENSMUSG00000042105	chr7	Inpp5f	1.29E+08	1.29E+08	8323	0.007383	1.631996	0.980602	0.99061	0.047037	0	37	25	82	53	50	31	75	63	61	47
ENSMUSG00000022546	chr15	Gpt	76696764	76697019	1749	0.006417	4.590116	0.980739	0.990673	0.06962	0	244	174	340	661	523	306	506	468	607	341
ENSMUSG00000038187	chr7	Btbd10	1.13E+08	1.13E+08	5801	0.008256	3.098164	0.98093	0.990791	0.027324	0	114	95	198	124	156	117	221	164	170	112
ENSMUSG00000024535	chr18	Snx24	53245662	53245852	1880	0.003994	3.656315	0.981301	0.99109	0.027722	0	183	114	275	189	263	172	242	204	336	201
ENSMUSG00000031144	chrX	Syp	7638471	7638728	5211	-0.00036	1.64333	0.98139	0.991104	0.050865	0	50	48	54	43	40	41	64	50	81	43
ENSMUSG00000001995	chr8	Sipa1l2	1.25E+08	1.25E+08	6365	0.006195	2.897677	0.981846	0.991346	0.10544	0	45	44	131	190	205	76	195	129	163	122
ENSMUSG00000006676	chr9	Usp19	1.08E+08	1.08E+08	7048	-0.00389	7.467985	0.981889	0.991346	0.029746	0	2411	1613	4413	2834	3421	2377	3551	2887	4333	3085
ENSMUSG00000028790	chr4	Khdrbs1	1.3E+08	1.3E+08	6419	-0.00299	5.101367	0.981929	0.991346	0.024933	0	445	462	752	500	587	433	793	605	706	601
ENSMUSG00000038324	chr2	Trpc4ap	1.56E+08	1.56E+08	8753	-0.0035	7.138905	0.981913	0.991346	0.026209	0	1984	1463	3174	2322	2538	1874	2837	2448	3535	2274
ENSMUSG00000019564	chr10	Arid3a	79927043	79927256	5562	-0.00243	1.758384	0.982254	0.9916	0.048056	0	32	37	87	48	67	53	61	73	55	52
ENSMUSG00000035967	chrX	Ddx26b	56454857	56455316	7173	-0.01039	3.02845	0.982716	0.991991	0.0387	0	134	72	197	110	150	147	201	129	142	111
ENSMUSG00000031246	chrX	Sh3bgrl	1.09E+08	1.09E+08	3298	0.007108	4.094109	0.983722	0.99293	0.055061	0	227	262	340	219	287	149	282	409	374	337
ENSMUSG00000026564	chr1	Dusp27	1.66E+08	1.66E+08	4049	0.00299	6.07509	0.984249	0.99316	0.029126	0	849	624	1536	1128	1421	856	1341	1197	1709	1114
ENSMUSG00000036435	chr5	Exoc1	76529311	76529462	9158	-0.00675	3.770156	0.984096	0.99316	0.025196	0	189	130	303	206	285	218	327	234	252	202
ENSMUSG00000060152	chr5	Pop5	1.15E+08	1.15E+08	2296	-0.00153	4.571599	0.984139	0.99316	0.026556	0	369	316	476	330	385	341	584	446	498	315
ENSMUSG00000102824	chr1	RP23-411B11.2	1.89E+08	1.89E+08	381	0.000693	3.252118	0.984245	0.99316	0.034169	0	139	139	169	146	144	130	239	146	202	152
ENSMUSG00000023047	chr15	Amhr2	1.02E+08	1.02E+08	2002	-0.00384	3.099866	0.984515	0.993353	0.108897	0	163	102	127	156	105	162	164	131	292	47
ENSMUSG00000031545	chr8	Agpat6	23172946	23174660	3944	0.0032	5.861664	0.984673	0.993437	0.028223	0	761	595	1081	1115	1124	864	1101	1082	1346	909
ENSMUSG00000004788	chr12	Eif2b2	85219481	85219724	1885	0.003957	5.350254	0.984983	0.993667	0.024081	0	628	511	880	573	653	610	869	662	943	651
ENSMUSG00000028540	chr4	Dph2	1.18E+08	1.18E+08	3030	-0.00923	2.037783	0.985051	0.993667	0.047715	0	65	32	85	60	86	54	109	79	62	61
ENSMUSG00000046962	chr16	Zbtb21	97947435	97950869	6010	0.005578	2.266861	0.985251	0.993793	0.033738	0	55	52	95	69	112	63	108	77	108	78
ENSMUSG00000045503	chr2	Sys1	1.64E+08	1.64E+08	4958	0.005062	4.753381	0.985551	0.99402	0.025738	0	408	342	495	447	423	399	597	440	583	443
ENSMUSG00000021770	chr14	Samd8	21750531	21750780	7638	0.002801	6.155291	0.985968	0.994365	0.030884	0	1080	675	1940	902	1312	903	1680	1193	1638	1179
ENSMUSG00000034480	chrX	Diap2	1.3E+08	1.3E+08	11553	-0.01319	2.25904	0.986142	0.99439	0.040583	0	54	43	117	68	109	56	107	101	93	71
ENSMUSG00000039349	chr1	C130074G19Rik	1.85E+08	1.85E+08	3035	0.005466	4.34565	0.986101	0.99439	0.037158	0	305	287	406	257	341	305	352	474	453	260
ENSMUSG00000040532	chr5	Abhd11	1.35E+08	1.35E+08	2172	-0.00211	5.266881	0.986788	0.994965	0.026213	0	559	416	675	697	721	540	939	587	885	600
ENSMUSG00000051335	chr13	Gfod1	43195519	43201244	6654	-0.01186	2.107305	0.987215	0.99532	0.063722	0	49	24	82	90	105	51	98	70	89	76
ENSMUSG00000053536	chr19	Cstf2t	31082841	31086590	3750	-0.00264	4.564732	0.987294	0.995324	0.021792	0	279	271	512	390	467	308	550	379	553	387
ENSMUSG00000039244	chr5	E130309D02Rik	1.43E+08	1.43E+08	4639	0.001368	3.453429	0.987802	0.995761	0.026479	0	139	106	246	192	204	166	199	197	251	175
ENSMUSG00000049950	chr2	Rpp38	3328949	3329873	1042	0.014262	2.379255	0.988169	0.996055	0.049452	0	81	81	97	58	80	75	144	78	104	73
ENSMUSG00000029038	chr4	Ssu72	1.56E+08	1.56E+08	2689	-0.00106	4.969509	0.988575	0.996316	0.028697	0	491	436	614	444	470	489	758	504	664	454
ENSMUSG00000033909	chr11	Usp36	1.18E+08	1.18E+08	7689	-0.00605	4.301745	0.988578	0.996316	0.026383	0	263	162	486	329	394	280	402	361	410	331
ENSMUSG00000022377	chr15	Asap1	64086857	64089521	7482	-0.00887	3.632557	0.988763	0.996426	0.034969	0	139	106	312	193	284	177	228	202	264	239
ENSMUSG00000034353	chr1	Ramp1	91179822	91180140	3022	-0.00451	5.650374	0.989841	0.997437	0.10132	0	416	272	833	1393	1278	852	1106	546	1378	748
ENSMUSG00000031652	chr8	N4bp1	86841139	86845041	6469	-0.00348	4.982173	0.990544	0.99807	0.025188	0	414	269	775	552	607	440	707	561	736	462
ENSMUSG00000040738	chr4	Ints8	11199158	11199451	7472	0.002863	3.690802	0.990787	0.998238	0.030078	0	199	140	346	166	196	189	313	239	252	184
ENSMUSG00000027519	chr2	Rab22a	1.74E+08	1.74E+08	7206	0.001714	6.100661	0.990903	0.998279	0.024327	0	901	707	1547	1168	1270	1032	1462	1141	1628	1039
ENSMUSG00000018481	chr11	Appbp2	85187262	85191899	6463	-0.00512	3.896326	0.991441	0.998745	0.025193	0	200	137	377	235	276	195	359	272	285	244
ENSMUSG00000049760	chr17	2410015M20Rik	56607452	56607841	755	-0.00118	5.238357	0.991556	0.998785	0.03074	0	493	446	616	739	690	585	899	575	891	529
ENSMUSG00000028060	chr3	2810403A07Rik	88685794	88685887	2999	-0.002	4.466458	0.991698	0.998853	0.022925	0	320	250	525	310	385	298	531	432	439	323
ENSMUSG00000041577	chr1	Prelp	1.34E+08	1.34E+08	3615	-0.00324	5.920633	0.992044	0.999125	0.043682	0	591	556	1559	928	1485	862	1231	1261	984	1091
ENSMUSG00000023960	chr17	Enpp5	44078813	44078898	4858	0.00405	4.161726	0.992209	0.99919	0.024589	0	281	218	370	250	300	255	420	347	344	265
ENSMUSG00000037993	chr8	Dhx38	1.1E+08	1.1E+08	4197	5.39E-05	4.008803	0.992259	0.99919	0.025499	0	210	145	337	265	357	256	320	271	360	251
ENSMUSG00000028093	chr3	Acp6	97158777	97159365	4592	-0.00221	4.248563	0.99315	0.999996	0.021881	0	271	190	381	314	378	267	408	312	445	305
ENSMUSG00000070934	chr4	Rraga	86575668	86577285	1618	-0.00083	5.48128	0.993286	0.999996	0.021948	0	659	539	942	679	752	618	1007	814	964	691
ENSMUSG00000079562	chr5	Maea	33335572	33335645	2128	-0.00137	5.902114	0.993245	0.999996	0.022309	0	780	677	1308	990	1086	877	1298	997	1398	918
ENSMUSG00000002617	chr17	Zfp40	23173869	23177364	4482	-0.01524	0.036204	1	1	0.052333	0	12	12	18	12	20	12	21	22	16	12
ENSMUSG00000002847	chr16	Pla1a	38396119	38396535	1972	-0.00658	3.378294	0.995371	1	0.091926	0	166	111	288	117	167	256	121	233	203	90
ENSMUSG00000003235	chr16	Eif2b5	20498817	20499096	3209	-0.00061	6.197358	0.996184	1	0.024777	0	1017	847	1465	1244	1307	1058	1579	1199	1762	1148
ENSMUSG00000004791	chr12	Pgf	85166639	85167414	1582	0.001804	0.222859	1	1	0.097364	0	10	15	28	9	25	24	12	15	19	23
ENSMUSG00000007603	chr17	Dus3l	56764751	56764941	2303	-0.00269	4.293505	0.993534	1	0.021677	0	291	194	428	315	359	283	403	317	452	329
ENSMUSG00000009905	chr1	Kdsr	1.07E+08	1.07E+08	8147	0.004093	2.668361	1	1	0.068176	0	95	106	116	61	109	60	117	157	135	105
ENSMUSG00000018263	chr5	Tbx5	1.2E+08	1.2E+08	3941	-0.03023	0.084367	1	1	0.114359	0	9	16	32	4	18	8	16	22	24	16
ENSMUSG00000018395	chr11	Kif3a	53567379	53567531	3586	-0.005	2.594672	1	1	0.030479	0	68	74	145	80	119	86	135	112	123	87
ENSMUSG00000020630	chr12	Rnaseh1	28649602	28649816	1457	0.00531	2.670025	1	1	0.035741	0	103	82	124	74	114	100	136	97	130	107
ENSMUSG00000021136	chr12	Smoc1	81026808	81027158	3496	-0.00607	2.480046	0.994126	1	0.200444	0	105	92	120	38	72	51	59	243	63	69
ENSMUSG00000021189	chr12	Atxn3	1.02E+08	1.02E+08	5407	0.003249	2.843011	1	1	0.038018	0	96	103	160	86	120	115	131	122	186	95
ENSMUSG00000021596	chr13	Mctp1	76384535	76385251	8193	0.010426	0.218681	1	1	0.081367	0	12	14	30	8	22	9	34	23	18	14

ENSMUSG00000022103	chr14	Gfra2	70890130	70890894	3462	0.002798	1.566361	1	1	0.061829	0	25	42	65	35	65	36	46	55	58	62
ENSMUSG00000022414	chr15	Tab1	80133154	80133188	2931	0.000971	4.287853	0.99667	1	0.033662	0	221	173	414	353	445	214	503	312	452	332
ENSMUSG00000022537	chr16	Tmem44	30511855	30514822	8822	-0.00649	1.394722	1	1	0.051049	0	35	20	53	35	65	42	69	40	43	36
ENSMUSG00000022751	chr16	Nit2	57156671	57157166	1280	0.003095	4.265452	0.998909	1	0.025937	0	255	234	419	310	320	250	542	339	386	265
ENSMUSG00000023066	chr18	Rttn	88971790	88972078	7268	-0.01553	0.760224	1	1	0.052862	0	19	19	30	29	31	21	41	31	21	29
ENSMUSG00000023828	chr17	Slc22a3	12419972	12421497	3501	0.002762	0.774581	1	1	0.215043	0	49	25	15	9	22	28	21	52	23	20
ENSMUSG00000024067	chr17	Dpy30	74299474	74299824	974	0.004836	4.349512	0.994091	1	0.041733	0	318	306	389	245	327	353	460	289	547	236
ENSMUSG00000024232	chr18	Bambi	3507957	3508285	5040	-0.01001	0.434664	1	1	0.044734	0	19	15	28	21	17	14	33	21	26	20
ENSMUSG00000024534	chr18	Sncaip	52767709	52767950	4522	-0.01069	1.2202	1	1	0.044818	0	27	18	46	45	46	38	45	41	50	28
ENSMUSG00000026707	chr2	Nsun6	14995131	14996546	5006	0.019923	0.768843	1	1	0.052755	0	23	23	31	30	18	23	34	32	31	26
ENSMUSG00000027030	chr2	Stk39	68210445	68211993	4955	-0.0019	1.623938	1	1	0.04805	0	33	31	49	59	68	44	79	50	52	47
ENSMUSG00000027193	chr2	Api5	94411682	94413781	4545	0.000849	4.959873	0.999676	1	0.024425	0	439	371	678	428	590	479	764	597	575	426
ENSMUSG00000027551	chr2	Zfp64	1.69E+08	1.69E+08	5918	-0.00497	2.54095	1	1	0.033151	0	65	60	148	98	100	75	121	117	123	87
ENSMUSG00000027775	chr3	Mfsd1	67582741	67582977	3042	0.000497	4.793236	1	1	0.023565	0	408	349	608	362	492	445	630	460	580	411
ENSMUSG00000027778	chr3	Ift80	68892499	68894181	12428	0.006002	2.147726	1	1	0.034673	0	60	45	103	60	85	55	120	76	81	68
ENSMUSG00000027799	chr3	Nbea	55625205	55626994	10976	-0.00613	1.374618	1	1	0.039083	0	34	23	59	38	50	27	60	53	53	36
ENSMUSG00000028741	chr4	Mrto4	1.39E+08	1.39E+08	2611	0.003489	4.577981	0.99504	1	0.023583	0	363	298	469	321	445	355	559	417	548	320
ENSMUSG00000029106	chr5	Add1	34573664	34573913	6066	-0.00174	6.29358	0.994483	1	0.028306	0	958	742	1718	1457	1565	1121	1638	1369	1670	1343
ENSMUSG00000029576	chr5	Radil	1.42E+08	1.42E+08	4803	0.000137	0.823782	1	1	0.074862	0	16	24	32	22	40	21	26	48	31	24
ENSMUSG00000030272	chr6	Camk1	1.13E+08	1.13E+08	6067	0.001538	5.247382	0.999405	1	0.026496	0	614	482	742	545	612	613	867	618	784	579
ENSMUSG00000030528	chr7	Blm	80454993	80455436	4946	-0.00376	0.68559	1	1	0.088554	0	14	29	38	16	23	27	47	21	21	21
ENSMUSG00000030621	chr7	Me3	89632392	89632569	14624	-0.00072	6.374403	0.996634	1	0.028856	0	1008	918	1639	1584	1539	1144	1886	1260	1982	1377
ENSMUSG00000030671	chr7	Pde3b	1.14E+08	1.14E+08	6899	0.003548	2.766238	1	1	0.342952	0	198	126	74	34	48	76	57	316	58	82
ENSMUSG00000030718	chr7	Ppme1	1E+08	1E+08	2361	0.000865	4.873271	1	1	0.023286	0	417	298	577	505	563	412	628	504	729	427
ENSMUSG00000031883	chr8	Car7	1.05E+08	1.05E+08	2459	-0.01423	0.486446	1	1	0.045679	0	17	13	28	24	23	20	35	15	27	21
ENSMUSG00000032584	chr9	Mst1r	1.08E+08	1.08E+08	5007	-0.02087	0.851944	1	1	0.121593	0	22	18	51	18	33	17	30	63	20	21
ENSMUSG00000032727	chr13	Mier3	1.12E+08	1.12E+08	5846	0.0018	2.770735	1	1	0.033968	0	74	81	161	113	118	75	150	124	146	123
ENSMUSG00000032846	chr13	Zswim6	1.08E+08	1.08E+08	5456	0.005522	0.808518	1	1	0.068626	0	14	22	51	23	25	14	33	33	39	32
ENSMUSG00000033124	chr1	Atg9a	75180860	75181931	5762	-7.8E-05	7.752915	0.999779	1	0.028405	0	2688	2000	5529	3569	4162	2922	4582	3611	4933	3734
ENSMUSG00000033356	chr15	Pus7l	94522688	94523651	3291	0.006313	1.125361	1	1	0.063496	0	37	34	39	27	24	23	57	39	44	30
ENSMUSG00000033644	chr14	Piwil2	70372480	70374436	4913	-0.01103	0.238547	1	1	0.05768	0	10	12	22	21	22	20	26	18	14	18
ENSMUSG00000033933	chr6	Vhl	1.14E+08	1.14E+08	2997	0.001758	3.13286	1	1	0.028242	0	123	112	196	121	144	119	169	180	196	129
ENSMUSG00000034111	chr12	Tmed8	87166242	87172631	7179	-0.01337	2.226557	1	1	0.038192	0	69	40	101	63	104	69	89	89	88	77
ENSMUSG00000034926	chr4	Dhcr24	1.07E+08	1.07E+08	4028	-0.005	2.528676	1	1	0.044796	0	72	51	150	89	109	90	92	106	163	69
ENSMUSG00000035266	chr5	Helq	1.01E+08	1.01E+08	5056	0.014405	1.898416	1	1	0.048313	0	58	51	67	50	58	53	90	42	97	56
ENSMUSG00000036898	chr5	Zfp157	1.38E+08	1.38E+08	8782	0.012646	1.51981	1	1	0.049116	0	31	42	59	38	50	27	80	48	58	45
ENSMUSG00000038007	chr4	Acer2	86874396	86874596	7159	-0.00495	1.909432	1	1	0.103773	0	50	39	71	64	71	64	55	123	54	29
ENSMUSG00000038256	chr3	Bcl9	97203662	97205977	8285	-0.00803	2.044062	1	1	0.03952	0	41	48	88	61	91	49	78	83	88	68
ENSMUSG00000038628	chr2	Polr3k	1.82E+08	1.82E+08	3124	0.003545	4.582092	0.997115	1	0.031683	0	432	307	470	289	380	343	538	395	589	344
ENSMUSG00000038836	chr6	Agbl3	34780432	34781059	11075	-0.00071	0.100707	1	1	0.073535	0	11	17	20	8	21	10	24	23	16	15
ENSMUSG00000039697	chr10	Ncoa7	30645584	30647651	5336	0.001849	1.498491	1	1	0.063843	0	31	31	73	27	63	32	82	59	46	33
ENSMUSG00000041696	chr9	Rasl12	65398488	65398667	3877	0.007396	2.552114	1	1	0.050348	0	108	77	104	77	83	78	94	118	134	100
ENSMUSG00000043572	chr4	Pars2	1.07E+08	1.07E+08	3094	-0.00502	2.012247	1	1	0.041322	0	54	34	70	74	87	50	99	63	94	58
ENSMUSG00000045075	chr11	Gm9796	95696894	95699143	2250	-0.02391	0.119454	1	1	0.065001	0	16	6	23	20	15	13	17	13	30	16
ENSMUSG00000045932	chr19	Ifit2	34550694	34551022	3927	-0.01001	2.152245	1	1	0.082762	0	35	56	97	79	88	69	122	74	40	83
ENSMUSG00000046207	chr11	Pik3r6	68503019	68503247	3622	-0.00059	1.083736	1	1	0.043308	0	22	19	41	37	45	29	36	43	45	30
ENSMUSG00000047905	chr6	Gm8566	67205619	67206083	465	0.026367	0.331685	1	1	0.089135	0	16	21	20	23	8	15	24	26	28	14
ENSMUSG00000048218	chr15	Amigo2	97244074	97246597	2871	0.015974	1.293005	1	1	0.070308	0	41	28	32	36	46	21	48	63	51	34
ENSMUSG00000049562	chr19	Ap5b1	5568074	5568607	3092	-0.00899	0.502577	1	1	0.066005	0	26	10	23	23	23	25	20	27	31	15
ENSMUSG00000051116	chr5	Gm8121	57608567	57609067	501	0.006852	1.813631	1	1	0.069175	0	57	63	55	42	43	57	87	48	71	51
ENSMUSG00000051323	chrX	Pcdh19	1.34E+08	1.34E+08	10464	-0.01073	2.468377	1	1	0.05369	0	48	55	139	92	120	69	91	96	109	121
ENSMUSG00000051427	chr11	Ccdc157	4141123	4143935	5589	0.001996	2.168228	1	1	0.036265	0	64	53	105	46	89	64	100	75	101	64
ENSMUSG00000051736	chr10	Fam229b	39118804	39119034	3331	0.013005	0.926248	1	1	0.045894	0	27	20	40	26	31	24	43	27	54	20
ENSMUSG00000052374	chr13	Actn2	12269426	12269652	3694	-0.00248	8.968307	0.99662	1	0.388144	0	1221	1021	3791	21296	14520	4293	14336	4041	16397	9193
ENSMUSG00000053094	chr5	Tmem248	1.3E+08	1.3E+08	3845	0.000697	5.885946	0.999388	1	0.023701	0	908	678	1333	825	1021	868	1318	1058	1337	853
ENSMUSG00000055707	chr8	Klhl26	70450228	70453019	3069	-0.00198	3.735512	1	1	0.024503	0	166	128	288	230	271	213	265	222	287	214
ENSMUSG00000057554	chr13	Lgals8	12439415	12440994	3688	0.00112	4.783253	0.994733	1	0.022035	0	336	292	638	480	496	394	661	469	577	424
ENSMUSG00000063286	chr7	Gm8995	1.07E+08	1.07E+08	7280	-0.00847	1.975631	1	1	0.070628	0	29	42	129	48	78	59	101	71	55	60
ENSMUSG00000066491	chr12	Gm6265	56373593	56373823	231	0.026364	0.428491	1	1	0.070217	0	22	18	13	20	22	17	33	15	33	18
ENSMUSG00000067367	chr5	Lyar	38220470	38220635	2401	0.00299	4.213574	1	1	0.026188	0	249	261	355	289	302	290	426	282	440	264
ENSMUSG00000068015	chr14	Lrch1	74754674	74757143	4706	0.000364	1.768512	1	1	0.055646	0	21	42	83	56	70	43	76	57	68	58
ENSMUSG00000068206	chr15	Pick1	79229173	79229420	7770	0.001371	5.505556	0.996773	1	0.028294	0	589	489	909	855	812	739	1041	674	1156	591
ENSMUSG00000070343	chr3	Gm10288	1.47E+08	1.47E+08	537	0.005857	2.850306	1	1	0.058399	0	122	118	113	87	104	135	173	107	139	95
ENSMUSG00000075419	chr2	Dolk	30284231	30286334	2104	0.000839	4.742812	1	1	0.02186	0	371	312	549	429	483	379	555	532	584	393
ENSMUSG00000075569	chr5	Rsph10b	1.44E+08	1.44E+08	3101	0.044142	0.028323	1	1	0.070888	0	10	16	24	8	14	14	28	15	17	11

ENSMUSG00000075592	chr14	Nynrin	55854036	55854059	7436	-0.01015	1.892118	1	1	0.096125	0	23	43	110	49	80	29	57	79	78	82
ENSMUSG00000078234	chr4	Klhdc7a	1.4E+08	1.4E+08	7807	0.01331	1.789009	0.99447	1	0.583771	0	126	61	24	10	13	39	28	180	12	37
ENSMUSG00000085436	chr2	Zfp335os	1.65E+08	1.65E+08	1273	0.002453	1.540535	1	1	0.051647	0	52	34	61	36	40	47	58	33	69	49
ENSMUSG00000085493	chr5	Gm15469	31135753	31136302	961	-0.04759	-0.4909	1	1	0.44755	0	1	0	26	18	8	2	2	13	25	11
ENSMUSG00000086779	chr2	Gm13562	26352645	26352731	1344	-0.01232	-0.27305	1	1	0.172519	0	13	3	10	20	11	3	30	8	11	15
ENSMUSG00000097059	chr13	Fam120aos	48968287	48968604	1780	0.017419	1.554371	1	1	0.046889	0	36	45	52	41	48	40	60	41	83	40
ENSMUSG00000097099	chr9	Gm9917	1.08E+08	1.08E+08	6021	0.005095	0.311597	1	1	0.067635	0	9	12	26	23	22	9	27	28	27	14
ENSMUSG00000097195	chr9	Snhg5	88521050	88521448	1730	0.001361	3.219392	1	1	0.049801	0	171	132	191	92	137	163	222	140	199	121
ENSMUSG00000097204	chr3	Gm17690	96167464	96169652	3467	0.007978	1.193022	1	1	0.067537	0	32	28	35	34	43	23	62	20	56	43
ENSMUSG00000097919	chr8	Gm27021	1.21E+08	1.21E+08	758	0.007307	1.476789	1	1	0.06739	0	54	31	36	37	51	45	43	62	51	40
ENSMUSG00000100254	chr7	TRPC2	1.02E+08	1.02E+08	2874	-0.02713	0.821671	1	1	0.056416	0	23	15	42	20	38	33	32	23	28	31
ENSMUSG00000104204	chr6	RP23-291E6.6	57684739	57687580	2842	0.016393	0.795077	1	1	0.069998	0	11	20	30	39	30	26	37	26	43	19

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Table S7. RNA sequencing analysis and differential expression data of D2-mdx vs D2-WT mice at 1 month of age. Raw reads were mapped to chromosomes and gene identifiers and subsequent differential analysis was completed (n = 5 per group).

Ensembl ID	Chromosome	Gene Name	logFC_D2-*mdx* 1mo_D2-WT 1mo	P-value_D2-*mdx* 1mo_D2-WT 1mo	FDR_D2-*mdx* 1mo_D2-WT 1mo	logCPM_D2-*mdx* 1mo_D2-WT 1mo	Tgw.Disp	UpDown.Tgw	D2-WT.1mo_Rep1_raw	D2-WT.1mo_Rep2_raw	D2-WT.1mo_Rep3_raw	D2-WT.1mo_Rep4_raw	D2-WT.1mo_Rep5_raw	D2-mdx.1mo_Rep1_raw	D2-mdx.1mo_Rep2_raw	D2-mdx.1mo_Rep3_raw	D2-mdx.1mo_Rep4_raw	D2-mdx.1mo_Rep5_raw
ENSMUSG00000033182	chr6	Kbtbd12	-4.009307	7.9522E-110	1.1114E-105	5.716352967	0.027790128	-1	1508	1263	1358	1664	1546	106	102	87	118	87
ENSMUSG00000036905	chr4	C1qb	4.09870189	4.6745E-109	3.2665E-105	6.749217356	0.031132364	1	174	191	155	168	185	3866	2883	3161	2893	3813
ENSMUSG00000046805	chr19	Mpeg1	5.96210608	9.4498E-107	4.4023E-103	6.465311643	0.053699233	1	39	41	34	50	43	2915	3275	1458	2409	4310
ENSMUSG00000045103	chrX	Dmd	-4.9271752	2.2742E-104	7.9461E-101	6.516270261	0.042147371	-1	2697	2124	2488	3331	2593	65	113	62	102	133
ENSMUSG00000050335	chr14	Lgals3	6.91034544	5.0177E-99	1.40254E-95	7.81252739	0.07405657	1	54	48	46	78	52	7865	11337	2709	7507	7476
ENSMUSG00000040552	chr6	C3ar1	4.54596572	1.36163E-88	3.17169E-85	4.886996136	0.040181265	1	36	36	33	34	39	1022	1013	499	963	1154
ENSMUSG00000038642	chr3	Ctss	6.1388276	6.52372E-85	1.30251E-81	7.699245979	0.07390093	1	89	118	76	90	58	9129	7337	3106	4595	10045
ENSMUSG00000023992	chr17	Trem2	6.84713226	4.14183E-77	7.23577E-74	5.274500147	0.085193167	1	6	8	10	14	11	2118	1148	508	856	1789
ENSMUSG00000026956	chr2	Uap1l1	4.16762175	4.07179E-76	6.32304E-73	4.339310332	0.039520628	1	36	34	29	34	24	643	781	387	748	555
ENSMUSG00000044811	chr11	AF251705	6.32067261	5.07318E-76	7.09028E-73	3.577653197	0.062245411	1	1	9	5	4	2	513	352	217	305	541
ENSMUSG00000069515	chr10	Lyz1	5.89167095	9.95064E-74	1.26427E-70	4.750442446	0.070935941	1	14	20	9	11	11	1243	1116	346	815	858
ENSMUSG00000031394	chrX	Opn1mw	-7.7047945	1.406E-72	1.63752E-69	2.250356591	0.052181837	-1	120	132	149	188	109	1	0	1	1	0
ENSMUSG00000030579	chr7	Tyrobp	4.73749567	1.55537E-71	1.67214E-68	5.834842644	0.057828089	1	53	72	72	47	56	2392	2121	855	1695	2042
ENSMUSG00000018774	chr11	Cd68	5.33687956	9.231E-71	9.21517E-68	6.354600876	0.071187562	1	52	65	60	52	60	3863	3172	1089	1891	3320
ENSMUSG00000034947	chr11	Tmem106a	4.14420262	1.82925E-67	1.70437E-64	4.397562494	0.045565748	1	33	40	29	37	27	918	738	329	620	678
ENSMUSG00000060586	chr17	H2-Eb1	4.3786562	5.25804E-67	4.5929E-64	5.52171255	0.054303065	1	66	68	45	70	63	1764	975	1956	913	1497
ENSMUSG00000037280	chr15	Galnt6	5.91722031	1.15804E-66	9.52043E-64	2.954100842	0.059612146	1	2	3	3	8	2	362	277	157	171	271
ENSMUSG00000031827	chr8	Cotl1	4.14968846	1.61001E-66	1.25009E-63	6.184379985	0.051503455	1	112	132	94	109	123	3336	2484	1211	2446	1899
ENSMUSG00000058715	chr1	Fcer1g	4.76670467	1.95797E-66	1.44024E-63	5.706520148	0.06289693	1	40	74	59	43	53	2484	1729	932	1884	1272
ENSMUSG00000004730	chr17	Emr1	3.36152685	6.77909E-66	4.73722E-63	4.800094889	0.03395661	1	75	68	82	70	67	919	955	502	853	924
ENSMUSG00000000682	chr4	Cd52	6.06771473	2.45603E-65	1.63455E-62	4.250055749	0.080847522	1	8	9	6	12	6	1114	637	257	640	453
ENSMUSG00000024300	chr17	Myo1f	4.79037648	2.94077E-65	1.86819E-62	4.640534819	0.060532164	1	24	28	33	24	18	1101	1009	370	597	906
ENSMUSG00000048163	chr5	Selplg	5.15334146	5.55661E-64	3.37649E-61	4.020251496	0.064638313	1	4	11	14	20	16	853	514	291	390	556
ENSMUSG00000073421	chr17	H2-Ab1	4.29841944	7.89681E-64	4.59857E-61	5.81473132	0.056329486	1	86	84	57	102	77	2226	1184	2455	1097	1724
ENSMUSG00000093327	chr18	Mir5107	4.54051932	2.47945E-63	1.38611E-60	5.111219291	0.059920002	1	42	39	38	52	40	1459	698	1467	601	1159
ENSMUSG00000076036	chr7	Gm22133	3.85158169	3.72071E-63	2.00002E-60	8.589759396	0.050078316	1	765	748	615	905	693	17696	14804	6173	11042	10153
ENSMUSG00000015947	chr3	Fcgr1	4.95565805	5.29133E-63	2.73895E-60	3.800405616	0.060261377	1	9	17	9	12	16	493	608	236	507	347
ENSMUSG00000000290	chr10	Itgb2	5.46360467	1.00381E-62	5.01044E-60	5.432900502	0.081115664	1	29	33	23	35	22	2001	1887	472	1020	1666
ENSMUSG00000046718	chr8	Bst2	2.7386467	2.87173E-62	1.38398E-59	4.942853048	0.025237761	1	147	113	101	128	104	1063	830	811	685	979
ENSMUSG00000059422	chr9	Gm8116	-3.0240037	5.1023E-61	2.37699E-58	4.469849366	0.03007737	-1	585	509	593	779	483	97	80	49	99	71
ENSMUSG00000056069	chr15	Fam105a	4.08194254	1.38457E-60	6.24219E-58	3.134965479	0.041192156	1	11	15	14	17	14	355	322	210	242	209
ENSMUSG00000022488	chr15	Nckap1l	3.85624302	3.26104E-60	1.42426E-57	4.759984834	0.047609894	1	49	58	47	63	42	1312	859	417	755	851
ENSMUSG00000089929	chr9	Bcl2a1b	5.77981867	5.14201E-60	2.17772E-57	2.668278183	0.061943183	1	3	6	1	5	1	259	226	111	205	202
ENSMUSG00000007617	chr13	Homer1	-2.7310568	5.50304E-60	2.26207E-57	5.853477108	0.028393948	-1	1485	1243	1434	1807	1506	234	281	177	247	299
ENSMUSG00000026177	chr1	Slc11a1	3.9658889	5.90876E-60	2.35945E-57	3.87798568	0.045622365	1	19	30	31	28	21	581	563	262	354	503
ENSMUSG00000024965	chr19	Fermt3	4.44251106	1.79101E-59	6.9531E-57	3.975919732	0.056153338	1	21	21	13	21	25	826	531	301	447	366
ENSMUSG00000016256	chr2	Ctsz	3.28822911	3.73363E-59	1.4103E-56	7.009579899	0.040754891	1	374	325	321	455	314	6033	4150	2479	2774	4003
ENSMUSG00000006519	chr8	Cyba	4.14616925	1.14209E-58	4.2005E-56	5.943506969	0.058487443	1	89	103	82	125	91	3359	2130	931	1598	1699
ENSMUSG00000043336	chr16	Filip1l	-2.7710832	1.695E-58	6.0742E-56	6.416297133	0.030310538	-1	2157	2102	2126	2669	2037	428	303	253	362	447
ENSMUSG00000033777	chrX	Tlr13	4.9684052	3.52712E-58	1.23237E-55	3.254329417	0.061475763	1	9	7	9	13	5	302	380	146	360	304
ENSMUSG00000034708	chr11	Grn	3.29236043	6.02355E-58	2.0533E-55	7.995958349	0.041988258	1	643	725	576	878	705	12166	7834	5524	5367	7601
ENSMUSG00000021998	chr14	Lcp1	4.49080622	1.69165E-57	5.62916E-55	6.476766759	0.068676801	1	98	122	126	123	91	4288	3254	1098	2953	2580
ENSMUSG00000021423	chr13	Ly86	4.13992994	2.00464E-57	6.51556E-55	4.103468345	0.053312508	1	32	27	25	27	24	946	450	488	366	418
ENSMUSG00000028599	chr4	Tnfrsf1b	3.3188916	2.34033E-57	7.43375E-55	4.791222074	0.038959	1	74	66	69	85	78	1051	953	459	656	1031
ENSMUSG00000032322	chr9	Pstpip1	4.80907031	3.7562E-57	1.16659E-54	3.086118436	0.057582883	1	8	13	10	8	3	406	261	196	180	289
ENSMUSG00000052160	chr12	Pld4	3.71895656	4.12459E-57	1.25316E-54	4.764298857	0.04748082	1	48	58	61	58	56	1465	731	573	690	715
ENSMUSG00000040907	chr7	Atp1a3	7.77344628	5.87427E-57	1.74678E-54	3.503809809	0.10936592	1	1	3	1	2	0	480	451	149	191	589
ENSMUSG00000002111	chr2	Spi1	4.16469394	3.48715E-56	1.01534E-53	4.17203217	0.05575552	1	27	23	27	40	24	897	632	264	507	518
ENSMUSG00000034652	chr11	Cd300a	4.69627793	4.5118E-56	1.28688E-53	4.203553312	0.067534596	1	17	16	15	23	29	933	640	278	402	686
ENSMUSG00000024672	chr19	Ms4a7	4.24120775	1.3246E-55	3.70253E-53	4.058436118	0.056979286	1	26	30	31	17	17	851	395	454	365	527
ENSMUSG00000036594	chr17	H2-Aa	4.38543663	7.27339E-55	1.99319E-52	6.04798996	0.068852586	1	89	99	61	90	106	2858	1276	2767	1222	2163
ENSMUSG00000037902	chr2	Sirpa	3.62656311	8.26041E-55	2.22015E-52	6.714008858	0.051987628	1	219	237	214	265	230	4881	3578	1508	2655	3560
ENSMUSG00000040659	chr4	Efhd2	3.14237813	1.33912E-54	3.53122E-52	5.946179875	0.040352819	1	221	156	162	194	194	2633	1928	1097	1831	1652
ENSMUSG00000040751	chr5	Lat2	5.74709728	1.4587E-54	3.77533E-52	4.335295767	0.094112419	1	9	16	9	13	7	943	831	199	749	544
ENSMUSG00000028843	chr4	Sh3bgrl3	3.54124087	1.96808E-54	5.00107E-52	5.87131747	0.048780984	1	154	129	114	181	115	2807	2180	969	1542	1449
ENSMUSG00000053205	chr14	Styx	-4.5956886	4.65278E-54	1.1612E-51	2.725969293	0.054369384	-1	197	160	179	183	208	5	12	3	8	14
ENSMUSG00000030707	chr7	Coro1a	5.04659277	1.54572E-53	3.79E-51	5.354333629	0.085495758	1	37	37	27	38	38	2174	1418	559	1670	738
ENSMUSG00000024610	chr18	Cd74	4.52216696	1.71331E-53	4.12848E-51	7.481594475	0.076679217	1	202	215	167	255	266	7499	3343	7978	2955	6124

ENSMUSG00000004266	chr6	Ptpn6	4.63473484	2.83442E-53	6.61319E-51	4.289308982	0.070607393	1	25	21	21	19	24	932	851	282	603	427
ENSMUSG00000030786	chr7	Itgam	4.57903369	2.83909E-53	6.61319E-51	4.965655953	0.072874044	1	34	32	27	44	48	1335	1395	365	932	936
ENSMUSG00000021190	chr12	Lgmn	2.89360965	7.26867E-53	1.66536E-50	7.65764419	0.036828607	1	720	756	652	833	604	7934	5640	3941	6743	5005
ENSMUSG00000036908	chr19	Unc93b1	3.11135313	1.06866E-52	2.40896E-50	5.790585139	0.040227282	1	147	162	175	169	189	2445	1348	1332	1179	1885
ENSMUSG00000050708	chr7	Ftl1	3.36038425	1.11157E-52	2.46591E-50	9.634154967	0.048182255	1	2129	2187	1757	2549	1905	32720	30855	12204	21423	23049
ENSMUSG00000036896	chr4	C1qc	3.48442262	1.94362E-52	4.24438E-50	6.428482422	0.050733295	1	198	197	202	227	219	4382	1859	2468	1694	2668
ENSMUSG00000038594	chr10	Cep85l	-4.4317933	3.27514E-52	7.04205E-50	2.680174792	0.053305023	-1	184	174	189	210	144	3	14	5	15	8
ENSMUSG00000006731	chr10	B4galnt1	4.14475106	4.36458E-52	9.24233E-50	3.347033927	0.054180965	1	9	19	18	19	14	489	330	183	249	323
ENSMUSG00000079227	chr9	Ccr5	4.98153383	5.17181E-52	1.07882E-49	2.957868535	0.066633295	1	8	7	9	6	4	383	272	129	231	207
ENSMUSG00000026480	chr1	Ncf2	4.15662748	6.1375E-52	1.26144E-49	4.183444412	0.061010694	1	30	30	19	39	25	918	617	251	544	510
ENSMUSG00000027907	chr3	S100a11	2.79089565	8.69405E-52	1.76099E-49	6.11882792	0.034641401	1	264	271	228	294	244	2608	2418	1729	1789	1403
ENSMUSG00000040613	chr6	Apobec1	3.47580917	9.78791E-52	1.95423E-49	4.021686658	0.044345735	1	44	42	41	39	30	468	581	293	414	674
ENSMUSG00000049625	chr13	Tifab	4.25631696	1.26501E-51	2.4901E-49	2.765296305	0.050455195	1	7	9	10	16	7	245	265	145	212	168
ENSMUSG00000029322	chr5	Plac8	5.6385041	2.89798E-51	5.6253E-49	2.786955244	0.077214704	1	2	5	2	3	7	366	208	117	181	226
ENSMUSG00000038147	chr1	Cd84	5.05255906	4.34999E-51	8.32814E-49	4.256445215	0.084113139	1	6	25	16	16	18	759	696	235	540	827
ENSMUSG00000020437	chr11	Myo1g	4.48664713	2.64989E-50	5.0047E-48	3.257812312	0.063369411	1	13	12	11	12	11	436	356	135	299	266
ENSMUSG00000003484	chr8	Cyp4f18	6.63310199	2.97521E-50	5.54421E-48	1.96398577	0.07145523	1	1	0	2	2	0	88	126	117	148	120
ENSMUSG00000021665	chr13	Hexb	2.88929003	3.16243E-50	5.81554E-48	5.528808326	0.036797983	1	181	174	142	173	142	2034	1402	860	1118	1314
ENSMUSG00000024737	chr19	Slc15a3	4.76551965	3.47805E-50	6.29154E-48	4.122553957	0.078232664	1	15	13	14	26	23	803	651	202	424	701
ENSMUSG00000061436	chr6	Hipk2	-3.086945	3.51131E-50	6.29154E-48	4.89934585	0.040365746	-1	732	571	815	866	949	72	109	94	117	116
ENSMUSG00000004707	chr1	Ly9	6.11754309	5.10424E-50	9.02999E-48	3.098994498	0.094354094	1	3	4	1	2	7	369	349	100	235	324
ENSMUSG00000015355	chr1	Cd48	4.50415211	5.86201E-50	1.02409E-47	3.096617663	0.062244308	1	9	12	11	11	9	292	347	132	315	234
ENSMUSG00000102573	chr9	RP23-296I6.8	-4.7276332	7.2517E-49	1.25123E-46	2.56489628	0.062597134	-1	179	121	174	195	168	5	7	2	15	5
ENSMUSG00000040212	chr7	Emp3	3.26154509	1.19607E-48	2.03856E-46	5.276961943	0.046803545	1	115	80	92	145	114	1757	1446	782	1010	795
ENSMUSG00000024679	chr19	Ms4a6d	4.45620135	1.30564E-48	2.17234E-46	3.41210438	0.067461975	1	11	11	14	21	11	555	346	169	346	248
ENSMUSG00000028581	chr4	Laptm5	4.5132984	1.29479E-48	2.17234E-46	6.365117621	0.082497884	1	81	109	83	118	120	5028	1963	1538	1411	3321
ENSMUSG00000049130	chr7	C5ar1	4.36227462	3.21414E-48	5.2848E-46	4.397300344	0.073066198	1	14	28	36	40	26	758	900	323	823	473
ENSMUSG00000024298	chr17	Zfp871	-3.8231279	3.73784E-48	6.07443E-46	2.528732954	0.044767818	-1	137	145	156	174	175	13	14	7	13	14
ENSMUSG00000056737	chr6	Capg	4.2762556	4.48567E-48	7.20594E-46	6.226157226	0.076598496	1	134	80	106	143	87	3677	3176	893	2191	1922
ENSMUSG00000093938	chr11	Evi2b	4.74578451	6.77598E-48	1.07615E-45	2.781483382	0.066046483	1	5	5	10	6	9	272	253	107	225	210
ENSMUSG00000069516	chr10	Lyz2	4.21898667	6.90554E-48	1.0844E-45	9.065200679	0.077314875	1	826	1029	869	631	634	22379	20686	6635	17179	17581
ENSMUSG00000029762	chr6	Akr1b8	4.23181185	9.35435E-48	1.45263E-45	3.468945473	0.064417834	1	13	18	10	29	13	474	353	417	238	210
ENSMUSG00000021699	chr13	Pde4d	-3.1477243	1.30746E-47	2.00803E-45	5.702084119	0.045885723	-1	1264	1128	1202	1961	1464	180	161	87	222	215
ENSMUSG00000020961	chr12	Ston2	-3.0517118	3.82489E-47	5.8105E-45	3.678147599	0.037941401	-1	315	282	362	436	301	31	59	29	50	54
ENSMUSG00000001750	chr19	Tcirg1	3.08419287	4.7514E-47	7.14038E-45	4.947782787	0.043246056	1	101	90	95	105	89	1330	1084	472	736	948
ENSMUSG00000049988	chr8	Lrrc25	4.00135589	7.57679E-47	1.12652E-44	2.873344547	0.053499881	1	11	12	10	14	15	350	230	142	189	206
ENSMUSG00000053063	chr6	Clec12a	4.92092984	8.39691E-47	1.23532E-44	3.930206251	0.08729171	1	16	16	20	15	4	943	374	262	383	481
ENSMUSG00000031760	chr8	Mt3	3.93431271	1.16032E-46	1.68923E-44	3.003808338	0.054074687	1	20	11	10	20	11	343	218	271	203	171
ENSMUSG00000049103	chr9	Ccr2	4.90705321	2.04218E-46	2.94242E-44	4.113730456	0.08939238	1	16	17	14	20	15	511	594	358	959	261
ENSMUSG00000021779	chr14	Thrb	-2.6818105	5.34248E-46	7.61903E-44	3.861185202	0.031283111	-1	346	310	374	556	301	62	71	44	61	81
ENSMUSG00000051984	chr19	Sec31b	-2.5887429	9.16733E-46	1.29417E-43	4.81737699	0.032276063	-1	678	553	663	999	727	176	105	88	145	145
ENSMUSG00000058099	chr15	Nfam1	4.00224317	1.03756E-45	1.45009E-43	3.15005105	0.058556649	1	15	16	17	20	8	391	321	149	276	219
ENSMUSG00000064344	chrMT	mt-Tm	-3.2681627	1.4668E-45	2.02971E-43	4.305359962	0.047834795	-1	373	497	489	900	452	52	48	58	87	54
ENSMUSG00000026786	chr2	Apbb1ip	3.55821426	3.43347E-45	4.70453E-43	3.134164971	0.047673652	1	19	25	28	17	10	271	314	199	219	300
ENSMUSG00000024397	chr17	Aif1	4.27014636	4.65021E-45	6.30983E-43	3.109150785	0.065497734	1	6	14	12	12	17	352	213	241	333	172
ENSMUSG00000033220	chr15	Rac2	4.82905561	4.92563E-45	6.61929E-43	4.532390787	0.092934115	1	26	17	31	29	13	1591	629	369	533	614
ENSMUSG00000024885	chr19	Aldh3b1	3.20396131	5.007E-45	6.66456E-43	3.312860771	0.04105746	1	28	23	25	40	27	406	348	219	263	217
ENSMUSG00000029925	chr6	Tbxas1	3.71336375	9.79186E-45	1.29105E-42	2.838161784	0.049808046	1	12	14	15	24	9	298	223	149	224	175
ENSMUSG00000028874	chr4	Fgr	6.0993105	3.10564E-44	4.05649E-42	2.803501608	0.105182955	1	2	7	2	3	0	343	325	112	187	148
ENSMUSG00000039168	chr15	Dap	2.25314048	9.38234E-44	1.21414E-41	5.085220274	0.026893203	1	183	176	157	213	146	1245	934	913	712	781
ENSMUSG00000033713	chr12	Foxn3	-2.6891331	2.63053E-43	3.37287E-41	4.232005947	0.035081552	-1	428	403	458	616	511	72	56	82	100	97
ENSMUSG00000018008	chr15	Cyth4	3.47087842	3.54546E-43	4.50467E-41	4.79140088	0.057981477	1	74	68	62	66	66	1506	919	444	627	728
ENSMUSG00000060063	chr5	Alox5ap	4.28241166	3.84716E-43	4.84396E-41	4.645192943	0.081779843	1	29	36	32	48	36	1324	890	353	930	428
ENSMUSG00000063193	chr11	Cd300lb	4.93869801	5.85889E-43	7.31106E-41	3.15587705	0.087438981	1	8	5	10	6	11	372	329	104	232	372
ENSMUSG00000036887	chr4	C1qa	3.32145554	6.51922E-43	8.06307E-41	6.448558045	0.057714868	1	184	248	257	255	226	4737	1889	2388	1999	2119
ENSMUSG00000040540	chr10	Gm9770	-3.6990584	1.07856E-42	1.32227E-40	2.366532196	0.047962669	-1	124	137	133	170	138	18	8	6	16	11
ENSMUSG00000060036	chr15	Rpl3	2.19834762	1.51529E-42	1.84154E-40	7.022590373	0.027891615	1	753	700	616	778	610	3927	3999	3245	3355	2893
ENSMUSG00000021886	chr12	Gpr65	5.15547467	1.6162E-42	1.94724E-40	1.906376725	0.067384252	1	1	2	5	4	2	165	126	73	100	112
ENSMUSG00000002204	chr7	Napsa	5.95571051	5.85515E-42	6.99416E-40	2.217019492	0.094224306	1	2	4	0	2	2	151	186	61	143	187
ENSMUSG00000058818	chr7	Pirb	3.84928831	8.31935E-42	9.85349E-40	4.224004177	0.069146034	1	28	37	32	38	42	1063	494	284	421	641
ENSMUSG00000031387	chrX	Renbp	3.42322267	1.31675E-41	1.54646E-39	3.661959156	0.053869518	1	30	26	37	38	27	589	412	202	390	301
ENSMUSG00000054659	chr4	Pm20d2	-3.5595696	1.38529E-41	1.6134E-39	3.127813635	0.054349472	-1	162	199	234	407	210	20	17	16	26	31
ENSMUSG00000050556	chr2	Kcnb1	-2.1802553	2.71985E-41	3.14154E-39	4.367067466	0.024839108	-1	557	435	477	581	457	120	116	123	138	106
ENSMUSG00000027514	chr2	Zbp1	4.49090345	3.00453E-41	3.44192E-39	1.951679636	0.058969496	1	8	4	1	5	5	146	139	91	89	119
ENSMUSG00000028986	chr5	Klhl7	-2.1078251	7.69935E-41	8.74847E-39	5.271856844	0.025815381	-1	962	832	837	1195	859	227	237	181	227	317

ENSMUSG00000025473	chr7	Adam8	5.5773491	7.79878E-41	8.78998E-39	4.495780621	0.12791078	1	2	16	12	26	13	1171	964	233	739	554
ENSMUSG00000022831	chr16	Hcls1	3.33466794	9.61852E-41	1.07543E-38	4.461588882	0.05682579	1	53	64	36	83	60	1100	704	355	635	515
ENSMUSG00000048612	chr19	Myof	2.76089233	1.5815E-40	1.75421E-38	4.772116849	0.041512062	1	109	87	99	155	77	856	1141	522	553	838
ENSMUSG00000100838	chr9	Gm29094	3.63668821	2.21998E-40	2.44302E-38	2.820119508	0.054352874	1	19	21	12	16	8	250	228	124	233	215
ENSMUSG00000059498	chr1	Fcgr3	3.32468988	3.27242E-40	3.57307E-38	5.073831284	0.059051741	1	112	95	96	75	69	1617	950	502	818	1200
ENSMUSG00000015950	chr5	Ncf1	3.995148	4.71298E-40	5.1061E-38	4.036873112	0.076487861	1	23	19	24	41	36	875	512	219	533	408
ENSMUSG00000040345	chr10	Arhgap9	3.86110844	4.7611E-40	5.11855E-38	3.202254286	0.065708902	1	14	23	17	20	12	487	278	155	215	275
ENSMUSG00000001473	chr18	Tubb6	2.93336303	4.98537E-40	5.31874E-38	6.288877916	0.049945213	1	288	211	237	355	263	2080	2109	3284	1982	1634
ENSMUSG00000103888	chr1	AC123072.1	-2.5573159	1.06524E-39	1.12787E-37	7.590319867	0.039865836	-1	4140	4046	4579	7030	4950	686	958	777	944	1188
ENSMUSG00000023826	chr17	Park2	-2.5677004	1.09914E-39	1.15501E-37	3.827458547	0.034291707	-1	365	381	328	400	321	110	56	59	59	51
ENSMUSG00000060216	chr11	Arrb2	2.6855322	1.68165E-39	1.75393E-37	4.334219682	0.039212433	1	81	86	68	95	71	868	531	424	623	406
ENSMUSG00000034116	chr17	Vav1	4.08026904	1.89497E-39	1.96179E-37	3.380206435	0.074962494	1	12	18	25	18	11	539	359	164	305	241
ENSMUSG00000073982	chr7	Rhog	2.34251496	2.10599E-39	2.16421E-37	5.262450116	0.032830058	1	169	168	161	254	191	1631	968	863	826	994
ENSMUSG00000052776	chr5	Oas1a	4.42155108	2.35289E-39	2.40029E-37	2.41981804	0.072394588	1	4	8	7	10	5	209	222	86	123	181
ENSMUSG00000021486	chr13	Prelid1	2.04783243	8.77961E-39	8.89158E-37	5.573857555	0.026040896	1	300	255	253	327	244	1588	1406	1044	1200	1037
ENSMUSG00000031443	chr8	F7	10.727083	1.10533E-38	1.11137E-36	2.800657625	0.190402012	1	0	0	0	0	0	313	355	37	171	261
ENSMUSG00000051506	chr14	Wdfy4	3.60521393	1.16623E-38	1.16423E-36	2.673684058	0.055246773	1	13	14	9	18	16	223	243	131	207	138
ENSMUSG00000005054	chr10	Cstb	3.80705072	1.3185E-38	1.3069E-36	5.452373756	0.078780888	1	91	100	73	79	85	2205	1777	557	1344	903
ENSMUSG00000054342	chr7	Kcnn4	5.07551617	1.51879E-38	1.49483E-36	2.69666458	0.09790016	1	6	2	3	11	5	271	308	86	189	163
ENSMUSG00000026100	chr1	Mstn	-3.2444756	2.10466E-38	2.05697E-36	5.591993521	0.060884287	-1	1534	1148	1062	1274	1421	137	170	63	156	232
ENSMUSG00000004360	chr10	9330159F19Rik	-2.4017706	2.44483E-38	2.37285E-36	4.664364062	0.033916228	-1	522	524	551	954	654	185	122	87	120	150
ENSMUSG00000059326	chr19	Csf2ra	4.41112207	2.49428E-38	2.40414E-36	3.75425819	0.091551049	1	19	20	12	12	24	664	520	150	326	469
ENSMUSG00000072620	chr11	Slfn2	4.80520284	2.69575E-38	2.58053E-36	4.28433906	0.109208285	1	15	21	11	21	30	1157	623	232	711	389
ENSMUSG00000057191	chr9	AB124611	4.30034152	2.78876E-38	2.6335E-36	2.691156492	0.074967638	1	10	8	11	5	10	354	191	133	148	169
ENSMUSG00000079547	chr17	H2-DMb1	4.30385324	2.78706E-38	2.6335E-36	2.749007158	0.076876671	1	10	10	3	6	17	179	161	259	216	191
ENSMUSG00000039419	chr6	Cntnap2	-2.6671273	3.46469E-38	3.24984E-36	4.143044516	0.040050146	-1	536	423	364	447	479	109	79	46	59	103
ENSMUSG00000030798	chr7	Cd37	4.15339176	3.61815E-38	3.37115E-36	3.518555309	0.081886215	1	24	9	17	21	18	687	309	174	279	342
ENSMUSG00000026288	chr1	Inpp5d	2.84110809	4.53512E-38	4.19754E-36	4.086039407	0.044783987	1	54	52	57	98	50	754	500	318	499	370
ENSMUSG00000061132	chr19	Blnk	3.28117516	4.78512E-38	4.39979E-36	3.190136937	0.052217281	1	29	24	20	28	23	390	287	162	180	332
ENSMUSG00000009185	chr11	Ccl8	4.76258723	5.11972E-38	4.67668E-36	3.505605317	0.101865974	1	21	9	8	7	13	646	218	351	365	194
ENSMUSG00000024338	chr17	Psmb8	2.49006466	5.38796E-38	4.88975E-36	3.97858347	0.034116043	1	50	61	63	92	85	588	426	320	419	429
ENSMUSG00000081194	chrX	Gm8424	-4.1140607	5.91937E-38	5.33737E-36	3.054372651	0.077370859	-1	163	205	229	361	215	5	20	9	27	11
ENSMUSG00000013707	chr3	Tnfaip8l2	3.90392988	7.50951E-38	6.72775E-36	2.592066697	0.0640294	1	10	11	7	12	14	288	170	117	129	209
ENSMUSG00000020901	chr11	Pik3r5	4.60234034	1.69504E-37	1.50891E-35	3.150558974	0.094760424	1	9	13	7	14	8	476	309	93	253	268
ENSMUSG00000032359	chr9	Ctsh	2.36539888	1.73842E-37	1.53773E-35	5.493218991	0.03549331	1	213	238	261	180	176	1339	1365	996	1243	1209
ENSMUSG00000089672	chr10	Gp49a	4.70516078	2.74392E-37	2.41189E-35	3.420138417	0.101144947	1	6	19	10	12	10	407	386	103	424	357
ENSMUSG00000025647	chr9	Shisa5	2.26453979	2.91806E-37	2.53309E-35	5.515854579	0.03297627	1	198	229	228	295	221	1834	1216	915	943	1347
ENSMUSG00000061232	chr17	H2-K1	2.43488458	2.91779E-37	2.53309E-35	7.194149371	0.038849745	1	589	833	564	788	621	5730	3335	3445	3093	4785
ENSMUSG00000005413	chr8	Hmox1	3.01319734	4.00403E-37	3.45434E-35	5.101482786	0.054387998	1	99	134	120	123	82	1462	1031	600	1243	673
ENSMUSG00000056888	chr10	Glipr1	5.79279699	4.36856E-37	3.7457E-35	2.679629278	0.12192452	1	2	1	0	6	7	309	169	89	141	315
ENSMUSG00000001020	chr3	S100a4	4.33714071	4.61405E-37	3.93207E-35	6.262590515	0.103458656	1	182	86	65	141	73	3233	3023	1370	3274	1087
ENSMUSG00000053199	chr9	Arhgap20	-2.3419606	6.24744E-37	5.29177E-35	4.614641839	0.033528592	-1	536	415	547	884	684	145	121	107	124	162
ENSMUSG00000073684	chr4	2610002J02Rik	2.53890895	6.61608E-37	5.57026E-35	3.111714209	0.031842254	1	33	42	39	43	28	260	245	247	201	228
ENSMUSG00000020634	chr12	Ubxn2a	-3.1419484	7.5093E-37	6.28443E-35	6.153515038	0.061504432	-1	1818	1663	1771	2411	1877	149	296	128	344	259
ENSMUSG00000032122	chr9	Slc37a2	4.59780299	7.95072E-37	6.61424E-35	4.752810667	0.109241143	1	49	31	24	19	32	1214	1159	244	706	981
ENSMUSG00000043157	chr14	Arl11	5.30951478	8.33579E-37	6.89355E-35	2.241095129	0.098351381	1	7	3	3	1	2	162	184	58	157	173
ENSMUSG00000023845	chr17	Lnpep	-2.4877204	8.86028E-37	7.28419E-35	4.156083138	0.036432674	-1	329	375	427	627	496	75	88	72	87	116
ENSMUSG00000027994	chr3	Ccdc109b	4.49969914	1.23406E-36	1.00861E-34	2.171094761	0.077922317	1	6	6	6	8	1	202	149	85	152	97
ENSMUSG00000025877	chr13	Hk3	4.21897316	1.31062E-36	1.06496E-34	3.850172511	0.091292503	1	18	15	17	35	24	538	618	137	380	580
ENSMUSG00000032231	chr9	Anxa2	2.71245694	1.4037E-36	1.13399E-34	7.934364185	0.048360041	1	1026	932	881	1214	792	10700	8205	5331	6571	4211
ENSMUSG00000033685	chr7	Ucp2	3.12166609	1.52186E-36	1.22239E-34	6.818128129	0.061626035	1	267	383	357	419	300	6104	3229	2060	2093	3449
ENSMUSG00000048677	chr7	Tpcn2	3.44519749	1.53313E-36	1.2244E-34	2.843487857	0.056963458	1	23	11	15	24	15	235	276	118	179	253
ENSMUSG00000030220	chr6	Arhgdib	2.68946439	2.07668E-36	1.64907E-34	5.201589083	0.045442385	1	131	135	158	176	131	1552	1119	625	1191	751
ENSMUSG00000020865	chr11	Abcc3	4.03436557	2.37794E-36	1.86708E-34	1.885667086	0.058606356	1	2	4	5	11	8	100	114	112	93	124
ENSMUSG00000024621	chr18	Csf1r	2.37049481	2.37268E-36	1.86708E-34	6.276367813	0.03753366	1	318	380	403	390	358	3166	1999	1556	1684	2337
ENSMUSG00000031838	chr8	Ifi30	2.50468722	2.66522E-36	2.08096E-34	5.795694532	0.04127118	1	247	271	190	253	266	2302	1853	1151	1317	1163
ENSMUSG00000039704	chr15	Lmbrd2	-4.1478825	2.79293E-36	2.16855E-34	2.377238589	0.074078537	-1	134	115	143	185	146	4	10	1	16	13
ENSMUSG00000034786	chr17	Gpsm3	3.33134502	3.87541E-36	2.99241E-34	3.436508854	0.059255867	1	30	32	23	33	25	592	281	210	226	309
ENSMUSG00000025283	chrX	Sat1	2.23238487	3.90362E-36	2.99764E-34	5.167996756	0.032757598	1	165	217	183	210	157	1394	987	658	826	1022
ENSMUSG00000026395	chr1	Ptprc	3.46146537	4.91423E-36	3.74453E-34	3.735501343	0.065631744	1	40	33	44	23	20	422	497	229	291	555
ENSMUSG00000054555	chr7	Adam12	2.75908779	4.92983E-36	3.74453E-34	3.058322038	0.038938481	1	23	40	22	37	34	286	258	201	178	247
ENSMUSG00000023004	chr15	Tuba1b	2.80003979	7.98746E-36	6.0342E-34	6.749410815	0.051935181	1	356	337	401	464	441	3821	3686	3099	3093	1619
ENSMUSG00000052920	chr19	Prkg1	-3.3212619	9.7092E-36	7.29547E-34	3.356180002	0.060089832	-1	179	321	323	391	172	37	20	23	32	39
ENSMUSG00000043091	chr15	Tuba1c	3.17119643	1.01521E-35	7.58744E-34	4.408730243	0.060177648	1	69	71	48	87	42	796	842	406	723	349
ENSMUSG00000103405	chr1	Unspecified	-3.5844369	1.04205E-35	7.74661E-34	2.744151583	0.062855141	-1	154	127	201	242	188	11	12	13	28	18

ENSMUSG00000021457	chr13	Syk	3.13391787	1.35645E-35	1.00306E-33	3.998661718	0.057259285	1	48	38	55	47	50	726	483	223	391	544
ENSMUSG00000001128	chrX	Cfp	3.40613086	1.55783E-35	1.1459E-33	4.632875535	0.06924093	1	52	67	63	61	69	1205	717	380	942	481
ENSMUSG00000047798	chr11	Cd300lf	8.40316406	1.82948E-35	1.33868E-33	1.926582553	0.143670917	1	0	0	1	0	0	99	186	57	177	72
ENSMUSG00000031101	chrX	Sash3	4.26291803	2.68162E-35	1.952E-33	2.550607511	0.082584335	1	3	9	11	16	3	247	199	88	177	185
ENSMUSG00000022500	chr16	Litaf	2.21063713	2.81223E-35	2.03646E-33	5.220899112	0.033146272	1	190	163	181	283	176	1275	1296	652	824	1004
ENSMUSG00000055541	chr7	Lair1	4.91598564	2.92496E-35	2.10718E-33	2.408789204	0.098150397	1	1	7	2	7	7	259	182	86	101	202
ENSMUSG00000040747	chr3	Cd53	3.80653899	3.02071E-35	2.165E-33	4.141902465	0.0822045	1	25	40	43	38	26	520	798	198	478	709
ENSMUSG00000026547	chr1	Tagln2	2.34475606	3.08003E-35	2.19625E-33	6.759500095	0.038305633	1	498	567	523	656	413	4034	3750	2187	2693	2244
ENSMUSG00000034993	chr11	Vat1	2.59386648	5.25209E-35	3.72605E-33	6.424752291	0.046253431	1	328	326	294	503	378	3429	2951	1328	1844	2693
ENSMUSG00000062382	chr13	Gm10116	3.22811245	5.87619E-35	4.14776E-33	3.725869551	0.060507593	1	40	40	28	57	25	553	506	176	349	379
ENSMUSG00000043832	chr6	Clec4a3	3.33652994	6.15885E-35	4.32543E-33	3.015880505	0.057936009	1	20	25	25	14	20	378	205	177	236	193
ENSMUSG00000020143	chr11	Dock2	3.43216841	6.28811E-35	4.39413E-33	3.481100493	0.065588346	1	25	37	27	30	19	396	391	136	369	372
ENSMUSG00000001025	chr3	S100a6	2.89158223	6.965E-35	4.84293E-33	7.009180678	0.056697804	1	509	436	370	610	374	5162	4393	3296	3937	1784
ENSMUSG00000048865	chr1	Arhgap30	3.29070742	7.01376E-35	4.85269E-33	3.662701594	0.062202809	1	27	34	29	43	39	548	451	160	382	342
ENSMUSG00000009687	chr7	Fxyd5	3.54253961	7.14315E-35	4.91786E-33	5.501177893	0.078160126	1	114	83	100	144	94	2269	1921	542	1253	959
ENSMUSG00000073412	chr17	Lst1	4.40736079	8.83342E-35	6.05176E-33	2.879573875	0.092589235	1	8	5	15	8	11	374	196	132	285	146
ENSMUSG00000049723	chr9	Mmp12	7.10505879	1.34662E-34	9.18066E-33	4.555704241	0.212575873	1	6	4	2	9	4	1461	508	132	385	1458
ENSMUSG00000035697	chr10	Hmha1	3.16551878	1.37718E-34	9.34342E-33	3.78249637	0.059241696	1	28	51	43	43	36	658	385	224	438	322
ENSMUSG00000035273	chr5	Hpse	3.31301211	1.96419E-34	1.32616E-32	2.712152428	0.055393414	1	22	20	16	15	13	198	202	120	164	272
ENSMUSG00000101389	chr19	Ms4a4a	4.11128706	4.20747E-34	2.8271E-32	2.993729983	0.085695872	1	7	16	12	10	17	431	166	217	244	156
ENSMUSG00000021238	chr12	Aldh6a1	-2.4512738	4.35085E-34	2.90945E-32	6.435304861	0.042958515	-1	1962	2210	1867	2907	2013	312	488	300	493	587
ENSMUSG00000096764	chr2	Gm21985	-3.3076282	6.64532E-34	4.42262E-32	3.672073162	0.065728266	-1	321	353	330	397	310	15	60	20	43	51
ENSMUSG00000047180	chr1	Neurl3	3.29641563	8.45223E-34	5.5985E-32	3.187635233	0.060973674	1	27	29	27	24	15	380	230	261	142	327
ENSMUSG00000052384	chr16	Nrros	2.79678522	8.58047E-34	5.65664E-32	4.317423651	0.05051808	1	73	86	72	72	64	822	691	292	593	465
ENSMUSG00000063856	chr9	Gpx1	2.15919574	9.39989E-34	6.16774E-32	7.312376915	0.034591806	1	943	853	844	942	731	6182	4537	2924	3701	4140
ENSMUSG00000053687	chr8	Dpep2	6.50329783	1.05488E-33	6.88922E-32	3.60184598	0.180752333	1	7	3	3	5	1	948	363	105	185	417
ENSMUSG00000079419	chr19	Ms4a6c	3.20876127	1.51365E-33	9.83942E-32	3.506240861	0.061515363	1	34	40	29	40	20	455	386	185	410	228
ENSMUSG00000030306	chr6	Tmtc1	-2.0926227	1.54667E-33	1.00075E-31	7.078175042	0.032807754	-1	3401	3163	2852	3248	3483	823	995	683	927	756
ENSMUSG00000033624	chr8	Pdpr	-4.5439288	2.1032E-33	1.35458E-31	5.909230492	0.123688263	-1	1438	1467	1717	2355	1647	27	87	37	164	81
ENSMUSG00000021728	chr13	Emb	3.79560364	2.16182E-33	1.38594E-31	3.459737191	0.082205417	1	25	22	24	20	16	546	378	118	316	329
ENSMUSG00000019122	chr11	Ccl9	5.24846591	2.3165E-33	1.47833E-31	5.803927309	0.153481178	1	33	33	31	59	57	3091	2375	492	2372	708
ENSMUSG00000061086	chr11	Myl4	5.72553141	2.49924E-33	1.5877E-31	7.056350489	0.177485801	1	42	89	74	104	60	4778	2049	9273	1290	3444
ENSMUSG00000025351	chr10	Cd63	2.17944506	2.52765E-33	1.59848E-31	7.692194245	0.03578886	1	1298	1035	933	1376	956	7658	5828	4071	5899	4407
ENSMUSG00000026656	chr1	Fcgr2b	2.83697811	2.93651E-33	1.84868E-31	4.35974591	0.052995005	1	62	87	77	77	66	1042	433	524	396	569
ENSMUSG00000073411	chr17	H2-D1	2.71390973	2.9643E-33	1.85781E-31	8.124594705	0.053549788	1	924	1309	972	1242	1026	11652	6963	5324	5151	11215
ENSMUSG00000026131	chr1	Dst	-2.0379981	3.31168E-33	2.06625E-31	7.804210856	0.031732834	-1	4557	4400	4939	7735	5391	1350	1437	1306	1351	1695
ENSMUSG00000015027	chr8	Galns	2.9947994	3.33925E-33	2.07419E-31	3.30025957	0.053748772	1	35	32	27	56	14	404	291	175	254	302
ENSMUSG00000026728	chr2	Vim	2.19964152	3.47186E-33	2.14702E-31	8.712000994	0.036728038	1	2459	2268	2087	2624	1747	15179	14178	8322	9198	10001
ENSMUSG00000003363	chr7	Pld3	2.99589178	3.49025E-33	2.14889E-31	6.422303514	0.063351946	1	313	231	234	369	282	3340	2528	1595	1273	3948
ENSMUSG00000053040	chr9	Aph1c	4.30314636	4.09822E-33	2.51214E-31	2.285277421	0.084355208	1	5	10	7	6	5	231	142	81	98	194
ENSMUSG00000070354	chr11	Gm21975	3.46905367	4.40933E-33	2.69104E-31	3.228096771	0.069045664	1	12	21	29	25	25	326	342	125	306	294
ENSMUSG00000015745	chr3	Plekho1	1.75586954	4.50778E-33	2.73916E-31	5.504769024	0.022858783	1	347	290	264	377	268	1351	1052	1030	1120	1161
ENSMUSG00000052812	chr12	Atad2b	-3.3999036	4.80994E-33	2.89757E-31	2.646986277	0.062048337	-1	162	145	164	198	171	10	27	6	22	22
ENSMUSG00000087410	chr11	2310065F04Rik	-2.6487193	4.80035E-33	2.89757E-31	6.582017914	0.051219525	-1	2984	2465	2969	2152	1582	461	538	291	479	389
ENSMUSG00000050919	chr13	Zfp366	-5.0565162	5.30873E-33	3.18433E-31	1.082693041	0.073136253	-1	50	43	58	83	61	0	4	3	1	1
ENSMUSG00000028931	chr4	Kcnab2	4.36377945	6.93496E-33	4.14201E-31	2.960550409	0.099499985	1	13	9	10	12	8	405	297	85	250	173
ENSMUSG00000021384	chr13	Susd3	4.97855028	7.94557E-33	4.72542E-31	1.305711584	0.076741851	1	3	4	2	1	0	92	77	55	87	56
ENSMUSG00000022014	chr14	Epsti1	3.55710002	8.6478E-33	5.12126E-31	2.149212672	0.058794649	1	11	13	6	8	11	151	133	91	100	174
ENSMUSG00000033192	chr8	Lpcat2	4.1634542	8.77237E-33	5.17311E-31	1.963475004	0.074690184	1	3	5	7	9	5	173	102	120	67	121
ENSMUSG00000018927	chr11	Ccl6	5.15164901	1.25015E-32	7.34124E-31	6.239350931	0.154017587	1	40	64	60	65	74	3938	3104	789	3516	801
ENSMUSG00000018415	chr11	Gid4	-1.9230961	1.51378E-32	8.8521E-31	6.398085619	0.028597791	-1	2085	1667	1706	2423	2067	574	638	450	631	579
ENSMUSG00000035133	chr12	Arhgap5	-3.4792616	1.66367E-32	9.68813E-31	4.101698767	0.077854973	-1	434	415	429	647	431	20	82	20	55	52
ENSMUSG00000056201	chr19	Cfl1	2.19214063	2.30992E-32	1.33956E-30	7.713828221	0.037322492	1	1109	1107	1030	1462	937	8031	6790	4025	5178	4409
ENSMUSG00000041992	chr12	Rapgef5	-3.8281124	2.48047E-32	1.43252E-30	1.505097416	0.056769137	-1	66	82	70	108	60	7	4	3	8	7
ENSMUSG00000026600	chr1	Soat1	2.68382322	3.10232E-32	1.78428E-30	4.620132086	0.050555257	1	113	84	71	144	85	870	907	328	599	806
ENSMUSG00000029580	chr5	Actb	2.18251539	4.0605E-32	2.3258E-30	9.443841523	0.037539835	1	3675	3375	3236	4795	3720	23551	23090	13049	19451	14723
ENSMUSG00000039496	chr2	Cdnf	-1.9523726	4.40719E-32	2.51407E-30	5.068942443	0.028726263	-1	775	746	746	981	723	165	257	192	258	244
ENSMUSG00000087555	chr2	Gm13997	-4.9378358	4.77547E-32	2.71309E-30	1.222000979	0.079786593	-1	59	49	67	75	73	0	2	1	1	7
ENSMUSG00000022197	chr15	Pdzd2	-1.7527006	4.88083E-32	2.76172E-30	4.889357434	0.022908776	-1	638	667	672	786	623	204	258	211	188	242
ENSMUSG00000041702	chr12	Btbd7	-2.6807306	5.36468E-32	3.02326E-30	3.283041371	0.045252444	-1	185	222	230	355	260	34	35	33	46	64
ENSMUSG00000046223	chr7	Plaur	4.95028725	5.43311E-32	3.04952E-30	3.876189474	0.137075516	1	13	13	5	21	16	984	586	139	312	356
ENSMUSG00000023169	chr15	Slc38a1	2.89508826	6.0651E-32	3.39064E-30	3.002465107	0.050213779	1	26	23	25	44	22	224	331	191	219	166
ENSMUSG00000002603	chr7	Tgfb1	2.31615394	1.11148E-31	6.18886E-30	4.555378722	0.038914438	1	94	117	83	195	104	931	661	495	462	672
ENSMUSG00000025326	chr7	Ube3a	-1.9415073	1.18263E-31	6.5589E-30	4.907130547	0.028615658	-1	669	637	664	927	656	149	252	191	194	218
ENSMUSG00000021242	chr12	Npc2	2.23788423	1.23208E-31	6.80616E-30	7.013428328	0.039512809	1	713	719	586	732	602	5216	3537	2332	2532	4085

ENSMUSG00000037649	chr17	H2-DMa	2.77337264	2.06025E-31	1.12918E-29	3.477226478	0.050226099	1	38	52	28	43	46	515	273	285	250	257
ENSMUSG00000067212	chr17	H2-T23	2.51084679	2.05712E-31	1.12918E-29	5.046841599	0.046840063	1	138	163	148	177	106	1286	871	622	567	1308
ENSMUSG00000025232	chr9	Hexa	2.10126671	2.07644E-31	1.13361E-29	6.697211223	0.035276632	1	616	605	551	665	478	4120	2868	1881	2266	2802
ENSMUSG00000034641	chr11	Cd300ld	3.77064916	2.30946E-31	1.25591E-29	2.951134963	0.082488354	1	12	17	15	17	15	368	229	94	175	312
ENSMUSG00000032508	chr9	Myd88	2.14104189	2.57181E-31	1.39316E-29	3.864179632	0.031403391	1	67	72	76	107	76	574	370	310	333	351
ENSMUSG00000049866	chr1	Arl4c	2.81799981	3.17846E-31	1.71514E-29	3.644520966	0.053338801	1	67	43	39	52	28	569	383	310	258	267
ENSMUSG00000028573	chr4	Fggy	6.31786655	3.76344E-31	2.02299E-29	1.673103147	0.13090401	1	3	0	1	0	1	46	97	144	85	108
ENSMUSG00000011884	chr5	Gltp	2.13434939	4.64298E-31	2.48622E-29	4.727932025	0.034171244	1	124	160	110	191	146	665	750	509	616	984
ENSMUSG00000019947	chr10	Arid5b	-2.6453517	5.52772E-31	2.94868E-29	2.866607826	0.042776344	-1	176	177	151	254	175	19	38	31	30	43
ENSMUSG00000038663	chr7	Fsd2	-1.8770101	6.03172E-31	3.2053E-29	8.277751844	0.029371383	-1	7193	6383	6583	9178	7106	1949	2179	2032	2066	2592
ENSMUSG00000000244	chr7	Tspan32	4.83644291	7.3291E-31	3.87998E-29	1.294589848	0.081155932	1	2	1	3	3	2	105	92	55	63	50
ENSMUSG00000059089	chr1	Fcgr4	5.58787693	8.22288E-31	4.33672E-29	2.419862742	0.139555858	1	3	5	4	2	1	201	133	116	65	328
ENSMUSG00000030844	chr7	Rgs10	2.57180748	8.26263E-31	4.3413E-29	3.686222947	0.045473724	1	53	73	53	56	36	540	379	239	329	313
ENSMUSG00000039879	chr10	Heca	-2.4924617	8.67334E-31	4.54002E-29	3.667141867	0.043228178	-1	294	267	325	413	302	47	60	38	70	96
ENSMUSG00000006360	chr12	Crip1	2.67836843	8.98366E-31	4.68491E-29	6.520774687	0.056302542	1	408	356	318	487	292	4243	3077	1809	2529	1466
ENSMUSG00000040699	chr11	Limd2	2.23427055	9.61387E-31	4.99492E-29	3.580880646	0.034029243	1	72	53	47	90	50	461	269	254	295	327
ENSMUSG00000006095	chr7	Tbcb	1.7362681	1.04027E-30	5.38474E-29	4.733331128	0.023255309	1	198	169	158	231	158	737	714	652	665	548
ENSMUSG00000005087	chr2	Cd44	2.84989596	1.05549E-30	5.44335E-29	5.739988453	0.062528032	1	238	184	186	232	131	2468	2138	810	1202	1187
ENSMUSG00000024074	chr17	Crim1	-1.9870918	1.20565E-30	6.19492E-29	4.38742793	0.02945127	-1	457	563	415	602	446	112	150	114	130	179
ENSMUSG00000031762	chr8	Mt2	6.39128415	1.35409E-30	6.93215E-29	6.477353625	0.22547289	1	37	21	20	43	36	8028	1272	1780	3112	607
ENSMUSG00000062593	chr10	Lilrb4	4.22760706	1.37822E-30	7.02994E-29	3.98776717	0.113590178	1	13	19	27	33	26	671	630	123	614	435
ENSMUSG00000022383	chr15	Ppara	-3.9863381	1.45779E-30	7.40875E-29	2.065177427	0.080889515	-1	64	90	136	186	105	8	7	8	10	6
ENSMUSG00000028108	chr3	Ecm1	2.21370187	1.51791E-30	7.68635E-29	5.28566371	0.039045653	1	190	177	208	301	162	1382	992	1138	627	1111
ENSMUSG00000026355	chr1	Mcm6	3.20019505	1.62013E-30	8.17436E-29	3.848378428	0.070216243	1	50	38	44	34	39	398	676	313	475	232
ENSMUSG00000020120	chr11	Plek	4.07152609	1.85883E-30	9.34496E-29	5.013778255	0.11240216	1	49	44	60	62	52	1341	1762	256	954	745
ENSMUSG00000079293	chr6	Clec7a	4.38070819	2.21677E-30	1.11045E-28	3.540015342	0.117143612	1	23	18	15	7	13	477	282	201	177	688
ENSMUSG00000063142	chr14	Kcnma1	-2.0523391	2.35611E-30	1.17603E-28	4.176401997	0.03118091	-1	391	360	410	645	381	131	110	105	137	86
ENSMUSG00000022439	chr15	Parvg	4.0918349	2.74489E-30	1.36521E-28	2.22773531	0.087584385	1	9	3	4	11	10	207	192	78	125	105
ENSMUSG00000040433	chr9	Zbtb38	-1.6771457	2.86964E-30	1.4222E-28	4.779484755	0.022166413	-1	584	615	648	746	513	220	211	191	194	250
ENSMUSG00000032383	chr9	Ppib	1.83850063	3.57496E-30	1.7655E-28	6.45297905	0.028455993	1	568	569	518	701	498	2929	2478	2049	1896	1871
ENSMUSG00000054958	chr4	Nt5c1a	-4.1673467	4.71308E-30	2.31937E-28	2.549892849	0.098278659	-1	170	128	182	146	178	2	20	4	15	8
ENSMUSG00000029771	chr6	Irf5	2.56205291	4.80784E-30	2.3577E-28	4.390850587	0.049580396	1	71	97	112	126	46	768	671	382	594	520
ENSMUSG00000037321	chr17	Tap1	2.34516586	5.07294E-30	2.479E-28	3.334880474	0.037031426	1	64	43	46	48	41	342	301	222	190	313
ENSMUSG00000021948	chr14	Prkcd	2.23800366	5.49243E-30	2.67464E-28	4.21911814	0.037725913	1	86	92	83	141	84	699	602	295	412	520
ENSMUSG00000002985	chr7	Apoe	3.74362017	5.88581E-30	2.85625E-28	9.536596949	0.104042538	1	1229	1830	1287	1527	1717	37325	13332	17885	9436	37567
ENSMUSG00000079575	chr6	Rbpsuh-rs3	-4.0327226	6.59465E-30	3.18916E-28	1.046590654	0.057970944	-1	54	49	55	65	54	5	1	4	3	5
ENSMUSG00000026796	chr2	Fam129b	2.65880746	7.29744E-30	3.51686E-28	5.809285136	0.056869865	1	227	210	241	260	197	2406	1892	667	1363	1731
ENSMUSG00000098112	chr15	Bin2	4.2499552	7.40471E-30	3.5563E-28	1.549390387	0.07672639	1	4	6	3	4	3	88	118	47	88	91
ENSMUSG00000027533	chr3	Fabp5	3.46663203	9.52167E-30	4.55736E-28	6.012327192	0.090301208	1	165	216	152	152	104	1602	3148	722	2036	2228
ENSMUSG00000085939	chr18	Cd63-ps	2.48586534	9.96756E-30	4.75449E-28	3.74455657	0.044817192	1	79	59	41	71	50	544	405	273	372	258
ENSMUSG00000078771	chr11	Evi2a	2.67333648	1.19264E-29	5.66948E-28	3.571396182	0.050614144	1	39	51	44	52	49	390	365	156	368	394
ENSMUSG00000023927	chr17	Satb1	-1.8621688	1.30786E-29	6.19617E-28	6.009108559	0.029544444	-1	1498	1318	1310	1809	1580	406	443	374	463	579
ENSMUSG00000018507	chr11	Trpv2	3.08692304	1.36024E-29	6.42256E-28	3.211405202	0.064104951	1	24	31	24	34	29	459	283	132	244	238
ENSMUSG00000097328	chr11	Tnfsf12	1.91986851	1.45079E-29	6.82701E-28	4.554272103	0.028942116	1	138	152	119	192	130	610	772	427	526	700
ENSMUSG00000020097	chr10	Sgpl1	1.98439385	1.52127E-29	7.13467E-28	5.467601247	0.032965764	1	274	282	227	339	211	1371	1379	719	1006	1341
ENSMUSG00000026321	chr1	Tnfrsf11a	3.45732001	1.94107E-29	9.07304E-28	2.292653559	0.06811286	1	8	8	14	13	15	170	187	78	147	133
ENSMUSG00000020340	chr11	Cyfip2	3.37648202	2.36389E-29	1.10126E-27	2.449046982	0.068595078	1	11	10	14	25	10	133	210	188	105	150
ENSMUSG00000031146	chrX	Plp2	1.99468435	3.52161E-29	1.63515E-27	5.533192554	0.033779102	1	334	245	252	274	265	1747	1296	1026	1019	993
ENSMUSG00000045763	chr15	Basp1	2.79038723	3.99408E-29	1.84839E-27	3.717754862	0.057263181	1	48	53	26	62	56	462	509	191	375	339
ENSMUSG00000020256	chr10	Aldh1l2	-2.0409811	4.09444E-29	1.88858E-27	3.794104896	0.031155249	-1	394	314	331	325	277	91	108	69	95	77
ENSMUSG00000022372	chr15	Sla	3.73104218	4.43694E-29	2.03314E-27	2.574053622	0.083811351	1	10	16	17	9	7	284	187	86	156	182
ENSMUSG00000032041	chr9	Tirap	-2.1669639	4.42697E-29	2.03314E-27	4.410017688	0.037488335	-1	580	475	532	470	492	124	141	79	115	175
ENSMUSG00000002699	chr11	Lcp2	3.0955861	4.81669E-29	2.19994E-27	2.541389946	0.059177076	1	23	12	10	21	22	233	206	116	136	146
ENSMUSG00000038170	chr3	Pde4dip	-1.8586173	5.2274E-29	2.37974E-27	11.58275831	0.031070407	-1	67210	58528	62485	95228	76535	25956	21801	16821	21385	22941
ENSMUSG00000078453	chr10	Abracl	2.59757542	5.47111E-29	2.4826E-27	3.288489755	0.047644783	1	43	53	34	47	26	361	339	240	225	190
ENSMUSG00000076138	chr9	Gm26377	2.13839376	5.53661E-29	2.50419E-27	6.795803534	0.039775765	1	721	664	594	554	495	3948	3176	2909	2007	2833
ENSMUSG00000032393	chr9	Dpp8	-1.8352555	6.32633E-29	2.85215E-27	7.156634486	0.030011318	-1	3282	3014	2970	4100	3258	997	1030	738	1093	1253
ENSMUSG00000025531	chrX	Chm	-2.3518205	6.59424E-29	2.96338E-27	3.894922441	0.04248187	-1	362	317	346	443	374	67	89	40	104	96
ENSMUSG00000045246	chr8	Kcng4	-2.3037038	7.20814E-29	3.22888E-27	5.361324447	0.044939072	-1	1081	897	1384	953	703	192	240	220	245	224
ENSMUSG00000030793	chr7	Pycard	3.66954942	7.71752E-29	3.44601E-27	3.264908592	0.091271378	1	33	20	14	25	11	425	319	158	383	157
ENSMUSG00000025498	chr7	Irf7	2.87205184	7.91389E-29	3.52244E-27	3.698641898	0.061155112	1	52	37	40	58	43	439	315	301	194	617
ENSMUSG00000031010	chrX	Usp9x	-2.4826868	8.19155E-29	3.63445E-27	6.088020493	0.052431876	-1	1696	1481	1620	2072	1716	202	369	228	432	444
ENSMUSG00000015340	chrX	Cybb	3.16190915	1.10273E-28	4.87715E-27	4.951800048	0.078302799	1	86	96	109	85	78	1618	777	500	481	1276
ENSMUSG00000037966	chr13	Ninj1	1.85267721	1.25141E-28	5.51728E-27	4.475654868	0.027645398	1	162	153	134	140	120	712	638	405	513	583
ENSMUSG00000028859	chr4	Csf3r	4.07373356	1.26748E-28	5.57053E-27	2.183406188	0.094974739	1	6	4	6	17	4	189	113	69	182	128

ENSMUSG00000003283	chr2	Hck	3.84460841	1.29671E-28	5.66713E-27	2.747989647	0.093830879	1	8	13	7	23	13	333	268	99	181	138
ENSMUSG00000025534	chr5	Gusb	2.76441673	1.29757E-28	5.66713E-27	5.939958736	0.064025505	1	197	207	229	312	229	2871	2115	759	1266	1935
ENSMUSG00000032518	chr9	Rpsa	2.03180264	1.38841E-28	6.04497E-27	8.806534315	0.03714642	1	2728	2517	2270	3224	2404	9284	13726	11614	13440	10108
ENSMUSG00000069792	chr11	Wfdc17	3.47237273	1.42225E-28	6.1731E-27	3.830416788	0.087485861	1	33	47	39	27	24	529	463	286	626	200
ENSMUSG00000003882	chr15	Il7r	6.56236585	1.58503E-28	6.85832E-27	2.667649709	0.197321417	1	0	4	2	2	1	216	266	43	113	385
ENSMUSG00000021939	chr14	Ctsb	2.05786671	1.60253E-28	6.91265E-27	10.12432207	0.038216292	1	6084	6645	5711	7951	5874	35805	33696	17047	27901	34344
ENSMUSG00000017697	chr2	Ada	3.56939318	1.783E-28	7.66746E-27	1.922568035	0.067944848	1	7	6	7	6	15	102	103	83	129	129
ENSMUSG00000022575	chr15	Gsdmd	2.29902606	1.86528E-28	7.99667E-27	3.403043851	0.038628311	1	60	47	46	61	48	443	278	219	259	231
ENSMUSG00000090778	chr8	Gm3235	-3.3304516	2.22766E-28	9.52103E-27	1.839413864	0.060236018	-1	103	110	74	119	70	8	10	5	14	14
ENSMUSG00000029304	chr5	Spp1	8.12253691	2.29591E-28	9.78282E-27	9.465840767	0.342817144	1	36	51	107	123	63	27112	64356	1674	11759	13779
ENSMUSG00000005580	chr16	Adcy9	-3.3903763	2.30655E-28	9.7983E-27	4.217546216	0.087276471	-1	484	432	493	571	529	19	53	27	70	93
ENSMUSG00000027366	chr2	Sppl2a	-1.7457504	2.4142E-28	1.02245E-26	6.78029184	0.027744165	-1	2548	2204	2296	3287	2340	840	812	643	794	1046
ENSMUSG00000029994	chr6	Anxa4	1.91912326	2.45701E-28	1.03744E-26	5.254388897	0.032098602	1	280	235	207	284	183	1311	1148	631	865	1019
ENSMUSG00000027712	chr3	Anxa5	2.03433191	2.89373E-28	1.21816E-26	7.098646512	0.037346344	1	666	748	702	1131	788	5062	4450	2678	2822	3192
ENSMUSG00000028630	chr10	Dyrk2	-1.8963623	3.02022E-28	1.26759E-26	4.330331793	0.02931142	-1	476	396	385	532	554	125	131	137	133	164
ENSMUSG00000028238	chr4	Atp6v0d2	7.90730453	3.54169E-28	1.482E-26	4.404711057	0.302897919	1	1	3	0	8	1	923	878	130	151	1464
ENSMUSG00000004591	chr3	Pkn2	-1.8093011	3.64779E-28	1.52183E-26	5.087164823	0.028651556	-1	702	661	712	1061	815	251	295	162	253	274
ENSMUSG00000031444	chr8	F10	7.89670254	4.44897E-28	1.85056E-26	2.886948007	0.253873708	1	0	0	1	3	0	371	457	33	208	136
ENSMUSG00000039891	chr10	Txlnb	-2.10122	4.6353E-28	1.92234E-26	8.242817435	0.040264364	-1	6879	6691	6428	9857	6987	1375	2048	1449	2287	2140
ENSMUSG00000046841	chr10	Ckap4	1.9472222	5.34545E-28	2.2103E-26	5.884872314	0.034098783	1	394	288	339	472	326	2044	1839	1408	1279	1117
ENSMUSG00000021482	chr13	Aaed1	-2.3233443	5.4243E-28	2.23628E-26	3.546989146	0.041696688	-1	329	284	293	329	207	78	73	30	71	66
ENSMUSG00000032089	chr9	Il10ra	3.27010508	6.50462E-28	2.67378E-26	3.392109017	0.077976464	1	22	40	36	20	23	518	281	215	177	369
ENSMUSG00000049037	chr6	Clec4a1	3.0811245	6.64547E-28	2.72367E-26	3.083882494	0.067415012	1	24	35	25	23	22	432	191	150	244	217
ENSMUSG00000030654	chr7	Arl6ip1	1.79106717	7.1865E-28	2.9368E-26	4.95861016	0.028037625	1	169	229	198	216	212	801	982	659	736	748
ENSMUSG00000024644	chr18	Cndp2	2.1851719	7.46364E-28	3.03601E-26	5.703562379	0.042558777	1	279	274	242	343	260	1953	1577	793	1617	1090
ENSMUSG00000042284	chr13	Itga1	-1.9221299	7.47272E-28	3.03601E-26	3.681989939	0.028470856	-1	299	278	304	418	218	105	90	89	69	82
ENSMUSG00000001751	chr11	Naglu	2.27780622	7.51709E-28	3.04518E-26	3.906855958	0.041366359	1	93	78	65	89	54	556	419	278	273	515
ENSMUSG00000026384	chr1	Ptpn4	-2.6193623	7.70702E-28	3.1131E-26	4.759545153	0.057568626	-1	424	503	666	1197	735	113	151	86	97	174
ENSMUSG00000070034	chr1	Sp110	2.39130673	7.76982E-28	3.12942E-26	2.888607006	0.039656396	1	29	29	36	52	28	259	190	140	182	233
ENSMUSG00000102627	chr7	Snurf	-1.8067163	8.0288E-28	3.22444E-26	3.875108501	0.025721156	-1	338	294	293	466	314	128	117	71	101	116
ENSMUSG00000027639	chr2	Samhd1	1.62775619	8.45947E-28	3.38767E-26	5.25346431	0.023597101	1	284	278	217	378	240	1089	992	709	896	1032
ENSMUSG00000031662	chr8	Snx20	4.09312607	8.74945E-28	3.49378E-26	1.895138283	0.09228254	1	7	2	7	9	4	169	138	68	111	69
ENSMUSG00000026932	chr2	Nacc2	-1.6763439	9.07196E-28	3.61224E-26	5.458669648	0.025354797	-1	990	929	960	1121	962	397	295	288	376	354
ENSMUSG00000030144	chr6	Clec4d	6.66097428	1.03468E-27	4.10816E-26	3.234693208	0.225384009	1	2	5	2	4	0	477	475	41	356	178
ENSMUSG00000022952	chr16	Runx1	2.71270934	1.08288E-27	4.28736E-26	3.492421588	0.056448416	1	57	50	32	49	31	410	377	361	228	197
ENSMUSG00000024659	chr19	Anxa1	2.5551235	1.10513E-27	4.36309E-26	6.329567619	0.057797486	1	349	357	345	435	259	3117	2887	974	1835	2625
ENSMUSG00000021091	chr12	Serpina3n	3.73962985	1.28287E-27	5.05053E-26	3.92652526	0.103846592	1	25	38	26	31	34	843	420	407	486	149
ENSMUSG00000002222	chr6	Rmnd5a	-1.7037083	1.34957E-27	5.29821E-26	7.171005123	0.027380797	-1	3385	3103	2841	4161	3004	1103	1132	862	1076	1369
ENSMUSG00000054008	chr18	Ndst1	-1.8824719	1.42246E-27	5.56872E-26	5.840930913	0.032493919	-1	1169	1182	1315	1808	1268	323	431	310	410	519
ENSMUSG00000098364	chr4	Gm27646	-2.3495486	1.62436E-27	6.34137E-26	3.998022771	0.045305743	-1	305	344	352	576	419	64	65	72	105	117
ENSMUSG00000030148	chr6	Clec4a2	3.86576266	1.63656E-27	6.37118E-26	3.164733858	0.104199341	1	20	22	19	15	7	505	239	111	298	220
ENSMUSG00000056529	chr4	Ptafr	2.92240938	1.69942E-27	6.59752E-26	3.945838169	0.067734584	1	41	73	47	36	61	628	552	241	322	497
ENSMUSG00000001281	chr15	Itgb7	4.19273218	1.72539E-27	6.67978E-26	2.591541277	0.111355888	1	7	12	9	13	4	273	302	82	147	120
ENSMUSG00000000305	chr2	Cdh4	-3.5934618	2.12399E-27	8.1825E-26	3.500853448	0.096109497	-1	454	360	258	149	288	31	33	19	40	17
ENSMUSG00000025355	chr10	Mmp19	3.36986655	2.12525E-27	8.1825E-26	4.604992649	0.090920649	1	66	69	64	57	57	1406	933	303	410	664
ENSMUSG00000051236	chr10	Msrb3	-1.7554153	2.41631E-27	9.27757E-26	7.323260925	0.029331099	-1	3968	3513	3404	4128	3347	1093	1349	930	1216	1391
ENSMUSG00000021188	chr12	Trip11	-1.6818211	2.43757E-27	9.33357E-26	4.920712814	0.025314456	-1	596	565	704	942	643	226	262	187	236	262
ENSMUSG00000050721	chr9	Plekho2	2.03293789	3.04365E-27	1.16224E-25	5.066115907	0.037267512	1	169	174	222	247	164	1012	1133	514	750	1021
ENSMUSG00000020657	chr12	Dnajc27	-1.6503529	3.21955E-27	1.22606E-25	5.907023991	0.025506593	-1	1248	1318	1325	1681	1207	428	549	418	476	488
ENSMUSG00000002992	chr7	Apoc2	6.1237696	3.75657E-27	1.42668E-25	1.71881737	0.157771128	1	1	4	0	1	0	159	108	57	141	42
ENSMUSG00000090290	chr8	Gm17296	-2.8542588	4.50315E-27	1.70558E-25	2.510539517	0.056457779	-1	117	103	144	210	165	19	30	14	24	24
ENSMUSG00000078970	chr11	Wdr92	-1.8231053	4.52278E-27	1.70839E-25	5.350419115	0.03069884	-1	956	899	796	1127	952	237	337	219	333	336
ENSMUSG00000030218	chr6	Mgp	2.81538264	4.69409E-27	1.76832E-25	7.073480239	0.070865684	1	414	558	398	612	511	6529	5031	3427	1878	2721
ENSMUSG00000063171	chr6	Rps4l	3.11683275	5.21887E-27	1.96073E-25	2.633870557	0.068709978	1	15	21	9	36	14	127	178	208	158	207
ENSMUSG00000030789	chr7	Itgax	7.22665109	6.12968E-27	2.29674E-25	4.554154881	0.288060931	1	5	8	0	8	2	1475	636	237	125	1478
ENSMUSG00000030276	chr6	Ttll3	2.28092599	6.34671E-27	2.3717E-25	5.200163223	0.047327723	1	233	168	167	201	160	1681	994	763	934	651
ENSMUSG00000000058	chr6	Cav2	-1.8925853	6.36949E-27	2.37386E-25	4.741861513	0.03192346	-1	534	624	657	846	488	165	200	130	191	240
ENSMUSG00000001555	chr11	Fkbp10	1.79638725	7.90727E-27	2.93915E-25	5.282415403	0.029968245	1	294	216	225	316	244	1388	940	988	755	875
ENSMUSG00000071203	chr13	Naip5	3.8416491	8.36624E-27	3.1015E-25	1.235675893	0.067688377	1	6	2	3	7	3	96	70	45	64	64
ENSMUSG00000033880	chr11	Lgals3bp	2.13558896	1.04363E-26	3.85868E-25	5.443573049	0.04241712	1	220	245	189	312	237	1323	1048	1115	676	1650
ENSMUSG00000021624	chr13	Cd180	4.72519304	1.07083E-26	3.93841E-25	2.58597538	0.138957408	1	2	6	8	8	7	112	296	63	220	231
ENSMUSG00000022584	chr15	Ly6c2	5.52466304	1.07003E-26	3.93841E-25	2.046575005	0.156663153	1	3	2	3	3	1	216	173	83	132	37
ENSMUSG00000022292	chr15	Rrm2b	-2.012866	1.32991E-26	4.87844E-25	3.746962959	0.033630833	-1	311	296	290	441	269	64	97	65	87	119
ENSMUSG00000024696	chr19	Lpxn	4.34025564	1.37158E-26	5.01813E-25	2.766827278	0.124789283	1	11	13	14	4	3	328	252	80	229	161
ENSMUSG00000050022	chr5	Amz1	3.88490138	1.43769E-26	5.24625E-25	1.856581485	0.08783774	1	9	7	4	6	6	188	106	57	87	101

ENSMUSG00000030830	chr7	Itgal	3.51464037	1.57673E-26	5.73865E-25	1.735964516	0.071485217	1	3	11	7	14	3	120	117	85	78	79
ENSMUSG00000028402	chr4	Mpdz	-1.9928316	1.66719E-26	6.05213E-25	6.089674245	0.038040259	-1	1308	1257	1473	2600	1595	358	505	397	443	520
ENSMUSG00000030761	chr7	Myo7a	2.268176	1.77878E-26	6.44049E-25	2.861768365	0.037509533	1	41	32	26	43	40	196	238	166	190	172
ENSMUSG00000026812	chr2	Tsc1	-1.6093904	1.79176E-26	6.47072E-25	5.118562619	0.02426718	-1	770	625	680	959	857	317	265	229	290	299
ENSMUSG00000028780	chr5	Sema3c	-1.8639216	2.03569E-26	7.33269E-25	5.845253193	0.03342668	-1	1416	1189	1180	1409	1469	355	455	299	383	534
ENSMUSG00000030263	chr6	Lrmp	3.41855099	2.17599E-26	7.81792E-25	2.057088058	0.072970162	1	9	12	11	9	9	201	116	71	114	104
ENSMUSG00000041515	chr8	Irf8	1.90006744	2.44184E-26	8.75054E-25	3.737908293	0.029808964	1	84	67	80	110	76	431	357	258	258	413
ENSMUSG00000022969	chr16	Il10rb	1.92892204	2.45E-26	8.75734E-25	4.446326688	0.033234714	1	126	128	130	186	106	735	705	351	477	569
ENSMUSG00000062901	chr16	Klhl24	-2.5251187	2.67987E-26	9.55457E-25	6.617032748	0.059975091	-1	2207	2240	2171	3532	2417	284	431	381	457	812
ENSMUSG00000042759	chr7	Apobr	3.18577402	3.22614E-26	1.14729E-24	2.643625135	0.073374483	1	17	19	17	20	16	244	223	72	183	187
ENSMUSG00000034801	chr12	Sos2	-1.9266051	3.25595E-26	1.15495E-24	5.413139126	0.035543313	-1	882	921	902	1355	985	224	335	246	238	404
ENSMUSG00000031264	chrX	Btk	4.18876294	3.65272E-26	1.29241E-24	2.491679519	0.114987894	1	8	6	11	6	10	303	198	72	184	103
ENSMUSG00000037818	chr3	3110057O12Rik	-2.0368347	4.07445E-26	1.43799E-24	4.09515999	0.036485876	-1	311	384	381	711	298	108	108	102	106	119
ENSMUSG00000047810	chr19	Ccdc88b	2.91306633	4.12683E-26	1.45281E-24	2.057491206	0.053499756	1	19	10	18	12	10	155	115	90	109	112
ENSMUSG00000056394	chr7	Lig1	2.5980521	4.35627E-26	1.52973E-24	3.195069682	0.053620677	1	38	35	40	42	34	301	315	243	264	136
ENSMUSG00000006589	chr8	Aprt	2.35827605	4.45324E-26	1.55986E-24	5.225506358	0.05226439	1	184	168	162	230	165	1625	1198	589	1104	648
ENSMUSG00000053158	chr7	Fes	2.35498467	4.67147E-26	1.63221E-24	3.764848254	0.047399394	1	71	64	59	81	53	594	387	201	364	320
ENSMUSG00000087107	chr11	AI662270	4.81534123	4.76466E-26	1.66062E-24	2.440459717	0.144171625	1	3	3	10	5	5	216	220	63	247	89
ENSMUSG00000084516	chr2	Mir1902	-2.4575636	5.09319E-26	1.77071E-24	3.050451989	0.047760703	-1	202	183	175	282	199	22	49	34	40	60
ENSMUSG00000047045	chrX	Tmem164	1.82137411	5.25648E-26	1.82294E-24	4.174351753	0.029146202	1	125	114	116	128	103	632	516	325	390	442
ENSMUSG00000029810	chr6	Tmem176b	2.5007195	5.45954E-26	1.88868E-24	5.844265265	0.05912675	1	249	258	233	285	251	2586	1258	1921	809	1445
ENSMUSG00000074519	chr2	Etohi1	-2.7311404	6.38549E-26	2.20355E-24	2.161611565	0.049889315	-1	119	104	104	157	89	13	29	15	19	17
ENSMUSG00000061393	chr9	Acvr2b	-2.7980347	7.12916E-26	2.45412E-24	1.894934725	0.048366407	-1	82	94	100	103	91	17	12	17	12	16
ENSMUSG00000027365	chr2	Trpm7	-1.889538	7.42881E-26	2.55098E-24	5.141738001	0.034452964	-1	808	776	855	1077	638	208	264	164	247	343
ENSMUSG00000045165	chr7	AI467606	3.02829878	1.07809E-25	3.693E-24	2.170071116	0.061895596	1	14	14	13	16	13	206	140	100	88	106
ENSMUSG00000033467	chr5	Crlf2	2.35755091	1.10736E-25	3.78398E-24	3.14719731	0.044641196	1	45	41	40	48	37	328	204	210	151	309
ENSMUSG00000033278	chr17	Ptprm	-1.7908918	1.12957E-25	3.85045E-24	4.923710175	0.03096621	-1	554	651	652	1045	637	303	199	184	168	265
ENSMUSG00000062210	chr18	Tnfaip8	2.01193508	1.18377E-25	4.0254E-24	3.329118598	0.03301673	1	52	55	53	89	47	331	295	178	236	268
ENSMUSG00000006585	chr8	Cdt1	3.12838821	1.20467E-25	4.08653E-24	2.487270656	0.071190592	1	13	13	20	23	14	244	197	103	160	103
ENSMUSG00000029470	chr5	P2rx4	2.71053627	1.29225E-25	4.37299E-24	4.299475473	0.065677216	1	105	85	69	84	43	828	513	302	387	796
ENSMUSG00000047419	chr13	Cmya5	-1.8362828	1.31037E-25	4.42362E-24	10.48389338	0.034652899	-1	30392	27662	27617	46993	35490	10311	10082	7775	10866	12251
ENSMUSG00000021589	chr13	Rhobtb3	-1.7412962	1.36969E-25	4.61271E-24	5.019311917	0.029492749	-1	716	570	579	1098	794	295	258	186	202	285
ENSMUSG00000032436	chr9	Cmtm7	2.17530377	1.37923E-25	4.62727E-24	3.839716597	0.041593496	1	108	51	61	92	72	517	393	313	394	286
ENSMUSG00000036820	chr17	Amdhd2	2.2038586	1.38063E-25	4.62727E-24	3.672051593	0.041780012	1	81	76	60	67	49	362	418	233	403	276
ENSMUSG00000044308	chr2	Ubr3	-2.0028206	1.50713E-25	5.03915E-24	7.80774151	0.040633385	-1	5255	4581	4722	7033	5264	1124	1600	1047	1532	2004
ENSMUSG00000057948	chr11	Unc13d	4.18602593	1.55971E-25	5.19883E-24	1.178858591	0.083561958	1	3	1	4	7	1	103	57	44	63	63
ENSMUSG00000090231	chr17	Cfb	3.19631611	1.56233E-25	5.19883E-24	4.133497159	0.088093377	1	28	63	42	70	52	987	283	483	306	548
ENSMUSG00000032661	chr5	Oas3	5.24570568	1.63046E-25	5.41267E-24	1.393919886	0.13372185	1	1	0	1	5	2	98	100	48	34	119
ENSMUSG00000047497	chr15	Adamts12	-2.9660352	1.70064E-25	5.63227E-24	3.035006626	0.071088269	-1	209	220	203	197	229	13	43	18	43	32
ENSMUSG00000042129	chr6	Rassf4	2.26610106	1.71907E-25	5.67985E-24	4.167838068	0.046547374	1	102	89	79	103	83	790	438	268	398	564
ENSMUSG00000103779	chr17	RP24-490B17.7	-2.5027803	1.76017E-25	5.80193E-24	2.271867296	0.043491858	-1	120	115	113	127	122	26	24	14	28	24
ENSMUSG00000029007	chr4	Agtrap	2.29434431	1.78956E-25	5.88491E-24	4.14642316	0.047737392	1	73	82	83	122	85	321	459	629	392	548
ENSMUSG00000033863	chr19	Klf9	-2.6040412	1.99748E-25	6.55323E-24	5.902617787	0.065346998	-1	1342	1483	1487	1888	1445	146	353	162	304	412
ENSMUSG00000031165	chrX	Was	3.36647027	2.04927E-25	6.70741E-24	2.257579988	0.078694513	1	8	17	6	13	16	196	164	74	140	122
ENSMUSG00000066026	chr4	Dhrs3	2.07842319	2.18327E-25	7.12929E-24	5.402831296	0.042555546	1	227	232	166	327	259	1677	1196	733	785	1278
ENSMUSG00000043740	chr17	B430306N03Rik	5.40123333	2.30735E-25	7.51692E-24	1.562762781	0.143821093	1	2	1	1	2	3	92	146	29	65	120
ENSMUSG00000021068	chr12	Nin	-1.5350171	2.43487E-25	7.9139E-24	5.277304409	0.023348444	-1	813	784	767	1089	845	334	341	250	309	393
ENSMUSG00000037731	chr4	Themis2	2.58289214	2.68075E-25	8.69283E-24	2.767402065	0.051570527	1	16	36	29	35	25	204	200	126	163	245
ENSMUSG00000046230	chr19	Vps13a	-1.9517142	2.7715E-25	8.96633E-24	3.677202691	0.033128535	-1	285	276	294	392	263	61	110	79	94	79
ENSMUSG00000091562	chr16	Gm9581	-4.3956044	2.89427E-25	9.34187E-24	1.789332067	0.117342611	-1	57	82	124	117	97	0	4	5	12	3
ENSMUSG00000028053	chr3	Ash1l	-1.9248875	2.91244E-25	9.37886E-24	5.333075359	0.036912738	-1	800	766	914	1361	943	265	299	184	239	392
ENSMUSG00000000278	chr11	Scpep1	1.76707893	3.11594E-25	1.00111E-23	5.22839273	0.03097248	1	234	284	211	280	249	1146	1114	621	795	1091
ENSMUSG00000078763	chr11	Slfn1	5.68547934	3.56899E-25	1.14404E-23	1.076591212	0.13523495	1	0	2	0	2	1	54	80	26	95	58
ENSMUSG00000035004	chr7	Igsf6	3.31029605	3.96986E-25	1.26963E-23	2.42683152	0.080769762	1	17	10	11	19	14	168	202	72	116	227
ENSMUSG00000028832	chr4	Stmn1	2.59387131	4.11857E-25	1.31418E-23	3.764074511	0.059610705	1	60	77	51	54	40	323	548	397	360	239
ENSMUSG00000027022	chr2	Xirp2	-1.7131156	4.26897E-25	1.35907E-23	10.32257305	0.031052315	-1	28748	24149	26973	38005	28953	9930	11577	8200	10191	8975
ENSMUSG00000002897	chr6	Il17ra	2.5667443	4.4732E-25	1.42085E-23	3.246866773	0.055697918	1	24	42	33	56	46	400	282	204	254	176
ENSMUSG00000079523	chr6	Tmsb10	3.20602451	4.71627E-25	1.49466E-23	6.985398941	0.096484794	1	450	354	374	389	271	4645	3847	6194	1918	1842
ENSMUSG00000052688	chr1	5430435G22Rik	2.89794994	4.74665E-25	1.50089E-23	4.253545434	0.075846441	1	64	82	60	61	62	492	799	210	686	553
ENSMUSG00000043263	chr1	Pyhin1	5.72043777	4.78861E-25	1.51074E-23	1.325196157	0.150948949	1	0	0	1	3	2	31	120	56	71	97
ENSMUSG00000041959	chr3	S100a10	2.11165446	5.15233E-25	1.62182E-23	6.147450347	0.045201637	1	399	381	384	455	357	2443	2235	1434	2196	1104
ENSMUSG00000028414	chr4	Fktn	-1.6000893	5.36286E-25	1.6843E-23	4.205171257	0.023433216	-1	360	382	411	557	358	146	168	125	141	164
ENSMUSG00000001131	chrX	Timp1	5.14296369	5.78914E-25	1.8141E-23	5.558871184	0.203299951	1	34	36	33	68	26	3425	1216	1022	1736	208
ENSMUSG00000052336	chr9	Cx3cr1	3.4314152	6.57388E-25	2.0554E-23	2.877098074	0.093563387	1	10	10	23	35	14	368	221	217	145	134
ENSMUSG00000045594	chr9	Glb1	2.18355797	6.64037E-25	2.07156E-23	3.41289831	0.041317993	1	75	49	56	72	32	242	326	268	236	331

ENSMUSG00000038451	chr6	Spsb2	2.93916551	6.81728E-25	2.12201E-23	2.999991854	0.070412883	1	42	22	29	21	19	358	230	223	186	143
ENSMUSG00000055639	chr14	Dach1	-2.4421938	7.23262E-25	2.24629E-23	2.300950893	0.043171326	-1	133	121	106	135	113	26	24	17	20	36
ENSMUSG00000028673	chr4	Fuca1	1.51616771	7.41944E-25	2.2992E-23	5.208840824	0.02307267	1	309	287	254	304	262	952	981	688	865	989
ENSMUSG00000047036	chr9	Zfp445	-2.8492019	7.70546E-25	2.38255E-23	3.309975724	0.070087717	-1	257	235	261	292	238	21	44	16	57	57
ENSMUSG00000008475	chr1	Arpc5	2.24806676	7.72292E-25	2.38268E-23	5.88861512	0.051044038	1	294	361	300	367	211	2232	1933	866	1787	1250
ENSMUSG00000056413	chr5	Adap1	2.80282285	7.89335E-25	2.4299E-23	2.650624108	0.060702049	1	22	24	20	17	29	247	211	109	171	145
ENSMUSG00000025188	chr19	Hps1	2.98610567	9.57197E-25	2.94017E-23	1.983411504	0.058969254	1	18	8	17	7	12	130	116	100	104	101
ENSMUSG00000046785	chr9	Epm2aip1	-1.665005	1.08411E-24	3.3227E-23	5.730855166	0.02878413	-1	1319	1100	1130	1339	1103	361	433	338	408	536
ENSMUSG00000031903	chr8	Pla2g15	2.21663174	1.24431E-24	3.80535E-23	4.437660143	0.047180343	1	97	145	104	118	99	954	529	415	390	658
ENSMUSG00000103866	chr18	Setbp1	-4.2737664	1.41844E-24	4.32842E-23	0.735712927	0.077684665	-1	43	39	39	50	51	1	2	0	6	3
ENSMUSG00000103319	chrX	AC055766.1	-4.8653302	1.43921E-24	4.38221E-23	0.397641666	0.079245091	-1	39	42	32	33	29	0	1	1	1	3
ENSMUSG00000004530	chr5	Coro1c	1.90773676	1.58197E-24	4.796E-23	5.639330589	0.03769432	1	275	284	281	424	303	1892	1494	817	1202	1092
ENSMUSG00000004849	chr5	Ap1s1	1.84685785	1.58063E-24	4.796E-23	5.331682185	0.035055124	1	340	239	222	278	220	1349	1088	898	1069	738
ENSMUSG00000020399	chr11	Havcr2	5.49979314	1.633E-24	4.94001E-23	0.897124208	0.124209578	1	0	0	0	4	1	96	60	28	50	43
ENSMUSG00000032353	chr9	Tmed3	1.69437307	1.66408E-24	5.02315E-23	5.391558886	0.029663872	1	284	308	249	378	259	1555	988	926	874	924
ENSMUSG00000034854	chr10	Mfsd12	2.82429206	1.67183E-24	5.03566E-23	4.41385265	0.074784556	1	77	78	88	83	61	699	717	226	472	973
ENSMUSG00000013033	chr8	Lphn1	-1.6732103	1.74078E-24	5.23207E-23	5.487918991	0.029127046	-1	835	825	932	1457	1072	371	369	302	298	412
ENSMUSG00000024781	chr19	Lipa	2.51163012	1.74637E-24	5.2376E-23	5.532535718	0.063324462	1	199	214	205	248	160	1201	1498	605	1020	2178
ENSMUSG00000074677	chr3	Sirpb1c	7.43570575	1.85101E-24	5.53955E-23	1.025091347	0.179126318	1	0	0	1	0	0	113	67	17	69	44
ENSMUSG00000029082	chr5	Bst1	5.60826278	1.97176E-24	5.88831E-23	1.438573421	0.152856693	1	3	0	2	1	1	125	122	25	75	68
ENSMUSG00000018761	chr11	Mpdu1	1.80838281	2.06938E-24	6.16667E-23	3.976137763	0.030280965	1	106	129	91	101	85	504	430	334	375	346
ENSMUSG00000031765	chr8	Mt1	4.64114524	2.4774E-24	7.3512E-23	6.299362901	0.180349182	1	57	92	90	144	74	6621	1401	1389	2586	734
ENSMUSG00000073490	chr1	AI607873	2.59652577	2.47644E-24	7.3512E-23	3.499390999	0.060556124	1	34	38	56	52	53	420	370	143	305	348
ENSMUSG00000021690	chr13	Jmy	-1.5358589	2.54077E-24	7.51605E-23	4.939023298	0.024044896	-1	594	605	654	933	625	239	289	213	240	301
ENSMUSG00000022139	chr14	Mbnl2	-1.879944	2.54371E-24	7.51605E-23	6.878396847	0.037775153	-1	2488	2242	2529	3986	2673	654	1036	603	880	926
ENSMUSG00000004798	chr11	Ulk2	-1.5693124	2.61242E-24	7.70277E-23	6.895518052	0.026705318	-1	2595	2275	2363	3414	2662	956	1056	788	970	1135
ENSMUSG00000027035	chr2	Cers6	2.5959158	2.85062E-24	8.38742E-23	2.717739228	0.054436946	1	25	23	20	32	35	278	204	129	138	163
ENSMUSG00000047141	chr16	Zfp654	-1.8786233	3.57955E-24	1.051E-22	3.397428422	0.031233771	-1	235	228	217	350	207	65	85	51	76	88
ENSMUSG00000036617	chr2	Etl4	-1.8277257	3.6535E-24	1.07047E-22	5.467421844	0.035164766	-1	911	1040	902	1433	894	286	289	226	340	447
ENSMUSG00000025920	chr1	Stau2	-1.4816881	3.86981E-24	1.13148E-22	5.083277525	0.022704302	-1	724	670	689	1069	602	357	285	256	297	264
ENSMUSG00000038034	chr1	Igsf8	2.07853991	4.1115E-24	1.19963E-22	4.672958132	0.043295242	1	101	154	120	199	152	1087	711	495	524	584
ENSMUSG00000020733	chr11	Slc9a3r1	1.91798572	4.68212E-24	1.36044E-22	3.477761641	0.032892739	1	70	59	76	76	60	323	316	184	283	323
ENSMUSG00000037416	chr18	Dmxl1	-2.2479612	4.67606E-24	1.36044E-22	4.940545894	0.051253175	-1	768	657	695	921	733	99	191	116	201	260
ENSMUSG00000034330	chr8	Plcg2	3.22461115	5.5446E-24	1.6077E-22	2.609875138	0.084252009	1	15	15	12	27	17	279	225	81	180	126
ENSMUSG00000047230	chrX	Cldn2	4.60582078	5.60243E-24	1.62111E-22	1.646058399	0.129034913	1	4	4	3	4	2	99	48	162	64	87
ENSMUSG00000020091	chr10	Eif4ebp2	-2.1018929	5.80279E-24	1.67561E-22	5.137421143	0.046127238	-1	733	776	699	1031	997	171	251	123	260	280
ENSMUSG00000044734	chr13	Serpinb1a	2.35125281	6.42821E-24	1.85239E-22	5.339067465	0.057314432	1	281	136	172	232	168	1484	910	1037	1399	663
ENSMUSG00000026360	chr1	Rgs2	2.09959814	6.72347E-24	1.93348E-22	4.295742134	0.043533587	1	137	123	127	93	63	568	617	384	480	545
ENSMUSG00000042460	chr6	C1galt1	-2.4432995	6.74134E-24	1.93464E-22	2.657391865	0.049782959	-1	121	135	159	231	144	34	41	17	36	30
ENSMUSG00000041801	chr1	Phlda3	2.67636348	7.23363E-24	2.07166E-22	6.105066407	0.073708309	1	200	267	183	574	216	1131	2279	2194	1939	2024
ENSMUSG00000026571	chr1	Dcaf6	-1.7109741	7.25896E-24	2.07467E-22	7.854572771	0.032475439	-1	5076	4626	4994	7207	4710	2416	1700	1208	1717	1899
ENSMUSG00000040616	chr4	Tmem51	2.2780332	7.34267E-24	2.09431E-22	2.763417372	0.04252889	1	18	35	36	42	37	214	189	151	162	186
ENSMUSG00000024477	chr18	Pggt1b	-2.3318647	8.00236E-24	2.27782E-22	2.802472646	0.046121021	-1	155	141	161	242	164	31	38	22	47	48
ENSMUSG00000020620	chr11	Abca8b	-1.5257869	8.37099E-24	2.37791E-22	4.769086988	0.024050915	-1	551	646	542	644	602	262	223	210	243	205
ENSMUSG00000027784	chr3	Ppm1l	-1.6619453	9.18291E-24	2.60325E-22	7.206447908	0.030693648	-1	3273	3056	3101	3909	3340	957	1188	1068	1141	1414
ENSMUSG00000022102	chr14	Dok2	3.91927807	9.55147E-24	2.70225E-22	3.771856471	0.132852605	1	21	20	28	27	27	710	526	144	557	163
ENSMUSG00000004626	chr8	Stxbp2	3.215592	9.62675E-24	2.71805E-22	2.958048267	0.088563967	1	18	27	16	34	16	341	283	86	252	178
ENSMUSG00000026979	chr2	Psd4	4.17950224	1.01014E-23	2.84631E-22	2.45928815	0.133061895	1	3	10	6	18	5	281	196	53	170	143
ENSMUSG00000021745	chr14	Ptprg	-1.6121744	1.01335E-23	2.84962E-22	4.485008647	0.026125287	-1	477	431	444	775	418	167	203	154	190	182
ENSMUSG00000060147	chr13	Serpinb6a	1.94480114	1.02196E-23	2.86805E-22	7.481408076	0.041558428	1	1351	1098	1017	1097	894	4101	3489	4564	4715	6171
ENSMUSG00000019942	chr10	Cdk1	2.94677662	1.02721E-23	2.877E-22	3.523119702	0.079245859	1	54	43	39	24	30	410	489	270	305	171
ENSMUSG00000025019	chr19	Lcor	-3.0960745	1.08329E-23	3.02801E-22	2.003132985	0.071046641	-1	68	90	107	130	126	12	10	16	18	10
ENSMUSG00000031304	chrX	Il2rg	2.57654449	1.11114E-23	3.09965E-22	3.466125707	0.061514794	1	47	51	49	57	29	554	332	214	208	246
ENSMUSG00000044827	chr5	Tlr1	5.32198607	1.11415E-23	3.10187E-22	1.727189585	0.163768649	1	0	3	3	4	1	30	135	104	128	97
ENSMUSG00000023031	chr15	Cela1	5.57634418	1.34422E-23	3.73496E-22	0.715934297	0.123320296	1	0	1	0	2	1	70	50	23	64	33
ENSMUSG00000021182	chr12	Ccdc88c	-2.2040133	1.3617E-23	3.77601E-22	5.320925048	0.051548876	-1	1037	829	890	1055	1045	131	218	200	271	332
ENSMUSG00000029570	chr5	Lfng	2.07878396	1.47349E-23	4.07589E-22	3.638750962	0.040865337	1	52	79	46	86	87	450	336	265	304	281
ENSMUSG00000029622	chr5	Arpc1b	1.8080422	1.47567E-23	4.07589E-22	6.126986616	0.035879522	1	433	466	426	545	435	2271	2094	1103	1957	1510
ENSMUSG00000029919	chr6	Hpgds	2.7876521	1.49149E-23	4.11146E-22	2.571114687	0.063806154	1	25	23	30	16	13	230	144	110	149	201
ENSMUSG00000070031	chr1	Sp140	3.05664064	1.67044E-23	4.59568E-22	1.895976065	0.067387245	1	7	11	9	19	11	148	118	70	71	120
ENSMUSG00000029401	chr5	Rilpl2	2.43576823	1.77313E-23	4.86862E-22	3.521984549	0.055907891	1	55	54	52	53	47	389	457	153	249	338
ENSMUSG00000031506	chr1	Ptpn7	3.9639089	1.83245E-23	5.02164E-22	2.209366647	0.11653195	1	7	12	9	6	5	203	186	64	164	75
ENSMUSG00000053332	chr1	Gas5	1.73025243	1.94845E-23	5.32906E-22	5.116689339	0.032188467	1	293	234	216	284	170	1032	977	781	917	629
ENSMUSG00000037111	chr3	Setd7	-1.7910491	1.96636E-23	5.36754E-22	8.247814774	0.036194991	-1	8001	7052	5978	7298	6627	1850	2599	1730	2237	2711
ENSMUSG00000023827	chr17	Agpat4	2.22556618	1.99334E-23	5.43059E-22	3.452231485	0.046425244	1	55	43	67	71	47	406	374	257	212	215

ENSMUSG00000044461	chr14	Shisa2	-1.630335	2.17552E-23	5.91538E-22	6.707650816	0.02993244	-1	2557	2095	2211	2501	2331	999	898	573	846	879
ENSMUSG00000071547	chr14	Nt5dc2	2.27029853	2.34426E-23	6.36181E-22	3.535688877	0.048955134	1	56	66	65	63	41	405	394	273	293	188
ENSMUSG00000027589	chr2	Pcmtd2	-1.8362322	2.35135E-23	6.3687E-22	5.094884055	0.03644166	-1	799	768	711	1110	624	203	250	165	238	366
ENSMUSG00000024675	chr19	Ms4a4c	5.45091525	2.35858E-23	6.37591E-22	1.449704449	0.159084961	1	2	0	1	2	3	64	135	37	122	52
ENSMUSG00000102049	chr1	Zbed6	-4.3626693	2.44992E-23	6.61005E-22	4.514516653	0.166669323	-1	600	537	610	752	726	11	42	4	56	59
ENSMUSG00000003812	chr8	Dnase2a	2.25787243	2.48135E-23	6.68196E-22	4.510604574	0.052313368	1	146	126	83	131	98	986	651	319	619	536
ENSMUSG00000035232	chrX	Pdk3	2.36347071	2.54989E-23	6.85331E-22	2.239756463	0.041709265	1	26	25	21	22	16	157	116	113	111	130
ENSMUSG00000020766	chr11	Galk1	2.25765682	2.55523E-23	6.85448E-22	3.172294439	0.046507468	1	44	39	39	66	42	345	237	256	204	158
ENSMUSG00000039477	chr5	Tnrc18	-2.3743075	2.60321E-23	6.96982E-22	3.755683366	0.05532817	-1	286	335	306	416	334	42	73	43	79	117
ENSMUSG00000041736	chr15	Tspo	1.84424527	2.6443E-23	7.0663E-22	5.70835968	0.037409949	1	351	434	257	384	267	1885	1162	1276	1272	1092
ENSMUSG00000042390	chr3	Gatad2b	-2.6189111	2.68985E-23	7.1743E-22	2.659194025	0.059347711	-1	98	132	146	244	185	26	36	21	30	29
ENSMUSG00000038056	chr5	Kmt2c	-1.7048599	2.95438E-23	7.86484E-22	4.926075885	0.031347131	-1	582	582	630	934	743	200	268	185	207	304
ENSMUSG00000042363	chr11	Lgalsl	-1.9510773	3.1037E-23	8.24664E-22	6.002740589	0.042127805	-1	1510	1394	1377	2027	1328	289	505	311	532	501
ENSMUSG00000019876	chr10	Pkib	4.6518667	3.13902E-23	8.32465E-22	0.724480571	0.092594358	1	1	3	2	2	0	49	59	29	60	39
ENSMUSG00000059182	chr6	Skap2	2.32903582	3.26443E-23	8.64084E-22	4.087946794	0.054478826	1	83	94	61	92	85	683	589	231	456	372
ENSMUSG00000068335	chr6	Dok1	2.3869415	3.29339E-23	8.70103E-22	3.369012997	0.053890462	1	52	54	31	66	42	473	311	192	195	250
ENSMUSG00000041697	chr5	Cox6a1	1.95516816	3.55379E-23	9.37127E-22	5.897532642	0.042296687	1	318	404	371	463	266	2094	1462	1789	1305	1065
ENSMUSG00000037234	chr8	Hook3	-1.6166897	3.61972E-23	9.52716E-22	6.773149456	0.029769974	-1	2336	2037	2362	3165	2417	782	962	732	840	1074
ENSMUSG00000029561	chr5	Oasl2	2.55754913	3.76988E-23	9.90373E-22	3.384011219	0.061807002	1	45	43	25	53	56	315	314	255	150	414
ENSMUSG00000024677	chr19	Ms4a6b	2.8316139	3.81091E-23	9.97402E-22	2.397698777	0.065988884	1	13	20	20	28	13	189	163	78	175	133
ENSMUSG00000049382	chr15	Krt8	5.25633164	3.80774E-23	9.97402E-22	1.554871737	0.158382585	1	3	1	1	3	2	124	55	53	42	176
ENSMUSG00000022651	chr16	Retnlg	5.41744738	3.96492E-23	1.03577E-21	1.23682809	0.154590386	1	2	2	0	3	0	141	39	51	81	43
ENSMUSG00000027490	chr2	E2f1	2.31968746	4.41754E-23	1.15186E-21	3.027811435	0.048612677	1	43	48	38	42	27	306	208	173	248	158
ENSMUSG00000048960	chr1	Prex2	-2.3757993	4.87884E-23	1.26977E-21	3.215911527	0.053223147	-1	171	216	248	296	219	29	61	33	53	66
ENSMUSG00000059248	chr11	Sept9	1.5244867	4.93242E-23	1.28133E-21	5.41513423	0.025746847	1	327	290	312	417	294	1255	1215	957	865	881
ENSMUSG00000026126	chr1	Ptpn18	2.97276118	5.62752E-23	1.45919E-21	3.151022683	0.081046269	1	25	38	31	24	26	474	219	152	269	170
ENSMUSG00000047466	chr18	8030462N17Rik	-2.7217577	5.72724E-23	1.48229E-21	3.792076554	0.073167761	-1	309	298	369	473	339	29	66	31	63	107
ENSMUSG00000040061	chr2	Plcb2	4.16112186	5.79589E-23	1.49729E-21	0.99314964	0.091164199	1	4	1	3	4	2	67	66	33	75	44
ENSMUSG00000014496	chr14	Ankrd28	-1.8512563	5.95582E-23	1.53577E-21	5.519938984	0.038203225	-1	1035	865	977	1462	1043	239	340	246	414	375
ENSMUSG00000033793	chr1	Atp6v1h	1.71617499	5.98814E-23	1.54126E-21	4.630630343	0.031179887	1	180	150	153	225	153	800	741	387	623	563
ENSMUSG00000056629	chr19	Fkbp2	1.81923095	6.20877E-23	1.59511E-21	3.816739107	0.032680147	1	100	90	73	109	87	486	404	289	344	262
ENSMUSG00000041134	chr16	Cyyr1	-2.294376	6.71443E-23	1.72185E-21	2.843183732	0.047361298	-1	153	153	161	240	175	27	43	26	50	49
ENSMUSG00000035711	chr13	Dok3	3.53343366	7.31946E-23	1.87357E-21	2.190797664	0.097844906	1	13	8	16	8	6	234	129	80	140	88
ENSMUSG00000021027	chr12	Ralgapa1	-1.3828884	7.5494E-23	1.92889E-21	5.268126595	0.021186487	-1	811	701	790	1057	794	373	365	291	336	379
ENSMUSG00000020590	chr12	Snx13	-1.6025486	7.66779E-23	1.95557E-21	5.564755897	0.028957361	-1	1041	965	984	1382	951	350	425	270	450	416
ENSMUSG00000030554	chr7	Synm	-1.5091559	7.71497E-23	1.96401E-21	9.084337036	0.026909833	-1	12413	10509	10767	14308	11862	5049	5059	3908	4382	4710
ENSMUSG00000063382	chr9	Bcl9l	-1.6200848	9.53091E-23	2.42189E-21	4.777057967	0.028731566	-1	541	485	583	800	669	203	198	210	207	275
ENSMUSG00000060802	chr2	B2m	1.86532613	1.06784E-22	2.70855E-21	7.538098453	0.040294729	1	1126	1491	1053	1293	972	6333	4744	3372	3613	6073
ENSMUSG00000030538	chr7	Cib1	2.01147486	1.10795E-22	2.80521E-21	3.603236836	0.039968326	1	91	76	56	81	52	453	331	278	291	227
ENSMUSG00000036067	chr2	Slc2a6	4.14740395	1.11212E-22	2.81066E-21	1.324583433	0.10443553	1	4	7	2	2	3	97	85	89	47	45
ENSMUSG00000037106	chr15	Fer1l6	-2.1418495	1.133E-22	2.85827E-21	3.057152582	0.043122004	-1	193	198	186	237	186	65	31	33	50	71
ENSMUSG00000056116	chr17	H2-T22	1.65271223	1.15337E-22	2.90442E-21	4.343905422	0.028602504	1	152	157	128	165	122	477	499	483	383	658
ENSMUSG00000025372	chr11	Baiap2	2.26006888	1.15969E-22	2.91508E-21	3.029497395	0.047224578	1	38	39	34	52	43	324	226	180	130	237
ENSMUSG00000002043	chr7	Trappc6a	2.53991423	1.16217E-22	2.91607E-21	2.275719467	0.052021925	1	22	22	24	23	11	125	110	127	122	168
ENSMUSG00000017830	chr11	Dhx58	2.39388959	1.33684E-22	3.34833E-21	2.09883084	0.043154887	1	16	18	23	25	16	126	136	92	98	117
ENSMUSG00000024236	chr18	Svil	-1.59154	1.3558E-22	3.38974E-21	7.970318074	0.030010791	-1	5262	4701	5015	7305	5866	2011	2123	1703	1883	2505
ENSMUSG00000033488	chr1	BC026585	3.77098032	1.47784E-22	3.68828E-21	1.665688873	0.098777016	1	10	6	7	4	3	51	100	116	84	102
ENSMUSG00000040430	chr11	Pitpnc1	-1.644953	1.59939E-22	3.98451E-21	6.19710514	0.031474327	-1	1233	1479	1577	2397	1654	628	561	492	525	704
ENSMUSG00000025044	chr8	Msr1	4.56979883	1.61889E-22	4.02592E-21	3.985613568	0.182212576	1	18	14	16	25	21	1175	567	115	495	189
ENSMUSG00000018752	chr11	Tnfsf12Tnfsf13	1.70307541	1.62651E-22	4.03768E-21	4.161889756	0.030188991	1	124	140	95	157	108	451	563	314	399	504
ENSMUSG00000096145	chr7	Vkorc1	1.60396249	1.65794E-22	4.10839E-21	4.548460627	0.027489063	1	178	185	159	180	151	769	530	581	464	524
ENSMUSG00000040528	chr11	Milr1	4.12035065	1.75259E-22	4.33525E-21	1.729940464	0.118583514	1	6	5	5	6	3	177	105	39	106	69
ENSMUSG00000091649	chr14	Phf11b	4.12037117	2.05648E-22	5.07799E-21	1.255837603	0.106796388	1	4	1	1	10	2	96	81	38	49	86
ENSMUSG00000018377	chr11	Vezf1	-1.5152464	2.07146E-22	5.10595E-21	6.050179459	0.026837947	-1	1335	1357	1284	1954	1417	550	585	481	485	707
ENSMUSG00000021573	chr13	Tppp	-2.0008467	2.3383E-22	5.75354E-21	3.934273894	0.041913354	-1	356	476	382	309	263	93	100	98	89	115
ENSMUSG00000025255	chr3	Zfhx4	-1.7074264	2.69229E-22	6.6129E-21	3.919263022	0.030077487	-1	305	339	324	352	378	119	129	123	86	118
ENSMUSG00000001270	chr12	Ckb	2.99818086	2.7304E-22	6.69475E-21	5.497523276	0.095650533	1	121	116	121	242	158	2475	888	1432	497	1360
ENSMUSG00000020326	chr11	Ccng1	-1.7781519	2.90436E-22	7.10883E-21	9.58323604	0.037857515	-1	19552	15957	15774	20909	16389	4495	5641	4639	5717	7747
ENSMUSG00000038811	chr11	Gngt2	2.01641294	3.64447E-22	8.90474E-21	2.752133756	0.035867674	1	42	44	34	49	26	208	192	155	144	167
ENSMUSG00000029217	chr5	Tec	2.50399542	3.78414E-22	9.22988E-21	2.641059825	0.056362112	1	33	21	35	29	17	201	192	124	199	130
ENSMUSG00000027327	chr2	1700037H04Rik	1.93770167	4.32832E-22	1.05388E-20	3.270327624	0.036361945	1	60	72	54	59	46	310	274	238	219	191
ENSMUSG00000003178	chr6	Mical3	-2.1864963	4.35933E-22	1.05958E-20	2.998699733	0.045859189	-1	158	170	156	247	235	54	32	39	57	50
ENSMUSG00000022708	chr16	Zbtb20	-1.6011201	4.6625E-22	1.1313E-20	6.590045389	0.030749896	-1	1878	1915	2143	2606	2219	763	779	796	611	946
ENSMUSG00000031666	chr8	Rbl2	-1.548341	4.72728E-22	1.14503E-20	5.405633405	0.027989148	-1	975	887	776	1039	1002	353	426	266	315	408
ENSMUSG00000005142	chr8	Man2b1	2.63293237	4.79225E-22	1.15876E-20	5.677931724	0.077507718	1	206	206	201	214	218	2635	1070	910	723	2043

ENSMUSG00000038024	chr4	Dennd4c	-3.0133589	5.51817E-22	1.33198E-20	4.165553987	0.094618678	-1	403	452	435	582	495	35	75	19	88	105
ENSMUSG00000028337	chr4	Coro2a	4.01365186	5.86998E-22	1.41446E-20	1.563026347	0.114399139	1	3	2	1	9	9	87	133	44	88	81
ENSMUSG00000101152	chr9	Gm28305	-2.8342817	6.0927E-22	1.4656E-20	2.070725913	0.067853492	-1	104	93	102	133	106	8	16	9	20	29
ENSMUSG00000054717	chr8	Hmgb2	2.03785049	6.63969E-22	1.59444E-20	3.82931998	0.043799053	1	106	70	77	82	73	443	485	315	371	236
ENSMUSG00000074994	chr2	Qser1	-1.8732276	6.67858E-22	1.60103E-20	6.116392936	0.041661534	-1	1577	1295	1306	2309	1707	340	581	380	536	580
ENSMUSG00000031875	chr8	Cmtm3	1.67697613	6.78145E-22	1.6229E-20	4.798269485	0.032131532	1	213	213	213	207	132	885	724	516	559	795
ENSMUSG00000023921	chr17	Mut	-1.4686388	6.94097E-22	1.65824E-20	6.027909838	0.025878604	-1	1351	1501	1354	1727	1205	556	579	456	604	630
ENSMUSG00000059456	chr14	Ptk2b	2.46282252	7.04255E-22	1.67964E-20	3.332344803	0.061329343	1	49	46	42	56	34	476	276	132	231	286
ENSMUSG00000021200	chr12	Asb2	-1.6131032	7.8313E-22	1.86457E-20	8.064836648	0.03198299	-1	6142	5546	4441	8083	6098	2882	1910	1770	1953	2343
ENSMUSG00000085438	chr2	1700020I14Rik	-1.5659517	7.91274E-22	1.88076E-20	9.346732494	0.030353062	-1	13291	13245	13574	19818	13115	4833	6202	5037	5290	5391
ENSMUSG00000027750	chr3	Postn	2.00690941	8.19549E-22	1.94465E-20	7.868800204	0.048362855	1	1542	1326	1337	1650	1094	6370	4867	6862	3750	8740
ENSMUSG00000031376	chrX	Atp2b3	-1.711115	8.28321E-22	1.96214E-20	3.821039443	0.030665564	-1	356	322	252	329	334	102	104	106	125	96
ENSMUSG00000102869	chr2	RP24-114E18.7	-2.4566627	8.30933E-22	1.96499E-20	3.968851256	0.064842281	-1	442	344	320	482	382	37	86	48	97	122
ENSMUSG00000049606	chr5	Zfp644	-1.7506469	9.0326E-22	2.13243E-20	3.957844858	0.032818784	-1	359	312	322	499	301	98	127	78	119	157
ENSMUSG00000042349	chr1	Ikbke	2.82912763	9.47288E-22	2.2326E-20	2.394303936	0.071404768	1	24	16	17	20	16	249	163	80	125	126
ENSMUSG00000026771	chr2	Spopl	-1.7024556	1.02322E-21	2.4075E-20	3.668070683	0.030031992	-1	311	233	253	388	265	90	108	66	106	115
ENSMUSG00000026153	chr1	Fam135a	-1.6221709	1.04935E-21	2.46483E-20	3.941135978	0.028002158	-1	310	295	344	442	330	118	123	91	118	163
ENSMUSG00000090100	chr2	Ttbk2	-1.7129238	1.06189E-21	2.49009E-20	3.337153762	0.029115173	-1	216	192	221	295	223	95	88	57	59	86
ENSMUSG00000027499	chr3	Pkia	-1.9378449	1.1002E-21	2.57562E-20	8.639802089	0.045706886	-1	9628	8787	8774	11207	8731	1879	3119	1862	3052	3547
ENSMUSG00000075470	chr15	Alg10b	-2.4095366	1.14906E-21	2.68549E-20	3.706118243	0.061658515	-1	299	294	288	404	342	38	88	37	101	69
ENSMUSG00000056515	chr17	Rab31	1.62261935	1.16429E-21	2.71656E-20	4.814494714	0.030486417	1	208	197	164	258	199	1035	721	512	526	707
ENSMUSG00000027177	chr2	Hipk3	-1.6572008	1.16903E-21	2.72306E-20	7.7762772	0.03391601	-1	4744	4117	4381	6933	4841	1555	1873	1469	1445	2293
ENSMUSG00000032046	chr2	Abhd12	1.45554108	1.24193E-21	2.88807E-20	5.53105132	0.025283887	1	377	367	328	435	329	1460	1066	830	992	1222
ENSMUSG00000042717	chr6	Ppp1r3a	-2.4496218	1.29094E-21	2.99704E-20	7.585083705	0.070462775	-1	4951	4400	4338	6487	4194	495	1193	615	1011	1532
ENSMUSG00000021262	chr12	Evl	1.91734268	1.29776E-21	3.00789E-20	4.440285808	0.041443475	1	146	134	108	193	100	761	676	318	425	652
ENSMUSG00000028961	chr4	Pgd	1.64516655	1.33686E-21	3.09337E-20	5.410833284	0.03222355	1	258	343	262	334	323	1447	1180	847	901	919
ENSMUSG00000073468	chr17	Sft2d1	1.9025722	1.34052E-21	3.09672E-20	3.248529292	0.035675409	1	48	54	60	56	72	276	271	198	243	219
ENSMUSG00000090066	chr3	1110002E22Rik	-1.7823693	1.40715E-21	3.24528E-20	8.735862024	0.039265001	-1	9851	7975	8379	13406	9982	2457	3117	2811	2939	4319
ENSMUSG00000049313	chr9	Sorl1	-1.6073561	1.45052E-21	3.33978E-20	5.900639986	0.031359436	-1	1039	1107	1130	1960	1515	513	500	423	464	510
ENSMUSG00000025492	chr7	Ifitm3	1.85921869	1.47592E-21	3.39268E-20	6.190589107	0.041810099	1	447	438	470	638	371	3117	1867	1571	1319	1603
ENSMUSG00000027272	chr2	Ubr1	-1.4890364	1.59149E-21	3.65233E-20	4.891187028	0.025902628	-1	643	582	569	835	634	216	270	200	289	291
ENSMUSG00000035849	chr11	Krt222	-1.9362592	1.65025E-21	3.78097E-20	3.244870184	0.037902802	-1	257	191	191	255	215	45	80	51	72	68
ENSMUSG00000030516	chr7	Tjp1	-1.6858973	1.67492E-21	3.83121E-20	4.890083144	0.033432339	-1	632	634	585	909	624	171	210	222	208	329
ENSMUSG00000007041	chr17	Clic1	2.06369725	1.72654E-21	3.94282E-20	5.986090733	0.05099768	1	368	367	377	424	281	2717	1807	1127	1738	1053
ENSMUSG00000052414	chr15	Gm28047	-2.2172856	1.75957E-21	4.00516E-20	2.792681214	0.047392494	-1	145	159	163	189	178	33	39	32	58	34
ENSMUSG00000091712	chr16	Sec14l5	-2.9478135	1.75948E-21	4.00516E-20	3.346889703	0.088645759	-1	279	230	238	283	293	13	38	24	69	42
ENSMUSG00000045205	chr4	Dpy19l4	-1.5045136	1.81296E-21	4.11998E-20	4.236565162	0.024887024	-1	423	370	343	534	407	151	187	120	155	187
ENSMUSG00000024556	chr18	Me2	2.02766487	1.99734E-21	4.53162E-20	3.208186331	0.041582391	1	57	34	52	68	56	270	262	262	218	176
ENSMUSG00000022636	chr16	Alcam	3.90912428	2.00622E-21	4.5444E-20	2.685844951	0.13668732	1	10	10	13	11	13	256	288	40	184	211
ENSMUSG00000020100	chr10	Slc29a3	2.11439899	2.03695E-21	4.60654E-20	3.670902267	0.047882873	1	84	45	66	86	71	410	442	200	246	395
ENSMUSG00000087370	chr13	Tmem170b	-1.420796	2.06853E-21	4.6704E-20	4.718865742	0.023387762	-1	603	585	474	714	485	237	276	203	186	267
ENSMUSG00000104453	chr7	Wl1-1616M8.3	-1.6910851	2.19644E-21	4.9512E-20	6.15093763	0.035128494	-1	1646	1480	1464	2033	1480	412	532	509	511	767
ENSMUSG00000037759	chr14	Ptger2	4.74453277	2.22444E-21	5.00625E-20	0.451405234	0.099505337	1	1	1	0	3	1	60	35	20	37	42
ENSMUSG00000028494	chr4	Plin2	2.27914769	2.24048E-21	5.03424E-20	7.03141228	0.062340052	1	559	725	578	865	611	5085	4499	1408	3416	3640
ENSMUSG00000075702	chr11	Selm	1.56618471	2.32883E-21	5.22436E-20	4.35403401	0.027444413	1	177	140	149	181	118	666	494	485	429	414
ENSMUSG00000024030	chr17	Abcg1	3.82099048	2.33453E-21	5.22876E-20	3.38218054	0.141771198	1	19	15	22	38	9	539	255	143	124	553
ENSMUSG00000033960	chr18	9430020K01Rik	-1.5159893	2.37307E-21	5.30656E-20	5.192463955	0.027577893	-1	658	778	833	1193	612	377	321	262	288	302
ENSMUSG00000097391	chr12	Mirg	3.38263245	2.38901E-21	5.33368E-20	3.341153775	0.113842457	1	39	27	22	15	24	385	162	201	184	578
ENSMUSG00000035561	chr4	Aldh1b1	4.51408815	2.48264E-21	5.53387E-20	0.756630631	0.106081527	1	2	2	4	1	0	32	67	47	35	59
ENSMUSG00000023150	chr1	Ivns1abp	-1.4563178	2.63845E-21	5.8718E-20	7.132478637	0.026753615	-1	3282	2671	2627	3705	3053	1375	1316	933	1242	1277
ENSMUSG00000039987	chr5	Phtf2	-1.6139312	2.6679E-21	5.92792E-20	7.152230587	0.032669203	-1	2849	2691	2870	4642	3086	1019	1166	945	1116	1473
ENSMUSG00000039208	chr11	Metrnl	2.42306206	2.7199E-21	6.03386E-20	4.795066584	0.06723681	1	118	103	142	191	99	1340	889	368	741	542
ENSMUSG00000058064	chr18	Gm10036	5.2763519	2.85827E-21	6.33077E-20	3.184733126	0.229044608	1	6	8	7	8	4	26	374	309	358	322
ENSMUSG00000031266	chrX	Gla	2.79076214	3.12203E-21	6.90404E-20	3.346096892	0.08086905	1	50	26	38	39	34	337	360	100	264	391
ENSMUSG00000091089	chr14	A930018M24Rik	-2.4541506	3.18104E-21	7.02342E-20	4.738502764	0.06910373	-1	582	650	699	778	631	61	152	94	132	230
ENSMUSG00000079426	chr6	Arpc4	1.74514592	3.40446E-21	7.50486E-20	6.253838065	0.037742161	1	617	490	464	614	429	2892	2023	1474	1866	1423
ENSMUSG00000021773	chr14	Comtd1	2.03983187	3.46101E-21	7.61749E-20	2.735845347	0.03944069	1	43	31	35	53	29	226	157	171	158	145
ENSMUSG00000044066	chr11	Cep68	-1.689977	3.4675E-21	7.61978E-20	4.81179492	0.034049578	-1	571	595	608	889	548	149	240	184	224	280
ENSMUSG00000073664	chr1	Nbeal1	-1.5696627	3.69446E-21	8.10577E-20	4.504223152	0.028387246	-1	414	466	463	742	461	167	194	179	157	232
ENSMUSG00000026271	chr1	Gpr35	5.03375335	3.9283E-21	8.60531E-20	1.796461554	0.180646233	1	2	3	1	4	4	240	134	40	66	60
ENSMUSG00000102351	chr16	AC107830.1	1.64859592	4.26973E-21	9.33862E-20	4.233395688	0.030734441	1	132	154	121	165	102	628	540	384	340	442
ENSMUSG00000002020	chr12	Ltbp2	3.55532984	4.54323E-21	9.92127E-20	2.686788976	0.119528636	1	15	15	13	19	11	350	289	115	129	81
ENSMUSG00000020988	chr12	L2hgdh	-1.3761277	4.69528E-21	1.02373E-19	5.179578142	0.022946029	-1	810	762	710	949	667	311	367	260	324	382
ENSMUSG00000052397	chr17	Ezr	1.86117131	4.8777E-21	1.06185E-19	3.662394596	0.037734257	1	99	77	60	112	59	430	380	236	315	254
ENSMUSG00000063632	chr12	Sox11	3.60151259	5.08384E-21	1.105E-19	2.069262593	0.111368946	1	16	8	4	7	10	148	144	140	46	134

ENSMUSG00000042155	chr2	Klhl23	-1.6653372	5.76498E-21	1.25111E-19	5.148133041	0.033912345	-1	857	830	800	822	671	200	309	266	318	279
ENSMUSG00000033355	chr16	Rtp4	1.95929227	5.96507E-21	1.29253E-19	2.830929457	0.037126226	1	43	42	43	56	29	205	202	140	147	217
ENSMUSG00000079057	chr8	Cyp4v3	2.65896674	6.34998E-21	1.3738E-19	2.691433343	0.069842086	1	25	25	23	32	23	236	168	101	115	284
ENSMUSG00000023367	chr6	Tmem176a	2.61296711	6.40262E-21	1.38304E-19	4.161701687	0.076868205	1	77	79	68	83	63	952	365	559	235	416
ENSMUSG00000073489	chr1	Ifi204	2.37612959	7.02517E-21	1.51518E-19	3.347564037	0.060680441	1	76	42	36	54	34	276	359	148	327	269
ENSMUSG00000000594	chr11	Gm2a	1.92974669	7.08543E-21	1.52348E-19	5.242605005	0.045591539	1	250	277	213	225	193	1493	875	637	702	1263
ENSMUSG00000037337	chr7	Map4k1	3.69098342	7.08403E-21	1.52348E-19	2.020449523	0.115636445	1	7	6	12	10	6	181	160	39	116	105
ENSMUSG00000025366	chr10	Esyt1	1.46156964	7.37326E-21	1.58293E-19	5.841071087	0.026871669	1	446	414	380	597	445	1664	1647	1064	1082	1457
ENSMUSG00000038121	chr18	Fam210a	-1.6912406	7.76019E-21	1.66344E-19	6.820021458	0.036491969	-1	2088	2268	2652	3857	2135	697	942	799	948	948
ENSMUSG00000022525	chr16	Hrasls	-1.5895857	7.84802E-21	1.67969E-19	5.546215644	0.031569475	-1	1200	1091	980	1067	851	314	467	370	365	374
ENSMUSG00000030729	chr7	Pgm2l1	-1.7431196	8.10135E-21	1.73126E-19	4.218748616	0.035229048	-1	399	324	374	570	469	118	180	97	140	162
ENSMUSG00000024121	chr17	Atp6v0c	1.89239505	8.15235E-21	1.7395E-19	5.853819624	0.04471889	1	379	329	291	497	344	981	2050	1154	1347	1883
ENSMUSG00000005886	chr1	Ncoa2	-1.7619901	8.23129E-21	1.75367E-19	4.478735256	0.03669106	-1	492	456	429	636	546	114	186	130	165	229
ENSMUSG00000099974	chr9	Bcl2a1d	8.17057423	8.53449E-21	1.81549E-19	0.378552668	0.181495532	1	0	0	0	0	0	24	69	17	51	26
ENSMUSG00000029616	chr5	Erp29	1.77888362	8.60827E-21	1.82841E-19	6.215691118	0.03997741	1	473	516	422	630	461	2912	2005	1388	1851	1330
ENSMUSG00000024909	chr19	Efemp2	1.99017188	9.34684E-21	1.98227E-19	4.619629444	0.0471482	1	177	162	107	153	131	1039	605	646	463	464
ENSMUSG00000024521	chr18	Pmaip1	5.17364195	9.79882E-21	2.07497E-19	1.367477332	0.174117135	1	2	2	5	0	0	109	56	121	30	68
ENSMUSG00000010461	chr10	Eya4	-2.1078975	1.00837E-20	2.13208E-19	4.402794894	0.052429324	-1	590	435	440	540	531	83	159	78	175	150
ENSMUSG00000103229	chr3	Dcun1d1	-2.7000704	1.02964E-20	2.17376E-19	3.58231626	0.080249454	-1	376	259	269	338	292	17	68	33	64	75
ENSMUSG00000034653	chr18	Ythdc2	-2.6188428	1.07049E-20	2.25659E-19	2.440850096	0.066795304	-1	154	126	115	173	120	9	34	17	28	33
ENSMUSG00000103268	chr9	AC161246.1	-2.6936389	1.16724E-20	2.45683E-19	6.879560573	0.087542183	-1	2915	2636	2725	3864	3087	219	555	297	758	722
ENSMUSG00000019966	chr10	Kitl	-1.5266621	1.17402E-20	2.46738E-19	4.477291055	0.027514754	-1	410	455	459	717	438	167	190	152	190	234
ENSMUSG00000000957	chr14	Mmp14	2.11601095	1.18209E-20	2.48062E-19	6.355646072	0.056091182	1	411	400	449	581	445	2792	1630	2368	1109	3030
ENSMUSG00000031441	chr8	Atp11a	-1.5828869	1.19942E-20	2.51321E-19	5.342263109	0.031441002	-1	837	736	806	1156	995	292	398	251	310	407
ENSMUSG00000028641	chr4	Lepre1	1.51880995	1.25893E-20	2.63396E-19	4.882788302	0.028251419	1	251	213	197	252	216	689	771	831	541	705
ENSMUSG00000090150	chr9	Acad11	-1.5496365	1.27386E-20	2.66121E-19	5.754545657	0.030536107	-1	1148	1199	1017	1566	1090	335	514	410	461	509
ENSMUSG00000024663	chr19	Rab3il1	1.68161889	1.35776E-20	2.83225E-19	4.527361481	0.033685672	1	168	161	155	182	143	872	545	429	584	450
ENSMUSG00000048779	chr7	P2ry6	2.98341368	1.55637E-20	3.2417E-19	3.462126942	0.096014177	1	25	28	44	40	42	677	291	155	254	241
ENSMUSG00000008036	chr7	Ap2s1	1.66944195	1.57402E-20	3.27358E-19	6.039081606	0.035723588	1	506	465	416	521	425	2503	1511	1316	1636	1260
ENSMUSG00000032575	chr9	Manf	2.01386779	1.57932E-20	3.27973E-19	5.350261325	0.050644945	1	239	196	205	323	246	1692	1242	740	1075	636
ENSMUSG00000040945	chr4	Rcc2	1.55650864	1.62559E-20	3.37081E-19	5.134511319	0.030280725	1	258	254	265	325	222	1120	1000	854	639	670
ENSMUSG00000072812	chr12	Ahnak2	2.36679223	1.6615E-20	3.44016E-19	3.936485275	0.064472475	1	98	64	67	92	48	584	362	329	207	626
ENSMUSG00000030249	chr6	Abcc9	-1.7662223	1.67266E-20	3.45815E-19	7.807960979	0.040657099	-1	5177	4663	4476	6015	5418	1195	1844	1416	1554	2285
ENSMUSG00000060591	chr7	Ifitm2	1.7736073	1.81939E-20	3.75595E-19	6.25602452	0.040462235	1	467	501	481	623	498	3193	1902	1619	1608	1441
ENSMUSG00000054520	chr5	Sh3bp2	2.14835981	1.90589E-20	3.92873E-19	3.915091409	0.053270551	1	109	78	98	62	56	543	462	249	404	352
ENSMUSG00000052087	chr13	Rgs14	4.03773601	2.05022E-20	4.22E-19	1.160866402	0.110414168	1	4	3	5	2	3	116	68	33	60	48
ENSMUSG00000040462	chr10	Os9	1.39655777	2.07991E-20	4.27482E-19	5.373906226	0.024692616	1	334	311	271	437	349	1247	949	857	804	1068
ENSMUSG00000010307	chr7	Tmem86a	2.1753677	2.11681E-20	4.34427E-19	4.180522585	0.055820242	1	70	138	107	105	62	633	449	499	288	551
ENSMUSG00000020169	chr10	Best3	-2.3185899	2.35595E-20	4.82797E-19	2.660718127	0.054679694	-1	144	133	148	196	154	18	49	31	27	44
ENSMUSG00000022089	chr14	Bin3	1.76919582	2.36578E-20	4.84102E-19	3.577688348	0.034745989	1	91	90	56	88	73	427	304	271	238	260
ENSMUSG00000027288	chr2	Zfp106	-1.5920791	2.38712E-20	4.87755E-19	9.503400675	0.033814585	-1	13476	13112	14589	24402	16586	5785	6160	5451	6125	5922
ENSMUSG00000029373	chr5	Pf4	3.2277138	2.45917E-20	5.01743E-19	4.787519624	0.118285785	1	72	100	82	68	66	1044	1017	420	1300	276
ENSMUSG00000051285	chr1	Pcmtd1	-1.3763101	2.58542E-20	5.26733E-19	5.678334406	0.024443201	-1	1129	1055	1046	1381	909	462	493	368	485	516
ENSMUSG00000024640	chr19	Psat1	2.22430759	2.60826E-20	5.30612E-19	3.980711667	0.05783912	1	76	97	73	79	81	461	614	360	443	223
ENSMUSG00000034595	chr17	Ppp1r18	1.66669934	2.63659E-20	5.35596E-19	4.505735826	0.033651926	1	145	167	179	195	119	834	586	441	491	481
ENSMUSG00000017716	chr11	Birc5	3.75701739	2.6907E-20	5.45794E-19	3.020896753	0.141649073	1	17	22	19	13	9	382	344	164	264	66
ENSMUSG00000063296	chr15	Tmem117	-1.2675242	2.71791E-20	5.50515E-19	5.187397541	0.0201887	-1	809	707	722	953	649	409	364	310	308	357
ENSMUSG00000020354	chr11	Sgcd	-1.8291775	2.9476E-20	5.96174E-19	3.863219365	0.03908578	-1	372	253	356	423	284	162	90	75	112	84
ENSMUSG00000034525	chr13	Ice1	-1.4889472	2.97783E-20	6.01419E-19	5.172312813	0.028185296	-1	828	681	712	929	798	261	277	279	339	380
ENSMUSG00000029233	chr5	Srd5a3	1.76802736	3.19971E-20	6.45298E-19	3.447962773	0.034345385	1	75	73	78	87	51	364	303	185	246	275
ENSMUSG00000034910	chr9	Pygo1	-1.6085386	3.41242E-20	6.87204E-19	3.946169389	0.030014848	-1	260	322	332	486	330	120	113	131	107	145
ENSMUSG00000041859	chr1	Mcm3	2.26453695	3.63511E-20	7.30997E-19	3.835855836	0.059927637	1	78	56	54	95	81	484	552	298	383	201
ENSMUSG00000072501	chr15	Phf20l1	-1.5470691	3.76273E-20	7.55573E-19	4.853623086	0.030214013	-1	636	574	588	831	586	181	297	185	248	287
ENSMUSG00000090272	chr1	Mndal	4.07593813	3.80711E-20	7.63388E-19	2.466044438	0.156153995	1	11	10	6	14	4	47	167	136	164	307
ENSMUSG00000006498	chr10	Ptbp1	1.52333992	3.81833E-20	7.64542E-19	5.283862114	0.029799041	1	274	311	243	387	284	1278	1124	715	842	788
ENSMUSG00000006728	chr10	Cdk4	1.49853248	3.9674E-20	7.93254E-19	5.847790769	0.029404604	1	476	440	396	551	382	1828	1599	1212	1285	1041
ENSMUSG00000029413	chr5	Naaa	1.56620279	4.04581E-20	8.07775E-19	3.985529973	0.028394471	1	108	133	89	132	126	481	407	337	367	330
ENSMUSG00000085295	chr4	4930430E12Rik	6.39258523	4.05382E-20	8.08219E-19	0.688644188	0.188918955	1	0	0	0	2	0	54	80	11	51	42
ENSMUSG00000030657	chr7	Xylt1	-2.8916365	4.09213E-20	8.14695E-19	1.348749801	0.064791959	-1	69	44	56	92	64	9	15	7	10	6
ENSMUSG00000053318	chr1	Slamf8	6.333051	4.23968E-20	8.42869E-19	0.663207568	0.171282376	1	0	1	1	0	0	36	68	19	28	82
ENSMUSG00000031529	chr8	Tnks	-1.9811196	4.29769E-20	8.5319E-19	3.376207908	0.044282772	-1	274	192	227	293	239	47	72	46	77	97
ENSMUSG00000006390	chr4	Elovl1	1.71351333	4.32664E-20	8.57717E-19	4.514294771	0.036022303	1	150	132	129	190	188	838	652	443	468	473
ENSMUSG00000026950	chr2	Neb	-2.3592914	4.45741E-20	8.8239E-19	11.82866157	0.071603101	-1	79684	69412	76060	122399	107946	10609	20931	14340	20026	30698
ENSMUSG00000022263	chr15	Trio	-1.5379682	4.73152E-20	9.35328E-19	5.082493565	0.030343407	-1	678	602	672	1050	772	232	361	237	289	291
ENSMUSG00000063506	chr14	Arhgap22	2.31445455	4.81898E-20	9.51272E-19	2.212113377	0.050028797	1	27	15	18	30	22	159	143	113	101	96

ENSMUSG00000022587	chr15	Ly6e	1.96475307	5.01765E-20	9.89093E-19	7.347308952	0.050872531	1	857	1000	887	1247	960	6867	3408	4413	2421	4301
ENSMUSG00000071379	chr12	Hpcal1	1.7894381	5.11007E-20	1.00589E-18	4.04715409	0.038300853	1	84	110	93	155	109	591	446	271	322	477
ENSMUSG00000023973	chr17	Cnpy3	1.38566684	5.18911E-20	1.02001E-18	4.231883417	0.022473259	1	163	148	142	172	142	541	471	353	437	410
ENSMUSG00000030804	chr7	Gm21974	1.47523488	5.63231E-20	1.10533E-18	4.517983151	0.026913286	1	188	185	170	183	165	733	527	544	450	491
ENSMUSG00000036792	chr2	Mbd5	-1.5659339	5.63893E-20	1.10533E-18	3.533864175	0.027228556	-1	220	234	244	353	237	106	103	67	90	110
ENSMUSG00000008668	chr17	Rps18	1.65910297	5.96123E-20	1.16687E-18	7.637549889	0.037123413	1	1540	1389	1357	1596	1233	3742	5788	4615	5735	4585
ENSMUSG00000021366	chr13	Hivep1	-1.6060152	6.15061E-20	1.20177E-18	4.179776611	0.031135536	-1	376	324	423	514	388	120	165	125	126	192
ENSMUSG00000029056	chr4	Pank4	-1.3868905	6.15675E-20	1.20177E-18	4.953576866	0.024566605	-1	606	648	668	825	586	368	255	215	299	266
ENSMUSG00000092463	chrX	Gm20489	2.48190867	6.55656E-20	1.27803E-18	2.579999456	0.063397131	1	24	28	26	36	18	269	190	120	115	125
ENSMUSG00000049775	chrX	Tmsb4x	2.07322372	6.64144E-20	1.29277E-18	8.841288088	0.056896173	1	2813	2929	2701	2966	1704	18187	13250	8269	13587	7803
ENSMUSG00000032312	chr9	Csk	1.51670436	7.37664E-20	1.43388E-18	4.477573778	0.028253725	1	152	145	163	206	186	728	600	462	417	494
ENSMUSG00000071713	chr15	Csf2rb	2.74641733	7.40679E-20	1.43774E-18	3.460555635	0.085906469	1	39	40	34	47	48	486	342	117	194	444
ENSMUSG00000052142	chr17	Rasal3	4.15412667	7.46692E-20	1.4474E-18	0.79043415	0.10550315	1	2	4	2	4	0	65	55	22	42	63
ENSMUSG00000039701	chr3	Usp53	-2.3615388	8.05317E-20	1.55743E-18	2.196691065	0.054235382	-1	92	116	107	155	94	16	31	15	26	31
ENSMUSG00000093674	chr10	Rpl41	1.67553405	8.05684E-20	1.55743E-18	8.352443437	0.038234215	1	2869	2184	2233	2356	1907	11699	7518	7890	7015	6751
ENSMUSG00000093989	chr11	Rnasek	1.34792189	8.5368E-20	1.64793E-18	5.932393402	0.024292428	1	532	507	415	622	490	1754	1415	1369	1184	1449
ENSMUSG00000078945	chr13	Naip2	3.2083771	8.92716E-20	1.72091E-18	1.482964271	0.084965746	1	7	10	4	10	7	102	106	39	80	66
ENSMUSG00000015094	chr2	Npdc1	1.4818974	9.07525E-20	1.74705E-18	5.00297277	0.02838423	1	262	240	227	272	247	938	606	828	611	860
ENSMUSG00000035569	chr8	Ankrd11	-1.4295721	9.29698E-20	1.78727E-18	5.756468283	0.027318009	-1	1050	1037	1020	1638	1167	511	539	359	418	574
ENSMUSG00000015501	chr10	Hivep2	-1.3179298	9.58885E-20	1.84085E-18	5.823097902	0.023231448	-1	1184	1165	1037	1537	1114	506	582	508	461	583
ENSMUSG00000055737	chr15	Ghr	-1.6871124	9.66242E-20	1.85243E-18	6.70829654	0.038503163	-1	2456	2446	2164	2598	2169	580	1017	708	707	1023
ENSMUSG00000028367	chr4	Txn1	1.63470531	9.68508E-20	1.85423E-18	6.712567424	0.03620121	1	802	759	754	866	615	3785	2899	1923	2455	2014
ENSMUSG00000036931	chr7	Nfkbid	5.3992873	9.95214E-20	1.90275E-18	0.554938382	0.150396469	1	2	0	0	2	0	56	72	16	33	36
ENSMUSG00000027765	chr3	P2ry1	-1.6127518	1.00096E-19	1.91112E-18	3.692491165	0.030207463	-1	266	314	304	349	209	95	123	99	96	102
ENSMUSG00000061462	chr11	Obscn	-1.6355067	1.014E-19	1.93338E-18	10.37165113	0.036870583	-1	24689	23356	25321	41199	35516	10880	10933	9700	9144	12108
ENSMUSG00000030047	chr6	Arhgap25	2.99931573	1.02066E-19	1.94343E-18	3.355513004	0.101778493	1	28	37	30	54	20	432	295	117	164	493
ENSMUSG00000018363	chr11	Smurf2	-1.5141901	1.02433E-19	1.94776E-18	4.743962615	0.029498149	-1	494	508	566	766	618	281	206	177	269	200
ENSMUSG00000020186	chr10	Csrp2	2.39104531	1.06584E-19	2.02394E-18	3.708102832	0.067924493	1	49	54	45	89	73	497	328	484	190	272
ENSMUSG00000027239	chr2	Mdk	2.29762077	1.1235E-19	2.13054E-18	3.445711605	0.061512891	1	56	67	48	52	45	320	205	306	177	455
ENSMUSG00000036202	chr2	Rif1	-1.9987411	1.16806E-19	2.21204E-18	3.440194931	0.046630621	-1	247	228	218	329	265	50	95	46	94	65
ENSMUSG00000043252	chr4	Tmem64	-1.3148322	1.16997E-19	2.21265E-18	6.898894498	0.023835195	-1	2532	2423	2266	3058	2404	1110	1162	1064	1039	1202
ENSMUSG00000092511	chr17	Gm20547	2.67249212	1.20045E-19	2.26722E-18	4.440164895	0.087081914	1	44	99	76	114	101	1115	350	584	351	694
ENSMUSG00000034636	chr4	Zyg11b	-1.4604763	1.22991E-19	2.31973E-18	6.27481665	0.029042727	-1	1598	1591	1622	2189	1488	567	780	667	584	757
ENSMUSG00000062753	chr17	AI413582	2.70448142	1.40384E-19	2.64422E-18	2.387406972	0.075247486	1	16	24	21	30	10	241	162	99	122	105
ENSMUSG00000040407	chr5	Akap9	-1.4295875	1.4716E-19	2.76811E-18	5.773875732	0.027622716	-1	1098	1196	1102	1527	1036	419	469	428	473	622
ENSMUSG00000033307	chr10	Mif	1.58144094	1.53207E-19	2.87799E-18	5.625908151	0.033659357	1	369	300	272	540	380	1496	1289	1296	953	1000
ENSMUSG00000030745	chr7	Il21r	4.18331458	1.63717E-19	3.07128E-18	0.993233628	0.125135203	1	2	2	1	7	2	90	53	64	23	57
ENSMUSG00000029730	chr5	Mcm7	1.70049094	1.68738E-19	3.16124E-18	4.107779685	0.035644968	1	100	122	107	145	124	579	508	351	411	298
ENSMUSG00000025888	chr9	Casp1	3.10228594	1.73685E-19	3.24955E-18	1.920302176	0.089251399	1	7	15	13	9	11	140	118	45	111	123
ENSMUSG00000038506	chr8	Dcun1d2	-1.5967457	1.80788E-19	3.37794E-18	6.285993634	0.034934566	-1	1720	1589	1565	2131	1730	465	751	529	721	679
ENSMUSG00000033991	chr13	Ttc37	-1.6715222	1.86586E-19	3.48161E-18	3.921000153	0.034109286	-1	329	302	329	370	366	119	130	70	142	128
ENSMUSG00000071540	chr14	3425401B19Rik	-1.7268724	1.87618E-19	3.4962E-18	7.875745455	0.041265315	-1	4374	4568	5117	7826	5237	1714	1965	1909	1149	2162
ENSMUSG00000025790	chr7	Slco3a1	-1.6554596	1.92171E-19	3.57628E-18	5.633495381	0.037107595	-1	969	999	1081	1504	1078	623	316	369	309	352
ENSMUSG00000042312	chr3	S100a13	1.70193193	1.94983E-19	3.62377E-18	4.435855107	0.036845146	1	157	148	148	178	122	806	481	526	518	365
ENSMUSG00000020859	chr11	Spag9	-1.5102279	1.97041E-19	3.65717E-18	7.425686258	0.031851301	-1	3413	3333	3702	5289	3370	1296	1622	1131	1553	1689
ENSMUSG00000021298	chr12	Gpr132	5.06684293	2.00739E-19	3.72087E-18	0.539739769	0.131405783	1	1	0	1	1	2	84	39	24	29	34
ENSMUSG00000020644	chr12	Id2	2.28584085	2.06532E-19	3.82317E-18	3.493662578	0.06230999	1	61	63	51	68	39	457	427	169	268	208
ENSMUSG00000025241	chr9	Fyco1	-1.6709554	2.10728E-19	3.89568E-18	8.029190919	0.038889897	-1	5628	5133	5313	8125	5645	1463	2283	1712	2123	2572
ENSMUSG00000024339	chr17	Tap2	1.52797482	2.32843E-19	4.29882E-18	4.187227106	0.028907767	1	124	148	110	168	143	558	421	465	330	423
ENSMUSG00000025262	chrX	Fam120c	-2.9291573	2.51293E-19	4.63333E-18	3.02166061	0.097373892	-1	177	145	194	292	255	15	33	12	52	39
ENSMUSG00000039981	chr10	Zc3h12d	4.8228887	2.53905E-19	4.67533E-18	0.713737496	0.135873877	1	0	0	3	3	1	69	59	16	43	51
ENSMUSG00000032717	chr17	Mdfi	3.48355374	2.5843E-19	4.75239E-18	2.544705056	0.125613951	1	16	21	10	9	12	70	120	198	201	247
ENSMUSG00000021796	chr14	Bmpr1a	-1.4900985	2.60755E-19	4.78257E-18	6.278509584	0.030793782	-1	1592	1533	1498	2330	1631	552	726	561	643	839
ENSMUSG00000022971	chr16	Ifnar2	1.56674594	2.60457E-19	4.78257E-18	4.157414032	0.030505079	1	122	153	120	153	116	642	413	347	355	428
ENSMUSG00000038650	chr7	Rnh1	1.57232377	2.67559E-19	4.90093E-18	6.400015606	0.034267148	1	764	571	567	696	559	2385	2364	1524	2376	1681
ENSMUSG00000027995	chr3	Tlr2	2.90973113	2.68926E-19	4.91951E-18	2.994769612	0.095134895	1	31	35	19	25	25	407	302	107	191	143
ENSMUSG00000039968	chr5	Rsbn1l	-1.601226	2.71659E-19	4.96302E-18	3.170710814	0.028045442	-1	200	167	177	273	189	73	85	61	65	77
ENSMUSG00000060143	chr14	Gm10076	1.64777693	2.76456E-19	5.04406E-18	4.280465209	0.034463937	1	179	121	125	175	100	554	486	497	498	344
ENSMUSG00000054428	chr4	Atpif1	1.68172853	2.77196E-19	5.05097E-18	5.216712767	0.038039989	1	352	288	249	229	182	1160	894	935	822	806
ENSMUSG00000024013	chr17	Fgd2	2.62070522	2.85221E-19	5.19043E-18	1.824423877	0.062101457	1	17	14	16	8	14	117	71	84	90	115
ENSMUSG00000040455	chr4	Usp45	-1.7031208	2.89719E-19	5.26543E-18	3.941087608	0.036033243	-1	372	275	323	458	323	96	148	77	142	122
ENSMUSG00000066861	chr5	Oas1g	3.74369682	3.0212E-19	5.48367E-18	0.334910872	0.065559842	1	1	2	2	3	3	39	35	29	28	39
ENSMUSG00000097705	chr10	Gm26740	-2.2699331	3.03684E-19	5.50492E-18	2.905259085	0.058470789	-1	213	200	132	191	175	26	58	25	48	50
ENSMUSG00000001525	chr17	Tubb5	1.71195646	3.07283E-19	5.56294E-18	7.283512633	0.040931371	1	1160	996	875	1410	1019	5367	4824	3116	3763	2547
ENSMUSG00000070632	chr5	Btbd8	-5.0953331	3.17315E-19	5.73712E-18	-0.184844218	0.092514395	-1	30	18	24	20	20	1	1	0	0	1

ENSMUSG00000030867	chr7	Plk1	3.31413634	3.20846E-19	5.79347E-18	2.128098019	0.107671835	1	9	14	13	9	11	172	182	123	99	51
ENSMUSG00000098021	chr15	Gm9522	-4.2828939	3.31539E-19	5.97883E-18	0.808726212	0.131372	-1	42	51	45	48	48	11	1	0	0	1
ENSMUSG00000036606	chr15	Plxnb2	1.62815675	3.34391E-19	6.02249E-18	5.673745507	0.036346065	1	394	327	356	413	357	1904	1307	958	850	1363
ENSMUSG00000020736	chr11	Nt5c	1.75016683	3.54388E-19	6.37442E-18	3.495933744	0.036212875	1	82	74	63	94	68	420	278	211	284	221
ENSMUSG00000020649	chr12	Rrm2	2.4223916	3.63198E-19	6.52449E-18	3.399283323	0.070099613	1	57	55	49	49	32	292	487	202	280	174
ENSMUSG00000002233	chr3	Rhoc	1.62970957	3.7694E-19	6.76266E-18	6.173791933	0.03694061	1	589	407	478	681	483	2788	1737	1498	1300	1692
ENSMUSG00000020300	chr11	Cpeb4	-2.0283552	3.77956E-19	6.77219E-18	5.605717625	0.055826165	-1	1014	912	1080	1764	1123	196	406	214	283	466
ENSMUSG00000024660	chr19	Incenp	2.19803708	3.8147E-19	6.82641E-18	3.049214262	0.055571971	1	50	41	36	39	48	300	286	182	192	136
ENSMUSG00000020647	chr12	Ncoa1	-1.3225176	4.02321E-19	7.19033E-18	5.156822302	0.023590726	-1	719	695	650	953	778	311	320	295	349	381
ENSMUSG00000082536	chr2	Gm13456	1.55849731	4.08997E-19	7.30031E-18	3.758723563	0.029091873	1	111	102	85	110	96	386	342	349	232	326
ENSMUSG00000043483	chr12	Gm6863	1.54843312	4.10832E-19	7.3237E-18	3.825628784	0.029078091	1	112	86	86	144	108	413	318	373	310	291
ENSMUSG00000032690	chr5	Oas2	2.60928065	4.12569E-19	7.3453E-18	2.159707034	0.068528638	1	14	21	19	17	18	202	115	74	96	128
ENSMUSG00000015335	chr2	Zdhhc12	2.21830203	4.23226E-19	7.51675E-18	2.176395584	0.047961151	1	21	22	21	30	21	164	141	90	91	107
ENSMUSG00000032245	chr9	Cln6	1.46220796	4.23274E-19	7.51675E-18	4.260766858	0.026914069	1	139	174	108	181	153	583	427	422	392	466
ENSMUSG00000028873	chr4	Cdca8	2.96153301	4.25994E-19	7.55544E-18	1.982600064	0.085565332	1	11	15	14	10	13	116	164	84	123	62
ENSMUSG00000063953	chr10	Amd2	-3.0784219	4.50355E-19	7.97739E-18	1.868233767	0.094227154	-1	123	79	99	72	95	21	10	3	16	12
ENSMUSG00000062082	chr16	Cd200r4	5.99882981	4.51664E-19	7.99045E-18	0.349612198	0.16272585	1	0	0	1	1	0	31	61	11	40	39
ENSMUSG00000023349	chr6	Clec4n	4.18853455	4.82597E-19	8.52689E-18	3.18878806	0.18474702	1	18	19	9	16	7	646	409	98	168	114
ENSMUSG00000071342	chr12	Lsmem1	-1.7403933	4.83778E-19	8.53697E-18	5.488519368	0.041773513	-1	1323	1017	835	918	996	442	333	200	331	400
ENSMUSG00000087543	chr15	Gm16576	-2.109	4.90072E-19	8.63712E-18	2.460204289	0.047023053	-1	111	118	130	154	139	22	35	33	33	42
ENSMUSG00000097295	chr10	Hmgb1-ps8	-3.4156152	4.96514E-19	8.73965E-18	1.092925284	0.093544302	-1	61	74	43	50	48	3	3	3	8	11
ENSMUSG00000042254	chr9	Cilp	2.41496353	4.98457E-19	8.76282E-18	7.016502926	0.078672034	1	808	509	481	761	509	3031	3011	4813	1585	5257
ENSMUSG00000079104	chr12	Prps1l3	-1.7132409	5.10864E-19	8.96964E-18	3.719852025	0.036226356	-1	366	306	269	300	246	80	106	82	93	138
ENSMUSG00000022253	chr15	Nadk2	-1.4547023	5.40145E-19	9.47186E-18	4.593259811	0.02813092	-1	507	528	469	735	414	240	193	146	202	276
ENSMUSG00000061577	chr8	Gpr114	4.91261471	5.55704E-19	9.73247E-18	0.12215472	0.105900959	1	1	0	0	2	1	29	25	39	35	20
ENSMUSG00000058070	chr12	Eml1	-1.3602267	5.73876E-19	1.00382E-17	7.10236499	0.026597582	-1	3104	2684	2606	3444	2880	1336	1342	1030	1090	1519
ENSMUSG00000017418	chr2	Arl5b	-1.5437714	6.2726E-19	1.09582E-17	4.159814108	0.030548985	-1	339	407	384	509	340	143	182	96	146	178
ENSMUSG00000004933	chr10	Matk	4.82521279	6.33216E-19	1.10485E-17	1.878201747	0.197357304	1	0	3	1	4	9	199	102	40	59	169
ENSMUSG00000036198	chrX	Arhgap36	4.57057258	6.3439E-19	1.10552E-17	2.680647505	0.202278415	1	5	4	13	5	9	327	72	152	70	379
ENSMUSG00000025907	chr1	Rb1cc1	-1.3953381	6.47202E-19	1.12644E-17	6.04830508	0.027538449	-1	1337	1418	1370	1820	1215	538	642	485	576	734
ENSMUSG00000005410	chr8	Mcm5	2.39205276	6.59731E-19	1.14682E-17	3.351479574	0.069264144	1	63	44	43	42	45	330	384	200	326	141
ENSMUSG00000072594	chr14	Gm16439	-2.7505202	6.65064E-19	1.15465E-17	1.189619337	0.06090123	-1	48	54	47	77	59	16	9	5	9	7
ENSMUSG00000033066	chr11	Gas7	1.6767425	6.68495E-19	1.15917E-17	4.782088783	0.038101367	1	152	156	190	272	206	1082	663	543	519	646
ENSMUSG00000035992	chr11	Fnip1	-1.585537	6.74546E-19	1.16821E-17	5.121810076	0.034622556	-1	756	705	812	1018	611	223	351	221	242	383
ENSMUSG00000020248	chr10	Nfyb	-1.2308742	6.85711E-19	1.18608E-17	5.045487746	0.020460999	-1	682	675	563	867	666	358	320	261	336	335
ENSMUSG00000003762	chr7	Adck4	1.85195563	6.94351E-19	1.19954E-17	3.240282809	0.040308924	1	51	58	60	69	61	329	181	217	266	198
ENSMUSG00000029816	chr6	Gpnmb	7.86012021	7.07011E-19	1.2199E-17	8.208537952	0.505251272	1	18	15	17	86	60	650	15071	1965	3821	27443
ENSMUSG00000061111	chr11	Fam195b	1.49702012	7.92453E-19	1.36564E-17	5.624710031	0.031423734	1	430	339	384	420	338	1623	943	1214	1107	1058
ENSMUSG00000017400	chr11	Stac2	4.96486729	7.94241E-19	1.36703E-17	1.990737154	0.215337895	1	3	3	2	4	5	180	72	161	19	176
ENSMUSG00000010830	chr15	Kdelr3	1.48114383	7.99292E-19	1.37404E-17	4.187569956	0.0279008	1	145	131	149	143	136	539	460	444	331	405
ENSMUSG00000042599	chr6	Kdm7a	-1.2750684	8.11524E-19	1.39335E-17	5.05853024	0.02218933	-1	608	653	655	961	650	384	354	254	276	329
ENSMUSG00000025132	chr11	Arhgdia	1.50650557	8.13455E-19	1.39495E-17	7.643153187	0.032884356	1	1412	1411	1342	2108	1528	6938	5204	3980	3864	4412
ENSMUSG00000029223	chr5	Uchl1	3.53358594	8.30611E-19	1.42263E-17	2.456830283	0.132571106	1	7	13	21	18	4	97	157	262	102	169
ENSMUSG00000055493	chr10	Epm2a	-1.5115404	8.8894E-19	1.52066E-17	6.122326468	0.032572758	-1	1535	1562	1356	1977	1288	463	609	483	676	707
ENSMUSG00000025597	chrX	Klhl4	-2.5979537	9.03827E-19	1.54424E-17	1.476224882	0.059222745	-1	64	71	78	83	48	16	10	7	15	14
ENSMUSG00000004698	chr12	Hdac9	-2.0486756	9.12435E-19	1.55704E-17	3.010501989	0.049398567	-1	152	203	186	267	155	51	66	31	66	39
ENSMUSG00000034266	chr12	Batf	4.59744546	9.21494E-19	1.57058E-17	0.694666416	0.132082844	1	1	2	3	1	1	86	51	25	44	27
ENSMUSG00000028497	chr4	Ptplad2	1.90794046	9.25828E-19	1.57605E-17	3.150342463	0.042687644	1	37	69	61	58	46	219	238	182	202	287
ENSMUSG00000046138	chr19	9930021J03Rik	-1.6664784	9.31636E-19	1.58401E-17	3.990107831	0.03555514	-1	288	319	354	501	339	86	145	114	130	139
ENSMUSG00000037712	chr14	Fermt2	-1.4294633	9.48205E-19	1.61022E-17	7.531494712	0.029803484	-1	3886	3529	3497	5289	3999	1526	1779	1260	1763	1852
ENSMUSG00000039512	chr17	Uhrf1bp1	-1.338295	9.55746E-19	1.62106E-17	5.02271692	0.024572029	-1	630	557	673	883	722	283	324	260	320	310
ENSMUSG00000028518	chr4	Prkaa2	-1.6879607	9.57181E-19	1.62152E-17	7.746102326	0.041118005	-1	4711	3839	4251	6843	4978	1178	1846	1424	1715	2102
ENSMUSG00000034041	chr8	Lyl1	2.31227103	9.62018E-19	1.62774E-17	2.920371417	0.062343607	1	39	33	49	36	26	345	174	136	161	209
ENSMUSG00000029333	chr5	Rasgef1b	2.89803909	1.05255E-18	1.77877E-17	2.137716795	0.087909328	1	18	23	10	14	9	173	176	74	109	86
ENSMUSG00000027797	chr3	Dclk1	2.85867208	1.09859E-18	1.85433E-17	4.47388819	0.104395511	1	79	60	72	102	86	671	531	1171	232	514
ENSMUSG00000025903	chr1	Lypla1	-2.0844308	1.11208E-18	1.87282E-17	5.737291386	0.060530387	-1	1344	1096	1185	1679	1157	178	377	230	335	537
ENSMUSG00000053291	chr7	Rab4b	1.5527602	1.11222E-18	1.87282E-17	4.019599492	0.030618817	1	139	112	113	120	120	558	397	320	314	388
ENSMUSG00000031897	chr8	Psmb10	1.60207322	1.11638E-18	1.87755E-17	4.426845103	0.034117769	1	125	137	161	226	145	723	514	475	539	382
ENSMUSG00000022534	chr16	Mefv	5.60698363	1.12717E-18	1.89344E-17	0.009343263	0.120928224	1	0	1	0	1	0	43	32	13	31	20
ENSMUSG00000070780	chr5	Rbm47	3.71825537	1.25548E-18	2.10644E-17	1.590690954	0.124560695	1	2	13	6	4	4	114	125	39	85	75
ENSMUSG00000026832	chr2	Cytip	4.14116977	1.2618E-18	2.11449E-17	0.976706143	0.127730266	1	6	4	1	3	0	83	73	30	62	35
ENSMUSG00000033209	chr5	Ttc28	-1.5652739	1.29741E-18	2.17157E-17	4.620099853	0.033576774	-1	495	485	449	669	629	232	182	208	135	257
ENSMUSG00000028164	chr3	Manba	1.51000332	1.3057E-18	2.18284E-17	3.648837791	0.027627801	1	87	78	113	112	88	352	298	296	268	285
ENSMUSG00000099023	chr11	Gm27456	-3.2049741	1.31072E-18	2.18861E-17	1.062349033	0.08074541	-1	60	42	52	74	42	3	7	4	13	4
ENSMUSG00000021775	chr14	Nr1d2	-1.4422087	1.31588E-18	2.19461E-17	6.685616221	0.030304012	-1	2378	2206	2265	2547	1790	813	1015	720	881	1094

ENSMUSG00000037742	chr9	Eef1a1	1.46165181	1.34633E-18	2.2427E-17	9.983773182	0.031680404	1	9199	8529	7409	8153	6667	28871	25447	22681	19716	25112
ENSMUSG00000028278	chr4	Rragd	-1.5710032	1.35746E-18	2.25856E-17	7.749599215	0.036155793	-1	5159	4494	4151	5580	4594	1410	2026	1326	2046	2017
ENSMUSG00000035385	chr11	Ccl2	6.40778913	1.46302E-18	2.43129E-17	4.797826046	0.376474826	1	5	8	7	16	12	1208	1572	149	1515	60
ENSMUSG00000038179	chr1	Slamf7	5.55181596	1.50894E-18	2.50293E-17	1.942186677	0.257949436	1	1	3	0	4	3	23	182	71	81	232
ENSMUSG00000039745	chr7	Htatip2	1.87329614	1.50971E-18	2.50293E-17	3.138096258	0.041583508	1	66	64	47	50	47	221	229	189	277	189
ENSMUSG00000038312	chr2	Edem2	1.66041031	1.65069E-18	2.73341E-17	3.783326559	0.03508956	1	107	96	91	124	72	487	385	244	244	354
ENSMUSG00000029004	chr5	Kmt2e	-1.4232017	1.65997E-18	2.74553E-17	4.688291382	0.027870907	-1	539	525	465	753	527	239	213	169	205	320
ENSMUSG00000021712	chr13	Trim23	-1.9684196	1.68133E-18	2.7746E-17	4.495762746	0.052588778	-1	572	525	462	684	441	84	182	102	149	229
ENSMUSG00000042529	chr11	Kcnj12	-1.6480114	1.68152E-18	2.7746E-17	5.175453284	0.03838166	-1	900	726	767	860	796	217	360	188	328	330
ENSMUSG00000098701	chr10	Mir6914	-3.7426512	1.70777E-18	2.81459E-17	0.728368184	0.100335216	-1	30	31	45	61	50	0	5	2	7	3
ENSMUSG00000064267	chr5	Hvcn1	2.90461079	1.80377E-18	2.96931E-17	3.052245267	0.100101564	1	24	39	31	24	22	346	241	91	154	368
ENSMUSG00000057722	chr4	Lepr	-2.0508616	1.87808E-18	3.088E-17	2.0332573	0.041417607	-1	105	89	88	111	87	29	26	16	28	28
ENSMUSG00000027843	chr3	Ptpn22	3.49792406	1.89918E-18	3.11903E-17	0.941231571	0.093375392	1	2	5	5	7	2	70	69	26	53	50
ENSMUSG00000023908	chr17	Pkmyt1	2.89061582	1.90197E-18	3.11995E-17	1.595202355	0.078584533	1	12	12	4	9	13	112	94	67	88	53
ENSMUSG00000003206	chr17	Ebi3	3.38915327	1.93846E-18	3.17607E-17	1.338828744	0.098536569	1	1	6	6	7	10	116	75	42	57	69
ENSMUSG00000031540	chr8	Kat6a	-1.4039735	1.94273E-18	3.17934E-17	5.003338129	0.027679539	-1	644	594	566	844	808	307	320	210	301	299
ENSMUSG00000021061	chr12	Sptb	-1.5518051	2.00937E-18	3.28456E-17	7.67615553	0.035657929	-1	3871	3710	3689	6313	5276	1783	1590	1373	1648	2126
ENSMUSG00000067288	chr17	Rps28	1.58972884	2.11887E-18	3.4595E-17	7.199731051	0.037261827	1	1156	999	867	1353	1100	5454	3646	3369	2911	2781
ENSMUSG00000028459	chr4	Cd72	5.0031419	2.12593E-18	3.46698E-17	2.629148041	0.241152329	1	0	9	4	5	8	464	118	130	46	228
ENSMUSG00000043019	chr1	Edem3	-1.3807507	2.12851E-18	3.46715E-17	5.104672501	0.026920861	-1	733	683	676	871	727	251	360	258	301	383
ENSMUSG00000043991	chr18	Pura	-1.3585271	2.24789E-18	3.65733E-17	5.225484266	0.026237372	-1	754	672	743	1061	790	319	386	289	288	432
ENSMUSG00000095538	chr7	Gm21983	1.54606297	2.28554E-18	3.71426E-17	4.012571393	0.030977813	1	141	115	113	118	116	557	396	317	315	380
ENSMUSG00000025323	chr12	Sp4	-2.5052694	2.29089E-18	3.71863E-17	2.379538091	0.070709104	-1	129	125	90	180	130	17	24	13	25	46
ENSMUSG00000030592	chr7	Ryr1	-1.6278664	2.38014E-18	3.85902E-17	11.28740639	0.039548756	-1	49123	45415	44501	75400	68072	21284	20485	17154	15868	25534
ENSMUSG00000032334	chr9	Loxl1	1.67584873	2.5895E-18	4.1936E-17	6.039388553	0.040891917	1	409	410	408	608	502	2156	1493	1947	1035	1549
ENSMUSG00000062054	chr12	Iah1	1.70505997	2.90087E-18	4.69242E-17	3.105099199	0.03417662	1	51	77	55	68	44	265	210	176	196	215
ENSMUSG00000026430	chr1	Rassf5	2.50016613	2.91896E-18	4.71623E-17	2.014281853	0.064853575	1	16	14	20	25	12	169	102	64	98	114
ENSMUSG00000024087	chr17	Cyp1b1	3.33997227	3.00287E-18	4.8462E-17	2.100824512	0.117551024	1	17	13	5	7	12	232	133	73	65	125
ENSMUSG00000027322	chr2	Siglec1	2.45652289	3.0732E-18	4.95399E-17	2.944184826	0.073264111	1	24	37	25	42	44	323	189	130	128	292
ENSMUSG00000038970	chr5	Lmtk2	-1.2457683	3.09057E-18	4.97625E-17	4.80443514	0.021535789	-1	513	534	536	774	574	289	290	245	228	300
ENSMUSG00000102418	chr1	Sh2d1b1	5.70828265	3.1062E-18	4.99566E-17	0.086441431	0.141430074	1	0	0	0	1	1	17	37	19	47	26
ENSMUSG00000028656	chr4	Cap1	1.69237939	3.26755E-18	5.24911E-17	6.301392974	0.042104534	1	482	565	509	707	515	2827	2261	1119	2073	1669
ENSMUSG00000024835	chr19	Coro1b	1.44424029	3.3887E-18	5.43749E-17	5.469508198	0.030232339	1	349	387	381	371	269	1410	1039	838	1001	1026
ENSMUSG00000073647	chr18	Gm10557	-3.576339	3.48326E-18	5.5828E-17	0.405167635	0.081381739	-1	42	41	28	32	25	4	4	1	2	4
ENSMUSG00000034021	chr5	Pds5b	-1.472966	3.52573E-18	5.64439E-17	5.014944271	0.031045759	-1	682	613	586	913	751	233	325	198	311	327
ENSMUSG00000068220	chr15	Lgals1	1.87973147	3.54333E-18	5.66609E-17	8.832217687	0.052310484	1	4065	3198	2592	2554	1992	11873	13475	11978	12282	8571
ENSMUSG00000020592	chr12	Sdc1	1.79630751	3.79935E-18	6.06854E-17	4.300974052	0.044086338	1	128	131	131	138	119	733	547	395	268	578
ENSMUSG00000019841	chr10	Rev3l	-1.7316512	3.82664E-18	6.10514E-17	5.27875501	0.043398617	-1	818	811	962	969	844	213	293	200	339	417
ENSMUSG00000000708	chr17	Kat2b	-1.3560934	3.86003E-18	6.1514E-17	5.894604865	0.027172859	-1	1219	1098	1111	1836	1174	589	599	389	569	591
ENSMUSG00000066232	chr7	Ipo7	-1.6590525	3.91655E-18	6.23436E-17	6.154397191	0.040651385	-1	1545	1366	1375	2314	1541	418	678	414	702	568
ENSMUSG00000033943	chr2	Mga	-1.2888945	3.98269E-18	6.33243E-17	5.054823044	0.023704352	-1	665	687	603	932	640	311	336	237	296	398
ENSMUSG00000050310	chr15	Rictor	-1.5180463	4.23048E-18	6.71115E-17	3.484132476	0.028610972	-1	232	191	214	331	264	101	96	75	90	108
ENSMUSG00000078949	chr2	R3hdml	9.02202007	4.22984E-18	6.71115E-17	1.143147549	0.344496069	1	0	0	0	0	0	47	49	174	13	43
ENSMUSG00000028822	chr4	Tmem50a	1.41754595	4.5824E-18	7.26118E-17	5.817617739	0.029707008	1	532	498	383	502	367	1874	1293	1051	1177	1358
ENSMUSG00000098234	chr1	Snhg6	2.10439979	4.69438E-18	7.4302E-17	2.87160307	0.053067558	1	44	40	43	36	36	145	259	159	215	166
ENSMUSG00000021339	chr13	Mrs2	-1.6681192	4.71111E-18	7.44825E-17	3.440792051	0.03517381	-1	199	210	243	332	241	86	90	72	105	66
ENSMUSG00000052155	chr2	Acvr2a	-1.8157888	4.72789E-18	7.46633E-17	4.795618864	0.047245691	-1	749	625	547	637	632	144	192	139	204	322
ENSMUSG00000067851	chr1	Arfgef1	-1.39736	4.76738E-18	7.52019E-17	6.081094824	0.029136153	-1	1296	1256	1264	2031	1509	554	711	508	612	651
ENSMUSG00000020101	chr10	4632428N05Rik	1.8670837	4.81884E-18	7.59279E-17	5.658388367	0.050859901	1	393	368	317	303	221	1730	1377	903	815	1736
ENSMUSG00000033107	chr18	Rnf125	-3.8157546	4.83051E-18	7.60261E-17	0.332542422	0.087607192	-1	26	31	33	31	39	0	4	1	3	4
ENSMUSG00000035735	chr19	Dagla	-1.4340701	4.86577E-18	7.64949E-17	3.793007763	0.02641002	-1	287	241	282	357	327	124	122	119	102	140
ENSMUSG00000032431	chr9	Crtap	1.42171815	5.29908E-18	8.32135E-17	5.149342847	0.029300062	1	320	284	269	330	229	1236	805	709	640	862
ENSMUSG00000001998	chr2	Ap4e1	-2.0739907	5.5366E-18	8.68457E-17	3.06559523	0.053988887	-1	206	170	176	263	188	34	58	30	76	60
ENSMUSG00000041075	chr1	Fzd7	-1.8140465	5.76962E-18	9.03993E-17	5.582752603	0.048387049	-1	1054	974	1065	1222	1199	252	372	268	274	569
ENSMUSG00000026928	chr2	Card9	3.92871556	5.91385E-18	9.25554E-17	1.693515419	0.151133886	1	7	4	6	9	2	167	117	43	111	40
ENSMUSG00000033526	chr2	Ppip5k1	-1.6803105	5.95851E-18	9.31501E-17	5.576261356	0.041699972	-1	722	1058	1080	1695	926	414	373	304	461	294
ENSMUSG00000025362	chr10	Rps26	1.63831587	6.0333E-18	9.42138E-17	7.475952272	0.040666556	1	1447	1137	1103	1498	1260	6821	4564	4002	3702	3103
ENSMUSG00000034617	chr13	Mtrr	-1.4042976	6.3E-18	9.82688E-17	4.22781197	0.026808146	-1	392	372	372	487	393	165	178	116	202	174
ENSMUSG00000045954	chr1	Sdpr	-1.3143971	6.38523E-18	9.94872E-17	5.804931868	0.025789337	-1	1061	1101	1176	1686	965	544	499	443	569	558
ENSMUSG00000020821	chr11	Kif1c	-1.4336968	6.6299E-18	1.03184E-16	9.535839874	0.031799634	-1	14222	13511	14083	23072	16573	7246	6587	5116	6949	6948
ENSMUSG00000025898	chr9	Cwf19l2	-1.6835929	6.72765E-18	1.04589E-16	3.895925188	0.03826734	-1	353	332	307	409	284	81	133	79	147	131
ENSMUSG00000055805	chr11	Fmnl1	1.79858835	6.9972E-18	1.08659E-16	3.986723031	0.044126375	1	87	103	104	156	78	599	442	308	394	267
ENSMUSG00000021767	chr14	Kat6b	-1.5579812	7.05924E-18	1.095E-16	3.762074387	0.03196955	-1	263	274	268	419	286	97	117	114	82	147
ENSMUSG00000017057	chrX	Il13ra1	1.5350827	7.57712E-18	1.17403E-16	3.629363738	0.030367265	1	90	108	82	118	71	409	317	257	247	266
ENSMUSG00000076236	chr13	Mir682	1.54674305	7.78432E-18	1.2048E-16	3.934566922	0.03201952	1	148	113	110	120	83	500	333	318	369	331

ENSMUSG00000027346	chr2	Gpcpd1	-1.671991	8.14162E-18	1.25871E-16	6.664404847	0.042369438	-1	2149	2367	1976	3096	1994	562	897	565	854	1071
ENSMUSG00000069892	chr11	9930111J21Rik2	-3.8529301	8.24409E-18	1.27314E-16	0.352478469	0.099150266	-1	21	38	28	46	32	7	2	1	0	2
ENSMUSG00000022048	chr14	Dpysl2	1.59935569	8.54193E-18	1.31768E-16	4.417992415	0.035925277	1	208	149	146	158	121	758	549	457	453	410
ENSMUSG00000090942	chr18	F830016B08Rik	-3.1556422	8.87345E-18	1.36731E-16	4.793628021	0.132562494	-1	1296	648	833	401	453	39	74	90	145	98
ENSMUSG00000046402	chr9	Rbp1	2.20887204	8.89589E-18	1.36926E-16	3.398418601	0.064099442	1	58	59	55	60	42	496	210	297	162	247
ENSMUSG00000023505	chr6	Cdca3	2.78093903	9.65101E-18	1.48386E-16	2.542701362	0.092687831	1	38	16	15	21	17	154	249	153	163	86
ENSMUSG00000037270	chr3	4932438A13Rik	-1.4016731	9.71503E-18	1.49206E-16	4.97180286	0.028804214	-1	583	626	632	918	642	292	273	191	344	305
ENSMUSG00000035357	chr6	Pdzrn3	-1.5701754	9.73472E-18	1.49344E-16	5.653714529	0.037059154	-1	828	920	1117	1754	1057	384	423	328	486	442
ENSMUSG00000068663	chr16	Clec16a	-1.7286287	1.02553E-17	1.57157E-16	6.244578352	0.045276978	-1	1559	1320	1603	2485	1781	989	483	445	450	548
ENSMUSG00000032271	chr9	Nnmt	2.75776474	1.02945E-17	1.57585E-16	3.303565206	0.097754594	1	30	58	35	29	31	181	256	235	483	203
ENSMUSG00000034613	chr10	Ppm1h	2.01049147	1.06273E-17	1.62503E-16	2.519359147	0.04675682	1	23	34	33	48	28	168	192	106	131	138
ENSMUSG00000037151	chr10	Lrrc20	-1.5565088	1.09855E-17	1.67797E-16	7.433768708	0.037456723	-1	4146	3889	3564	4129	3408	1079	1745	1118	1508	1695
ENSMUSG00000056608	chr8	Chd9	-1.2322948	1.11025E-17	1.69398E-16	4.486879631	0.021257625	-1	409	440	436	605	450	251	199	199	221	219
ENSMUSG00000036478	chr10	Btg1	1.54017793	1.14134E-17	1.73952E-16	5.173260249	0.035243003	1	333	314	259	285	176	1199	886	736	683	906
ENSMUSG00000056492	chr17	Gpr116	-1.4044953	1.14652E-17	1.74551E-16	5.946421448	0.030072398	-1	991	1263	1251	1945	1270	629	558	476	463	645
ENSMUSG00000045312	chr13	Lhfpl2	1.79858934	1.15043E-17	1.74956E-16	4.708802437	0.047242996	1	218	141	169	200	138	866	791	364	471	866
ENSMUSG00000040809	chr3	Chil3	9.46525689	1.16609E-17	1.77145E-16	4.065713232	0.60155351	1	0	0	0	2	1	104	889	84	1511	46
ENSMUSG00000041058	chr4	Wwp1	-1.7059535	1.16892E-17	1.77382E-16	7.448995346	0.044736221	-1	3521	3558	3573	5739	3734	942	1430	975	1607	1712
ENSMUSG00000037601	chr11	Nme1	1.65949181	1.21686E-17	1.84456E-16	5.996411265	0.041818822	1	449	407	435	619	389	1913	1833	1540	1689	910
ENSMUSG00000060791	chr7	Gmfg	3.0026772	1.33356E-17	2.01927E-16	2.624909678	0.108767068	1	17	20	23	16	21	336	154	94	208	94
ENSMUSG00000059355	chr8	Wdr83os	1.33261909	1.34181E-17	2.02956E-16	5.360415349	0.026614241	1	393	324	252	424	347	1078	937	1009	877	875
ENSMUSG00000023951	chr17	Vegfa	-1.478141	1.35573E-17	2.0484E-16	6.18317959	0.033568496	-1	1178	1485	1647	2374	1357	586	657	594	673	606
ENSMUSG00000099703	chr18	Gm28285	-1.4830274	1.39281E-17	2.10215E-16	3.784742394	0.029348705	-1	307	283	289	381	248	94	129	92	136	136
ENSMUSG00000072945	chrX	Ripply1	6.31022239	1.39913E-17	2.10941E-16	1.075581875	0.253890052	1	0	0	2	0	1	76	38	123	14	61
ENSMUSG00000015575	chr17	Atp6v0e	1.87342418	1.49841E-17	2.25666E-16	5.11508924	0.052143135	1	244	255	235	184	168	1385	1074	540	783	718
ENSMUSG00000022357	chr15	Klhl38	-2.2000264	1.53346E-17	2.30696E-16	3.565033008	0.065846271	-1	280	416	278	254	193	65	41	57	82	97
ENSMUSG00000044583	chrX	Tlr7	2.50903422	1.53552E-17	2.30758E-16	2.292255771	0.07281443	1	19	22	23	20	20	188	129	60	123	169
ENSMUSG00000058672	chr13	Tubb2a	2.16658251	1.57892E-17	2.37025E-16	5.444294254	0.069569079	1	173	207	197	399	225	1402	1224	1663	802	658
ENSMUSG00000040511	chr7	Pvr	1.45004603	1.59164E-17	2.38678E-16	3.62669052	0.027321642	1	103	88	86	124	88	353	302	312	226	268
ENSMUSG00000039062	chr7	Anpep	2.68018639	1.60952E-17	2.411E-16	5.821042557	0.103200349	1	232	199	158	272	272	2646	1247	898	630	2784
ENSMUSG00000028583	chr4	Pdpn	2.00898345	1.7325E-17	2.59244E-16	4.590099981	0.058529489	1	176	131	97	189	124	752	965	425	645	363
ENSMUSG00000026630	chr1	Batf3	3.81275331	1.81911E-17	2.71913E-16	0.156680362	0.072058515	1	1	2	2	1	3	36	27	30	24	31
ENSMUSG00000028525	chr4	Pde4b	-1.4535432	1.86248E-17	2.78099E-16	5.839137082	0.032547378	-1	1069	1134	982	1762	1344	611	454	376	590	473
ENSMUSG00000026981	chr2	Il1rn	6.92366232	1.86932E-17	2.78822E-16	4.788948351	0.448567763	1	1	1	1	21	11	1718	1921	104	389	503
ENSMUSG00000031129	chr9	Slc9a9	1.84427491	1.87375E-17	2.79184E-16	3.011947785	0.042597025	1	49	64	55	47	39	226	186	163	245	190
ENSMUSG00000005534	chr8	Insr	-1.3264567	1.95436E-17	2.90885E-16	5.897417616	0.027192503	-1	1102	1034	1179	1805	1273	672	597	507	462	545
ENSMUSG00000021898	chr14	Asb14	-1.5479017	1.97599E-17	2.93791E-16	5.938949356	0.036977234	-1	1434	1344	1258	1532	1219	413	617	364	649	497
ENSMUSG00000038205	chr3	Prkab2	-1.8646703	2.0502E-17	3.04502E-16	8.358049382	0.053955538	-1	8691	7421	6701	8237	7163	1578	2664	1528	3231	2468
ENSMUSG00000067653	chr1	Ankrd23	-1.7050884	2.05303E-17	3.04598E-16	11.48987467	0.045733183	-1	68557	59410	62926	76225	60460	26566	28804	15478	25196	14672
ENSMUSG00000094441	chr17	Zfp955a	-3.1271487	2.09069E-17	3.09856E-16	1.436613747	0.098497609	-1	60	75	68	87	60	5	6	3	20	9
ENSMUSG00000030677	chr7	Kif22	2.77549002	2.15032E-17	3.18356E-16	2.491282591	0.093375034	1	24	26	14	21	18	207	223	138	149	64
ENSMUSG00000059149	chr1	Mfsd4	-2.135914	2.22108E-17	3.28486E-16	2.765964722	0.057863538	-1	136	176	147	210	148	53	17	43	37	53
ENSMUSG00000034898	chr9	Filip1	-1.8738922	2.27548E-17	3.36175E-16	5.041991695	0.052825081	-1	764	581	696	1052	781	132	192	222	242	352
ENSMUSG00000015214	chrX	Mtmr1	-1.2737582	2.31854E-17	3.42174E-16	4.600518044	0.02359634	-1	496	468	431	670	496	212	255	185	232	271
ENSMUSG00000038059	chr18	Smim3	2.40629209	2.36365E-17	3.48303E-16	2.773887181	0.072995555	1	42	29	33	27	25	344	164	141	148	136
ENSMUSG00000040118	chr5	Cacna2d1	-1.6570382	2.36505E-17	3.48303E-16	8.678313259	0.043353515	-1	10097	8481	8368	10508	8805	2219	3830	2469	3410	4134
ENSMUSG00000061046	chr17	Haghl	1.50177254	2.40371E-17	3.53624E-16	3.79120302	0.030529481	1	129	111	91	107	92	324	274	340	316	393
ENSMUSG00000024588	chr18	Fech	-1.4783262	2.41748E-17	3.55275E-16	6.960168326	0.034495493	-1	2658	2674	2636	3305	2380	806	1063	945	1237	1281
ENSMUSG00000057181	chr11	5730455P16Rik	-1.4822516	2.42445E-17	3.55926E-16	5.712060524	0.033966182	-1	1201	1016	1078	1315	1119	324	514	384	458	564
ENSMUSG00000033083	chr14	Tbc1d4	-1.4508613	2.42852E-17	3.56148E-16	5.256547425	0.032140497	-1	668	726	654	1207	943	416	377	245	310	333
ENSMUSG00000020700	chr11	Map3k3	-1.3960497	2.50231E-17	3.66586E-16	4.547996814	0.028665592	-1	478	457	466	626	492	187	219	146	229	268
ENSMUSG00000068284	chr16	Gm608	-1.3072686	2.62179E-17	3.83687E-16	5.818927651	0.026562577	-1	1031	956	1104	1703	1235	574	528	479	478	595
ENSMUSG00000042228	chr4	Lyn	1.64201874	2.7095E-17	3.96109E-16	4.263035751	0.038872371	1	132	149	143	174	93	656	548	297	482	399
ENSMUSG00000031858	chr8	Mau2	-1.4180674	2.77966E-17	4.05941E-16	4.854577811	0.030260599	-1	676	591	613	666	565	284	206	181	292	324
ENSMUSG00000051910	chr7	Sox6	-1.6004789	2.8434E-17	4.14816E-16	6.697418987	0.040318445	-1	2094	1768	2199	3073	2522	632	977	665	860	1058
ENSMUSG00000034297	chr11	Med13	-1.445467	2.86404E-17	4.17392E-16	5.369343897	0.032146998	-1	773	742	829	1257	925	308	427	314	305	456
ENSMUSG00000059791	chr17	Nrm	2.01380503	2.93526E-17	4.27325E-16	2.274832353	0.046011316	1	29	25	27	37	21	161	146	111	88	112
ENSMUSG00000030341	chr6	Tnfrsf1a	1.35649096	3.27972E-17	4.76975E-16	5.623586466	0.0286145	1	354	415	364	614	337	1557	1197	984	1046	1030
ENSMUSG00000022474	chr15	Pmm1	1.46254957	3.3107E-17	4.80981E-16	3.842684451	0.029393315	1	117	117	115	131	83	303	341	376	319	351
ENSMUSG00000057322	chr11	Rpl38	1.57088215	3.40929E-17	4.9479E-16	6.572930337	0.039003736	1	772	685	605	860	653	3753	2361	1936	1985	1721
ENSMUSG00000032889	chr11	Gm6685	-7.1356654	3.41648E-17	4.95319E-16	-0.589899592	0.104553152	-1	20	12	17	13	20	0	0	0	0	0
ENSMUSG00000079445	chr1	B3gnt7	5.07875056	3.47592E-17	5.03414E-16	0.525832664	0.174600318	1	2	1	0	2	0	71	38	23	58	16
ENSMUSG00000010142	chr11	Tnfrsf13b	3.01544412	3.60503E-17	5.21572E-16	1.986768815	0.104028321	1	7	19	12	16	8	137	137	62	153	66
ENSMUSG00000027827	chr3	Kcnab1	-1.9683688	3.80842E-17	5.5043E-16	2.059538677	0.042211258	-1	90	95	95	114	89	35	28	17	24	32
ENSMUSG00000021945	chr14	Zmym2	-1.299088	3.90999E-17	5.64174E-16	5.134509433	0.025835862	-1	705	643	652	1035	709	295	368	256	339	396

ENSMUSG00000103661	chr1	ANKRD23	-1.6891823	3.9116E-17	5.64174E-16	11.45940352	0.045733342	-1	67016	58027	61519	74363	58961	26288	28437	15322	24821	14455
ENSMUSG00000021556	chr13	Golm1	2.10313703	4.0009E-17	5.76459E-16	3.18186241	0.059449918	1	49	61	44	60	37	159	267	158	247	351
ENSMUSG00000028005	chr3	Gucy1b3	-1.807326	4.04415E-17	5.82091E-16	2.940477706	0.041853643	-1	137	175	171	253	150	41	61	52	49	71
ENSMUSG00000027130	chr2	Slc12a6	-1.1867077	4.06099E-17	5.83914E-16	5.053180346	0.021336794	-1	649	716	656	802	600	398	342	264	286	371
ENSMUSG00000003873	chr7	Bax	1.49509702	4.11427E-17	5.90966E-16	4.473686327	0.032913063	1	187	183	154	193	143	736	603	374	555	415
ENSMUSG00000028081	chr3	Rps3a1	1.33022604	4.11904E-17	5.91044E-16	8.558930986	0.028827653	1	3401	3135	2875	3687	2877	10142	9402	8056	9093	7356
ENSMUSG00000024349	chr18	Tmem173	2.00343677	4.46414E-17	6.3925E-16	3.578877617	0.056193871	1	53	78	87	82	49	505	336	274	216	230
ENSMUSG00000044749	chr11	Abca6	-2.5889133	4.46054E-17	6.3925E-16	2.280670433	0.082009575	-1	112	162	133	108	87	19	12	18	34	27
ENSMUSG00000020154	chr10	Ptprb	-1.5187447	4.67162E-17	6.68276E-16	5.752689248	0.036369447	-1	918	1005	1039	1721	1310	397	492	357	438	593
ENSMUSG00000035373	chr11	Ccl7	6.7474049	4.71182E-17	6.73338E-16	4.554415641	0.441058387	1	4	4	2	16	7	1164	1037	128	1440	38
ENSMUSG00000003355	chr15	Fkbp11	2.42693041	4.72372E-17	6.74348E-16	2.220666886	0.069400748	1	20	21	22	21	20	207	141	109	82	89
ENSMUSG00000012017	chr16	Scarf2	1.50860085	4.80803E-17	6.85684E-16	3.991986558	0.032194296	1	133	108	118	119	127	530	389	363	283	353
ENSMUSG00000033684	chr1	Qsox1	1.38346987	5.01876E-17	7.15006E-16	5.264027591	0.029710962	1	329	278	292	375	306	1286	716	892	732	922
ENSMUSG00000024695	chr19	Zfp91	-1.326053	5.07245E-17	7.21855E-16	7.379423978	0.028613151	-1	3509	3189	3341	4681	3115	1496	1782	1184	1658	1637
ENSMUSG00000056602	chr5	Fry	-1.475297	5.07716E-17	7.21855E-16	5.876724229	0.034514459	-1	1040	1068	1229	1818	1318	428	534	440	455	677
ENSMUSG00000093701	chr16	Gm21970	1.49373191	5.12401E-17	7.27776E-16	3.82068853	0.031275227	1	107	112	96	153	83	457	397	239	302	308
ENSMUSG00000025747	chr5	Tyms	2.72747192	5.25514E-17	7.45643E-16	2.3068266	0.090888383	1	18	21	19	21	14	156	215	104	144	62
ENSMUSG00000054640	chr17	Slc8a1	-2.7321913	5.38414E-17	7.63172E-16	2.256859382	0.091213006	-1	111	77	109	179	137	8	25	11	30	25
ENSMUSG00000000275	chr11	Trim25	1.18092366	5.4289E-17	7.68737E-16	4.765323946	0.020748871	1	243	235	220	301	236	659	635	515	540	729
ENSMUSG00000036918	chr17	Ttc7	1.35200595	5.48956E-17	7.76539E-16	5.076854004	0.028215222	1	309	271	229	357	251	715	815	577	939	894
ENSMUSG00000078671	chr7	Chd2	-1.3266447	5.50543E-17	7.77997E-16	5.486573741	0.027646262	-1	950	827	897	1129	957	365	406	406	378	522
ENSMUSG00000035164	chr9	Zc3h12c	-1.8465341	5.94768E-17	8.39644E-16	2.305314045	0.038845117	-1	105	110	101	132	116	35	32	26	38	41
ENSMUSG00000049791	chr7	Fzd4	-2.4284642	6.00171E-17	8.46417E-16	5.062665396	0.088087829	-1	687	1331	863	643	582	87	240	138	205	175
ENSMUSG00000067189	chr17	Gm7335	-3.665203	6.15192E-17	8.66726E-16	0.199324236	0.088083251	-1	29	23	27	43	24	7	0	1	1	3
ENSMUSG00000027078	chr2	Ube2l6	1.72604695	6.2586E-17	8.80868E-16	3.666780374	0.042226079	1	85	85	85	123	60	477	367	203	241	312
ENSMUSG00000026469	chr1	Xpr1	-1.3124292	6.65811E-17	9.36154E-16	6.246267738	0.027814559	-1	1578	1592	1372	1901	1606	805	832	586	542	815
ENSMUSG00000028273	chr3	Pdlim5	-1.3282428	6.77423E-17	9.51524E-16	8.682871454	0.029173324	-1	9303	7721	8407	11635	7065	4130	3731	3164	3494	4674
ENSMUSG00000035208	chr11	Slfn8	2.51243406	6.851E-17	9.61342E-16	1.531903763	0.064994494	1	12	16	6	18	9	85	90	49	65	95
ENSMUSG00000021816	chr14	Ppp3cb	-1.3735792	6.93558E-17	9.72234E-16	7.42156328	0.030937795	-1	3889	3241	3244	4505	3581	1358	1738	1252	1507	1943
ENSMUSG00000006740	chr18	Kif5b	-1.5300935	7.07554E-17	9.90859E-16	6.783316472	0.037960542	-1	2415	2123	2130	3193	2386	774	1081	601	1059	1113
ENSMUSG00000025754	chr7	Agbl1	-3.6917707	7.15523E-17	1.00102E-15	1.397029465	0.139504999	-1	25	82	72	118	59	2	5	4	9	9
ENSMUSG00000029204	chr5	Rhoh	3.13069697	7.16504E-17	1.00139E-15	0.989955304	0.087429983	1	1	3	8	13	3	67	52	41	47	64
ENSMUSG00000038618	chr7	Rassf7	4.02189856	7.42352E-17	1.03647E-15	1.57085453	0.167728718	1	5	5	1	7	6	125	43	140	34	90
ENSMUSG00000096146	chr7	Kcnj11	-1.7216293	7.64229E-17	1.06595E-15	5.036981846	0.046364613	-1	737	687	678	900	741	140	299	214	224	362
ENSMUSG00000029571	chr6	Tmem106b	-1.2462885	7.66276E-17	1.06774E-15	5.588823875	0.024679	-1	878	1004	965	1345	870	457	455	399	471	544
ENSMUSG00000028906	chr4	Epb4.1	-1.2656228	7.73439E-17	1.07665E-15	6.233350974	0.025953729	-1	1581	1431	1416	2049	1470	651	773	622	736	817
ENSMUSG00000085925	chr12	Rtl1	6.70437085	7.95203E-17	1.10585E-15	1.438068563	0.333187005	1	0	1	0	1	1	202	24	75	14	108
ENSMUSG00000092470	chr16	Gm20518	-1.6687285	7.98628E-17	1.1095E-15	3.834511479	0.04034319	-1	290	279	295	421	327	79	113	80	119	162
ENSMUSG00000025138	chr11	Sirt7	1.57227627	8.52533E-17	1.18322E-15	3.545798732	0.034327123	1	104	77	75	111	68	404	297	196	275	252
ENSMUSG00000028063	chr3	Lmna	1.47393963	8.63114E-17	1.19576E-15	7.364584753	0.035686289	1	1360	1075	1117	1882	1147	5537	4295	3751	3281	3033
ENSMUSG00000059108	chr7	Ifitm6	5.1601245	8.63284E-17	1.19576E-15	0.605065746	0.193221742	1	3	0	1	1	0	54	62	24	64	14
ENSMUSG00000027782	chr3	Kpna4	-1.4417623	8.89496E-17	1.23085E-15	6.55520583	0.033939688	-1	1986	1604	1667	2826	2230	842	940	567	859	939
ENSMUSG00000039395	chr1	Mreg	-1.5093742	9.28887E-17	1.28409E-15	4.619558957	0.035245536	-1	430	518	566	841	386	205	222	148	213	255
ENSMUSG00000039294	chr11	BC017643	1.4854513	9.94793E-17	1.37384E-15	3.705933739	0.03088844	1	115	106	82	111	91	423	317	216	317	293
ENSMUSG00000060550	chr17	H2-Q7	3.0096614	9.99321E-17	1.37873E-15	1.754011887	0.101068433	1	7	15	13	4	12	145	58	93	75	99
ENSMUSG00000034218	chr9	Atm	-2.3347421	1.09307E-16	1.50658E-15	2.626868884	0.07173757	-1	148	154	133	185	138	16	40	24	55	27
ENSMUSG00000074800	chr13	Gm4149	1.39782977	1.11101E-16	1.5298E-15	4.752862684	0.030321987	1	260	229	196	236	176	895	553	550	651	542
ENSMUSG00000045767	chr13	B230219D22Rik	-1.775802	1.13311E-16	1.55869E-15	5.402339197	0.050299969	-1	922	867	908	1220	958	175	393	243	300	442
ENSMUSG00000001027	chr11	Scn4a	-1.5152373	1.14003E-16	1.56667E-15	8.287748236	0.038137543	-1	6055	5490	5609	9200	8260	2264	2839	2401	2565	3121
ENSMUSG00000035885	chr19	Cox8a	1.44388882	1.14814E-16	1.57627E-15	6.060871263	0.033963223	1	476	561	554	662	418	2108	1556	1728	1193	1393
ENSMUSG00000037348	chr4	Paqr7	1.9050579	1.15069E-16	1.57822E-15	3.028899272	0.048836425	1	70	53	53	37	35	219	214	158	233	209
ENSMUSG00000063550	chr7	Nup98	-1.6887625	1.17128E-16	1.60489E-15	3.161902565	0.038627579	-1	176	198	159	269	210	53	84	53	79	72
ENSMUSG00000049339	chr1	Fam134a	1.35667932	1.18811E-16	1.62635E-15	4.785276438	0.028624986	1	187	244	204	303	214	908	597	515	517	721
ENSMUSG00000100975	chr12	Gm28875	2.43661356	1.191E-16	1.62872E-15	1.810593879	0.067184294	1	15	13	10	22	18	117	119	78	92	58
ENSMUSG00000026640	chr1	Plxna2	-1.6080648	1.21204E-16	1.65587E-15	4.313994851	0.039307536	-1	348	313	365	688	534	170	175	132	133	192
ENSMUSG00000002458	chr2	Rgs19	2.15417089	1.25571E-16	1.71385E-15	2.460555538	0.058170538	1	25	29	31	32	28	217	139	81	154	131
ENSMUSG00000007891	chr7	Ctsd	1.48195343	1.26992E-16	1.73155E-15	10.09688333	0.03680022	1	9221	8615	7478	10179	7581	30053	30072	15823	25466	31645
ENSMUSG00000029915	chr6	Clec5a	4.03935187	1.27981E-16	1.74334E-15	1.842204075	0.176786324	1	5	8	4	3	8	171	178	26	80	84
ENSMUSG00000018654	chr11	Ikzf1	2.91276787	1.31223E-16	1.78427E-15	1.963110381	0.099733833	1	13	12	6	11	22	147	156	57	97	89
ENSMUSG00000063524	chr4	Eno1	1.79922635	1.31241E-16	1.78427E-15	7.874030953	0.053054268	1	1745	1547	1258	1772	1473	3896	5878	7312	4399	7958
ENSMUSG00000006611	chr13	Hfe	2.17293651	1.3167E-16	1.78836E-15	4.628356279	0.072215428	1	130	167	105	155	108	310	578	623	701	1040
ENSMUSG00000027470	chr2	Mylk2	-1.2836417	1.32517E-16	1.79812E-15	9.040337077	0.027861508	-1	11755	11125	10637	11870	9931	5030	5112	4612	4984	5261
ENSMUSG00000027248	chr2	Pdia3	1.47232595	1.36049E-16	1.84425E-15	7.438355678	0.0360922	1	1346	1331	1208	1726	1254	5658	5077	3074	4078	3098
ENSMUSG00000031433	chrX	Rbm41	-2.8613424	1.42275E-16	1.92678E-15	1.405601837	0.087960406	-1	82	69	59	74	51	8	9	2	18	13
ENSMUSG00000036943	chr9	Rab8b	1.44867285	1.47922E-16	2.00132E-15	4.462346139	0.032402272	1	158	171	151	224	173	686	610	310	526	515

ENSMUSG00000047945	chr4	Marcksl1	2.29790705	1.48182E-16	2.00289E-15	4.106519435	0.078940079	1	97	88	76	93	74	1009	433	344	300	289
ENSMUSG00000027889	chr3	Ampd2	1.43652525	1.50298E-16	2.02953E-15	3.644191828	0.028876337	1	109	88	98	123	80	382	330	279	244	245
ENSMUSG00000036054	chr8	Sugp2	-1.2123116	1.53596E-16	2.07207E-15	5.567824769	0.023800994	-1	904	842	855	1344	1014	536	441	426	439	493
ENSMUSG00000039976	chr11	Tbc1d16	-1.3335671	1.57151E-16	2.11798E-15	5.145942065	0.028478592	-1	763	644	622	957	794	389	272	241	367	376
ENSMUSG00000038582	chr5	Pptc7	-1.5191371	1.61164E-16	2.16997E-15	6.396572733	0.038146273	-1	1337	1630	1935	2854	1651	618	764	641	803	710
ENSMUSG00000043241	chr2	Upf2	-1.3278634	1.62511E-16	2.186E-15	4.579290873	0.027339009	-1	480	500	439	613	505	188	230	176	262	248
ENSMUSG00000006442	chr4	Srm	1.95810591	1.65738E-16	2.22727E-15	4.162925412	0.058452243	1	114	88	91	154	100	767	563	322	432	255
ENSMUSG00000035239	chr7	Neu3	-1.6459068	1.7011E-16	2.2811E-15	2.678542788	0.033771304	-1	167	131	113	178	127	56	55	41	42	56
ENSMUSG00000070691	chr4	Runx3	4.01141886	1.70233E-16	2.2811E-15	0.556158782	0.122542234	1	3	3	2	3	0	55	60	40	29	20
ENSMUSG00000094446	chr13	Gm6344	5.93061435	1.69994E-16	2.2811E-15	1.297555894	0.292405249	1	2	1	1	1	0	7	107	91	80	78
ENSMUSG00000011008	chr3	Mcoln2	4.20648559	1.73059E-16	2.31674E-15	0.727466877	0.150976824	1	1	4	1	4	1	77	52	13	44	51
ENSMUSG00000027339	chr2	Rassf2	1.44219077	1.73579E-16	2.32147E-15	4.294741076	0.031422857	1	144	159	155	157	158	675	388	404	454	419
ENSMUSG00000035439	chr8	Haus8	2.32309479	1.77487E-16	2.37148E-15	2.819155739	0.07369405	1	23	36	41	49	23	174	223	198	231	104
ENSMUSG00000040856	chr12	Dlk1	3.41181686	1.95624E-16	2.61131E-15	5.789863123	0.167467932	1	158	116	109	95	209	1719	721	1545	594	3759
ENSMUSG00000031147	chrX	Magix	-1.6658806	2.03599E-16	2.71517E-15	3.5552972	0.040387907	-1	205	303	257	375	193	110	82	101	61	103
ENSMUSG00000039126	chr19	Prune2	2.11003728	2.06545E-16	2.75184E-15	3.780867623	0.066828384	1	71	57	60	152	54	268	283	501	316	408
ENSMUSG00000043613	chr9	Mmp3	3.29959579	2.07561E-16	2.76274E-15	2.758680432	0.144180122	1	14	19	4	31	24	203	168	85	360	161
ENSMUSG00000026222	chr1	Sp100	1.29832495	2.09688E-16	2.78839E-15	4.249984831	0.025015666	1	152	175	166	168	146	512	493	355	364	482
ENSMUSG00000004319	chr8	Clcn3	-1.375556	2.18368E-16	2.90106E-15	5.431164514	0.030960307	-1	857	996	821	1124	836	317	472	305	392	469
ENSMUSG00000035933	chr12	Cog5	-1.6536309	2.28306E-16	3.03021E-15	2.766762898	0.035238184	-1	138	131	144	199	149	50	52	46	64	51
ENSMUSG00000028478	chr4	Clta	1.37570436	2.28752E-16	3.03325E-15	6.283756012	0.031650733	1	651	692	575	814	507	2514	2048	1460	1729	1490
ENSMUSG00000029156	chr5	Sgcb	-1.2911933	2.31673E-16	3.06906E-15	7.588952514	0.028432412	-1	4431	3741	3457	4869	3892	1803	2031	1438	2001	1845
ENSMUSG00000095028	chr3	Sirpb1b	7.12618101	2.35107E-16	3.1116E-15	-0.509694861	0.12517068	1	0	0	0	0	0	32	15	8	18	19
ENSMUSG00000035284	chr9	Vps13c	-1.5885739	2.37642E-16	3.14218E-15	4.527964631	0.039592871	-1	393	449	480	761	511	127	198	168	205	232
ENSMUSG00000021579	chr13	Lrrc14b	-1.5166326	2.38325E-16	3.14824E-15	6.620925186	0.038585125	-1	2066	2197	2079	2699	1841	627	917	600	994	1009
ENSMUSG00000025764	chr3	Jade1	-1.6537675	2.42444E-16	3.19962E-15	4.655949685	0.043713878	-1	491	485	514	762	600	116	238	175	199	255
ENSMUSG00000073016	chrX	Uprt	-2.4253211	2.50415E-16	3.30169E-15	1.600608168	0.066064656	-1	54	58	78	96	83	15	19	8	19	14
ENSMUSG00000063659	chr1	Zbtb18	-1.4785285	2.57719E-16	3.3948E-15	6.252997172	0.03660245	-1	1643	1437	1514	2185	1615	453	743	665	610	791
ENSMUSG00000022844	chr16	Pdia5	1.82769874	2.61817E-16	3.44553E-15	2.991892381	0.04603487	1	50	47	50	75	36	300	208	190	146	159
ENSMUSG00000016319	chrX	Slc25a5	1.35627981	2.73233E-16	3.59239E-15	6.409236512	0.031016709	1	604	656	678	1021	626	2199	2357	2027	1701	1676
ENSMUSG00000017760	chr2	Ctsa	1.54328555	2.75014E-16	3.61241E-15	7.248833583	0.040297408	1	1281	1119	966	1332	1086	5704	3766	2250	3078	4019
ENSMUSG00000072596	chr14	Ear2	5.34018259	2.7667E-16	3.63074E-15	1.194022261	0.244940524	1	3	3	0	0	1	49	90	14	126	60
ENSMUSG00000033910	chr3	Gucy1a3	-1.5394658	2.78181E-16	3.64715E-15	3.444350371	0.033821976	-1	218	238	201	332	217	71	83	89	84	122
ENSMUSG00000026739	chr2	Bmi1	-1.5371165	2.78766E-16	3.65139E-15	4.521785086	0.037685476	-1	457	460	439	753	459	164	278	131	161	228
ENSMUSG00000064109	chr7	Hcst	4.7353475	2.82835E-16	3.70122E-15	0.236181215	0.148338051	1	2	1	0	2	0	69	25	17	25	29
ENSMUSG00000079110	chr2	Capn3	-1.2800297	2.87893E-16	3.76389E-15	7.104874922	0.027997219	-1	2903	2512	2391	3926	2898	1310	1238	1136	1450	1407
ENSMUSG00000034361	chr8	Cpne2	1.65401333	2.88331E-16	3.76609E-15	4.000062587	0.041727005	1	167	90	85	119	108	554	357	294	324	459
ENSMUSG00000050410	chr17	Tcf19	2.07553526	2.92434E-16	3.81611E-15	2.487185822	0.055546921	1	39	34	28	26	27	187	146	116	170	102
ENSMUSG00000030589	chr7	Rasgrp4	2.72179851	2.94277E-16	3.83658E-15	1.887778	0.088858267	1	15	13	12	16	13	173	84	73	120	57
ENSMUSG00000050965	chr11	Prkca	-1.2891067	2.98668E-16	3.8902E-15	5.891041409	0.027804003	-1	1171	1008	1055	1664	1395	563	633	537	500	575
ENSMUSG00000001418	chr3	Glmp	1.29870315	3.00815E-16	3.91451E-15	5.421421686	0.027738194	1	384	380	329	411	331	1419	1010	783	813	991
ENSMUSG00000014956	chr5	Ppp1cb	-1.6180806	3.09719E-16	4.02663E-15	7.992763685	0.044488717	-1	5580	5152	5192	8187	4844	1391	2437	1540	2176	2649
ENSMUSG00000041624	chr9	Gucy1a2	-4.4197088	3.16536E-16	4.11144E-15	-0.437555873	0.076769782	-1	18	16	17	21	18	1	2	0	1	0
ENSMUSG00000030068	chr6	Gm20696	-1.7592295	3.1998E-16	4.15232E-15	2.687073854	0.040465388	-1	165	118	139	172	136	35	58	42	49	51
ENSMUSG00000089832	chr7	Shkbp1	1.68352955	3.26054E-16	4.22721E-15	2.96507662	0.038209967	1	49	53	56	68	45	275	177	155	195	158
ENSMUSG00000054000	chr4	Tusc1	2.53487466	3.30807E-16	4.28486E-15	1.739918319	0.073482182	1	10	19	10	14	16	62	115	73	83	110
ENSMUSG00000037490	chr10	Slc2a12	-1.5929581	3.39795E-16	4.39719E-15	3.393117036	0.036402203	-1	223	234	183	300	230	62	88	74	80	118
ENSMUSG00000040584	chr5	Abcb1a	-1.7893611	3.43604E-16	4.44237E-15	3.111821911	0.045428404	-1	202	202	133	292	174	60	53	44	63	94
ENSMUSG00000001056	chr11	Nhp2	1.45671473	3.51864E-16	4.54496E-15	4.546698827	0.033885589	1	226	160	161	217	162	692	662	471	580	382
ENSMUSG00000060572	chr4	Mfap2	2.1160583	3.67074E-16	4.73706E-15	5.177313893	0.07246426	1	227	175	145	215	239	1424	637	946	453	1388
ENSMUSG00000020914	chr11	Top2a	2.15802832	3.72571E-16	4.8012E-15	4.141823924	0.071955742	1	98	88	101	77	104	531	713	439	436	214
ENSMUSG00000036879	chr8	Phkb	-1.7742253	3.72732E-16	4.8012E-15	8.190966441	0.053339813	-1	6707	5962	5867	8537	6722	1345	2420	1482	2589	2917
ENSMUSG00000042810	chr6	Krba1	-1.3185644	3.74766E-16	4.82295E-15	4.636035948	0.027784372	-1	634	523	450	518	492	242	230	199	269	215
ENSMUSG00000021477	chr13	Ctsl	2.17142013	3.79946E-16	4.88511E-15	8.39094439	0.077861124	1	1716	2106	1495	2176	1599	11584	9709	3671	5973	14997
ENSMUSG00000034295	chr18	Fhod3	-1.4841437	3.83272E-16	4.91433E-15	5.561601167	0.036786239	-1	941	973	871	1527	929	274	491	394	412	440
ENSMUSG00000039840	chr18	Epg5	-1.2080387	3.82635E-16	4.91433E-15	4.896395244	0.023490752	-1	585	557	528	816	617	264	337	245	287	331
ENSMUSG00000099088	chr10	Gm27920	-3.621145	3.83226E-16	4.91433E-15	0.279139136	0.094213193	-1	32	27	38	34	22	1	4	2	6	0
ENSMUSG00000036894	chr3	Rap2b	1.74319381	3.87943E-16	4.96965E-15	3.956510689	0.046715455	1	118	120	80	124	86	374	489	206	466	407
ENSMUSG00000031375	chrX	Bgn	1.87170317	3.94714E-16	5.05176E-15	8.338864171	0.05911667	1	2405	1833	1885	2496	1764	13705	7987	9268	4388	6617
ENSMUSG00000103508	chr9	Map4	-1.5026046	3.98575E-16	5.0965E-15	7.442576249	0.038764768	-1	3825	3350	3407	4793	3820	1057	1496	1291	1541	1988
ENSMUSG00000032754	chr5	Slc8b1	1.32803763	4.07816E-16	5.2099E-15	4.265746682	0.027075045	1	187	161	152	191	121	567	463	397	327	493
ENSMUSG00000045896	chr6	Paip2b	-1.2898905	4.089E-16	5.2161E-15	6.328798846	0.028401034	-1	1730	1881	1640	1832	1372	781	855	600	784	793
ENSMUSG00000059555	chr2	Tor4a	1.8770076	4.09047E-16	5.2161E-15	2.5357964	0.045933949	1	35	30	36	56	25	210	147	108	126	142
ENSMUSG00000031813	chr8	Mvb12a	1.29957487	4.12321E-16	5.25305E-15	4.205723144	0.025755297	1	144	153	134	232	134	471	374	447	432	395
ENSMUSG00000001082	chr5	Mfsd10	1.81511004	4.17016E-16	5.30802E-15	3.022780327	0.046237508	1	56	53	46	63	45	338	197	140	171	184

ENSMUSG00000032009	chr9	Sesn3	-1.742558	4.30066E-16	5.46916E-15	2.454473138	0.038165472	-1	115	95	117	164	129	41	41	37	37	46
ENSMUSG00000039523	chr4	Cep104	-1.2655685	4.49007E-16	5.70484E-15	5.071132994	0.026296068	-1	653	601	698	960	638	275	359	260	326	387
ENSMUSG00000023043	chr15	Krt18	4.37115116	4.55977E-16	5.78813E-15	1.496010288	0.204720628	1	5	3	0	7	3	172	83	37	26	109
ENSMUSG00000029299	chr5	Abcg3	4.49534062	4.56629E-16	5.79115E-15	1.094671725	0.191811641	1	5	0	2	2	3	22	89	45	101	49
ENSMUSG00000030029	chr6	Lrig1	-1.4057232	4.57411E-16	5.79581E-15	6.198234323	0.033698912	-1	1588	1438	1630	1724	1505	503	756	552	700	758
ENSMUSG00000027408	chr2	Cpxm1	2.03389238	4.57831E-16	5.79587E-15	4.662393712	0.066097476	1	175	192	114	86	151	760	610	688	396	865
ENSMUSG00000016757	chr15	Ttll12	1.34871247	4.59886E-16	5.81663E-15	4.351048763	0.028295529	1	190	158	145	180	174	429	458	546	434	491
ENSMUSG00000062661	chr2	Ncs1	1.43735675	4.91476E-16	6.21055E-15	3.989077945	0.031477456	1	120	110	99	164	141	391	352	447	310	367
ENSMUSG00000019990	chr10	Pde7b	-1.6440784	4.95718E-16	6.2585E-15	4.808643711	0.044457211	-1	610	527	635	864	541	133	262	179	214	314
ENSMUSG00000032300	chr9	1700017B05Rik	1.75166174	5.03821E-16	6.35505E-15	3.652503282	0.04629553	1	68	67	79	103	105	490	320	237	300	234
ENSMUSG00000029202	chr5	Pds5a	-1.7465529	5.0661E-16	6.38448E-15	4.140298202	0.048185549	-1	366	393	344	540	383	85	168	79	164	160
ENSMUSG00000024242	chr17	Map4k3	-1.4258264	5.10633E-16	6.42937E-15	4.266129785	0.031942167	-1	393	413	392	528	360	151	169	118	165	248
ENSMUSG00000025743	chr4	Sdc3	1.47995928	5.22573E-16	6.57378E-15	6.096938588	0.037343244	1	475	572	526	667	449	2335	1516	1308	1112	2058
ENSMUSG00000045636	chr8	Mtus1	-1.3236338	5.26421E-16	6.61624E-15	7.130681914	0.03046405	-1	2979	3224	2794	3654	2303	1210	1299	1111	1245	1668
ENSMUSG00000047878	chr15	A4galt	2.28774927	5.29034E-16	6.6431E-15	2.241726518	0.067152347	1	29	18	29	24	15	195	107	115	80	130
ENSMUSG00000026253	chr1	Chrng	4.82150709	5.34379E-16	6.7042E-15	3.897249171	0.290797008	1	24	20	13	11	6	511	307	1178	89	170
ENSMUSG00000040952	chr7	Rps19	1.33698275	5.45392E-16	6.83624E-15	7.463977528	0.031185929	1	1686	1407	1265	1838	1293	5571	4314	3664	3934	3262
ENSMUSG00000029560	chr5	Snx8	1.62048793	5.66837E-16	7.09867E-15	4.572088915	0.042842179	1	174	199	151	200	140	919	605	356	612	461
ENSMUSG00000026414	chr1	Tnnt2	4.06156681	5.74499E-16	7.18819E-15	5.752310142	0.230635166	1	165	85	77	61	59	2283	1012	3507	305	1050
ENSMUSG00000045404	chr12	Kcnk13	2.70105137	5.76934E-16	7.2122E-15	1.580656661	0.082128611	1	12	13	10	7	13	108	113	71	58	54
ENSMUSG00000074129	chr7	Rpl13a	1.25761452	5.89951E-16	7.36833E-15	8.324861468	0.027894537	1	3202	2611	2596	3229	2446	8620	7875	6457	7405	6624
ENSMUSG00000006398	chr4	Cdc20	2.91114941	6.02154E-16	7.51402E-15	2.661560237	0.116709299	1	22	25	27	23	10	204	305	173	138	70
ENSMUSG00000046432	chrX	Ngfrap1	1.74623753	6.08681E-16	7.58869E-15	2.913957075	0.042056622	1	54	41	37	63	58	241	201	194	142	154
ENSMUSG00000045690	chr12	Wdr89	1.64218626	6.10711E-16	7.60722E-15	4.583557998	0.043726311	1	156	172	126	226	185	968	529	575	478	424
ENSMUSG00000019832	chr10	Rab32	2.76614559	6.16673E-16	7.67464E-15	2.757427536	0.107095367	1	29	34	26	20	15	303	246	93	211	100
ENSMUSG00000049550	chr5	Clip1	-1.2642834	6.2015E-16	7.71105E-15	7.595649036	0.028108878	-1	4472	3605	3475	5141	3753	2189	2178	1532	1491	1958
ENSMUSG00000047888	chr15	Tnrc6b	-1.5674336	6.24585E-16	7.75929E-15	5.606542092	0.04167561	-1	849	971	982	1659	1028	286	466	362	342	543
ENSMUSG00000021306	chr13	Gpr137b	2.92120833	6.26963E-16	7.78191E-15	3.080087394	0.12238037	1	39	28	29	29	18	355	256	99	101	419
ENSMUSG00000019768	chr10	Esr1	-1.5966327	6.44633E-16	7.99413E-15	4.767031024	0.042165012	-1	445	584	549	833	640	141	240	234	209	267
ENSMUSG00000050211	chr2	Pla2g4e	-1.3666239	6.4914E-16	8.04006E-15	6.026895847	0.032126507	-1	1445	1334	1163	1494	1514	612	587	412	633	740
ENSMUSG00000089669	chr11	Tnfsf13	2.55541175	6.49487E-16	8.04006E-15	2.294737179	0.08662493	1	25	27	17	19	14	79	190	87	154	151
ENSMUSG00000031168	chrX	Ebp	1.45644148	6.50752E-16	8.0486E-15	4.027320073	0.032861685	1	125	105	106	180	132	559	422	333	315	323
ENSMUSG00000025007	chr19	Aldh18a1	1.34944413	6.54478E-16	8.08047E-15	3.53943407	0.025905568	1	103	90	88	104	95	286	299	277	236	246
ENSMUSG00000053398	chr3	Phgdh	1.95153956	6.54485E-16	8.08047E-15	3.403704586	0.057244048	1	45	86	57	70	59	258	386	284	241	178
ENSMUSG00000020386	chr11	Sar1b	-1.7427988	6.69127E-16	8.25394E-15	7.929785555	0.052437995	-1	6347	5607	4787	6023	5117	1322	2201	1084	2066	2500
ENSMUSG00000004207	chr10	Psap	1.37909735	6.71999E-16	8.27477E-15	10.81164579	0.033679473	1	14223	14676	12789	18639	14241	47771	52329	29043	36224	48698
ENSMUSG00000068922	chr3	Msto1	1.29273555	6.71877E-16	8.27477E-15	3.777949489	0.024470209	1	108	116	120	156	89	355	310	320	277	312
ENSMUSG00000029167	chr5	Ppargc1a	-1.55656	6.72931E-16	8.27895E-15	4.420838343	0.039019407	-1	340	444	495	733	389	132	179	169	194	203
ENSMUSG00000006411	chr1	Pvrl4	3.5631439	6.87312E-16	8.44844E-15	0.401544648	0.094378744	1	1	5	4	2	1	53	31	33	22	39
ENSMUSG00000000804	chr11	Usp32	-1.3703881	7.58706E-16	9.3127E-15	3.889970393	0.028633816	-1	293	321	301	428	251	126	162	108	109	168
ENSMUSG00000022742	chr16	Cpox	-1.3299965	7.58956E-16	9.3127E-15	4.150691799	0.027496216	-1	357	345	333	499	359	129	180	141	173	195
ENSMUSG00000057396	chr13	Zfp759	-1.9579882	7.76058E-16	9.5142E-15	1.924949795	0.045202492	-1	93	90	74	112	72	29	32	15	23	25
ENSMUSG00000090841	chr10	Myl6	1.42313361	7.86471E-16	9.63341E-15	7.712075715	0.0356723	1	1742	1712	1557	2070	1421	7066	5156	4348	4935	3564
ENSMUSG00000032412	chr9	Atp1b3	1.24041195	7.98677E-16	9.77435E-15	6.043931492	0.026604254	1	559	591	543	729	503	1936	1664	1274	1165	1582
ENSMUSG00000034342	chr9	Cbl	-2.3187318	8.07783E-16	9.87714E-15	2.085460313	0.069602192	-1	69	86	107	135	118	22	27	11	31	22
ENSMUSG00000039476	chr2	Prrx2	2.27591124	8.14441E-16	9.94984E-15	2.239413252	0.068640969	1	26	20	18	38	16	207	132	106	81	101
ENSMUSG00000002028	chr9	Kmt2a	-1.3251822	8.28983E-16	1.01187E-14	4.574156543	0.028790448	-1	408	458	493	665	509	278	263	165	171	239
ENSMUSG00000048758	chr9	Rpl29	3.32993114	8.34668E-16	1.01792E-14	6.637347597	0.169539189	1	270	257	219	306	284	400	3889	3632	3105	3382
ENSMUSG00000078193	chr1	Gm2000	1.49075584	8.45788E-16	1.03058E-14	3.918037333	0.034300556	1	142	103	108	110	117	527	369	304	317	301
ENSMUSG00000018042	chr15	Cyb5r3	1.298724	8.50854E-16	1.03585E-14	6.354751729	0.029434134	1	768	663	669	878	556	2408	1633	1992	1571	1902
ENSMUSG00000048279	chr14	Sacs	-1.452531	8.79532E-16	1.06983E-14	4.863535945	0.035306582	-1	470	606	684	945	495	205	258	264	242	291
ENSMUSG00000028132	chr3	Tmem56	-1.9252277	9.11353E-16	1.10757E-14	4.876814536	0.061947878	-1	750	551	516	839	804	125	245	109	259	257
ENSMUSG00000073418	chr17	C4b	3.5944956	9.57943E-16	1.16318E-14	4.390905614	0.187573906	1	22	68	32	36	72	1343	281	697	198	689
ENSMUSG00000018412	chr11	Kansl1	-1.3160872	9.97207E-16	1.20981E-14	4.5017193	0.028377425	-1	427	430	438	614	494	220	198	159	192	292
ENSMUSG00000095788	chr3	Sirpb1a	7.06492335	1.01128E-15	1.22581E-14	-0.566579311	0.128841105	1	0	0	0	0	0	19	24	8	24	12
ENSMUSG00000046480	chr9	Scn4b	-1.3369277	1.02673E-15	1.24346E-14	8.623894568	0.032004072	-1	7045	8887	7752	11510	7206	3392	4339	3210	3698	3595
ENSMUSG00000047867	chr6	Gimap6	-1.4706885	1.03249E-15	1.24936E-14	5.008541229	0.036719039	-1	834	671	641	793	577	465	216	235	235	256
ENSMUSG00000083992	chr11	Gm11478	1.75364849	1.0501E-15	1.26957E-14	3.199560748	0.045432833	1	57	66	41	80	65	283	177	219	277	179
ENSMUSG00000072941	chr5	Sod3	1.86718853	1.05794E-15	1.27794E-14	5.076620331	0.058898693	1	166	226	156	333	211	1506	865	838	494	668
ENSMUSG00000040097	chr17	Flywch1	-1.4743304	1.05951E-15	1.27873E-14	4.363871196	0.035285022	-1	450	403	438	522	428	133	160	138	214	237
ENSMUSG00000041362	chr19	4930506M07Rik	2.61114643	1.06612E-15	1.2856E-14	2.230336676	0.091852351	1	14	13	18	28	22	158	156	46	126	160
ENSMUSG00000024742	chr19	Fen1	1.53209431	1.06716E-15	1.28574E-14	3.243465413	0.033913106	1	62	61	69	96	70	249	257	186	258	181
ENSMUSG00000018750	chr11	Zbtb4	-1.1400791	1.07693E-15	1.2964E-14	5.284212137	0.022007111	-1	782	715	764	982	746	402	402	326	386	469
ENSMUSG00000007480	chr18	Mc5r	-2.6858312	1.12774E-15	1.3564E-14	1.149253225	0.076656536	-1	60	54	39	70	52	5	7	5	12	17
ENSMUSG00000026502	chr1	Desi2	-1.1885273	1.17281E-15	1.40938E-14	5.703598222	0.024481125	-1	1063	1126	968	1295	941	490	583	461	460	598

ENSMUSG00000037754	chr2	Ppp1r16b	-1.8489125	1.186E-15	1.42402E-14	3.283936062	0.052224693	-1	194	236	239	265	189	124	56	63	41	63
ENSMUSG00000026358	chr1	Rgs1	5.89128209	1.19038E-15	1.42805E-14	1.987051412	0.347129626	1	0	1	3	5	0	206	231	10	65	117
ENSMUSG00000029862	chr6	Clcn1	-1.5073174	1.19865E-15	1.43674E-14	6.920291882	0.0401718	-1	2691	2688	2403	2952	2555	718	1119	870	977	1447
ENSMUSG00000025289	chrX	Prdx4	1.42871942	1.21361E-15	1.45342E-14	4.22872039	0.032737826	1	140	159	153	178	120	593	520	336	447	334
ENSMUSG00000041828	chr11	Abca8a	-1.2922774	1.22171E-15	1.46187E-14	6.010320831	0.029296745	-1	1170	1487	1411	1416	1261	634	623	558	515	724
ENSMUSG00000025533	chr5	Asl	1.28206164	1.28914E-15	1.54123E-14	3.584217876	0.023684264	1	122	97	91	110	93	310	275	234	270	285
ENSMUSG00000067274	chr5	Rplp0	1.59268787	1.32862E-15	1.58707E-14	8.986322202	0.045228853	1	4377	3454	3359	4251	3363	7881	14751	12263	13655	12969
ENSMUSG00000022876	chr16	Samsn1	3.73522282	1.33877E-15	1.59783E-14	0.44480389	0.111993238	1	5	2	1	1	3	41	54	20	43	27
ENSMUSG00000030451	chr7	Herc2	-1.3513046	1.35528E-15	1.61616E-14	5.951460442	0.03207963	-1	1242	1200	1179	1579	1404	458	632	494	521	733
ENSMUSG00000084899	chr10	Gm15344	1.81836331	1.35859E-15	1.61872E-14	5.62509622	0.057009055	1	327	295	255	476	289	1852	1620	880	1309	660
ENSMUSG00000016559	chr11	H3f3b	1.27404732	1.36546E-15	1.62553E-14	6.955840468	0.029033725	1	1244	1126	932	1326	807	3558	3239	2383	2573	2662
ENSMUSG00000021213	chr13	Akr1c13	3.99134945	1.3714E-15	1.63121E-14	0.16294389	0.105000562	1	2	2	1	1	2	34	39	17	39	21
ENSMUSG00000031807	chr8	Pgls	1.31965443	1.47777E-15	1.75624E-14	5.020893042	0.02967213	1	269	254	249	351	259	1110	637	768	621	654
ENSMUSG00000056758	chr10	Hmga2	6.09239262	1.55238E-15	1.84334E-14	0.423696471	0.250225016	1	0	1	0	1	0	32	90	29	31	10
ENSMUSG00000054263	chr15	Lifr	-1.2750003	1.57863E-15	1.87291E-14	5.278403412	0.028084909	-1	714	858	900	952	646	358	450	336	325	380
ENSMUSG00000046865	chr7	Fbl	1.61252055	1.60123E-15	1.89811E-14	4.778919426	0.044310056	1	185	167	180	288	192	944	800	549	700	386
ENSMUSG00000022221	chr14	Ripk3	2.48297885	1.62019E-15	1.91897E-14	1.852584918	0.077729367	1	14	21	15	20	8	136	116	61	104	66
ENSMUSG00000008226	chr2	Scrn3	-1.4585489	1.62692E-15	1.9253E-14	5.387239966	0.037040809	-1	1008	809	812	1123	826	262	445	263	389	458
ENSMUSG00000039478	chr8	Micu3	-1.4732767	1.6773E-15	1.98325E-14	4.179529477	0.035362483	-1	446	363	351	435	375	145	156	96	164	222
ENSMUSG00000004677	chr8	Myo9b	1.27122256	1.68431E-15	1.98984E-14	4.52476882	0.026707223	1	190	175	200	247	187	688	610	378	507	481
ENSMUSG00000090118	chr8	Gm16163	-2.4145145	1.74087E-15	2.05494E-14	2.880836781	0.087081713	-1	135	186	158	245	192	14	29	31	54	57
ENSMUSG00000006273	chr8	Atp6v1b2	1.37183252	1.75656E-15	2.07171E-14	7.050637534	0.033869982	1	1001	1003	981	1457	1084	4084	3703	1973	2856	3179
ENSMUSG00000014932	chr5	Yes1	-1.6213002	1.76332E-15	2.07792E-14	3.14663455	0.038901367	-1	217	189	200	239	143	58	81	61	55	96
ENSMUSG00000072294	chr14	Klf12	-3.4112068	1.76774E-15	2.08138E-14	0.500683871	0.100662773	-1	33	35	46	35	29	5	2	0	8	3
ENSMUSG00000028327	chr4	Stra6l	5.54316124	1.77924E-15	2.09315E-14	0.972988906	0.256889297	1	1	1	0	1	2	88	64	15	17	112
ENSMUSG00000022449	chr15	Adamts20	-1.8045084	1.80304E-15	2.11871E-14	3.970749783	0.053056881	-1	505	273	414	276	309	99	146	93	101	128
ENSMUSG00000026458	chr1	Ppfia4	2.12207824	1.804E-15	2.11871E-14	3.387831737	0.070294212	1	91	58	42	61	36	273	202	396	196	289
ENSMUSG00000095930	chr13	Nim1k	-1.7401122	1.81268E-15	2.12712E-14	2.462362942	0.040249169	-1	130	122	128	137	102	44	30	38	46	45
ENSMUSG00000034226	chr2	Rhov	7.88119906	1.86125E-15	2.18229E-14	0.144169842	0.269790133	1	0	0	0	0	0	71	25	4	27	32
ENSMUSG00000022945	chr16	Chaf1b	2.39213669	1.914E-15	2.24226E-14	1.649574425	0.06787633	1	16	16	10	17	12	80	101	70	103	54
ENSMUSG00000030980	chr7	Knop1	-1.259067	1.92444E-15	2.25259E-14	5.589056789	0.027911834	-1	1018	880	967	1217	968	626	478	343	362	531
ENSMUSG00000040904	chr11	Gm21988	1.19276003	2.02499E-15	2.36831E-14	6.343350687	0.025514263	1	757	704	623	893	705	2354	1794	1742	1561	1800
ENSMUSG00000031833	chr8	Mast3	1.49855509	2.05774E-15	2.40459E-14	3.171307532	0.032543386	1	66	64	67	89	60	283	182	219	169	220
ENSMUSG00000030126	chr6	Tmcc1	-1.2505215	2.10689E-15	2.45997E-14	5.709579505	0.027693345	-1	1138	1045	947	1248	1091	641	502	362	558	476
ENSMUSG00000028041	chr3	Adam15	1.34097859	2.12363E-15	2.47746E-14	5.616086603	0.031743659	1	422	374	337	542	400	1705	1158	939	1069	908
ENSMUSG00000010492	chr2	Uckl1os	-1.4479118	2.12936E-15	2.48206E-14	5.547390007	0.036973663	-1	1266	1042	835	1071	865	311	404	346	447	528
ENSMUSG00000040253	chr3	Gbp7	-2.1106772	2.14877E-15	2.5026E-14	3.565872293	0.071172768	-1	308	296	307	245	246	34	92	50	71	113
ENSMUSG00000008658	chr16	Rbfox1	-1.27851	2.16037E-15	2.51402E-14	6.973817047	0.029683192	-1	2624	2325	2196	3176	2924	1188	1209	935	1269	1395
ENSMUSG00000060477	chr6	Irak2	1.54738927	2.17801E-15	2.53243E-14	3.453615004	0.036949443	1	76	74	63	136	69	229	286	218	241	343
ENSMUSG00000078485	chr4	Plekhn1	3.2804445	2.21812E-15	2.57693E-14	0.473643077	0.091976486	1	3	5	1	7	1	38	34	23	37	53
ENSMUSG00000097451	chr12	Rian	2.64843266	2.22225E-15	2.57958E-14	7.621185578	0.117576506	1	1044	938	755	620	615	4273	3182	4022	3770	12707
ENSMUSG00000006304	chr1	Arpc2	1.25054886	2.22839E-15	2.58456E-14	6.781345187	0.028350723	1	1025	875	866	1212	884	3355	2781	1971	2404	2220
ENSMUSG00000034744	chr6	Nagk	1.62103642	2.23202E-15	2.58663E-14	3.675591405	0.041540808	1	116	97	85	90	71	470	323	200	262	325
ENSMUSG00000019987	chr10	Arg1	7.60633866	2.3254E-15	2.6926E-14	1.861541042	0.462614925	1	0	1	1	0	0	302	70	36	162	7
ENSMUSG00000091955	chr7	Gm9844	3.54485702	2.36356E-15	2.73453E-14	1.785510408	0.156382291	1	12	6	9	6	5	101	99	185	42	61
ENSMUSG00000024601	chr18	Isoc1	-1.3053145	2.37507E-15	2.74558E-14	4.257493125	0.027838957	-1	378	367	388	511	379	159	195	126	196	220
ENSMUSG00000027329	chr2	Spef1	2.49940185	2.43319E-15	2.80812E-14	1.741092595	0.078151398	1	12	9	20	18	12	55	115	82	90	98
ENSMUSG00000040322	chr3	Slc25a24	1.5602568	2.43289E-15	2.80812E-14	3.553835769	0.037853088	1	112	89	83	98	56	276	347	298	215	276
ENSMUSG00000034761	chr12	Map4k5	-1.1953286	2.47285E-15	2.85153E-14	4.716412635	0.024160888	-1	515	481	534	702	494	234	298	218	238	313
ENSMUSG00000026213	chr1	Stk11ip	1.30980725	2.5212E-15	2.90489E-14	3.752665054	0.026268548	1	118	120	107	129	96	365	274	313	248	355
ENSMUSG00000073590	chr18	3222401L13Rik	-2.6106543	2.57272E-15	2.9618E-14	1.107723437	0.073229505	-1	72	56	49	41	43	12	10	9	7	9
ENSMUSG00000054178	chr19	Gm9938	-3.4192956	2.62863E-15	3.02368E-14	0.008477195	0.073683129	-1	23	23	24	30	23	0	4	1	3	4
ENSMUSG00000026341	chr1	Actr3	1.36049227	2.63388E-15	3.02723E-14	6.304633979	0.033421199	1	602	656	585	890	585	2262	2265	1165	1888	1780
ENSMUSG00000020954	chr12	Strn3	-1.6580455	2.67482E-15	3.06923E-14	7.1585418	0.049587102	-1	3210	2786	2885	4336	3052	655	1240	927	1213	1542
ENSMUSG00000059775	chr8	Rps26-ps1	1.43716212	2.6737E-15	3.06923E-14	3.39188604	0.030979704	1	97	83	59	95	82	326	248	232	200	235
ENSMUSG00000028800	chr4	Hdac1	1.3307825	2.82405E-15	3.23781E-14	4.222526222	0.028944703	1	139	164	142	192	148	366	545	406	439	398
ENSMUSG00000060923	chr11	Acyp2	-1.2916222	2.89812E-15	3.32001E-14	5.905191183	0.030008143	-1	1272	1222	1092	1645	1136	567	570	392	698	609
ENSMUSG00000034845	chr8	Plvap	1.782634	2.98161E-15	3.41286E-14	4.74765191	0.055191291	1	125	147	123	314	206	1088	620	608	471	638
ENSMUSG00000023809	chr17	Rps6ka2	-1.4386814	3.00253E-15	3.43399E-14	6.836899419	0.037727687	-1	2325	2179	2322	3355	2331	684	1062	1065	970	1200
ENSMUSG00000097141	chr18	Gm10524	-1.9975132	3.13964E-15	3.58787E-14	2.24442186	0.054660567	-1	108	76	107	172	98	26	31	34	21	39
ENSMUSG00000055024	chr15	Ep300	-1.3800137	3.25761E-15	3.71964E-14	5.013410355	0.033484934	-1	541	585	663	943	747	274	344	216	250	383
ENSMUSG00000092787	chrX	Mir5116	-2.5159048	3.33311E-15	3.80274E-14	0.953967307	0.061207012	-1	44	46	45	61	38	5	8	7	11	13
ENSMUSG00000081344	chr2	Gm14303	1.33481912	3.56829E-15	4.06774E-14	5.607817095	0.031956584	1	433	414	360	461	384	1605	1095	1085	1091	832
ENSMUSG00000063428	chr10	Ddo	-1.2849243	3.69427E-15	4.20792E-14	5.120306802	0.029142855	-1	734	725	683	1017	544	307	345	244	401	349
ENSMUSG00000024981	chr19	Acsl5	1.42667585	3.70898E-15	4.22123E-14	4.359993566	0.034305582	1	155	181	158	215	119	687	552	359	475	376

ENSMUSG00000039004	chr13	Bmp6	-1.7584212	3.72246E-15	4.23313E-14	2.826604483	0.045771605	-1	132	162	158	235	126	38	65	44	47	66
ENSMUSG00000050299	chr16	Gm9843	1.46824828	3.8539E-15	4.37903E-14	4.424334031	0.03658342	1	195	186	152	174	133	791	431	468	472	415
ENSMUSG00000091964	chr5	BC037034	1.86112503	3.85776E-15	4.37986E-14	3.030597091	0.052505328	1	56	38	59	50	52	333	179	164	199	162
ENSMUSG00000036948	chr5	BC037034	1.8611239	3.88047E-15	4.40207E-14	3.030597091	0.052516904	1	56	38	59	50	52	333	179	164	199	162
ENSMUSG00000049686	chr5	Orai1	1.54575296	3.92171E-15	4.44524E-14	6.079173842	0.043340802	1	543	426	461	652	493	1131	1491	2010	1440	2037
ENSMUSG00000020440	chr6	Arf5	1.36339388	3.93914E-15	4.46138E-14	6.39434521	0.034046956	1	767	719	645	829	549	2820	1779	1791	1988	1545
ENSMUSG00000021880	chr14	Rnase6	3.46464469	4.09787E-15	4.63739E-14	0.211327131	0.085048685	1	3	2	1	3	3	46	26	19	29	33
ENSMUSG00000038023	chr5	Atp6v0a2	-1.1830151	4.20381E-15	4.75343E-14	4.070468903	0.022318165	-1	340	315	300	434	343	169	191	156	146	172
ENSMUSG00000055320	chr7	Tead1	-1.5709884	4.22498E-15	4.77351E-14	7.268564189	0.045400721	-1	2564	2956	3235	5734	3026	1281	1235	1530	869	1400
ENSMUSG00000002799	chr12	Jag2	-1.2432551	4.24199E-15	4.788E-14	4.647878153	0.026596593	-1	467	443	475	769	491	213	251	225	268	248
ENSMUSG00000025006	chr19	Sorbs1	-2.546285	4.24466E-15	4.788E-14	3.724122075	0.105034833	-1	153	298	331	649	285	30	65	45	96	73
ENSMUSG00000039967	chr4	Zfp292	-1.3060321	4.36746E-15	4.92255E-14	3.446251036	0.025654752	-1	244	206	218	279	201	94	99	92	100	122
ENSMUSG00000037405	chr9	Icam1	2.10906015	4.42823E-15	4.98702E-14	2.83064691	0.068121858	1	28	35	26	67	42	311	200	124	128	177
ENSMUSG00000037573	chr11	Tob1	-1.6017226	4.50631E-15	5.07087E-14	6.920070414	0.047116256	-1	2402	2408	3032	3202	2471	701	1097	790	821	1494
ENSMUSG00000063065	chr7	Mapk3	1.40655696	4.6229E-15	5.19788E-14	5.777986238	0.0359659	1	470	458	378	541	392	2119	1117	1032	999	1323
ENSMUSG00000067869	chr15	Tcea1-ps1	-2.6339232	4.63333E-15	5.20542E-14	0.814300555	0.066046191	-1	43	36	37	63	36	10	8	6	10	3
ENSMUSG00000028514	chr4	Usp24	-1.2333329	4.68583E-15	5.26017E-14	6.464954767	0.028130255	-1	1601	1572	1600	2655	1885	911	975	749	803	870
ENSMUSG00000014547	chr14	Wdfy2	-3.0460083	4.73006E-15	5.30557E-14	1.036131783	0.104142234	-1	60	41	54	55	49	5	7	0	14	8
ENSMUSG00000059495	chr9	Arhgef12	-1.249387	4.78646E-15	5.36452E-14	6.040962619	0.028634399	-1	1171	1162	1304	1896	1402	668	628	621	518	748
ENSMUSG00000021820	chr14	Camk2g	-1.2828905	4.95729E-15	5.55153E-14	7.37856685	0.030814595	-1	3712	3344	3155	4184	3187	1412	1699	1221	1848	1716
ENSMUSG00000043895	chr9	S1pr2	1.38170367	5.03255E-15	5.63129E-14	3.539347267	0.029558138	1	105	93	83	108	85	317	284	193	228	345
ENSMUSG00000002325	chr14	Irf9	1.23987523	5.04692E-15	5.64286E-14	3.7604445	0.023854546	1	114	115	94	156	118	368	314	238	310	316
ENSMUSG00000045665	chr15	Mfsd5	1.23357803	5.16271E-15	5.76771E-14	4.856726293	0.026668429	1	237	253	224	337	237	965	633	592	560	581
ENSMUSG00000037098	chr17	Rab11fip3	-1.3840695	5.22253E-15	5.82988E-14	6.061341544	0.035221755	-1	1176	1252	1148	2231	1483	594	589	624	469	739
ENSMUSG00000020309	chr11	Chac2	-1.5402985	5.32477E-15	5.93927E-14	3.124714315	0.035997546	-1	179	188	196	235	159	52	73	67	79	87
ENSMUSG00000035776	chrX	Cd99l2	-1.1903444	5.36158E-15	5.97555E-14	6.900698427	0.026512637	-1	2869	2388	2107	2615	2342	1267	1224	1104	1204	1135
ENSMUSG00000028010	chr3	Gar1	1.80085192	5.41318E-15	6.02825E-14	3.336948513	0.052171445	1	61	58	42	102	72	299	311	278	215	158
ENSMUSG00000018293	chr11	Pfn1	1.26415597	5.43488E-15	6.0476E-14	8.24811492	0.030193449	1	2785	2411	2512	2963	2590	9483	7286	5954	6377	6192
ENSMUSG00000024431	chr18	Nr3c1	-1.3912177	5.45305E-15	6.06299E-14	6.359456327	0.035817774	-1	1825	1645	1572	2256	1592	570	811	563	748	1004
ENSMUSG00000035969	chr4	Rusc2	-1.1951336	5.52426E-15	6.13728E-14	5.113249291	0.025467418	-1	629	661	735	851	694	470	309	306	283	358
ENSMUSG00000014498	chr10	Ankrd52	-1.6347976	5.66308E-15	6.28652E-14	6.370415839	0.049109087	-1	1591	1517	1570	2643	2067	414	736	546	713	860
ENSMUSG00000021952	chr14	Xpo4	-2.3800053	6.06248E-15	6.72203E-14	2.532966207	0.085626699	-1	87	110	108	309	125	36	38	18	31	27
ENSMUSG00000042286	chr14	Stab1	1.83546672	6.06502E-15	6.72203E-14	6.215426535	0.061311927	1	427	455	453	576	501	2921	1930	1443	2290	935
ENSMUSG00000034165	chr17	Ccnd3	1.37082682	6.25365E-15	6.92559E-14	6.043975465	0.034712185	1	558	533	488	634	519	2044	1275	1784	1102	1565
ENSMUSG00000078780	chr3	Gm5150	5.73994074	6.29179E-15	6.96232E-14	-0.473760958	0.13282775	1	0	0	1	0	0	23	18	10	30	12
ENSMUSG00000027601	chr3	Mtfr1	-1.1764056	6.29935E-15	6.96517E-14	4.561566107	0.023829509	-1	423	452	468	714	400	257	216	224	224	257
ENSMUSG00000030536	chr7	Iqgap1	1.5333961	6.74919E-15	7.45666E-14	6.275096895	0.043555225	1	576	504	553	783	557	2956	2201	1080	1580	1745
ENSMUSG00000031229	chrX	Atrx	-1.5700121	6.78332E-15	7.48845E-14	5.274755528	0.044820148	-1	929	778	758	1024	820	212	381	226	292	480
ENSMUSG00000025508	chr7	Rplp2	1.48420668	6.84571E-15	7.55135E-14	7.998832967	0.041492013	1	2011	1798	1617	2772	1929	9682	6056	5663	5217	4427
ENSMUSG00000061603	chr12	Akap6	-1.1652272	6.97896E-15	7.69226E-14	5.672372168	0.024896028	-1	1023	959	978	1237	1040	498	500	546	476	532
ENSMUSG00000049470	chr11	Aff4	-1.2954847	7.05748E-15	7.77268E-14	6.009753731	0.031167644	-1	1262	1118	1220	1849	1404	547	639	489	578	793
ENSMUSG00000066647	chr7	Gm5113	-2.1281646	7.07352E-15	7.78421E-14	1.960432365	0.060890405	-1	85	78	92	130	79	16	27	12	28	32
ENSMUSG00000025932	chr1	Eya1	-1.379233	7.08702E-15	7.79293E-14	4.097964885	0.032093082	-1	365	326	317	444	381	111	175	132	171	179
ENSMUSG00000028671	chr4	Gale	2.56227753	7.42586E-15	8.1591E-14	1.850625185	0.087361107	1	16	19	15	10	13	117	110	120	81	52
ENSMUSG00000034377	chr17	Tulp4	-1.2185852	7.62016E-15	8.36602E-14	6.164719883	0.027736295	-1	1400	1355	1495	1870	1358	642	730	685	598	857
ENSMUSG00000038384	chr5	Setd1b	-1.7854238	7.72128E-15	8.47038E-14	3.376609724	0.052036251	-1	180	194	239	356	231	47	80	83	61	104
ENSMUSG00000042404	chr3	Dennd4b	-1.2856321	7.77359E-15	8.52107E-14	6.72615217	0.03118558	-1	1806	1828	1935	3270	2442	1087	1057	849	980	1063
ENSMUSG00000101585	chr7	1600010M07Rik	5.88196889	7.94409E-15	8.70115E-14	-0.357228968	0.156172694	1	0	0	0	1	0	35	18	6	17	28
ENSMUSG00000037313	chr5	Tacc3	2.40866772	8.07181E-15	8.83411E-14	2.968722499	0.091492119	1	47	35	34	31	32	228	324	231	182	85
ENSMUSG00000046688	chr3	Tifa	2.09584402	8.10973E-15	8.86867E-14	2.108772229	0.059701849	1	25	31	25	20	15	154	118	77	86	122
ENSMUSG00000033792	chrX	Atp7a	-2.9335433	8.21056E-15	8.97191E-14	2.370305294	0.12710306	-1	120	120	109	179	145	5	33	6	31	20
ENSMUSG00000010609	chr1	Psen2	1.22929828	8.39123E-15	9.16217E-14	4.02855658	0.024738926	1	150	152	119	161	137	379	330	356	358	426
ENSMUSG00000027652	chr2	Ralgapb	-1.1547894	8.99163E-15	9.81007E-14	5.167091459	0.024137822	-1	708	632	669	920	760	338	432	309	352	382
ENSMUSG00000028064	chr3	Sema4a	1.96525343	9.50933E-15	1.03668E-13	2.80245742	0.059634185	1	25	37	53	47	43	279	189	131	139	161
ENSMUSG00000062822	chr13	4833420G17Rik	2.0030019	9.76306E-15	1.06351E-13	3.052066135	0.064072165	1	68	47	44	37	43	127	241	230	215	239
ENSMUSG00000027215	chr2	Cd82	1.40252057	9.79075E-15	1.0657E-13	4.915948118	0.035658825	1	322	209	189	260	246	757	761	850	531	647
ENSMUSG00000006800	chr2	Sulf2	1.48303632	1.03309E-14	1.12362E-13	4.871633425	0.039874078	1	196	211	227	233	263	704	695	712	445	957
ENSMUSG00000079304	chr6	4933413G19Rik	3.63897701	1.04261E-14	1.13309E-13	0.007966033	0.084690419	1	2	2	3	2	0	30	35	21	18	27
ENSMUSG00000015396	chr13	Cd83	2.52115076	1.05576E-14	1.14649E-13	2.930437202	0.101113846	1	32	43	33	41	16	379	183	143	90	269
ENSMUSG00000044533	chr17	Rps2	1.36174117	1.05781E-14	1.14706E-13	8.633142656	0.035720448	1	3108	2952	2797	4523	3309	7332	10982	9633	9151	9205
ENSMUSG00000099411	chr16	2310015D24Rik	-1.6149045	1.05793E-14	1.14706E-13	4.852973812	0.047568512	-1	929	585	605	591	505	343	246	191	232	154
ENSMUSG00000015652	chr5	Steap1	4.14614255	1.06696E-14	1.15582E-13	0.280887836	0.147884044	1	4	1	1	2	0	52	41	27	34	12
ENSMUSG00000037475	chrX	Thoc2	-1.3770681	1.06766E-14	1.15582E-13	3.928146366	0.031914619	-1	341	277	318	391	301	113	143	97	158	175
ENSMUSG00000084796	chr11	Mir142hg	4.53579334	1.07915E-14	1.16735E-13	0.495953655	0.180346301	1	0	2	5	0	0	80	35	20	40	25
ENSMUSG00000029177	chr5	Cenpa	2.2954986	1.08294E-14	1.17055E-13	2.861261587	0.083150768	1	39	47	40	26	24	240	265	196	166	98

ENSMUSG00000028557	chr4	Rnf11	-1.3897478	1.0978E-14	1.18569E-13	6.962408204	0.036847437	-1	2675	2374	2304	3646	2548	833	1174	992	1062	1545
ENSMUSG00000020476	chr11	Dbnl	1.29803766	1.10958E-14	1.19749E-13	4.732766551	0.030335312	1	245	203	196	337	175	911	554	497	565	574
ENSMUSG00000032238	chr9	Rora	-1.3786693	1.12598E-14	1.21425E-13	5.974086839	0.03580006	-1	1288	1148	1144	1837	1385	455	571	443	604	771
ENSMUSG00000033940	chr6	Brk1	1.15042715	1.13112E-14	1.21885E-13	6.010069094	0.024919534	1	648	599	517	759	472	1778	1440	1275	1417	1354
ENSMUSG00000099697	chr7	Gm4790	-2.9845604	1.15115E-14	1.23948E-13	0.420434225	0.075996162	-1	30	31	40	36	26	2	6	5	6	3
ENSMUSG00000057551	chr9	Zfp317	-2.3299975	1.16995E-14	1.25876E-13	2.69302174	0.085892019	-1	147	158	170	180	135	17	55	15	34	52
ENSMUSG00000072235	chr15	Tuba1a	1.65476244	1.19697E-14	1.28684E-13	6.882499992	0.051755108	1	756	788	793	1125	791	2646	2945	4399	2188	2206
ENSMUSG00000051735	chr7	Rinl	2.53944235	1.22926E-14	1.32053E-13	1.946938826	0.090015652	1	6	20	17	20	17	172	104	59	102	86
ENSMUSG00000022540	chr16	Rogdi	1.69142575	1.2464E-14	1.33791E-13	3.301695443	0.046634961	1	78	67	61	83	54	236	180	332	198	253
ENSMUSG00000006386	chr4	Tek	-1.2069126	1.25204E-14	1.34294E-13	4.617602784	0.025922495	-1	434	539	508	621	439	221	225	223	241	294
ENSMUSG00000035692	chr4	Isg15	2.14691291	1.28658E-14	1.37892E-13	2.408830348	0.069651139	1	29	29	21	43	21	179	151	125	64	176
ENSMUSG00000039652	chr19	Cpeb3	-1.4647114	1.28976E-14	1.38128E-13	4.816473898	0.039260899	-1	510	569	504	945	588	177	263	195	238	345
ENSMUSG00000001228	chr17	Uhrf1	2.45177956	1.34913E-14	1.44376E-13	3.166259205	0.097962698	1	35	29	50	36	49	275	396	176	268	105
ENSMUSG00000096842	chr13	Gm10736	1.280697	1.36123E-14	1.45559E-13	5.476497108	0.030666333	1	442	340	313	499	348	1333	1010	1107	863	827
ENSMUSG00000096910	chr17	Zfp955b	-3.1383318	1.38943E-14	1.48461E-13	1.619753468	0.132290595	-1	76	71	101	91	59	1	12	3	15	18
ENSMUSG00000025314	chr2	Ptprj	1.56518874	1.44259E-14	1.54023E-13	3.713738932	0.041567316	1	74	103	72	137	105	453	382	214	269	286
ENSMUSG00000067158	chr1	Col4a4	-2.2510158	1.45695E-14	1.55438E-13	1.752044186	0.067917914	-1	83	68	105	68	73	14	20	21	17	20
ENSMUSG00000062585	chr4	Cnr2	3.31562193	1.4699E-14	1.567E-13	1.124562182	0.132338654	1	4	8	7	7	1	92	77	21	51	65
ENSMUSG00000021268	chr12	Meg3	2.53139332	1.48313E-14	1.57869E-13	7.016406106	0.115084159	1	792	598	494	345	548	5191	1445	3021	2411	6206
ENSMUSG00000024978	chr19	Gpam	-2.3717222	1.48215E-14	1.57869E-13	6.567839935	0.102151758	-1	1942	2176	1941	3416	2474	192	523	285	766	716
ENSMUSG00000030681	chr7	Mvp	1.35451005	1.48663E-14	1.58122E-13	5.445336851	0.034473992	1	374	294	283	612	300	1408	911	944	891	977
ENSMUSG00000038342	chr5	Mlxip	-1.3647099	1.51062E-14	1.60551E-13	6.812956617	0.035899557	-1	2260	1979	1844	3063	2932	1043	1062	808	926	1316
ENSMUSG00000033382	chr18	Trappc8	-1.4034084	1.54663E-14	1.64253E-13	4.792502361	0.03618453	-1	567	566	548	773	545	183	299	164	286	304
ENSMUSG00000051000	chr3	Fam160a1	-1.4241714	1.5904E-14	1.68773E-13	5.976747669	0.038625113	-1	1342	1136	1325	1676	1350	405	563	456	570	787
ENSMUSG00000060419	chr5	Rps16-ps2	1.57147135	1.61427E-14	1.71176E-13	4.404916429	0.044219452	1	176	155	117	186	156	868	533	426	418	360
ENSMUSG00000038775	chr9	Vill	3.10733142	1.6285E-14	1.72555E-13	1.316183131	0.122716521	1	8	6	7	11	4	119	68	33	87	39
ENSMUSG00000037369	chrX	Kdm6a	-1.6063685	1.64979E-14	1.74677E-13	3.700355953	0.044378412	-1	219	213	236	503	307	140	96	78	108	102
ENSMUSG00000049173	chr18	Myoz3	-2.7510076	1.6631E-14	1.75953E-13	5.314980405	0.132104823	-1	1229	873	1018	1028	968	48	136	94	252	301
ENSMUSG00000041845	chr19	Rhod	2.68536192	1.66487E-14	1.76007E-13	1.084169416	0.080196489	1	10	7	5	8	9	64	35	68	44	67
ENSMUSG00000087579	chr19	1500017E21Rik	-1.7011511	1.69263E-14	1.78807E-13	3.694649164	0.049699322	-1	295	181	277	499	246	82	106	110	112	78
ENSMUSG00000020098	chr10	Pcbd1	3.2876811	1.75938E-14	1.85718E-13	1.936651576	0.150289766	1	19	10	10	1	9	82	74	152	79	151
ENSMUSG00000008683	chr7	Rps15a	1.20550713	1.79659E-14	1.89503E-13	7.519662055	0.028486352	1	1667	1643	1457	2030	1487	4504	4558	3960	4424	3388
ENSMUSG00000098265	chr11	Gm27517	-2.5581401	1.84334E-14	1.94288E-13	1.181874743	0.078641306	-1	47	37	67	78	49	7	14	9	6	15
ENSMUSG00000023959	chr17	Clic5	-1.614789	1.89192E-14	1.99257E-13	7.373238022	0.050316578	-1	3608	3255	3529	4872	3440	806	1718	989	1594	1514
ENSMUSG00000015755	chr10	Tab2	-1.1536297	1.9016E-14	2.00126E-13	6.644966552	0.025892803	-1	1925	1728	1861	2687	2116	1066	1109	870	937	1093
ENSMUSG00000039835	chr10	Nhsl1	-1.6467589	2.01746E-14	2.1216E-13	3.157597641	0.044420296	-1	207	217	186	184	192	63	67	56	56	108
ENSMUSG00000022436	chr15	Sh3bp1	1.27281185	2.0294E-14	2.13255E-13	3.713770334	0.026458896	1	112	101	114	115	119	383	304	270	253	296
ENSMUSG00000062232	chr3	Rapgef2	-1.2641074	2.03598E-14	2.13785E-13	3.950873633	0.027214039	-1	303	293	313	405	305	133	184	110	141	171
ENSMUSG00000062098	chr2	Btbd3	-1.2349467	2.04159E-14	2.14214E-13	4.143144353	0.026436141	-1	358	369	321	447	345	191	200	109	174	187
ENSMUSG00000101086	chr14	Gm28651	-2.3900973	2.08714E-14	2.18829E-13	1.463578122	0.073894486	-1	63	63	76	90	43	16	19	18	8	8
ENSMUSG00000028619	chr4	Tceanc2	3.56717922	2.09016E-14	2.18981E-13	2.538781389	0.189998871	1	9	13	14	21	9	25	213	199	188	209
ENSMUSG00000066456	chr9	Hmgn3	2.03094753	2.19305E-14	2.29589E-13	2.367171369	0.061747245	1	30	25	32	33	26	86	155	157	105	148
ENSMUSG00000026880	chr2	Stom	1.24400366	2.26073E-14	2.36497E-13	6.166212295	0.029994112	1	708	681	482	834	496	1757	1470	1369	1833	1803
ENSMUSG00000036676	chr10	Tmtc3	-1.6178945	2.29312E-14	2.39706E-13	3.316151119	0.043690056	-1	223	210	206	265	205	61	123	51	82	79
ENSMUSG00000029119	chr5	Man2b2	1.35199188	2.34689E-14	2.45143E-13	3.7908758	0.030971003	1	107	123	106	141	98	429	303	238	251	405
ENSMUSG00000027287	chr2	Snap23	-1.3143149	2.37223E-14	2.47605E-13	5.275719805	0.032749982	-1	868	736	686	1014	814	290	399	266	444	405
ENSMUSG00000040761	chr4	Spen	-1.3486151	2.56841E-14	2.67882E-13	4.512798196	0.033455379	-1	388	361	474	684	538	198	203	185	193	268
ENSMUSG00000025759	chr3	Mfsd8	-1.2483247	2.57584E-14	2.68455E-13	3.859573429	0.026347395	-1	340	280	263	349	280	128	155	106	155	153
ENSMUSG00000051439	chr18	Cd14	4.08167669	2.62577E-14	2.73455E-13	4.622600181	0.258730671	1	41	39	50	39	31	2627	528	194	298	359
ENSMUSG00000046828	chr1	Mettl21e	-3.0302215	2.64183E-14	2.74923E-13	5.267263989	0.159348633	-1	894	1002	1030	1269	911	390	56	51	78	142
ENSMUSG00000018819	chr7	Lsp1	1.47215668	2.66734E-14	2.77371E-13	6.502046177	0.042227206	1	944	689	640	563	683	2928	1959	2182	1745	2101
ENSMUSG00000075602	chr15	Ly6a	1.36895717	2.69779E-14	2.80329E-13	6.054472624	0.03640212	1	519	543	497	710	500	2547	1400	1301	1369	1286
ENSMUSG00000028111	chr3	Ctsk	2.76059133	2.71006E-14	2.81395E-13	5.707840568	0.136269442	1	251	242	206	155	129	2783	1063	692	586	2559
ENSMUSG00000038664	chr9	Herc1	-1.2095461	2.76452E-14	2.86837E-13	6.078373253	0.02850906	-1	1303	1325	1286	1762	1356	590	704	530	669	835
ENSMUSG00000020737	chr11	Hn1	1.43970214	2.79773E-14	2.90067E-13	6.354970068	0.040437536	1	813	634	569	680	572	2285	1778	2496	1493	1649
ENSMUSG00000020415	chr11	Pttg1	2.00346537	2.79987E-14	2.90073E-13	2.366111983	0.060454158	1	35	36	28	25	23	188	150	110	122	88
ENSMUSG00000006395	chr4	Hyi	1.4704252	2.814E-14	2.91229E-13	3.321626765	0.035268049	1	83	94	59	74	76	321	204	203	219	242
ENSMUSG00000038274	chr19	Fau	1.32154925	2.81519E-14	2.91229E-13	7.240630137	0.034550897	1	1440	1238	1234	1455	1061	5364	3441	2951	3047	3011
ENSMUSG00000026944	chr2	Abca2	-1.0896636	2.82548E-14	2.92078E-13	4.699107948	0.021590795	-1	461	472	516	653	521	301	295	229	259	270
ENSMUSG00000038843	chr19	Gcnt1	3.3909141	2.87819E-14	2.97306E-13	1.212692225	0.140269645	1	4	7	7	3	6	86	81	30	94	33
ENSMUSG00000027996	chr3	Sfrp2	3.32286932	2.94299E-14	3.03775E-13	3.557889933	0.178865233	1	25	43	7	14	62	406	598	214	225	304
ENSMUSG00000057101	chr7	Zfp180	-1.2437502	3.09806E-14	3.19546E-13	3.880075256	0.026535963	-1	250	289	294	385	314	173	158	111	141	129
ENSMUSG00000005447	chr7	Pafah1b3	2.58090381	3.10847E-14	3.20383E-13	1.639840858	0.093469027	1	15	14	9	21	5	119	81	92	79	44
ENSMUSG00000027002	chr2	Nckap1	-1.1800339	3.1756E-14	3.27061E-13	6.15384196	0.027317869	-1	1322	1242	1296	2119	1447	902	707	640	600	727
ENSMUSG00000066735	chr5	Vkorc1l1	-1.206074	3.2819E-14	3.3776E-13	4.251108756	0.025827698	-1	400	363	341	496	376	188	215	126	207	202

ENSMUSG00000056268	chr1	Dennd1b	-1.3544749	3.29583E-14	3.38944E-13	4.303015048	0.033240625	-1	447	354	369	520	419	133	193	150	175	249
ENSMUSG00000015882	chr5	Lcorl	-1.8139572	3.42883E-14	3.52363E-13	1.896194734	0.043867923	-1	77	76	77	115	78	26	28	22	20	35
ENSMUSG00000034751	chr13	Mast4	-1.4870818	3.47627E-14	3.56975E-13	5.590586722	0.042894257	-1	1024	805	809	1352	1304	317	450	361	363	572
ENSMUSG00000027293	chr2	Ehd4	1.3014241	3.74715E-14	3.84509E-13	6.271334101	0.033468705	1	613	501	508	1014	727	1744	1885	1532	1844	1948
ENSMUSG00000030753	chr7	Prkrir	-1.2737361	3.80998E-14	3.9067E-13	6.942513764	0.032399915	-1	2696	2259	2292	3446	2358	971	1386	904	1301	1300
ENSMUSG00000009585	chr15	Apobec3	2.07538077	3.90358E-14	3.99974E-13	2.531789103	0.068658541	1	37	17	33	41	33	120	205	170	98	147
ENSMUSG00000005958	chr16	Ephb3	1.87444867	3.95455E-14	4.04899E-13	3.092112021	0.059581841	1	40	46	41	92	53	305	160	241	136	239
ENSMUSG00000040133	chr2	Gpr176	3.15913934	3.95774E-14	4.04929E-13	1.242525672	0.129265074	1	5	3	4	12	9	105	99	32	40	55
ENSMUSG00000031626	chr8	Sorbs2	-1.2327684	4.04386E-14	4.13438E-13	4.218117919	0.027215121	-1	431	390	350	417	341	162	206	139	170	227
ENSMUSG00000032418	chr9	Me1	-1.1771505	4.07812E-14	4.16636E-13	6.960313178	0.027804667	-1	2912	2476	2078	2938	2453	1273	1432	990	1305	1239
ENSMUSG00000016206	chr17	H2-M3	1.9191102	4.12413E-14	4.21028E-13	2.298616048	0.055689811	1	21	34	26	47	22	182	103	95	127	114
ENSMUSG00000071042	chr17	Rasgrp3	-1.5610457	4.16419E-14	4.24808E-13	5.523182735	0.04744057	-1	986	968	1118	1180	842	266	466	233	439	493
ENSMUSG00000038080	chr13	Kdm1b	-1.45184	4.27628E-14	4.35924E-13	3.480366739	0.035939034	-1	207	229	233	292	244	71	121	76	105	109
ENSMUSG00000032601	chr9	Prkar2a	-1.4922884	4.3134E-14	4.39069E-13	7.231771437	0.044429742	-1	2928	2755	2660	4732	3595	923	1489	1022	1261	1729
ENSMUSG00000041297	chr13	Cdk13	-1.1736135	4.3104E-14	4.39069E-13	3.918825073	0.023638431	-1	294	271	282	411	301	158	161	112	152	173
ENSMUSG00000064356	chrMT	mt-Atp8	-2.2201421	4.40556E-14	4.48123E-13	1.960089989	0.07319006	-1	88	85	93	128	75	12	20	14	23	40
ENSMUSG00000025511	chr7	Tspan4	1.6341295	4.5008E-14	4.57478E-13	4.728528839	0.050829898	1	191	235	203	197	125	1065	701	397	594	555
ENSMUSG00000024481	chr18	4833403I15Rik	-3.8157829	4.78426E-14	4.85937E-13	0.102580057	0.129022221	-1	27	27	38	16	25	0	1	2	2	5
ENSMUSG00000021018	chr16	Polr2h	1.42124587	4.9373E-14	5.00958E-13	3.616719864	0.034872202	1	106	96	79	115	95	390	284	287	283	199
ENSMUSG00000032050	chr9	Rdx	-1.5698261	4.93932E-14	5.00958E-13	7.004279913	0.049147057	-1	2688	2415	2365	3909	3024	679	1231	840	984	1537
ENSMUSG00000073139	chrX	BC023829	-1.1759088	4.99861E-14	5.06603E-13	4.815349019	0.026165221	-1	645	552	465	675	563	240	321	242	259	343
ENSMUSG00000071573	chr19	Rnls	-1.576856	5.00478E-14	5.06861E-13	2.353247151	0.035632171	-1	101	112	104	148	97	49	41	31	39	46
ENSMUSG00000059839	chr13	Zfp874b	-1.4461397	5.05611E-14	5.11688E-13	3.493194677	0.036178677	-1	252	235	176	346	223	153	93	79	73	97
ENSMUSG00000046541	chr7	Zfp526	-2.1194473	5.06113E-14	5.11826E-13	1.926092261	0.06548923	-1	73	85	94	95	98	15	27	18	17	36
ENSMUSG00000023021	chr15	Cers5	1.23547641	5.16644E-14	5.22098E-13	3.984668436	0.026739886	1	152	156	118	168	105	457	371	284	362	334
ENSMUSG00000020640	chr12	Itsn2	-1.5196192	5.29446E-14	5.34649E-13	3.789252015	0.041459791	-1	253	261	291	418	302	92	157	80	143	106
ENSMUSG00000024789	chr19	Jak2	-1.1987157	5.32742E-14	5.37588E-13	5.048577867	0.027679147	-1	632	745	696	809	540	319	419	243	319	340
ENSMUSG00000027068	chr2	Dhrs9	5.35504176	5.43337E-14	5.47884E-13	1.49779904	0.332285149	1	4	2	0	3	0	139	158	9	35	96
ENSMUSG00000039908	chr11	Slc26a11	1.96959692	5.49859E-14	5.54061E-13	1.984294725	0.05520287	1	35	16	23	24	17	87	101	88	104	114
ENSMUSG00000021175	chr12	Cdca7l	2.49349582	5.58385E-14	5.62247E-13	1.413152507	0.080089434	1	17	10	14	5	9	78	94	48	65	65
ENSMUSG00000025911	chr1	Adhfe1	-1.467664	5.72913E-14	5.76123E-13	4.65785914	0.041335636	-1	406	647	415	726	568	204	248	142	270	227
ENSMUSG00000030621	chr7	Me3	-1.1688504	5.7299E-14	5.76123E-13	6.461652057	0.027538878	-1	1609	1870	1753	2237	1616	1040	899	685	966	851
ENSMUSG00000021702	chr13	Thbs4	1.89872153	5.89893E-14	5.92692E-13	8.633754472	0.071390902	1	3223	1747	2141	4104	1638	17652	11034	9226	7318	6638
ENSMUSG00000046330	chr1	Rpl37a	1.31734572	5.96804E-14	5.99204E-13	7.72291875	0.035372898	1	1995	1804	1636	2037	1530	7276	4512	4472	4637	3874
ENSMUSG00000074093	chr7	Svip	-1.4367859	6.08173E-14	6.10182E-13	4.149971861	0.038076714	-1	392	369	384	482	301	108	188	115	190	173
ENSMUSG00000020986	chr12	Sec23a	-1.3508313	6.08621E-14	6.10193E-13	6.456241354	0.036752415	-1	2043	1708	1591	2291	1782	644	919	572	966	925
ENSMUSG00000000340	chr3	Dbt	-1.4247774	6.11357E-14	6.12496E-13	4.963197727	0.039451714	-1	637	737	619	768	606	175	314	221	319	341
ENSMUSG00000058755	chr11	Osm	5.84499989	6.21004E-14	6.21716E-13	0.65257067	0.309495742	1	0	1	0	1	1	111	52	9	47	14
ENSMUSG00000060131	chr2	Atp8b4	4.052535	6.21771E-14	6.22038E-13	1.764032307	0.226354382	1	10	8	3	6	0	194	108	23	119	65
ENSMUSG00000022665	chr16	Ccdc80	1.3156558	6.23422E-14	6.23244E-13	5.87008521	0.034498547	1	543	508	495	532	403	1539	1324	1519	883	1542
ENSMUSG00000032534	chr9	Cep63	-1.2867497	6.39759E-14	6.39119E-13	5.122993564	0.032389796	-1	779	798	612	845	640	524	278	293	263	310
ENSMUSG00000000204	chr11	Slfn4	4.12893845	6.55263E-14	6.5414E-13	0.977422045	0.200722857	1	6	3	2	2	1	78	80	14	80	31
ENSMUSG00000038145	chr9	Snrk	-1.2625735	6.76528E-14	6.74886E-13	5.055076514	0.031100717	-1	639	720	636	861	635	298	288	230	319	463
ENSMUSG00000022148	chr15	Fyb	1.30765517	6.7925E-14	6.77118E-13	3.691474291	0.029661104	1	106	86	117	146	95	410	306	229	252	304
ENSMUSG00000024597	chr18	Slc12a2	-1.2823902	6.89138E-14	6.86486E-13	6.138650272	0.033149258	-1	1503	1348	1419	1993	1224	750	598	439	792	784
ENSMUSG00000024073	chr17	Birc6	-1.3275079	6.95774E-14	6.92602E-13	5.317220091	0.034804114	-1	789	710	727	1126	906	292	409	299	343	508
ENSMUSG00000024811	chr19	Tnks2	-1.1983736	7.00347E-14	6.96658E-13	7.314346298	0.02947346	-1	2875	2762	2918	4664	3423	1637	1778	1401	1346	1743
ENSMUSG00000032035	chr9	Ets1	-1.1273286	7.1279E-14	7.08531E-13	4.943925818	0.024439091	-1	558	711	569	839	481	326	317	300	276	355
ENSMUSG00000076387	chr5	Mir671	2.12576003	7.40295E-14	7.3535E-13	2.240251663	0.071168446	1	35	28	17	34	14	204	110	107	89	105
ENSMUSG00000021140	chr12	Pcnx	-1.2826447	7.59687E-14	7.54075E-13	5.96395763	0.033150342	-1	1013	1102	1373	1696	1394	579	641	596	468	680
ENSMUSG00000030748	chr7	Il4ra	2.15719828	7.96954E-14	7.90506E-13	4.5755459	0.088081999	1	100	125	102	206	123	1422	592	421	426	389
ENSMUSG00000072692	chr5	Rpl37rt	1.14007038	8.0884E-14	8.01727E-13	5.096055805	0.025299256	1	376	321	261	357	270	960	843	655	741	643
ENSMUSG00000021871	chr14	Pnp	1.45152208	8.2E-14	8.12213E-13	4.417761053	0.039981095	1	153	149	144	208	192	653	624	322	572	386
ENSMUSG00000002871	chr6	Tpra1	1.14358164	8.27558E-14	8.19119E-13	4.517971137	0.024610149	1	190	180	175	322	204	552	490	434	503	587
ENSMUSG00000038267	chr13	Slc22a23	-1.4825554	8.30234E-14	8.21186E-13	3.733593603	0.039670854	-1	196	264	297	431	273	102	106	127	125	103
ENSMUSG00000066687	chr9	Zbtb16	-1.7332307	8.40045E-14	8.30302E-13	4.084019436	0.05652617	-1	310	277	366	406	548	87	135	111	142	158
ENSMUSG00000023274	chr6	Cd4	3.47109175	9.04623E-14	8.93499E-13	1.007193921	0.148693951	1	3	5	4	3	7	90	24	67	29	70
ENSMUSG00000050347	chr7	Gm9844	3.48088708	9.17406E-14	9.05485E-13	1.61490775	0.173152351	1	11	4	9	6	5	83	90	169	35	52
ENSMUSG00000031400	chrX	G6pdx	1.85225325	9.2147E-14	9.08855E-13	3.716639198	0.063127629	1	47	101	66	121	87	476	405	169	328	309
ENSMUSG00000008496	chr7	Pou2f2	3.23798418	9.49532E-14	9.35872E-13	1.548806701	0.149065795	1	2	14	7	11	5	169	58	68	41	81
ENSMUSG00000001123	chr11	Lgals9	1.09837228	9.85476E-14	9.70614E-13	4.709074439	0.022994729	1	269	236	219	315	202	683	631	422	590	587
ENSMUSG00000035934	chr9	Pknox2	-1.1683974	1.01645E-13	9.99707E-13	5.353568497	0.027247104	-1	890	705	675	1027	916	397	441	325	403	489
ENSMUSG00000092274	chr19	Neat1	1.76767882	1.01624E-13	9.99707E-13	7.981886013	0.063494907	1	2098	2185	1425	1465	1285	4444	5604	5344	8798	7379
ENSMUSG00000036850	chr2	Mrpl41	1.14561799	1.02357E-13	1.00601E-12	4.43514807	0.024695929	1	215	195	185	254	153	534	469	463	535	409
ENSMUSG00000001247	chr7	Lsr	2.97970847	1.02611E-13	1.00708E-12	0.318573668	0.078720727	1	3	7	3	4	1	31	40	24	34	31

ENSMUSG00000015852	chr3	Fcrls	1.84680483	1.02558E-13	1.00708E-12	3.73106388	0.063039378	1	80	81	93	86	81	547	254	380	314	186
ENSMUSG00000025261	chrX	Huwe1	-1.1887083	1.0282E-13	1.00843E-12	7.326050341	0.029408875	-1	3052	2681	2998	4308	3613	1610	1725	1528	1366	1759
ENSMUSG00000043154	chr9	Ppp2r3a	-1.2363061	1.03019E-13	1.00911E-12	7.924949914	0.031907597	-1	4699	4220	4985	6747	4877	2053	2442	2038	2398	2870
ENSMUSG00000045752	chr7	Tssc4	1.48292269	1.03034E-13	1.00911E-12	4.143970286	0.041478896	1	152	139	111	195	100	640	382	422	387	288
ENSMUSG00000022489	chr15	Pde1b	2.1483344	1.03277E-13	1.01079E-12	1.383246481	0.057675118	1	15	14	10	15	13	83	52	47	64	84
ENSMUSG00000057135	chr11	Scimp	5.52588581	1.06297E-13	1.03961E-12	-0.049247919	0.218686473	1	0	1	0	1	0	68	21	15	12	18
ENSMUSG00000000787	chrX	Ddx3x	-1.5614071	1.08008E-13	1.05487E-12	6.989349549	0.050009	-1	2042	2058	2294	4889	3146	998	1176	761	961	1378
ENSMUSG00000042476	chr5	Abcb4	-1.4756252	1.07943E-13	1.05487E-12	5.931022796	0.044254108	-1	1015	1177	1337	2109	1139	356	590	485	602	575
ENSMUSG00000027200	chr2	Sema6d	-1.3066948	1.11318E-13	1.08644E-12	4.18603808	0.032041973	-1	263	403	360	591	328	184	176	167	150	174
ENSMUSG00000052698	chr9	Tln2	-1.2874566	1.14533E-13	1.11704E-12	6.968794657	0.034421679	-1	2170	2021	2252	3647	3201	1258	1210	1083	1077	1321
ENSMUSG00000096606	chr7	Gm4980	2.08370825	1.16314E-13	1.13361E-12	5.93042949	0.086068198	1	335	222	215	634	376	791	1457	1473	1904	2322
ENSMUSG00000039242	chr13	B3galnt2	-1.2403863	1.16948E-13	1.139E-12	6.270425335	0.031686223	-1	1561	1455	1432	2044	1602	618	840	586	857	833
ENSMUSG00000028249	chr4	Sdcbp	1.30077764	1.17772E-13	1.14623E-12	6.43076373	0.034906617	1	696	748	684	989	613	2119	2493	1227	2106	2128
ENSMUSG00000022270	chr15	Fam134b	-1.222389	1.18323E-13	1.15079E-12	6.173429251	0.030754631	-1	1583	1508	1267	2088	1162	773	788	482	656	860
ENSMUSG00000042066	chr1	Tmcc2	-1.2015256	1.19469E-13	1.16112E-12	5.46313111	0.029130524	-1	1014	747	799	1060	947	381	433	384	448	527
ENSMUSG00000020919	chr11	Stat5b	-1.2718579	1.20548E-13	1.17079E-12	7.368698609	0.033798743	-1	2965	3276	2878	4619	3739	1723	1471	1152	1545	2057
ENSMUSG00000033400	chr3	Agl	-1.323353	1.22346E-13	1.18744E-12	9.480026124	0.036838	-1	15303	13530	13052	19063	15287	5501	6688	5339	6698	9059
ENSMUSG00000049719	chr9	Prss46	7.56847671	1.23819E-13	1.20089E-12	-0.129909973	0.286035857	1	0	0	0	0	0	46	25	17	2	37
ENSMUSG00000042719	chr5	Naa25	-1.1369592	1.24734E-13	1.20893E-12	5.094559336	0.025628072	-1	696	606	619	899	684	302	411	274	374	376
ENSMUSG00000031075	chr7	Ano1	-1.756228	1.29207E-13	1.25142E-12	2.444098562	0.049732956	-1	114	121	110	194	86	53	28	32	38	49
ENSMUSG00000059811	chr17	Atl2	-1.2128772	1.31545E-13	1.27318E-12	7.401813186	0.030893505	-1	4116	3563	3002	3778	3093	1537	1925	1329	1639	1898
ENSMUSG00000096727	chr17	Psmb9	1.8489465	1.32855E-13	1.28497E-12	2.77182999	0.057651798	1	38	42	45	45	44	302	143	125	141	156
ENSMUSG00000000386	chr16	Mx1	3.38009832	1.34432E-13	1.29932E-12	0.629548049	0.127031659	1	3	3	2	7	3	26	69	21	43	50
ENSMUSG00000033475	chr17	Tomm6	1.07984518	1.36757E-13	1.32089E-12	5.835990204	0.023821401	1	578	475	453	702	533	1543	1264	1146	1238	1141
ENSMUSG00000046245	chr5	Pilra	3.86930165	1.37364E-13	1.32583E-12	1.590750398	0.210168218	1	8	5	1	2	10	183	97	35	90	40
ENSMUSG00000052889	chr7	Prkcb	2.83698869	1.37566E-13	1.32686E-12	1.489125221	0.114105807	1	7	9	13	13	6	143	79	63	33	69
ENSMUSG00000076128	chr14	Mir686	1.8052412	1.38423E-13	1.33421E-12	5.404404158	0.065480631	1	322	278	245	309	243	471	1219	1058	1328	1198
ENSMUSG00000030659	chr7	Nucb2	1.43920275	1.40053E-13	1.34899E-12	3.269400349	0.035760812	1	72	77	87	92	53	287	237	171	247	196
ENSMUSG00000084817	chr1	Gm5526	2.49940146	1.40312E-13	1.35055E-12	1.733047349	0.093852046	1	10	16	16	20	9	124	68	92	109	46
ENSMUSG00000040010	chr8	Slc7a5	1.8612062	1.42056E-13	1.3664E-12	3.588458176	0.064415174	1	62	67	75	99	79	446	344	365	210	159
ENSMUSG00000026737	chr2	Pip4k2a	1.30555159	1.45125E-13	1.39496E-12	4.002599685	0.031571744	1	160	149	125	140	105	497	379	278	298	415
ENSMUSG00000074916	chr2	Chst14	1.46122344	1.47304E-13	1.41492E-12	3.127243529	0.036276391	1	62	67	72	89	52	281	195	195	146	220
ENSMUSG00000022265	chr15	Ank	-1.1606334	1.49337E-13	1.43347E-12	6.503205468	0.028125435	-1	1482	1755	1776	2696	1706	957	1017	822	891	887
ENSMUSG00000005362	chr6	Crbn	-1.2154782	1.50718E-13	1.44573E-12	4.523025122	0.028750669	-1	491	497	425	539	428	184	254	173	229	285
ENSMUSG00000000982	chr11	Ccl3	4.55496828	1.51334E-13	1.45065E-12	1.97177897	0.290669739	1	0	2	0	12	9	221	175	38	110	58
ENSMUSG00000059883	chr15	Irak4	1.74691969	1.51683E-13	1.453E-12	2.063496248	0.043748791	1	20	27	28	32	30	111	108	89	82	119
ENSMUSG00000023015	chr15	Racgap1	1.76802125	1.54799E-13	1.48182E-12	3.327314192	0.056702452	1	76	67	62	67	60	265	393	219	225	147
ENSMUSG00000037225	chr3	Fgf2	-3.0947478	1.55765E-13	1.49005E-12	0.400282825	0.097693151	-1	23	28	24	52	37	2	2	8	4	4
ENSMUSG00000009555	chr2	Cdk9	1.1002458	1.57459E-13	1.50523E-12	5.044624645	0.024001887	1	333	317	278	358	271	1021	724	600	669	676
ENSMUSG00000039883	chr5	Lrrc17	1.68154728	1.57666E-13	1.50617E-12	4.050892931	0.053993979	1	106	119	143	90	111	374	404	525	270	458
ENSMUSG00000021466	chr13	Ptch1	-1.1816246	1.6127E-13	1.53801E-12	3.628276128	0.02428885	-1	239	248	259	297	223	128	140	102	125	118
ENSMUSG00000027848	chr3	Olfml3	1.23361846	1.61328E-13	1.53801E-12	4.949798432	0.030366037	1	315	279	256	290	223	1013	731	661	542	606
ENSMUSG00000028047	chr3	Thbs3	1.42381823	1.61274E-13	1.53801E-12	4.80195971	0.040497758	1	240	206	198	242	231	774	484	713	437	904
ENSMUSG00000027900	chr3	Dram2	-1.135005	1.62442E-13	1.54757E-12	5.393197278	0.026176956	-1	921	845	752	996	779	414	475	317	413	531
ENSMUSG00000028044	chr3	Cks1b	2.10848819	1.62615E-13	1.54817E-12	3.204989599	0.08060083	1	67	56	38	41	49	355	314	219	212	109
ENSMUSG00000002289	chr17	Angptl4	2.79365572	1.63127E-13	1.55199E-12	4.533550712	0.145096321	1	24	140	35	83	141	851	800	614	454	587
ENSMUSG00000041774	chr16	Ydjc	2.83227974	1.76274E-13	1.67593E-12	0.819289837	0.094111636	1	6	4	3	6	10	64	64	38	35	32
ENSMUSG00000014850	chr13	Msh3	-1.1362508	1.79846E-13	1.70872E-12	4.075072774	0.023781955	-1	321	332	343	416	304	182	194	127	164	192
ENSMUSG00000036257	chr12	Pnpla8	-1.4534885	1.80326E-13	1.71211E-12	6.052455904	0.043881438	-1	1387	1413	1463	1828	1166	385	626	434	641	800
ENSMUSG00000057762	chr13	Gm6169	1.91260017	1.83283E-13	1.73901E-12	1.831366496	0.051931902	1	26	15	21	23	21	113	105	74	80	70
ENSMUSG00000035620	chr10	Ric8b	-1.2146102	1.88264E-13	1.78506E-12	5.046504057	0.02977926	-1	574	626	640	992	632	272	285	306	349	400
ENSMUSG00000022193	chr14	Psmb5	1.56762699	1.88709E-13	1.78807E-12	6.792058856	0.051318738	1	940	766	760	984	717	1478	2940	2693	3210	3009
ENSMUSG00000044452	chr7	Zfp507	-1.1372127	1.89071E-13	1.79028E-12	4.061321291	0.02381576	-1	337	299	345	368	340	173	171	158	163	181
ENSMUSG00000047454	chr12	Gphn	-1.3224639	1.90682E-13	1.80431E-12	4.959510295	0.035385629	-1	677	604	572	795	656	210	360	209	342	321
ENSMUSG00000032218	chr9	Ccnb2	2.64051773	1.93113E-13	1.82608E-12	2.12788032	0.113304893	1	13	17	20	15	20	159	161	130	101	42
ENSMUSG00000021390	chr13	Ogn	-1.2497209	1.952E-13	1.84457E-12	5.746662722	0.03244422	-1	1297	1078	1068	1126	1014	546	516	358	490	699
ENSMUSG00000022772	chr16	Senp5	-1.5091854	1.95367E-13	1.8449E-12	2.713516758	0.037090342	-1	146	130	131	172	134	47	59	39	61	68
ENSMUSG00000044676	chr8	Zfp612	-3.0631698	1.96975E-13	1.85883E-12	1.747326024	0.144654007	-1	118	88	70	87	71	2	13	3	23	15
ENSMUSG00000081519	chr2	Gm13331	-2.5777023	1.99497E-13	1.88136E-12	1.004714859	0.086809364	-1	47	36	44	61	56	19	7	3	6	10
ENSMUSG00000071866	chr11	Ppia	1.3175003	2.01179E-13	1.89594E-12	7.532192902	0.036908232	1	1791	1685	1526	1604	1241	5103	5183	3494	4555	3280
ENSMUSG00000033855	chr17	Ston1	-2.5700918	2.0165E-13	1.8991E-12	1.498534898	0.095976833	-1	54	61	61	98	76	4	11	9	23	16
ENSMUSG00000033964	chr1	Zbtb41	-1.4159418	2.04914E-13	1.92854E-12	3.708854611	0.037330118	-1	231	262	239	421	270	81	135	108	108	143
ENSMUSG00000024816	chr19	Frmd8	1.37645045	2.06131E-13	1.93869E-12	3.525215405	0.034028354	1	83	96	86	112	93	387	309	196	232	231
ENSMUSG00000030223	chr6	Ptpro	2.52531923	2.08148E-13	1.9553E-12	2.231916246	0.104804378	1	21	22	20	21	15	260	109	55	92	133
ENSMUSG00000051457	chr7	Spn	3.42777204	2.08178E-13	1.9553E-12	1.017991109	0.150700238	1	2	2	9	6	4	107	64	31	53	29

ENSMUSG00000025862	chrX	Stag2	-1.3504682	2.08697E-13	1.95886E-12	6.118114284	0.038219389	-1	1615	1280	1299	1918	1358	462	725	500	624	877
ENSMUSG00000024122	chr17	Pdpk1	-1.1290363	2.11607E-13	1.98485E-12	5.181811955	0.025895176	-1	655	629	715	1003	719	340	400	299	380	436
ENSMUSG00000037278	chr11	Tmem97	1.64733685	2.15392E-13	2.01899E-12	3.008645105	0.04756455	1	58	56	46	79	48	267	225	163	206	121
ENSMUSG00000057596	chr7	Trim30d	8.55189793	2.20477E-13	2.06527E-12	0.71390759	0.468152085	1	0	0	0	0	0	0	70	53	51	65
ENSMUSG00000057719	chr18	Sh3rf2	-1.5270353	2.22964E-13	2.08717E-12	5.141979877	0.047898516	-1	897	942	597	778	663	275	267	179	313	456
ENSMUSG00000029417	chr5	Cxcl9	4.39248805	2.23715E-13	2.0928E-12	1.506453391	0.266436275	1	4	6	1	6	1	19	79	94	40	184
ENSMUSG00000046532	chrX	Ar	-1.2844935	2.28682E-13	2.13783E-12	4.586639214	0.032924685	-1	418	461	540	617	486	166	269	226	218	251
ENSMUSG00000031592	chr8	Pcm1	-1.1916939	2.29149E-13	2.14076E-12	6.006587481	0.02983044	-1	1473	1140	1086	1677	1309	572	653	524	622	823
ENSMUSG00000037563	chr7	Rps16	1.37685153	2.35901E-13	2.20237E-12	7.319884226	0.040398859	1	1365	1233	1104	1606	1315	5978	3919	3472	2672	3008
ENSMUSG00000040715	chr4	Rsc1a1	-1.413849	2.37101E-13	2.2121E-12	4.450489736	0.040070424	-1	474	412	359	569	545	179	203	120	188	286
ENSMUSG00000030168	chr6	Adipor2	-1.1225631	2.37701E-13	2.21622E-12	7.058959242	0.027000412	-1	2439	2551	2397	3592	2689	1338	1462	1119	1397	1538
ENSMUSG00000051469	chr18	Zfp191	-1.1929564	2.38505E-13	2.22223E-12	5.208045957	0.029207998	-1	755	656	718	1005	708	317	425	282	327	486
ENSMUSG00000079592	chr9	C1qtnf5	1.48839257	2.38697E-13	2.22254E-12	3.6407617	0.041243406	1	107	89	80	115	92	455	318	291	220	212
ENSMUSG00000022453	chr15	Naga	1.41080479	2.52838E-13	2.35264E-12	4.159322746	0.038724778	1	139	155	119	182	129	616	420	307	270	525
ENSMUSG00000036155	chr1	Mgat5	1.64114314	2.54681E-13	2.36821E-12	2.964951955	0.047210058	1	57	46	58	73	44	273	225	114	148	202
ENSMUSG00000025195	chr19	Dnmbp	-1.4771229	2.55453E-13	2.37381E-12	3.516171632	0.040497242	-1	215	245	190	321	276	77	94	83	91	144
ENSMUSG00000040466	chr7	Blvrb	1.39362434	2.61358E-13	2.42707E-12	3.606837415	0.035653845	1	96	96	107	109	84	393	256	213	331	238
ENSMUSG00000028378	chr4	Ptgr1	1.35425951	2.62695E-13	2.43787E-12	3.525402328	0.033102236	1	105	99	95	86	86	352	303	212	249	227
ENSMUSG00000032491	chr9	Nradd	2.32460958	2.63096E-13	2.43996E-12	1.545412337	0.078120391	1	16	14	15	14	9	109	85	81	59	44
ENSMUSG00000030720	chr7	Cln3	1.45701576	2.63427E-13	2.44142E-12	3.374907281	0.038323343	1	95	84	59	93	76	353	250	157	214	267
ENSMUSG00000026548	chr1	Slamf9	3.23804892	2.69372E-13	2.49486E-12	2.261046782	0.17321557	1	12	21	10	18	5	358	93	88	72	95
ENSMUSG00000032528	chr9	Vipr1	-2.1043967	2.71069E-13	2.50891E-12	1.544440615	0.064076877	-1	57	62	78	71	70	25	23	16	12	11
ENSMUSG00000030104	chr6	Edem1	1.51327878	2.73756E-13	2.5321E-12	4.583390597	0.046365203	1	168	193	174	216	168	671	850	327	619	438
ENSMUSG00000029634	chr5	Rnf6	-1.2180944	2.7434E-13	2.53583E-12	5.418328522	0.0308749	-1	980	792	790	1142	770	351	439	312	457	535
ENSMUSG00000078866	chr2	Gm14420	8.63112111	2.77185E-13	2.56044E-12	0.783758459	0.486810555	1	0	0	0	0	0	0	78	56	69	48
ENSMUSG00000021294	chr12	Kif26a	-1.5234484	2.83513E-13	2.61715E-12	3.380380831	0.04279548	-1	174	211	242	319	201	102	58	93	69	113
ENSMUSG00000038250	chr8	Usp38	-1.1815225	2.84516E-13	2.62468E-12	4.571614876	0.027807231	-1	460	459	388	649	506	194	266	207	260	251
ENSMUSG00000064367	chrMT	mt-Nd5	-1.6355239	2.85534E-13	2.63234E-12	11.35577432	0.057115057	-1	51447	54772	52507	96675	46230	15413	18497	14472	26480	29018
ENSMUSG00000093456	chr9	Gm20662	-1.6376023	2.89923E-13	2.67104E-12	2.529768558	0.044111172	-1	128	113	121	162	118	43	41	29	61	51
ENSMUSG00000044951	chr13	Mylk4	-2.1979276	3.04832E-13	2.80654E-12	9.046080465	0.099361128	-1	13331	16251	17495	9664	6601	1792	4684	2536	2544	3862
ENSMUSG00000069972	chr7	Rps13-ps2	1.61770395	3.08808E-13	2.84128E-12	2.880752996	0.045330828	1	57	55	38	61	53	273	156	161	165	140
ENSMUSG00000090553	chr1	Snrpe	1.22525497	3.10488E-13	2.85486E-12	4.780506588	0.030452088	1	272	243	219	270	214	856	677	531	628	451
ENSMUSG00000075391	chr2	Gm13443	-1.5784689	3.14915E-13	2.89365E-12	3.041986447	0.044767761	-1	182	171	189	209	156	110	56	68	46	56
ENSMUSG00000048264	chr13	Dip2c	-1.122013	3.15985E-13	2.90158E-12	4.314411698	0.02445563	-1	387	340	340	560	410	187	206	185	211	226
ENSMUSG00000019907	chr10	Ppp1r12a	-1.2975453	3.19945E-13	2.93409E-12	3.642348784	0.031086892	-1	248	245	209	355	264	99	132	87	122	145
ENSMUSG00000025068	chr19	Gsto1	1.21156891	3.19838E-13	2.93409E-12	4.536862645	0.029426417	1	169	203	191	308	177	459	650	492	518	503
ENSMUSG00000022285	chr15	Ywhaz	1.24578052	3.23626E-13	2.9659E-12	6.534264786	0.033318529	1	850	828	734	1013	680	3183	2297	1766	1753	1750
ENSMUSG00000040550	chr4	Otud6b	-1.2395895	3.25444E-13	2.9806E-12	5.685646498	0.032456222	-1	1014	960	997	1486	965	408	574	369	568	573
ENSMUSG00000001687	chr5	Ubl3	-1.1216498	3.31533E-13	3.03438E-12	5.936967635	0.026738658	-1	1202	1182	1140	1589	1153	631	703	453	609	764
ENSMUSG00000005233	chr2	Spc25	2.47106203	3.32568E-13	3.03994E-12	1.607467034	0.092108898	1	16	15	9	11	14	80	112	70	96	41
ENSMUSG00000041707	chr14	1810011H11Rik	3.17970795	3.32575E-13	3.03994E-12	0.320635456	0.099151382	1	2	4	2	6	2	40	45	35	18	25
ENSMUSG00000051316	chr18	Taf7	-1.5167285	3.34897E-13	3.05917E-12	3.602458704	0.043793088	-1	269	300	273	322	170	92	101	66	133	117
ENSMUSG00000058056	chr8	Palld	-1.8708508	3.35605E-13	3.06363E-12	5.84017956	0.072928534	-1	1175	914	1102	1976	1594	185	522	335	420	528
ENSMUSG00000020521	chr11	Rnft1	-1.3880715	3.38183E-13	3.0841E-12	4.953714663	0.03991942	-1	592	511	617	1048	616	220	326	191	338	317
ENSMUSG00000039197	chr14	Adk	-1.2298224	3.38289E-13	3.0841E-12	5.720705007	0.032015624	-1	866	1080	1032	1614	965	441	601	425	557	539
ENSMUSG00000068758	chr14	Il3ra	2.07458707	3.48775E-13	3.17762E-12	3.270760281	0.080780375	1	64	53	52	49	50	524	191	170	151	250
ENSMUSG00000022811	chr16	Zfp148	-1.0820723	3.49638E-13	3.18342E-12	4.364139348	0.022792377	-1	428	406	341	528	381	201	262	184	210	216
ENSMUSG00000064127	chrX	Med14	-1.0666319	3.52484E-13	3.20724E-12	4.751031258	0.022829118	-1	489	487	491	749	510	268	329	252	256	311
ENSMUSG00000032725	chr7	Folr2	1.76813406	3.56971E-13	3.24595E-12	4.132133899	0.062027663	1	100	143	124	95	114	746	477	330	400	271
ENSMUSG00000022124	chr14	Fbxl3	-1.0049117	3.5842E-13	3.25701E-12	5.244056104	0.020767406	-1	751	737	643	1005	652	443	427	347	414	425
ENSMUSG00000025794	chr9	Rpl14	1.15301071	3.59154E-13	3.26156E-12	7.807518077	0.02910375	1	2243	1924	1683	2618	1935	5917	5360	5264	4109	4591
ENSMUSG00000035683	chr4	Melk	2.81535334	3.65102E-13	3.31342E-12	1.363911233	0.115625601	1	13	10	8	6	7	58	120	65	65	37
ENSMUSG00000028480	chr4	Glipr2	1.51652838	3.66052E-13	3.31989E-12	3.930468987	0.044929874	1	103	107	114	139	118	609	380	298	321	241
ENSMUSG00000009394	chr6	Syn2	2.2710667	3.68509E-13	3.34E-12	2.299427079	0.087830775	1	21	33	27	25	15	85	102	177	104	169
ENSMUSG00000020460	chr11	Rps27a	1.21178809	3.8083E-13	3.44944E-12	7.916386712	0.032173335	1	2506	2128	1958	2333	1892	7144	5832	4753	5507	4419
ENSMUSG00000027665	chr3	Pik3ca	-1.1224003	3.98823E-13	3.61007E-12	5.868698377	0.026888672	-1	1060	1001	1012	1690	1245	633	609	583	610	556
ENSMUSG00000022228	chr13	Zscan26	-1.142359	4.04125E-13	3.6557E-12	3.834523828	0.024177063	-1	254	302	266	360	272	156	149	118	126	175
ENSMUSG00000079444	chr17	Gm21981	1.05310794	4.07378E-13	3.68274E-12	5.855893826	0.023609967	1	588	492	468	717	548	1549	1277	1155	1252	1148
ENSMUSG00000029163	chr5	Emilin1	1.28950672	4.10494E-13	3.70851E-12	5.227137674	0.034930796	1	349	259	330	408	274	1158	919	859	520	905
ENSMUSG00000026068	chr1	Il18rap	4.69302007	4.12234E-13	3.72182E-12	-0.032863847	0.171829457	1	0	1	1	1	1	53	35	11	19	15
ENSMUSG00000027247	chr2	Arhgap1	1.10022365	4.14661E-13	3.74132E-12	4.371435433	0.023772706	1	180	174	177	264	185	593	513	372	374	457
ENSMUSG00000026281	chr1	Dtymk	1.3138281	4.16311E-13	3.75378E-12	3.794780528	0.032718883	1	112	141	107	125	99	389	379	293	304	237
ENSMUSG00000031519	chr8	Asb5	-1.357869	4.18746E-13	3.7733E-12	6.596301034	0.039924275	-1	2198	1920	1795	2392	2045	740	908	585	1155	1034
ENSMUSG00000020220	chr4	Vps13d	-1.1018606	4.23341E-13	3.81225E-12	5.718004037	0.025854357	-1	913	974	872	1512	1115	603	562	461	520	589
ENSMUSG00000090213	chr2	Tmem189	1.10179378	4.25393E-13	3.82827E-12	5.294096581	0.025365579	1	361	354	331	447	359	1104	1041	676	749	822

ENSMUSG00000004446	chr6	Bid	2.46067157	4.40882E-13	3.9651E-12	1.926697222	0.097828541	1	20	22	8	12	20	125	146	56	108	73
ENSMUSG00000026520	chr1	Pycr2	1.10712123	4.44349E-13	3.99371E-12	4.253475067	0.023912896	1	181	172	179	229	137	400	472	409	421	402
ENSMUSG00000018585	chr11	Atox1	1.40665002	4.46136E-13	4.0072E-12	5.011347545	0.041466716	1	261	303	206	312	230	1316	617	629	577	729
ENSMUSG00000034739	chr9	Mfrp	1.4623587	4.58859E-13	4.11883E-12	3.648405618	0.040936364	1	108	91	83	117	93	456	318	291	220	212
ENSMUSG00000073705	chr4	Apitd1	2.69741588	4.60953E-13	4.13497E-12	0.838237178	0.08925417	1	8	5	6	6	7	69	51	39	49	25
ENSMUSG00000000605	chr7	Clcn4-2	-1.0088942	4.64781E-13	4.16664E-12	5.778412506	0.021696767	-1	1063	1034	1023	1374	976	639	655	498	585	599
ENSMUSG00000042680	chr18	Garem	-1.8930238	4.77642E-13	4.27918E-12	2.098009727	0.058101134	-1	77	91	77	143	107	23	24	32	38	26
ENSMUSG00000062627	chr4	Mysm1	-1.5419863	4.82857E-13	4.32313E-12	2.817010725	0.041703903	-1	149	156	147	180	138	53	60	36	59	83
ENSMUSG00000040204	chr9	2810417H13Rik	2.98283908	5.03445E-13	4.50457E-12	2.552265759	0.155607829	1	21	20	32	8	11	221	275	139	135	62
ENSMUSG00000042903	chrX	Foxo4	-1.0738044	5.05985E-13	4.5244E-12	6.902139078	0.025378261	-1	2366	2180	2027	3210	2367	1348	1161	1090	1269	1425
ENSMUSG00000022800	chr16	Fyttd1	-1.1673511	5.08706E-13	4.54583E-12	6.135736395	0.029586125	-1	1549	1304	1286	1852	1288	599	789	555	764	821
ENSMUSG00000013160	chr8	Atp6v0d1	1.18482335	5.10859E-13	4.56215E-12	5.804029242	0.030219335	1	523	495	404	645	482	1810	1432	930	1072	1155
ENSMUSG00000020794	chr11	Ube2g1	-1.17013	5.14036E-13	4.58759E-12	6.378588001	0.029887353	-1	1642	1587	1568	2236	1582	719	979	698	750	1033
ENSMUSG00000056124	chr18	B4galt6	1.66378145	5.17826E-13	4.61846E-12	3.297442428	0.052635305	1	51	40	66	108	84	285	268	157	267	232
ENSMUSG00000037112	chr9	Sik2	-1.5264313	5.26339E-13	4.6914E-12	3.330144173	0.043951133	-1	234	251	171	211	225	65	80	80	72	121
ENSMUSG00000041483	chr1	Zfp281	-1.2544627	5.3196E-13	4.73848E-12	3.537749612	0.02917121	-1	250	233	228	320	187	138	138	78	93	113
ENSMUSG00000001983	chr11	Taco1	-1.2873674	5.43976E-13	4.84243E-12	5.404370496	0.035429643	-1	1009	904	847	1020	688	284	416	367	436	489
ENSMUSG00000029512	chr5	Ulk1	-1.0739369	5.46662E-13	4.86324E-12	5.76558304	0.024835172	-1	999	1108	976	1383	1033	689	584	494	443	666
ENSMUSG00000023048	chr15	Prr13	1.26259648	5.77429E-13	5.13368E-12	4.916594564	0.033453498	1	306	246	230	290	243	1095	716	505	553	649
ENSMUSG00000068122	chrX	Agtr2	2.94903591	5.81598E-13	5.16746E-12	1.988688509	0.146457545	1	12	11	9	19	14	196	43	86	55	182
ENSMUSG00000044224	chr15	Dnajc21	-1.2258042	5.84E-13	5.1855E-12	5.150195903	0.03187458	-1	643	592	667	1086	747	289	396	294	399	346
ENSMUSG00000095362	chr2	Gm14325	-2.0903508	5.86105E-13	5.2009E-12	2.813840128	0.080864876	-1	190	150	165	187	144	16	54	29	63	51
ENSMUSG00000040548	chr11	Tex2	-1.1924302	5.89297E-13	5.2259E-12	5.670105386	0.030703911	-1	842	912	946	1569	1056	495	606	409	513	505
ENSMUSG00000005893	chr6	Nr2c2	-1.0640786	5.92636E-13	5.25217E-12	4.801081509	0.023296168	-1	489	474	508	790	561	299	327	251	274	319
ENSMUSG00000050714	chr2	Zbtb26	-1.5175776	6.00041E-13	5.31443E-12	2.347266133	0.036724345	-1	119	99	100	129	104	42	44	31	43	51
ENSMUSG00000042350	chr12	Arel1	-1.0391267	6.00984E-13	5.31941E-12	4.912401183	0.022322049	-1	584	550	619	642	591	330	310	287	329	347
ENSMUSG00000065497	chr12	Mir410	4.83239319	6.06665E-13	5.3663E-12	0.335371681	0.225899842	1	1	1	1	1	1	41	16	17	18	86
ENSMUSG00000040022	chr19	Rab11fip2	-1.5392018	6.10207E-13	5.39422E-12	3.043585824	0.043506193	-1	168	174	177	235	153	48	70	55	64	103
ENSMUSG00000017291	chr11	Taok1	-1.0792028	6.12979E-13	5.41529E-12	5.834932805	0.02522684	-1	1000	1062	1080	1605	1060	562	679	539	552	656
ENSMUSG00000028670	chr4	Lypla2	1.07596778	6.13828E-13	5.41937E-12	5.405534497	0.024627346	1	438	377	351	464	393	1200	883	836	938	837
ENSMUSG00000042515	chrX	Mum1l1	-1.9538149	6.14601E-13	5.42277E-12	2.399359757	0.066675827	-1	120	117	131	136	107	15	48	28	40	41
ENSMUSG00000052085	chr19	Dock8	1.61604135	6.32279E-13	5.57522E-12	3.163483663	0.049029738	1	55	62	52	96	61	276	253	111	236	221
ENSMUSG00000030180	chr6	Kdm5a	-1.2032858	6.39067E-13	5.63153E-12	4.541381665	0.029851131	-1	440	440	434	637	469	188	223	186	238	310
ENSMUSG00000045679	chr12	Pqlc3	2.03952266	6.39799E-13	5.63442E-12	2.511890144	0.074291449	1	40	32	33	39	18	154	192	68	129	195
ENSMUSG00000099398	chr19	Ms4a14	3.22545583	6.47317E-13	5.69704E-12	0.202956817	0.099830988	1	2	5	1	3	3	30	20	40	23	35
ENSMUSG00000036611	chr9	Eepd1	-1.2869023	6.4896E-13	5.7079E-12	6.112370511	0.036291228	-1	1039	1578	1408	2004	1310	854	565	475	656	758
ENSMUSG00000038366	chr11	Lasp1	1.17164662	6.52748E-13	5.73761E-12	5.928352532	0.029927604	1	526	523	458	730	560	1844	1629	1024	1227	1216
ENSMUSG00000025823	chr6	Pdia4	1.28353042	6.57765E-13	5.77808E-12	5.136152678	0.035173591	1	286	267	243	439	301	910	1076	581	883	619
ENSMUSG00000036138	chr9	Acaa1a	1.23547263	6.69317E-13	5.87587E-12	5.367094224	0.032816215	1	369	357	348	462	298	710	922	1074	941	1016
ENSMUSG00000030465	chr8	Psd3	-1.2229999	6.71568E-13	5.89193E-12	4.515642403	0.030878241	-1	453	369	512	599	445	186	236	194	267	226
ENSMUSG00000005871	chr18	Apc	-1.1149726	6.72741E-13	5.89852E-12	5.108823382	0.026330998	-1	586	634	649	910	735	354	354	328	291	451
ENSMUSG00000058690	chr14	Ccser2	-1.0653232	6.74716E-13	5.91212E-12	6.561057414	0.025117956	-1	1878	1606	1753	2519	1809	1066	1051	910	841	1126
ENSMUSG00000024924	chr19	Vldlr	-1.3106963	6.75264E-13	5.91321E-12	6.603062482	0.037936786	-1	1543	2137	1846	3020	1873	736	1077	753	863	1125
ENSMUSG00000091498	chr12	Mpc1-ps	-1.3978514	6.8185E-13	5.96715E-12	4.724211696	0.041225485	-1	522	528	570	797	453	163	255	181	319	256
ENSMUSG00000021375	chr13	Kif13a	-1.1582979	6.89079E-13	6.02664E-12	6.593687943	0.029722652	-1	1841	1602	1750	2930	1927	921	947	860	996	1145
ENSMUSG00000035247	chr12	Hectd1	-1.2141572	6.90908E-13	6.03885E-12	7.107570768	0.032840795	-1	2597	2501	2418	4128	2856	1118	1426	1212	1348	1655
ENSMUSG00000040363	chrX	Bcor	-1.0928245	6.96273E-13	6.08195E-12	4.513827852	0.024331353	-1	395	420	427	643	439	238	257	197	210	287
ENSMUSG00000056498	chr3	Tmem154	2.51386174	7.05501E-13	6.15871E-12	1.905470999	0.105805116	1	14	23	17	17	8	76	139	45	105	137
ENSMUSG00000079197	chr14	Psme2	1.11128892	7.106E-13	6.19934E-12	5.157652504	0.02621482	1	305	357	324	432	265	1009	824	690	805	654
ENSMUSG00000036246	chr8	Gmip	1.61150354	7.18626E-13	6.26545E-12	3.188435144	0.048778012	1	74	60	66	67	60	369	226	141	184	202
ENSMUSG00000024228	chr17	Nudt12	-1.7416123	7.20849E-13	6.28091E-12	2.032860054	0.047747295	-1	85	81	88	121	85	27	31	18	35	39
ENSMUSG00000040524	chr9	Zfp609	-1.4632061	7.32194E-13	6.37579E-12	4.492608612	0.045004376	-1	395	482	428	620	527	144	219	176	138	298
ENSMUSG00000028634	chr4	Hivep3	1.8768822	7.34758E-13	6.39413E-12	2.195181079	0.059250912	1	18	25	21	49	30	149	130	97	76	122
ENSMUSG00000039000	chr5	Ube3c	-1.0984786	7.35238E-13	6.39433E-12	5.967200452	0.026437888	-1	1293	1153	1143	1589	1186	560	688	572	673	745
ENSMUSG00000032463	chr9	Faim	2.09648146	7.3883E-13	6.42158E-12	1.720693513	0.067831331	1	18	21	12	24	14	109	112	51	84	64
ENSMUSG00000034957	chr7	Cebpa	2.02714239	7.42491E-13	6.44938E-12	4.487750976	0.08466541	1	73	244	103	91	126	672	757	420	507	589
ENSMUSG00000002835	chr17	Chaf1a	1.95720184	7.46243E-13	6.47795E-12	2.342519182	0.066501917	1	33	27	28	31	30	149	175	95	147	74
ENSMUSG00000068373	chr2	D430041D05Rik	-1.6894299	7.5601E-13	6.55865E-12	2.398658819	0.048245367	-1	125	103	97	146	119	35	41	39	54	29
ENSMUSG00000001424	chr6	Snd1	1.10073179	7.60025E-13	6.5894E-12	6.033715981	0.026610116	1	595	538	493	790	690	1603	1593	1346	1333	1415
ENSMUSG00000020170	chr10	Frs2	-1.2873336	7.6119E-13	6.59541E-12	3.663413242	0.031865101	-1	276	251	219	342	248	101	136	86	112	163
ENSMUSG00000021413	chr13	Prpf4b	-1.2455042	7.76472E-13	6.72365E-12	4.37388889	0.03205031	-1	426	386	384	524	443	165	236	134	225	240
ENSMUSG00000044328	chr11	Trp53i13	1.46141405	7.77304E-13	6.72669E-12	2.953900246	0.038352648	1	56	67	45	84	52	245	173	188	136	173
ENSMUSG00000062760	chr15	1810041L15Rik	2.20766969	7.78596E-13	6.7337E-12	3.264003966	0.094249204	1	86	41	33	29	57	178	185	296	259	336
ENSMUSG00000029309	chr5	Sparcl1	-1.129743	7.8505E-13	6.78532E-12	7.992933038	0.028846822	-1	4937	4948	4756	6955	4619	3209	2390	2506	2050	2954
ENSMUSG00000051853	chr15	Arf3	1.09361186	7.86946E-13	6.7975E-12	5.277278946	0.025589528	1	345	340	331	464	361	1173	809	758	669	926

ENSMUSG00000069917	chr11	Hba-a2	3.79593527	8.05473E-13	6.95324E-12	3.539743478	0.255320656	1	6	40	5	42	24	113	215	258	398	751
ENSMUSG00000027961	chr3	Lrrc39	-1.3337095	8.20896E-13	7.082E-12	6.11980966	0.039264883	-1	1506	1360	1305	1898	1374	428	656	595	803	705
ENSMUSG00000028991	chr4	Mtor	-1.093665	8.23221E-13	7.09768E-12	5.195693843	0.025608987	-1	650	582	671	1038	793	423	376	327	357	427
ENSMUSG00000101904	chr1	Gm29427	-2.1830048	8.34437E-13	7.18994E-12	1.374578677	0.069570873	-1	64	65	64	82	32	12	17	10	16	18
ENSMUSG00000039323	chr1	Igfbp2	3.28526545	8.41255E-13	7.24423E-12	0.50340032	0.121771767	1	0	3	7	4	3	48	31	52	21	36
ENSMUSG00000072704	chr6	2700089E24Rik	-1.1143941	8.51759E-13	7.33016E-12	6.973226657	0.027903482	-1	2621	2245	2190	3480	2372	1158	1384	1110	1308	1510
ENSMUSG00000037012	chr10	Hk1	1.33068366	8.60666E-13	7.40225E-12	4.825694351	0.037811009	1	217	180	188	355	269	627	568	721	514	859
ENSMUSG00000041347	chr12	Bdkrb1	5.58914776	8.70347E-13	7.48091E-12	-0.588241312	0.166937586	1	1	0	0	0	0	35	18	15	7	10
ENSMUSG00000043262	chr7	Uevld	-1.4608742	8.72477E-13	7.49461E-12	3.177125056	0.040156943	-1	195	205	194	230	154	63	91	52	77	107
ENSMUSG00000030082	chr6	Sec61a1	1.19294057	8.82449E-13	7.57562E-12	5.751722392	0.031270996	1	481	454	433	657	430	1729	1443	954	1056	987
ENSMUSG00000092035	chr6	Peg10	2.10645416	9.09498E-13	7.80303E-12	3.12948581	0.085800156	1	47	45	51	44	51	243	198	388	127	168
ENSMUSG00000005732	chr16	Ranbp1	1.39542361	9.27438E-13	7.95207E-12	4.588036582	0.041328425	1	189	174	185	264	175	683	795	448	564	350
ENSMUSG00000032253	chr9	Phip	-1.3361003	9.28957E-13	7.96021E-12	4.080533816	0.036343977	-1	299	330	273	545	372	150	182	102	154	195
ENSMUSG00000020623	chr11	Map2k6	-1.5791645	9.29901E-13	7.96342E-12	4.745578211	0.053432954	-1	685	723	500	508	531	132	217	221	208	308
ENSMUSG00000020571	chr12	Pdia6	1.3871022	9.36361E-13	8.01382E-12	6.949865126	0.043062918	1	1004	929	769	1321	1091	3538	3545	2157	3436	1953
ENSMUSG00000011257	chr4	Pabpc4	-1.0759933	9.50401E-13	8.12901E-12	7.873761419	0.026375644	-1	4783	4318	4351	5832	4455	2547	2692	2482	2156	2426
ENSMUSG00000030697	chr7	Ppp4c	1.08753795	1.00392E-12	8.58153E-12	5.089406857	0.02532979	1	330	344	274	411	266	1036	760	607	731	659
ENSMUSG00000021223	chr12	Papln	-2.3796164	1.02979E-12	8.79727E-12	2.052565451	0.098562173	-1	84	71	109	186	69	9	18	22	22	34
ENSMUSG00000079017	chr12	Ifi27l2a	2.63709373	1.03322E-12	8.82119E-12	4.859104283	0.141173612	1	109	215	81	63	110	1881	573	583	625	507
ENSMUSG00000031887	chr8	Tradd	1.6904886	1.03404E-12	8.8228E-12	2.553136526	0.050334537	1	51	32	33	54	33	209	127	110	157	115
ENSMUSG00000034127	chr10	Tspan8	-1.2572786	1.04305E-12	8.89424E-12	5.965890717	0.035193414	-1	1674	1384	930	1425	1149	720	658	443	661	537
ENSMUSG00000024241	chr17	Sos1	-1.0960605	1.05861E-12	9.02146E-12	4.466669259	0.024833225	-1	420	391	387	633	425	224	266	195	188	276
ENSMUSG00000031618	chr8	Nr3c2	-1.6123603	1.06475E-12	9.06823E-12	2.930643304	0.048302468	-1	134	183	168	244	124	46	53	58	77	66
ENSMUSG00000039218	chr17	Srrm2	-1.1338803	1.07625E-12	9.16055E-12	7.376909765	0.029281723	-1	3411	2905	3016	4003	3641	2012	1592	1467	1416	2058
ENSMUSG00000046311	chr11	Zfp62	-1.5095347	1.08522E-12	9.2313E-12	3.658123111	0.045826489	-1	278	231	253	392	242	80	123	60	128	141
ENSMUSG00000000134	chrX	Tfe3	1.2755059	1.08943E-12	9.2615E-12	4.346138864	0.034017926	1	141	183	154	239	167	728	474	358	396	408
ENSMUSG00000027323	chr2	Rad51	2.30680058	1.09504E-12	9.30349E-12	1.624833114	0.082671919	1	18	15	17	10	12	86	112	45	93	64
ENSMUSG00000035093	chr2	Secisbp2l	-1.0877081	1.11196E-12	9.44154E-12	4.603356735	0.024783948	-1	428	429	492	660	456	305	282	192	212	284
ENSMUSG00000037306	chr4	Man1c1	1.12883606	1.12615E-12	9.55621E-12	4.171883295	0.025493184	1	165	142	163	203	163	518	379	311	343	471
ENSMUSG00000046006	chr13	Gapt	4.26802372	1.14432E-12	9.7045E-12	0.025922849	0.178255676	1	1	1	0	3	1	24	35	21	46	9
ENSMUSG00000049164	chr19	Zfp518a	-1.5024154	1.14544E-12	9.70811E-12	2.702010784	0.03979007	-1	150	149	123	159	124	51	49	39	61	73
ENSMUSG00000041642	chr1	Kif21b	1.99979241	1.14614E-12	9.70818E-12	1.825230817	0.063772691	1	18	17	19	27	20	142	80	77	55	95
ENSMUSG00000004317	chrX	Clcn5	1.16880054	1.15531E-12	9.77991E-12	3.956326541	0.026878403	1	126	130	135	156	154	378	370	368	308	310
ENSMUSG00000029765	chr6	Plxna4	-1.4562865	1.17595E-12	9.94858E-12	3.137454865	0.040110606	-1	157	185	193	244	173	105	70	77	45	85
ENSMUSG00000035914	chr9	Cd276	1.56228675	1.19516E-12	1.0105E-11	4.083491328	0.050747461	1	135	136	113	145	104	369	422	495	216	544
ENSMUSG00000022019	chr14	Tdrd3	-1.0745281	1.19953E-12	1.01358E-11	4.246636426	0.023454305	-1	459	350	355	425	318	226	202	164	178	227
ENSMUSG00000002227	chr3	Mov10	1.6842585	1.20355E-12	1.01636E-11	2.498928616	0.049677519	1	28	30	38	50	48	179	124	127	101	159
ENSMUSG00000047986	chr8	Palm3	3.63639945	1.26943E-12	1.07135E-11	0.955952494	0.181599137	1	5	2	2	2	8	81	26	84	25	54
ENSMUSG00000093485	chr11	Gm20708	-1.1556753	1.27146E-12	1.07241E-11	4.089461097	0.026882089	-1	364	353	286	361	365	160	159	163	178	193
ENSMUSG00000079465	chr1	Col4a3	-2.7767657	1.30099E-12	1.09666E-11	1.358263881	0.122979413	-1	71	59	76	53	58	4	24	5	10	8
ENSMUSG00000018846	chr11	Pank3	-1.1700737	1.30279E-12	1.09752E-11	4.765670938	0.029413117	-1	449	524	472	809	568	262	329	213	236	327
ENSMUSG00000018930	chr11	Ccl4	4.00447788	1.31147E-12	1.10416E-11	1.037932513	0.230953778	1	3	1	0	12	1	112	68	25	62	30
ENSMUSG00000057469	chr12	E2f6	-1.0876116	1.33177E-12	1.12058E-11	6.615025883	0.026910058	-1	1940	1847	1982	2541	1652	958	1073	900	1118	1053
ENSMUSG00000037466	chr12	4930427A07Rik	2.62301037	1.33844E-12	1.12552E-11	0.919279783	0.091887374	1	11	6	3	9	7	55	75	34	48	34
ENSMUSG00000034037	chr6	Fgd5	-1.1273309	1.37751E-12	1.15767E-11	3.733849295	0.02442259	-1	241	274	273	351	216	153	129	116	125	156
ENSMUSG00000015133	chr7	Lrrk1	1.25895138	1.38067E-12	1.15963E-11	3.440789624	0.029796065	1	106	78	87	104	94	272	288	241	183	253
ENSMUSG00000018923	chr11	Med11	1.69748268	1.3881E-12	1.16517E-11	2.653972627	0.051906712	1	54	39	41	36	43	162	188	105	181	132
ENSMUSG00000022440	chr15	C1qtnf6	1.28561128	1.42086E-12	1.19195E-11	5.439734504	0.036682686	1	411	391	384	363	309	1311	942	1057	656	1071
ENSMUSG00000022905	chr16	Kpna1	-1.2384693	1.43709E-12	1.20484E-11	7.218755356	0.035174694	-1	3281	2679	2673	3885	3109	1141	1791	1150	1576	1558
ENSMUSG00000071226	chr6	Cecr2	-1.3259206	1.44921E-12	1.21428E-11	3.867069074	0.035692171	-1	228	315	275	448	291	116	111	135	142	167
ENSMUSG00000026853	chr2	Crat	-1.1805041	1.47518E-12	1.2353E-11	9.107885776	0.032363847	-1	9552	10542	10546	16031	10817	7440	4831	4642	5083	5793
ENSMUSG00000015659	chr17	Serac1	-1.7387061	1.52088E-12	1.27281E-11	2.580707067	0.055011885	-1	136	132	115	170	124	24	46	38	61	50
ENSMUSG00000020773	chr11	Trim47	1.31199861	1.53698E-12	1.2855E-11	4.361179663	0.036761481	1	158	129	162	275	162	721	442	439	410	383
ENSMUSG00000026471	chr1	Mr1	-1.1286756	1.54473E-12	1.29122E-11	3.744035318	0.02454548	-1	259	246	265	378	223	160	120	137	132	132
ENSMUSG00000084416	chr1	Rpl10a-ps1	1.09664765	1.62872E-12	1.36061E-11	5.075287982	0.026250362	1	357	282	310	359	283	998	737	727	685	600
ENSMUSG00000060961	chr5	Slc4a4	-1.4847966	1.64478E-12	1.3732E-11	2.888280299	0.040868117	-1	132	135	162	218	158	46	74	59	66	67
ENSMUSG00000104217	chr1	RP24-426M1.3	-2.7229616	1.65893E-12	1.38419E-11	4.564950472	0.151917443	-1	612	567	620	692	552	26	136	35	183	121
ENSMUSG00000036565	chr5	Ttyh3	1.15039086	1.66694E-12	1.39004E-11	4.769166529	0.028568554	1	246	207	238	310	255	785	586	564	421	723
ENSMUSG00000033970	chr5	Rfc3	1.73740976	1.67789E-12	1.39834E-11	2.328516192	0.052226591	1	44	27	26	36	34	167	137	93	126	93
ENSMUSG00000008855	chr11	Hdac5	-1.018746	1.68008E-12	1.39934E-11	5.728934031	0.023282486	-1	979	1003	930	1412	990	697	534	477	533	631
ENSMUSG00000048949	chrX	Gm6206	-1.5887132	1.68512E-12	1.40269E-11	2.90838699	0.048079344	-1	181	129	139	226	161	95	57	35	66	52
ENSMUSG00000040481	chr11	Bptf	-1.0674901	1.70133E-12	1.41535E-11	4.928912701	0.024745355	-1	571	526	513	818	651	343	390	250	288	338
ENSMUSG00000068227	chr15	Il2rb	4.37273772	1.71206E-12	1.42342E-11	-0.307298714	0.152880611	1	2	0	1	1	0	40	10	18	12	25
ENSMUSG00000025017	chr19	Pik3ap1	3.18046956	1.74473E-12	1.44972E-11	1.757290366	0.169105936	1	6	13	8	11	9	46	139	31	94	167
ENSMUSG00000020680	chr11	Taf15	1.01714415	1.75693E-12	1.45899E-11	4.836603242	0.022150055	1	248	262	248	380	271	707	658	626	560	556

ENSMUSG00000057789	chr17	Bak1	1.01586382	1.75958E-12	1.46033E-11	4.871568608	0.022151435	1	317	258	220	366	283	657	610	638	591	682
ENSMUSG00000013974	chr8	Mcemp1	8.15918057	1.76796E-12	1.46641E-11	0.384557476	0.450815769	1	0	0	0	0	0	80	50	4	52	5
ENSMUSG00000030031	chr6	Kbtbd8	-2.3565134	1.77442E-12	1.47089E-11	0.882701642	0.072073194	-1	46	34	50	39	46	8	13	10	8	7
ENSMUSG00000031596	chr8	Slc7a2	-1.1992807	1.77981E-12	1.47449E-11	6.031986505	0.032763703	-1	1489	1386	1093	1418	1361	600	667	515	584	881
ENSMUSG00000049658	chr13	Bdp1	-1.2486262	1.79114E-12	1.48299E-11	3.650625289	0.030929067	-1	246	221	238	388	230	135	135	84	141	109
ENSMUSG00000021374	chr13	Nup153	-1.188835	1.80857E-12	1.49654E-11	4.873738503	0.030961604	-1	535	530	520	844	620	236	331	227	341	315
ENSMUSG00000062456	chr19	Rpl9-ps6	1.49374465	1.81247E-12	1.49888E-11	2.839689466	0.041097207	1	65	47	57	65	40	233	152	131	181	153
ENSMUSG00000025860	chrX	Xiap	-1.1458929	1.82198E-12	1.50586E-11	4.898079194	0.028764571	-1	560	552	574	820	562	276	383	210	282	366
ENSMUSG00000052102	chr18	Gnpda1	1.31659696	1.84415E-12	1.52328E-11	4.285658419	0.036634916	1	155	176	172	181	138	538	493	286	562	386
ENSMUSG00000068748	chr6	Ptprz1	-2.6406167	1.85177E-12	1.52867E-11	0.310273395	0.070294787	-1	30	27	31	29	28	2	5	6	6	6
ENSMUSG00000049225	chr4	Pdp1	-1.4044881	1.89593E-12	1.5642E-11	6.126738039	0.044970785	-1	1764	1542	1471	1683	1086	452	606	472	750	832
ENSMUSG00000014856	chr8	Tmem208	1.2010644	1.89825E-12	1.56519E-11	4.602757533	0.0311724	1	267	205	175	248	197	731	540	519	560	404
ENSMUSG00000063450	chr12	Syne2	-1.1729207	1.93165E-12	1.59179E-11	4.588491113	0.029701615	-1	493	486	461	557	468	189	240	196	281	291
ENSMUSG00000031207	chrX	Msn	1.26202954	1.94271E-12	1.59996E-11	6.747834282	0.036767473	1	871	855	857	1365	813	3451	3043	1699	2266	2059
ENSMUSG00000041328	chr7	Pcf11	-1.2491547	1.98161E-12	1.63104E-11	3.744540037	0.031447433	-1	239	253	256	396	263	115	164	92	122	152
ENSMUSG00000018459	chr2	Slc13a3	4.30697428	1.99888E-12	1.64381E-11	1.363594935	0.279633056	1	5	4	0	5	3	131	32	29	155	30
ENSMUSG00000020580	chr12	Rock2	-1.1307645	1.99949E-12	1.64381E-11	7.059323635	0.029747817	-1	2646	2214	2223	3921	2782	1542	1351	1044	1420	1495
ENSMUSG00000038943	chr7	Prc1	1.9877291	2.02177E-12	1.66116E-11	2.930930434	0.077485845	1	43	36	51	47	45	248	281	166	196	86
ENSMUSG00000034460	chr12	Six4	-1.1610607	2.10618E-12	1.72949E-11	4.052847033	0.027752198	-1	299	317	367	478	252	202	178	143	149	164
ENSMUSG00000036672	chr8	Cenpt	1.9266092	2.11256E-12	1.73372E-11	2.128301663	0.065817201	1	30	21	17	43	22	161	117	99	104	68
ENSMUSG00000075705	chr17	Msrb1	1.26600417	2.13535E-12	1.75139E-11	6.972437679	0.037214308	1	1125	1213	1016	1285	854	2216	2591	2808	3133	3614
ENSMUSG00000093402	chr3	Gm18588	-2.5054842	2.15937E-12	1.77005E-11	0.887294494	0.08648009	-1	50	45	40	52	35	1	11	6	11	13
ENSMUSG00000040084	chr2	Bub1b	2.41254851	2.164E-12	1.7728E-11	2.298645245	0.10737229	1	28	25	22	15	20	111	245	117	109	72
ENSMUSG00000085980	chr4	Gm12408	4.94587413	2.18521E-12	1.78913E-11	0.423809744	0.264464967	1	1	1	1	0	2	7	23	65	38	52
ENSMUSG00000028469	chr4	Npr2	-1.0732961	2.19584E-12	1.79678E-11	5.320793687	0.025785858	-1	649	767	744	1195	718	488	425	406	367	415
ENSMUSG00000048271	chr5	Rbm33	-1.0357142	2.24742E-12	1.83791E-11	4.728626176	0.023164068	-1	489	454	511	618	564	300	276	241	268	332
ENSMUSG00000036769	chrX	Wdr44	-1.2225821	2.25741E-12	1.845E-11	3.781195756	0.030131633	-1	265	261	251	391	266	107	155	106	157	141
ENSMUSG00000044147	chr12	Arf6	1.14563674	2.28518E-12	1.86661E-11	5.473224279	0.029704107	1	409	407	367	575	318	1264	1116	714	1044	877
ENSMUSG00000031848	chr8	Lsm4	1.00583961	2.33939E-12	1.90977E-11	5.233226515	0.022425734	1	354	387	320	447	349	913	858	793	811	705
ENSMUSG00000046312	chr4	AI464131	-1.1953968	2.3424E-12	1.91111E-11	7.471471874	0.033537717	-1	3221	3450	3022	4539	4158	2162	1566	1432	1495	2221
ENSMUSG00000040167	chr7	Ikzf5	-1.2719301	2.36298E-12	1.92678E-11	3.324358244	0.031195078	-1	213	204	156	288	194	87	113	70	93	112
ENSMUSG00000029718	chr5	Pcolce	1.25789545	2.38355E-12	1.94242E-11	7.41259863	0.037047616	1	1580	1373	1268	1772	1489	5717	3763	4041	2675	3562
ENSMUSG00000000056	chr11	Narf	-1.2774334	2.41271E-12	1.96504E-11	6.645550058	0.037941175	-1	2185	2095	1997	2481	1795	652	1069	824	1020	1179
ENSMUSG00000045136	chr13	Tubb2b	2.57578103	2.42129E-12	1.97087E-11	3.964821598	0.137114652	1	60	61	60	91	61	478	403	875	159	205
ENSMUSG00000047721	chr7	Bola2	1.38380293	2.46075E-12	2.00183E-11	4.024696522	0.040491223	1	168	121	121	149	107	544	462	298	352	265
ENSMUSG00000028245	chr4	Nsmaf	-1.0047729	2.4675E-12	2.00615E-11	4.965310618	0.022129462	-1	623	636	521	781	549	329	377	266	351	370
ENSMUSG00000022105	chr14	Rb1	-1.1048034	2.56537E-12	2.08451E-11	4.549192044	0.026459706	-1	546	428	410	553	437	244	273	177	212	309
ENSMUSG00000030172	chr6	Erc1	-1.086789	2.57293E-12	2.08944E-11	4.868708752	0.026041493	-1	525	499	516	821	610	317	303	310	235	358
ENSMUSG00000062980	chr6	Cped1	-1.1349642	2.57671E-12	2.09129E-11	4.419655514	0.027733614	-1	457	408	399	557	371	205	252	149	257	226
ENSMUSG00000063011	chr17	Msln	3.42694692	2.63589E-12	2.13808E-11	1.618319484	0.196612131	1	3	9	8	13	4	136	61	148	23	67
ENSMUSG00000050812	chr4	AI314180	-1.1420399	2.68194E-12	2.17417E-11	8.125128627	0.030948675	-1	5981	4923	4883	7230	5712	2640	2901	2239	3131	3296
ENSMUSG00000041827	chr5	Oasl1	2.70070764	2.69247E-12	2.18145E-11	1.330138916	0.118410978	1	8	7	7	16	9	80	66	49	27	117
ENSMUSG00000008976	chr16	Gabpa	-1.1658763	2.72327E-12	2.20513E-11	4.623739395	0.029839009	-1	478	454	438	725	463	196	277	208	232	322
ENSMUSG00000023982	chr17	Guca1a	3.53154596	2.7522E-12	2.22726E-11	0.050937268	0.122557265	1	5	2	0	1	2	40	36	19	25	15
ENSMUSG00000018924	chr11	Alox15	2.83409909	2.75747E-12	2.23024E-11	0.785578511	0.113522682	1	4	3	2	13	7	77	35	31	49	36
ENSMUSG00000002015	chrX	Bcap31	1.09165126	2.79169E-12	2.2566E-11	6.084676619	0.027619	1	679	674	495	769	612	1962	1613	1306	1366	1325
ENSMUSG00000035835	chr10	Lppr3	3.74102066	2.80046E-12	2.26238E-11	-0.383195821	0.103313072	1	0	2	0	3	1	30	14	17	13	22
ENSMUSG00000074238	chr3	Ap1ar	-1.1420347	2.82906E-12	2.28417E-11	4.524097826	0.02841879	-1	525	500	368	527	428	197	250	190	253	274
ENSMUSG00000041453	chr5	Rpl21	1.27905242	2.90289E-12	2.34242E-11	7.811891562	0.038679151	1	2110	1969	1733	2242	1708	3817	6247	5429	5540	4665
ENSMUSG00000063077	chr4	Kif1b	-1.2689533	2.93895E-12	2.37015E-11	8.971270287	0.038271021	-1	8962	8348	9778	15730	10624	3869	5011	4744	4619	5663
ENSMUSG00000047675	chr4	Rps8	1.12342593	2.97521E-12	2.39802E-11	8.306470403	0.030114031	1	3085	2792	2549	3682	2775	9182	7538	6363	6764	5716
ENSMUSG00000100826	chr7	D7Ertd715e	-2.0831251	3.03483E-12	2.44465E-11	1.370647475	0.065830567	-1	46	59	49	92	57	10	21	11	14	21
ENSMUSG00000026491	chr1	Ahctf1	-1.0785376	3.03722E-12	2.44517E-11	5.114063974	0.026204345	-1	754	655	693	743	629	390	418	247	347	422
ENSMUSG00000026207	chr1	Speg	-1.2930222	3.13233E-12	2.52029E-11	8.045985156	0.039680185	-1	5118	4344	4621	7502	6503	2113	2520	2450	2151	3240
ENSMUSG00000029465	chr5	Arpc3	1.32206334	3.1618E-12	2.54254E-11	6.080071409	0.040716884	1	577	571	571	759	416	2278	1762	1134	1657	1116
ENSMUSG00000039191	chr5	Rbpj	1.35052402	3.17011E-12	2.54775E-11	4.694869469	0.040874406	1	187	193	204	288	213	416	844	500	654	591
ENSMUSG00000050503	chr9	Fbxl22	1.47537157	3.19485E-12	2.56617E-11	4.879728448	0.04914963	1	322	222	178	177	239	533	642	749	713	850
ENSMUSG00000038463	chr1	Olfml2b	1.25807879	3.20088E-12	2.56953E-11	5.512233459	0.036439582	1	454	353	337	483	377	936	1206	1153	679	1257
ENSMUSG00000025804	chr9	Ccr1	3.83768	3.21152E-12	2.57659E-11	2.667606726	0.262735005	1	20	4	14	5	15	287	286	41	279	64
ENSMUSG00000045411	chr7	2410002F23Rik	1.37201172	3.22397E-12	2.5851E-11	3.364186882	0.037277694	1	101	100	81	63	70	265	257	212	226	237
ENSMUSG00000024907	chr19	Gal	4.67612142	3.22763E-12	2.58655E-11	2.259085346	0.349856396	1	7	1	4	9	5	73	348	189	93	14
ENSMUSG00000057375	chr4	Yipf1	1.16060407	3.23921E-12	2.59434E-11	3.653863712	0.026768284	1	121	118	88	142	106	381	291	242	243	257
ENSMUSG00000029186	chr5	Pi4k2b	1.86718854	3.24711E-12	2.59918E-11	1.800088973	0.057735272	1	29	15	19	32	13	72	101	75	83	96
ENSMUSG00000073209	chr6	Klf14	3.06082607	3.27005E-12	2.61604E-11	0.516935119	0.119354975	1	1	8	3	5	3	34	29	47	22	55
ENSMUSG00000009563	chr2	Tor2a	1.25244259	3.31387E-12	2.64918E-11	3.426570819	0.031006026	1	111	81	76	124	79	333	242	181	213	264

ENSMUSG00000029860	chr6	Zyx	1.20471602	3.31527E-12	2.64918E-11	5.765904555	0.033669157	1	416	417	466	671	490	1862	1194	1102	917	1176
ENSMUSG00000036599	chr5	Chst12	1.25011434	3.38967E-12	2.70709E-11	3.7692798	0.032021567	1	130	112	98	126	126	434	299	282	221	329
ENSMUSG00000023118	chr7	Sympk	-1.0253003	3.39324E-12	2.70839E-11	6.608131193	0.024840155	-1	1848	1680	1726	2588	1948	1218	1027	935	1027	1047
ENSMUSG00000029190	chr5	D5Ertd579e	-1.1737979	3.39601E-12	2.70906E-11	6.679355612	0.032563816	-1	2082	1951	1950	2799	1857	806	1073	874	1190	1165
ENSMUSG00000017493	chr11	Igfbp4	1.59889258	3.46597E-12	2.76329E-11	6.964515002	0.059705122	1	877	952	812	981	958	5178	2004	3057	1779	3523
ENSMUSG00000018334	chr11	Ksr1	-1.1263765	3.5215E-12	2.80595E-11	7.084589883	0.030213804	-1	2778	2279	2408	3258	3109	1512	1221	1186	1445	1604
ENSMUSG00000071748	chrX	Gm14698	-2.3560231	3.57414E-12	2.84628E-11	1.09866169	0.083081338	-1	65	66	42	44	36	7	12	10	9	16
ENSMUSG00000028048	chr3	Gba	1.13836104	3.57874E-12	2.84832E-11	4.684805735	0.028723804	1	252	252	210	269	206	762	646	401	589	498
ENSMUSG00000022255	chr15	Mtdh	-1.3565102	3.6086E-12	2.87045E-11	6.406778255	0.043287451	-1	1725	1629	1666	2316	1772	521	934	593	765	1069
ENSMUSG00000066324	chr4	Impad1	-1.1237902	3.77929E-12	3.00451E-11	6.167909378	0.029738209	-1	1394	1289	1275	2012	1421	639	889	596	716	849
ENSMUSG00000018920	chr11	Cxcl16	2.41661903	3.78827E-12	3.00994E-11	3.926578394	0.124132679	1	69	70	84	85	45	895	238	405	135	449
ENSMUSG00000078238	chr4	Gm12854	3.01826987	3.91499E-12	3.10886E-11	0.183144764	0.100538778	1	4	1	3	7	1	46	23	29	26	21
ENSMUSG00000034792	chr10	Gna15	2.76260697	3.92414E-12	3.11436E-11	0.522619136	0.091422299	1	8	4	5	3	4	55	45	27	34	24
ENSMUSG00000022601	chr16	Zbtb11	-1.3658805	4.02195E-12	3.19017E-11	3.164353732	0.036841029	-1	146	176	173	282	184	74	87	61	82	101
ENSMUSG00000031149	chrX	Praf2	1.52100024	4.03877E-12	3.20169E-11	3.127051696	0.04663632	1	57	64	61	94	57	297	259	195	143	155
ENSMUSG00000042323	chr14	Pbrm1	-1.1323954	4.07435E-12	3.22807E-11	5.425439218	0.02967726	-1	849	763	904	1103	777	354	456	388	428	562
ENSMUSG00000027962	chr3	Vcam1	1.28293997	4.09736E-12	3.24446E-11	3.77419342	0.034398632	1	139	141	95	122	89	318	399	304	265	280
ENSMUSG00000052760	chr1	A630001G21Rik	2.89521751	4.1146E-12	3.25626E-11	1.051871745	0.125320715	1	7	2	9	6	9	100	48	31	64	37
ENSMUSG00000062785	chr7	Kcnc3	-1.8062258	4.13564E-12	3.27107E-11	3.169610804	0.067904552	-1	230	161	207	186	234	49	80	51	38	107
ENSMUSG00000059159	chr6	Gm8129	2.25806554	4.2209E-12	3.33661E-11	1.789472711	0.089674621	1	31	13	14	12	14	138	69	73	99	70
ENSMUSG00000020572	chr12	Nampt	-1.3347318	4.23828E-12	3.34657E-11	6.264865504	0.042130399	-1	1584	1508	1546	2316	1329	538	816	477	889	832
ENSMUSG00000038914	chr2	Dido1	-1.0698313	4.23714E-12	3.34657E-11	4.231931268	0.024550589	-1	384	300	359	452	390	216	186	159	190	237
ENSMUSG00000040390	chr7	Map3k10	-0.9696405	4.29484E-12	3.38931E-11	5.037277201	0.02110062	-1	639	596	546	769	677	371	383	359	320	372
ENSMUSG00000029763	chr6	Exoc4	-1.0539134	4.29919E-12	3.39083E-11	5.601316042	0.02582711	-1	1039	858	823	1219	951	447	556	456	526	580
ENSMUSG00000028789	chr4	Azin2	1.97174766	4.37148E-12	3.4459E-11	1.78274002	0.066075097	1	25	20	8	26	21	115	64	86	73	92
ENSMUSG00000071068	chr17	Treml2	3.50015991	4.42352E-12	3.48496E-11	0.130085294	0.130575362	1	1	2	1	4	3	45	44	21	18	16
ENSMUSG00000031333	chrX	Abcb7	-1.1553138	4.42851E-12	3.48692E-11	5.697984183	0.031292453	-1	941	962	936	1508	1029	427	647	438	501	606
ENSMUSG00000019877	chr10	Serinc1	-1.4818694	4.44471E-12	3.49771E-11	7.034879153	0.052157961	-1	2977	2631	2389	3686	2769	744	1270	735	1186	1711
ENSMUSG00000003233	chr16	Dvl3	-1.7675149	4.4864E-12	3.52853E-11	3.794253183	0.068005931	-1	296	273	311	418	296	51	91	76	106	185
ENSMUSG00000050232	chrX	Cxcr3	4.06909255	4.53395E-12	3.56392E-11	-0.545791773	0.109486174	1	1	0	0	1	2	25	19	9	11	21
ENSMUSG00000023791	chr16	Pigx	1.25965477	4.60873E-12	3.62067E-11	3.132555895	0.030288527	1	77	75	71	97	60	181	224	202	195	187
ENSMUSG00000032652	chr6	Crebl2	-1.2305757	4.6218E-12	3.62889E-11	3.389661609	0.030330578	-1	191	234	206	268	187	126	90	75	92	127
ENSMUSG00000060002	chr10	Chpt1	-1.3383327	4.66171E-12	3.65817E-11	6.181308955	0.042459275	-1	1226	1591	1447	2241	1312	454	684	669	646	877
ENSMUSG00000039988	chr3	Ankrd13c	-1.2661212	4.76288E-12	3.73337E-11	3.718766407	0.033541933	-1	302	231	252	343	252	106	122	90	158	149
ENSMUSG00000049526	chr9	Tmem202	3.22151244	4.76246E-12	3.73337E-11	0.020958688	0.099085457	1	4	3	2	2	1	41	27	13	23	26
ENSMUSG00000028572	chr4	Hook1	-1.372057	4.80823E-12	3.76523E-11	3.126126322	0.037269367	-1	162	180	150	243	196	72	75	57	98	90
ENSMUSG00000039158	chr4	Akna	1.77383351	4.80891E-12	3.76523E-11	2.759391249	0.063013543	1	46	45	33	77	27	274	166	105	151	154
ENSMUSG00000024725	chr19	Ostf1	1.25790323	4.81502E-12	3.7679E-11	5.544096584	0.037082379	1	462	418	385	469	311	1538	1200	687	1101	893
ENSMUSG00000031799	chr8	Tpm4	1.19633334	4.84267E-12	3.78742E-11	6.274061665	0.034107366	1	679	623	686	969	571	2072	2341	1306	1687	1431
ENSMUSG00000039219	chr13	Arid4b	-1.3763803	4.86955E-12	3.80631E-11	3.647600979	0.040215779	-1	242	234	243	377	253	94	127	84	88	174
ENSMUSG00000052430	chr3	Bmpr1b	-1.6345792	4.91824E-12	3.84222E-11	2.297534713	0.048497263	-1	123	86	75	163	104	46	39	40	36	30
ENSMUSG00000039747	chr5	Orai2	1.62835336	4.94045E-12	3.85741E-11	2.193824404	0.045972729	1	33	38	32	32	25	151	116	96	88	99
ENSMUSG00000043004	chr14	Gng2	1.18731604	4.94454E-12	3.85845E-11	3.698557177	0.02896679	1	107	107	122	154	96	394	288	216	298	272
ENSMUSG00000055172	chr6	C1ra	1.23892488	4.96802E-12	3.87461E-11	4.751907547	0.034897495	1	205	253	186	254	281	745	520	543	481	806
ENSMUSG00000055612	chr2	Cdca7	2.58578162	4.98394E-12	3.88486E-11	2.058025588	0.125282431	1	14	13	13	23	22	155	170	68	131	41
ENSMUSG00000035941	chr9	Ibtk	-1.2144818	5.00444E-12	3.89866E-11	6.669342763	0.035397724	-1	2109	1825	1947	2684	2056	744	1221	846	1116	1047
ENSMUSG00000028744	chr4	Pqlc2	1.44529279	5.10978E-12	3.97851E-11	2.91498322	0.040308861	1	65	75	42	62	51	159	202	146	187	188
ENSMUSG00000038127	chr16	Ccdc50	-1.1897273	5.12231E-12	3.98605E-11	6.363677575	0.03387412	-1	1720	1530	1422	2138	1736	729	869	590	1010	889
ENSMUSG00000027342	chr2	Pcna	1.39198661	5.24403E-12	4.07849E-11	4.937579121	0.044858292	1	282	203	213	339	228	849	975	492	842	462
ENSMUSG00000022769	chr16	Sdf2l1	2.09307435	5.36856E-12	4.17206E-11	3.274324546	0.092459342	1	62	56	47	44	56	341	344	117	335	133
ENSMUSG00000040675	chr10	Mthfd1l	2.14387239	5.37329E-12	4.17206E-11	2.084960381	0.085027384	1	17	29	25	22	18	120	160	70	130	66
ENSMUSG00000048047	chrX	Zbtb33	-1.530079	5.3732E-12	4.17206E-11	2.800422131	0.045966797	-1	166	114	142	197	145	48	64	45	46	86
ENSMUSG00000057133	chr2	Chd6	-1.1296297	5.39656E-12	4.1878E-11	4.058579071	0.027312567	-1	271	321	345	390	357	190	163	159	145	193
ENSMUSG00000048920	chr7	Fkrp	-1.0733577	5.4838E-12	4.25314E-11	5.465519791	0.02697044	-1	869	737	787	1174	908	423	482	389	491	531
ENSMUSG00000025330	chr4	Padi4	5.22188477	5.57308E-12	4.31999E-11	-0.318536045	0.197029314	1	0	1	1	0	0	8	25	16	40	15
ENSMUSG00000025268	chrX	Maged2	1.89516384	5.57878E-12	4.32201E-11	7.147921626	0.084177645	1	1105	766	777	919	883	2336	2098	4149	2900	6614
ENSMUSG00000031299	chrX	Pdha1	-1.1824809	5.58971E-12	4.32808E-11	9.442853101	0.03428082	-1	12838	14052	14308	20928	10720	6432	6748	6300	7740	7393
ENSMUSG00000054675	chr5	Tmem119	1.34764139	5.60624E-12	4.33847E-11	3.73645968	0.038755619	1	104	97	93	141	120	324	283	350	196	393
ENSMUSG00000061983	chr10	Rps12	1.35297737	5.61154E-12	4.34017E-11	8.064042586	0.044375604	1	2439	2188	1914	2686	2011	10038	6636	5376	5564	4114
ENSMUSG00000017002	chr2	Slpi	4.21237767	5.66097E-12	4.37598E-11	1.049788502	0.259988688	1	2	6	1	4	1	155	64	15	39	33
ENSMUSG00000037487	chr15	Ubr5	-1.08096	5.72516E-12	4.42316E-11	6.457478572	0.028160979	-1	1488	1541	1672	2377	1837	1000	1011	785	789	1036
ENSMUSG00000007050	chr17	Lsm2	1.19372968	5.76474E-12	4.45127E-11	3.565058199	0.029002071	1	111	93	93	136	99	321	311	242	256	201
ENSMUSG00000005881	chr2	Ergic3	1.06665457	5.83366E-12	4.502E-11	5.982354395	0.027111944	1	664	596	520	711	549	1870	1267	1364	1172	1333
ENSMUSG00000039599	chr14	Fam149b	-1.1596775	5.94301E-12	4.58386E-11	3.930455564	0.028613799	-1	296	270	318	379	295	135	148	123	187	169
ENSMUSG00000052248	chr2	Zeb2os	1.95946504	6.10767E-12	4.70827E-11	1.980633591	0.068102208	1	27	34	25	17	11	111	108	81	101	93

ENSMUSG00000021928	chr14	Ebpl	1.37619582	6.14293E-12	4.73283E-11	3.076811388	0.037539474	1	63	82	53	89	58	272	164	173	198	175
ENSMUSG00000033009	chr8	Ogfod1	-1.0647916	6.14976E-12	4.73549E-11	4.674034692	0.025572785	-1	466	459	452	703	501	243	298	219	303	277
ENSMUSG00000025935	chr1	Tram1	1.14153362	6.26408E-12	4.82086E-11	5.109200698	0.030348216	1	386	302	258	411	254	1056	924	611	656	653
ENSMUSG00000062006	chr3	Rpl34	1.1175256	6.2963E-12	4.84299E-11	6.921492085	0.030394655	1	1233	1142	1083	1291	937	2647	3183	2307	3038	2326
ENSMUSG00000012819	chr10	Cdh23	-2.1613845	6.40125E-12	4.92101E-11	1.852681082	0.08537114	-1	61	70	77	107	112	22	17	32	10	23
ENSMUSG00000006134	chr16	Crkl	-1.4071532	6.42228E-12	4.93446E-11	4.474834201	0.045476009	-1	417	406	460	717	425	129	227	139	216	277
ENSMUSG00000020803	chr11	Txndc17	1.09347289	6.44869E-12	4.95203E-11	5.187213496	0.027852327	1	415	348	316	377	268	897	939	682	847	674
ENSMUSG00000028033	chr1	Kcnq5	-1.7523627	6.46372E-12	4.96085E-11	3.007639663	0.064044897	-1	97	197	249	219	145	60	55	50	61	71
ENSMUSG00000001036	chr11	Epn2	-0.9707625	6.56041E-12	5.03229E-11	4.907883944	0.021393999	-1	551	582	552	754	523	371	329	255	359	341
ENSMUSG00000042747	chr3	Krtcap2	1.11357377	6.66052E-12	5.10628E-11	5.036117909	0.028802618	1	316	269	230	418	318	1004	781	686	566	638
ENSMUSG00000061119	chr7	Prcp	1.54430351	6.75447E-12	5.17546E-11	4.43296118	0.054332193	1	176	210	186	158	80	775	502	380	434	553
ENSMUSG00000003680	chr19	Taf6l	1.23580201	6.96255E-12	5.33198E-11	3.860535662	0.032721042	1	137	134	88	149	131	472	358	266	275	294
ENSMUSG00000086712	chr4	AI427809	3.74540702	7.0676E-12	5.40947E-11	0.09894222	0.150835229	1	1	1	3	3	1	44	25	14	13	47
ENSMUSG00000026193	chr1	Fn1	1.43610587	7.0932E-12	5.42609E-11	8.565559919	0.050359057	1	2776	2597	2784	3769	3297	15270	10222	6986	5938	7594
ENSMUSG00000029361	chr5	Nos1	-1.7520852	7.15691E-12	5.47183E-11	4.374750501	0.069979441	-1	285	420	408	867	451	117	196	214	107	128
ENSMUSG00000056612	chr19	Ppp1r14b	1.18821195	7.18213E-12	5.4881E-11	6.265074165	0.034180994	1	772	731	677	726	565	2186	1898	1671	1711	1255
ENSMUSG00000039886	chr5	Tmem120a	1.43127214	7.22695E-12	5.51934E-11	3.565708835	0.043858057	1	92	106	66	106	100	341	322	183	338	215
ENSMUSG00000048440	chr17	Cyp4f16	1.8548673	7.26194E-12	5.54303E-11	2.250208794	0.064590261	1	30	35	28	33	22	188	133	83	113	79
ENSMUSG00000017754	chr2	Pltp	2.05095478	7.27758E-12	5.55194E-11	5.913399982	0.098012736	1	282	339	335	455	334	2876	819	1617	622	2130
ENSMUSG00000045975	chr16	C2cd2	-1.1007305	7.32451E-12	5.58469E-11	7.053519575	0.029751522	-1	2788	2255	2383	3192	2859	1340	1466	1056	1489	1550
ENSMUSG00000010277	chr11	2610507B11Rik	-1.1449958	7.40979E-12	5.64356E-11	8.67707017	0.032507056	-1	7111	7118	7803	11024	9034	3776	4461	3779	4338	4388
ENSMUSG00000028643	chr4	Ccdc23	1.42035676	7.40895E-12	5.64356E-11	4.244654178	0.045563124	1	190	153	139	150	126	561	359	599	338	368
ENSMUSG00000021929	chr14	Kpna3	-1.1754387	7.48987E-12	5.70144E-11	6.868294834	0.033842387	-1	2330	2117	2061	3243	2387	989	1412	843	1208	1406
ENSMUSG00000023025	chr15	Larp4	-1.1833136	7.52049E-12	5.72163E-11	4.88468032	0.032656441	-1	505	518	566	942	558	267	367	210	323	304
ENSMUSG00000035891	chr15	Cerk	1.38850123	7.58304E-12	5.76608E-11	4.192153347	0.043297221	1	107	140	151	184	162	513	581	244	399	430
ENSMUSG00000025993	chr1	Slc40a1	-1.2663782	7.94278E-12	6.03634E-11	4.111238595	0.035668606	-1	290	345	374	574	255	163	145	163	146	206
ENSMUSG00000083307	chrX	AA414768	2.24300455	7.9624E-12	6.04796E-11	0.979756028	0.070301564	1	11	8	8	11	9	61	65	28	50	44
ENSMUSG00000024750	chr19	Zfand5	-1.1853459	8.08275E-12	6.13593E-11	7.444177177	0.034701137	-1	3698	3472	3004	4556	3365	1421	2027	1314	1676	2255
ENSMUSG00000036591	chr2	Arhgap21	-1.0306142	8.08699E-12	6.13593E-11	4.293067423	0.023445584	-1	353	380	375	508	343	237	212	156	192	256
ENSMUSG00000003824	chr8	Syce2	3.08250538	8.30245E-12	6.29599E-11	0.668620009	0.132690408	1	5	6	2	3	6	44	60	34	55	17
ENSMUSG00000027806	chr3	Tsc22d2	-1.2722171	8.42501E-12	6.38547E-11	4.564548406	0.037582251	-1	508	365	393	718	528	195	273	152	227	283
ENSMUSG00000040446	chr18	Rprd1a	-1.443856	8.4954E-12	6.43532E-11	3.450121695	0.044661984	-1	263	203	210	288	219	56	87	97	110	120
ENSMUSG00000037221	chr5	Mospd3	1.20807538	8.59603E-12	6.50803E-11	3.502719151	0.030052799	1	99	83	86	134	104	285	232	268	195	297
ENSMUSG00000040850	chr11	Psme4	-1.1295397	8.61936E-12	6.52215E-11	7.682013692	0.031698259	-1	4079	3751	4089	5329	3806	1800	2232	1685	2370	2403
ENSMUSG00000022770	chr16	Dlg1	-1.0188792	8.62542E-12	6.5232E-11	5.516492465	0.024783524	-1	860	773	793	1255	911	571	534	378	456	541
ENSMUSG00000090187	chr13	AK157302	-1.7687375	8.65162E-12	6.53949E-11	1.902881123	0.05515558	-1	70	75	77	132	71	20	33	20	32	29
ENSMUSG00000028969	chr5	Cdk5	1.10440033	8.7246E-12	6.59108E-11	3.998987254	0.02617249	1	151	145	151	185	119	429	291	363	312	373
ENSMUSG00000054404	chr11	Slfn5	-1.8605971	8.74754E-12	6.60484E-11	4.297117188	0.079414339	-1	332	370	460	683	462	68	174	76	158	213
ENSMUSG00000028333	chr4	Anp32b	1.12698019	8.95723E-12	6.75951E-11	6.352745171	0.031124708	1	810	707	593	1031	712	2438	2098	1625	1538	1502
ENSMUSG00000095253	chr17	Zfp799	-1.5810574	9.0236E-12	6.80593E-11	2.338079396	0.046631378	-1	122	109	103	133	88	38	36	27	43	59
ENSMUSG00000001348	chr9	Acp5	3.51886226	9.06511E-12	6.83355E-11	4.191471873	0.251610624	1	12	93	28	28	48	1223	405	330	133	732
ENSMUSG00000039763	chr16	Dnajc28	-1.1569386	9.09889E-12	6.85531E-11	4.259305788	0.030175125	-1	396	417	354	504	300	164	166	172	228	228
ENSMUSG00000062997	chr2	Rpl35	1.09790928	9.12396E-12	6.8705E-11	7.09921127	0.029876515	1	1391	1358	1122	1526	1110	3937	3303	2861	2764	2436
ENSMUSG00000021094	chr12	Dhrs7	1.33929839	9.19175E-12	6.91782E-11	4.511355426	0.041743572	1	135	212	175	259	179	563	504	703	398	465
ENSMUSG00000033386	chr3	Frrs1	1.9623122	9.22366E-12	6.9381E-11	2.101399708	0.072385561	1	18	35	20	33	20	138	153	75	103	73
ENSMUSG00000024177	chr17	Nme4	1.75147735	9.40542E-12	7.07102E-11	2.045527918	0.05444124	1	32	29	27	22	24	128	96	93	110	74
ENSMUSG00000039519	chr3	Cyp7b1	2.92050697	9.4526E-12	7.10266E-11	0.651611943	0.117708646	1	8	7	1	3	5	73	42	24	37	32
ENSMUSG00000018501	chr11	Ncor1	-1.1555498	9.49538E-12	7.13098E-11	6.422392967	0.032842992	-1	1593	1513	1626	2297	1809	685	981	776	841	1038
ENSMUSG00000078619	chr11	Smarcd2	0.9716162	9.94933E-12	7.46787E-11	4.690207681	0.021376244	1	246	253	255	299	236	678	568	451	555	537
ENSMUSG00000027895	chr3	Kcnc4	-1.3822353	1.00149E-11	7.51304E-11	7.216712551	0.047224961	-1	3315	3103	2750	3622	3181	2021	1839	1047	876	1052
ENSMUSG00000054871	chr9	Tmem158	2.21231582	1.01435E-11	7.60548E-11	1.949176444	0.091833079	1	13	27	10	21	26	133	80	101	56	132
ENSMUSG00000059479	chr7	B3gnt8	1.95244116	1.04573E-11	7.83654E-11	1.812497951	0.067398493	1	20	19	27	22	14	120	108	69	84	58
ENSMUSG00000091549	chr17	Gm6548	1.4141767	1.05002E-11	7.86447E-11	2.314682507	0.034497718	1	40	37	37	46	36	121	110	98	116	129
ENSMUSG00000021097	chr12	Clmn	-1.6686095	1.08087E-11	8.09121E-11	2.177979983	0.051564104	-1	73	88	92	127	121	43	38	35	27	30
ENSMUSG00000025150	chr11	Cbr2	1.82277744	1.10068E-11	8.23504E-11	4.81376356	0.078462413	1	195	229	161	151	168	1415	542	586	681	393
ENSMUSG00000071657	chr19	Bscl2	1.07987827	1.1015E-11	8.23682E-11	4.310924893	0.026275107	1	181	161	164	248	193	597	426	400	334	445
ENSMUSG00000036273	chr15	Lrrk2	-1.3540156	1.11538E-11	8.33615E-11	3.10926594	0.037586301	-1	179	166	189	247	139	78	99	53	90	72
ENSMUSG00000025937	chr1	Lactb2	-1.128785	1.11691E-11	8.34312E-11	4.512350555	0.029502951	-1	460	491	443	554	377	214	268	157	264	263
ENSMUSG00000003402	chr9	Prkcsh	1.20810742	1.12486E-11	8.39537E-11	5.302563587	0.035176823	1	340	307	324	406	386	1316	986	837	678	704
ENSMUSG00000042558	chr4	Adprhl2	1.12381864	1.12511E-11	8.39537E-11	3.744144546	0.026814832	1	135	113	110	162	105	383	302	244	314	247
ENSMUSG00000003429	chr7	Rps11	1.15544592	1.13844E-11	8.48579E-11	7.810054817	0.033558792	1	2309	1978	1634	2480	1980	7263	5151	4647	4007	4428
ENSMUSG00000071793	chr8	2610005L07Rik	-2.2685183	1.13835E-11	8.48579E-11	1.150694275	0.082562782	-1	65	49	31	54	62	12	6	10	15	16
ENSMUSG00000030022	chr6	Adamts9	-1.2658409	1.1495E-11	8.56362E-11	3.936770463	0.035961076	-1	259	261	277	441	371	204	161	112	108	153
ENSMUSG00000027983	chr3	Cyp2u1	-1.7415505	1.15926E-11	8.63179E-11	1.642954816	0.04991759	-1	71	52	63	86	75	25	17	21	27	23
ENSMUSG00000036990	chr8	Otud4	-1.2585337	1.16451E-11	8.66623E-11	6.021072453	0.039010561	-1	1272	1231	1194	1734	1400	454	727	528	536	875

ENSMUSG00000090862	chr7	Rps13	1.17478109	1.16862E-11	8.69223E-11	7.250370566	0.034573694	1	1418	1328	1130	1861	1277	5128	3498	3082	2956	2702
ENSMUSG00000051212	chr14	Gpr183	2.87383933	1.16947E-11	8.69388E-11	1.374082786	0.145774158	1	11	8	9	9	6	103	89	31	101	29
ENSMUSG00000052299	chr16	Ltn1	-1.0556237	1.17523E-11	8.73207E-11	4.854795089	0.026178705	-1	523	527	540	749	570	258	364	247	311	348
ENSMUSG00000047415	chr12	Gpr68	5.2561584	1.18728E-11	8.81694E-11	-0.278238754	0.245256148	1	0	0	1	1	0	23	35	8	5	39
ENSMUSG00000027613	chr2	Eif6	1.04518201	1.19148E-11	8.84338E-11	5.404955791	0.026303943	1	435	381	373	468	393	1208	982	855	868	749
ENSMUSG00000034327	chr14	Kctd9	-1.0871221	1.21862E-11	9.04001E-11	5.296717872	0.028493225	-1	787	848	756	972	619	420	388	328	508	401
ENSMUSG00000078783	chr3	Gm9733	7.33326451	1.24785E-11	9.25193E-11	-0.351264938	0.337978942	1	0	0	0	0	0	25	19	5	50	5
ENSMUSG00000031007	chrX	Atp6ap2	1.25286251	1.24964E-11	9.26036E-11	4.911642501	0.037561638	1	275	270	218	335	228	916	861	370	606	747
ENSMUSG00000022385	chr15	Gtse1	2.48776067	1.25806E-11	9.31778E-11	0.892073337	0.090450938	1	9	5	9	8	7	43	70	44	51	28
ENSMUSG00000025959	chr1	Klf7	-1.0524572	1.26043E-11	9.33037E-11	3.97520858	0.023963022	-1	306	277	304	402	287	171	201	157	133	169
ENSMUSG00000018076	chr5	Med13l	-1.0508905	1.26412E-11	9.35275E-11	4.465137319	0.025342418	-1	385	382	377	654	437	247	242	200	200	284
ENSMUSG00000021838	chr14	Samd4	-1.1115949	1.27108E-11	9.39926E-11	5.264605779	0.029823819	-1	752	624	744	1100	721	329	389	434	357	459
ENSMUSG00000019539	chr7	Rcn3	1.30147623	1.28765E-11	9.51673E-11	5.905652357	0.041746714	1	571	418	497	595	488	2075	1319	1549	913	1135
ENSMUSG00000038708	chr9	Golga4	-1.265875	1.29895E-11	9.59522E-11	8.222290029	0.040427699	-1	5128	4881	5012	10506	6533	2621	3103	2528	3119	2901
ENSMUSG00000007039	chr17	Ddah2	1.2414618	1.3003E-11	9.59903E-11	4.665887934	0.036479899	1	227	218	243	254	173	744	546	702	415	488
ENSMUSG00000045098	chr19	Suv420h1	-1.0213401	1.30084E-11	9.59903E-11	4.461401086	0.023851565	-1	385	389	374	616	443	267	242	194	205	280
ENSMUSG00000052146	chr17	Rps10	1.18658796	1.3271E-11	9.78342E-11	7.311806751	0.035467734	1	1561	1467	1275	1754	1187	5417	3844	3029	3090	2818
ENSMUSG00000061207	chr17	Stk19	1.35931268	1.32723E-11	9.78342E-11	2.893006124	0.036762229	1	69	69	46	77	45	193	187	167	169	139
ENSMUSG00000028334	chr4	Nans	1.09176222	1.32895E-11	9.79096E-11	4.57967664	0.027687911	1	278	202	186	241	221	569	620	386	549	528
ENSMUSG00000026977	chr2	March7	-1.0864762	1.35245E-11	9.95882E-11	4.325875525	0.026981917	-1	431	387	346	550	327	182	226	163	241	229
ENSMUSG00000033152	chr6	Podxl2	-1.0362178	1.36548E-11	1.00495E-10	5.414746545	0.02606379	-1	862	719	738	1088	871	427	441	387	475	546
ENSMUSG00000015533	chr13	Itga2	-2.851624	1.41091E-11	1.03784E-10	0.240171022	0.103568027	-1	32	16	26	33	34	3	9	1	3	5
ENSMUSG00000074622	chr2	Mafb	1.64164455	1.41456E-11	1.03997E-10	5.505740657	0.065581682	1	204	374	456	275	289	1636	1089	704	1218	1018
ENSMUSG00000037395	chr1	Rcor3	-1.1433092	1.42734E-11	1.04827E-10	4.085804804	0.029475257	-1	329	298	329	466	320	175	175	112	182	219
ENSMUSG00000046985	chr5	Tapt1	-1.0058628	1.42731E-11	1.04827E-10	5.702060013	0.02483739	-1	1022	928	975	1295	961	533	676	463	537	615
ENSMUSG00000043631	chr13	Ecm2	-1.049123	1.46868E-11	1.07806E-10	4.542010523	0.025599384	-1	458	425	442	631	392	326	208	237	195	275
ENSMUSG00000057230	chr6	Aak1	-1.9762184	1.47303E-11	1.08069E-10	2.324799556	0.079336583	-1	93	98	119	137	134	14	33	25	43	46
ENSMUSG00000078532	chr4	Nkain1	-1.3644917	1.47885E-11	1.08438E-10	3.653867742	0.041404696	-1	279	273	239	292	252	69	115	109	119	154
ENSMUSG00000028692	chr4	Akr1a1	1.13840092	1.49347E-11	1.09453E-10	8.305597009	0.033060022	1	3397	2989	2642	3148	2501	8066	8258	5083	7607	6670
ENSMUSG00000067336	chr1	Bmpr2	-1.0426131	1.49446E-11	1.09469E-10	5.972318238	0.027006586	-1	1100	1065	1156	1786	1235	701	740	563	582	772
ENSMUSG00000035606	chr9	Ky	-1.5911863	1.52187E-11	1.11418E-10	8.747681703	0.063346515	-1	12786	9737	9344	7672	7868	2194	4028	2865	3404	4943
ENSMUSG00000027708	chr3	Dcun1d1	-1.2139981	1.54066E-11	1.12735E-10	5.562777168	0.036391539	-1	1199	861	858	1045	933	372	590	335	493	530
ENSMUSG00000034614	chr11	Pik3ip1	-1.4269944	1.56537E-11	1.14482E-10	4.771985811	0.049361336	-1	693	717	553	473	478	397	191	180	208	247
ENSMUSG00000002808	chr13	Epdr1	-1.1007136	1.57767E-11	1.15322E-10	6.87275935	0.030672539	-1	2197	2344	2202	3166	2063	1011	1341	1063	1400	1233
ENSMUSG00000020057	chr10	Dram1	2.08416155	1.5797E-11	1.1541E-10	3.054702815	0.095036487	1	22	76	32	58	43	382	226	128	152	213
ENSMUSG00000028792	chr4	Ak2	1.08284181	1.59051E-11	1.16139E-10	5.405336386	0.028681378	1	401	479	346	465	327	1117	1131	826	822	809
ENSMUSG00000102692	chr3	Dchs2	-2.223117	1.59153E-11	1.16153E-10	0.592053509	0.063217196	-1	34	28	33	46	32	8	13	5	8	6
ENSMUSG00000018567	chr11	Gabarap	1.06410684	1.59754E-11	1.16531E-10	7.518264822	0.028892045	1	1830	1837	1481	2187	1531	5172	4068	3286	4262	3541
ENSMUSG00000021057	chr12	Akap5	-2.0705766	1.60575E-11	1.17068E-10	1.76484156	0.079898801	-1	62	95	93	110	40	19	24	23	14	23
ENSMUSG00000048096	chr1	Lmod1	-1.7956034	1.6102E-11	1.17331E-10	3.205254845	0.071514197	-1	122	254	125	262	290	65	65	57	57	90
ENSMUSG00000006333	chr7	Rps9	1.24261537	1.62554E-11	1.18387E-10	8.68531298	0.039429577	1	3960	3570	3258	4449	3043	14614	9514	8347	8315	6898
ENSMUSG00000038248	chr10	Sobp	-1.1296178	1.62977E-11	1.18634E-10	5.029954789	0.030901989	-1	640	531	504	888	785	296	338	313	311	407
ENSMUSG00000075700	chr3	Selt	-1.1108317	1.63544E-11	1.18984E-10	7.176154748	0.031398378	-1	3112	2525	2746	3749	2655	1281	1797	1163	1514	1716
ENSMUSG00000050199	chr2	Lgr4	-1.2081412	1.64219E-11	1.19413E-10	4.571148138	0.034766686	-1	519	478	402	635	443	171	245	181	241	328
ENSMUSG00000079588	chr1	Tmem182	-1.1201685	1.67156E-11	1.21486E-10	7.875364315	0.032121148	-1	4470	4335	4109	6705	4558	2030	2605	2339	2162	2905
ENSMUSG00000020697	chr11	Lig3	-1.0456778	1.68246E-11	1.22214E-10	4.862709928	0.026090541	-1	613	474	480	746	610	282	374	268	318	300
ENSMUSG00000038859	chr5	Baiap2l1	2.58003964	1.69036E-11	1.22725E-10	1.366392186	0.118457238	1	15	8	8	14	7	66	70	110	30	61
ENSMUSG00000074785	chr10	Plxnc1	1.7497071	1.69615E-11	1.23081E-10	2.618726164	0.062590114	1	32	51	45	25	46	176	156	103	147	177
ENSMUSG00000002804	chr12	Nudt14	1.19643364	1.72424E-11	1.25055E-10	3.344796107	0.029802459	1	97	101	70	121	68	232	205	236	214	249
ENSMUSG00000089714	chr1	Gm16092	-3.5048348	1.73814E-11	1.25997E-10	0.146349265	0.166200882	-1	20	25	38	37	18	10	0	0	2	1
ENSMUSG00000029752	chr6	Asns	2.11244926	1.76084E-11	1.27576E-10	2.665975382	0.094564039	1	30	36	24	33	48	212	155	226	147	75
ENSMUSG00000052373	chr11	Mpp3	-1.2281941	1.76326E-11	1.27686E-10	4.951246927	0.036798982	-1	683	698	579	659	581	460	215	300	229	315
ENSMUSG00000026581	chr1	Sell	3.46660378	1.80581E-11	1.30699E-10	1.045972545	0.200767618	1	1	7	5	6	4	103	57	27	84	18
ENSMUSG00000041258	chr18	Zfp236	-1.0630846	1.82793E-11	1.32232E-10	3.811845239	0.02450103	-1	271	244	267	342	281	159	150	110	142	179
ENSMUSG00000033538	chr9	Casp4	2.28454121	1.8317E-11	1.32436E-10	1.001597362	0.080236953	1	8	11	9	14	5	80	38	42	54	39
ENSMUSG00000031320	chrX	Rps4x	1.11341499	1.84102E-11	1.33041E-10	8.676877928	0.031991136	1	4242	3771	3215	4609	3480	12450	9308	8622	8057	7491
ENSMUSG00000038485	chr11	Socs7	-1.0452215	1.86338E-11	1.34587E-10	6.268502717	0.02759365	-1	1502	1303	1429	1898	1598	752	827	727	820	972
ENSMUSG00000099200	chr4	Mir7019	-1.3665099	1.90813E-11	1.37748E-10	3.035041818	0.0390189	-1	156	161	176	238	144	103	63	65	84	55
ENSMUSG00000006058	chr11	Snf8	1.08022985	1.91297E-11	1.3797E-10	4.685352509	0.027788471	1	236	253	202	316	223	734	618	550	518	424
ENSMUSG00000062093	chr14	Gm10110	-1.1685255	1.91318E-11	1.3797E-10	3.58709733	0.029440678	-1	251	239	174	320	252	110	135	126	103	123
ENSMUSG00000061410	chr8	Zcchc14	-1.0416992	1.93311E-11	1.39336E-10	4.770186007	0.025940492	-1	443	453	516	790	548	341	313	261	238	305
ENSMUSG00000049932	chr9	H2afx	1.34460919	1.94931E-11	1.40431E-10	3.642343435	0.040364346	1	112	83	87	114	121	402	335	269	243	205
ENSMUSG00000038886	chr7	Man2a2	-1.2712373	1.97944E-11	1.42486E-10	7.769905251	0.041434772	-1	5006	3898	3964	5277	4804	1603	2044	1664	2132	2982
ENSMUSG00000045725	chr6	Prr15	2.66361496	1.97988E-11	1.42486E-10	0.76503364	0.106700382	1	9	7	4	5	6	27	34	39	65	52
ENSMUSG00000083405	chr16	Gm15725	-2.4136487	2.00944E-11	1.44539E-10	1.602823151	0.109248435	-1	57	72	73	83	82	6	17	6	28	18

ENSMUSG00000079297	chrX	Gm2223	-1.898504	2.06079E-11	1.48156E-10	1.814236494	0.06753216	-1	63	65	53	129	97	19	23	22	26	27
ENSMUSG00000060012	chr14	Kif13b	-2.0450589	2.10549E-11	1.51292E-10	2.479907066	0.089147706	-1	113	139	130	148	125	17	50	16	34	58
ENSMUSG00000096474	chr1	Gm5561	6.25457363	2.12653E-11	1.52725E-10	0.550593277	0.445713956	1	0	0	0	1	1	0	56	56	52	44
ENSMUSG00000033159	chr1	Cnppd1	1.11214359	2.15797E-11	1.54904E-10	4.757297827	0.029849983	1	227	284	217	334	213	841	600	511	427	659
ENSMUSG00000041841	chr15	Rpl37	1.12317095	2.15937E-11	1.54925E-10	7.011136986	0.032417553	1	1315	1196	1027	1462	1059	4201	2839	2613	2588	2285
ENSMUSG00000006575	chr11	Rundc3a	2.96988141	2.16407E-11	1.55182E-10	-0.002595446	0.090249845	1	2	3	2	4	3	20	24	27	17	36
ENSMUSG00000043126	chr10	D830039M14Rik	-1.3506435	2.16944E-11	1.55488E-10	2.848923523	0.037055857	-1	146	151	142	190	133	53	67	53	82	70
ENSMUSG00000026649	chr1	1700009P17Rik	3.09872452	2.18585E-11	1.56584E-10	0.100442053	0.111190514	1	4	0	5	3	2	18	27	36	22	32
ENSMUSG00000072940	chr6	Gm10443	1.97074359	2.18851E-11	1.56694E-10	1.805910622	0.07250519	1	25	13	13	29	22	130	79	95	73	60
ENSMUSG00000035226	chr2	Rims4	-2.3080832	2.20908E-11	1.58085E-10	1.498816309	0.098473989	-1	31	51	61	128	74	15	13	15	15	16
ENSMUSG00000021768	chr14	Dusp13	-1.340918	2.24598E-11	1.60644E-10	6.561652844	0.045859926	-1	2243	1835	1709	2320	1971	1487	814	637	867	617
ENSMUSG00000030682	chr7	Cdipt	0.9974826	2.27149E-11	1.62386E-10	5.44893848	0.024654329	1	461	382	400	535	393	1198	864	940	862	883
ENSMUSG00000031004	chr7	Mki67	1.6352059	2.27929E-11	1.6286E-10	4.176221271	0.063496187	1	135	147	140	92	122	538	639	363	434	248
ENSMUSG00000005973	chr2	Rcn1	1.06618683	2.28081E-11	1.62885E-10	5.098710907	0.027874581	1	371	331	285	380	278	974	842	750	634	583
ENSMUSG00000091900	chr7	Gm4353	-2.6842933	2.30735E-11	1.64612E-10	0.729200629	0.111768185	-1	37	27	32	45	59	9	11	2	9	3
ENSMUSG00000100862	chr1	Gm10925	-1.1926389	2.30717E-11	1.64612E-10	3.470202589	0.030642592	-1	235	211	228	314	161	97	129	94	107	118
ENSMUSG00000031600	chr8	Vps37a	-1.0733166	2.31371E-11	1.64981E-10	5.877297372	0.029154472	-1	1463	1200	1016	1163	1050	752	597	476	607	674
ENSMUSG00000002477	chr18	Snrpd1	1.32456729	2.32779E-11	1.65901E-10	4.15345794	0.041372516	1	181	136	128	193	118	551	497	342	426	253
ENSMUSG00000040321	chr2	Zfp770	-1.1707662	2.33831E-11	1.66566E-10	4.349974894	0.032633905	-1	359	342	386	650	387	170	219	173	187	270
ENSMUSG00000044783	chr1	Hjurp	1.46463609	2.37024E-11	1.68754E-10	4.091404362	0.050669283	1	164	115	124	120	139	247	422	461	435	432
ENSMUSG00000021959	chr14	Lats2	-1.1065442	2.40568E-11	1.7119E-10	4.47996367	0.02924026	-1	408	379	396	633	462	207	303	198	190	254
ENSMUSG00000001864	chr2	Aif1l	1.8684388	2.44667E-11	1.74007E-10	4.196388652	0.083196941	1	149	118	123	97	88	503	551	713	224	320
ENSMUSG00000030203	chr6	Dusp16	-1.0904572	2.44775E-11	1.74007E-10	4.461579959	0.02837146	-1	375	370	402	577	503	296	257	199	185	215
ENSMUSG00000002668	chr17	Dennd1c	2.64131141	2.48905E-11	1.76853E-10	1.4249342	0.127949136	1	9	11	13	10	8	154	60	35	66	49
ENSMUSG00000033530	chr12	Ttc7b	-1.01807	2.49312E-11	1.76962E-10	5.965904554	0.026307148	-1	1067	1111	1098	1834	1186	686	685	658	637	697
ENSMUSG00000058569	chr13	Tmed9	0.97334575	2.49289E-11	1.76962E-10	6.89675413	0.024492987	1	1299	1088	1010	1461	1143	2686	2839	2363	2501	2484
ENSMUSG00000099471	chr1	Gm8451	2.22897251	2.50144E-11	1.77463E-10	1.179816979	0.081758172	1	12	7	10	13	13	86	48	48	68	36
ENSMUSG00000103409	chr9	RP23-456B9.23	-1.2916632	2.5482E-11	1.80688E-10	3.414843635	0.036678961	-1	218	185	221	271	222	75	133	84	109	97
ENSMUSG00000028693	chr4	Nasp	1.37278215	2.56218E-11	1.81587E-10	4.408047688	0.045758913	1	166	193	187	200	127	584	669	406	529	300
ENSMUSG00000074264	chr3	Amy1	-1.2040076	2.58184E-11	1.82888E-10	3.379670497	0.031439659	-1	181	249	178	275	192	121	110	71	93	118
ENSMUSG00000034485	chr9	Uaca	-1.0644275	2.60295E-11	1.8429E-10	6.815455704	0.029325399	-1	2111	1949	1956	3339	2132	1479	1186	1204	972	1120
ENSMUSG00000059070	chr7	Rpl18	1.2290939	2.62674E-11	1.8588E-10	7.752543553	0.039269026	1	1885	1754	1660	2440	1896	7805	4986	4413	4004	3732
ENSMUSG00000039100	chr15	March6	-1.0567802	2.65291E-11	1.87637E-10	7.124349729	0.029044833	-1	2649	2559	2206	3778	2933	1487	1656	1266	1266	1740
ENSMUSG00000044617	chr10	Zbtb39	-1.211784	2.65549E-11	1.87724E-10	3.021374669	0.030037425	-1	179	137	147	208	166	100	80	67	63	87
ENSMUSG00000036391	chr11	Sec24a	-1.3476925	2.72575E-11	1.92594E-10	4.166894257	0.043360386	-1	266	308	332	551	465	156	180	112	189	187
ENSMUSG00000066258	chr7	Trim12a	5.91050876	2.76992E-11	1.95616E-10	1.468458775	0.501336979	1	1	1	0	3	1	0	94	100	83	135
ENSMUSG00000056900	chr3	Usp13	-1.0814631	2.80605E-11	1.98067E-10	7.972460199	0.030681822	-1	5044	4177	4580	6694	5045	2257	2817	2481	2655	2891
ENSMUSG00000068101	chr15	Cenpm	2.92262319	2.81759E-11	1.98782E-10	0.481822692	0.11844163	1	5	4	6	2	4	35	43	45	40	16
ENSMUSG00000098462	chr19	Gm27694	-1.6163612	2.85933E-11	2.01625E-10	2.827077944	0.056702427	-1	163	158	174	131	148	52	48	37	59	86
ENSMUSG00000038658	chr19	Ric1	-1.060579	2.86381E-11	2.01838E-10	4.657782402	0.027286617	-1	439	462	496	685	464	273	327	183	252	303
ENSMUSG00000035493	chr13	Tgfbi	1.6009776	2.87536E-11	2.0255E-10	6.322032933	0.06519083	1	621	589	481	640	606	3646	2246	1379	1617	1112
ENSMUSG00000022020	chr14	Naa16	-1.1673004	2.89291E-11	2.03684E-10	3.583322655	0.030168189	-1	245	208	219	307	249	137	114	83	148	117
ENSMUSG00000090799	chr14	Klhl33	-1.507142	2.89895E-11	2.04006E-10	5.930532244	0.057825999	-1	1075	1434	1325	1561	1288	324	509	413	459	882
ENSMUSG00000034773	chr11	BC030867	3.34411095	2.90315E-11	2.04199E-10	0.202773995	0.141771155	1	3	1	4	4	1	37	48	26	28	11
ENSMUSG00000080921	chr6	Rpl38-ps2	1.26398116	2.93334E-11	2.06219E-10	4.271358617	0.038342959	1	173	186	114	246	133	668	446	373	405	338
ENSMUSG00000024014	chr17	Pim1	1.311196	2.94164E-11	2.06699E-10	3.983190551	0.040201166	1	125	136	153	127	121	450	426	329	217	418
ENSMUSG00000024308	chr17	Tapbp	1.18078526	2.99525E-11	2.1036E-10	5.965678972	0.035761996	1	534	520	525	754	526	2215	1295	1177	986	1498
ENSMUSG00000020124	chr10	Usp15	-1.1978378	3.02764E-11	2.12528E-10	6.699728147	0.037256864	-1	2113	1923	1958	2937	1933	797	1106	761	1253	1214
ENSMUSG00000071302	chr8	2610044O15Rik8	-1.1294563	3.04567E-11	2.13687E-10	4.127750475	0.029796687	-1	354	403	324	436	266	175	170	137	218	189
ENSMUSG00000015085	chr2	Entpd2	1.36943474	3.05236E-11	2.14048E-10	4.294066427	0.045203656	1	146	160	160	164	171	402	328	543	370	635
ENSMUSG00000021470	chr13	Ercc6l2	-1.0975733	3.0689E-11	2.151E-10	4.205374216	0.028396727	-1	373	296	353	483	365	157	230	179	201	182
ENSMUSG00000028152	chr3	Tspan5	1.35778749	3.1372E-11	2.19777E-10	3.14093807	0.039711542	1	62	88	67	71	71	237	230	136	178	247
ENSMUSG00000062115	chr11	Rai1	-1.0841605	3.14102E-11	2.19934E-10	4.373486156	0.028085386	-1	343	383	462	516	381	196	214	230	189	246
ENSMUSG00000030660	chr7	Pik3c2a	-1.2626902	3.18064E-11	2.22597E-10	3.228070202	0.034727014	-1	193	165	186	248	186	117	110	56	87	79
ENSMUSG00000094392	chr3	Gm3788	4.26119458	3.18391E-11	2.22715E-10	-0.161077361	0.184828093	1	3	1	0	0	1	24	31	38	14	9
ENSMUSG00000058603	chr1	Rpl28-ps1	1.51689991	3.20864E-11	2.2422E-10	3.039879803	0.050545247	1	61	60	53	78	60	333	154	184	165	151
ENSMUSG00000079471	chr17	Gm7325	3.81989406	3.20758E-11	2.2422E-10	2.934161349	0.294035263	1	25	24	12	2	8	262	150	460	45	208
ENSMUSG00000025223	chr19	Ldb1	1.04958489	3.21778E-11	2.24746E-10	4.968152589	0.027196664	1	293	323	311	337	243	943	589	638	570	714
ENSMUSG00000046798	chr5	Cldn12	-1.1043897	3.23064E-11	2.25532E-10	4.2508757	0.029037608	-1	401	439	340	433	311	178	262	167	176	199
ENSMUSG00000026810	chr2	Dpm2	1.20215201	3.23363E-11	2.25628E-10	3.878612232	0.033227691	1	149	129	127	140	110	512	322	261	287	295
ENSMUSG00000052144	chr6	Ppp4r2	-1.2173678	3.25025E-11	2.26674E-10	4.975852503	0.037169273	-1	661	550	556	875	649	233	382	209	310	409
ENSMUSG00000035448	chr9	Ccr3	3.77512478	3.25452E-11	2.26859E-10	-0.542686212	0.096599919	1	2	0	1	0	2	12	19	18	19	15
ENSMUSG00000029575	chr5	Mmab	-1.0288945	3.27001E-11	2.27825E-10	4.900153058	0.026075206	-1	665	631	535	601	525	281	319	295	336	361
ENSMUSG00000053799	chr19	Exoc6	-1.1759691	3.3143E-11	2.30795E-10	5.460962252	0.03520292	-1	825	840	848	1220	833	306	466	398	471	547
ENSMUSG00000060716	chr12	Plekhh1	2.14362364	3.3202E-11	2.31091E-10	1.413421282	0.082301645	1	17	17	7	16	12	75	63	84	36	77

ENSMUSG00000085342	chr11	Gm12254	1.12864596	3.334E-11	2.31936E-10	3.885275049	0.028959253	1	151	132	123	140	134	448	293	322	298	284
ENSMUSG00000037361	chr12	Sf3b6	1.0973573	3.39552E-11	2.35989E-10	4.492137858	0.029137308	1	221	206	198	257	181	636	549	432	521	357
ENSMUSG00000040351	chr5	Ankib1	-1.1752196	3.39564E-11	2.35989E-10	3.779274256	0.031640032	-1	258	235	254	396	276	122	165	96	156	144
ENSMUSG00000051495	chr8	Irf2bp2	0.9752205	3.39758E-11	2.36007E-10	4.994540693	0.023363506	1	317	349	282	351	290	864	738	604	544	709
ENSMUSG00000037493	chr9	Cib2	-1.2022527	3.41612E-11	2.37177E-10	7.320305747	0.037960226	-1	4531	3190	2870	3101	2792	1524	1706	1208	1676	1799
ENSMUSG00000037816	chr13	Fbxw17	1.4842184	3.44256E-11	2.38894E-10	2.099356637	0.039718788	1	37	26	31	37	31	107	107	102	81	101
ENSMUSG00000031902	chr8	Nfatc3	-0.9436921	3.47775E-11	2.41216E-10	5.193446818	0.022163338	-1	627	655	646	916	740	432	440	355	369	447
ENSMUSG00000027858	chr3	Tspan2	-1.2129502	3.48778E-11	2.41792E-10	3.325944141	0.032012817	-1	160	230	206	264	175	110	91	88	81	120
ENSMUSG00000033502	chr3	Cdc14a	-1.3220141	3.51748E-11	2.4373E-10	3.998249044	0.04181609	-1	332	273	405	423	260	141	161	97	130	217
ENSMUSG00000074361	chr7	C5ar2	4.12103759	3.56856E-11	2.47147E-10	-0.267336252	0.161970976	1	2	0	2	0	1	7	32	18	22	27
ENSMUSG00000023272	chr15	Creld2	1.63744986	3.58247E-11	2.47987E-10	3.789913813	0.063966445	1	101	100	71	115	108	553	368	199	394	198
ENSMUSG00000028007	chr3	Snx7	1.46653641	3.60785E-11	2.4962E-10	2.477523731	0.043004052	1	42	50	35	58	31	161	140	125	91	137
ENSMUSG00000057280	chr4	Musk	-1.4157116	3.72986E-11	2.57934E-10	2.786850791	0.042124511	-1	149	147	173	140	120	57	57	63	64	60
ENSMUSG00000044795	chr11	Cyb5d1	-1.8995599	3.75552E-11	2.5958E-10	2.881721217	0.081203682	-1	161	168	172	185	164	26	64	23	74	63
ENSMUSG00000031392	chrX	Irak1	-0.9705709	3.76602E-11	2.60177E-10	5.918190087	0.02429911	-1	1201	1113	1151	1462	1040	632	746	551	659	745
ENSMUSG00000031885	chr8	Cbfb	-1.117529	3.79934E-11	2.6235E-10	6.171665512	0.032545366	-1	1706	1450	1065	1677	1451	684	864	609	640	922
ENSMUSG00000045838	chr2	A430105I19Rik	-1.0964663	3.82822E-11	2.64213E-10	4.299347194	0.028854342	-1	457	389	392	442	306	178	213	221	212	187
ENSMUSG00000024854	chr19	Pold4	1.11085961	3.8525E-11	2.65758E-10	4.073669929	0.028804662	1	211	139	135	178	126	474	347	352	347	349
ENSMUSG00000042817	chr5	Flt3	3.48171189	3.86938E-11	2.6679E-10	-0.107828903	0.131123653	1	1	2	3	1	2	36	20	18	33	11
ENSMUSG00000036052	chr4	Dnajb5	-1.1207098	3.92954E-11	2.70805E-10	7.616416515	0.033350057	-1	3742	3650	3662	5100	3919	2795	2078	1408	2128	1774
ENSMUSG00000025151	chrX	Maged1	1.1308572	3.96014E-11	2.72779E-10	6.387995575	0.033480967	1	812	753	719	910	709	1931	1756	2313	1382	1945
ENSMUSG00000028530	chr4	Jak1	-1.1447924	4.00108E-11	2.75463E-10	7.161296865	0.034671969	-1	3315	2684	2476	3311	2873	1216	1768	1089	1597	1598
ENSMUSG00000034855	chr5	Cxcl10	2.97975958	4.01068E-11	2.75989E-10	0.977731953	0.155215663	1	4	6	3	15	3	44	87	38	22	75
ENSMUSG00000073889	chr4	Il11ra1	1.15383069	4.04213E-11	2.78016E-10	5.961898646	0.03460394	1	556	550	520	699	550	2240	1245	1181	1245	1175
ENSMUSG00000027953	chr3	Slc50a1	1.05307192	4.0758E-11	2.80194E-10	3.860745812	0.024957058	1	148	141	124	166	119	425	323	279	290	277
ENSMUSG00000037946	chr13	Fgd3	2.7014144	4.08555E-11	2.80726E-10	2.341610135	0.158649432	1	17	3	19	54	10	182	113	171	127	100
ENSMUSG00000029713	chr5	Gnb2	1.05609209	4.09162E-11	2.81005E-10	6.882972036	0.029477226	1	1075	1075	1076	1469	1031	3700	2652	2273	2273	2207
ENSMUSG00000060019	chr8	Gm10073	1.70507196	4.16575E-11	2.85956E-10	3.459224478	0.068291029	1	93	89	61	56	74	452	202	255	280	175
ENSMUSG00000001794	chr7	Capns1	1.02659826	4.25477E-11	2.91923E-10	7.874690401	0.028191226	1	2348	2066	1831	3017	2317	5967	4787	5131	4409	5438
ENSMUSG00000071715	chr15	Ncf4	2.78757271	4.26571E-11	2.9253E-10	3.109124902	0.174119327	1	66	28	25	19	19	562	255	93	136	206
ENSMUSG00000027852	chr3	Nras	0.98668183	4.28697E-11	2.93699E-10	6.049496754	0.025336125	1	729	645	604	714	599	1455	1334	1404	1350	1619
ENSMUSG00000092486	chr5	2610524H06Rik	1.90949421	4.28629E-11	2.93699E-10	1.496896012	0.064766051	1	21	23	12	21	7	90	72	54	68	63
ENSMUSG00000022016	chr14	Akap11	-1.059239	4.32965E-11	2.96478E-10	4.671394891	0.027782395	-1	472	453	429	658	551	295	276	181	298	300
ENSMUSG00000040396	chr8	Abhd13	-1.0024041	4.34432E-11	2.97191E-10	3.985400524	0.022819003	-1	327	282	300	395	266	160	194	150	165	186
ENSMUSG00000084929	chr4	Foxo6os	3.94033288	4.34309E-11	2.97191E-10	3.964994148	0.323980251	1	34	30	27	29	20	13	616	615	475	590
ENSMUSG00000021870	chr14	Slmap	-1.0458197	4.38254E-11	2.99659E-10	5.77518913	0.0283927	-1	911	946	967	1670	1066	651	618	439	573	647
ENSMUSG00000033004	chr14	Mycbp2	-1.0407343	4.39997E-11	3.00704E-10	5.444263242	0.027808612	-1	761	686	801	1274	878	511	454	379	455	529
ENSMUSG00000029552	chr6	Tes	2.10557704	4.40545E-11	3.00931E-10	2.508697218	0.09736386	1	21	34	23	50	29	268	166	59	116	143
ENSMUSG00000052681	chr10	Rap1b	1.19757006	4.43416E-11	3.02745E-10	5.83730965	0.037370638	1	467	460	492	747	442	1802	1618	807	1221	1123
ENSMUSG00000033316	chr5	Galnt9	5.37830217	4.44515E-11	3.03347E-10	-0.144745059	0.298203476	1	0	0	0	0	2	56	32	4	10	22
ENSMUSG00000001542	chr13	Ell2	-1.4919706	4.45496E-11	3.03868E-10	3.813079491	0.053747955	-1	263	259	297	373	339	111	138	52	140	161
ENSMUSG00000041669	chr12	Prima1	-2.4792312	4.47811E-11	3.05298E-10	0.923060118	0.106134684	-1	35	31	53	53	54	17	13	3	5	7
ENSMUSG00000022280	chr15	Rnf19a	-0.9755427	4.62501E-11	3.15159E-10	4.251124778	0.022493045	-1	395	337	319	513	325	252	211	156	203	227
ENSMUSG00000024442	chr18	0610009O20Rik	-1.1417054	4.63072E-11	3.15394E-10	6.664561654	0.03452794	-1	2029	2083	1938	2623	1757	864	1087	759	1268	1170
ENSMUSG00000056708	chr1	Ier5	1.51690154	4.83952E-11	3.29455E-10	4.041927027	0.056504452	1	99	97	114	220	113	593	482	204	364	367
ENSMUSG00000099083	chr15	Atf7	-1.0282537	4.87951E-11	3.32015E-10	5.768078554	0.027547281	-1	1072	1082	982	1289	1012	507	610	554	499	749
ENSMUSG00000030313	chr6	Dennd5b	-1.3851754	4.88511E-11	3.32235E-10	2.679963823	0.040073475	-1	134	117	114	199	124	80	62	38	46	62
ENSMUSG00000074862	chr10	BC025920	-1.6684054	4.90783E-11	3.33618E-10	2.212932663	0.056688759	-1	129	99	109	98	76	28	48	26	36	39
ENSMUSG00000092607	chr3	Scnm1	1.06799455	4.92386E-11	3.34545E-10	4.20161644	0.02742135	1	191	152	151	239	153	343	404	416	441	399
ENSMUSG00000096740	chr19	Lbhd1	1.16153878	4.98738E-11	3.38696E-10	3.897860821	0.031578941	1	152	142	115	144	124	404	375	318	332	237
ENSMUSG00000037086	chrX	Prr32	3.9127074	5.03861E-11	3.42009E-10	0.817932309	0.241211999	1	4	5	3	0	2	61	23	50	13	102
ENSMUSG00000020897	chr11	Aurkb	2.18565434	5.08805E-11	3.45197E-10	1.692444686	0.09266905	1	23	20	11	15	13	91	133	59	82	49
ENSMUSG00000029538	chr5	Srsf9	1.44044665	5.09524E-11	3.45517E-10	4.067819985	0.050829531	1	148	128	126	164	103	662	471	263	357	262
ENSMUSG00000085711	chrX	Gm15163	-2.1909335	5.21422E-11	3.53414E-10	0.721680268	0.070273456	-1	28	39	32	59	33	13	9	5	11	7
ENSMUSG00000015702	chr3	Anxa9	3.11217895	5.33632E-11	3.61408E-10	-0.168061327	0.095628486	1	4	3	1	1	2	23	19	13	26	29
ENSMUSG00000099764	chr16	Rps10-ps2	1.2054548	5.33734E-11	3.61408E-10	3.469691957	0.032885503	1	103	97	100	126	69	346	256	203	243	206
ENSMUSG00000022150	chr15	Dab2	1.6156414	5.35637E-11	3.62521E-10	5.578791484	0.067650542	1	333	384	352	363	301	1628	1435	635	1564	650
ENSMUSG00000040451	chr19	Sgms1	-0.9919327	5.36606E-11	3.63001E-10	5.214191453	0.025188387	-1	778	672	645	929	664	440	419	286	373	519
ENSMUSG00000041685	chr13	Fcho2	-1.0950099	5.51014E-11	3.72567E-10	4.063634095	0.028656279	-1	315	305	299	488	299	190	190	118	154	220
ENSMUSG00000038084	chr16	Opa1	-1.0216787	5.56302E-11	3.75961E-10	6.613744523	0.027876189	-1	1814	1854	1720	2718	1750	924	1157	1033	1048	1085
ENSMUSG00000027207	chr2	Galk2	1.41409018	5.56774E-11	3.76099E-10	3.101707314	0.044790035	1	88	58	66	77	54	183	256	143	239	180
ENSMUSG00000032307	chr9	Ube2q2	-1.075342	5.6234E-11	3.79675E-10	4.850933941	0.029319112	-1	597	524	527	762	514	241	379	227	309	355
ENSMUSG00000098900	chr7	Gm18190	-2.7138881	5.69198E-11	3.8412E-10	0.212226271	0.093759547	-1	31	17	19	44	27	3	6	4	7	2
ENSMUSG00000032267	chr9	Usp28	-0.9725854	5.77059E-11	3.89236E-10	6.377106121	0.025188424	-1	1691	1347	1445	2148	1610	997	877	811	893	1005
ENSMUSG00000019261	chr8	Map1s	1.15684536	5.91361E-11	3.98499E-10	3.843974905	0.031255414	1	123	130	103	134	160	374	316	315	251	351

ENSMUSG00000051486	chr18	Pcdhb11	-3.2013081	5.91133E-11	3.98499E-10	-0.187482171	0.124802901	-1	23	17	16	25	23	9	1	0	2	0
ENSMUSG00000050592	chr2	Fam78a	-1.1061117	5.92269E-11	3.98918E-10	5.695936211	0.03215941	-1	1118	1028	1008	1126	957	428	524	616	482	607
ENSMUSG00000075415	chr2	Fnbp1	0.98669522	5.92919E-11	3.99164E-10	4.682398358	0.024119389	1	245	258	234	301	237	762	485	500	493	549
ENSMUSG00000067547	chr15	Gm7666	-1.0973299	5.97056E-11	4.01755E-10	4.392042938	0.029901632	-1	435	407	440	509	333	326	189	201	184	195
ENSMUSG00000039262	chr2	Prrc2b	-1.0295534	6.07915E-11	4.08865E-10	7.574142818	0.028757265	-1	3587	3280	3394	4851	3981	1937	2117	2001	1798	2359
ENSMUSG00000030934	chr7	Oat	-1.0416783	6.17225E-11	4.14927E-10	7.661052845	0.029479658	-1	4199	4031	3565	4648	3817	2334	2223	1532	2164	2612
ENSMUSG00000033589	chr14	Reep4	1.67274559	6.20337E-11	4.16819E-10	2.697027348	0.062282704	1	45	38	38	69	38	255	201	106	123	115
ENSMUSG00000030861	chr7	Acadsb	-1.0515791	6.21072E-11	4.17112E-10	6.385561564	0.029592647	-1	1571	1662	1408	2276	1542	1014	836	626	990	993
ENSMUSG00000006494	chr2	Pdk1	-1.0780893	6.24269E-11	4.19058E-10	5.925186873	0.030808906	-1	1029	1189	1101	1900	1012	664	578	509	717	718
ENSMUSG00000026687	chr1	Aldh9a1	1.53988932	6.3417E-11	4.25296E-10	3.372637284	0.056050723	1	52	107	61	97	72	286	316	146	287	213
ENSMUSG00000089762	chr2	Ier5l	1.48537453	6.34029E-11	4.25296E-10	2.665603221	0.047340847	1	46	46	49	70	34	221	154	132	101	146
ENSMUSG00000046364	chr7	Rpl27a	1.0822288	6.3505E-11	4.25682E-10	7.336675095	0.031728764	1	1708	1497	1378	1769	1366	4977	3693	3165	3372	2815
ENSMUSG00000016503	chr5	Gtf3a	1.15411696	6.42284E-11	4.30324E-10	4.335439883	0.03321057	1	186	196	144	247	160	323	503	421	497	498
ENSMUSG00000078920	chr11	Ifi47	1.91989649	6.46314E-11	4.32817E-10	2.15136988	0.078145255	1	25	35	18	35	21	115	146	73	64	163
ENSMUSG00000004100	chr9	Ppan	1.3512912	6.50247E-11	4.35242E-10	3.394307742	0.042347319	1	95	76	70	112	84	353	305	183	215	173
ENSMUSG00000035173	chr19	Ccdc186	-0.9577666	6.51169E-11	4.3565E-10	4.585179633	0.02264651	-1	483	431	428	516	482	256	285	231	248	307
ENSMUSG00000002059	chr11	Rab34	1.22211838	6.53596E-11	4.37065E-10	3.204605047	0.032937717	1	81	93	77	101	55	262	232	180	168	202
ENSMUSG00000024726	chr19	2410127L17Rik	-1.7005587	6.68892E-11	4.47079E-10	5.55808032	0.075513718	-1	1053	920	1023	1548	879	159	389	243	499	500
ENSMUSG00000028597	chr4	Gpx7	1.15391687	6.72212E-11	4.49084E-10	4.020573102	0.032036988	1	169	153	147	151	119	484	350	381	285	318
ENSMUSG00000021196	chr13	Pfkp	1.35895209	6.82051E-11	4.55439E-10	3.651328623	0.0443611	1	86	95	70	162	113	419	351	211	212	287
ENSMUSG00000028495	chr4	Rps6	1.04105977	6.8361E-11	4.56263E-10	7.460805861	0.029519412	1	1776	1610	1522	2088	1598	5354	4068	3403	3391	3271
ENSMUSG00000095677	chr17	Dynlt1f	1.75195091	6.84576E-11	4.56689E-10	1.860939786	0.058719244	1	33	17	26	23	19	101	111	69	89	70
ENSMUSG00000031337	chrX	Mtm1	-1.4562831	6.87468E-11	4.584E-10	3.373581525	0.050106955	-1	227	220	192	297	193	56	110	56	114	110
ENSMUSG00000090093	chr2	Gm14399	-2.4042825	6.89625E-11	4.59619E-10	0.176792079	0.067113265	-1	31	24	23	33	18	6	4	6	5	5
ENSMUSG00000024059	chr17	Clip4	-1.2370373	6.90833E-11	4.60204E-10	5.997719727	0.040840091	-1	868	1231	1311	2351	1067	662	660	575	557	653
ENSMUSG00000060913	chr3	Trim55	-1.2335027	7.12238E-11	4.74237E-10	6.530782002	0.040969944	-1	2190	1857	1794	2015	1750	584	1007	858	911	1107
ENSMUSG00000036430	chr17	Tbcc	1.15941232	7.13339E-11	4.74744E-10	3.510419828	0.030887624	1	131	79	77	147	91	286	235	253	242	253
ENSMUSG00000097415	chr7	AU020206	1.98887533	7.1828E-11	4.77805E-10	1.949981192	0.081630201	1	22	22	21	33	14	182	86	67	63	96
ENSMUSG00000062380	chr8	Tubb3	4.63282374	7.2129E-11	4.79579E-10	0.694233163	0.31985045	1	2	1	1	2	2	30	84	79	29	5
ENSMUSG00000026000	chr1	Lancl1	1.45647945	7.21716E-11	4.79634E-10	4.786686016	0.055033859	1	230	208	200	263	193	345	592	621	737	957
ENSMUSG00000059263	chr7	Usp47	-1.0662547	7.2556E-11	4.8196E-10	8.032847364	0.031167033	-1	4892	4283	4346	7709	5476	2784	2810	2320	2823	3091
ENSMUSG00000024251	chr17	Thada	-1.3599184	7.29357E-11	4.84252E-10	3.102917677	0.042392495	-1	147	171	167	218	205	98	101	49	60	85
ENSMUSG00000021096	chr12	Ppm1a	-1.008936	7.32647E-11	4.85986E-10	6.917208261	0.027670155	-1	2300	2151	2138	3280	2245	1196	1300	1131	1334	1578
ENSMUSG00000079553	chr17	Kifc1	2.41249634	7.32664E-11	4.85986E-10	1.564569308	0.11364405	1	16	15	16	10	8	66	124	66	90	38
ENSMUSG00000021772	chr14	Nkiras1	-0.9780711	7.33357E-11	4.86214E-10	5.502826781	0.025144555	-1	885	852	843	1143	768	688	455	421	437	507
ENSMUSG00000026773	chr2	Pfkfb3	-1.6745187	7.47061E-11	4.95065E-10	7.06462479	0.07459435	-1	2897	4911	2549	2585	2041	707	1149	1051	809	1474
ENSMUSG00000000628	chr6	Hk2	-1.0051261	7.55177E-11	5.00206E-10	7.540154192	0.027691837	-1	3260	3321	3662	5183	3228	2271	2215	1927	1810	1891
ENSMUSG00000046722	chr3	Cdc42se1	1.14373833	7.6162E-11	5.04235E-10	5.279127204	0.034380799	1	339	387	328	448	299	1348	870	706	814	656
ENSMUSG00000005698	chr8	Ctcf	-0.9902923	7.64541E-11	5.05929E-10	5.056492225	0.025288776	-1	694	570	531	842	667	317	409	300	383	402
ENSMUSG00000064145	chr9	Arih2	-0.9831097	7.65819E-11	5.06535E-10	6.050589593	0.025898937	-1	1475	1208	1146	1534	1193	831	677	563	784	788
ENSMUSG00000025899	chr9	Alkbh8	-1.9044731	7.66233E-11	5.06569E-10	2.745218535	0.08431641	-1	150	116	123	241	159	26	62	22	43	75
ENSMUSG00000098906	chr11	Mir7652	-2.4556007	7.8164E-11	5.16511E-10	0.479101832	0.088537904	-1	35	41	27	26	32	3	9	7	4	9
ENSMUSG00000071653	chr19	1810009A15Rik	1.17475425	7.84088E-11	5.17883E-10	3.798328352	0.032785048	1	131	133	107	135	121	383	339	309	311	215
ENSMUSG00000022867	chr16	Usp25	-1.3314064	7.86722E-11	5.19378E-10	6.389157465	0.047759381	-1	1549	1585	1615	2398	1823	481	853	626	842	1067
ENSMUSG00000040263	chr8	Klhdc4	1.13205264	8.15105E-11	5.37862E-10	3.682266523	0.029987173	1	106	104	112	163	111	312	341	251	300	219
ENSMUSG00000025656	chrX	Arhgef9	-1.2198067	8.19754E-11	5.40674E-10	3.56824085	0.034941908	-1	214	221	244	319	231	88	104	102	140	139
ENSMUSG00000027520	chr1	Zdbf2	1.36690567	8.22619E-11	5.42307E-10	4.137586711	0.046877526	1	146	110	124	168	176	392	317	511	296	527
ENSMUSG00000034892	chr12	Rps29	1.21049858	8.24567E-11	5.43336E-10	8.221858164	0.040234036	1	2871	2754	2364	3115	2318	10748	6284	5932	6372	5011
ENSMUSG00000037674	chr9	Rfx7	-1.03871	8.27363E-11	5.44921E-10	4.345556017	0.026844603	-1	430	303	393	566	355	212	241	164	218	249
ENSMUSG00000039087	chr13	Rreb1	-1.1617399	8.29372E-11	5.45987E-10	4.827956223	0.035062118	-1	537	498	495	832	581	212	316	263	239	395
ENSMUSG00000048373	chr5	Fgfbp1	6.202727	8.39587E-11	5.52451E-10	-0.096707127	0.385949979	1	0	0	1	0	0	0	37	33	23	33
ENSMUSG00000020948	chr12	Klhl28	-2.0207529	8.40258E-11	5.52633E-10	2.061526595	0.087297047	-1	90	86	83	131	100	10	38	17	39	26
ENSMUSG00000044042	chr2	Fmn1	2.43190417	8.49903E-11	5.58713E-10	1.258794662	0.11175746	1	9	5	7	16	15	102	70	29	42	72
ENSMUSG00000026492	chr1	Tfb2m	-0.9443278	8.55991E-11	5.62451E-10	4.647945021	0.022359994	-1	484	462	444	649	425	294	262	223	314	302
ENSMUSG00000043122	chr12	A530016L24Rik	-2.3579104	8.58833E-11	5.64053E-10	1.455133666	0.111830567	-1	39	95	60	68	65	24	6	13	8	20
ENSMUSG00000022912	chr16	Pros1	1.16879927	8.66635E-11	5.6891E-10	4.63267347	0.035212515	1	223	219	207	306	185	914	559	416	453	489
ENSMUSG00000003731	chr4	Kpna6	-1.0324543	8.67518E-11	5.69222E-10	6.606799271	0.029071489	-1	1757	1832	1872	2460	1839	879	1183	922	1084	1135
ENSMUSG00000009112	chr6	Bcl2l13	-1.0653456	8.68354E-11	5.69504E-10	6.199118655	0.030731308	-1	1285	1297	1330	2077	1467	669	756	686	841	908
ENSMUSG00000078862	chr2	Gm14326	-1.6468217	8.68977E-11	5.69645E-10	2.722105428	0.061605288	-1	154	118	142	188	135	28	67	35	68	57
ENSMUSG00000002324	chr14	Rec8	4.59483759	8.69677E-11	5.69836E-10	-0.134794315	0.230473573	1	1	3	0	0	0	7	25	41	15	31
ENSMUSG00000001333	chr4	Sync	-1.3999858	8.8635E-11	5.80489E-10	5.061598426	0.051816888	-1	863	561	627	871	688	201	247	226	336	480
ENSMUSG00000068036	chr17	Mllt4	-1.0373084	8.87369E-11	5.80884E-10	5.683304569	0.028793425	-1	903	1033	1116	1341	766	597	505	457	555	636
ENSMUSG00000022295	chr15	Atp6v1c1	1.10538629	8.8826E-11	5.81195E-10	5.253567278	0.032310111	1	371	358	315	501	272	988	1001	514	889	882
ENSMUSG00000076437	chr2	2700094K13Rik	1.36722865	8.94557E-11	5.85041E-10	3.350507718	0.044210395	1	95	76	59	113	79	305	290	204	240	148
ENSMUSG00000030087	chr6	Klf15	-1.3993688	9.13327E-11	5.96992E-10	4.185589765	0.049834902	-1	373	450	312	378	422	189	102	119	160	248

ENSMUSG00000056054	chr3	S100a8	5.91614853	9.13685E-11	5.96992E-10	1.536289736	0.541102444	1	3	1	0	1	1	281	61	4	94	17
ENSMUSG00000066442	chr9	Mthfs	1.73336268	9.19608E-11	6.00582E-10	1.803591098	0.05718342	1	24	24	24	22	20	102	87	50	100	83
ENSMUSG00000027386	chr2	Fbln7	2.16096181	9.39937E-11	6.13571E-10	3.966533558	0.116295518	1	82	89	63	71	109	163	403	503	248	728
ENSMUSG00000047996	chrX	Prrg1	-2.1269931	9.48594E-11	6.18933E-10	2.302827229	0.102227154	-1	90	85	110	154	148	13	34	20	24	56
ENSMUSG00000060636	chr16	Rpl35a	1.12059003	9.54853E-11	6.22726E-10	7.207812351	0.034605798	1	1509	1493	1268	1621	1053	4627	3434	2770	3230	2572
ENSMUSG00000036501	chr18	Fam13b	-1.1410213	9.60532E-11	6.25846E-10	3.201993218	0.028827029	-1	197	185	165	212	173	127	89	70	85	96
ENSMUSG00000052459	chr16	Atp6v1a	1.21247829	9.60489E-11	6.25846E-10	5.580334153	0.039480309	1	400	442	391	553	366	1311	1396	568	1036	1203
ENSMUSG00000012640	chr7	Zfp715	-1.5534532	9.67646E-11	6.30187E-10	3.445820665	0.059043239	-1	232	247	203	333	197	66	102	47	139	92
ENSMUSG00000003226	chr10	Ranbp2	-1.0765958	9.72705E-11	6.33187E-10	6.239650603	0.03159254	-1	1462	1433	1350	1967	1448	658	925	597	848	934
ENSMUSG00000032826	chr3	Ank2	-1.1702259	9.82468E-11	6.38955E-10	5.741508056	0.036955386	-1	832	990	1054	1804	929	436	570	517	578	564
ENSMUSG00000033213	chr2	AA467197	3.69839208	9.82479E-11	6.38955E-10	-0.408354106	0.122203315	1	2	0	3	1	0	21	18	13	29	12
ENSMUSG00000029371	chr5	Cxcl5	7.96827349	9.83989E-11	6.39639E-10	0.210749871	0.536214555	1	0	0	0	0	0	75	24	8	58	1
ENSMUSG00000035840	chr13	Lysmd3	-2.2205959	9.96849E-11	6.47697E-10	1.977725254	0.106950413	-1	63	107	102	122	78	9	32	10	32	27
ENSMUSG00000037826	chr6	Ppm1k	-1.1465229	1.01295E-10	6.57854E-10	3.684255705	0.031309679	-1	220	305	260	307	214	110	130	130	136	138
ENSMUSG00000022744	chr16	Cldn25	-1.0490688	1.03226E-10	6.70084E-10	4.991508938	0.028887312	-1	655	599	542	768	625	273	423	262	365	361
ENSMUSG00000031709	chr8	Tbc1d9	1.8333276	1.04649E-10	6.79004E-10	2.088432171	0.070946002	1	31	26	25	33	19	184	87	64	107	89
ENSMUSG00000055782	chr15	Abcd2	-1.4522061	1.05188E-10	6.82187E-10	5.525795605	0.056722128	-1	923	1147	911	1105	908	212	473	302	478	531
ENSMUSG00000022577	chr15	Ly6h	4.12763645	1.05812E-10	6.85277E-10	0.290103769	0.241234222	1	4	2	1	0	1	31	20	36	8	72
ENSMUSG00000022946	chr16	Dopey2	-1.0945003	1.05765E-10	6.85277E-10	5.140534396	0.031821242	-1	742	595	547	834	846	357	346	286	369	478
ENSMUSG00000023047	chr15	Amhr2	2.06102379	1.05757E-10	6.85277E-10	1.988899147	0.091154687	1	34	11	12	30	24	61	111	104	101	122
ENSMUSG00000020137	chr10	Thap2	-1.6446039	1.06059E-10	6.86562E-10	2.363989504	0.059207929	-1	77	103	106	167	121	47	47	25	50	31
ENSMUSG00000024856	chr19	Cdk2ap2	1.01184217	1.06145E-10	6.86795E-10	4.506406807	0.025905123	1	220	234	189	265	208	685	471	417	483	425
ENSMUSG00000040722	chr9	Scamp5	1.37693236	1.07462E-10	6.94997E-10	3.403868375	0.045248703	1	96	100	85	79	68	379	183	216	202	263
ENSMUSG00000042686	chr1	Jph1	-1.2167721	1.08175E-10	6.99285E-10	8.196299248	0.041164698	-1	6732	5663	5061	7037	6044	2042	3288	2376	2842	3821
ENSMUSG00000026349	chr1	Ccnt2	-0.9127797	1.11166E-10	7.18285E-10	4.816288087	0.021340638	-1	595	551	506	571	494	338	315	275	323	340
ENSMUSG00000037857	chr11	Nufip2	-1.0425021	1.11359E-10	7.19203E-10	4.553672393	0.027936497	-1	433	435	452	607	427	229	299	178	231	316
ENSMUSG00000002210	chr7	Smg9	1.06055493	1.12141E-10	7.23916E-10	4.058038507	0.027536784	1	147	140	134	217	164	323	403	344	392	352
ENSMUSG00000014361	chr2	Mertk	1.62784207	1.13908E-10	7.34984E-10	2.448655645	0.05839456	1	36	32	31	62	35	118	145	77	135	184
ENSMUSG00000100679	chr1	Gm28778	-1.8573625	1.141E-10	7.35885E-10	3.216355544	0.084501978	-1	237	243	221	227	143	30	77	38	99	78
ENSMUSG00000035278	chr10	Plekhj1	1.19016222	1.15832E-10	7.4671E-10	4.343623686	0.036407834	1	217	164	174	191	165	743	410	372	408	383
ENSMUSG00000020133	chr10	2310011J03Rik	1.07826735	1.16954E-10	7.53595E-10	4.073704402	0.028594621	1	162	166	148	190	134	507	346	290	399	319
ENSMUSG00000020695	chr11	Mrc2	1.14964149	1.18735E-10	7.64018E-10	5.491844009	0.035734228	1	407	370	361	505	434	1291	991	1163	639	979
ENSMUSG00000036875	chr10	Dna2	2.33282454	1.18632E-10	7.64018E-10	1.193547489	0.101476991	1	11	8	6	17	11	67	93	35	63	35
ENSMUSG00000047443	chr1	Fam132b	-2.3511377	1.18684E-10	7.64018E-10	1.648386557	0.115450505	-1	86	58	48	71	112	6	25	18	18	13
ENSMUSG00000053062	chr16	Jam2	-0.9271663	1.20282E-10	7.73611E-10	4.895343926	0.022279556	-1	543	536	556	838	457	381	348	276	336	333
ENSMUSG00000092907	chrX	Mir5132	-2.7748401	1.20478E-10	7.74519E-10	0.064623136	0.096975335	-1	29	19	19	33	23	1	3	1	5	9
ENSMUSG00000078139	chr13	AK157302	-1.6229495	1.21609E-10	7.8143E-10	2.0101466	0.053311317	-1	75	79	80	135	78	21	41	28	33	33
ENSMUSG00000032562	chr9	Gnai2	0.99917548	1.22831E-10	7.88918E-10	7.139159413	0.027877847	1	1479	1327	1302	1689	1213	4242	2888	2678	2593	3056
ENSMUSG00000063488	chr9	Zkscan7	-2.2438433	1.24529E-10	7.99457E-10	1.104995725	0.09202381	-1	72	51	43	55	32	8	10	6	13	21
ENSMUSG00000023074	chrX	Mospd1	-1.199855	1.24859E-10	8.01205E-10	5.4293534	0.039033682	-1	1044	872	786	992	766	311	405	407	375	624
ENSMUSG00000085208	chr11	Brip1os	1.07374481	1.25607E-10	8.05635E-10	3.936611186	0.027869831	1	124	162	147	165	127	443	371	264	306	308
ENSMUSG00000047213	chr3	Ythdf3	-1.2493286	1.25865E-10	8.06921E-10	5.326705435	0.042277828	-1	780	652	771	1197	838	308	455	268	342	571
ENSMUSG00000035455	chr11	Fignl1	2.67542355	1.27624E-10	8.17823E-10	1.314176768	0.141823711	1	10	9	5	13	10	63	119	40	81	27
ENSMUSG00000015342	chrX	Xk	-1.6553045	1.29842E-10	8.31654E-10	2.483774541	0.062412635	-1	115	103	106	155	143	45	37	25	36	75
ENSMUSG00000064493	chr12	Snora28	-3.2731741	1.30514E-10	8.35574E-10	-0.322128207	0.119360877	-1	11	13	24	29	17	0	4	0	3	3
ENSMUSG00000022987	chr15	Zfp641	-1.1685499	1.31095E-10	8.38912E-10	4.387099247	0.035537993	-1	574	382	381	414	384	197	215	148	228	261
ENSMUSG00000033808	chr2	Tmem87a	-1.061389	1.31271E-10	8.39656E-10	5.717864166	0.030800388	-1	1344	1028	886	1072	941	611	544	410	550	679
ENSMUSG00000071176	chr8	Arhgef10	-1.0845932	1.36449E-10	8.72372E-10	3.453459344	0.027225239	-1	217	200	201	257	222	107	112	98	105	146
ENSMUSG00000024429	chr17	Gnl1	0.96728827	1.36674E-10	8.73415E-10	5.171290277	0.024921994	1	408	307	327	474	307	985	766	751	731	653
ENSMUSG00000039449	chr2	Prpf18	-0.9525021	1.37524E-10	8.78443E-10	5.282686133	0.024281593	-1	774	765	703	937	645	383	473	373	410	520
ENSMUSG00000091462	chr13	Gm17084	1.48490367	1.39147E-10	8.88403E-10	2.728839678	0.049812667	1	42	60	48	53	49	234	179	106	130	141
ENSMUSG00000097971	chr17	Gm26917	2.33307491	1.39242E-10	8.88603E-10	5.921922132	0.141901431	1	239	138	206	399	508	3383	2129	1185	786	988
ENSMUSG00000031601	chr8	Cnot7	-0.9759311	1.39508E-10	8.89899E-10	4.959090177	0.025159279	-1	615	544	544	838	548	318	428	283	287	395
ENSMUSG00000030986	chr7	Dhx32	-1.0422091	1.41138E-10	8.99885E-10	4.806632695	0.028640276	-1	535	449	509	762	560	240	301	264	321	356
ENSMUSG00000034610	chr4	Zcchc11	-1.3043171	1.41571E-10	9.0223E-10	3.577905291	0.041849204	-1	198	218	218	388	250	77	115	100	119	143
ENSMUSG00000038178	chr11	Slc43a2	1.04973548	1.43359E-10	9.13212E-10	5.387779204	0.029927903	1	318	375	369	662	338	1059	888	852	776	1037
ENSMUSG00000052212	chr7	Cd177	6.4834862	1.4448E-10	9.1993E-10	0.144053803	0.453854187	1	0	0	0	1	0	62	51	6	36	2
ENSMUSG00000028447	chr4	Dctn3	0.99068803	1.4527E-10	9.24545E-10	4.397739009	0.024978082	1	224	202	180	263	180	382	495	448	440	499
ENSMUSG00000045193	chr10	Cirbp	1.03708739	1.45889E-10	9.28058E-10	4.934403705	0.028568228	1	339	306	259	348	237	841	528	698	537	747
ENSMUSG00000030301	chr6	Ccdc91	-1.1175365	1.50028E-10	9.53951E-10	6.28557401	0.034785647	-1	1869	1416	1395	1738	1510	664	920	618	952	847
ENSMUSG00000000711	chr10	Rab5b	-0.9965179	1.50301E-10	9.55258E-10	6.647378094	0.027830596	-1	1921	1900	1821	2458	1857	988	1185	895	1050	1347
ENSMUSG00000027406	chr2	Idh3b	-1.1385261	1.5072E-10	9.57482E-10	8.814195998	0.036798898	-1	8769	9265	9478	11986	6857	4451	4340	3481	5740	4904
ENSMUSG00000024912	chr19	Fosl1	5.42005246	1.50825E-10	9.57716E-10	0.535947384	0.415952299	1	0	0	1	3	0	35	92	31	47	2
ENSMUSG00000025558	chr14	Dock9	-0.927145	1.53268E-10	9.72787E-10	4.666612658	0.022183535	-1	413	479	450	684	461	328	293	270	254	281
ENSMUSG00000032246	chr9	Calml4	1.65970332	1.55007E-10	9.83374E-10	2.324524697	0.060426667	1	28	36	34	45	31	196	89	79	118	129

ENSMUSG00000027134	chr2	Lpcat4	1.98060174	1.58524E-10	1.00523E-09	1.57114625	0.079210496	1	15	12	13	30	16	126	80	58	52	57
ENSMUSG00000043733	chr5	Ptpn11	-0.9411887	1.58917E-10	1.00727E-09	6.939493708	0.024999081	-1	2208	2075	2291	3170	2324	1473	1376	1191	1297	1537
ENSMUSG00000031253	chrX	Srpx2	1.41798998	1.59434E-10	1.01009E-09	3.78541036	0.051023167	1	125	121	112	90	97	488	322	337	187	302
ENSMUSG00000006262	chr5	Mob1b	-1.1059401	1.63921E-10	1.03804E-09	5.370232084	0.033478124	-1	785	736	825	1159	726	337	471	385	358	585
ENSMUSG00000087038	chr9	2900079G21Rik	2.50554652	1.66113E-10	1.05145E-09	1.25098802	0.123288671	1	10	10	7	9	13	42	33	81	51	100
ENSMUSG00000062933	chr9	Gm10123	1.2838025	1.69267E-10	1.07093E-09	4.23146579	0.042965563	1	189	192	149	167	109	507	583	292	446	343
ENSMUSG00000050732	chr6	Vamp8	1.07591349	1.70014E-10	1.07517E-09	5.32013647	0.031614337	1	372	374	372	491	308	1263	819	707	948	701
ENSMUSG00000021822	chr14	Plau	1.92116103	1.73994E-10	1.09984E-09	5.975807223	0.10002159	1	354	488	407	397	291	1891	3016	744	1729	820
ENSMUSG00000060992	chr15	Copz1	1.01338574	1.74641E-10	1.10343E-09	6.044106061	0.028636694	1	687	643	556	822	559	1965	1507	1268	1331	1163
ENSMUSG00000015846	chr2	Rxra	-1.026639	1.78696E-10	1.12817E-09	6.94216724	0.029913235	-1	2162	2054	2114	3258	2738	1415	1291	1106	1213	1606
ENSMUSG00000058230	chr7	Arhgap35	-0.9265998	1.78719E-10	1.12817E-09	5.196266514	0.023130284	-1	646	586	658	940	752	445	410	366	383	458
ENSMUSG00000062190	chr6	Lancl2	-1.1501981	1.78846E-10	1.12847E-09	3.27517504	0.030879865	-1	218	159	173	265	177	87	110	74	100	115
ENSMUSG00000037736	chr5	Limch1	-0.9437288	1.79673E-10	1.13317E-09	6.818705325	0.0252373	-1	2089	1887	1981	2920	2233	1333	1303	1113	1227	1330
ENSMUSG00000016344	chr2	Ppdpf	1.2003368	1.79816E-10	1.13356E-09	4.608689189	0.03859849	1	227	204	209	289	174	356	571	593	617	588
ENSMUSG00000019188	chr2	H13	1.03995796	1.80747E-10	1.13892E-09	5.9272322	0.030151739	1	613	515	439	811	609	1821	1456	1100	1132	1222
ENSMUSG00000062078	chr17	Qk	-1.2380166	1.82534E-10	1.14966E-09	6.935976809	0.043343152	-1	1795	2050	2106	4690	2504	1159	1316	1067	1077	1333
ENSMUSG00000085334	chr4	Gm12940	1.29565341	1.82762E-10	1.15058E-09	3.010556482	0.038793476	1	65	74	56	90	58	256	144	171	193	157
ENSMUSG00000022978	chr16	Mis18a	2.16139615	1.82918E-10	1.15104E-09	1.6674534	0.097682423	1	13	17	19	16	16	134	94	42	90	49
ENSMUSG00000067736	chr1	Gm10222	-2.2010737	1.85911E-10	1.16935E-09	1.040404564	0.086649565	-1	46	27	52	80	38	7	9	13	12	15
ENSMUSG00000078877	chr2	Gm14295	-1.7375529	1.86598E-10	1.17314E-09	2.042005825	0.065505488	-1	118	73	70	118	85	18	40	23	39	30
ENSMUSG00000037725	chr8	Ckap2	2.03527944	1.886E-10	1.18466E-09	1.72228066	0.086010969	1	18	22	22	12	16	92	113	73	89	46
ENSMUSG00000056130	chr18	Ticam2	2.40961926	1.88527E-10	1.18466E-09	0.68665974	0.093241056	1	10	7	6	7	4	62	48	19	34	41
ENSMUSG00000042851	chr2	Zc3h6	-1.6303668	1.89526E-10	1.18995E-09	2.348390528	0.059461853	-1	116	128	107	127	84	32	34	25	46	62
ENSMUSG00000019820	chr10	Utrn	-0.9440346	1.90173E-10	1.19293E-09	5.030488718	0.023889239	-1	541	612	558	886	620	330	379	349	343	414
ENSMUSG00000049517	chr13	Rps23	1.03808604	1.90171E-10	1.19293E-09	7.714249	0.030877669	1	2222	1876	1846	2459	1856	5922	4990	3860	4741	3631
ENSMUSG00000024548	chr18	Setbp1	-1.4259905	1.9055E-10	1.19476E-09	2.390841515	0.043763511	-1	115	106	92	138	109	38	56	31	44	59
ENSMUSG00000030689	chr7	Ino80e	1.06689103	1.94232E-10	1.2173E-09	3.947458545	0.028386161	1	146	118	128	189	157	473	342	289	304	294
ENSMUSG00000086841	chr11	2410006H16Rik	1.62627598	1.9536E-10	1.22383E-09	3.747068028	0.068378155	1	130	118	73	80	78	588	253	319	264	232
ENSMUSG00000042744	chr5	Gm15800	-0.9873339	1.96559E-10	1.23078E-09	4.591385925	0.025645156	-1	401	421	424	625	513	279	292	251	206	289
ENSMUSG00000101523	chr1	Csnk2a1	-1.6628573	1.9758E-10	1.23662E-09	1.804828673	0.055336137	-1	64	73	71	100	77	18	24	22	32	36
ENSMUSG00000022141	chr15	Nipbl	-0.9297915	1.98467E-10	1.24123E-09	4.888566327	0.023002412	-1	523	490	516	802	575	337	381	293	284	368
ENSMUSG00000096493	chr1	Gm10031	-1.6628564	1.98494E-10	1.24123E-09	1.804828673	0.055353212	-1	64	73	71	100	77	18	24	22	32	36
ENSMUSG00000035150	chrX	Eif2s3x	-1.1419654	2.01683E-10	1.26061E-09	5.406965413	0.036171609	-1	738	688	670	1330	973	502	450	299	482	433
ENSMUSG00000060538	chr7	Tmem219	1.29920741	2.01933E-10	1.26161E-09	3.714196769	0.042758195	1	145	101	106	120	86	471	246	224	319	262
ENSMUSG00000029221	chr5	Slc30a9	-0.9443921	2.09012E-10	1.30525E-09	6.349457908	0.025235916	-1	1605	1509	1487	2114	1326	880	928	793	931	1012
ENSMUSG00000027010	chr2	Slc25a12	-1.1304608	2.10363E-10	1.3131E-09	8.582995097	0.036850728	-1	6934	7324	7581	10906	6788	3044	3809	3591	4193	4887
ENSMUSG00000043940	chr5	Wdfy3	-1.013287	2.12296E-10	1.32458E-09	5.072739294	0.027996368	-1	538	545	601	1014	685	384	431	296	327	384
ENSMUSG00000020315	chr11	Sptbn1	-0.9746225	2.1319E-10	1.32956E-09	7.17029728	0.027273878	-1	2562	2868	2780	3608	2434	1576	1644	1449	1371	1898
ENSMUSG00000066571	chr7	4931406P16Rik	-0.9972935	2.14871E-10	1.33945E-09	5.314572683	0.027421383	-1	689	776	706	1048	742	612	424	379	334	435
ENSMUSG00000025816	chr2	Sec61a2	-0.8975402	2.16336E-10	1.34798E-09	5.180308972	0.021800648	-1	717	660	678	799	643	390	462	385	399	422
ENSMUSG00000062248	chr13	Cks2	2.44912516	2.17537E-10	1.35486E-09	1.481192333	0.124420931	1	22	14	9	8	7	91	107	74	59	34
ENSMUSG00000034390	chr8	Cmip	1.31055931	2.17836E-10	1.35611E-09	4.433117149	0.046292979	1	149	164	163	253	194	781	518	345	300	603
ENSMUSG00000057036	chr3	Gm7536	1.07418052	2.18658E-10	1.36063E-09	5.28015109	0.031862899	1	416	350	336	449	312	1151	950	699	899	609
ENSMUSG00000021256	chr12	Vash1	-1.7890435	2.19467E-10	1.36505E-09	2.560438779	0.076058799	-1	122	121	126	193	115	20	30	42	49	69
ENSMUSG00000024053	chr17	Emilin2	1.5166449	2.20299E-10	1.36961E-09	4.976527048	0.06324124	1	204	218	238	271	269	1342	852	381	763	531
ENSMUSG00000058997	chr14	Vwa8	-1.0469276	2.22652E-10	1.38363E-09	6.82844603	0.031387405	-1	1803	1997	1932	3542	2291	1287	1167	1098	1155	1346
ENSMUSG00000037656	chr8	Slc20a2	-0.9402074	2.22857E-10	1.38429E-09	6.057293184	0.02491535	-1	1219	1238	1069	1785	1255	817	675	676	714	843
ENSMUSG00000002870	chr6	Mcm2	1.28157303	2.23277E-10	1.38628E-09	3.635320301	0.041324653	1	95	114	85	116	120	276	403	252	275	213
ENSMUSG00000079508	chrX	Apoo	-1.0877602	2.24975E-10	1.3962E-09	6.132932637	0.033527968	-1	1481	1485	1303	1765	1098	592	808	564	820	870
ENSMUSG00000030147	chr6	Clec4b1	2.77990202	2.26137E-10	1.40279E-09	0.09874835	0.100855614	1	2	7	2	3	3	40	20	19	32	22
ENSMUSG00000032939	chr8	Nup93	0.96243638	2.26808E-10	1.40633E-09	4.394763807	0.02394606	1	208	195	198	259	197	543	483	465	348	421
ENSMUSG00000039001	chr2	Rps21	1.20872345	2.28297E-10	1.41493E-09	7.203674804	0.041877748	1	1510	1376	1208	1422	1092	5346	3381	2748	3080	2420
ENSMUSG00000032279	chr9	Idh3a	-1.1360655	2.28399E-10	1.41494E-09	9.179670048	0.037417025	-1	10766	11305	11424	16311	10038	4515	6389	5335	5655	7620
ENSMUSG00000053746	chr2	Ptrh1	2.11501313	2.29384E-10	1.42041E-09	1.777612267	0.096134626	1	13	18	26	18	15	140	121	57	67	56
ENSMUSG00000037358	chrX	4930578C19Rik	-1.9640326	2.31511E-10	1.43295E-09	1.568115624	0.079559609	-1	70	85	61	77	47	24	7	16	26	22
ENSMUSG00000042489	chr4	Clspn	2.10230026	2.33163E-10	1.44253E-09	1.177680375	0.083015055	1	14	7	13	13	12	48	91	49	49	43
ENSMUSG00000063511	chr7	Snrnp70	1.09089906	2.33782E-10	1.44573E-09	6.076388709	0.033727846	1	717	538	539	778	641	2127	1485	1480	1273	1157
ENSMUSG00000029819	chr6	Npy	6.4626666	2.34264E-10	1.44806E-09	0.819620585	0.564347374	1	0	0	0	0	2	112	36	3	7	111
ENSMUSG00000026875	chr2	Traf1	2.24250863	2.42907E-10	1.50082E-09	1.201696747	0.095131362	1	12	12	9	10	12	99	68	49	46	31
ENSMUSG00000027742	chr3	Cog6	-1.0423197	2.43677E-10	1.50492E-09	5.924711671	0.030754924	-1	1401	1219	1149	1372	942	593	694	494	753	699
ENSMUSG00000069729	chr17	Arid1b	-1.0406224	2.44397E-10	1.5087E-09	5.174990392	0.029939762	-1	665	621	637	936	764	399	322	368	315	524
ENSMUSG00000020230	chr10	Prmt2	1.25765882	2.4649E-10	1.52095E-09	3.424029701	0.03892229	1	103	84	92	108	78	322	175	226	288	208
ENSMUSG00000049421	chr7	Zfp260	-0.8652456	2.46851E-10	1.5225E-09	5.101711171	0.020221413	-1	689	639	626	821	531	451	395	326	390	426
ENSMUSG00000002332	chr14	Dhrs1	0.93589145	2.48055E-10	1.52925E-09	5.331037478	0.024154252	1	423	447	366	508	316	903	846	892	766	887
ENSMUSG00000006344	chr10	Ggt5	1.32667381	2.51877E-10	1.55213E-09	3.278783476	0.043072076	1	66	85	72	80	98	335	183	180	199	230

ENSMUSG00000039179	chr16	Tekt5	4.76655815	2.56266E-10	1.57848E-09	-0.675868903	0.204965488	1	1	1	0	0	0	23	7	24	4	19
ENSMUSG00000102742	chr18	PCDHGB6	1.11870264	2.56961E-10	1.58207E-09	5.933370738	0.035534114	1	605	562	448	675	576	1657	1321	1526	852	1482
ENSMUSG00000025429	chr18	Pstpip2	-1.6352647	2.57167E-10	1.58263E-09	4.601771815	0.073397506	-1	599	455	452	647	575	93	192	118	271	281
ENSMUSG00000026580	chr1	Selp	1.93616462	2.58335E-10	1.58905E-09	1.186713953	0.068431778	1	17	15	12	18	4	62	57	39	60	59
ENSMUSG00000085156	chr11	Gm11974	2.18334163	2.58437E-10	1.58905E-09	1.208375511	0.093198553	1	10	15	9	16	8	100	67	42	50	34
ENSMUSG00000028179	chr3	Cth	-2.2905519	2.58861E-10	1.59096E-09	0.962925393	0.098221154	-1	48	65	36	35	42	12	4	8	12	15
ENSMUSG00000028383	chr4	Hsdl2	-1.2178052	2.67996E-10	1.64638E-09	5.561561124	0.041899325	-1	681	968	915	1631	809	382	438	396	527	561
ENSMUSG00000032011	chr9	Thy1	1.19882571	2.69222E-10	1.65319E-09	5.172592333	0.040136111	1	321	280	306	394	323	1106	858	979	537	613
ENSMUSG00000051518	chr15	Rps19bp1	1.12521178	2.72401E-10	1.67197E-09	3.303819283	0.030004252	1	77	90	82	133	78	272	245	182	209	187
ENSMUSG00000056234	chr14	Ncoa4	-1.6414215	2.74214E-10	1.68236E-09	4.17443355	0.07277218	-1	383	388	400	499	359	83	152	69	159	251
ENSMUSG00000024515	chr18	Smad4	-0.9735858	2.76653E-10	1.69658E-09	4.99652983	0.025984343	-1	592	529	531	888	631	330	383	312	295	436
ENSMUSG00000019579	chr17	D17Wsu104e	1.07691317	2.81976E-10	1.72846E-09	5.038773747	0.032112375	1	387	301	282	334	261	919	847	592	755	527
ENSMUSG00000013663	chr19	Pten	-0.9334742	2.85614E-10	1.75E-09	4.931156435	0.023713318	-1	528	565	571	809	520	321	403	287	307	391
ENSMUSG00000022759	chr16	Lrrc74b	-2.803421	2.86247E-10	1.75311E-09	-0.058077709	0.099524241	-1	16	26	25	18	25	2	2	3	4	6
ENSMUSG00000021760	chr13	Gpx8	1.0960447	2.89988E-10	1.77508E-09	4.257525365	0.031861453	1	234	175	180	181	128	521	449	413	375	358
ENSMUSG00000033458	chr7	Fan1	-1.482606	2.9009E-10	1.77508E-09	2.218129272	0.047251963	-1	92	103	83	114	106	35	30	34	46	50
ENSMUSG00000026192	chr1	Atic	1.03260392	2.93954E-10	1.79795E-09	5.168760233	0.029702174	1	329	313	277	478	368	955	968	746	635	641
ENSMUSG00000038894	chr8	Irs2	-2.4196041	2.95962E-10	1.80943E-09	2.36062163	0.141178891	-1	77	144	178	123	102	15	42	8	20	46
ENSMUSG00000000693	chr6	Loxl3	1.42671979	2.99455E-10	1.82999E-09	3.743448764	0.053457987	1	116	94	104	127	94	544	372	256	227	202
ENSMUSG00000062031	chr7	Athl1	1.10257485	3.06226E-10	1.87055E-09	3.356055506	0.028934981	1	95	100	71	127	88	292	190	211	200	237
ENSMUSG00000054843	chr19	Atrnl1	-1.0197161	3.07692E-10	1.87868E-09	3.838046339	0.026064065	-1	297	307	261	287	255	150	182	136	137	161
ENSMUSG00000025058	chrX	5430427O19Rik	2.62675807	3.08463E-10	1.88257E-09	0.235498085	0.098674466	1	3	7	3	5	3	27	45	16	30	28
ENSMUSG00000041836	chr7	Ptpre	1.47671323	3.09449E-10	1.88776E-09	2.765538536	0.051995878	1	47	48	46	71	51	192	185	80	155	197
ENSMUSG00000089075	chr3	Gm23820	-2.8957025	3.11234E-10	1.89782E-09	-0.136518856	0.105160899	-1	19	20	22	22	22	0	7	0	5	3
ENSMUSG00000042505	chr6	Acn9	-1.1988026	3.14447E-10	1.91658E-09	3.130116758	0.034284826	-1	194	170	158	213	164	74	90	61	104	99
ENSMUSG00000054648	chr8	Zfp869	-1.4920868	3.15412E-10	1.92162E-09	2.776685566	0.053581198	-1	137	141	131	201	137	35	62	42	78	70
ENSMUSG00000044968	chr5	Napepld	-1.154596	3.16074E-10	1.92481E-09	3.727644271	0.033958521	-1	223	219	254	396	272	114	143	102	142	164
ENSMUSG00000081926	chr10	Gm15536	2.43527802	3.19187E-10	1.94292E-09	0.753770434	0.101458471	1	8	5	8	5	9	52	31	49	54	25
ENSMUSG00000074896	chr19	Ifit3	1.74116818	3.20908E-10	1.95255E-09	3.074341156	0.077354908	1	70	57	52	78	30	155	213	176	134	366
ENSMUSG00000047747	chr8	Rnf150	-1.0552812	3.28517E-10	1.99798E-09	5.375851773	0.031525538	-1	614	715	746	1333	823	485	479	358	436	446
ENSMUSG00000056211	chr1	R3hdm1	-0.95159	3.29491E-10	2.00303E-09	5.369586541	0.025457276	-1	722	709	712	1133	807	452	514	387	409	539
ENSMUSG00000019066	chr9	Rab3d	1.08117842	3.32963E-10	2.02326E-09	3.584204285	0.028707953	1	94	133	105	144	92	346	246	225	253	251
ENSMUSG00000023036	chr18	Pcdhgc4	1.11176796	3.34889E-10	2.03408E-09	5.935193075	0.035567691	1	610	564	449	677	579	1656	1319	1526	854	1481
ENSMUSG00000083563	chr2	Gm13340	-1.4034887	3.35438E-10	2.03653E-09	3.108140113	0.048916334	-1	155	176	154	303	151	56	63	73	96	90
ENSMUSG00000103749	chr18	Pcdhgb5	1.10538122	3.38141E-10	2.05205E-09	5.939539918	0.035180311	1	609	566	455	689	579	1661	1319	1528	859	1480
ENSMUSG00000038244	chr7	Mical2	-1.2457633	3.43002E-10	2.08064E-09	6.832958159	0.045234385	-1	2523	1770	1797	3331	2637	1208	1181	1054	648	1464
ENSMUSG00000024776	chr19	Stambpl1	1.81302557	3.43355E-10	2.08173E-09	1.458043263	0.063204389	1	19	21	16	16	13	77	83	66	40	66
ENSMUSG00000042042	chr6	Csgalnact2	-1.1819815	3.4348E-10	2.08173E-09	4.791305382	0.039038975	-1	602	510	519	730	507	214	386	172	270	341
ENSMUSG00000092397	chr2	C130080G10Rik	-2.1791839	3.44622E-10	2.08775E-09	5.55239295	0.130552353	-1	1428	911	1294	1028	988	70	283	262	235	521
ENSMUSG00000020834	chr11	Dhrs13	1.82502071	3.44845E-10	2.0882E-09	1.339096608	0.063501202	1	13	18	10	26	12	65	61	55	75	47
ENSMUSG00000038025	chr13	Phf2	-1.0099262	3.45036E-10	2.08844E-09	5.412061458	0.028921142	-1	713	719	779	1190	859	488	465	423	358	576
ENSMUSG00000031751	chr8	Amfr	-0.9455244	3.4529E-10	2.08908E-09	7.182141303	0.026299415	-1	2900	2691	2506	3533	2645	1556	1688	1332	1656	1872
ENSMUSG00000030142	chr6	Clec4e	5.02062218	3.48418E-10	2.1069E-09	2.212304907	0.499086661	1	0	0	1	16	4	307	250	17	100	58
ENSMUSG00000104346	chr18	PCDHGB6	1.11031543	3.48538E-10	2.1069E-09	5.935339699	0.035547483	1	612	563	450	680	577	1656	1325	1524	851	1479
ENSMUSG00000017009	chr2	Sdc4	1.16677068	3.4932E-10	2.11072E-09	5.181659105	0.038555518	1	294	279	297	492	317	1309	784	642	783	613
ENSMUSG00000103897	chr18	PCDHGB6	1.10972376	3.49479E-10	2.11077E-09	5.933464423	0.035511745	1	605	566	451	677	579	1656	1316	1524	851	1478
ENSMUSG00000020664	chr12	Dld	-1.1538828	3.50933E-10	2.11863E-09	7.963168545	0.039244165	-1	4815	5326	5099	6882	3717	1977	2500	2109	2850	3142
ENSMUSG00000000318	chr11	Clec10a	1.76173388	3.51131E-10	2.11892E-09	3.806466595	0.083010781	1	69	121	83	79	108	702	236	261	325	253
ENSMUSG00000036835	chr7	Psenen	0.97661328	3.53624E-10	2.13304E-09	5.19203471	0.02666813	1	402	359	346	369	339	749	826	669	916	770
ENSMUSG00000060681	chrX	Slc9a6	-0.9107958	3.56455E-10	2.14918E-09	5.166988864	0.023070867	-1	687	617	576	976	663	403	449	339	426	414
ENSMUSG00000036412	chr18	Arsi	1.14561244	3.56941E-10	2.15119E-09	3.560256238	0.032948491	1	100	81	96	143	122	247	241	282	226	310
ENSMUSG00000102440	chr18	PCDHGA9	1.10812475	3.60263E-10	2.17027E-09	5.935016041	0.035465865	1	607	565	452	681	579	1656	1319	1524	852	1479
ENSMUSG00000000958	chr14	Slc7a7	2.05860931	3.6363E-10	2.18961E-09	2.419359328	0.103266957	1	21	29	28	38	33	285	125	67	131	92
ENSMUSG00000093930	chr13	Hmgcs1	-1.0053151	3.65476E-10	2.19978E-09	5.501702954	0.028813052	-1	919	808	916	1111	752	432	633	403	489	496
ENSMUSG00000032177	chr9	Pde4a	-1.0546487	3.66675E-10	2.20605E-09	5.961090698	0.032161499	-1	970	1109	1201	1870	1174	615	687	723	611	645
ENSMUSG00000091037	chr2	Gm17661	-2.968347	3.67178E-10	2.20812E-09	-0.15968303	0.114416148	-1	17	22	18	17	29	3	1	6	3	1
ENSMUSG00000027331	chr2	Knstrn	2.45403232	3.69754E-10	2.22266E-09	2.167971414	0.141733387	1	17	18	19	14	29	183	165	120	99	35
ENSMUSG00000045658	chr1	Pid1	1.45631997	3.7062E-10	2.22691E-09	3.971990006	0.057111512	1	107	124	130	115	133	510	501	190	394	289
ENSMUSG00000103081	chr18	Pcdhgb8	1.10528665	3.72844E-10	2.23931E-09	5.935657157	0.035346807	1	607	565	455	686	577	1659	1316	1524	852	1478
ENSMUSG00000042043	chr13	Tbca	1.02294006	3.80409E-10	2.28376E-09	4.611783064	0.028638091	1	256	257	216	288	181	634	619	462	547	403
ENSMUSG00000069495	chr2	Epc2	-1.081471	3.85567E-10	2.31373E-09	3.618978866	0.029344251	-1	230	226	231	322	229	113	160	94	118	155
ENSMUSG00000022673	chr16	Mcm4	1.26463053	3.92273E-10	2.35296E-09	3.53822689	0.041173561	1	105	109	85	124	81	319	376	209	242	184
ENSMUSG00000036533	chr17	Cdc42ep3	-1.1210892	3.92716E-10	2.35461E-09	4.646072441	0.034934755	-1	557	443	513	661	388	182	304	234	233	325
ENSMUSG00000033590	chr9	Myo5c	-1.2730548	3.93574E-10	2.35874E-09	2.949095553	0.038748515	-1	154	137	141	204	169	74	70	49	95	76
ENSMUSG00000029577	chr5	Ube3b	-0.9513231	3.99632E-10	2.39402E-09	7.579127561	0.02692536	-1	3594	3376	3151	4956	3797	2124	2096	1886	2118	2413

ENSMUSG00000005514	chr5	Por	1.04437282	4.04075E-10	2.4196E-09	4.912127965	0.030544141	1	217	282	273	395	296	581	757	549	747	651
ENSMUSG00000026490	chr1	Cdc42bpa	-0.8851813	4.04993E-10	2.42406E-09	4.809252161	0.02136253	-1	504	473	499	730	511	333	321	302	276	372
ENSMUSG00000022427	chr15	Tomm22	0.97245362	4.06053E-10	2.42936E-09	5.94925824	0.02742602	1	652	586	588	791	500	1323	1494	1430	1226	1165
ENSMUSG00000034587	chr11	8430429K09Rik	-3.138257	4.06566E-10	2.43139E-09	0.50070867	0.185826895	-1	33	39	35	47	23	16	1	0	3	2
ENSMUSG00000031488	chr8	Rab11fip1	2.9093458	4.09867E-10	2.45009E-09	0.344003077	0.137832533	1	2	2	4	5	6	62	33	12	25	33
ENSMUSG00000010290	chr1	AI597479	-0.9110162	4.11397E-10	2.45818E-09	4.371883082	0.021901815	-1	415	366	375	489	362	213	229	231	223	268
ENSMUSG00000022856	chr16	Tmem41a	1.24955513	4.12313E-10	2.4626E-09	2.681533468	0.034908263	1	62	49	50	62	53	167	126	152	121	155
ENSMUSG00000022516	chr16	Nudt16l1	0.92738334	4.12575E-10	2.46311E-09	4.569077597	0.02317292	1	251	252	226	296	190	648	442	455	469	523
ENSMUSG00000102428	chr18	PCDHGA12	1.10614491	4.13439E-10	2.46722E-09	5.937520098	0.035590094	1	613	563	453	679	583	1657	1320	1525	853	1484
ENSMUSG00000041654	chr11	Slc39a11	1.37124876	4.17241E-10	2.48885E-09	2.69707215	0.043883625	1	72	49	46	51	44	160	167	104	140	180
ENSMUSG00000067081	chr1	Asb18	-1.1956449	4.18986E-10	2.49818E-09	4.652325959	0.040070198	-1	484	499	555	610	444	159	270	212	311	280
ENSMUSG00000046982	chr18	Tshz1	-1.4229517	4.22445E-10	2.51773E-09	3.598850063	0.053787924	-1	221	205	259	324	293	66	116	115	78	155
ENSMUSG00000021373	chr13	Cap2	-1.1020786	4.2489E-10	2.53123E-09	8.007530675	0.036213637	-1	5975	4270	4592	6489	4932	2080	2971	2396	3088	2722
ENSMUSG00000030868	chr7	Dctn5	0.89336455	4.32458E-10	2.57522E-09	4.74516398	0.021732919	1	315	289	236	342	216	667	594	476	527	581
ENSMUSG00000029804	chr6	Herc3	-1.2142785	4.36658E-10	2.59912E-09	5.336973563	0.042461018	-1	713	666	767	1303	810	260	422	372	409	506
ENSMUSG00000022485	chr15	Hoxc5	-1.0806424	4.39316E-10	2.61383E-09	4.025218727	0.030953026	-1	325	257	274	515	295	192	191	137	131	203
ENSMUSG00000103332	chr18	Pcdhga2	1.1026104	4.42554E-10	2.63197E-09	5.940033512	0.035488109	1	616	567	456	681	581	1661	1321	1525	854	1485
ENSMUSG00000021245	chr12	Mlh3	-1.0292776	4.43521E-10	2.6366E-09	3.617588598	0.02637722	-1	256	245	216	287	214	116	136	104	139	158
ENSMUSG00000020432	chr11	Tcn2	0.95215595	4.44715E-10	2.64257E-09	5.132048692	0.025559408	1	280	397	315	463	324	915	740	695	602	828
ENSMUSG00000000183	chr6	Fgf6	-2.4567383	4.45304E-10	2.64495E-09	0.214082061	0.088500091	-1	34	22	22	30	25	3	7	1	9	6
ENSMUSG00000042439	chr18	Zfp532	-1.0684785	4.45782E-10	2.64666E-09	3.813007448	0.029404414	-1	272	250	274	348	265	140	133	161	112	188
ENSMUSG00000039195	chr2	1110008P14Rik	1.03417685	4.47417E-10	2.65525E-09	4.705807269	0.029735511	1	280	250	214	293	232	634	484	700	466	550
ENSMUSG00000000902	chr10	Smarcb1	0.91431955	4.54929E-10	2.69868E-09	4.608882363	0.022679156	1	238	237	247	332	206	661	501	498	451	487
ENSMUSG00000103088	chr18	Pcdhgb6	1.09988811	4.69102E-10	2.78157E-09	5.943183265	0.035422055	1	614	571	456	688	583	1656	1321	1534	860	1484
ENSMUSG00000037926	chr11	Ssh2	-0.9486489	4.69853E-10	2.78485E-09	5.810617943	0.026188994	-1	953	923	976	1619	1089	740	611	556	538	692
ENSMUSG00000028234	chr4	Rps20	1.02286345	4.70221E-10	2.78585E-09	7.678942351	0.03135785	1	2336	1913	1852	2235	1716	5940	4385	4144	4354	3668
ENSMUSG00000103472	chr18	Pcdhga7	1.10327144	4.72004E-10	2.79522E-09	5.941320889	0.035649534	1	610	568	455	681	588	1661	1324	1527	854	1487
ENSMUSG00000029669	chr6	Tspan12	-1.3981066	4.74533E-10	2.80901E-09	3.776271943	0.05279129	-1	205	278	280	501	235	86	124	114	104	181
ENSMUSG00000059796	chr11	Eif4a1	1.25710377	4.76823E-10	2.82137E-09	7.052562316	0.046875167	1	1196	1156	1094	1472	937	2542	4550	2189	3560	2395
ENSMUSG00000006191	chr13	Cdkal1	-1.0967928	4.78501E-10	2.8301E-09	3.75550592	0.03117587	-1	296	254	277	314	219	114	160	115	166	139
ENSMUSG00000026669	chr2	Mcm10	2.99741954	4.80267E-10	2.83814E-09	1.012500305	0.181755481	1	10	7	4	3	6	75	75	30	76	16
ENSMUSG00000031167	chrX	Rbm3	1.11770279	4.80211E-10	2.83814E-09	5.729200813	0.036480821	1	565	538	434	628	340	1085	1435	877	1407	1102
ENSMUSG00000000948	chr7	Snrpn	-1.0043449	4.83774E-10	2.85645E-09	5.154303792	0.028840049	-1	668	661	635	933	654	592	340	314	352	351
ENSMUSG00000023953	chr17	Polh	-1.0644977	4.83672E-10	2.85645E-09	3.526777893	0.028157167	-1	252	198	211	273	218	101	131	101	126	143
ENSMUSG00000025871	chr13	4833439L19Rik	-0.9391172	4.84267E-10	2.85816E-09	7.577818219	0.026498917	-1	3731	3437	3356	4751	3496	2019	2204	1846	2219	2388
ENSMUSG00000015854	chr3	Cd5l	3.90853943	4.88607E-10	2.88141E-09	-0.050068286	0.209994083	1	1	1	1	1	3	46	27	10	36	8
ENSMUSG00000102543	chr18	PCDHGC5	1.10374617	4.88619E-10	2.88141E-09	5.940023217	0.035743762	1	611	571	453	680	584	1660	1321	1530	853	1483
ENSMUSG00000036450	chr19	Hif1an	-0.9677131	4.90529E-10	2.89145E-09	7.810163076	0.028198406	-1	4547	3792	3965	5615	4283	2635	2252	2150	2319	3071
ENSMUSG00000104063	chr18	Pcdhgb7	1.09699448	4.90878E-10	2.89229E-09	5.93940889	0.035314489	1	612	566	461	687	582	1657	1321	1526	852	1478
ENSMUSG00000032525	chr9	Nktr	-0.91457	4.91938E-10	2.89732E-09	5.369303651	0.023946817	-1	802	686	713	1004	818	547	507	367	479	443
ENSMUSG00000032932	chr16	Hspa13	-1.0168187	4.93557E-10	2.90562E-09	3.895709494	0.02682641	-1	315	261	256	370	278	189	178	102	164	171
ENSMUSG00000018899	chr11	Irf1	0.99304473	5.05394E-10	2.97406E-09	4.253509605	0.026517828	1	195	204	155	230	162	445	445	408	292	474
ENSMUSG00000017776	chr11	Crk	-1.049296	5.06197E-10	2.97753E-09	5.75987705	0.032251877	-1	853	951	1059	1599	1025	666	680	397	599	553
ENSMUSG00000102748	chr18	Pcdhgb2	1.10012832	5.06749E-10	2.97952E-09	5.942571599	0.035581797	1	618	570	453	696	576	1663	1318	1530	855	1488
ENSMUSG00000028678	chr4	Kif2c	2.60665816	5.12854E-10	3.01415E-09	1.314634455	0.145955506	1	12	13	8	7	8	84	115	39	67	25
ENSMUSG00000023104	chr5	Rfc2	1.05189933	5.1667E-10	3.0353E-09	4.124887823	0.029542918	1	189	164	156	188	141	522	388	318	393	295
ENSMUSG00000034664	chr11	Itga2b	1.67387426	5.18248E-10	3.04329E-09	1.343251723	0.050661039	1	19	16	15	21	14	66	45	59	65	62
ENSMUSG00000006356	chr12	Crip2	1.27652818	5.21485E-10	3.06102E-09	6.155318885	0.04809959	1	631	590	478	839	586	2414	1506	2012	1004	1317
ENSMUSG00000032328	chr9	Tmem30a	-1.0035664	5.23798E-10	3.0733E-09	6.377537955	0.029912332	-1	1793	1469	1427	2111	1503	802	1142	718	890	963
ENSMUSG00000021982	chr14	Cdadc1	-0.9163932	5.24167E-10	3.07417E-09	4.387334942	0.022583466	-1	423	339	418	520	337	265	261	205	226	223
ENSMUSG00000037060	chr7	Prkcdbp	1.05037209	5.24555E-10	3.07516E-09	4.88922711	0.031301431	1	297	255	280	353	249	976	616	623	562	493
ENSMUSG00000024791	chr19	Cdca5	2.82241399	5.25192E-10	3.0776E-09	0.861074164	0.155755262	1	3	1	13	7	6	54	77	43	41	24
ENSMUSG00000102222	chr18	Pcdhga10	1.10053803	5.26256E-10	3.08255E-09	5.939482391	0.035672673	1	611	564	453	685	590	1659	1317	1525	854	1485
ENSMUSG00000103037	chr18	Pcdhgb1	1.09690862	5.27191E-10	3.08673E-09	5.938139161	0.035438588	1	613	564	459	684	585	1657	1316	1524	852	1479
ENSMUSG00000054065	chr7	Pkp3	3.82935328	5.28035E-10	3.09038E-09	-0.730571206	0.104573033	1	1	2	1	0	0	19	11	15	17	9
ENSMUSG00000055865	chr3	Fam19a3	-1.3397189	5.50911E-10	3.22291E-09	3.396897182	0.047014863	-1	260	209	228	231	181	59	115	78	105	123
ENSMUSG00000003037	chr8	Rab8a	0.96776857	5.61126E-10	3.28129E-09	4.572316244	0.025875342	1	228	225	237	308	199	690	538	362	455	539
ENSMUSG00000063457	chr10	Rps15	1.08952002	5.63579E-10	3.29426E-09	8.177298533	0.035941996	1	3161	2631	2453	3054	2462	9455	6030	5604	6245	5041
ENSMUSG00000022339	chr15	Ebag9	-1.1616059	5.67124E-10	3.3136E-09	3.26550802	0.033644072	-1	190	154	177	271	195	86	114	72	88	121
ENSMUSG00000027312	chr2	Atrn	-0.9528556	5.67864E-10	3.31654E-09	4.735250012	0.025444872	-1	495	452	466	666	535	321	329	247	222	366
ENSMUSG00000046908	chr14	Ltb4r1	4.44317025	5.71877E-10	3.33858E-09	0.170957822	0.304687038	1	1	1	0	4	0	78	23	8	36	11
ENSMUSG00000078515	chr4	Ddi2	-1.0204594	5.73488E-10	3.34659E-09	6.301217264	0.031056975	-1	1580	1415	1212	1976	1702	1059	814	669	692	1053
ENSMUSG00000020077	chr10	Srgn	1.72929634	5.82119E-10	3.39553E-09	4.318785231	0.084046819	1	96	120	148	188	133	1009	596	245	353	354
ENSMUSG00000022671	chr16	Mzt2	1.15087324	5.86264E-10	3.41686E-09	3.771714915	0.03503164	1	150	113	109	145	109	353	246	280	386	251
ENSMUSG00000053175	chr7	Bcl3	2.3118241	5.86036E-10	3.41686E-09	2.423909728	0.134365329	1	12	28	19	43	29	324	136	92	80	96

ENSMUSG00000028584	chr4	Lrrc38	-1.0608628	5.9417E-10	3.46149E-09	5.051030688	0.03246526	-1	653	623	632	705	691	285	307	335	328	488
ENSMUSG00000040732	chr16	Erg	-1.260323	5.94565E-10	3.46235E-09	3.298937385	0.0409655	-1	175	249	227	250	124	97	94	88	89	100
ENSMUSG00000048027	chr17	Rgmb	-0.9788033	5.96724E-10	3.4731E-09	4.960802944	0.027326474	-1	606	569	605	756	537	280	366	312	298	448
ENSMUSG00000055447	chr16	Cd47	0.99488807	5.96908E-10	3.4731E-09	5.600191556	0.028985394	1	512	553	437	535	368	1327	1185	807	871	1120
ENSMUSG00000103677	chr18	Pcdhga4	1.09282257	5.98753E-10	3.48239E-09	5.941925516	0.035413041	1	622	569	457	691	581	1656	1318	1529	856	1480
ENSMUSG00000103567	chr18	Pcdhga5	1.08911465	5.99869E-10	3.48742E-09	5.946359409	0.035175252	1	619	569	467	685	591	1662	1319	1527	862	1485
ENSMUSG00000041028	chr14	Ghitm	-0.9812566	6.01268E-10	3.49266E-09	8.666679348	0.02941472	-1	7939	7960	7575	10544	6428	4213	4575	3767	4824	4896
ENSMUSG00000053830	chr10	Gm9923	-2.9954271	6.01039E-10	3.49266E-09	-0.227118497	0.116402179	-1	25	11	22	16	24	1	2	5	2	3
ENSMUSG00000030604	chr7	Zfp626	-3.5125586	6.03983E-10	3.50696E-09	-0.391263985	0.159681243	-1	27	24	15	19	5	0	2	0	3	3
ENSMUSG00000064357	chrMT	mt-Atp6	-1.2876042	6.17419E-10	3.58349E-09	3.707076203	0.044692067	-1	218	261	261	424	225	81	122	106	139	163
ENSMUSG00000071415	chr11	Rpl23	1.02229974	6.24121E-10	3.62088E-09	8.261280805	0.031889422	1	3385	3183	2617	3402	2489	9111	6794	5846	6296	5720
ENSMUSG00000003623	chr5	Crot	-1.3802813	6.26209E-10	3.62848E-09	5.375480455	0.055985886	-1	1060	854	745	841	917	248	420	239	397	575
ENSMUSG00000004233	chr3	Wars2	-1.1366398	6.26041E-10	3.62848E-09	2.940520072	0.030320667	-1	159	165	140	178	133	89	80	76	77	64
ENSMUSG00000103585	chr18	Pcdhgb4	1.08986608	6.26003E-10	3.62848E-09	5.941712836	0.035300015	1	614	581	464	683	579	1659	1317	1527	854	1477
ENSMUSG00000034842	chr5	Art3	-0.9621863	6.33685E-10	3.67028E-09	7.004190593	0.028041022	-1	2665	2735	2431	2716	2034	1722	1586	1142	1285	1416
ENSMUSG00000061455	chr4	Stx17	-0.9718321	6.52696E-10	3.77883E-09	4.848765592	0.026872138	-1	586	564	537	605	526	263	310	275	350	379
ENSMUSG00000010721	chr5	Lmbr1	-1.1492539	6.56907E-10	3.80163E-09	3.871261014	0.035725596	-1	313	321	268	278	296	129	150	105	161	193
ENSMUSG00000000420	chr18	Galnt1	-0.9070113	6.6118E-10	3.82477E-09	6.12781615	0.024549313	-1	1299	1229	1323	1810	1167	939	848	628	776	795
ENSMUSG00000035673	chr10	Sbno2	1.36732244	6.63761E-10	3.83811E-09	3.894202227	0.05168552	1	116	92	118	172	119	602	383	288	232	256
ENSMUSG00000026028	chr1	Trak2	-1.119156	6.75943E-10	3.90694E-09	6.639648711	0.037805575	-1	1815	1829	2036	2880	1698	718	1123	1019	1070	1154
ENSMUSG00000005800	chr9	Mmp8	5.33884493	6.83932E-10	3.95148E-09	0.208537316	0.383884531	1	0	1	2	0	0	29	40	5	77	9
ENSMUSG00000071714	chr15	Csf2rb2	2.38052071	6.84253E-10	3.95171E-09	3.010473252	0.149288901	1	34	40	34	47	34	321	144	94	81	474
ENSMUSG00000031157	chrX	Pqbp1	0.87135247	6.87144E-10	3.96676E-09	4.6714205	0.020988934	1	264	245	224	351	258	659	513	482	465	570
ENSMUSG00000101746	chr1	2310043L19Rik	2.72682541	6.90999E-10	3.98736E-09	0.438775314	0.131918616	1	7	2	3	11	1	36	26	53	22	34
ENSMUSG00000032382	chr9	Snx1	1.03074947	6.92097E-10	3.99104E-09	4.898314427	0.030578418	1	312	293	219	367	270	885	787	487	605	520
ENSMUSG00000033020	chr15	Polr2f	1.03871419	6.92208E-10	3.99104E-09	4.63401981	0.030651746	1	256	201	205	326	226	771	536	529	479	410
ENSMUSG00000015869	chr11	Prpsap1	0.99687431	6.95356E-10	4.00754E-09	4.20787242	0.027085311	1	209	194	143	200	165	525	356	395	333	394
ENSMUSG00000029438	chr5	Bcl7a	-0.9455968	6.9591E-10	4.00908E-09	4.33711659	0.024486876	-1	431	379	367	448	345	193	250	194	214	270
ENSMUSG00000084329	chr11	Gm6733	-2.0645834	6.98876E-10	4.02451E-09	1.118098284	0.085892974	-1	52	50	28	53	65	10	17	7	13	18
ENSMUSG00000026426	chr1	Arl8a	0.89865366	7.07401E-10	4.07193E-09	4.619042789	0.022406148	1	261	259	219	330	210	650	535	394	489	549
ENSMUSG00000031103	chrX	Elf4	1.13488706	7.1024E-10	4.08659E-09	3.457707324	0.033186682	1	80	97	90	144	98	318	272	165	216	259
ENSMUSG00000049349	chr3	Gm5105	-1.6856692	7.10698E-10	4.08754E-09	1.315141171	0.053635549	-1	48	51	52	61	58	16	16	16	17	27
ENSMUSG00000044424	chr19	Gm9493	3.93217223	7.13169E-10	4.10006E-09	0.097162612	0.251468916	1	2	2	2	2	0	5	55	18	36	27
ENSMUSG00000024276	chr18	Zfp397	-1.1747131	7.21891E-10	4.14679E-09	3.903442054	0.037811471	-1	333	295	256	376	280	132	170	84	179	182
ENSMUSG00000032565	chr9	Nudt16	1.34557265	7.21659E-10	4.14679E-09	2.704859031	0.043477415	1	60	57	53	56	41	131	134	128	153	200
ENSMUSG00000024900	chr19	Cpt1a	1.14191639	7.23171E-10	4.15244E-09	4.477799537	0.03722404	1	161	187	160	322	213	559	627	312	510	499
ENSMUSG00000079435	chrX	Rpl36a	1.10499024	7.25885E-10	4.16631E-09	6.558181065	0.036942007	1	1073	921	817	850	754	2721	2091	1919	2229	1545
ENSMUSG00000066684	chr5	Pilrb1	3.31091126	7.27422E-10	4.17342E-09	-0.246954419	0.132846874	1	2	0	1	2	4	36	23	13	22	11
ENSMUSG00000042734	chr12	Ttc9	1.55984083	7.30272E-10	4.18634E-09	3.881651914	0.068451189	1	92	71	114	211	79	260	254	443	380	417
ENSMUSG00000096472	chr9	Cdkn2d	1.01350793	7.30248E-10	4.18634E-09	4.226405487	0.02821787	1	210	207	171	192	134	453	363	431	366	412
ENSMUSG00000056941	chr2	Commd7	0.94069705	7.31823E-10	4.1935E-09	4.369868501	0.024226356	1	220	215	190	231	189	557	470	397	428	359
ENSMUSG00000058975	chr7	Kcnc1	-1.1454395	7.34976E-10	4.20985E-09	6.338627791	0.039607093	-1	1358	1381	1684	2526	1452	662	915	928	658	920
ENSMUSG00000027692	chr3	Tnik	-1.2255821	7.39424E-10	4.23359E-09	5.681042712	0.044831662	-1	812	767	990	1628	1204	372	593	490	465	571
ENSMUSG00000022789	chr16	Dnm1l	-1.0545806	7.45388E-10	4.26599E-09	6.145573891	0.033495944	-1	1370	1308	1287	1911	1284	543	886	705	785	807
ENSMUSG00000022305	chr15	Lrp12	1.36219876	7.46437E-10	4.2685E-09	3.235586024	0.048773453	1	67	66	77	108	71	261	249	119	174	303
ENSMUSG00000040113	chr1	Mettl11b	3.30936096	7.4631E-10	4.2685E-09	2.332655794	0.263742812	1	4	8	13	37	8	24	145	123	206	214
ENSMUSG00000037849	chr1	Gm4955	5.49394466	7.49236E-10	4.28275E-09	-0.69816604	0.279129244	1	0	0	0	1	0	1	19	19	11	26
ENSMUSG00000009207	chr2	Lnp	-1.2314748	7.55197E-10	4.31506E-09	4.851305467	0.044339211	-1	601	582	520	803	523	172	345	223	252	409
ENSMUSG00000054206	chr10	Gzmm	-1.5637388	7.57791E-10	4.32811E-09	1.700279063	0.049997004	-1	80	53	61	95	64	23	23	22	33	28
ENSMUSG00000002257	chr17	Def6	1.55685774	7.59864E-10	4.33768E-09	2.220762945	0.055916233	1	39	30	40	38	23	173	108	90	91	94
ENSMUSG00000034591	chr10	Slc41a2	1.77634941	7.60088E-10	4.33768E-09	2.216275423	0.076390339	1	32	23	31	42	24	183	148	56	94	98
ENSMUSG00000022180	chr14	Slc7a8	1.22246119	7.70626E-10	4.39603E-09	4.556400535	0.043137175	1	196	176	143	274	260	727	597	331	580	465
ENSMUSG00000030704	chr7	Rab6a	-0.9568261	7.73286E-10	4.4094E-09	6.160503621	0.027613707	-1	1539	1268	1278	1707	1251	780	922	581	835	858
ENSMUSG00000057924	chr8	Gm10033	-2.3968205	7.77529E-10	4.43179E-09	0.92342699	0.115130288	-1	55	46	42	55	28	3	11	3	17	12
ENSMUSG00000001829	chr7	Clpb	-0.9391271	8.06855E-10	4.59707E-09	5.672148298	0.026273032	-1	819	947	890	1398	967	657	510	515	585	584
ENSMUSG00000019659	chr9	Ccdc12	0.86054808	8.0919E-10	4.60849E-09	5.232502923	0.021452539	1	389	389	358	513	343	943	755	779	751	718
ENSMUSG00000031622	chr8	Sin3b	0.86297708	8.09671E-10	4.60935E-09	5.221735045	0.021571076	1	403	385	327	510	352	987	743	709	753	739
ENSMUSG00000040618	chr14	Pck2	1.07486785	8.1893E-10	4.66016E-09	3.455942877	0.029485737	1	107	94	112	131	77	303	238	240	209	212
ENSMUSG00000047153	chr14	Khnyn	-1.1556498	8.2996E-10	4.72101E-09	3.227525403	0.033911716	-1	185	223	191	203	146	86	95	97	83	106
ENSMUSG00000057605	chr19	Gm6807	2.32795374	8.57084E-10	4.87332E-09	0.743859596	0.097746916	1	9	10	6	5	7	65	28	50	28	38
ENSMUSG00000078439	chr10	Smim24	2.80250929	8.67097E-10	4.92824E-09	0.649255355	0.151433509	1	4	5	5	7	5	85	26	43	15	37
ENSMUSG00000011148	chr12	Adssl1	-1.1088425	8.6905E-10	4.93733E-09	9.208338945	0.038164903	-1	9291	10338	10735	17822	12626	5140	6726	5661	6415	6507
ENSMUSG00000022186	chr15	Oxct1	-1.0448338	8.79243E-10	4.98916E-09	8.664291483	0.033939379	-1	8177	8946	8069	9727	5853	4172	4495	4160	4798	3884
ENSMUSG00000058542	chr17	Gm15590	4.0607765	8.78927E-10	4.98916E-09	-0.547442696	0.18849026	1	0	2	1	1	0	34	22	8	15	6
ENSMUSG00000103793	chr18	Pcdhga6	1.08529469	8.787E-10	4.98916E-09	5.942504536	0.035636528	1	622	571	463	681	591	1657	1316	1525	853	1480

ENSMUSG00000099375	chr1	Gm28187	-2.8629176	8.91529E-10	5.05682E-09	-0.429608306	0.085296206	-1	20	19	15	18	11	4	4	1	2	1
ENSMUSG00000041926	chr1	Rnpep	0.9918584	8.96875E-10	5.08508E-09	4.83197993	0.028468946	1	247	278	242	353	294	839	725	499	534	509
ENSMUSG00000021485	chr13	Mxd3	2.26418379	9.0869E-10	5.14998E-09	1.062090272	0.10213249	1	15	9	8	7	10	44	80	50	57	30
ENSMUSG00000035953	chr14	Tmem55b	0.97103009	9.14694E-10	5.18191E-09	4.251031814	0.026013591	1	196	191	184	205	171	571	433	333	351	374
ENSMUSG00000007659	chr2	Bcl2l1	1.6422148	9.38199E-10	5.31291E-09	4.691648656	0.079322789	1	155	149	109	288	240	1256	603	406	540	444
ENSMUSG00000058443	chr9	Rpl10-ps3	1.93629786	9.44154E-10	5.34447E-09	1.507172986	0.081749373	1	20	17	10	14	21	110	46	59	75	61
ENSMUSG00000024516	chr18	Sec11c	1.16602655	9.51394E-10	5.38109E-09	4.442537481	0.039351596	1	246	187	157	240	167	637	622	301	518	385
ENSMUSG00000063895	chr14	Nupl1	-1.1707858	9.51135E-10	5.38109E-09	3.818142548	0.037738826	-1	294	264	256	365	271	103	176	93	156	175
ENSMUSG00000022614	chr15	Lmf2	1.00080269	9.54856E-10	5.39849E-09	4.473565274	0.028474193	1	192	191	194	291	232	640	472	470	343	495
ENSMUSG00000046186	chr9	Cd109	1.77361535	9.61222E-10	5.43228E-09	3.792189507	0.089013828	1	146	89	101	93	33	458	413	240	196	453
ENSMUSG00000027706	chr3	Sec62	-0.9859647	9.62214E-10	5.43569E-09	5.902119122	0.029507757	-1	1271	1245	1087	1245	1034	619	607	571	604	873
ENSMUSG00000003031	chr6	Cdkn1b	-0.983658	9.73875E-10	5.49935E-09	5.212327543	0.028732188	-1	828	725	693	794	609	364	458	326	355	530
ENSMUSG00000028690	chr4	Mmachc	-0.9912817	9.74434E-10	5.50028E-09	4.767328936	0.028527216	-1	558	465	489	760	448	243	368	242	285	344
ENSMUSG00000025437	chr3	Usp33	-1.046048	9.83549E-10	5.54725E-09	4.411612883	0.031304472	-1	449	394	384	523	382	166	267	177	236	280
ENSMUSG00000025967	chr1	Eef1b2	1.00707389	9.83319E-10	5.54725E-09	7.869739461	0.031630112	1	2593	2293	2102	2571	1995	6705	4980	5055	4671	4143
ENSMUSG00000092203	chr17	1110038B12Rik	1.44422965	9.92749E-10	5.59688E-09	3.242302576	0.056177507	1	100	64	72	78	58	336	252	198	205	129
ENSMUSG00000064246	chr1	Chil1	3.20786129	1.00361E-09	5.65582E-09	0.946250622	0.211131376	1	9	3	6	4	3	127	17	30	51	42
ENSMUSG00000007892	chr9	Rplp1	1.12791811	1.00928E-09	5.68549E-09	9.206360918	0.03976454	1	6234	5285	5006	6109	4936	19664	12928	11694	12936	9398
ENSMUSG00000055204	chr5	Ankrd17	-0.9847758	1.01352E-09	5.70707E-09	5.624201724	0.029277563	-1	861	871	850	1331	990	462	610	457	502	667
ENSMUSG00000022361	chr15	Zhx1	-0.8886958	1.01554E-09	5.71383E-09	4.836750418	0.022725172	-1	564	537	523	652	479	288	345	279	344	371
ENSMUSG00000022533	chr16	Atp13a3	-1.2145422	1.01528E-09	5.71383E-09	5.524763448	0.044662918	-1	1064	778	834	1090	1009	314	540	336	416	655
ENSMUSG00000046034	chr15	Otulin	1.32210226	1.01997E-09	5.73645E-09	4.301654411	0.050751364	1	153	134	142	301	126	747	417	356	459	330
ENSMUSG00000078452	chr10	Raet1d	3.96300095	1.04121E-09	5.85356E-09	-0.622807942	0.145521977	1	2	1	1	0	0	26	20	8	18	7
ENSMUSG00000038374	chr3	Rbm8a	0.96758671	1.04552E-09	5.87545E-09	5.366350543	0.02798699	1	446	427	393	487	322	1179	953	824	788	719
ENSMUSG00000022408	chr15	Fam83f	2.73615373	1.05246E-09	5.91204E-09	0.659149723	0.143296914	1	9	6	6	3	3	33	39	19	34	80
ENSMUSG00000036810	chr8	Cnep1r1	-1.0334033	1.05301E-09	5.91276E-09	4.768040571	0.03130237	-1	562	494	463	683	525	230	311	215	314	384
ENSMUSG00000020629	chr12	Adi1	-0.9115862	1.05456E-09	5.91906E-09	5.484227896	0.024915992	-1	920	809	723	1104	811	678	502	436	477	453
ENSMUSG00000024068	chr17	Spast	-0.9388214	1.08141E-09	6.06736E-09	5.645471839	0.026648648	-1	1011	812	800	1318	988	528	568	497	542	660
ENSMUSG00000047215	chr5	Rpl9	0.98522786	1.08202E-09	6.06835E-09	8.107205234	0.030487141	1	2833	2743	2503	3400	2347	8084	6239	5036	5811	4918
ENSMUSG00000029406	chr5	Pitpnm2	-0.9837133	1.08641E-09	6.09051E-09	5.040892118	0.028663365	-1	491	548	648	901	674	374	373	371	291	390
ENSMUSG00000039153	chr17	Runx2	2.23778078	1.09966E-09	6.15984E-09	1.050483089	0.103313334	1	12	11	4	13	10	58	76	50	22	55
ENSMUSG00000057841	chr6	Rpl32	0.92565953	1.09949E-09	6.15984E-09	7.669276569	0.026883912	1	2208	2028	1747	2486	1996	5347	4659	3540	4249	4081
ENSMUSG00000045045	chr19	Lrfn4	1.4493208	1.10154E-09	6.16789E-09	2.330489632	0.0499549	1	37	39	23	58	40	154	97	124	101	109
ENSMUSG00000056290	chr19	Ms4a4b	3.68492663	1.1098E-09	6.21166E-09	-0.602973484	0.124881936	1	0	3	1	0	1	17	9	16	11	26
ENSMUSG00000030987	chr7	Stim1	-1.1198408	1.11223E-09	6.22114E-09	7.517212749	0.039167273	-1	3249	3326	3375	5178	3690	1458	1854	1836	1621	2624
ENSMUSG00000091661	chr9	Gm17021	-1.2935367	1.11238E-09	6.22114E-09	3.574599263	0.046161984	-1	238	216	216	362	232	63	127	101	114	150
ENSMUSG00000018537	chr11	Pcgf2	1.44939776	1.11557E-09	6.23649E-09	2.505394604	0.051090592	1	36	41	47	48	47	187	126	126	83	145
ENSMUSG00000057113	chr11	Npm1	1.10361779	1.1464E-09	6.40627E-09	7.100765876	0.037996044	1	1383	1321	1092	1647	1084	3738	4167	2392	2882	2193
ENSMUSG00000021156	chr13	Zmynd11	-0.8863682	1.14938E-09	6.42035E-09	6.007343747	0.024048044	-1	1137	1149	1143	1627	1181	807	756	628	648	858
ENSMUSG00000102252	chr7	Snrpn	-1.0015954	1.1551E-09	6.44973E-09	5.717707768	0.030642849	-1	941	1045	902	1388	974	868	504	489	493	532
ENSMUSG00000048327	chr2	Ckap2l	1.92565856	1.15721E-09	6.45895E-09	1.851946964	0.087550095	1	21	20	31	15	18	107	119	70	100	52
ENSMUSG00000103144	chr18	Pcdhga1	1.07944679	1.16761E-09	6.51435E-09	5.948246755	0.035800812	1	622	578	460	695	595	1667	1320	1528	855	1480
ENSMUSG00000040706	chr4	Agmat	3.13052369	1.16903E-09	6.51712E-09	0.2889843	0.172167501	1	1	3	2	4	6	10	25	35	43	43
ENSMUSG00000048490	chr16	Nrip1	-1.2165644	1.16887E-09	6.51712E-09	4.562607424	0.043808773	-1	480	362	412	655	555	167	284	160	242	303
ENSMUSG00000081643	chr1	Gm11605	2.7860001	1.17595E-09	6.55305E-09	-0.31699895	0.081515036	1	2	5	1	2	2	24	22	17	16	16
ENSMUSG00000040681	chr16	Hmgn1	0.9544138	1.17783E-09	6.56092E-09	5.524556959	0.027549779	1	505	473	405	545	402	1239	1140	962	757	868
ENSMUSG00000035459	chr10	Stab2	-2.5876778	1.18747E-09	6.61201E-09	4.02209963	0.186766158	-1	428	470	242	614	347	233	35	32	31	64
ENSMUSG00000070385	chr3	Ampd1	-1.0843678	1.1955E-09	6.65406E-09	10.1724133	0.037204442	-1	27062	22744	19510	23663	23126	10848	15496	10026	12624	11296
ENSMUSG00000046027	chr7	Stard5	1.25030435	1.21137E-09	6.73969E-09	2.693489708	0.037636104	1	46	69	50	64	49	171	153	126	116	165
ENSMUSG00000041132	chr5	N4bp2l1	1.91228953	1.21998E-09	6.78487E-09	1.53324105	0.080493571	1	20	17	15	17	16	109	53	60	40	97
ENSMUSG00000033799	chr13	Fam208b	-1.4844927	1.22445E-09	6.80436E-09	3.220217274	0.060517182	-1	182	216	189	260	169	40	100	59	78	118
ENSMUSG00000046058	chr7	Eid2	1.37840933	1.2242E-09	6.80436E-09	2.679311687	0.048260983	1	47	62	35	81	38	152	118	147	136	185
ENSMUSG00000030282	chr6	Cmas	0.90341638	1.23388E-09	6.854E-09	5.029808563	0.024022203	1	404	343	321	337	274	803	672	664	649	676
ENSMUSG00000034210	chr4	Efcab14	-1.0030284	1.2348E-09	6.8564E-09	5.570636657	0.030658686	-1	927	827	920	1139	900	384	574	477	545	582
ENSMUSG00000024818	chr19	Slc25a45	1.89739872	1.25567E-09	6.96952E-09	2.366596423	0.092774073	1	34	43	36	33	11	200	99	77	145	131
ENSMUSG00000053768	chr6	Chchd3	-1.0361351	1.25735E-09	6.97607E-09	7.753743031	0.033876791	-1	4043	4100	4228	5974	3454	1945	2347	1968	2727	2503
ENSMUSG00000028757	chr4	Ddost	0.91632281	1.27223E-09	7.05585E-09	6.344674721	0.026062833	1	844	789	689	1036	839	2098	1892	1511	1665	1524
ENSMUSG00000024327	chr17	Slc39a7	0.92402862	1.27881E-09	7.08953E-09	6.355255999	0.02652315	1	831	761	745	1066	814	2249	1856	1581	1583	1512
ENSMUSG00000045382	chr1	Cxcr4	1.45234824	1.31204E-09	7.27083E-09	3.587396603	0.059766519	1	106	116	66	117	71	483	325	251	180	202
ENSMUSG00000038390	chr6	Gpr162	3.12224545	1.3464E-09	7.4583E-09	-0.17007809	0.131409334	1	3	1	1	3	3	16	19	16	16	43
ENSMUSG00000026883	chr2	Dab2ip	-0.9604643	1.36025E-09	7.53203E-09	6.27991797	0.028755257	-1	1415	1322	1408	1875	1615	959	769	877	697	1005
ENSMUSG00000020546	chr11	Stxbp4	-1.2970086	1.36496E-09	7.54613E-09	4.374204373	0.049979487	-1	537	459	382	357	420	124	221	157	216	252
ENSMUSG00000027429	chr2	Sec23b	0.92451319	1.36472E-09	7.54613E-09	3.980393315	0.023164655	1	177	142	127	217	148	345	358	277	337	359
ENSMUSG00000027715	chr3	Ccna2	1.84049448	1.36347E-09	7.54613E-09	3.223413761	0.09437865	1	69	72	55	38	58	250	389	200	228	106
ENSMUSG00000028710	chr4	Atpaf1	-0.9968896	1.36388E-09	7.54613E-09	4.871711562	0.029579154	-1	557	530	580	746	494	241	344	266	359	373

ENSMUSG00000079165	chr5	Sap25	1.63347685	1.37473E-09	7.59714E-09	2.268178954	0.065546369	1	36	31	35	24	40	176	99	97	120	88
ENSMUSG00000023861	chr17	Mpc1	-1.1707063	1.37764E-09	7.61025E-09	6.50550381	0.042857527	-1	1707	1940	1945	2404	1404	678	955	698	1200	998
ENSMUSG00000038740	chr2	Mvb12b	-0.9579148	1.40979E-09	7.78473E-09	5.703560306	0.028239616	-1	1005	836	992	1236	1043	546	515	506	608	707
ENSMUSG00000052270	chr17	Fpr2	6.83163551	1.4176E-09	7.82482E-09	0.452858479	0.611122889	1	0	0	0	1	0	113	36	6	46	1
ENSMUSG00000032812	chr7	Arap1	1.16312451	1.42015E-09	7.83576E-09	5.538124917	0.041669554	1	434	400	364	547	396	1858	906	822	815	920
ENSMUSG00000023067	chr17	Cdkn1a	2.25123438	1.44149E-09	7.95037E-09	6.381483803	0.149887639	1	360	267	235	863	506	4180	1504	3093	715	1860
ENSMUSG00000033222	chr3	Ttf2	-1.0483338	1.4778E-09	8.14743E-09	3.331433338	0.028336671	-1	228	192	181	222	176	98	127	91	112	101
ENSMUSG00000022032	chr14	Scara5	-1.1515794	1.48405E-09	8.17868E-09	4.292020344	0.03910413	-1	398	394	421	411	362	184	163	170	160	314
ENSMUSG00000027107	chr2	Chrna1	1.47746669	1.50519E-09	8.29191E-09	6.219824601	0.067684374	1	593	616	551	559	576	2568	1542	2546	943	1331
ENSMUSG00000024247	chr17	Pkdcc	-0.95801	1.50971E-09	8.31352E-09	6.328569302	0.02879083	-1	1641	1341	1482	2048	1426	780	965	727	942	1035
ENSMUSG00000034584	chr9	Exph5	-3.1054321	1.54463E-09	8.50244E-09	-0.457130637	0.118244745	-1	20	12	15	13	22	0	4	0	4	2
ENSMUSG00000036499	chr10	Eea1	-1.0877375	1.56087E-09	8.58849E-09	4.811514691	0.035704287	-1	534	478	506	791	550	216	378	218	283	367
ENSMUSG00000027109	chr2	Sp3	-1.3917386	1.57145E-09	8.64326E-09	4.296018937	0.057614664	-1	370	367	387	622	387	89	237	134	176	241
ENSMUSG00000031748	chr8	Gnao1	-1.3306707	1.57297E-09	8.64821E-09	2.892422304	0.046698627	-1	123	172	117	169	194	68	71	58	57	87
ENSMUSG00000022559	chr15	Fbxl6	1.18566681	1.58743E-09	8.72431E-09	3.54228203	0.038818313	1	92	98	106	137	92	400	234	266	183	233
ENSMUSG00000032815	chr8	Fanca	2.47995675	1.58961E-09	8.72602E-09	0.474723834	0.111492272	1	8	4	4	8	4	41	48	21	45	18
ENSMUSG00000038812	chr19	Trmt112	1.00157169	1.58913E-09	8.72602E-09	4.419709214	0.029236671	1	261	159	190	236	208	611	474	436	412	392
ENSMUSG00000040521	chr10	Tsfm	0.98959708	1.58887E-09	8.72602E-09	4.577515172	0.02895176	1	243	208	211	359	182	611	460	578	467	456
ENSMUSG00000055228	chr13	Zfp935	-2.1131501	1.59348E-09	8.74381E-09	0.5500759	0.075844991	-1	43	36	30	32	23	5	7	9	9	11
ENSMUSG00000024007	chr17	Ppil1	1.0947925	1.595E-09	8.7487E-09	3.760079733	0.03329164	1	141	97	115	169	119	344	356	244	328	221
ENSMUSG00000000409	chr4	Lck	3.18805969	1.59845E-09	8.7642E-09	-0.487139742	0.117058464	1	3	3	0	2	0	24	11	20	10	20
ENSMUSG00000097715	chr13	Gpr137b-ps	2.01628378	1.61569E-09	8.85525E-09	2.015517926	0.102324347	1	23	27	22	25	17	129	138	33	82	137
ENSMUSG00000028030	chr3	Tbck	-2.1502919	1.6166E-09	8.85679E-09	1.758907597	0.114967062	-1	72	58	87	106	78	5	28	11	21	33
ENSMUSG00000026466	chr1	Tor1aip1	-0.981043	1.626E-09	8.90477E-09	6.494866522	0.030417975	-1	1692	1617	1600	2275	1753	843	1056	811	963	1274
ENSMUSG00000098404	chr7	Gm8086	-2.3506133	1.62942E-09	8.91998E-09	0.489943075	0.100846251	-1	27	21	32	48	35	2	9	4	12	7
ENSMUSG00000021112	chr12	Mpp5	-0.9069857	1.63131E-09	8.92686E-09	4.53953956	0.023951271	-1	482	425	455	540	352	293	291	201	231	307
ENSMUSG00000018672	chr11	Copz2	1.0292556	1.64466E-09	8.99639E-09	4.956108063	0.032067491	1	330	308	265	356	257	1007	609	698	496	601
ENSMUSG00000078122	chrX	F630028O10Rik	2.93762688	1.64992E-09	9.01897E-09	0.808672993	0.17717414	1	13	3	6	4	1	63	50	18	69	33
ENSMUSG00000082519	chr2	Vamp7-ps	-2.0953089	1.65008E-09	9.01897E-09	1.660678534	0.106136334	-1	79	72	52	81	85	12	28	8	33	13
ENSMUSG00000072082	chr17	Ccnf	1.7883264	1.65545E-09	9.04481E-09	1.947286505	0.077573822	1	28	29	16	29	22	99	142	72	102	55
ENSMUSG00000022307	chr15	Oxr1	-1.1857182	1.66353E-09	9.08538E-09	5.333259519	0.043501185	-1	924	830	727	1015	683	254	429	317	425	573
ENSMUSG00000036087	chr5	Slain2	-0.9392459	1.67402E-09	9.13911E-09	6.454514191	0.027889768	-1	1654	1505	1502	2326	1654	881	1118	853	926	1123
ENSMUSG00000020366	chr11	Mapk9	-0.9200337	1.68304E-09	9.18475E-09	5.626929157	0.026192722	-1	1035	865	793	1134	982	528	593	470	530	666
ENSMUSG00000029238	chr5	Clock	-1.3899271	1.72322E-09	9.40035E-09	4.403640523	0.058382564	-1	304	323	376	763	544	148	280	162	175	183
ENSMUSG00000030557	chr7	Mef2a	-1.0751116	1.74246E-09	9.50158E-09	6.621590347	0.036716837	-1	2043	1826	1606	2701	1854	745	1239	864	1062	1242
ENSMUSG00000031133	chrX	Arhgef6	-1.0429334	1.76281E-09	9.6088E-09	5.919868821	0.034165725	-1	1124	930	1162	1654	1229	534	705	518	767	688
ENSMUSG00000026849	chr2	Tor1a	1.11140281	1.7686E-09	9.63663E-09	3.11476589	0.031643729	1	86	91	62	89	73	242	196	157	192	168
ENSMUSG00000030760	chr7	Acer3	1.59565155	1.80544E-09	9.83351E-09	2.833384312	0.069155946	1	36	49	48	72	54	273	193	78	153	176
ENSMUSG00000037868	chr10	Egr2	2.34553529	1.80764E-09	9.84166E-09	2.402696864	0.146369367	1	28	22	37	25	12	190	243	54	63	167
ENSMUSG00000028756	chr4	Pink1	-1.0004807	1.80986E-09	9.84991E-09	9.056994351	0.032420731	-1	9569	10336	9602	14628	9222	6122	5206	4837	7030	5730
ENSMUSG00000046031	chr10	Fam26f	3.17033353	1.81498E-09	9.87395E-09	-0.139958516	0.142950404	1	1	3	1	4	2	27	14	29	9	34
ENSMUSG00000042496	chr9	Prdm10	-1.8078622	1.81676E-09	9.87979E-09	0.928448584	0.060314571	-1	39	34	40	43	51	15	15	12	11	12
ENSMUSG00000091931	chr12	AK010878	-1.2106569	1.81778E-09	9.88149E-09	3.017628843	0.0388721	-1	179	148	163	215	132	105	89	44	77	83
ENSMUSG00000059588	chr2	Calcrl	-1.3756879	1.82005E-09	9.88612E-09	3.51831606	0.054070258	-1	204	255	240	299	223	60	117	75	103	160
ENSMUSG00000093156	chr14	Mir3076	2.20450768	1.81939E-09	9.88612E-09	2.925231469	0.134284402	1	19	82	27	34	32	346	222	150	189	104
ENSMUSG00000041997	chr2	Tlk1	-0.9290568	1.83095E-09	9.94145E-09	5.303571516	0.026531146	-1	662	700	660	1084	774	462	505	331	437	489
ENSMUSG00000032112	chr9	Trappc4	1.08765185	1.8413E-09	9.99379E-09	4.718790429	0.035825176	1	238	250	197	326	244	944	529	512	499	456
ENSMUSG00000037572	chr14	Wdhd1	2.06843202	1.84276E-09	9.99783E-09	1.294289	0.092869762	1	14	17	14	10	10	48	95	47	70	43
ENSMUSG00000063316	chr11	Rpl27	0.9916273	1.84971E-09	1.00317E-08	7.214692281	0.031568433	1	1530	1514	1436	1727	1192	4332	3334	2754	3232	2555
ENSMUSG00000033781	chr13	Asb13	-0.996258	1.85335E-09	1.00475E-08	3.778428125	0.027336732	-1	300	275	225	326	230	130	181	121	137	174
ENSMUSG00000028463	chr4	Car9	2.42341901	1.8589E-09	1.00737E-08	0.29684519	0.091974858	1	8	3	3	5	6	20	34	23	38	34
ENSMUSG00000053565	chr7	Eif3k	0.94890469	1.87738E-09	1.01699E-08	6.431172206	0.028624656	1	876	799	729	1117	877	2541	1825	1721	1525	1720
ENSMUSG00000001376	chr6	Ccdc132	-1.0201879	1.87987E-09	1.01794E-08	4.668334099	0.031313908	-1	544	518	473	542	440	223	303	203	327	306
ENSMUSG00000033585	chr7	Ndn	0.89821917	1.89443E-09	1.02543E-08	4.673021552	0.023768649	1	281	220	246	310	262	586	508	535	439	632
ENSMUSG00000026775	chr2	Yme1l1	-1.0668688	1.90213E-09	1.0292E-08	5.705170101	0.035736493	-1	1165	977	954	1352	840	390	643	452	612	637
ENSMUSG00000038143	chr8	Stox2	-1.2832341	1.92537E-09	1.04137E-08	3.627104812	0.047165729	-1	213	215	201	430	260	106	106	134	79	156
ENSMUSG00000040592	chr11	Cd79b	2.63356113	1.96214E-09	1.06085E-08	0.247790683	0.111389382	1	5	4	2	4	6	46	16	18	35	33
ENSMUSG00000065947	chrMT	mt-Nd4l	-2.3971067	2.00874E-09	1.08562E-08	0.828338174	0.119798753	-1	28	40	49	56	37	1	14	7	6	15
ENSMUSG00000002980	chr7	Bcam	1.09830995	2.04934E-09	1.10713E-08	6.029828799	0.038313632	1	488	546	521	891	672	1420	1199	1727	1511	1328
ENSMUSG00000024889	chr19	Rce1	1.31854567	2.05069E-09	1.10744E-08	2.857424707	0.045629651	1	61	63	56	64	57	261	180	129	132	136
ENSMUSG00000031111	chrX	Igsf1	1.5577734	2.09724E-09	1.13214E-08	2.421011926	0.063118054	1	53	34	28	55	29	117	112	93	114	202
ENSMUSG00000051855	chr6	Mest	1.75570135	2.10376E-09	1.13522E-08	5.942181294	0.095801669	1	556	396	401	331	373	1819	1109	1813	561	2478
ENSMUSG00000074476	chr9	Spc24	1.85097899	2.12077E-09	1.14396E-08	1.743600226	0.082818734	1	21	25	15	28	15	85	127	77	75	45
ENSMUSG00000027863	chr3	Cd2	3.36884435	2.12271E-09	1.14456E-08	-0.47519841	0.124770763	1	1	3	1	0	2	29	8	15	14	21
ENSMUSG00000057236	chr4	Rbbp4	0.89486426	2.13931E-09	1.15307E-08	6.419468938	0.025606714	1	949	917	804	1055	735	1925	1964	1790	1709	1673

ENSMUSG00000041431	chr13	Ccnb1	2.4640543	2.19392E-09	1.18205E-08	1.867662051	0.153487526	1	26	12	21	9	10	114	178	71	83	40
ENSMUSG00000058706	chr6	0610030E20Rik	-0.8925932	2.19796E-09	1.18377E-08	4.285554086	0.023005339	-1	339	383	373	403	367	244	235	178	218	237
ENSMUSG00000022799	chr16	Arhgap31	-0.9086559	2.2116E-09	1.19065E-08	4.916756608	0.025154779	-1	527	529	570	751	557	446	361	242	291	387
ENSMUSG00000063904	chr19	Dpp3	0.84311596	2.21737E-09	1.1933E-08	5.163913019	0.021693412	1	384	324	341	522	349	764	768	712	766	726
ENSMUSG00000025630	chrX	Hprt	0.9028206	2.24618E-09	1.20834E-08	4.954437931	0.024801444	1	325	306	256	434	295	775	802	500	636	590
ENSMUSG00000028923	chr4	Necap2	0.88533885	2.26814E-09	1.21968E-08	5.075161899	0.023898086	1	406	347	329	365	302	933	686	587	681	692
ENSMUSG00000045817	chr17	Zfp36l2	1.10433155	2.28373E-09	1.22759E-08	4.453617616	0.03693322	1	208	202	197	266	162	476	715	303	456	493
ENSMUSG00000089862	chr6	Gm16039	-1.0189781	2.29084E-09	1.23094E-08	3.743604604	0.028999745	-1	291	234	232	309	260	129	168	106	134	182
ENSMUSG00000035215	chr10	Lsm7	1.05524756	2.32175E-09	1.24707E-08	3.466582782	0.03004854	1	112	121	100	102	89	290	261	231	213	210
ENSMUSG00000049687	chr15	Fam109b	1.60113684	2.35203E-09	1.26285E-08	1.808382506	0.058948409	1	26	21	23	26	27	122	84	84	55	70
ENSMUSG00000021709	chr13	Erbb2ip	-1.0232196	2.37883E-09	1.27675E-08	5.373163853	0.032950503	-1	791	743	752	1211	686	377	508	319	448	579
ENSMUSG00000020130	chr10	Tbc1d15	-0.9923646	2.38357E-09	1.2788E-08	4.352465721	0.029312242	-1	390	320	384	597	350	197	251	166	234	263
ENSMUSG00000040482	chr17	Dxo	1.20987455	2.38866E-09	1.28104E-08	3.032815392	0.038678426	1	71	76	64	70	77	251	153	168	190	157
ENSMUSG00000028803	chr4	Nipal3	-1.079424	2.39226E-09	1.28248E-08	3.699617449	0.033132677	-1	253	255	240	312	244	203	100	100	129	151
ENSMUSG00000063160	chr7	Numbl	1.10732582	2.41825E-09	1.29591E-08	3.401680237	0.033246439	1	101	82	95	104	107	264	230	267	185	214
ENSMUSG00000090264	chr18	Eif4ebp3	1.39767741	2.42271E-09	1.29781E-08	2.882901459	0.053412281	1	67	49	54	87	43	268	168	165	147	114
ENSMUSG00000032202	chr9	Rab27a	1.66136863	2.43532E-09	1.30406E-08	1.284918433	0.054978446	1	16	19	11	21	15	76	64	45	56	45
ENSMUSG00000030413	chr7	Pglyrp1	2.82563509	2.46688E-09	1.32045E-08	0.201940494	0.138206383	1	3	2	6	5	2	59	19	17	30	21
ENSMUSG00000068270	chrX	Shroom4	-1.1536956	2.46917E-09	1.32118E-08	3.285219449	0.036541574	-1	142	202	169	297	192	114	87	74	105	110
ENSMUSG00000004364	chr1	Cul3	-1.1069947	2.50874E-09	1.34183E-08	7.379889238	0.039973197	-1	3503	2973	2931	4586	3092	1207	2034	1360	1832	2159
ENSMUSG00000040325	chr9	Vprbp	-1.0240779	2.57122E-09	1.37473E-08	4.087740925	0.030594132	-1	297	276	281	489	361	157	208	157	194	191
ENSMUSG00000072955	chrX	Tmsb15l	2.66678157	2.59123E-09	1.3849E-08	-0.077397368	0.098666276	1	1	7	3	5	0	21	27	23	18	25
ENSMUSG00000018160	chr11	Med1	-0.9286527	2.61704E-09	1.39815E-08	4.866122274	0.026481372	-1	514	504	613	719	493	388	395	271	319	267
ENSMUSG00000038495	chr3	Otud7b	-0.9120653	2.64095E-09	1.41018E-08	6.091675155	0.026764189	-1	1243	1136	1191	1773	1320	842	779	577	778	901
ENSMUSG00000070436	chr7	Serpinh1	1.05289669	2.64156E-09	1.41018E-08	7.994326706	0.036449353	1	2426	2249	2206	3176	2346	6741	6599	6155	4475	4104
ENSMUSG00000018362	chr11	Kpna2	1.1461547	2.70146E-09	1.4415E-08	4.24766067	0.039796715	1	223	146	158	182	162	422	592	378	425	300
ENSMUSG00000081406	chr2	Rps6-ps4	1.03634485	2.70229E-09	1.4415E-08	4.320372055	0.032330411	1	215	193	146	252	170	641	464	360	399	333
ENSMUSG00000034940	chr11	Synrg	-0.8544638	2.73151E-09	1.45653E-08	5.659292187	0.023121157	-1	989	832	879	1190	956	593	583	563	557	633
ENSMUSG00000090112	chr10	Shprh	-1.0538604	2.74461E-09	1.46296E-08	3.401667125	0.030253647	-1	212	185	192	276	193	97	143	84	108	124
ENSMUSG00000037860	chr1	Aim2	2.53184746	2.76444E-09	1.47296E-08	0.96035324	0.14079806	1	5	10	11	11	2	82	63	18	38	54
ENSMUSG00000061288	chr5	Taok3	1.16432572	2.76748E-09	1.47402E-08	3.16347484	0.036857175	1	66	73	82	125	64	226	228	146	164	240
ENSMUSG00000026251	chr1	Chrnd	1.5414801	2.76908E-09	1.47431E-08	3.351822612	0.069248496	1	60	72	83	97	71	234	224	377	125	251
ENSMUSG00000036768	chr9	Kif15	2.59075003	2.77876E-09	1.4789E-08	1.155906109	0.155962434	1	16	9	8	4	6	58	91	34	81	27
ENSMUSG00000043535	chr2	Setx	-0.9469945	2.7908E-09	1.48475E-08	5.284086629	0.028246816	-1	647	634	721	1061	774	399	462	398	372	537
ENSMUSG00000029922	chr6	Mkrn1	0.8429214	2.79704E-09	1.4875E-08	4.681642358	0.021179653	1	269	259	251	328	255	664	509	441	476	604
ENSMUSG00000038201	chr7	Kcna7	-1.1717884	2.83704E-09	1.5082E-08	7.298680703	0.044976294	-1	3172	2917	3274	4382	2613	1018	1670	1726	1372	2044
ENSMUSG00000026915	chr2	Strbp	-1.1603906	2.84029E-09	1.50935E-08	4.104371822	0.040508384	-1	420	318	300	369	346	116	216	134	186	208
ENSMUSG00000087298	chr7	Gm9392	-1.6011996	2.84847E-09	1.51312E-08	1.714984272	0.059245814	-1	76	64	62	96	61	29	22	18	40	19
ENSMUSG00000029178	chr5	Klf3	-1.4280847	2.86429E-09	1.52095E-08	2.632103586	0.054837574	-1	103	125	139	149	142	51	48	32	70	69
ENSMUSG00000034973	chr9	Dopey1	-0.9423457	2.86989E-09	1.52334E-08	3.382309254	0.023173143	-1	193	201	187	257	177	128	115	96	115	124
ENSMUSG00000031821	chr8	Gins2	2.04240065	2.87411E-09	1.525E-08	1.115335948	0.091789231	1	15	8	13	17	6	57	78	38	60	33
ENSMUSG00000027536	chr3	Chmp4c	-3.0289294	2.88507E-09	1.53024E-08	1.964948402	0.239691039	-1	65	68	103	209	77	45	7	4	9	5
ENSMUSG00000031986	chr8	Sprtn	-1.755938	2.90921E-09	1.54245E-08	1.716569632	0.075550014	-1	58	65	84	92	67	14	22	15	33	34
ENSMUSG00000026238	chr1	Ptma	0.99621223	2.91394E-09	1.54438E-08	6.529485457	0.032409735	1	913	818	886	1246	763	2019	2808	1632	1687	1928
ENSMUSG00000027422	chr2	Rrbp1	0.96348945	2.9234E-09	1.5488E-08	6.471747368	0.030291202	1	868	704	763	1283	905	2326	2264	1557	1625	1863
ENSMUSG00000067924	chrX	Cxx1b	0.8996945	2.94836E-09	1.56144E-08	5.034233292	0.025102763	1	411	315	278	382	311	758	627	761	597	718
ENSMUSG00000027805	chr3	Pfn2	-0.9986162	2.95056E-09	1.56201E-08	7.061369544	0.032817035	-1	2844	2609	2393	3405	2091	1262	1794	1137	1308	1786
ENSMUSG00000020422	chr11	Tns3	0.94057859	2.95902E-09	1.56589E-08	4.626610104	0.026897181	1	251	240	221	308	236	607	664	394	401	596
ENSMUSG00000058290	chr15	Espl1	2.07113817	2.96144E-09	1.56658E-08	1.463634184	0.100561297	1	22	17	16	8	10	103	92	44	61	48
ENSMUSG00000003161	chr5	Sri	1.01224163	2.99996E-09	1.58636E-08	4.402317726	0.031009468	1	223	229	178	223	181	668	478	362	432	374
ENSMUSG00000022309	chr15	Angpt1	-1.4747286	3.02324E-09	1.59807E-08	3.513436768	0.064460257	-1	171	220	260	497	135	91	97	90	91	119
ENSMUSG00000031561	chr8	Tenm3	-1.0611206	3.05817E-09	1.61592E-08	3.376025814	0.031077813	-1	176	166	191	282	225	123	118	97	84	124
ENSMUSG00000050029	chrX	Rap2c	-0.9474357	3.06476E-09	1.61878E-08	5.048250301	0.028109087	-1	679	585	575	868	556	284	432	341	331	446
ENSMUSG00000027459	chr2	Fam110a	1.35749228	3.07571E-09	1.62396E-08	2.548105955	0.048045631	1	54	44	46	63	33	165	105	157	101	142
ENSMUSG00000030342	chr6	Cd9	1.7125719	3.08057E-09	1.62591E-08	6.021286096	0.093410489	1	457	436	416	564	391	2279	2774	592	845	1846
ENSMUSG00000052917	chr16	Senp7	-1.2042048	3.11742E-09	1.64474E-08	2.958947377	0.039025602	-1	167	133	140	236	132	58	91	71	66	92
ENSMUSG00000013662	chr19	Atad1	-1.088688	3.12174E-09	1.64613E-08	5.701015524	0.038274987	-1	978	982	1088	1385	855	371	638	458	631	595
ENSMUSG00000030655	chr7	Smg1	-1.0008136	3.12241E-09	1.64613E-08	5.533568861	0.032163625	-1	724	762	953	1270	905	507	602	359	507	550
ENSMUSG00000040785	chr16	Ttc3	-0.8859188	3.1339E-09	1.65156E-08	6.069433352	0.025443024	-1	1346	1167	1143	1627	1223	716	778	668	758	923
ENSMUSG00000091460	chr9	Gm7808	1.76049894	3.14225E-09	1.65534E-08	1.651794024	0.072582345	1	23	21	21	21	15	119	51	76	77	56
ENSMUSG00000032705	chr12	Exd2	-1.1781128	3.14704E-09	1.65724E-08	4.904701422	0.043942874	-1	691	574	602	653	550	188	316	226	371	384
ENSMUSG00000029725	chr5	Ppp1r35	1.46493475	3.14976E-09	1.65742E-08	2.696045505	0.058676181	1	59	43	40	64	46	231	180	118	146	91
ENSMUSG00000070469	chr7	Adamtsl3	-1.3246979	3.14888E-09	1.65742E-08	2.634560484	0.046743154	-1	122	135	121	153	119	74	75	31	58	49
ENSMUSG00000053510	chr4	Nrd1	-0.8640022	3.15195E-09	1.65795E-08	7.366877562	0.024758311	-1	3077	2988	2747	4150	2989	2218	1946	1670	1900	1840
ENSMUSG00000041355	chr3	Ssr2	0.931502	3.19371E-09	1.67928E-08	6.060890937	0.028176554	1	757	656	530	773	695	1705	1571	1308	1374	1192

ENSMUSG00000049401	chr2	Ogfr	0.8355828	3.25125E-09	1.70825E-08	4.991547189	0.021527157	1	356	325	282	431	309	652	645	689	644	671
ENSMUSG00000056342	chr11	Usp34	-0.8710755	3.25053E-09	1.70825E-08	5.837458972	0.02446334	-1	1023	890	1006	1468	1138	691	720	607	613	665
ENSMUSG00000055296	chr4	Tmem245	-0.9293645	3.26005E-09	1.71223E-08	4.882326506	0.026891531	-1	498	551	577	691	549	287	397	272	298	400
ENSMUSG00000026393	chr1	Nek7	-0.8954196	3.27928E-09	1.72169E-08	6.472501265	0.026312332	-1	1843	1522	1495	2300	1509	1020	1127	802	990	1139
ENSMUSG00000093076	chr17	Mir3082	0.87757721	3.28704E-09	1.72511E-08	4.246967906	0.022459697	1	197	184	166	242	202	495	437	326	374	372
ENSMUSG00000026511	chr1	Srp9	1.19082314	3.29404E-09	1.72814E-08	5.284268161	0.045515108	1	352	365	278	415	352	513	999	890	1034	915
ENSMUSG00000020516	chr11	Rps6kb1	-1.0033077	3.29822E-09	1.72968E-08	5.008420147	0.031782339	-1	711	580	603	744	553	263	377	271	388	440
ENSMUSG00000022788	chr16	Fgd4	-1.1341489	3.30195E-09	1.73098E-08	3.618744586	0.037295952	-1	267	221	254	261	236	96	158	89	123	157
ENSMUSG00000058905	chr5	Gm10051	1.87832418	3.32424E-09	1.74202E-08	1.116264541	0.074625236	1	15	15	10	14	10	84	34	46	43	55
ENSMUSG00000021893	chr14	Capn7	-0.982233	3.32815E-09	1.74341E-08	5.631712424	0.031123609	-1	994	989	858	1237	839	441	590	444	655	572
ENSMUSG00000084535	chr12	Mir1906-1	2.48552924	3.37445E-09	1.76701E-08	2.847516368	0.174825407	1	66	28	15	16	31	222	92	147	129	397
ENSMUSG00000030577	chr7	Cd22	3.58323489	3.38148E-09	1.77002E-08	1.221651373	0.303382135	1	2	10	3	9	1	13	86	56	33	140
ENSMUSG00000027602	chr2	Map1lc3a	1.03680465	3.3888E-09	1.77319E-08	7.937037304	0.035847075	1	2206	2052	2236	3373	2202	5579	4032	5392	4862	7007
ENSMUSG00000005575	chr7	Ube2m	0.89724941	3.41269E-09	1.78502E-08	6.796421753	0.026614172	1	1204	1097	1056	1404	1029	2350	2186	2559	2190	2456
ENSMUSG00000026459	chr1	Myog	1.87517434	3.43781E-09	1.79749E-08	6.362477344	0.111832017	1	777	557	473	423	365	2967	1904	3251	734	1669
ENSMUSG00000035847	chrX	Ids	-0.9942411	3.44616E-09	1.80118E-08	4.456759038	0.030374393	-1	386	379	390	574	448	220	267	188	194	329
ENSMUSG00000005481	chr8	Ddx39	1.16154819	3.462E-09	1.80878E-08	4.522467336	0.042329398	1	199	163	164	337	207	606	648	471	528	325
ENSMUSG00000081058	chr3	Hist2h3c2	1.67299997	3.49104E-09	1.82327E-08	1.484488888	0.061937316	1	21	11	18	28	17	69	54	70	80	55
ENSMUSG00000020814	chr11	Mxra7	0.94390678	3.53214E-09	1.84267E-08	4.089314624	0.026021058	1	165	174	154	218	152	405	399	397	288	323
ENSMUSG00000055022	chr15	Cntn1	-2.6143713	3.52965E-09	1.84267E-08	-0.190509789	0.094049358	-1	14	16	18	23	27	2	4	4	5	2
ENSMUSG00000071253	chr10	Slc25a16	-1.1017452	3.53093E-09	1.84267E-08	4.514810826	0.037889651	-1	515	438	395	551	419	159	261	185	247	326
ENSMUSG00000004846	chr5	Plod3	1.2059256	3.57444E-09	1.86405E-08	5.32844881	0.046916961	1	349	320	331	409	387	1588	971	761	642	674
ENSMUSG00000025395	chr10	Prim1	1.94544599	3.58291E-09	1.86776E-08	1.355173365	0.088731999	1	21	14	9	17	13	58	88	45	81	40
ENSMUSG00000086604	chr7	Gm15510	4.08381723	3.63462E-09	1.89401E-08	-0.554054998	0.222428477	1	1	1	1	1	0	2	24	15	24	18
ENSMUSG00000021815	chr14	Mss51	-2.5152891	3.6629E-09	1.90804E-08	5.994258518	0.192675976	-1	2215	1709	1832	912	1205	876	200	170	94	283
ENSMUSG00000024471	chr18	Myot	-1.0283522	3.67357E-09	1.91288E-08	9.419861243	0.035604893	-1	11033	11519	12178	22351	12673	7849	7630	6475	7897	6914
ENSMUSG00000036095	chr12	Dgkb	-2.6156831	3.68262E-09	1.91688E-08	-0.337204632	0.083905024	-1	17	18	20	18	14	0	3	4	4	4
ENSMUSG00000102051	chr15	l830127L07Rik	6.19558209	3.69787E-09	1.9241E-08	-0.059354433	0.513097001	1	0	0	1	0	0	64	44	2	21	3
ENSMUSG00000082745	chr1	Gm15181	-3.8944297	3.72691E-09	1.93849E-08	0.859811098	0.335378132	-1	39	35	49	65	53	17	0	1	0	0
ENSMUSG00000075122	chr16	Cd80	3.07351839	3.74891E-09	1.94921E-08	0.61011536	0.201333812	1	6	3	3	4	5	93	40	9	37	27
ENSMUSG00000025571	chr11	Tnrc6c	-0.9338826	3.78299E-09	1.96547E-08	4.954553711	0.0275278	-1	497	520	517	902	621	417	316	270	351	389
ENSMUSG00000031637	chr8	Lrp2bp	-1.630157	3.78265E-09	1.96547E-08	3.79546441	0.081614755	-1	557	280	308	210	180	91	116	87	107	149
ENSMUSG00000005150	chr8	Wdr83	0.91302007	3.79674E-09	1.97188E-08	4.423702549	0.025175443	1	198	200	224	261	216	502	456	501	361	451
ENSMUSG00000035352	chr11	Ccl12	3.76565511	3.83767E-09	1.99186E-08	1.580161599	0.34286764	1	9	3	4	11	2	278	67	28	56	19
ENSMUSG00000044712	chr12	Slc38a6	1.36009793	3.83806E-09	1.99186E-08	2.420128395	0.047151261	1	50	44	34	43	45	176	100	115	99	126
ENSMUSG00000040711	chr11	Sh3pxd2b	1.26963082	3.84384E-09	1.99412E-08	4.832045722	0.051543049	1	204	198	186	308	339	1028	587	573	413	718
ENSMUSG00000093661	chr6	Eif4e3	-0.9961591	3.94929E-09	2.04806E-08	4.992607061	0.031597308	-1	679	605	518	735	613	242	384	335	354	403
ENSMUSG00000031609	chr8	Sap30	1.09271772	3.96905E-09	2.05754E-08	3.571288112	0.034360177	1	123	111	80	131	114	204	312	256	236	292
ENSMUSG00000025192	chr19	Entpd7	1.87831375	3.99884E-09	2.07222E-08	1.891186213	0.091806068	1	28	21	15	31	19	164	106	49	86	60
ENSMUSG00000024642	chr19	Tle4	-1.0475876	4.12437E-09	2.13648E-08	4.394510813	0.034235807	-1	341	427	431	506	392	249	227	202	142	302
ENSMUSG00000058488	chr5	Kl	-2.5003945	4.12736E-09	2.13723E-08	-0.042677112	0.100664747	-1	23	23	22	15	25	8	3	1	4	5
ENSMUSG00000020018	chr10	Snrpf	1.06834551	4.1344E-09	2.14009E-08	4.751388034	0.036271403	1	244	234	217	351	252	703	726	521	642	371
ENSMUSG00000034354	chr11	Mtmr3	-0.8489409	4.14279E-09	2.14364E-08	6.242420694	0.023818535	-1	1408	1283	1392	1827	1352	980	863	748	827	1005
ENSMUSG00000026082	chr1	Rev1	-0.999034	4.15147E-09	2.14733E-08	4.235313788	0.030497101	-1	348	384	354	478	304	171	218	148	235	247
ENSMUSG00000030432	chr7	Rpl28	1.09483435	4.15794E-09	2.14988E-08	7.730889518	0.040317234	1	1987	1777	1684	2696	2011	7526	4429	4470	3388	4075
ENSMUSG00000017607	chr11	Tns4	2.79333443	4.16363E-09	2.15203E-08	-0.412187312	0.085243526	1	0	2	3	3	3	20	20	11	16	21
ENSMUSG00000000184	chr6	Ccnd2	-0.8811526	4.1773E-09	2.15769E-08	4.347215348	0.023411925	-1	340	391	372	475	376	255	283	192	193	246
ENSMUSG00000030788	chr7	Rnf141	-0.9027085	4.17766E-09	2.15769E-08	4.525022754	0.025052137	-1	473	446	352	512	441	272	318	197	263	258
ENSMUSG00000052139	chr5	Bre	0.82389119	4.18998E-09	2.16325E-08	4.73659828	0.020822302	1	298	275	240	382	243	632	501	529	506	604
ENSMUSG00000020044	chr10	Timp3	-0.9229713	4.19866E-09	2.16693E-08	6.941380489	0.028589029	-1	2302	2281	2280	2643	2408	1750	1587	1048	1164	1443
ENSMUSG00000078486	chr4	Perm1	-1.2594618	4.29498E-09	2.21582E-08	7.170526004	0.052975964	-1	1906	2549	3147	5418	2467	1123	1490	1400	1524	1329
ENSMUSG00000031954	chr8	Cfdp1	0.85765171	4.30417E-09	2.21974E-08	4.685097094	0.022674333	1	281	269	241	356	218	652	569	491	527	459
ENSMUSG00000056966	chr5	Gjc3	-1.7995375	4.32432E-09	2.22931E-08	1.32640661	0.075227505	-1	52	51	50	75	52	15	24	7	13	29
ENSMUSG00000067071	chr1	Hes6	1.22984673	4.32748E-09	2.23012E-08	4.332634413	0.047653001	1	212	193	184	173	123	621	382	574	317	396
ENSMUSG00000025381	chr10	Cnpy2	0.84976437	4.34231E-09	2.23694E-08	5.049348444	0.022746945	1	412	341	320	377	299	830	736	625	666	614
ENSMUSG00000074283	chr7	Zfp109	-2.640972	4.35227E-09	2.24124E-08	0.025340146	0.115999188	-1	15	30	19	29	24	1	3	1	7	8
ENSMUSG00000038204	chr5	Asb10	-1.1111324	4.35595E-09	2.24231E-08	6.026499073	0.040907538	-1	1504	1395	1094	1540	1109	556	723	551	935	570
ENSMUSG00000020407	chr11	Upp1	2.33767621	4.3942E-09	2.26117E-08	0.702839251	0.113125145	1	10	7	6	7	6	63	27	57	30	25
ENSMUSG00000012848	chr7	Rps5	0.94253765	4.42496E-09	2.27616E-08	8.331610122	0.030204978	1	3616	3110	2875	3793	3027	9335	6855	6163	6536	5886
ENSMUSG00000028364	chr4	Tnc	1.79487218	4.42733E-09	2.27654E-08	5.687253813	0.104054794	1	476	242	238	539	261	1656	1186	2212	661	727
ENSMUSG00000097799	chr2	Gm26899	-3.8300878	4.44223E-09	2.28336E-08	1.219875174	0.345183465	-1	19	28	27	106	134	3	3	11	0	6
ENSMUSG00000061755	chr5	Bod1l	-1.0470115	4.44552E-09	2.28421E-08	4.525249825	0.03454918	-1	416	401	415	619	463	192	247	191	239	352
ENSMUSG00000024083	chr17	Pja2	-1.0099375	4.50429E-09	2.31356E-08	7.008173904	0.034347911	-1	2554	2298	2167	3469	2422	1127	1409	1363	1177	1876
ENSMUSG00000033751	chr8	Gadd45gip1	0.96589338	4.5188E-09	2.32016E-08	5.234904254	0.030223257	1	343	311	375	549	334	666	758	824	854	921
ENSMUSG00000030107	chr6	Usp18	1.75490531	4.55158E-09	2.33613E-08	2.101158203	0.081408431	1	40	23	28	27	22	88	131	67	73	167

ENSMUSG00000083325	chr2	Gm14121	-1.7905533	4.64592E-09	2.38368E-08	0.879527695	0.060314102	-1	44	32	39	50	36	13	9	9	18	14
ENSMUSG00000039055	chr11	Eme1	2.76297745	4.67796E-09	2.39924E-08	-0.248212943	0.100883784	1	3	4	3	3	0	25	22	24	17	12
ENSMUSG00000028796	chr4	Phc2	0.95538266	4.70318E-09	2.41128E-08	5.20683944	0.029568644	1	346	313	340	540	346	1158	764	711	691	672
ENSMUSG00000022195	chr15	6030458C11Rik	-0.8820149	4.79687E-09	2.45798E-08	5.255735515	0.02513783	-1	781	701	685	828	677	476	548	336	438	398
ENSMUSG00000056071	chr3	S100a9	5.22035573	4.79777E-09	2.45798E-08	2.210663744	0.603273358	1	2	6	2	6	1	530	58	9	136	13
ENSMUSG00000028885	chr4	Smpdl3b	1.7346382	4.80677E-09	2.46169E-08	1.971603347	0.078360646	1	32	27	30	25	15	101	125	110	79	57
ENSMUSG00000047907	chr2	Tshz2	-0.8883652	4.8107E-09	2.4628E-08	3.724094518	0.022190498	-1	246	243	240	303	236	182	152	119	148	153
ENSMUSG00000074903	chr7	Gm2058	-2.6046197	4.81579E-09	2.4645E-08	-0.27981562	0.088436774	-1	22	15	21	17	16	3	1	2	4	6
ENSMUSG00000021460	chr13	Auh	-0.9324391	4.81974E-09	2.46562E-08	5.550271991	0.028551062	-1	905	991	889	1066	719	624	472	389	600	550
ENSMUSG00000037989	chr13	Wnk2	-1.2204625	4.86265E-09	2.48666E-08	5.801712697	0.049461449	-1	1048	1015	936	1542	1291	336	652	405	586	743
ENSMUSG00000022346	chr15	Myc	1.55064473	4.97199E-09	2.54164E-08	3.206651869	0.071801076	1	89	68	61	62	61	337	296	107	226	157
ENSMUSG00000098598	chr15	Pou6f1	-2.1295311	4.97944E-09	2.54452E-08	1.156912712	0.107153282	-1	38	42	59	71	49	10	13	4	25	12
ENSMUSG00000032511	chr9	Scn5a	3.07112199	5.02861E-09	2.56871E-08	1.365978491	0.23509938	1	9	6	2	9	12	83	124	98	30	18
ENSMUSG00000031226	chrX	Pbdc1	1.25775338	5.06976E-09	2.58878E-08	3.793677431	0.048437571	1	118	97	97	162	132	518	380	213	260	235
ENSMUSG00000080776	chr11	Gm12174	1.25817886	5.09982E-09	2.60318E-08	3.274406929	0.046127479	1	93	94	79	88	63	343	156	166	221	223
ENSMUSG00000021036	chr12	Sptlc2	1.04055412	5.22352E-09	2.66535E-08	4.289797262	0.033874844	1	169	184	162	264	175	649	464	294	392	363
ENSMUSG00000024440	chr18	Pcdh12	-1.3594502	5.239E-09	2.67227E-08	3.292878097	0.055215028	-1	153	225	203	357	125	86	71	100	76	109
ENSMUSG00000096252	chr13	Tes3-ps	-2.1280177	5.27384E-09	2.68906E-08	0.854995129	0.097159374	-1	51	36	39	47	34	2	11	7	15	16
ENSMUSG00000038521	chr6	C1s1	1.05540993	5.32821E-09	2.71579E-08	6.003862502	0.037283887	1	545	638	521	647	719	1330	1249	1338	1194	1951
ENSMUSG00000034673	chr17	Pbx2	0.91881542	5.33605E-09	2.7188E-08	4.985334041	0.027144049	1	369	314	296	404	251	959	598	567	561	717
ENSMUSG00000022961	chr16	Son	-0.8888361	5.37064E-09	2.73543E-08	7.060572437	0.026916605	-1	2565	2177	2273	3404	2559	1501	1636	1304	1409	1802
ENSMUSG00000029363	chr5	Rfc5	1.59264352	5.40002E-09	2.74939E-08	2.122751724	0.067029028	1	35	41	15	40	26	119	138	78	106	77
ENSMUSG00000030204	chr6	Ddx47	0.79106099	5.42473E-09	2.76096E-08	4.978585799	0.019681991	1	352	354	310	412	288	709	719	578	579	672
ENSMUSG00000030102	chr6	Itpr1	-0.9229385	5.4454E-09	2.77047E-08	4.090609121	0.025691719	-1	263	316	287	487	316	206	208	178	168	196
ENSMUSG00000001229	chr17	Dpp9	-0.9112243	5.45867E-09	2.77622E-08	5.312127644	0.027146512	-1	671	651	652	1099	815	493	452	432	466	399
ENSMUSG00000063628	chr18	Gm7665	2.46847568	5.50623E-09	2.79939E-08	0.117248174	0.101940741	1	6	4	2	4	5	35	37	24	21	14
ENSMUSG00000020605	chr12	Hs1bp3	1.07330112	5.52004E-09	2.80539E-08	3.634479854	0.034004883	1	129	121	79	156	109	394	256	216	216	293
ENSMUSG00000000823	chr2	Znf512b	-0.8190903	5.52336E-09	2.80605E-08	4.374854143	0.020221024	-1	354	375	369	514	359	258	235	219	238	270
ENSMUSG00000026672	chr2	Optn	-1.0122972	5.59366E-09	2.84073E-08	5.288579674	0.033777306	-1	623	722	668	1229	705	407	395	317	493	498
ENSMUSG00000002266	chr7	Zim1	-2.1709264	5.67139E-09	2.87916E-08	2.224659617	0.134358856	-1	126	105	88	59	165	10	32	25	26	42
ENSMUSG00000026833	chr2	Olfm1	1.37472364	5.84262E-09	2.96502E-08	3.838844602	0.059318659	1	97	79	99	174	143	544	315	343	263	217
ENSMUSG00000021221	chr12	Dpf3	-1.10623	5.86363E-09	2.97459E-08	3.220642477	0.034595809	-1	185	177	173	247	161	68	99	91	105	111
ENSMUSG00000024579	chr18	Pcyox1l	1.89419013	5.90446E-09	2.99422E-08	1.429036275	0.087308443	1	7	11	19	28	16	82	60	82	52	51
ENSMUSG00000025968	chr1	Ndufs1	-1.0349504	5.91547E-09	2.99872E-08	8.904559709	0.037000752	-1	8612	9840	10086	13006	6788	4489	5017	4447	5762	5850
ENSMUSG00000053113	chr11	Socs3	2.05555569	5.95043E-09	3.01534E-08	4.012997327	0.132809571	1	129	107	63	113	54	990	368	189	418	202
ENSMUSG00000025402	chr10	Nab2	1.12359766	5.97197E-09	3.02516E-08	3.85997471	0.038723074	1	159	117	129	172	101	486	344	246	314	235
ENSMUSG00000047146	chr10	Tet1	-1.3685727	6.01622E-09	3.04648E-08	3.027363751	0.054959061	-1	161	209	168	199	127	54	61	70	63	118
ENSMUSG00000021978	chr14	Extl3	-0.8391251	6.08677E-09	3.08108E-08	6.102321785	0.023702209	-1	1349	1220	1189	1461	1313	836	849	712	780	842
ENSMUSG00000028527	chr4	Ak4	-1.1174632	6.15166E-09	3.1128E-08	3.742593851	0.037964741	-1	306	286	224	278	254	162	156	112	164	90
ENSMUSG00000030281	chr6	Il17rc	1.48901782	6.15664E-09	3.1142E-08	2.380679988	0.060163423	1	34	37	45	40	40	135	107	161	115	86
ENSMUSG00000020627	chr12	Klhl29	-1.4397733	6.19687E-09	3.13341E-08	2.220261106	0.054765453	-1	123	93	115	95	67	54	40	36	37	34
ENSMUSG00000005763	chr1	Cd247	3.37962588	6.33263E-09	3.2009E-08	-0.484671028	0.145787058	1	3	2	2	0	0	7	15	23	21	19
ENSMUSG00000031987	chr8	Egln1	-0.9741777	6.37843E-09	3.22288E-08	7.476449929	0.032763227	-1	2794	3018	3196	5712	3174	2019	1936	1773	1998	2071
ENSMUSG00000078861	chr2	Zfp931	-1.7302709	6.38539E-09	3.22523E-08	1.558841932	0.073200852	-1	70	58	63	88	49	11	21	17	34	23
ENSMUSG00000009569	chr16	Mkl2	-0.9494272	6.40588E-09	3.23442E-08	5.245709065	0.029795751	-1	740	635	727	863	740	344	539	370	372	481
ENSMUSG00000027763	chr3	Mbnl1	-1.0665495	6.43823E-09	3.24958E-08	7.755711928	0.039278428	-1	4355	3578	3811	5738	4423	1892	2571	1549	2630	2761
ENSMUSG00000041797	chr11	Abca9	-1.0403578	6.47247E-09	3.26568E-08	4.511120263	0.034913269	-1	368	455	483	462	480	242	226	209	199	341
ENSMUSG00000037474	chr1	Dtl	1.8933195	6.51225E-09	3.28456E-08	1.440034646	0.087329292	1	21	17	16	13	13	69	101	60	63	37
ENSMUSG00000026622	chr1	Nek2	2.09113342	6.6224E-09	3.33891E-08	1.466783587	0.10986349	1	23	15	14	11	10	69	124	52	60	42
ENSMUSG00000041415	chr12	Dicer1	-0.8599331	6.62835E-09	3.34071E-08	5.741018099	0.02479244	-1	1047	944	869	1173	1083	666	654	516	543	731
ENSMUSG00000100801	chr5	Gm15459	-2.0609031	6.63346E-09	3.34208E-08	7.090658163	0.138927892	-1	3601	2832	2583	4097	3331	2438	559	515	448	526
ENSMUSG00000028992	chr4	Nmnat1	-0.9659275	6.63808E-09	3.3432E-08	4.22597931	0.029112207	-1	385	333	330	486	313	167	218	167	252	220
ENSMUSG00000002326	chr14	Gmpr2	1.31116588	6.6545E-09	3.34906E-08	2.493916073	0.045771209	1	48	48	51	52	35	160	156	88	130	109
ENSMUSG00000041638	chr5	Gcn1l1	-0.8790896	6.65316E-09	3.34906E-08	5.327019313	0.025526108	-1	704	627	653	1140	786	521	492	421	405	470
ENSMUSG00000093575	chr16	Gm20695	-1.3401065	6.90684E-09	3.4748E-08	2.788214882	0.051354051	-1	121	159	150	170	125	47	77	40	78	72
ENSMUSG00000022200	chr15	Golph3	-1.0204374	6.93252E-09	3.48647E-08	5.691018106	0.035211876	-1	986	876	922	1318	1059	455	692	428	475	738
ENSMUSG00000095306	chr8	Gm21807	-2.0980995	7.01451E-09	3.52643E-08	0.205769459	0.068710617	-1	24	27	21	34	21	11	4	6	4	7
ENSMUSG00000026223	chr1	Itm2c	0.99189052	7.03697E-09	3.53645E-08	6.097518265	0.033522997	1	800	665	673	698	553	2076	1285	1385	1143	1599
ENSMUSG00000049734	chr9	Trex1	0.85073909	7.0396E-09	3.5365E-08	4.407165393	0.02237183	1	257	225	190	252	196	542	433	423	395	427
ENSMUSG00000026536	chr1	Mnda	1.82587823	7.09843E-09	3.56477E-08	1.707537144	0.08613459	1	12	16	27	28	19	61	96	57	113	68
ENSMUSG00000046056	chr7	Sbsn	2.3361919	7.13508E-09	3.58189E-08	1.199956121	0.136121808	1	7	12	9	16	9	32	38	59	46	117
ENSMUSG00000035401	chr7	2210018M11Rik	-1.0778327	7.20835E-09	3.61608E-08	3.619577173	0.03486772	-1	238	203	255	315	224	101	107	146	139	140
ENSMUSG00000067279	chr19	Ppp1r3c	-1.2441983	7.20635E-09	3.61608E-08	7.378278646	0.053376565	-1	2780	2117	3430	4310	4700	2118	1424	1167	1742	1669
ENSMUSG00000025572	chr11	Tmc6	1.22900094	7.2523E-09	3.63552E-08	3.032293377	0.043350643	1	72	77	69	80	59	292	146	163	143	186
ENSMUSG00000029581	chr5	Fscn1	1.1616433	7.25213E-09	3.63552E-08	5.661962178	0.045746434	1	482	514	451	552	329	1573	1108	1337	657	1049

ENSMUSG00000027164	chr2	Traf6	-0.8405984	7.4518E-09	3.73418E-08	4.275808797	0.021689016	-1	343	344	362	461	335	244	225	197	193	272
ENSMUSG00000054203	chr1	Ifi205	2.20755319	7.46195E-09	3.73793E-08	0.919960019	0.111986154	1	4	10	13	13	6	40	60	27	69	38
ENSMUSG00000003970	chr15	Rpl8	0.97090017	7.70525E-09	3.85842E-08	8.609649914	0.033106765	1	3875	3478	3263	5268	3910	11765	8774	7491	7591	6895
ENSMUSG00000090389	chr14	Gm7236	-2.3691086	7.7312E-09	3.87003E-08	-0.00956588	0.090100391	-1	14	19	20	39	20	7	6	2	4	4
ENSMUSG00000025423	chr18	Pias2	-0.9137081	7.73557E-09	3.87083E-08	5.396812737	0.027990251	-1	819	749	699	1058	786	390	527	421	444	594
ENSMUSG00000039103	chr3	Nexn	-0.8707926	7.79857E-09	3.90096E-08	8.517290968	0.026712508	-1	7260	6305	6201	9073	6624	4492	4369	3609	4478	4205
ENSMUSG00000049580	chr7	Tsku	1.53401079	7.8553E-09	3.92793E-08	2.359295475	0.064955564	1	35	40	37	40	37	190	113	127	64	117
ENSMUSG00000027104	chr2	Atf2	-0.9530431	7.94672E-09	3.97222E-08	3.937186361	0.027641366	-1	264	325	265	379	266	156	179	126	180	206
ENSMUSG00000032038	chr9	St3gal4	1.29142225	7.97206E-09	3.98346E-08	3.321766602	0.050359122	1	85	95	84	80	77	385	246	153	169	210
ENSMUSG00000070390	chr11	Nlrp1b	3.89033856	7.99178E-09	3.99189E-08	-0.724520579	0.190216214	1	0	0	1	3	0	4	10	20	19	18
ENSMUSG00000039217	chr9	Il18	1.89778278	8.015E-09	4.00206E-08	0.50885951	0.061012545	1	9	9	8	9	5	42	34	23	32	35
ENSMUSG00000020829	chr11	Slc46a1	1.42067775	8.07921E-09	4.03268E-08	1.52922442	0.043426634	1	25	22	17	26	21	77	69	64	52	65
ENSMUSG00000045322	chr9	Tlr9	2.58404875	8.20369E-09	4.09335E-08	0.150040101	0.114084248	1	2	6	3	4	5	21	29	14	27	45
ENSMUSG00000029246	chr5	Ppat	-0.9276344	8.22579E-09	4.10291E-08	4.900158027	0.02839287	-1	685	593	484	635	506	328	338	238	349	427
ENSMUSG00000037805	chr17	Rpl10a	0.88015549	8.31001E-09	4.14345E-08	7.51036209	0.027192844	1	2041	1843	1744	2092	1801	4959	3867	3527	3451	3565
ENSMUSG00000003814	chr8	Calr	1.01989239	8.31463E-09	4.14427E-08	8.160113171	0.036576279	1	2749	2531	2182	3786	2924	7660	7548	4416	6663	5179
ENSMUSG00000035161	chr14	Ints6	-1.220401	8.33457E-09	4.15272E-08	2.662015547	0.040775934	-1	100	126	130	165	128	56	76	58	62	52
ENSMUSG00000024908	chr19	Ppp6r3	-0.8269284	8.34835E-09	4.15811E-08	6.261848027	0.023538717	-1	1354	1345	1346	1928	1366	986	984	810	850	888
ENSMUSG00000030059	chr6	Tmf1	-1.0472238	8.36495E-09	4.16489E-08	3.941175014	0.034229102	-1	328	253	258	396	305	130	159	122	197	202
ENSMUSG00000029759	chr6	Pon3	-0.9398598	8.47781E-09	4.21817E-08	4.754340338	0.029003388	-1	505	575	561	575	405	294	317	222	336	337
ENSMUSG00000036678	chr15	Aaas	1.09599119	8.47799E-09	4.21817E-08	2.942676003	0.033055296	1	65	72	62	91	69	207	191	133	172	140
ENSMUSG00000007783	chr7	Cpt1c	1.510712	8.56987E-09	4.26237E-08	1.685100401	0.053845296	1	28	22	25	18	24	98	69	70	57	79
ENSMUSG00000028444	chr4	Cntfr	-1.2097659	8.67488E-09	4.31306E-08	4.395900498	0.048532108	-1	347	533	442	353	459	301	224	152	145	226
ENSMUSG00000046743	chr3	Fat4	-1.1965669	8.75019E-09	4.34896E-08	3.553455733	0.044640911	-1	307	206	211	265	218	137	88	98	81	178
ENSMUSG00000048546	chr15	Tob2	-1.5518394	8.79424E-09	4.3693E-08	5.890333527	0.082146296	-1	806	996	1697	1293	1653	879	516	261	380	485
ENSMUSG00000025353	chr10	Ormdl2	1.3103498	8.81023E-09	4.37568E-08	2.695110861	0.04870828	1	54	47	48	76	48	224	175	104	127	116
ENSMUSG00000013419	chr9	Zfp651	-0.9642906	8.81647E-09	4.37723E-08	6.54097663	0.03240246	-1	1474	1431	1732	2688	1922	1254	998	816	1048	1057
ENSMUSG00000020810	chr11	Cygb	1.00109598	8.86283E-09	4.39868E-08	4.925364415	0.033437121	1	320	328	252	370	238	915	563	677	440	723
ENSMUSG00000092569	chr18	Gm20544	-2.4507841	8.96647E-09	4.44854E-08	0.057056836	0.101236907	-1	22	30	19	30	17	4	7	1	9	2
ENSMUSG00000020687	chr11	Cdc27	-0.8752271	9.00736E-09	4.46724E-08	4.617369677	0.024722469	-1	500	461	427	570	404	240	334	236	284	312
ENSMUSG00000068823	chr3	Csde1	-0.9571093	9.12572E-09	4.52273E-08	9.230445966	0.032568216	-1	12159	10557	9723	15615	11425	6088	7396	5143	7467	7227
ENSMUSG00000075595	chr11	Zfp652	-0.8886071	9.12471E-09	4.52273E-08	7.75301274	0.027940941	-1	4061	3585	3667	5268	4329	2566	2532	2401	2066	2794
ENSMUSG00000036469	chr8	March1	2.16489977	9.19393E-09	4.55492E-08	0.851170516	0.104620136	1	11	11	10	6	6	57	35	30	28	74
ENSMUSG00000030796	chr7	Tead2	1.41325042	9.24455E-09	4.57838E-08	2.733220157	0.058564224	1	44	50	58	70	43	229	155	177	97	118
ENSMUSG00000080848	chr9	Gm9385	0.85459279	9.33188E-09	4.61999E-08	4.275546783	0.022727116	1	211	213	161	237	198	465	423	367	409	359
ENSMUSG00000054196	chr15	Cthrc1	2.01870423	9.35818E-09	4.63137E-08	3.68833174	0.13027885	1	113	97	73	47	39	550	317	392	106	324
ENSMUSG00000017861	chr2	Mybl2	2.5422036	9.3621E-09	4.63167E-08	0.533336411	0.135465357	1	6	4	8	7	3	31	68	19	41	23
ENSMUSG00000030850	chr7	Ate1	-0.9291092	9.39577E-09	4.64668E-08	5.31522099	0.029231494	-1	807	658	626	1052	769	402	455	347	523	502
ENSMUSG00000006736	chr10	Tspan31	0.84966166	9.54666E-09	4.71963E-08	5.457339804	0.024386145	1	458	492	432	515	423	984	1024	894	757	946
ENSMUSG00000036819	chr11	Jmjd4	-1.1189289	9.61E-09	4.74927E-08	3.585076976	0.038721969	-1	242	194	256	292	229	110	151	75	150	127
ENSMUSG00000024608	chr18	Rps14	0.99019869	9.62507E-09	4.75503E-08	8.391795881	0.034836516	1	3736	3508	3104	3592	2757	10304	6900	6220	7279	6000
ENSMUSG00000038174	chr1	Fam126b	-1.3911121	9.65327E-09	4.76728E-08	2.609849908	0.055752269	-1	117	116	126	166	124	44	69	61	28	68
ENSMUSG00000063047	chr7	Zfp780b	-2.0669218	9.66653E-09	4.77214E-08	0.636939801	0.087960218	-1	32	25	33	41	43	3	14	7	10	11
ENSMUSG00000026627	chr1	Tmem206	1.40334382	9.68141E-09	4.77612E-08	2.287764834	0.053021216	1	46	42	36	36	32	133	126	66	127	113
ENSMUSG00000044337	chr1	Ackr3	-0.8896731	9.67967E-09	4.77612E-08	4.597962703	0.025782183	-1	372	461	503	527	455	335	282	227	247	297
ENSMUSG00000038773	chr18	Kdm3b	-0.826297	9.69897E-09	4.78309E-08	4.747910341	0.022153704	-1	483	459	460	712	459	327	336	250	294	375
ENSMUSG00000031513	chr8	Leprotl1	0.90954015	9.7335E-09	4.79843E-08	4.528684958	0.026768121	1	253	216	204	289	228	692	534	409	382	453
ENSMUSG00000025580	chr11	Eif4a3	0.87603479	9.7602E-09	4.80989E-08	5.243242934	0.025845657	1	433	343	303	532	389	979	853	800	652	716
ENSMUSG00000036779	chr8	Papd5	-0.9070836	9.80362E-09	4.82959E-08	3.832840818	0.024699166	-1	246	244	270	360	259	146	170	143	159	184
ENSMUSG00000040536	chr4	Necab1	-2.3838913	9.80901E-09	4.83054E-08	0.19669961	0.106661593	-1	32	25	32	28	13	5	9	1	5	7
ENSMUSG00000063838	chr7	Cdc42ep5	1.45829889	9.85283E-09	4.85041E-08	2.237199586	0.05811358	1	50	36	30	46	21	127	107	129	100	82
ENSMUSG00000037400	chr3	Atp11b	-0.9030684	9.864E-09	4.8542E-08	4.657003095	0.026701587	-1	491	423	485	587	453	244	358	231	291	304
ENSMUSG00000070737	chr4	Gm12942	1.68831268	9.87351E-09	4.85717E-08	2.024563898	0.079135188	1	26	36	21	47	11	105	83	66	108	129
ENSMUSG00000018554	chr11	Ybx2	-1.6962626	9.96284E-09	4.89939E-08	2.311954684	0.084347562	-1	69	122	126	156	84	70	25	33	35	26
ENSMUSG00000059552	chr11	Trp53	0.95722129	1.00184E-08	4.92498E-08	4.634154879	0.030183372	1	265	235	206	311	238	692	581	569	368	462
ENSMUSG00000033102	chr13	Cdc14b	-1.1600353	1.00324E-08	4.93014E-08	2.664717823	0.036619006	-1	147	128	128	145	94	66	64	49	68	68
ENSMUSG00000090935	chr12	Synj2bp	-0.8985292	1.00646E-08	4.94422E-08	5.575690421	0.027663544	-1	944	900	859	1142	784	462	628	426	584	610
ENSMUSG00000037876	chr10	Jmjd1c	-0.878616	1.00699E-08	4.94509E-08	4.541976539	0.025004544	-1	442	437	388	529	441	248	299	198	279	312
ENSMUSG00000053128	chr9	Rnf26	1.06277205	1.00771E-08	4.94582E-08	3.101082456	0.031978468	1	73	70	86	111	69	222	212	177	141	184
ENSMUSG00000075232	chr10	Amd1	-1.1362791	1.00785E-08	4.94582E-08	6.243836141	0.045101918	-1	1764	1358	1883	1548	1134	630	982	649	891	693
ENSMUSG00000047824	chr3	Pygo2	0.8630894	1.00833E-08	4.94642E-08	4.568206519	0.024034083	1	287	229	211	311	215	679	471	426	449	478
ENSMUSG00000061848	chr15	Gm5805	1.70227583	1.01537E-08	4.97924E-08	2.747450557	0.087637796	1	62	59	39	35	32	266	97	161	182	117
ENSMUSG00000016541	chr15	Atxn10	0.84745848	1.01705E-08	4.98567E-08	5.721848375	0.024649693	1	600	529	429	725	537	1299	1087	1112	997	1033
ENSMUSG00000033623	chr5	Pcgf3	-0.8661416	1.0174E-08	4.98567E-08	5.697204471	0.025773448	-1	942	907	835	1314	1010	590	572	533	557	746
ENSMUSG00000038206	chr8	Fbxo8	-1.052512	1.03387E-08	5.06464E-08	3.742005224	0.034399517	-1	282	303	244	293	210	125	136	124	118	203

ENSMUSG00000022246	chr15	Rai14	1.22140068	1.05957E-08	5.18868E-08	3.12555611	0.044716092	1	82	64	61	102	77	289	249	146	144	166
ENSMUSG00000033436	chrX	Armcx2	1.02712852	1.06726E-08	5.22453E-08	4.035942466	0.033491373	1	178	151	163	182	123	392	364	433	276	309
ENSMUSG00000041120	chr4	Nbl1	1.20096999	1.07758E-08	5.27321E-08	5.375245187	0.049780039	1	392	288	343	478	374	1291	877	1061	459	1055
ENSMUSG00000010095	chr19	Slc3a2	1.11846016	1.08448E-08	5.30509E-08	5.746626755	0.043507088	1	404	469	460	647	538	1998	1273	869	1016	927
ENSMUSG00000015968	chr14	Cacna1d	2.26203909	1.10304E-08	5.39402E-08	0.582183221	0.107795863	1	7	5	8	7	7	62	33	19	22	50
ENSMUSG00000028381	chr4	Ugcg	1.10422229	1.10536E-08	5.40348E-08	4.462682086	0.040647941	1	225	200	212	244	156	750	606	396	344	379
ENSMUSG00000068551	chr6	Zfp467	-1.1607536	1.1081E-08	5.41498E-08	4.672879364	0.045752564	-1	632	473	429	544	527	457	217	177	233	220
ENSMUSG00000095159	chr5	Tubb4b-ps1	-1.9589707	1.11649E-08	5.45408E-08	0.398365523	0.069621713	-1	23	28	25	45	24	7	10	4	9	10
ENSMUSG00000049751	chr12	Rpl36al	0.97194663	1.13909E-08	5.56251E-08	6.545712863	0.03340076	1	1105	888	806	1004	876	2343	2147	1673	2365	1561
ENSMUSG00000092885	chr11	Gm22123	-2.290409	1.14644E-08	5.59646E-08	-0.059077767	0.076100654	-1	22	24	21	22	16	3	5	7	3	5
ENSMUSG00000017491	chr14	Rarb	-1.109859	1.15417E-08	5.63221E-08	3.025372201	0.035560811	-1	172	164	138	185	158	70	99	90	63	92
ENSMUSG00000021180	chr12	Rps6ka5	-1.9312974	1.15496E-08	5.63411E-08	2.118624373	0.108500864	-1	69	138	106	113	73	12	25	24	29	53
ENSMUSG00000040813	chr9	Tex264	0.82841475	1.15849E-08	5.64936E-08	4.917462097	0.022734442	1	350	329	250	376	311	796	578	570	546	669
ENSMUSG00000009073	chr11	Nf2	-0.8170152	1.1748E-08	5.72687E-08	6.30453379	0.023476638	-1	1442	1436	1305	1915	1433	1027	914	875	835	1024
ENSMUSG00000009291	chr10	Pttg1ip	0.88935522	1.17945E-08	5.74755E-08	5.656384468	0.027399356	1	501	519	474	658	482	1423	1065	1063	805	1008
ENSMUSG00000050071	chrX	Bex1	1.56542294	1.19453E-08	5.81901E-08	4.504854009	0.082810821	1	230	110	157	214	144	642	388	938	333	415
ENSMUSG00000086584	chr11	Gm12002	-1.7487106	1.2106E-08	5.89526E-08	1.408114662	0.076879749	-1	50	65	53	76	50	13	18	9	28	27
ENSMUSG00000024792	chr19	Zfpl1	1.00756769	1.2142E-08	5.91074E-08	3.48448826	0.030391245	1	107	115	105	139	83	333	211	215	238	214
ENSMUSG00000100755	chr3	Rps23-ps	0.9071578	1.22542E-08	5.96327E-08	4.197626069	0.026250668	1	197	195	170	217	164	498	459	320	355	319
ENSMUSG00000021965	chr14	Ska3	2.16210503	1.22949E-08	5.98096E-08	0.353194675	0.086501117	1	3	4	7	13	4	36	38	27	30	21
ENSMUSG00000020593	chr12	Lpin1	-1.0514936	1.24929E-08	6.0752E-08	7.10602395	0.039547638	-1	2050	2285	2370	4638	2763	1327	1703	1314	1293	1679
ENSMUSG00000013275	chr1	Slc41a1	-1.0318324	1.27125E-08	6.17984E-08	6.237397974	0.037734343	-1	1146	1559	1668	2001	1189	757	728	945	696	889
ENSMUSG00000053347	chr17	Zfp943	-1.4884226	1.29119E-08	6.27455E-08	3.356036504	0.071201296	-1	231	207	208	283	190	45	140	47	92	111
ENSMUSG00000024026	chr17	Glo1	-1.0945456	1.29169E-08	6.27484E-08	7.148160888	0.042931657	-1	3225	2897	2742	3126	2356	2523	1285	1108	1314	1268
ENSMUSG00000020388	chr11	Pdlim4	1.66729336	1.29696E-08	6.29823E-08	4.309755265	0.093399852	1	136	128	144	159	132	851	393	709	220	281
ENSMUSG00000094638	chr1	Gm21972	0.85050476	1.3028E-08	6.32441E-08	5.763290039	0.025238004	1	675	523	513	671	502	1328	1237	1055	1114	962
ENSMUSG00000048410	chr18	Zfp407	-1.2474141	1.31643E-08	6.38833E-08	2.584328627	0.043903844	-1	131	98	139	144	105	48	53	48	67	68
ENSMUSG00000063236	chr15	1110038F14Rik	0.99517927	1.31989E-08	6.40289E-08	4.218594475	0.032450914	1	216	178	176	205	144	473	327	485	346	370
ENSMUSG00000025464	chr7	Paox	1.2655492	1.32513E-08	6.42611E-08	2.386339308	0.043218335	1	42	44	47	52	37	150	102	120	120	94
ENSMUSG00000025812	chr8	Pard3	-0.9551829	1.32836E-08	6.43954E-08	4.759560095	0.030855533	-1	524	426	476	705	536	251	290	296	253	406
ENSMUSG00000063439	chr7	B9d2	0.98942245	1.34271E-08	6.50683E-08	3.099766772	0.027202539	1	86	90	77	90	76	217	172	166	180	182
ENSMUSG00000039206	chr5	Daglb	1.17953838	1.34383E-08	6.50999E-08	4.555621921	0.047425163	1	209	202	160	275	225	801	449	314	401	735
ENSMUSG00000000374	chr10	Trappc10	-0.9378335	1.35885E-08	6.57822E-08	5.378379905	0.030574061	-1	803	703	775	1057	743	363	497	410	438	611
ENSMUSG00000035713	chr7	Usp35	1.89535911	1.35859E-08	6.57822E-08	1.230159251	0.089969706	1	27	8	5	18	12	57	52	57	52	65
ENSMUSG00000095098	chr19	Ccdc85b	1.02457442	1.36323E-08	6.59711E-08	4.797936641	0.035827432	1	357	296	264	275	164	683	565	588	628	561
ENSMUSG00000024851	chr19	Pitpnm1	1.15422384	1.37762E-08	6.66447E-08	2.944127063	0.038874245	1	65	70	61	95	60	221	134	158	129	215
ENSMUSG00000021598	chr13	Med10	0.99900052	1.38934E-08	6.71885E-08	3.343719783	0.029304557	1	120	90	89	106	91	270	220	169	233	202
ENSMUSG00000026027	chr1	Stradb	-0.8881184	1.40198E-08	6.7776E-08	6.724776797	0.028320658	-1	2100	1931	1862	2530	1828	1013	1411	1110	1180	1319
ENSMUSG00000078779	chr7	Zfp59	-2.4612534	1.40651E-08	6.79717E-08	0.310170571	0.128480887	-1	26	13	35	36	33	3	3	3	7	12
ENSMUSG00000005470	chr8	Asf1b	1.89476119	1.41587E-08	6.84005E-08	1.743123181	0.09848567	1	24	23	16	19	18	113	115	57	92	37
ENSMUSG00000098783	chr7	Mir7050	3.2037066	1.42103E-08	6.8626E-08	-0.337780075	0.170642977	1	5	1	0	2	1	24	32	5	18	18
ENSMUSG00000031697	chr8	Orc6	1.38725932	1.42711E-08	6.88955E-08	2.689365395	0.057130324	1	53	35	68	66	38	144	193	126	167	113
ENSMUSG00000038072	chr5	Galnt11	-0.9238278	1.43167E-08	6.90921E-08	4.032189657	0.027228824	-1	312	300	295	386	295	207	200	133	146	238
ENSMUSG00000052730	chr6	Gm5111	3.68815231	1.46557E-08	7.07033E-08	0.853007211	0.320146831	1	3	5	5	2	2	3	60	39	69	77
ENSMUSG00000045776	chr14	Lrtm1	-1.2786444	1.47862E-08	7.13083E-08	6.304652903	0.058318742	-1	1944	1438	1548	1903	1496	480	737	567	679	1303
ENSMUSG00000048442	chr11	Smim5	2.60088107	1.48382E-08	7.15346E-08	1.32225406	0.18308971	1	14	9	12	8	6	51	51	144	36	40
ENSMUSG00000025358	chr10	Cdk2	1.01020419	1.48508E-08	7.15707E-08	3.395109212	0.030458994	1	98	119	98	103	91	250	255	203	232	192
ENSMUSG00000021131	chr12	Erh	0.8845797	1.48857E-08	7.1714E-08	4.82798649	0.02647577	1	338	300	249	348	248	713	734	517	563	477
ENSMUSG00000022090	chr14	Pdlim2	1.3812027	1.49183E-08	7.18462E-08	2.568738599	0.055949881	1	45	51	44	58	41	227	153	109	92	112
ENSMUSG00000036564	chr8	Ndrg4	1.12026089	1.49636E-08	7.20397E-08	2.957575779	0.036693822	1	88	62	59	100	53	200	145	179	142	188
ENSMUSG00000098651	chr2	Mir6999	-2.5167368	1.51492E-08	7.29082E-08	-0.005926761	0.114204487	-1	19	27	31	22	13	1	4	3	7	6
ENSMUSG00000083161	chr11	Gm11427	3.51352132	1.52339E-08	7.32906E-08	-0.376037691	0.187544618	1	1	4	1	1	0	22	16	5	34	18
ENSMUSG00000053168	chr15	9030619P08Rik	3.28589569	1.52741E-08	7.34587E-08	0.793522441	0.260427314	1	5	4	4	2	6	11	29	35	43	116
ENSMUSG00000030208	chr6	Emp1	1.22011449	1.53177E-08	7.36431E-08	7.078353908	0.053636411	1	1455	1109	1098	1574	863	3648	4870	1955	2875	2224
ENSMUSG00000070003	chr8	Ssbp4	0.99953223	1.5468E-08	7.43399E-08	4.026916004	0.032330255	1	147	156	184	193	122	490	360	251	334	342
ENSMUSG00000024803	chr19	Ankrd1	2.81812119	1.55617E-08	7.47647E-08	5.878124376	0.255982412	1	467	152	223	163	76	4585	1739	1182	714	497
ENSMUSG00000021549	chr13	Rasa1	-1.1339443	1.5658E-08	7.51756E-08	4.069027201	0.042901628	-1	374	353	294	419	275	143	206	94	213	198
ENSMUSG00000098269	chr17	Mir8094	0.91855923	1.56569E-08	7.51756E-08	4.130354234	0.027301544	1	201	139	152	217	188	463	416	344	316	324
ENSMUSG00000061175	chr3	Fnip2	1.29159687	1.57414E-08	7.55502E-08	3.444207679	0.053903298	1	70	92	80	141	86	312	309	121	211	312
ENSMUSG00000064351	chrMT	mt-Co1	-1.2901923	1.57532E-08	7.55805E-08	14.12767984	0.060399654	-1	305175	383993	386709	574885	269277	111333	144707	148846	231242	202475
ENSMUSG00000083716	chr2	Gm13436	1.28926164	1.57842E-08	7.57034E-08	3.140121458	0.052298924	1	72	62	59	119	69	302	161	235	154	156
ENSMUSG00000070462	chr7	Mesdc1	1.07636184	1.58114E-08	7.5808E-08	3.568298477	0.03643776	1	105	100	104	144	110	411	262	196	234	211
ENSMUSG00000022033	chr14	Pbk	2.1200396	1.58225E-08	7.5835E-08	2.073621109	0.133823567	1	25	32	18	21	16	101	204	93	101	39
ENSMUSG00000025779	chr1	Ly96	2.0196249	1.58674E-08	7.60243E-08	0.524835757	0.07852359	1	4	4	11	12	7	39	31	27	42	31
ENSMUSG00000042010	chr5	Acacb	-1.0189938	1.59874E-08	7.65731E-08	7.337458337	0.037794668	-1	2511	2654	2600	5457	3244	1628	1784	1640	1737	1908

ENSMUSG00000038722	chr5	Bud31	0.90516124	1.6094E-08	7.7057E-08	5.464502765	0.028777511	1	530	434	415	514	389	1213	885	803	1018	780
ENSMUSG00000031736	chr8	Crnde	2.94629523	1.62099E-08	7.75853E-08	-0.411652519	0.119950956	1	1	1	3	2	3	9	23	20	22	14
ENSMUSG00000057278	chr6	Snrpg	1.08563692	1.63629E-08	7.82909E-08	3.681667977	0.037647845	1	124	120	100	141	120	378	342	230	280	186
ENSMUSG00000024248	chr17	Cox7a2l	1.01963183	1.63849E-08	7.83425E-08	6.610527623	0.037623004	1	998	1038	946	1082	731	1608	2142	2449	2088	2267
ENSMUSG00000070639	chr5	Lrrc8b	-2.030853	1.63801E-08	7.83425E-08	0.232635399	0.074418314	-1	26	26	23	31	22	6	9	3	4	12
ENSMUSG00000021177	chr12	Tdp1	1.32732784	1.64947E-08	7.88404E-08	2.234861277	0.04775081	1	44	42	24	41	42	123	123	86	111	91
ENSMUSG00000087523	chr11	Gm12319	-1.2421719	1.65204E-08	7.89364E-08	4.982747169	0.054205623	-1	741	638	635	663	600	157	347	272	302	441
ENSMUSG00000087153	chr8	Gm6483	-2.164155	1.65731E-08	7.91613E-08	0.617986613	0.104420229	-1	48	35	27	29	34	4	6	5	14	13
ENSMUSG00000031285	chrX	Dcx	3.17618366	1.66276E-08	7.93944E-08	-0.237391106	0.169373551	1	2	3	2	2	1	17	7	24	16	40
ENSMUSG00000042737	chr3	Dpm3	1.15936623	1.70436E-08	8.1353E-08	3.113685836	0.040628115	1	66	86	72	87	79	295	168	152	186	168
ENSMUSG00000089996	chrX	Tmsb15b2	2.75334791	1.70972E-08	8.15808E-08	-0.566797316	0.089198221	1	1	2	2	5	0	16	18	11	13	19
ENSMUSG00000041757	chr1	Plekha6	-0.9149671	1.72568E-08	8.23142E-08	3.768260608	0.025944724	-1	253	216	229	384	249	149	152	153	159	149
ENSMUSG00000032030	chr9	Cul5	-0.862169	1.74097E-08	8.30153E-08	6.198945103	0.026766944	-1	1483	1306	1202	1803	1295	763	946	735	922	873
ENSMUSG00000030060	chr6	Hmces	1.37437657	1.74328E-08	8.30972E-08	2.730250831	0.057447905	1	33	64	44	84	47	227	154	122	151	117
ENSMUSG00000001517	chr6	Foxm1	1.75402889	1.78774E-08	8.51874E-08	2.249695903	0.09226671	1	46	34	34	24	17	129	184	107	86	76
ENSMUSG00000037486	chr12	Asxl2	-1.0029455	1.80596E-08	8.60262E-08	3.852920479	0.0324606	-1	295	234	252	395	263	130	173	142	123	212
ENSMUSG00000029826	chr6	Zc3hav1	0.95674748	1.81187E-08	8.62733E-08	4.045304706	0.029762884	1	148	175	145	221	145	437	414	229	331	371
ENSMUSG00000032042	chr9	Srpr	-0.9692236	1.81238E-08	8.62733E-08	8.308063766	0.03469772	-1	7318	6015	4734	6493	6543	3563	3752	2594	3598	4048
ENSMUSG00000021738	chr14	Atxn7	-1.0431956	1.83371E-08	8.72587E-08	3.907557665	0.035570817	-1	263	228	259	431	327	126	182	130	169	186
ENSMUSG00000098274	chr16	Rpl24	0.85166458	1.85172E-08	8.80858E-08	7.867700241	0.026824816	1	2668	2352	2028	3227	2217	5793	4975	4569	4790	4431
ENSMUSG00000028496	chr4	Mllt3	-0.9883715	1.85796E-08	8.83524E-08	6.3378094	0.035509495	-1	2023	1437	1258	1856	1453	757	927	684	1041	1001
ENSMUSG00000029207	chr5	Apbb2	-0.8089429	1.86596E-08	8.87027E-08	5.235467841	0.022759244	-1	802	681	678	857	556	438	477	404	461	445
ENSMUSG00000038500	chr17	Prr3	1.53671637	1.87805E-08	8.92472E-08	2.155229512	0.067939073	1	46	36	19	38	26	170	86	100	81	91
ENSMUSG00000019558	chrX	Slc6a8	-0.8480629	1.88614E-08	8.96012E-08	6.839534924	0.026340792	-1	1969	1986	1962	3013	2110	1298	1400	1113	1368	1496
ENSMUSG00000071652	chr19	Ints5	0.85372074	1.89165E-08	8.98324E-08	4.847205952	0.024956738	1	338	275	271	367	273	788	625	564	569	475
ENSMUSG00000028159	chr3	Dapp1	1.49855178	1.89923E-08	9.01617E-08	1.948747842	0.060565662	1	27	23	37	34	23	134	88	73	91	65
ENSMUSG00000054978	chr9	Kbtbd13	-1.1301455	1.91268E-08	9.07697E-08	4.501887371	0.044261236	-1	422	492	481	604	320	166	217	305	228	221
ENSMUSG00000009214	chr2	Tmem8c	3.23711448	1.91623E-08	9.08971E-08	5.288555068	0.32724762	1	199	150	114	28	48	1134	745	2630	186	911
ENSMUSG00000027259	chr2	Adal	-0.9979589	1.91667E-08	9.08971E-08	4.023412493	0.032805831	-1	327	315	289	374	298	138	203	132	215	189
ENSMUSG00000026678	chr1	Rgs5	-0.9065358	1.93354E-08	9.16659E-08	8.332707155	0.030526799	-1	5710	6461	6327	8601	4490	4066	3476	3318	3543	3932
ENSMUSG00000009772	chr1	Nuak2	2.19801954	1.93723E-08	9.18038E-08	1.443048336	0.133968287	1	9	16	13	24	7	138	82	32	42	59
ENSMUSG00000022174	chr14	Dad1	0.92443841	1.93776E-08	9.18038E-08	5.642566046	0.030603502	1	550	461	426	639	495	1564	1087	901	943	882
ENSMUSG00000085888	chr11	Gm12224	-0.9178953	1.94398E-08	9.20675E-08	4.659665102	0.028912982	-1	556	465	470	536	419	301	346	254	306	213
ENSMUSG00000032845	chr18	Alpk2	-1.1360935	1.95306E-08	9.24661E-08	5.468833486	0.046340246	-1	636	681	685	1453	1134	499	460	487	367	441
ENSMUSG00000060519	chr1	Tor3a	1.05760943	1.96337E-08	9.29225E-08	4.184982813	0.037956987	1	184	158	161	237	140	633	400	336	254	398
ENSMUSG00000026069	chr1	Il1rl1	2.66316523	1.96941E-08	9.31769E-08	1.861425622	0.205915022	1	10	21	15	8	14	255	49	57	97	45
ENSMUSG00000038844	chr2	Kif16b	-1.3585597	1.97868E-08	9.35838E-08	5.012043698	0.065621361	-1	704	613	650	814	665	131	324	234	308	468
ENSMUSG00000024063	chr17	Lbh	1.0917606	1.98063E-08	9.36442E-08	4.821814182	0.041997242	1	240	269	225	407	218	941	614	690	408	496
ENSMUSG00000040943	chr3	Tet2	-0.9285222	2.00716E-08	9.48666E-08	4.121201769	0.028566217	-1	275	271	388	424	329	234	196	177	184	184
ENSMUSG00000038633	chr1	Degs1	0.98873984	2.02602E-08	9.57259E-08	5.420746394	0.035003833	1	455	372	356	591	380	1331	1086	585	752	957
ENSMUSG00000020048	chr10	Hsp90b1	1.10961618	2.02856E-08	9.58134E-08	7.894093919	0.045504073	1	2115	2073	1815	3155	2172	6898	6601	3660	5997	3543
ENSMUSG00000071347	chr14	C1qtnf9	-0.8396927	2.04318E-08	9.64712E-08	4.676884446	0.023977997	-1	443	542	448	591	413	367	255	285	292	294
ENSMUSG00000078578	chr3	Ube2d3	-0.9728551	2.046E-08	9.65719E-08	7.491432451	0.035057696	-1	3614	3082	3131	4894	3201	1611	2366	1502	1986	2453
ENSMUSG00000019970	chr10	Sgk1	-0.9929139	2.05078E-08	9.67648E-08	7.135279241	0.036424811	-1	2605	2850	3087	2840	2413	1734	1746	1110	1193	1968
ENSMUSG00000026683	chr1	Nuf2	1.90040949	2.05347E-08	9.68588E-08	1.712139552	0.102114761	1	22	20	25	17	13	103	128	66	69	39
ENSMUSG00000063663	chrX	Brwd3	-1.2879574	2.06139E-08	9.71996E-08	2.204899996	0.045848823	-1	92	100	86	120	80	37	54	37	30	56
ENSMUSG00000040297	chr1	Suco	-0.8553559	2.07597E-08	9.78542E-08	3.670498348	0.022136372	-1	233	231	225	314	214	169	142	124	155	145
ENSMUSG00000038000	chr8	Acd	1.08886509	2.07988E-08	9.80054E-08	3.176090253	0.036273871	1	108	78	69	108	64	267	197	190	179	159
ENSMUSG00000047459	chr2	Dynlrb1	0.85951928	2.08711E-08	9.83131E-08	6.021280061	0.026753584	1	746	685	654	705	619	1714	1249	1276	1328	1272
ENSMUSG00000073433	chr17	Arhgdig	2.2837737	2.1213E-08	9.98896E-08	1.343836108	0.142374691	1	11	7	7	8	26	71	43	96	52	59
ENSMUSG00000089857	chr8	Zfp882	-1.7855681	2.13623E-08	1.00559E-07	0.959633707	0.074388735	-1	42	39	46	58	29	25	12	9	8	14
ENSMUSG00000037103	chr8	Dcaf15	1.07254436	2.1405E-08	1.00726E-07	3.332550491	0.03600334	1	105	91	64	138	85	320	199	168	200	224
ENSMUSG00000042724	chr12	Map3k9	2.62229637	2.14747E-08	1.0102E-07	-0.124567144	0.121727845	1	4	2	2	7	1	33	16	25	10	26
ENSMUSG00000050370	chr19	Ch25h	4.18301196	2.1494E-08	1.01077E-07	0.127482	0.359313304	1	0	1	1	5	0	77	40	14	13	6
ENSMUSG00000035954	chr12	Dock4	-1.2758121	2.17972E-08	1.02468E-07	3.642517764	0.05465743	-1	236	227	241	351	258	64	145	84	129	167
ENSMUSG00000098371	chr16	Gm28037	0.84730248	2.18086E-08	1.02487E-07	7.86933032	0.026824166	1	2668	2359	2034	3242	2228	5792	4975	4570	4791	4431
ENSMUSG00000029440	chr5	Psmd9	0.77964656	2.19606E-08	1.03167E-07	4.553487897	0.020195265	1	257	242	236	321	228	483	492	445	500	484
ENSMUSG00000018830	chr16	Myh11	-1.3853622	2.2045E-08	1.03528E-07	4.982701618	0.068692676	-1	374	483	458	1224	929	318	269	240	244	361
ENSMUSG00000022812	chr16	Gsk3b	-0.9464934	2.26441E-08	1.06306E-07	5.75656265	0.032576397	-1	980	933	903	1473	1049	616	686	598	392	728
ENSMUSG00000070000	chr8	Fcho1	3.08825226	2.27917E-08	1.06963E-07	-0.394507646	0.144365458	1	2	1	3	0	3	32	23	6	15	16
ENSMUSG00000033790	chr7	Tubgcp5	-1.0262383	2.30139E-08	1.0797E-07	3.267885722	0.03241715	-1	168	184	165	259	182	89	113	75	115	120
ENSMUSG00000021254	chr12	Gpatch2l	-0.9588294	2.30862E-08	1.08273E-07	3.803411117	0.029773767	-1	247	270	240	368	247	121	175	124	162	185
ENSMUSG00000030201	chr6	Lrp6	-0.8954814	2.31787E-08	1.0867E-07	6.05500477	0.029381378	-1	1112	1298	1241	1584	1198	1044	757	693	565	764
ENSMUSG00000061273	chrX	Mmgt1	-0.838016	2.33111E-08	1.09254E-07	5.365756362	0.025039974	-1	833	724	682	967	735	442	571	412	514	465
ENSMUSG00000027067	chr2	Ssrp1	0.8663364	2.33522E-08	1.0941E-07	5.687725359	0.02715839	1	565	512	454	701	497	1294	1269	937	1078	857

ENSMUSG00000022359	chr15	Wdyhv1	1.29069523	2.35594E-08	1.10344E-07	2.596815955	0.05017151	1	50	36	50	82	41	178	141	121	149	97
ENSMUSG00000033379	chr4	Atp6v0b	1.10046828	2.35915E-08	1.10457E-07	6.479153894	0.044705452	1	971	894	813	873	651	3256	1910	1412	1913	1569
ENSMUSG00000024194	chr17	Cuta	0.86837182	2.3901E-08	1.11869E-07	5.872479661	0.027461861	1	655	622	532	699	570	1644	1070	1126	1262	1084
ENSMUSG00000043140	chr16	Tmem186	-0.8183241	2.41841E-08	1.13156E-07	4.256406168	0.022026626	-1	404	341	315	436	316	208	233	208	218	254
ENSMUSG00000024927	chr19	Rela	0.86795303	2.43673E-08	1.13975E-07	4.80153666	0.026246814	1	286	282	249	389	267	831	490	546	489	593
ENSMUSG00000034685	chr11	Fam171a2	1.8354264	2.45049E-08	1.1458E-07	2.934559754	0.111098021	1	54	52	38	63	39	227	113	333	78	196
ENSMUSG00000029471	chr5	Camkk2	0.95863192	2.46049E-08	1.1501E-07	3.533360241	0.028630692	1	124	118	104	130	102	286	292	212	251	194
ENSMUSG00000032783	chr15	Troap	2.45772122	2.47037E-08	1.15433E-07	0.282573957	0.123254134	1	8	3	5	3	5	33	42	33	28	12
ENSMUSG00000004285	chr6	Atp6v1f	0.88450348	2.49431E-08	1.16512E-07	5.874119647	0.028600145	1	681	626	546	708	505	1739	1180	953	1231	1149
ENSMUSG00000022885	chr16	St6gal1	1.00339261	2.50331E-08	1.16894E-07	3.547578105	0.03202586	1	85	124	126	146	92	334	246	207	222	259
ENSMUSG00000090157	chr2	Gm16534	-1.5825486	2.51222E-08	1.17271E-07	2.392748207	0.077686117	-1	136	135	114	97	87	36	41	66	26	39
ENSMUSG00000025583	chr11	Rptor	-0.8134623	2.51964E-08	1.17578E-07	5.301576692	0.023576399	-1	687	639	658	1028	750	503	460	465	411	490
ENSMUSG00000025225	chr19	Nfkb2	1.05642052	2.53379E-08	1.18198E-07	4.645115136	0.039564692	1	278	195	212	341	193	885	550	501	399	442
ENSMUSG00000079020	chr15	Slc45a4	-0.8599955	2.54196E-08	1.1854E-07	4.977906273	0.026140726	-1	627	588	506	667	619	407	302	313	332	475
ENSMUSG00000078870	chr2	Gm14410	-1.9361624	2.5555E-08	1.19132E-07	0.532689545	0.078834567	-1	43	33	28	31	23	14	5	8	11	7
ENSMUSG00000019461	chr11	Plscr3	1.13677848	2.55762E-08	1.19191E-07	4.764047932	0.046220366	1	249	276	217	316	206	1048	520	611	400	493
ENSMUSG00000066000	chr4	2610305D13Rik	-1.3959446	2.56168E-08	1.1934E-07	1.754740007	0.05080451	-1	54	79	65	92	64	27	34	25	23	38
ENSMUSG00000043518	chrX	Rai2	-0.9262438	2.56976E-08	1.19677E-07	4.250307416	0.029174479	-1	353	303	316	480	402	190	202	204	189	279
ENSMUSG00000031393	chrX	Mecp2	-0.8294999	2.58965E-08	1.20563E-07	5.144160689	0.024436533	-1	613	632	656	849	618	373	459	353	375	515
ENSMUSG00000078942	chr13	Naip6	2.88770182	2.59232E-08	1.20647E-07	-0.134590699	0.152868625	1	4	2	1	1	5	16	30	8	31	26
ENSMUSG00000051007	chr7	Pddc1	1.02890972	2.59446E-08	1.20706E-07	3.406582215	0.033389381	1	89	104	96	119	103	342	209	202	187	217
ENSMUSG00000097352	chr10	C920009B18Rik	2.59279368	2.62304E-08	1.21996E-07	0.392265178	0.146484678	1	5	8	4	4	3	60	38	12	36	20
ENSMUSG00000101678	chr5	Gm29609	-1.0566078	2.62556E-08	1.22072E-07	4.71679403	0.039778316	-1	568	499	505	584	472	183	309	208	333	349
ENSMUSG00000035900	chr15	Gramd4	-0.8762893	2.63282E-08	1.22369E-07	4.178641644	0.025730086	-1	315	326	295	424	376	204	232	157	210	236
ENSMUSG00000027201	chr2	Myef2	1.25719417	2.64144E-08	1.22729E-07	2.683547987	0.048162755	1	61	48	50	75	44	152	211	132	100	131
ENSMUSG00000030795	chr7	Fus	0.84842585	2.65038E-08	1.23103E-07	6.827380254	0.026931515	1	1324	1156	942	1554	1101	2565	2588	2298	2335	2106
ENSMUSG00000032280	chr9	Tle3	1.04116648	2.65371E-08	1.23217E-07	4.203283877	0.03740401	1	152	157	175	218	187	629	410	371	286	335
ENSMUSG00000029064	chr4	Gnb1	0.85943908	2.70778E-08	1.25686E-07	6.639301779	0.027580006	1	964	1049	959	1311	995	2808	2240	1780	1850	1880
ENSMUSG00000003348	chr10	Mob3a	1.18697362	2.70924E-08	1.25712E-07	3.739537131	0.047582316	1	111	125	135	122	102	524	279	218	226	279
ENSMUSG00000079215	chr5	Zfp664	-0.8258659	2.73057E-08	1.26659E-07	4.783557895	0.023749047	-1	509	494	510	728	398	307	334	278	318	379
ENSMUSG00000060441	chr7	Trim5	3.8611945	2.73428E-08	1.26789E-07	-0.095351508	0.286586495	1	1	4	2	0	0	3	23	30	24	40
ENSMUSG00000060487	chr10	Samd5	-2.8302542	2.75208E-08	1.27572E-07	-0.119450911	0.15252223	-1	26	21	16	28	16	11	0	4	1	0
ENSMUSG00000022299	chr15	Slc25a32	-1.2102532	2.75625E-08	1.27723E-07	2.371515519	0.041516674	-1	92	93	97	142	106	52	58	34	44	63
ENSMUSG00000097697	chr7	4833412C05Rik	3.24334195	2.79088E-08	1.29285E-07	-0.585084577	0.139905322	1	0	5	1	1	0	16	17	23	8	14
ENSMUSG00000045980	chr11	Tmem104	1.11598999	2.79251E-08	1.29318E-07	3.953109727	0.042602777	1	120	126	106	197	176	433	425	203	310	365
ENSMUSG00000026062	chr1	Slc9a2	-1.1572101	2.80925E-08	1.3005E-07	5.532115687	0.049248829	-1	835	826	775	1337	1016	261	513	459	485	593
ENSMUSG00000026972	chr2	Arrdc1	1.42575672	2.82504E-08	1.30737E-07	3.376076382	0.068237745	1	105	105	71	60	66	427	215	169	237	188
ENSMUSG00000021322	chr13	Aoah	2.45671807	2.83408E-08	1.31112E-07	0.005297946	0.104787878	1	5	3	6	1	4	34	15	16	24	31
ENSMUSG00000015757	chr10	Ppil4	-0.8817064	2.83508E-08	1.31115E-07	3.751575103	0.024736829	-1	245	234	259	319	235	180	154	110	165	162
ENSMUSG00000024294	chr18	Mib1	-0.9453931	2.83918E-08	1.31262E-07	5.050327311	0.032224359	-1	725	639	643	695	526	308	460	326	284	468
ENSMUSG00000040998	chr3	Npnt	1.33201259	2.84909E-08	1.31676E-07	4.371106827	0.063466845	1	158	148	160	259	156	377	362	743	304	581
ENSMUSG00000027808	chr3	Serp1	0.89554398	2.85576E-08	1.31941E-07	5.122432439	0.028831846	1	353	329	330	475	330	834	967	502	749	656
ENSMUSG00000021569	chr13	Trip13	2.68064727	2.8661E-08	1.32375E-07	0.711381871	0.181699966	1	6	1	3	11	9	43	75	25	51	17
ENSMUSG00000014599	chr3	Csf1	1.68824057	2.87946E-08	1.32948E-07	5.183994051	0.103004981	1	220	252	221	364	232	1519	1569	336	686	521
ENSMUSG00000047473	chr7	Zfp30	-1.2592327	2.88667E-08	1.33237E-07	2.989477113	0.050927705	-1	150	207	189	185	91	86	67	73	73	78
ENSMUSG00000026404	chr1	Ddx59	-1.0223892	2.89234E-08	1.33455E-07	3.348896213	0.033165388	-1	200	193	166	285	174	139	88	74	115	131
ENSMUSG00000032344	chr9	Mb21d1	2.08707754	2.89431E-08	1.33501E-07	0.357622574	0.083253378	1	3	7	7	9	6	36	32	20	40	23
ENSMUSG00000029638	chr6	Glcci1	-1.1711831	2.89765E-08	1.33611E-07	2.447701989	0.039325854	-1	109	94	96	137	117	65	49	46	41	69
ENSMUSG00000020808	chr11	Fam64a	2.24611076	2.9021E-08	1.33772E-07	1.695876181	0.147266256	1	17	20	19	4	17	93	118	97	71	36
ENSMUSG00000086290	chr4	Snhg12	1.54576974	2.91224E-08	1.34195E-07	2.405244935	0.072959917	1	42	39	40	25	45	188	153	88	115	89
ENSMUSG00000041650	chr14	Pcca	-0.8217378	2.91685E-08	1.34363E-07	5.126682614	0.024095663	-1	608	695	618	852	555	375	436	425	352	461
ENSMUSG00000031749	chr8	St3gal2	-0.8786808	2.92569E-08	1.34727E-07	5.810255528	0.028495083	-1	874	956	988	1551	1082	640	629	571	581	806
ENSMUSG00000024780	chr19	Cdc37l1	-0.9568571	2.93063E-08	1.34909E-07	5.137932086	0.033189922	-1	656	589	653	889	676	283	498	319	423	418
ENSMUSG00000098503	chr11	Gm27937	-2.1499778	2.96664E-08	1.36522E-07	-0.064008879	0.074332445	-1	17	21	20	25	20	6	4	2	8	5
ENSMUSG00000025102	chr7	3110040N11Rik	0.9780809	2.97244E-08	1.36744E-07	3.443816788	0.030013039	1	104	115	99	116	102	221	231	246	251	206
ENSMUSG00000079065	chr5	BC005561	-1.5513408	2.98703E-08	1.3737E-07	1.865595065	0.069100063	-1	85	79	74	92	64	42	47	15	19	26
ENSMUSG00000049303	chr19	Syt12	1.58573837	2.99474E-08	1.37679E-07	1.654883232	0.068547683	1	12	22	24	32	22	64	83	91	67	60
ENSMUSG00000006154	chr7	Eps8l1	7.11110328	3.00108E-08	1.37926E-07	-0.559458824	0.579813508	1	0	0	0	0	0	0	2	30	25	29
ENSMUSG00000053007	chr6	Creb5	-2.2747069	3.02696E-08	1.39069E-07	-0.086569505	0.08900253	-1	15	24	20	19	24	5	7	3	2	6
ENSMUSG00000014355	chr2	Anapc1	-0.8008005	3.04389E-08	1.39801E-07	5.706889427	0.023534153	-1	935	880	934	1260	940	747	694	503	582	595
ENSMUSG00000022906	chr16	Parp9	1.07605763	3.05546E-08	1.40286E-07	3.20738491	0.036491686	1	100	76	80	106	75	157	220	184	184	260
ENSMUSG00000046873	chrX	Mbtps2	-1.0210791	3.06239E-08	1.40558E-07	3.810803373	0.03499641	-1	281	262	224	345	282	114	188	110	148	191
ENSMUSG00000021003	chr12	Galc	1.33729672	3.08349E-08	1.4148E-07	3.049988313	0.058482116	1	51	53	61	89	89	244	196	101	175	249
ENSMUSG00000062373	chr15	Tmem65	-1.1329578	3.09054E-08	1.41757E-07	6.835809215	0.048368084	-1	1452	2199	2327	4124	1846	1006	1272	971	1211	1368
ENSMUSG00000047648	chr10	Fbxo30	-0.9681644	3.1059E-08	1.42415E-07	3.683859797	0.03075283	-1	209	253	219	390	205	143	137	117	128	181

ENSMUSG00000000142	chr11	Axin2	-1.2741236	3.14767E-08	1.44283E-07	2.850864216	0.051731176	-1	112	153	139	259	103	75	70	70	47	78
ENSMUSG00000037679	chr12	Inf2	0.9901215	3.15504E-08	1.44573E-07	4.053573286	0.033311131	1	143	153	180	182	158	526	381	291	273	338
ENSMUSG00000032369	chr9	Plscr1	1.6302499	3.17382E-08	1.45386E-07	1.345794813	0.067113263	1	13	19	15	23	17	78	81	45	37	58
ENSMUSG00000054400	chr8	Cklf	1.97260828	3.17546E-08	1.45414E-07	1.084011217	0.098303652	1	9	8	17	14	11	78	65	36	52	28
ENSMUSG00000099908	chr16	Gm28539	-0.9746442	3.19129E-08	1.46091E-07	4.277514536	0.033122302	-1	445	342	321	412	379	154	256	200	225	220
ENSMUSG00000021302	chr13	Ggps1	-1.0960515	3.20834E-08	1.46823E-07	2.703685781	0.035432197	-1	127	110	117	163	135	83	69	47	58	79
ENSMUSG00000035948	chr10	Acss3	-2.224729	3.22893E-08	1.47669E-07	0.424865625	0.111198722	-1	20	37	33	33	28	1	10	4	10	10
ENSMUSG00000042821	chr2	Snai1	1.85909519	3.22821E-08	1.47669E-07	1.726207216	0.100233521	1	25	11	19	22	24	108	116	85	56	41
ENSMUSG00000035024	chr9	Ncapd3	-1.0687202	3.30843E-08	1.51255E-07	3.093188407	0.035779225	-1	175	173	137	222	149	76	103	62	103	100
ENSMUSG00000097589	chr14	Dleu2	1.04547195	3.32623E-08	1.52019E-07	2.846957074	0.032317726	1	78	64	57	89	57	182	138	133	170	154
ENSMUSG00000032698	chr2	Lmo2	1.03584247	3.34115E-08	1.52651E-07	3.835345081	0.036334293	1	119	140	148	182	104	417	344	200	249	363
ENSMUSG00000046341	chr4	Gm11223	2.31899554	3.35455E-08	1.53213E-07	0.240877798	0.101424458	1	3	5	3	3	11	39	31	28	21	23
ENSMUSG00000018965	chr5	Ywhah	0.89205895	3.37372E-08	1.54038E-07	5.807408651	0.029654844	1	556	498	517	832	542	1607	1348	845	1111	1079
ENSMUSG00000032410	chr9	Xrn1	-0.8717435	3.37943E-08	1.54249E-07	3.933526001	0.02511052	-1	272	291	259	345	293	178	196	127	170	208
ENSMUSG00000008730	chr3	Hipk1	-0.8653183	3.43056E-08	1.56531E-07	5.441632311	0.027608625	-1	702	787	807	1044	831	584	576	368	432	570
ENSMUSG00000026409	chr1	Pfkfb2	-1.0629102	3.44692E-08	1.57226E-07	2.93149257	0.034244355	-1	145	146	158	195	117	68	87	72	73	97
ENSMUSG00000024369	chr17	Nelfe	0.9107135	3.45266E-08	1.57437E-07	3.601843874	0.026430203	1	141	127	109	159	89	300	254	216	272	240
ENSMUSG00000004655	chr6	Aqp1	-1.1078244	3.52353E-08	1.60616E-07	7.918929335	0.046975977	-1	3244	4066	4603	8135	4983	3587	2358	2223	2337	2102
ENSMUSG00000022947	chr16	Cbr3	1.54051306	3.5318E-08	1.6094E-07	1.72880115	0.065716443	1	30	27	10	29	25	109	78	71	58	72
ENSMUSG00000021947	chr14	Cryl1	1.22123318	3.53563E-08	1.61062E-07	2.650685599	0.045234542	1	53	56	48	60	56	221	137	104	118	130
ENSMUSG00000029254	chr5	Stap1	2.99510805	3.54054E-08	1.61234E-07	0.047156116	0.187274212	1	2	3	7	2	0	38	28	6	25	34
ENSMUSG00000047746	chr16	Fbxo40	-0.9851504	3.5545E-08	1.61817E-07	7.951923252	0.037314779	-1	4670	4000	4287	6571	5115	2220	2597	2228	3122	3349
ENSMUSG00000059436	chr12	Max	0.87223057	3.5775E-08	1.62811E-07	4.757265669	0.027120004	1	241	269	248	368	294	815	545	473	484	552
ENSMUSG00000058486	chr6	Wdr91	1.08746003	3.5873E-08	1.63204E-07	3.268623349	0.038204669	1	96	85	78	126	72	255	216	145	160	291
ENSMUSG00000050002	chr13	Idnk	1.18617483	3.59338E-08	1.63427E-07	2.841887579	0.043895434	1	59	72	60	79	50	243	136	136	156	132
ENSMUSG00000044550	chrX	Tceal3	2.51873235	3.61087E-08	1.64169E-07	1.472718659	0.186577458	1	14	10	11	18	6	46	46	162	35	67
ENSMUSG00000020570	chr12	Sypl	-0.8830319	3.6138E-08	1.64249E-07	7.014160683	0.029841228	-1	2553	2186	2170	3333	2329	1259	1689	1236	1469	1756
ENSMUSG00000038615	chr11	Nfe2l1	-0.8299881	3.6186E-08	1.64413E-07	8.876021963	0.026725778	-1	8793	8078	8263	12039	7948	5625	5455	5119	5301	6105
ENSMUSG00000022629	chr15	Kif21a	-1.3165752	3.62915E-08	1.64839E-07	3.59211664	0.059887901	-1	239	203	211	402	238	52	132	122	123	122
ENSMUSG00000037730	chr3	Mynn	-0.960413	3.6534E-08	1.65887E-07	3.349318567	0.029132061	-1	166	197	181	290	169	121	107	92	127	112
ENSMUSG00000024270	chr18	Slc39a6	1.0760114	3.65894E-08	1.66084E-07	3.362747446	0.037606631	1	76	98	100	109	100	313	263	166	205	187
ENSMUSG00000020836	chr11	Coro6	-1.0233059	3.66093E-08	1.66121E-07	6.980421407	0.040036526	-1	1892	2277	2268	4487	2004	1625	1211	1335	1393	1225
ENSMUSG00000081214	chr1	Rpl35a-ps2	1.90008913	3.69354E-08	1.67546E-07	0.874748723	0.084927233	1	15	11	8	12	7	61	35	36	57	29
ENSMUSG00000021557	chr13	Agtpbp1	-0.8444992	3.70529E-08	1.68025E-07	5.293844957	0.026162386	-1	755	639	655	968	744	408	480	383	513	495
ENSMUSG00000064043	chr17	Trerf1	1.40055354	3.85007E-08	1.74533E-07	2.290844061	0.05863073	1	44	22	41	37	48	147	93	91	103	132
ENSMUSG00000026778	chr2	Prkcq	-0.8914383	3.8518E-08	1.74555E-07	6.200632278	0.030155597	-1	1242	1409	1184	1970	1363	859	716	693	943	989
ENSMUSG00000022667	chr16	Cd200r1	2.7110494	3.87257E-08	1.7544E-07	1.00044218	0.20069129	1	6	6	9	4	10	56	85	8	51	66
ENSMUSG00000041225	chr18	Arhgap12	-0.815059	3.92467E-08	1.77742E-07	4.511611478	0.023223441	-1	370	418	397	586	399	281	297	214	244	313
ENSMUSG00000031778	chr8	Cx3cl1	1.8559896	3.95218E-08	1.7893E-07	1.717709376	0.104067195	1	15	13	15	47	15	97	68	114	57	64
ENSMUSG00000031880	chr8	Rrad	2.75922351	3.98927E-08	1.80551E-07	4.089974305	0.257547472	1	146	43	22	98	26	1084	256	669	146	282
ENSMUSG00000047591	chr15	Mafa	-1.2239171	4.00904E-08	1.81387E-07	5.019501111	0.055791542	-1	608	511	559	799	883	208	319	314	249	487
ENSMUSG00000022519	chr16	Srl	-0.9621395	4.0195E-08	1.81753E-07	10.94418538	0.036128847	-1	43350	36971	33928	42029	37039	17015	23508	22748	20213	24919
ENSMUSG00000033902	chr2	Mapkbp1	-0.9192243	4.01973E-08	1.81753E-07	3.699383162	0.027828	-1	220	223	261	285	260	183	142	138	113	155
ENSMUSG00000048416	chr3	Mlf1	-1.3950041	4.04988E-08	1.83057E-07	7.94454549	0.074202048	-1	5443	5438	5362	6202	4133	1022	2287	1644	2902	3119
ENSMUSG00000026608	chr1	Kctd3	-0.8741722	4.05265E-08	1.83123E-07	4.480747551	0.027059771	-1	461	354	431	491	401	225	284	198	267	307
ENSMUSG00000035764	chr16	Fbxo45	-0.8521392	4.06736E-08	1.83728E-07	4.686730241	0.0259427	-1	500	458	409	678	438	257	303	248	324	358
ENSMUSG00000072949	chr12	Acot1	1.88132203	4.0709E-08	1.83829E-07	0.277676026	0.062021677	1	5	7	6	11	5	28	26	25	26	33
ENSMUSG00000082361	chr5	Btc	-2.8149997	4.12998E-08	1.86436E-07	0.016839105	0.171204309	-1	36	30	27	14	10	6	1	6	1	4
ENSMUSG00000047557	chr3	Lxn	1.46270839	4.14473E-08	1.87042E-07	2.301796089	0.065439349	1	46	47	45	24	24	150	109	95	100	123
ENSMUSG00000038181	chr5	Chpf2	0.9921105	4.15375E-08	1.87327E-07	4.742451202	0.035975756	1	348	290	212	283	195	836	527	535	439	583
ENSMUSG00000042436	chr11	Mfap4	1.27871419	4.1531E-08	1.87327E-07	6.49962669	0.062308404	1	955	806	760	722	648	2788	1799	2580	982	2346
ENSMUSG00000042444	chr9	Fam63b	-0.8173607	4.17722E-08	1.88325E-07	4.899573276	0.024116784	-1	527	535	485	777	526	340	328	292	353	447
ENSMUSG00000066944	chr17	4921513D11Rik	-2.8256117	4.19385E-08	1.89014E-07	-0.465491154	0.131755174	-1	11	17	24	10	17	1	3	2	1	5
ENSMUSG00000003200	chr17	Sh3gl1	0.85818669	4.20571E-08	1.89488E-07	4.448869789	0.025878977	1	244	241	212	259	192	590	499	384	454	367
ENSMUSG00000054277	chr15	Arfgap3	0.87925911	4.23323E-08	1.90666E-07	3.573705222	0.024491586	1	141	131	102	141	103	295	252	214	216	274
ENSMUSG00000063605	chr8	Ccdc102a	1.03755024	4.23691E-08	1.9077E-07	2.948413742	0.033104503	1	84	59	63	102	65	211	140	163	156	164
ENSMUSG00000001300	chr8	Efnb2	-0.9993534	4.24874E-08	1.91241E-07	3.263692122	0.032043349	-1	173	203	175	248	150	137	106	83	75	121
ENSMUSG00000028552	chr4	Eps15	-0.8230334	4.26362E-08	1.91849E-07	6.092995183	0.025765065	-1	1393	1196	1078	1528	1296	898	847	602	810	882
ENSMUSG00000078878	chr2	Gm14305	-1.5434036	4.27205E-08	1.92167E-07	1.637352163	0.067371372	-1	69	73	57	78	57	28	24	9	32	33
ENSMUSG00000041346	chr11	Wrap53	1.31168598	4.28573E-08	1.9272E-07	2.38658107	0.051912952	1	37	41	39	57	44	99	114	152	118	102
ENSMUSG00000040254	chr5	Sema3d	-1.4436913	4.2892E-08	1.92814E-07	1.199173742	0.047877236	-1	50	47	42	63	38	25	21	19	14	17
ENSMUSG00000000439	chr6	Mkrn2	-0.7845026	4.33891E-08	1.94923E-07	5.445032234	0.022820828	-1	813	719	758	1117	723	543	525	446	527	568
ENSMUSG00000036932	chrX	Aifm1	-0.9432785	4.33869E-08	1.94923E-07	5.541471564	0.03353841	-1	796	922	924	1252	696	435	564	413	626	548
ENSMUSG00000024645	chr18	Timm21	-0.9293588	4.38739E-08	1.96975E-07	4.024795745	0.029753192	-1	259	329	305	449	252	162	190	155	198	202
ENSMUSG00000060675	chr19	Pla2g16	-0.8734179	4.38708E-08	1.96975E-07	7.015621234	0.02956392	-1	2051	2511	2316	3667	2065	1449	1510	1324	1580	1578

ENSMUSG00000007836	chr13	Hnrnpa0	0.85314791	4.38963E-08	1.97012E-07	5.847164466	0.027588006	1	605	503	542	885	551	1509	1281	1153	890	1240
ENSMUSG00000022548	chr16	Apod	1.35122351	4.41006E-08	1.97865E-07	5.556986818	0.068975174	1	349	339	379	487	413	2276	829	823	637	1088
ENSMUSG00000029814	chr6	Igf2bp3	2.24467772	4.44945E-08	1.99569E-07	0.856909897	0.131364573	1	17	10	4	9	3	53	61	18	44	51
ENSMUSG00000033014	chr3	Trim33	-0.9619565	4.46771E-08	2.00323E-07	3.59238209	0.030842193	-1	243	212	216	286	222	133	155	81	135	162
ENSMUSG00000007950	chr8	Abhd8	-0.8303909	4.50771E-08	2.02052E-07	4.99393137	0.025279031	-1	614	593	512	707	601	538	343	324	327	350
ENSMUSG00000036632	chr3	Alg5	0.86356557	4.51915E-08	2.025E-07	3.819279401	0.024536475	1	163	140	132	181	125	361	331	227	293	269
ENSMUSG00000022420	chr15	Dnal4	1.03748027	4.52894E-08	2.02874E-07	3.260745478	0.034814869	1	104	111	87	94	63	221	186	216	198	213
ENSMUSG00000021147	chr13	Wdr37	-0.9285291	4.56372E-08	2.04366E-07	4.766588336	0.031583552	-1	554	484	472	678	474	221	382	249	308	361
ENSMUSG00000034707	chr10	Gns	0.99403358	4.58687E-08	2.05336E-07	6.252394789	0.037994558	1	699	711	682	959	747	2378	1591	1159	1165	2120
ENSMUSG00000021133	chr12	4933426M11Rik	-0.8024405	4.65682E-08	2.08401E-07	5.878126357	0.024463576	-1	1123	1118	991	1302	1024	804	762	604	541	805
ENSMUSG00000040940	chr7	Arhgef1	0.84705505	4.67195E-08	2.09012E-07	5.608670137	0.027063635	1	533	439	473	659	496	1450	939	897	925	934
ENSMUSG00000030990	chr7	Pgap2	1.01943149	4.69165E-08	2.09826E-07	4.16741765	0.037253854	1	186	178	159	231	130	283	368	340	447	500
ENSMUSG00000024212	chr17	Mllt1	-0.7773273	4.69486E-08	2.09902E-07	4.946133912	0.021896994	-1	558	557	565	650	549	389	381	312	411	354
ENSMUSG00000020253	chr9	Ppm1m	1.17221063	4.71157E-08	2.10582E-07	2.904768695	0.04385282	1	71	79	65	62	56	248	172	125	142	153
ENSMUSG00000037697	chr14	Ddhd1	1.20356852	4.72475E-08	2.11103E-07	2.453174422	0.042900854	1	40	49	45	63	44	143	143	86	94	147
ENSMUSG00000018995	chr7	Nars2	-1.0668192	4.74456E-08	2.11921E-07	3.141900141	0.036887199	-1	159	155	185	257	133	75	105	79	93	107
ENSMUSG00000072772	chr6	Grcc10	0.8482565	4.74887E-08	2.12045E-07	6.208446127	0.027639849	1	834	765	718	964	659	2060	1321	1361	1584	1456
ENSMUSG00000046994	chr1	Mars2	-0.9879814	4.76458E-08	2.12679E-07	3.403915509	0.031790225	-1	214	164	196	288	185	99	147	111	101	114
ENSMUSG00000024598	chr18	Fbn2	1.9244857	4.79479E-08	2.13959E-07	2.637172751	0.125369801	1	43	20	36	51	39	297	134	132	47	193
ENSMUSG00000023947	chr17	Nfkbie	1.87642908	4.80446E-08	2.14322E-07	1.903466281	0.110403922	1	37	17	25	28	8	146	114	75	47	86
ENSMUSG00000032763	chr10	Ilvbl	0.81918792	4.83088E-08	2.15432E-07	3.806435418	0.021822909	1	139	140	125	197	149	328	292	248	289	290
ENSMUSG00000019139	chr8	Isyna1	1.62297026	4.88067E-08	2.17583E-07	3.775900862	0.094561232	1	121	120	96	55	90	416	307	494	154	293
ENSMUSG00000030403	chr7	Vasp	1.00200328	4.89124E-08	2.17985E-07	6.009704448	0.038604363	1	887	600	541	612	535	1777	1445	1494	1095	1206
ENSMUSG00000022887	chr16	Masp1	-1.6138228	4.90406E-08	2.18417E-07	1.762484065	0.076834057	-1	61	77	74	126	39	35	21	30	18	28
ENSMUSG00000027180	chr2	Fbxo3	-1.0199681	4.90254E-08	2.18417E-07	6.285844729	0.040223052	-1	1505	1646	1428	1968	1262	574	972	667	906	1068
ENSMUSG00000036550	chr8	Cnot1	-0.8071217	4.9224E-08	2.19164E-07	5.870950278	0.024838342	-1	1017	965	1014	1449	1115	818	789	552	664	664
ENSMUSG00000038976	chr11	Ppp1r9b	0.82624492	4.95755E-08	2.20658E-07	5.685004945	0.025886119	1	504	515	503	739	512	1336	1076	973	812	1198
ENSMUSG00000024976	chr19	Shoc2	-0.7803896	4.9679E-08	2.21049E-07	4.602782487	0.021641819	-1	432	462	419	545	420	314	314	219	283	330
ENSMUSG00000051748	chr11	Wfdc21	2.99658425	5.03865E-08	2.24125E-07	-0.47793797	0.139516551	1	0	7	1	0	1	12	21	18	13	20
ENSMUSG00000024421	chr18	Lama3	-1.6910655	5.06071E-08	2.25035E-07	1.175136305	0.075061914	-1	45	31	34	72	65	18	17	13	14	21
ENSMUSG00000045038	chr17	Prkce	-0.9201893	5.11423E-08	2.27342E-07	3.616056515	0.028168728	-1	256	212	209	253	249	132	149	103	145	158
ENSMUSG00000069662	chr10	Marcks	0.91532317	5.12502E-08	2.2775E-07	6.803850178	0.032711212	1	1308	1162	1040	1330	928	2794	2249	2275	1672	2990
ENSMUSG00000018572	chr11	Phf23	0.87371016	5.15409E-08	2.28969E-07	4.831523883	0.028087266	1	315	295	249	389	253	888	585	455	571	526
ENSMUSG00000032340	chr9	Neo1	-0.8612476	5.18353E-08	2.30203E-07	5.84204085	0.028452561	-1	1036	1035	885	1388	1172	720	668	610	498	839
ENSMUSG00000025616	chr16	Usp16	-0.7900431	5.18931E-08	2.30387E-07	4.942364812	0.022808361	-1	584	507	512	798	518	352	367	301	403	409
ENSMUSG00000043090	chr8	Zfp866	-0.8447031	5.19812E-08	2.30705E-07	3.657495275	0.023082045	-1	224	253	215	305	205	150	162	121	140	159
ENSMUSG00000039167	chr3	Eltd1	-0.9916837	5.22556E-08	2.31849E-07	4.419002786	0.03601245	-1	390	423	369	672	298	290	180	178	219	305
ENSMUSG00000026313	chr1	Hdac4	-0.8035847	5.2444E-08	2.32611E-07	5.209126671	0.02408608	-1	746	708	543	879	637	492	474	320	416	506
ENSMUSG00000032216	chr9	Nedd4	-0.9799254	5.24642E-08	2.32627E-07	8.763174072	0.037986529	-1	9007	7851	7335	10320	8485	3758	4716	4246	4404	6702
ENSMUSG00000036568	chr17	Gltscr1l	-0.9980373	5.30196E-08	2.35015E-07	3.47232044	0.033478361	-1	212	193	190	262	234	112	134	102	89	164
ENSMUSG00000032554	chr9	Trf	1.65723169	5.32309E-08	2.35877E-07	5.508407447	0.103721651	1	189	535	219	286	368	1345	791	1144	579	1815
ENSMUSG00000022037	chr14	Clu	1.63783224	5.3299E-08	2.36103E-07	6.646053636	0.102296691	1	1061	697	624	708	526	2104	2411	3187	3477	904
ENSMUSG00000081787	chr2	Gm13991	-2.5505754	5.34509E-08	2.36701E-07	-0.234885337	0.117936288	-1	12	24	15	29	15	3	1	1	8	4
ENSMUSG00000025103	chr7	Btbd1	-0.8208781	5.36954E-08	2.37709E-07	7.707815366	0.026654542	-1	3845	3809	3785	5053	3461	2426	2548	2055	2599	2706
ENSMUSG00000037286	chr9	Stag1	-0.8762679	5.38046E-08	2.38117E-07	4.748070211	0.028249479	-1	445	485	492	690	482	296	361	216	356	314
ENSMUSG00000043987	chr9	Cep164	1.14635151	5.4037E-08	2.3907E-07	2.432162055	0.038373617	1	48	53	54	50	37	136	124	113	101	118
ENSMUSG00000043683	chr17	Fem1a	-0.8399134	5.43182E-08	2.40238E-07	8.473366272	0.028049441	-1	6775	5895	5791	8833	6841	4115	4037	3765	4164	4697
ENSMUSG00000085411	chr2	Gm14319	-2.3629977	5.49822E-08	2.43097E-07	-0.030260522	0.110852339	-1	24	18	20	20	26	11	3	1	6	2
ENSMUSG00000033825	chr17	Tpsb2	1.74647136	5.50264E-08	2.43216E-07	3.007256553	0.106220622	1	21	43	56	72	76	349	111	188	150	207
ENSMUSG00000004383	chr8	Large	-0.8095732	5.51257E-08	2.43525E-07	4.642113947	0.023645767	-1	448	406	401	689	443	314	284	248	326	303
ENSMUSG00000038005	chr8	2700029M09Rik	1.17089624	5.51312E-08	2.43525E-07	3.396004182	0.047047797	1	100	91	88	105	90	319	302	171	245	145
ENSMUSG00000032727	chr13	Mier3	-1.0146855	5.57141E-08	2.46022E-07	3.141649806	0.033101977	-1	163	155	161	199	188	94	122	69	87	101
ENSMUSG00000022550	chr15	Adck5	1.19212601	5.58217E-08	2.4642E-07	2.349617516	0.041793692	1	46	47	35	60	38	122	90	94	128	129
ENSMUSG00000026385	chr1	Dbi	0.91700219	5.6606E-08	2.49787E-07	7.031409024	0.033145628	1	1190	1452	1157	1827	1166	3880	2506	2791	2511	2316
ENSMUSG00000098318	chr6	1190002F15Rik	2.58876745	5.66204E-08	2.49787E-07	0.020636	0.138889788	1	6	6	1	2	3	16	44	22	23	17
ENSMUSG00000027555	chr3	Car13	1.75581361	5.66409E-08	2.49799E-07	0.836590548	0.069789951	1	9	15	13	9	9	41	50	31	48	37
ENSMUSG00000060438	chr3	Rps10-ps1	1.53774897	5.6885E-08	2.50796E-07	2.117646434	0.073753732	1	29	29	29	41	32	178	95	100	82	59
ENSMUSG00000093133	chr11	Gm25994	-1.2121878	5.72087E-08	2.52144E-07	3.075499398	0.049848872	-1	180	169	154	171	185	84	84	43	111	89
ENSMUSG00000029311	chr5	Hsd17b11	1.13480986	5.7311E-08	2.52441E-07	4.105590828	0.046729205	1	180	170	132	140	164	581	325	256	292	494
ENSMUSG00000038763	chr7	Alpk3	-1.005532	5.73123E-08	2.52441E-07	7.378701264	0.039948703	-1	2780	2544	2659	5521	3379	2002	1574	2018	1508	1909
ENSMUSG00000028613	chr4	Lrp8	3.14717888	5.7723E-08	2.54171E-07	-0.253026497	0.186829396	1	2	2	3	2	1	25	34	8	29	7
ENSMUSG00000022801	chr16	Lrch3	-0.7864282	5.78968E-08	2.54855E-07	4.467391269	0.02197312	-1	405	379	363	574	374	282	296	199	257	291
ENSMUSG00000026822	chr2	Lcn2	4.23311217	5.81138E-08	2.5573E-07	1.765419047	0.50598532	1	2	5	1	9	7	373	56	35	55	7
ENSMUSG00000026317	chr8	Cln8	0.76431108	5.89974E-08	2.59537E-07	4.808566592	0.021211833	1	315	274	285	405	270	630	660	456	507	629
ENSMUSG00000044786	chr7	Zfp36	1.65197838	5.91286E-08	2.60032E-07	5.010643066	0.103218705	1	188	264	231	256	207	1571	1149	312	619	443

ENSMUSG00000024164	chr17	C3	1.68206152	5.96569E-08	2.62272E-07	5.928606789	0.107929729	1	189	549	280	441	655	2814	1017	1110	1259	1514
ENSMUSG00000047843	chr5	Bri3	0.89749064	5.9705E-08	2.62402E-07	4.670307936	0.029757564	1	253	294	221	343	215	791	563	413	435	523
ENSMUSG00000040021	chr10	Lats1	-0.8514608	5.98401E-08	2.62913E-07	4.379951174	0.026026185	-1	357	361	372	508	392	207	279	198	267	252
ENSMUSG00000018565	chr11	Elp5	0.80022077	6.00591E-08	2.63792E-07	5.191662711	0.024055883	1	433	370	331	516	343	733	733	798	779	711
ENSMUSG00000051639	chr17	Gm5812	1.66396548	6.04259E-08	2.6532E-07	1.465671322	0.077324968	1	21	18	23	15	15	97	75	51	64	40
ENSMUSG00000032020	chr9	Ubash3b	1.4764008	6.065E-08	2.6622E-07	2.85792337	0.074569971	1	78	62	44	52	42	287	204	88	144	147
ENSMUSG00000003184	chr7	Irf3	0.84589417	6.1607E-08	2.70336E-07	4.4559173	0.025770391	1	237	226	207	256	231	612	394	460	414	414
ENSMUSG00000045502	chr5	Hcar2	3.314395	6.17369E-08	2.70821E-07	-0.374568501	0.19321776	1	0	4	0	2	2	41	18	17	7	12
ENSMUSG00000044609	chr7	Gm9294	1.63188256	6.23561E-08	2.73451E-07	1.386623259	0.072253045	1	22	14	10	18	25	91	58	57	49	52
ENSMUSG00000065516	chr1	Mir214	2.77829492	6.26876E-08	2.74819E-07	-0.218251345	0.144170789	1	3	5	4	1	0	35	18	23	17	10
ENSMUSG00000013878	chr8	Rnf170	-1.0225444	6.2835E-08	2.75266E-07	4.565521121	0.039156583	-1	486	417	479	569	405	164	291	200	284	325
ENSMUSG00000028902	chr4	Sf3a3	0.87376705	6.28487E-08	2.75266E-07	4.350842247	0.027619217	1	239	191	163	296	189	571	475	359	399	351
ENSMUSG00000032997	chr1	Chpf	1.24490244	6.28224E-08	2.75266E-07	4.628096938	0.058754341	1	267	202	200	228	186	963	447	586	284	584
ENSMUSG00000022897	chr16	Dyrk1a	-0.7790255	6.31703E-08	2.76588E-07	6.12302127	0.023650599	-1	1301	1096	1282	1685	1212	899	869	768	762	892
ENSMUSG00000025869	chr13	Nop16	0.81466042	6.32406E-08	2.76809E-07	4.434302585	0.023774187	1	246	194	210	292	222	558	490	394	433	369
ENSMUSG00000058624	chr19	Gda	1.44889219	6.40612E-08	2.80313E-07	4.023131923	0.077821322	1	122	158	120	154	90	662	474	184	412	229
ENSMUSG00000020128	chr11	Vps54	-0.7893634	6.52928E-08	2.85613E-07	4.38429713	0.022156916	-1	368	396	373	500	331	243	271	204	256	270
ENSMUSG00000040560	chr18	Wdr7	-0.7987584	6.54576E-08	2.86244E-07	5.066952639	0.023964863	-1	699	534	547	723	654	398	414	321	378	486
ENSMUSG00000030474	chr7	Siglece	3.21108577	6.57391E-08	2.87385E-07	0.591036577	0.270338003	1	0	5	5	6	3	117	24	17	26	22
ENSMUSG00000025130	chr11	P4hb	0.88749755	6.59485E-08	2.8821E-07	8.305877933	0.031665702	1	3234	2931	2774	4618	3144	9079	7216	5090	6350	6103
ENSMUSG00000038991	chr13	Txndc5	0.84534677	6.62047E-08	2.8924E-07	6.264369448	0.028107341	1	831	780	730	1034	730	2065	1833	1514	1347	1329
ENSMUSG00000024180	chr17	Tmem8	2.54418028	6.62466E-08	2.89332E-07	2.338257049	0.215568705	1	27	17	15	11	33	379	80	78	109	59
ENSMUSG00000068114	chr15	Ccdc134	1.0588622	6.64829E-08	2.90273E-07	4.159323164	0.040951744	1	193	174	133	160	188	301	389	443	439	359
ENSMUSG00000035898	chr5	Uba6	-1.3743714	6.66737E-08	2.91016E-07	2.487814555	0.061382022	-1	103	115	92	150	133	32	63	39	69	45
ENSMUSG00000020817	chr11	Rabep1	-0.834593	6.69088E-08	2.9195E-07	5.359713074	0.026688937	-1	785	719	634	1000	789	523	505	351	556	473
ENSMUSG00000029061	chr4	Mmp23	1.4125677	6.72307E-08	2.93263E-07	3.025138911	0.068945172	1	65	75	77	50	52	309	168	203	113	165
ENSMUSG00000037628	chr14	Cdkn3	3.08936408	6.73545E-08	2.93712E-07	0.018375616	0.213236577	1	5	2	0	1	5	24	48	28	19	8
ENSMUSG00000040701	chr14	Ap1g2	1.08579005	6.7477E-08	2.94154E-07	3.164659892	0.03943627	1	88	61	81	125	71	283	182	156	200	166
ENSMUSG00000053317	chr4	Sec61b	1.19037227	6.7558E-08	2.94416E-07	4.791816927	0.054182806	1	247	266	226	261	242	1017	743	432	628	349
ENSMUSG00000008393	chr16	Carhsp1	0.80177068	6.79997E-08	2.96248E-07	4.925828118	0.02394922	1	328	367	281	389	280	808	557	615	576	592
ENSMUSG00000024887	chr19	Asah2	-1.0660696	6.81212E-08	2.96685E-07	3.107122939	0.037631867	-1	154	177	177	195	152	75	89	93	71	120
ENSMUSG00000046179	chr7	E2f8	1.98430091	6.81988E-08	2.9693E-07	1.227021707	0.112491973	1	10	19	12	12	12	46	97	67	35	40
ENSMUSG00000031274	chrX	Col4a5	-1.905593	6.82818E-08	2.97199E-07	3.669811778	0.132964275	-1	239	326	268	212	402	21	121	68	104	116
ENSMUSG00000021666	chr13	Gfm2	-0.7903309	6.84593E-08	2.97879E-07	6.112996638	0.024473709	-1	1214	1324	1218	1672	1122	820	824	835	798	844
ENSMUSG00000083669	chr7	Gm10169	1.71708858	6.89092E-08	2.99743E-07	1.011151573	0.073609093	1	14	18	10	16	7	63	46	54	33	39
ENSMUSG00000003119	chr11	Cdk12	-1.0209524	6.89321E-08	2.9975E-07	3.395076776	0.035413641	-1	178	178	211	272	203	111	136	82	135	97
ENSMUSG00000026987	chr2	Baz2b	-0.8452253	6.90876E-08	3.00332E-07	3.867333696	0.024503876	-1	244	298	245	357	248	184	182	136	146	202
ENSMUSG00000099292	chr10	Mir6916	2.61151665	6.94604E-08	3.01859E-07	-0.353758027	0.106244338	1	3	2	3	3	2	19	30	14	9	19
ENSMUSG00000075227	chr19	Znhit2	1.08848711	6.96686E-08	3.0267E-07	3.207604706	0.039949129	1	83	52	80	113	106	254	188	187	181	204
ENSMUSG00000005610	chr7	Eif4g2	-0.8545305	7.13228E-08	3.0976E-07	9.435497849	0.029645249	-1	12438	11184	11708	18584	13093	7860	8632	6989	7738	9063
ENSMUSG00000030061	chr6	Uba3	-1.0034252	7.1446E-08	3.10198E-07	5.198590985	0.03896539	-1	783	722	688	868	586	258	449	322	463	486
ENSMUSG00000038344	chrX	Txlng	-1.2344611	7.19964E-08	3.12491E-07	2.404615685	0.047538731	-1	127	99	92	120	104	41	44	40	58	69
ENSMUSG00000019823	chr10	Mical1	1.01967859	7.27776E-08	3.15784E-07	3.506395258	0.035931803	1	99	88	88	164	119	321	224	227	177	288
ENSMUSG00000032014	chr9	Oaf	0.91863797	7.28932E-08	3.16187E-07	4.317225208	0.030927001	1	216	191	213	226	171	458	479	461	279	439
ENSMUSG00000029263	chr5	Pigg	-1.1322116	7.31412E-08	3.17164E-07	2.553804684	0.039666172	-1	96	104	124	167	103	58	73	54	49	61
ENSMUSG00000026094	chr1	Stk17b	1.05281078	7.31676E-08	3.1718E-07	3.861154518	0.0398829	1	165	124	156	137	110	477	298	309	231	284
ENSMUSG00000028766	chr4	Alpl	-1.492131	7.32939E-08	3.1763E-07	3.36230908	0.080987296	-1	141	160	285	392	163	151	72	90	62	65
ENSMUSG00000023977	chr17	Ubr2	-0.7792408	7.34818E-08	3.18345E-07	6.072589815	0.023877278	-1	1161	1211	1073	1628	1275	876	776	746	768	877
ENSMUSG00000034290	chr12	Nek9	-0.8410289	7.3599E-08	3.18754E-07	7.153676183	0.028422584	-1	2729	2515	2326	3346	2714	1568	1751	1353	1890	1748
ENSMUSG00000089960	chr1	Ugt1a1	2.03845133	7.37645E-08	3.19372E-07	2.858825089	0.145483508	1	35	70	39	20	36	409	163	93	167	125
ENSMUSG00000030921	chr7	Trim30a	1.32261756	7.37898E-08	3.19383E-07	2.756891436	0.058806724	1	54	70	58	60	38	155	208	84	160	170
ENSMUSG00000094724	chr17	Rnaset2b	3.10217971	7.39692E-08	3.2006E-07	0.828915062	0.272722121	1	5	4	5	12	0	7	53	59	58	57
ENSMUSG00000031590	chr8	Frg1	0.82169098	7.43963E-08	3.21808E-07	4.449870102	0.024529045	1	240	280	200	262	186	546	474	420	410	421
ENSMUSG00000093315	chr19	Mir5114	-1.8894703	7.50439E-08	3.24509E-07	1.323901721	0.104931049	-1	47	53	52	61	67	7	18	15	10	33
ENSMUSG00000031389	chrX	Arhgap4	0.77364406	7.51409E-08	3.24828E-07	4.480320908	0.021545915	1	229	227	223	318	228	582	498	374	412	435
ENSMUSG00000069184	chr13	Zfp72	-2.2352526	7.53476E-08	3.25621E-07	0.104460606	0.102040182	-1	22	20	24	30	23	5	2	3	13	4
ENSMUSG00000050552	chr5	Lamtor4	0.90068461	7.548E-08	3.26092E-07	5.794171769	0.031904883	1	689	594	524	645	427	1522	1067	1052	1291	964
ENSMUSG00000022749	chr16	Tbc1d23	-0.8057322	7.58743E-08	3.2759E-07	4.286130921	0.023281786	-1	418	343	318	440	325	235	246	176	223	277
ENSMUSG00000090171	chr1	Ugt1a2	2.03680604	7.58861E-08	3.2759E-07	2.857539343	0.145539984	1	35	70	39	20	36	409	163	93	166	125
ENSMUSG00000100934	chr2	FMN1	2.52094907	7.58969E-08	3.2759E-07	-0.043451351	0.125744592	1	2	2	1	7	6	40	27	16	12	22
ENSMUSG00000089943	chr1	Ugt1a5	2.03680576	7.59275E-08	3.2762E-07	2.857539343	0.145545677	1	35	70	39	20	36	409	163	93	166	125
ENSMUSG00000003458	chr1	Ncstn	0.79798161	7.714E-08	3.3275E-07	5.596401291	0.024761519	1	547	517	434	655	482	929	1013	1030	882	1132
ENSMUSG00000072494	chr14	Ppp1r3e	2.78481884	7.77521E-08	3.3526E-07	0.611633759	0.209919588	1	3	8	2	8	5	7	44	42	41	61
ENSMUSG00000090124	chr1	Ugt1a7c	1.93873105	7.77701E-08	3.3526E-07	3.043771805	0.133941422	1	41	87	47	24	42	430	188	105	190	161
ENSMUSG00000037661	chr3	Gpr160	2.07623208	7.80124E-08	3.36201E-07	0.628812259	0.10108457	1	3	15	9	5	7	31	43	28	42	41

ENSMUSG00000090175	chr1	Ugt1a9	2.03957926	7.81131E-08	3.36532E-07	2.859769449	0.146082023	1	35	70	39	20	36	411	163	93	166	125
ENSMUSG00000015013	chr8	Trappc2l	0.86811423	7.83593E-08	3.37488E-07	4.918488731	0.028681738	1	370	320	252	382	270	853	643	604	605	481
ENSMUSG00000047343	chr1	Mettl21c	-1.147611	7.86626E-08	3.3869E-07	5.412791741	0.051736164	-1	662	663	800	1395	908	290	381	428	549	483
ENSMUSG00000020029	chr10	Nudt4	-0.9293802	7.89083E-08	3.39643E-07	8.116215786	0.035079174	-1	5290	5050	4600	7294	5071	2626	3373	2318	3666	3584
ENSMUSG00000034557	chr4	Zfyve9	-1.0115529	7.90737E-08	3.40251E-07	5.588668006	0.040337277	-1	986	912	830	1141	917	353	625	374	608	631
ENSMUSG00000034066	chr1	Farp2	-0.9507512	7.95782E-08	3.42316E-07	3.184475038	0.029473456	-1	179	177	147	210	170	116	94	96	74	122
ENSMUSG00000089847	chr7	Timm10b	0.91013129	7.97368E-08	3.42893E-07	4.756778276	0.031475693	1	313	265	220	356	247	841	563	528	526	427
ENSMUSG00000002778	chr7	Kdelr1	0.82477896	7.98186E-08	3.43139E-07	6.183262317	0.027020696	1	810	752	668	918	752	1961	1480	1487	1173	1509
ENSMUSG00000022822	chr16	Abcc5	-0.8172029	8.0057E-08	3.43952E-07	5.731709835	0.026233385	-1	1066	888	962	1112	992	658	561	548	589	786
ENSMUSG00000029001	chr4	Fbxo44	2.67328809	8.00395E-08	3.43952E-07	0.756083976	0.195579865	1	6	6	5	8	6	7	58	53	55	41
ENSMUSG00000021115	chr12	Vrk1	1.227117	8.00862E-08	3.43972E-07	2.764647271	0.050080194	1	61	65	46	76	50	208	165	124	170	97
ENSMUSG00000032254	chr9	Kif23	1.72167257	8.01277E-08	3.44044E-07	1.771214628	0.092652094	1	24	24	17	27	21	96	144	59	68	45
ENSMUSG00000061244	chr14	Exoc5	-0.8665926	8.01577E-08	3.44067E-07	4.620340137	0.028146027	-1	474	440	440	603	410	243	327	206	328	311
ENSMUSG00000076068	chr10	Mir678	1.7133409	8.06513E-08	3.4608E-07	1.321177712	0.081671209	1	20	16	15	20	11	82	37	63	71	41
ENSMUSG00000017831	chr17	Rab5a	-1.1550677	8.11376E-08	3.4806E-07	4.612517107	0.05144332	-1	516	474	434	665	435	150	297	154	273	358
ENSMUSG00000076033	chr13	Mir692-3	2.70371475	8.16256E-08	3.50046E-07	0.63876763	0.194117954	1	6	6	6	5	4	87	55	10	21	32
ENSMUSG00000030882	chr7	Dnhd1	0.92708854	8.18756E-08	3.5101E-07	4.613449211	0.032542204	1	286	243	197	321	212	758	507	489	485	380
ENSMUSG00000001323	chr11	Srr	-0.8733367	8.19165E-08	3.51078E-07	3.98872295	0.027010066	-1	342	279	307	343	247	174	158	177	177	221
ENSMUSG00000064326	chr12	Siva1	0.97448376	8.27886E-08	3.54707E-07	3.474745676	0.032399258	1	93	117	102	138	102	332	252	215	209	187
ENSMUSG00000036817	chr5	Sun1	-0.8214695	8.32915E-08	3.56752E-07	5.543806104	0.02639803	-1	912	871	702	1114	849	490	616	520	470	648
ENSMUSG00000006931	chr11	Leprel4	0.98512761	8.35819E-08	3.57886E-07	3.36953138	0.032621772	1	104	104	107	99	91	267	241	231	165	204
ENSMUSG00000010529	chr12	Gm266	1.72627978	8.37227E-08	3.58379E-07	0.953008373	0.074054676	1	16	10	13	9	13	36	38	45	44	61
ENSMUSG00000075585	chr5	6330403L08Rik	-0.8873428	8.40156E-08	3.59523E-07	4.382607605	0.029275036	-1	364	357	333	511	446	219	255	196	208	314
ENSMUSG00000027439	chr2	Gzf1	-0.8305269	8.52909E-08	3.64869E-07	4.495504166	0.025540274	-1	400	400	483	534	327	279	273	252	268	245
ENSMUSG00000000555	chr15	Itga5	1.14475373	8.53817E-08	3.65145E-07	5.439746205	0.05189075	1	351	337	368	690	309	1708	942	733	799	766
ENSMUSG00000039275	chr11	Foxk2	-0.8291898	8.55837E-08	3.65897E-07	5.414904586	0.026850232	-1	740	620	801	1034	866	514	554	427	495	515
ENSMUSG00000020171	chr10	Yeats4	0.8338477	8.6322E-08	3.68941E-07	4.118141485	0.024886071	1	191	168	164	242	163	497	356	309	337	315
ENSMUSG00000028896	chr4	Rcc1	1.04606402	8.70488E-08	3.71934E-07	4.23498302	0.041211117	1	204	162	186	205	150	514	540	302	443	267
ENSMUSG00000031891	chr8	Hsd11b2	2.09610363	8.75308E-08	3.73878E-07	0.794869	0.116081605	1	7	6	10	8	13	31	28	45	33	73
ENSMUSG00000050212	chr4	Eva1b	1.15377568	8.85308E-08	3.78034E-07	3.538865223	0.048160738	1	106	110	119	133	64	388	233	281	183	216
ENSMUSG00000049134	chr19	Nrap	-1.1221591	8.91054E-08	3.80372E-07	9.748528393	0.051402711	-1	13011	12893	14040	30795	19088	12807	8585	7723	7948	7515
ENSMUSG00000003847	chr8	Nfat5	-0.7361743	9.01746E-08	3.84818E-07	4.734131188	0.020067748	-1	492	435	471	634	446	385	333	293	315	301
ENSMUSG00000036053	chr2	Fmnl2	-1.1507583	9.05836E-08	3.86446E-07	3.128398234	0.04621904	-1	200	195	162	183	144	68	103	58	87	123
ENSMUSG00000053436	chr17	Mapk14	-0.8377527	9.14803E-08	3.90152E-07	6.828658413	0.028507116	-1	2060	1864	1938	2873	2171	1217	1392	1112	1403	1522
ENSMUSG00000027820	chr3	Mme	-1.0939128	9.16202E-08	3.9063E-07	2.963489391	0.040025884	-1	126	197	122	177	156	78	80	68	90	84
ENSMUSG00000071337	chr6	Tia1	-0.8276024	9.18851E-08	3.91401E-07	4.021178016	0.024397091	-1	329	249	282	353	321	203	198	160	195	194
ENSMUSG00000089675	chr1	Ugt1a8	2.02945309	9.18404E-08	3.91401E-07	2.858915677	0.14662456	1	35	71	39	20	36	409	163	93	166	125
ENSMUSG00000090165	chr1	Ugt1a10	2.02945286	9.18812E-08	3.91401E-07	2.858915677	0.146629285	1	35	71	39	20	36	409	163	93	166	125
ENSMUSG00000018547	chr11	Pip4k2b	-0.8034513	9.19609E-08	3.91605E-07	6.460733233	0.026053305	-1	1645	1514	1467	2032	1682	1150	903	990	1005	1187
ENSMUSG00000045983	chr16	Eif4g1	-0.825578	9.22893E-08	3.92883E-07	9.181801272	0.028160079	-1	11200	10080	9343	14108	10820	6668	7467	5965	7100	6964
ENSMUSG00000024736	chr19	Tmem132a	1.35466095	9.24701E-08	3.93533E-07	4.56544776	0.071555841	1	169	153	207	304	166	525	409	938	354	490
ENSMUSG00000044060	chr5	A830010M20Rik	-0.9070315	9.26767E-08	3.94292E-07	3.678753398	0.028666392	-1	237	200	249	295	251	128	157	116	147	173
ENSMUSG00000067870	chr15	Rpl31-ps8	0.89526451	9.3197E-08	3.96385E-07	4.846240205	0.030851697	1	392	268	259	319	252	679	676	501	693	491
ENSMUSG00000053038	chr8	Gm6180	1.6747722	9.35049E-08	3.97573E-07	1.581628783	0.084161735	1	25	27	8	22	19	67	87	41	86	74
ENSMUSG00000028653	chr4	Trit1	1.00164331	9.37703E-08	3.98581E-07	3.515430252	0.034897689	1	121	117	121	110	87	226	244	284	236	230
ENSMUSG00000043639	chr19	Rbm20	-0.8443674	9.49439E-08	4.03447E-07	5.613656897	0.028285993	-1	836	829	729	1440	915	663	544	507	482	672
ENSMUSG00000022100	chr14	Xpo7	-0.80553	9.56593E-08	4.06363E-07	5.452780463	0.025529842	-1	806	737	778	1004	816	505	611	409	486	593
ENSMUSG00000035585	chr7	Tsen34	0.77206125	9.58545E-08	4.07069E-07	5.217613112	0.02305671	1	442	440	349	485	329	860	692	771	697	797
ENSMUSG00000022194	chr14	Pabpn1	0.78357198	9.63218E-08	4.08855E-07	5.223511902	0.023797634	1	471	383	358	475	354	975	720	769	678	712
ENSMUSG00000036019	chr10	Tmtc2	-1.6078022	9.63336E-08	4.08855E-07	1.342137357	0.073362578	-1	33	61	44	92	47	27	19	14	21	17
ENSMUSG00000070565	chr1	Rasal2	-0.9811287	9.66912E-08	4.10248E-07	3.077320088	0.031919251	-1	165	179	167	182	129	105	109	73	75	98
ENSMUSG00000036985	chrX	Zdhhc9	0.83856341	9.6934E-08	4.11153E-07	3.896017254	0.024531814	1	144	156	135	191	162	397	326	238	277	319
ENSMUSG00000033953	chr11	Ppp3r1	-0.8855322	9.76472E-08	4.14053E-07	7.625003988	0.032252996	-1	4186	3346	3163	4563	3844	1984	2698	1947	1965	2732
ENSMUSG00000029703	chr5	Lrwd1	0.98773596	9.87418E-08	4.18567E-07	3.008940202	0.031643822	1	80	76	54	108	80	211	170	139	156	188
ENSMUSG00000085894	chr1	Gm15832	1.59176259	9.90556E-08	4.1977E-07	2.481516903	0.087007335	1	34	38	39	50	40	262	126	81	70	145
ENSMUSG00000033294	chr5	Noc4l	0.77878351	1.00592E-07	4.26151E-07	4.269722164	0.021806878	1	212	193	189	231	221	480	391	361	357	393
ENSMUSG00000037217	chrX	Syn1	2.59188305	1.0073E-07	4.26608E-07	-0.458274268	0.098622399	1	2	5	3	2	0	21	15	18	10	19
ENSMUSG00000021550	chr13	2210016F16Rik	0.83600336	1.00811E-07	4.2682E-07	4.410610537	0.026023327	1	252	234	206	264	176	498	439	388	506	378
ENSMUSG00000039176	chr7	Polg	-0.7819564	1.00915E-07	4.27133E-07	5.330182355	0.023967022	-1	760	709	648	965	715	625	491	365	485	460
ENSMUSG00000070520	chr7	Ndnl2	0.96664802	1.01466E-07	4.29335E-07	3.588953326	0.032857216	1	129	115	114	141	101	381	240	253	197	223
ENSMUSG00000032788	chr10	Pdxk	1.06491493	1.01985E-07	4.31397E-07	4.326013372	0.043483055	1	143	201	178	230	204	533	541	241	505	399
ENSMUSG00000020641	chr12	Rsad2	1.50952798	1.02036E-07	4.31482E-07	2.547075335	0.079113119	1	53	31	27	64	48	152	145	103	74	223
ENSMUSG00000023984	chr17	Gm20517	-1.1451778	1.03577E-07	4.37868E-07	2.938754604	0.044629551	-1	139	125	152	199	162	52	79	68	87	96
ENSMUSG00000047714	chr16	Ppp1r2	-0.7917399	1.03662E-07	4.38096E-07	6.516577606	0.025531666	-1	1708	1545	1601	2309	1534	1106	1139	871	1084	1282
ENSMUSG00000037443	chr4	Cep85	-0.7940567	1.03759E-07	4.3837E-07	5.346253411	0.024766204	-1	691	739	755	1048	629	464	469	443	525	515

ENSMUSG00000028857	chr4	Tmem222	0.86167201	1.0476E-07	4.42468E-07	4.615334552	0.028243861	1	244	288	225	285	242	733	454	454	491	451
ENSMUSG00000029684	chr6	Wasl	-0.805935	1.04957E-07	4.43166E-07	4.074375204	0.023392782	-1	286	300	309	414	284	238	217	149	185	212
ENSMUSG00000027316	chr2	Gfra4	1.61518735	1.05111E-07	4.43684E-07	1.346257494	0.072613416	1	12	16	19	20	20	97	54	48	39	61
ENSMUSG00000033578	chrX	Tmem35	2.40921949	1.05388E-07	4.44718E-07	0.94006606	0.169187474	1	10	5	5	12	10	48	31	99	22	40
ENSMUSG00000071655	chr19	Ubxn1	0.81508007	1.05773E-07	4.46208E-07	7.38907554	0.027433593	1	1839	1677	1617	2308	1644	3332	3186	3614	3301	3935
ENSMUSG00000074909	chr19	Ranbp6	-1.0590576	1.06634E-07	4.49704E-07	3.523300701	0.040385189	-1	224	185	214	350	191	83	157	108	123	129
ENSMUSG00000045273	chr13	Cenph	3.83214224	1.07236E-07	4.52105E-07	0.168321573	0.345985529	1	6	0	1	1	1	38	59	18	32	3
ENSMUSG00000084939	chr4	Gm830	2.69347815	1.07273E-07	4.52127E-07	0.010380383	0.159543572	1	0	3	4	7	3	45	13	30	21	14
ENSMUSG00000029249	chr5	Rest	-0.8272877	1.08096E-07	4.55456E-07	4.01027798	0.024572196	-1	332	294	254	374	277	217	219	158	145	209
ENSMUSG00000031286	chr3	Glt28d2	-1.1599029	1.08408E-07	4.56632E-07	2.908352664	0.046314225	-1	156	144	152	175	134	79	64	42	83	108
ENSMUSG00000025290	chr14	Rps24	0.92656735	1.08578E-07	4.57212E-07	8.357340608	0.035668723	1	3933	3387	3057	3739	2714	9448	7189	5795	7408	5413
ENSMUSG00000042302	chr11	Ehbp1	-0.9381999	1.09175E-07	4.59588E-07	3.612475725	0.031094054	-1	244	224	232	252	228	120	120	113	144	181
ENSMUSG00000049739	chr7	Zfp646	-0.9203634	1.09381E-07	4.60315E-07	3.676841022	0.030082393	-1	217	208	245	308	258	146	143	131	110	188
ENSMUSG00000030824	chr7	Nucb1	0.83752807	1.09769E-07	4.6181E-07	6.371087324	0.028633217	1	886	779	710	1174	898	2111	1686	1534	1344	2039
ENSMUSG00000025875	chr13	Tspan17	0.92418716	1.1046E-07	4.64577E-07	3.955023585	0.031153005	1	190	160	153	158	125	350	271	367	310	338
ENSMUSG00000058600	chr15	Rpl30	0.87007007	1.10519E-07	4.64683E-07	7.593600198	0.031395344	1	2208	1986	1681	2477	1852	5532	4225	3614	3908	3200
ENSMUSG00000024590	chr18	Lmnb1	0.89137462	1.11654E-07	4.69314E-07	4.15264674	0.029590458	1	204	209	140	224	148	372	478	348	344	329
ENSMUSG00000024767	chr19	Otub1	0.76832662	1.12395E-07	4.7229E-07	5.362112819	0.023262659	1	496	438	370	555	409	953	784	856	718	910
ENSMUSG00000032495	chr9	Lrrc2	-1.3777614	1.12505E-07	4.7261E-07	4.679272942	0.075266163	-1	386	540	532	984	375	369	220	231	236	106
ENSMUSG00000033059	chr2	Pygb	0.81484788	1.13409E-07	4.76263E-07	4.23167731	0.024327976	1	186	203	195	239	183	511	362	335	313	436
ENSMUSG00000024911	chr19	Fibp	0.78153012	1.13765E-07	4.77614E-07	4.641244316	0.023099722	1	289	245	250	357	228	651	466	411	536	511
ENSMUSG00000021814	chr14	Anxa7	0.93024548	1.13968E-07	4.78322E-07	6.063181231	0.035259065	1	847	750	562	671	574	1679	1381	1134	1699	1261
ENSMUSG00000048572	chr19	Tmem252	2.88301174	1.14603E-07	4.80843E-07	0.536498057	0.225569944	1	4	5	3	2	8	93	32	28	27	11
ENSMUSG00000092341	chr19	Malat1	-1.3053262	1.15298E-07	4.83614E-07	7.637284578	0.069898764	-1	4256	3568	4475	3786	4673	1217	1429	1634	2963	1973
ENSMUSG00000002732	chr2	Fkbp7	0.94184583	1.15704E-07	4.85173E-07	3.706440449	0.031732825	1	152	145	135	131	92	332	310	257	250	241
ENSMUSG00000036249	chr2	Rbm43	1.30336079	1.16806E-07	4.89648E-07	2.00217504	0.050880994	1	39	39	22	38	28	109	108	61	88	86
ENSMUSG00000020284	chr10	1810043G02Rik	1.13279987	1.1745E-07	4.92199E-07	2.692500941	0.041947405	1	64	70	51	53	54	195	128	120	135	135
ENSMUSG00000042572	chr3	Ube2q1	0.81681594	1.17997E-07	4.94343E-07	4.952371017	0.025975677	1	301	344	323	407	289	877	703	495	606	557
ENSMUSG00000030469	chr7	Zfp719	-1.2367017	1.18049E-07	4.94411E-07	2.231084238	0.047804471	-1	101	83	103	113	80	36	49	31	50	57
ENSMUSG00000020573	chr12	Pik3cg	1.65395343	1.1819E-07	4.94855E-07	1.931238984	0.088597655	1	27	20	28	21	33	129	109	38	92	93
ENSMUSG00000066682	chr5	Pilrb2	2.41583394	1.18466E-07	4.95861E-07	-0.269742487	0.097329667	1	2	4	1	6	3	23	12	20	24	16
ENSMUSG00000028127	chr3	Abcd3	-0.7858657	1.18617E-07	4.96347E-07	5.762831108	0.024880234	-1	928	942	911	1440	937	605	655	584	677	720
ENSMUSG00000035678	chr17	Tnfsf9	2.46571867	1.18874E-07	4.97272E-07	-0.002366105	0.130718213	1	4	4	3	4	4	39	33	9	25	14
ENSMUSG00000023963	chr17	Cyp39a1	-1.0662309	1.1944E-07	4.9949E-07	2.616942372	0.036000545	-1	131	122	110	141	104	55	74	54	71	63
ENSMUSG00000052926	chr8	Rnaseh2a	0.8740606	1.20517E-07	5.03844E-07	3.977522923	0.02786358	1	154	164	153	240	120	418	296	308	335	296
ENSMUSG00000024691	chr19	Fam111a	1.27542047	1.21027E-07	5.05672E-07	3.232089769	0.059533626	1	73	74	72	118	70	290	258	122	270	137
ENSMUSG00000064345	chrMT	mt-Nd2	-1.1735266	1.21014E-07	5.05672E-07	11.89730717	0.057326827	-1	64902	73620	72002	123425	66328	21869	38241	38048	40098	51119
ENSMUSG00000061360	chr15	Phf5a	0.76769358	1.21966E-07	5.09442E-07	5.337849859	0.023322638	1	512	415	384	525	391	1024	855	721	816	745
ENSMUSG00000028180	chr3	Zranb2	-0.8067117	1.23112E-07	5.14075E-07	5.383725203	0.025978579	-1	885	746	669	991	679	437	584	415	499	536
ENSMUSG00000032549	chr9	Rab6b	2.76036505	1.23931E-07	5.1734E-07	1.177121852	0.238201548	1	9	8	8	8	7	6	79	61	87	62
ENSMUSG00000042647	chr5	Acad12	-0.8850827	1.2422E-07	5.18394E-07	3.799276519	0.028156409	-1	255	273	234	367	218	177	134	147	190	142
ENSMUSG00000048583	chr7	Igf2	1.64888232	1.24502E-07	5.19417E-07	8.511342625	0.110201492	1	3103	2165	1843	2729	3224	6546	5282	10709	4697	17825
ENSMUSG00000099906	chr1	Gm28653	2.39088595	1.24551E-07	5.19465E-07	1.803796273	0.19608573	1	21	8	11	35	8	123	40	173	45	72
ENSMUSG00000025817	chr2	Nudt5	1.10275128	1.25254E-07	5.22238E-07	2.898181608	0.040881511	1	64	79	76	64	59	174	180	160	169	129
ENSMUSG00000024012	chr17	Mtch1	0.9080503	1.26219E-07	5.26106E-07	6.872707772	0.034276865	1	1166	1194	1086	1637	1028	3655	2086	2571	1939	2299
ENSMUSG00000030890	chr7	Ilk	0.80513441	1.26671E-07	5.27833E-07	6.315643916	0.026672215	1	840	881	774	1101	736	1949	1564	1761	1479	1497
ENSMUSG00000020250	chr10	Txnrd1	-0.7731444	1.2715E-07	5.29672E-07	6.002702793	0.024387666	-1	1254	1207	1089	1494	997	869	851	595	770	791
ENSMUSG00000031360	chrX	Ctps2	1.06724925	1.28496E-07	5.3512E-07	2.95478664	0.038568015	1	79	70	79	89	50	208	193	116	174	156
ENSMUSG00000090122	chrX	Kcne1l	2.02592628	1.28655E-07	5.35622E-07	4.810430961	0.159840593	1	76	91	154	346	180	323	533	498	729	1572
ENSMUSG00000046229	chr2	Scand1	1.01048709	1.28783E-07	5.35997E-07	4.489330527	0.040064729	1	199	182	182	308	240	755	369	504	365	462
ENSMUSG00000042712	chrX	Wbp5	0.71705487	1.29718E-07	5.39728E-07	4.926589938	0.019704839	1	376	335	296	387	311	711	630	544	593	603
ENSMUSG00000034574	chr12	Daam1	-0.8248315	1.29758E-07	5.3973E-07	4.341230517	0.025689935	-1	348	310	392	499	376	238	252	212	195	294
ENSMUSG00000029648	chr5	Flt1	-1.0971776	1.30435E-07	5.42387E-07	5.194288822	0.048822118	-1	420	630	630	1289	810	499	399	315	305	398
ENSMUSG00000029022	chr4	Miip	1.08023461	1.31142E-07	5.45163E-07	2.759085371	0.038322706	1	65	77	57	68	49	170	122	124	157	163
ENSMUSG00000034573	chr5	Ptpn13	-1.1729061	1.31385E-07	5.46012E-07	2.320997569	0.044045603	-1	100	94	89	120	102	68	58	34	34	54
ENSMUSG00000020671	chr12	Rab10	-1.0004867	1.32968E-07	5.52428E-07	7.917748712	0.042014011	-1	4709	4129	4253	6359	4703	1827	2886	2263	2489	3653
ENSMUSG00000030036	chr6	Mogs	1.00589732	1.35186E-07	5.61474E-07	4.08323274	0.038560245	1	152	149	148	208	176	562	419	261	338	275
ENSMUSG00000000740	chr8	Rpl13	0.8663689	1.36786E-07	5.67949E-07	8.170586386	0.031710734	1	3048	2756	2523	3909	3035	8470	6177	5436	5409	5088
ENSMUSG00000034593	chr9	Myo5a	1.32189583	1.38356E-07	5.74299E-07	4.4139887	0.069650449	1	166	167	158	201	204	236	683	348	498	697
ENSMUSG00000020826	chr11	Nos2	-1.2904403	1.38918E-07	5.76462E-07	2.558335539	0.057486933	-1	110	157	109	169	73	57	40	62	48	66
ENSMUSG00000025240	chr9	Sacm1l	-0.8537983	1.40018E-07	5.80851E-07	5.012482361	0.029072826	-1	685	584	575	772	486	359	416	249	438	413
ENSMUSG00000024066	chr17	Xdh	1.12774306	1.40381E-07	5.82186E-07	4.256653015	0.050077052	1	109	210	129	237	204	536	408	254	461	487
ENSMUSG00000022119	chr14	Rbm26	-0.7888506	1.4243E-07	5.90331E-07	4.375148534	0.023539553	-1	377	328	377	470	395	296	260	183	257	246
ENSMUSG00000038508	chr8	Gdf15	3.19972489	1.42426E-07	5.90331E-07	0.023632815	0.248214301	1	2	2	1	1	6	10	62	15	16	26
ENSMUSG00000005371	chr17	Fbxo11	-0.7736428	1.43859E-07	5.96081E-07	5.198032381	0.02387334	-1	676	645	649	888	599	433	480	327	475	495

ENSMUSG00000062963	chr1	Ufc1	0.73920894	1.43946E-07	5.96263E-07	5.609344582	0.022093996	1	553	516	483	698	481	1044	983	905	1058	974
ENSMUSG00000005882	chr2	Uqcc1	-0.8165679	1.44051E-07	5.96521E-07	6.966820675	0.028000939	-1	2212	2495	2320	2971	1912	1453	1525	1361	1639	1386
ENSMUSG00000025582	chr11	Nptx1	2.87702966	1.44237E-07	5.96979E-07	-0.170744669	0.189944165	1	3	5	1	4	0	25	41	15	20	7
ENSMUSG00000054519	chr11	Zfp867	-1.1594469	1.44247E-07	5.96979E-07	2.301350036	0.042204695	-1	119	89	94	128	70	56	41	47	52	47
ENSMUSG00000021676	chr13	Iqgap2	1.17990794	1.46901E-07	6.07781E-07	2.596200025	0.046018149	1	52	56	61	49	48	116	162	117	148	123
ENSMUSG00000029270	chr5	Fam69a	-0.8591282	1.47207E-07	6.08867E-07	5.225814064	0.029870862	-1	869	803	571	679	637	483	423	337	429	503
ENSMUSG00000046410	chr7	Kcnk6	1.53087734	1.48168E-07	6.12663E-07	2.727424625	0.084972296	1	38	52	42	61	54	303	175	75	122	130
ENSMUSG00000031245	chrX	Hmgn5	-1.0015039	1.48308E-07	6.13061E-07	3.310951731	0.03558712	-1	166	175	165	247	223	85	112	98	119	117
ENSMUSG00000021219	chr12	Rgs6	-2.2141058	1.48475E-07	6.13387E-07	-0.070355468	0.1033953	-1	18	17	25	23	20	9	1	8	2	4
ENSMUSG00000025266	chrX	Gnl3l	-0.802969	1.48457E-07	6.13387E-07	4.867108401	0.025398971	-1	611	533	469	668	482	289	424	318	317	378
ENSMUSG00000030016	chr6	Zfml	-0.9183732	1.49973E-07	6.1939E-07	4.960087369	0.033981119	-1	588	521	606	759	555	337	439	209	410	364
ENSMUSG00000026577	chr1	Blzf1	-0.8130985	1.51357E-07	6.24924E-07	4.222100166	0.024890449	-1	404	363	287	408	303	232	253	176	236	203
ENSMUSG00000001089	chr4	Luzp1	-0.792493	1.51698E-07	6.26148E-07	4.680067337	0.024492483	-1	455	411	461	656	445	359	365	249	238	326
ENSMUSG00000071083	chr8	Gm10311	-2.7230713	1.52326E-07	6.28554E-07	-0.189525243	0.162576291	-1	22	7	26	28	17	1	3	0	4	8
ENSMUSG00000004931	chr10	Apba3	-0.8184217	1.54751E-07	6.38332E-07	5.665006537	0.027506091	-1	798	807	882	1425	954	653	606	534	620	579
ENSMUSG00000023022	chr15	Lima1	0.76955685	1.54787E-07	6.38332E-07	5.002292929	0.023432842	1	370	328	343	441	283	801	716	604	492	692
ENSMUSG00000030319	chr6	Cand2	-1.0067051	1.5508E-07	6.39351E-07	6.721499495	0.042635154	-1	1972	1638	1666	2900	2390	878	1128	1209	961	1515
ENSMUSG00000028559	chr4	Osbpl9	-0.9054013	1.55381E-07	6.40401E-07	6.358049533	0.034352575	-1	1699	1722	1314	1801	1417	823	953	667	1063	1152
ENSMUSG00000035901	chr7	Dennd5a	-0.8501669	1.58148E-07	6.51614E-07	5.880842244	0.029987086	-1	974	961	1123	1601	1026	643	700	552	647	893
ENSMUSG00000047216	chr1	Cdh19	-2.1622789	1.58736E-07	6.53842E-07	-0.055548601	0.096245705	-1	12	21	19	28	24	4	10	3	4	4
ENSMUSG00000066149	chr4	Cdc26	0.81409837	1.59053E-07	6.54959E-07	4.167804911	0.024771215	1	222	183	182	197	174	364	388	361	386	350
ENSMUSG00000100131	chr1	Gm28439	-1.5232774	1.61965E-07	6.66752E-07	2.061287616	0.078292545	-1	80	63	92	141	80	18	30	30	38	54
ENSMUSG00000049323	chr11	Smcr8	-0.7893921	1.62219E-07	6.67601E-07	4.823973324	0.024606317	-1	527	493	451	719	494	309	422	266	318	377
ENSMUSG00000021610	chr13	Clptm1l	0.80977743	1.63537E-07	6.72828E-07	5.589244752	0.026948521	1	502	503	410	709	496	1363	1062	833	887	887
ENSMUSG00000022237	chr15	Ankrd33b	-0.9638865	1.63773E-07	6.73598E-07	4.77146799	0.037423752	-1	418	480	473	820	523	212	347	313	286	336
ENSMUSG00000096188	chr8	Cmtm4	-0.8134795	1.63998E-07	6.74326E-07	3.890867241	0.024091382	-1	278	272	245	394	225	229	172	143	158	176
ENSMUSG00000017561	chr11	Crlf3	1.02486836	1.65128E-07	6.78774E-07	3.188204224	0.037098601	1	67	86	96	115	77	261	219	188	150	170
ENSMUSG00000037190	chr9	Cyb561d2	1.27476692	1.65398E-07	6.79483E-07	2.13746367	0.051720318	1	52	29	36	39	29	131	114	78	91	81
ENSMUSG00000062825	chr11	Actg1	0.89695652	1.65357E-07	6.79483E-07	7.892037683	0.034372205	1	2646	2315	2243	3015	2174	6669	6128	3442	4904	4336
ENSMUSG00000004665	chr10	Cnn2	0.93237642	1.66751E-07	6.84842E-07	4.543412249	0.034631017	1	184	219	216	379	208	724	478	369	490	448
ENSMUSG00000027714	chr3	Exosc9	0.81689123	1.67288E-07	6.86843E-07	4.336171933	0.025601724	1	222	214	188	279	185	367	497	402	435	378
ENSMUSG00000021669	chr13	Col4a3bp	-0.8293745	1.68331E-07	6.90921E-07	5.351947871	0.02815975	-1	730	641	681	1090	776	476	521	376	415	619
ENSMUSG00000024622	chr18	Hmgxb3	-0.792776	1.69611E-07	6.95974E-07	4.243096769	0.023815856	-1	356	333	363	417	308	267	217	170	250	225
ENSMUSG00000020183	chr10	Cpm	-1.1207667	1.70954E-07	7.01278E-07	2.478259731	0.040842972	-1	105	89	117	147	102	49	68	50	47	67
ENSMUSG00000098926	chr1	Mir6904	-1.6377779	1.71095E-07	7.01649E-07	1.135893249	0.077020472	-1	45	42	50	52	46	11	21	7	19	25
ENSMUSG00000026116	chr1	Tmem131	-0.9476062	1.71667E-07	7.03788E-07	5.117714128	0.036831348	-1	483	607	628	1120	619	382	384	323	322	527
ENSMUSG00000001289	chr15	Pfdn5	0.81977753	1.7315E-07	7.0966E-07	6.491568006	0.028390476	1	1118	913	832	1194	809	2537	1727	1752	1706	1690
ENSMUSG00000061778	chrX	Mospd2	-1.1891116	1.73297E-07	7.10057E-07	2.921138874	0.051102475	-1	151	165	153	196	112	57	93	46	96	79
ENSMUSG00000020273	chr11	Papolg	-1.3721981	1.74381E-07	7.14286E-07	2.11075299	0.062401462	-1	98	78	93	106	78	24	39	25	48	55
ENSMUSG00000019899	chr10	Lama2	-0.9091289	1.74955E-07	7.16428E-07	6.282600629	0.034883828	-1	1339	1355	1401	1791	1649	720	955	901	718	1103
ENSMUSG00000029432	chr5	Gbas	-0.8171334	1.76471E-07	7.21791E-07	8.996932107	0.028850468	-1	9149	9874	9275	12922	7669	6313	5798	5227	5847	7069
ENSMUSG00000030750	chr7	Nsmce1	0.94980132	1.76462E-07	7.21791E-07	3.999176575	0.034490036	1	187	157	137	176	147	468	324	288	383	248
ENSMUSG00000031357	chrX	Syap1	-0.8719517	1.76367E-07	7.21791E-07	4.74358473	0.030481794	-1	501	464	501	657	457	234	361	253	292	398
ENSMUSG00000032396	chr9	Dis3l	-0.7249251	1.76412E-07	7.21791E-07	4.813208139	0.020523656	-1	517	460	483	683	471	346	330	321	363	360
ENSMUSG00000032586	chr9	Traip	1.92573498	1.77562E-07	7.2604E-07	0.554821872	0.087518979	1	11	6	10	3	10	42	42	27	35	26
ENSMUSG00000041096	chrX	Tspyl2	0.89876095	1.77917E-07	7.27279E-07	3.369912342	0.028056079	1	115	91	97	123	104	272	228	161	226	203
ENSMUSG00000037075	chr15	Rnf139	-0.8353599	1.80524E-07	7.3772E-07	5.423843906	0.028785979	-1	807	835	830	981	639	444	531	400	576	555
ENSMUSG00000026709	chr1	Dars2	-0.9332141	1.81216E-07	7.40332E-07	3.640246915	0.032176367	-1	224	256	235	307	191	122	169	108	163	130
ENSMUSG00000026096	chr1	Osgepl1	-0.9242114	1.81324E-07	7.40556E-07	4.771206024	0.034543704	-1	553	572	523	628	382	220	327	283	351	340
ENSMUSG00000097188	chr19	Snhg1	1.37245094	1.8382E-07	7.5053E-07	3.436317582	0.07289705	1	121	76	90	96	60	450	260	193	238	134
ENSMUSG00000038644	chr7	Pold1	1.1360188	1.83998E-07	7.51037E-07	2.828528049	0.045642694	1	63	57	44	101	64	167	176	133	185	119
ENSMUSG00000021994	chr14	Wnt5a	-1.1521963	1.84535E-07	7.53009E-07	3.719987656	0.051715984	-1	224	233	275	322	285	80	148	102	131	200
ENSMUSG00000020023	chr10	Tmcc3	-0.7286133	1.84695E-07	7.53253E-07	5.09883928	0.021297088	-1	598	647	544	803	593	444	430	362	362	509
ENSMUSG00000031871	chr8	Cdh5	-0.9302328	1.84702E-07	7.53253E-07	6.617651841	0.03685838	-1	1816	1992	1962	2387	1454	1234	835	1070	889	1503
ENSMUSG00000073155	chr6	1810058I24Rik	0.88021259	1.85187E-07	7.55009E-07	6.025945554	0.032655086	1	740	734	591	882	491	1930	1191	1324	1102	1382
ENSMUSG00000035370	chr10	Adat3	0.804742	1.85476E-07	7.55966E-07	4.992039861	0.026084065	1	364	299	284	392	376	894	681	571	553	617
ENSMUSG00000026004	chr1	Kansl1l	-1.0814839	1.87105E-07	7.62386E-07	4.250709874	0.046967472	-1	442	367	362	439	307	120	219	151	209	290
ENSMUSG00000067194	chrX	Eif1ax	-0.7880758	1.8758E-07	7.64097E-07	6.587793178	0.02641543	-1	1882	1580	1639	2368	1652	1079	1286	970	1217	1195
ENSMUSG00000020721	chr11	Helz	-0.8150595	1.88807E-07	7.68871E-07	4.360622294	0.025781361	-1	366	319	323	568	388	252	247	229	194	290
ENSMUSG00000027650	chr2	Tti1	-0.8115464	1.88933E-07	7.69159E-07	4.440080597	0.025709326	-1	410	357	360	525	406	222	269	208	257	324
ENSMUSG00000037991	chr16	Rmi2	-1.0967865	1.89425E-07	7.70937E-07	2.889779965	0.042533243	-1	153	115	135	176	162	56	91	68	69	95
ENSMUSG00000037709	chr6	Fam13a	-1.5058837	1.90988E-07	7.77074E-07	3.30388072	0.088149557	-1	127	263	163	370	177	50	76	63	77	149
ENSMUSG00000046636	chr18	Gm7729	-2.7616157	1.91298E-07	7.7811E-07	-0.041942025	0.194504218	-1	22	16	14	32	29	13	1	3	0	1
ENSMUSG00000031555	chr8	Adam9	-0.9169065	1.92725E-07	7.83686E-07	5.865723237	0.035452626	-1	1181	1078	994	1274	1127	513	783	490	810	682
ENSMUSG00000036061	chr15	Smug1	-0.9091487	1.94137E-07	7.89199E-07	3.382639804	0.029426355	-1	212	217	170	228	176	127	97	99	138	124

ENSMUSG00000024654	chr19	Asrgl1	-0.8350246	1.94226E-07	7.89329E-07	5.664823028	0.029169591	-1	876	820	800	1394	994	600	682	441	598	659
ENSMUSG00000023972	chr17	Ptk7	1.53611458	1.94665E-07	7.90885E-07	2.930436426	0.089534442	1	86	42	59	55	42	259	165	191	71	232
ENSMUSG00000039145	chr2	Camk1d	1.243628	1.95264E-07	7.93088E-07	2.458038662	0.052349797	1	39	35	52	59	51	165	139	76	128	112
ENSMUSG00000070858	chr5	Gm1673	2.3801551	1.95931E-07	7.95566E-07	-0.273645133	0.101453826	1	6	4	3	2	1	29	19	19	11	17
ENSMUSG00000021474	chr13	Sfxn1	1.08708282	1.9697E-07	7.99549E-07	2.922334071	0.041472574	1	73	93	60	68	58	162	212	140	148	165
ENSMUSG00000093565	chr17	Rab26os	2.26766981	1.97433E-07	8.01196E-07	0.022223034	0.111836308	1	4	8	1	5	4	36	25	18	27	13
ENSMUSG00000032402	chr9	Smad3	-0.9782739	1.97973E-07	8.03154E-07	6.566486777	0.040933075	-1	1464	1525	1517	3091	1937	1438	994	1046	790	969
ENSMUSG00000029559	chr5	2210016L21Rik	0.80752265	1.98452E-07	8.04863E-07	4.274080484	0.025156299	1	240	199	155	263	190	376	381	376	385	475
ENSMUSG00000023965	chr17	Fbxl17	-0.8392768	2.00552E-07	8.13146E-07	5.333892931	0.029190514	-1	652	659	662	1092	811	415	515	447	420	554
ENSMUSG00000032854	chr3	Ugt8a	-2.4105436	2.00895E-07	8.14299E-07	0.747851691	0.176481135	-1	14	27	60	58	39	4	15	11	4	6
ENSMUSG00000078441	chr10	Scamp4	0.80308519	2.01732E-07	8.17454E-07	4.939167161	0.026061637	1	359	284	271	379	362	857	660	545	535	598
ENSMUSG00000029196	chr5	Tada2b	-0.9094045	2.02516E-07	8.20396E-07	3.877970189	0.031609977	-1	274	247	311	360	231	163	195	108	168	198
ENSMUSG00000024892	chr19	Pcx	-1.0979944	2.02896E-07	8.21261E-07	5.721790059	0.050981519	-1	778	1110	795	1226	1403	395	508	566	556	691
ENSMUSG00000037544	chr14	Dlgap5	2.18731015	2.02906E-07	8.21261E-07	0.776596519	0.139186833	1	15	11	5	3	7	44	67	37	41	21
ENSMUSG00000042275	chr13	Pelo	0.81136285	2.02819E-07	8.21261E-07	3.804598161	0.023925477	1	145	133	137	207	132	345	257	296	260	282
ENSMUSG00000007815	chr9	Rhoa	0.78052809	2.04745E-07	8.28464E-07	7.342153757	0.02634481	1	1795	1717	1547	2227	1634	4211	3724	2729	3054	3128
ENSMUSG00000079278	chr5	Tmem233	-1.0081317	2.05184E-07	8.29999E-07	7.541106371	0.043899318	-1	4150	3565	3224	3750	3705	1430	1987	1625	2338	2666
ENSMUSG00000020840	chr11	Blmh	0.77329958	2.06402E-07	8.34688E-07	5.64037704	0.024943261	1	564	570	496	635	470	1157	1093	976	1023	872
ENSMUSG00000029422	chr5	Rsrc2	-0.7604008	2.06718E-07	8.35723E-07	5.228639592	0.023664184	-1	709	707	640	830	618	387	483	429	455	503
ENSMUSG00000042770	chr6	Hebp1	1.38423868	2.07767E-07	8.39721E-07	3.077418871	0.073041771	1	77	72	50	87	58	402	154	151	140	153
ENSMUSG00000066440	chr12	Zfyve26	-0.8052187	2.08678E-07	8.43156E-07	4.126140239	0.024800532	-1	313	308	275	403	347	214	227	167	175	253
ENSMUSG00000039952	chr9	Dag1	-0.9490628	2.09128E-07	8.44732E-07	8.310089783	0.039160391	-1	5520	5376	5187	8419	6812	2873	3622	3676	2915	4524
ENSMUSG00000025066	chr19	Sfr1	0.80156851	2.10703E-07	8.50847E-07	6.150791382	0.027343062	1	864	695	630	1036	665	1351	1723	1388	1363	1519
ENSMUSG00000042729	chr19	Wdr74	0.87068287	2.11305E-07	8.53031E-07	3.84292394	0.028448653	1	140	129	140	195	147	402	315	248	303	240
ENSMUSG00000066800	chr1	Rnasel	1.54163864	2.11657E-07	8.54208E-07	2.079183498	0.080686244	1	29	34	38	17	33	88	96	67	130	114
ENSMUSG00000034462	chr5	Pkd2	-0.7810675	2.12378E-07	8.56869E-07	4.542089079	0.02413098	-1	450	406	431	503	391	329	314	237	205	318
ENSMUSG00000021585	chr13	Cast	-0.7957893	2.13675E-07	8.61852E-07	5.849108799	0.026743875	-1	950	1009	1050	1589	904	658	708	577	684	809
ENSMUSG00000028945	chr5	Rheb	-0.7918786	2.14104E-07	8.63334E-07	5.795457068	0.026443415	-1	1086	990	945	1274	951	622	788	503	727	675
ENSMUSG00000097353	chr10	A430046D13Rik	-0.7374718	2.15644E-07	8.69293E-07	4.375366243	0.020840173	-1	414	347	354	483	333	296	234	240	257	237
ENSMUSG00000035666	chr2	Gtf3c4	-0.73425	2.16601E-07	8.72899E-07	4.697735473	0.021297182	-1	429	438	453	631	463	351	313	305	270	348
ENSMUSG00000026623	chr1	Lpgat1	-0.8418706	2.18711E-07	8.81149E-07	4.956947782	0.029105526	-1	460	558	511	958	526	425	406	334	290	363
ENSMUSG00000038039	chr10	Gcc2	-0.7678155	2.18871E-07	8.81541E-07	4.140087438	0.022284719	-1	332	328	259	425	310	209	240	196	199	214
ENSMUSG00000041445	chr14	Mmrn2	-0.9512187	2.20106E-07	8.86259E-07	4.486947166	0.03682364	-1	383	340	407	723	382	319	208	206	191	330
ENSMUSG00000036553	chr5	Sh3tc1	1.11063201	2.21099E-07	8.89998E-07	2.761244839	0.043086304	1	52	68	56	78	59	197	149	101	116	187
ENSMUSG00000019992	chr10	Mtfr2	2.79682011	2.22088E-07	8.93222E-07	-0.32696283	0.170241679	1	1	6	0	4	1	22	27	18	21	6
ENSMUSG00000040249	chr10	Lrp1	0.96499265	2.22091E-07	8.93222E-07	7.60734087	0.040501671	1	1657	1775	1656	2450	2290	6102	4508	2813	3375	4581
ENSMUSG00000097574	chr9	C920006O11Rik	3.48623513	2.21978E-07	8.93222E-07	-0.773640711	0.215681436	1	3	0	0	1	1	2	22	14	11	18
ENSMUSG00000034602	chr10	Mon2	-0.7935388	2.22432E-07	8.94335E-07	5.346934735	0.026231302	-1	782	649	668	954	791	515	508	347	482	586
ENSMUSG00000010066	chr9	Cacna2d2	-1.8199012	2.22508E-07	8.94383E-07	0.38794112	0.077365094	-1	39	19	25	34	23	12	12	7	6	6
ENSMUSG00000007872	chr4	Id3	1.04611563	2.23546E-07	8.98299E-07	4.848838174	0.045510614	1	232	299	308	349	207	1055	659	541	418	531
ENSMUSG00000027598	chr2	Itch	-0.8048188	2.23928E-07	8.99575E-07	4.722869837	0.026132533	-1	470	460	478	680	423	277	363	260	275	391
ENSMUSG00000036223	chr18	Ska1	2.83597756	2.24372E-07	9.01099E-07	0.072901205	0.206149563	1	6	5	3	1	1	24	44	19	36	7
ENSMUSG00000024939	chr19	Fam89b	0.75309881	2.25608E-07	9.05803E-07	5.199852836	0.023266658	1	411	392	386	467	372	952	640	715	654	807
ENSMUSG00000041180	chr19	Hectd2	-1.7998794	2.26025E-07	9.06955E-07	1.800641846	0.112391929	-1	79	52	63	107	93	17	27	20	46	11
ENSMUSG00000078622	chr11	Ccdc47	-0.8614585	2.25974E-07	9.06955E-07	6.637361297	0.032068718	-1	1867	1825	1628	2413	1856	924	1370	934	1219	1305
ENSMUSG00000000838	chrX	Fmr1	-1.0451157	2.29685E-07	9.21378E-07	2.994567686	0.039373846	-1	171	138	152	174	152	111	98	62	54	99
ENSMUSG00000030872	chr7	Gga2	0.77841581	2.29809E-07	9.21612E-07	5.064000559	0.024845403	1	378	323	334	440	354	585	685	718	637	793
ENSMUSG00000062519	chr6	Zfp398	-1.4126894	2.30536E-07	9.24258E-07	1.476036916	0.058843217	-1	52	64	47	75	53	18	37	20	18	26
ENSMUSG00000029153	chr5	Ociad2	-0.8241777	2.30805E-07	9.25072E-07	5.407359925	0.028523879	-1	890	743	665	849	862	503	464	413	490	630
ENSMUSG00000055093	chr6	Gm8430	1.55205589	2.3104E-07	9.25748E-07	2.837777694	0.09182229	1	90	53	52	37	30	225	208	117	199	108
ENSMUSG00000030122	chr6	Ptms	1.01370072	2.31964E-07	9.29187E-07	7.398661845	0.044718281	1	2081	1500	1463	1566	1637	5008	2830	3515	2574	4653
ENSMUSG00000022555	chr15	Dgat1	0.88417736	2.32551E-07	9.31003E-07	3.884989328	0.029725727	1	154	186	124	154	143	357	269	326	271	326
ENSMUSG00000028453	chr4	Fancg	1.39991884	2.32504E-07	9.31003E-07	1.74841319	0.061020051	1	30	25	24	28	24	117	62	63	84	57
ENSMUSG00000006715	chr13	Gmnn	1.63925141	2.3358E-07	9.34854E-07	2.263434991	0.097743108	1	32	47	35	42	13	124	157	84	144	66
ENSMUSG00000023960	chr17	Enpp5	-0.9189309	2.343E-07	9.37469E-07	3.580300335	0.031493341	-1	227	229	197	266	234	105	149	106	146	162
ENSMUSG00000031109	chrX	Enox2	-0.9139724	2.37321E-07	9.49285E-07	3.885426787	0.03252617	-1	331	259	233	303	297	231	164	108	157	180
ENSMUSG00000034075	chr2	Zdhhc5	-0.8162195	2.37816E-07	9.50993E-07	6.163672651	0.028618535	-1	1192	1181	1219	1967	1313	765	960	779	785	939
ENSMUSG00000032702	chr19	Kank1	-0.8451335	2.38141E-07	9.5202E-07	4.13605101	0.027941564	-1	383	328	217	431	327	243	219	167	194	202
ENSMUSG00000021943	chr14	Gdf10	1.07015605	2.3856E-07	9.53421E-07	3.3653486	0.042866308	1	87	91	123	76	101	263	237	230	182	213
ENSMUSG00000043192	chr8	Gm1840	-1.3120615	2.38822E-07	9.54197E-07	5.605047071	0.073413608	-1	1068	904	835	1211	1137	917	269	358	270	520
ENSMUSG00000064215	chr12	Ifi27	0.87545004	2.3894E-07	9.54395E-07	5.452586666	0.032358021	1	470	563	399	461	386	1090	821	977	725	1007
ENSMUSG00000006941	chr9	Eif1b	0.78593947	2.41903E-07	9.65951E-07	4.921854397	0.025287841	1	339	333	252	445	296	837	679	546	533	546
ENSMUSG00000068744	chr3	Psrc1	2.32953245	2.42191E-07	9.66828E-07	-0.034768463	0.110289977	1	6	7	4	2	1	36	27	18	14	20
ENSMUSG00000019979	chr10	Apaf1	1.05272138	2.42878E-07	9.69291E-07	3.067759874	0.040084882	1	64	83	76	103	74	253	215	136	171	141
ENSMUSG00000040596	chr1	Pogk	-0.9187206	2.4373E-07	9.72417E-07	3.854898429	0.032731093	-1	236	224	242	425	290	208	188	116	152	154

ENSMUSG00000035614	chr12	Fam179b	-1.124964	2.43802E-07	9.72425E-07	3.504215002	0.049252886	-1	208	234	202	313	200	64	147	94	120	149
ENSMUSG00000032849	chr14	Abcc4	-0.8943882	2.45378E-07	9.78432E-07	3.869064942	0.030794947	-1	269	237	232	371	303	147	213	135	143	192
ENSMUSG00000037905	chr5	Bri3bp	0.94618537	2.46915E-07	9.84278E-07	3.133248429	0.031439112	1	79	83	91	97	87	236	212	166	151	168
ENSMUSG00000084883	chr12	Ccdc85c	-2.0303207	2.4744E-07	9.86092E-07	0.889607056	0.124621198	-1	39	35	35	60	42	0	15	8	16	16
ENSMUSG00000029234	chr5	Tmem165	0.80636478	2.47916E-07	9.87424E-07	4.482732352	0.025975305	1	241	235	198	325	215	508	594	347	379	498
ENSMUSG00000092201	chr2	A530058N18Rik	-1.8008668	2.47911E-07	9.87424E-07	4.800892383	0.134432882	-1	783	502	712	608	579	47	196	192	177	390
ENSMUSG00000002718	chr2	Cse1l	-0.9104875	2.49595E-07	9.93827E-07	6.106892425	0.035796268	-1	1376	1116	1180	1726	1326	600	993	623	881	790
ENSMUSG00000042650	chr11	Alkbh5	-0.7768447	2.50903E-07	9.98753E-07	7.034884672	0.026403518	-1	2430	2161	2197	3160	2427	1601	1626	1374	1383	1923
ENSMUSG00000021067	chr12	Sav1	-0.841052	2.51622E-07	1.00133E-06	5.754210202	0.030261827	-1	1084	1057	925	1137	933	561	648	462	699	783
ENSMUSG00000036291	chr14	Ap5m1	-1.1008947	2.54263E-07	1.01136E-06	3.126602872	0.045363455	-1	142	163	200	226	147	70	93	66	92	127
ENSMUSG00000058883	chr13	Zfp708	-1.6592268	2.54287E-07	1.01136E-06	0.964352065	0.077409688	-1	46	39	40	49	35	8	22	7	18	17
ENSMUSG00000020782	chr11	Llgl2	-1.0708657	2.5552E-07	1.01575E-06	2.835784392	0.040859925	-1	147	130	108	163	161	83	84	47	82	76
ENSMUSG00000031358	chrX	Msl3	-0.7435163	2.55537E-07	1.01575E-06	5.113602734	0.022792589	-1	605	650	626	778	561	394	446	378	466	416
ENSMUSG00000041695	chr11	Kcnj2	-1.1368785	2.56704E-07	1.01985E-06	5.638331661	0.05550613	-1	1001	1389	820	1373	568	357	601	546	500	508
ENSMUSG00000041741	chr6	Pde3a	-1.0932795	2.56715E-07	1.01985E-06	2.932284649	0.043333147	-1	124	130	131	251	141	70	93	84	60	84
ENSMUSG00000045328	chr3	Cenpe	1.92556654	2.58237E-07	1.02561E-06	1.839598758	0.132175179	1	25	23	24	23	11	97	159	75	82	31
ENSMUSG00000042063	chr12	Zfp386	-1.1252683	2.58538E-07	1.02651E-06	4.055792297	0.051416391	-1	399	373	275	404	246	110	186	122	234	190
ENSMUSG00000015090	chr2	Ptgds	3.87589792	2.58752E-07	1.02678E-06	0.197780152	0.390120584	1	3	2	0	1	3	30	36	73	5	7
ENSMUSG00000071669	chr16	Snx29	-1.5685091	2.58707E-07	1.02678E-06	1.150788572	0.071019728	-1	44	46	39	59	48	12	14	13	29	18
ENSMUSG00000020185	chr10	E2f7	1.85794502	2.59201E-07	1.02827E-06	0.671256859	0.093741913	1	18	6	4	13	6	40	48	29	40	29
ENSMUSG00000057219	chr11	Armc7	1.4920086	2.59309E-07	1.02841E-06	1.896394886	0.075299023	1	34	28	18	29	30	136	104	57	82	57
ENSMUSG00000017843	chr12	Ppp2r5c	-0.7450739	2.59849E-07	1.03026E-06	6.187839797	0.023940879	-1	1280	1259	1233	1801	1259	925	978	730	861	959
ENSMUSG00000038507	chr6	Parp12	0.85840729	2.64247E-07	1.0474E-06	3.568596518	0.027073869	1	142	118	110	159	96	284	274	176	232	277
ENSMUSG00000079625	chr16	Tm4sf19	4.28652352	2.65957E-07	1.05387E-06	-0.368057784	0.409554162	1	1	2	0	1	0	17	35	1	5	42
ENSMUSG00000034201	chr11	Gas2l1	0.92165314	2.69349E-07	1.06701E-06	3.614231591	0.031968516	1	113	133	103	154	121	384	254	201	203	268
ENSMUSG00000050493	chr4	Fam167b	2.826568	2.70861E-07	1.0727E-06	0.364986444	0.220932866	1	5	8	1	1	5	69	16	34	12	35
ENSMUSG00000031907	chr8	Zfp90	1.21238698	2.71031E-07	1.07307E-06	1.886469256	0.044610395	1	39	33	27	38	23	97	68	75	84	82
ENSMUSG00000007827	chr6	Ankrd26	-1.1552169	2.71644E-07	1.07519E-06	2.030468733	0.041918908	-1	87	65	82	101	75	47	43	27	42	43
ENSMUSG00000027162	chr2	Lin7c	-0.7836429	2.72301E-07	1.07749E-06	4.530662113	0.024706702	-1	390	402	392	627	381	279	332	211	267	296
ENSMUSG00000076432	chr12	Ywhaq	0.83509055	2.73975E-07	1.0838E-06	4.580843941	0.028436332	1	206	256	260	346	212	542	630	367	475	489
ENSMUSG00000027469	chr2	Tpx2	1.52592814	2.74072E-07	1.08388E-06	3.284780641	0.092249978	1	102	87	73	49	51	306	348	204	202	109
ENSMUSG00000039585	chr9	Myo9a	-0.8356573	2.75957E-07	1.09103E-06	4.25008479	0.027867245	-1	364	312	306	443	384	212	239	156	241	264
ENSMUSG00000033228	chr15	Scaf11	-0.7241879	2.76546E-07	1.09304E-06	5.296959931	0.021911433	-1	702	694	641	1004	631	495	500	413	486	522
ENSMUSG00000031278	chrX	Acsl4	-0.887365	2.78449E-07	1.10026E-06	5.133967137	0.033348992	-1	798	683	609	760	537	299	483	367	350	502
ENSMUSG00000029161	chr5	Cgref1	1.36987533	2.80074E-07	1.10636E-06	2.646848607	0.069327724	1	74	48	56	38	35	127	144	184	141	116
ENSMUSG00000033161	chr3	Atp1a1	0.89548547	2.82566E-07	1.11589E-06	7.170623585	0.035441817	1	1486	1240	1226	2127	1499	4058	3818	2580	2320	2656
ENSMUSG00000031156	chrX	Slc35a2	0.87854367	2.82654E-07	1.11592E-06	3.828947868	0.029676111	1	138	150	136	184	132	438	284	277	231	271
ENSMUSG00000041408	chr14	Wapal	-0.7858025	2.83256E-07	1.11798E-06	5.368531109	0.026172289	-1	795	791	641	1045	649	454	599	405	466	549
ENSMUSG00000024897	chr19	Apba1	1.3110824	2.84098E-07	1.12078E-06	1.79236178	0.05293108	1	25	24	31	31	30	106	93	61	58	72
ENSMUSG00000040888	chr17	Gfer	0.86923807	2.84125E-07	1.12078E-06	4.070931835	0.029885172	1	162	180	165	211	160	274	368	355	385	362
ENSMUSG00000049482	chr8	Ctu2	0.96288137	2.84625E-07	1.12244E-06	3.135544419	0.033564071	1	89	74	74	129	76	228	183	203	165	154
ENSMUSG00000067847	chr2	Romo1	0.75612329	2.85323E-07	1.12487E-06	6.099802964	0.024768429	1	813	729	741	903	612	1674	1290	1351	1334	1380
ENSMUSG00000002346	chr8	Slc25a42	-0.801854	2.85925E-07	1.12693E-06	5.48250173	0.027472143	-1	813	880	735	999	795	560	491	417	490	710
ENSMUSG00000072640	chr11	Lyrm9	-0.830756	2.87506E-07	1.13284E-06	3.719476381	0.025687326	-1	264	254	201	285	241	150	141	141	174	159
ENSMUSG00000031985	chr8	Gnpat	-0.7875606	2.88758E-07	1.13745E-06	7.084246589	0.027432538	-1	2155	2428	2236	3684	2418	1665	1646	1602	1516	1680
ENSMUSG00000059900	chr6	Tmem40	3.02109695	2.90504E-07	1.14401E-06	-0.259617301	0.205475063	1	5	1	1	2	2	13	16	42	8	21
ENSMUSG00000036561	chr15	Ppp6r2	-0.8856385	2.91062E-07	1.14588E-06	5.27259811	0.033480402	-1	641	700	603	1037	774	335	444	419	434	568
ENSMUSG00000026754	chr2	Golga1	-0.7612625	2.9329E-07	1.15433E-06	3.924937127	0.02171552	-1	289	269	260	322	270	183	201	168	186	174
ENSMUSG00000024205	chr11	Rpl36-ps2	1.66703647	2.94944E-07	1.16051E-06	0.85046519	0.07375852	1	16	12	8	13	10	60	34	35	48	30
ENSMUSG00000089837	chr15	Npcd	-1.5957207	2.95616E-07	1.16283E-06	1.591969493	0.084186475	-1	62	53	45	85	82	11	26	18	30	32
ENSMUSG00000097317	chr2	Gm17281	-0.8498206	2.98239E-07	1.17282E-06	3.905571507	0.027920206	-1	281	269	263	387	237	159	194	135	209	168
ENSMUSG00000019254	chr7	Ppp1r12c	0.81535311	2.9845E-07	1.17332E-06	4.94054471	0.027804889	1	311	287	284	443	335	914	561	508	640	586
ENSMUSG00000028760	chr4	Eif4g3	-0.9028209	2.98856E-07	1.17458E-06	7.050848638	0.036133234	-1	2457	2184	2271	3148	2800	1172	1612	1300	1455	1985
ENSMUSG00000052151	chr10	Ppap2c	1.37957015	3.00414E-07	1.18037E-06	1.758375632	0.060815723	1	30	30	24	32	18	113	93	50	62	69
ENSMUSG00000045751	chr4	Mms22l	2.24257004	3.01522E-07	1.18439E-06	0.915901047	0.154727309	1	11	16	12	4	1	59	58	42	49	27
ENSMUSG00000051367	chr12	Six1	-0.7905627	3.03303E-07	1.19106E-06	5.864538334	0.027107178	-1	913	993	1068	1531	1024	701	701	690	569	819
ENSMUSG00000020444	chr11	Guk1	0.82942004	3.03718E-07	1.19235E-06	4.969643439	0.02889346	1	371	295	322	391	295	892	577	603	688	508
ENSMUSG00000024127	chr17	Prepl	-0.9866	3.04245E-07	1.19408E-06	4.951716804	0.041510056	-1	587	559	542	717	643	209	356	294	348	473
ENSMUSG00000034560	chr10	A230046K03Rik	-0.9953047	3.048E-07	1.19593E-06	3.896051386	0.039855776	-1	312	284	246	330	292	128	217	99	174	190
ENSMUSG00000051890	chr12	Klhdc1	-1.1864845	3.05714E-07	1.19917E-06	3.962412032	0.057951056	-1	319	329	276	382	298	75	196	120	203	170
ENSMUSG00000014353	chr2	Tmem87b	-0.8401046	3.08272E-07	1.20887E-06	4.536456707	0.029152012	-1	433	471	423	455	410	375	293	189	263	245
ENSMUSG00000034675	chr13	Dbn1	1.22109668	3.08553E-07	1.20963E-06	4.419022242	0.062994443	1	190	205	183	202	165	568	444	722	226	456
ENSMUSG00000074578	chr2	1500012F01Rik	1.16109744	3.138E-07	1.22986E-06	3.529353143	0.053654628	1	113	112	105	105	86	463	222	234	196	189
ENSMUSG00000002731	chr2	Prkra	1.10274613	3.17617E-07	1.24447E-06	3.225511382	0.046566546	1	114	102	82	92	46	266	187	170	210	198
ENSMUSG00000035704	chr7	Alg8	1.28822541	3.18359E-07	1.24703E-06	2.190823205	0.056635835	1	55	29	33	35	38	92	124	83	118	94

ENSMUSG00000078937	chr15	Cpt1b	-0.8142382	3.1876E-07	1.24825E-06	7.963655753	0.029767624	-1	3929	4617	4037	7085	4341	3093	2871	2780	2962	3048
ENSMUSG00000048118	chr12	Arid4a	-1.0478309	3.20005E-07	1.25277E-06	3.345412615	0.042513944	-1	193	167	193	259	201	101	109	59	122	147
ENSMUSG00000030393	chr7	Zik1	-1.6802782	3.20375E-07	1.25387E-06	0.734079192	0.074008662	-1	29	39	29	39	40	7	17	8	13	15
ENSMUSG00000074064	chr8	Mlycd	0.88578579	3.21425E-07	1.25763E-06	5.628488866	0.034175848	1	422	468	421	809	501	944	954	968	1234	1096
ENSMUSG00000030680	chr7	Pagr1a	0.7152823	3.21788E-07	1.25869E-06	4.631823672	0.020591174	1	285	265	248	347	250	619	473	468	479	469
ENSMUSG00000096696	chr17	Zfp960	-1.6941446	3.23742E-07	1.26598E-06	1.185245772	0.08939484	-1	66	33	61	50	36	10	23	12	20	18
ENSMUSG00000074749	chr2	Kiz	-0.8407975	3.24421E-07	1.26828E-06	3.859006641	0.027254841	-1	268	276	263	369	211	158	185	144	195	158
ENSMUSG00000027306	chr2	Nusap1	1.53834263	3.26486E-07	1.276E-06	1.584856141	0.077132174	1	25	18	23	27	16	79	101	65	65	37
ENSMUSG00000031143	chrX	Ccdc22	0.75472257	3.27328E-07	1.27893E-06	4.3361786	0.022676113	1	228	192	181	311	211	509	390	354	420	391
ENSMUSG00000074671	chr2	Tspyl3	1.62401922	3.33565E-07	1.30294E-06	1.11234824	0.075544567	1	11	13	20	16	13	41	37	61	49	59
ENSMUSG00000027187	chr2	Cat	-0.9211845	3.34802E-07	1.3074E-06	6.097017545	0.037463728	-1	972	1348	1102	2013	1310	657	811	622	822	940
ENSMUSG00000004891	chr3	Nes	1.07156513	3.35971E-07	1.31144E-06	6.996553872	0.051149999	1	1340	1153	1258	1393	976	2555	2650	4056	1754	2953
ENSMUSG00000029715	chr5	Pop7	1.00509665	3.36025E-07	1.31144E-06	3.25762765	0.038145306	1	114	74	84	112	84	269	196	209	207	146
ENSMUSG00000041420	chr7	Meis3	1.51495748	3.36391E-07	1.31251E-06	1.221364067	0.066908906	1	19	13	17	19	16	79	45	40	36	68
ENSMUSG00000026457	chr1	Adipor1	-0.7603675	3.36963E-07	1.31437E-06	8.039329916	0.026100848	-1	5293	4483	4176	6104	4671	3581	3191	2674	2949	3614
ENSMUSG00000021591	chr13	Glrx	-0.9007807	3.37187E-07	1.31469E-06	4.888438403	0.034601387	-1	617	586	595	679	392	371	339	221	425	329
ENSMUSG00000056153	chr18	Socs6	-0.9144364	3.37234E-07	1.31469E-06	4.615225845	0.035200628	-1	478	376	427	700	426	213	291	212	290	374
ENSMUSG00000005373	chr5	Mlxipl	-0.8465585	3.3946E-07	1.32267E-06	5.681214688	0.031302129	-1	835	784	834	1465	1042	728	632	590	522	522
ENSMUSG00000041406	chr1	BC055324	2.18844847	3.3947E-07	1.32267E-06	0.39226599	0.131819044	1	9	8	2	7	5	47	43	17	36	15
ENSMUSG00000027379	chr2	Bub1	2.24483868	3.40583E-07	1.32664E-06	0.771980897	0.157740691	1	10	12	2	7	9	33	76	35	47	19
ENSMUSG00000097119	chr17	B230354K17Rik	-0.8624859	3.42673E-07	1.33441E-06	3.325269796	0.027046873	-1	195	183	177	241	161	108	127	87	121	132
ENSMUSG00000033416	chr10	Gucd1	-0.7935391	3.45229E-07	1.34399E-06	5.741038277	0.027509394	-1	966	1080	922	1236	850	723	556	478	691	754
ENSMUSG00000041130	chr17	Zfp598	-0.7416136	3.46094E-07	1.34698E-06	4.492960614	0.022272153	-1	382	379	390	504	432	322	275	217	276	285
ENSMUSG00000025521	chr8	Tmem192	0.81721756	3.47862E-07	1.35349E-06	3.776629658	0.025355076	1	154	128	128	187	138	384	280	216	271	274
ENSMUSG00000025234	chr9	Arih1	-0.8220258	3.48166E-07	1.35422E-06	6.527851562	0.030095863	-1	1818	1574	1564	2183	1659	927	1246	863	1061	1344
ENSMUSG00000027770	chr3	Dhx36	-0.726721	3.48244E-07	1.35422E-06	4.87045575	0.021893136	-1	543	543	481	688	464	320	387	334	338	410
ENSMUSG00000020132	chr10	Rab21	-0.781447	3.52012E-07	1.36849E-06	4.998338762	0.025878987	-1	542	599	571	836	480	402	465	276	359	422
ENSMUSG00000039187	chr7	Fanci	2.76370353	3.53712E-07	1.37433E-06	0.005072166	0.197376475	1	5	0	1	3	7	12	41	19	34	16
ENSMUSG00000086247	chr5	Gm15787	-1.5419749	3.53698E-07	1.37433E-06	0.808516008	0.059632797	-1	40	32	40	41	29	13	17	15	13	10
ENSMUSG00000024395	chr18	Lims2	-0.870606	3.54131E-07	1.37558E-06	4.461849178	0.031613492	-1	344	405	428	514	417	304	209	251	183	325
ENSMUSG00000032263	chr9	Bckdhb	-0.8320763	3.54686E-07	1.37735E-06	4.215649706	0.028092403	-1	402	400	266	357	329	259	207	195	225	200
ENSMUSG00000001285	chr15	Myg1	0.82712907	3.55469E-07	1.38001E-06	3.704740991	0.025760002	1	141	137	125	147	139	321	272	227	292	237
ENSMUSG00000041958	chr11	Pigs	0.73368207	3.58582E-07	1.39171E-06	4.944261365	0.022427852	1	357	352	316	347	330	766	592	573	547	660
ENSMUSG00000016637	chr15	Ift27	1.35844375	3.59138E-07	1.39348E-06	4.932387269	0.080002043	1	396	252	231	205	175	343	770	700	725	995
ENSMUSG00000079109	chr5	Pms2	-1.0801038	3.60619E-07	1.39884E-06	3.086811587	0.044700272	-1	217	199	157	150	119	85	91	73	89	102
ENSMUSG00000031963	chr9	Bmper	1.25201853	3.61498E-07	1.40186E-06	3.247411951	0.06182842	1	72	87	94	51	96	333	216	175	171	193
ENSMUSG00000017485	chr14	Top2b	-0.8022346	3.6215E-07	1.404E-06	5.5445747	0.028041728	-1	873	819	779	1150	813	473	630	428	571	670
ENSMUSG00000017747	chr11	Ghdc	0.95029021	3.62269E-07	1.40407E-06	3.438644183	0.034460986	1	136	103	113	117	74	245	211	215	195	288
ENSMUSG00000041351	chr4	Rap1gap	-1.2899991	3.63555E-07	1.40866E-06	3.363706245	0.067582083	-1	189	162	286	310	140	173	67	74	85	91
ENSMUSG00000035798	chr10	Zdhhc17	-0.8547867	3.64227E-07	1.41087E-06	4.027678514	0.029256074	-1	317	263	255	415	315	165	210	147	185	236
ENSMUSG00000035476	chrX	Tab3	-0.974088	3.65137E-07	1.41401E-06	2.74194513	0.033004446	-1	127	108	115	171	132	79	78	55	67	85
ENSMUSG00000041733	chr5	Coq5	-0.7766048	3.67748E-07	1.42372E-06	6.609573114	0.026978565	-1	1582	1769	1714	2661	1553	1343	1103	1107	1041	1291
ENSMUSG00000006014	chr1	Prg4	2.59927134	3.68406E-07	1.42588E-06	4.614566135	0.271551381	1	145	50	87	208	47	1565	668	307	867	85
ENSMUSG00000027680	chr3	Fxr1	-0.9701201	3.70736E-07	1.4345E-06	8.361839305	0.042653155	-1	7189	6128	5769	7542	5831	2458	3735	3036	4125	4689
ENSMUSG00000034807	chr8	Colgalt1	0.7286323	3.71898E-07	1.4386E-06	6.124642847	0.023441103	1	741	775	665	978	756	1586	1510	1229	1246	1550
ENSMUSG00000027423	chr2	Snx5	0.8452776	3.72163E-07	1.43922E-06	6.421274484	0.031929785	1	1002	902	758	1113	801	1686	2108	1268	2045	1879
ENSMUSG00000038533	chr2	Cbfa2t2	-0.7243016	3.72615E-07	1.44057E-06	4.43900185	0.021144125	-1	396	364	383	488	374	333	242	245	225	290
ENSMUSG00000050312	chr16	Nsun3	-1.1429938	3.73068E-07	1.44193E-06	2.855640606	0.049280335	-1	151	150	142	176	114	61	68	59	57	119
ENSMUSG00000034858	chr9	Fam214a	-0.8731714	3.73548E-07	1.44338E-06	4.492041921	0.031979736	-1	455	478	328	503	397	249	220	224	232	369
ENSMUSG00000019370	chr7	Calm3	-0.8899185	3.74216E-07	1.44556E-06	8.318052521	0.036000863	-1	7469	6159	4991	5771	6203	3584	3919	2812	3897	4075
ENSMUSG00000019838	chr10	Slc16a10	-0.8239695	3.74374E-07	1.44577E-06	5.293149091	0.029474175	-1	689	596	653	899	879	471	509	363	426	545
ENSMUSG00000033082	chr6	Clec1a	-1.3944544	3.81227E-07	1.47183E-06	1.456497158	0.060335182	-1	56	55	63	69	42	15	25	21	23	34
ENSMUSG00000039232	chr10	Stx11	1.80909928	3.86164E-07	1.49048E-06	0.270646854	0.070122167	1	10	7	3	8	7	30	33	20	28	25
ENSMUSG00000097431	chr14	Gm26782	1.92174185	3.86467E-07	1.49124E-06	1.228133899	0.121963228	1	16	17	13	14	8	21	69	49	73	69
ENSMUSG00000047832	chr12	Cdca4	1.19070012	3.90858E-07	1.50777E-06	2.770474782	0.053325328	1	47	69	56	80	52	175	195	112	176	102
ENSMUSG00000025485	chr7	Ric8	0.79208069	3.93326E-07	1.51687E-06	4.870372994	0.0266169	1	349	342	273	365	260	685	556	673	578	509
ENSMUSG00000078716	chr4	Tmem8b	-0.92409	3.93937E-07	1.5188E-06	4.405195403	0.035981664	-1	308	346	379	673	386	242	271	266	194	211
ENSMUSG00000028207	chr4	Asph	-0.7840077	3.97681E-07	1.53282E-06	8.544903451	0.028162187	-1	7633	6008	5864	8687	7110	4845	4623	3740	4149	5128
ENSMUSG00000000320	chr11	Alox12	2.65506805	3.98382E-07	1.53509E-06	0.297855596	0.202399723	1	5	3	2	6	6	7	22	45	28	49
ENSMUSG00000025792	chr11	Slc25a10	1.18238243	4.00338E-07	1.54221E-06	3.483706786	0.05654825	1	64	154	81	94	103	258	242	273	191	286
ENSMUSG00000007655	chr6	Cav1	-0.8145326	4.07227E-07	1.56831E-06	7.534024557	0.030254562	-1	3131	3924	3542	4390	2649	2259	2096	2055	2009	2550
ENSMUSG00000025574	chr11	Tk1	1.44331586	4.08927E-07	1.57442E-06	3.090957344	0.08407822	1	80	79	61	64	49	268	274	132	241	90
ENSMUSG00000027751	chr3	Supt20	-1.1948813	4.12363E-07	1.58722E-06	2.500962545	0.052251491	-1	114	121	118	117	102	51	68	29	61	68
ENSMUSG00000044876	chr7	Zfp444	0.96533109	4.14449E-07	1.59448E-06	2.888395356	0.033294262	1	70	68	64	101	66	186	134	164	160	139
ENSMUSG00000059901	chr10	Adamts14	1.5115715	4.14479E-07	1.59448E-06	2.559470289	0.088496813	1	33	47	46	42	51	166	121	217	74	112

ENSMUSG00000033392	chr9	Clasp2	-0.8161819	4.14655E-07	1.59472E-06	5.646046963	0.029448202	-1	856	909	735	1377	927	535	633	586	506	690
ENSMUSG00000018143	chr5	Mafk	-0.8906668	4.15568E-07	1.59779E-06	4.167641602	0.03304451	-1	316	304	345	452	319	329	196	156	168	187
ENSMUSG00000022508	chr16	Bcl6	-1.3262911	4.15738E-07	1.59801E-06	5.627980059	0.078142651	-1	919	710	1089	677	1684	544	455	305	442	574
ENSMUSG00000037349	chr19	Nudt22	0.94950415	4.18126E-07	1.60675E-06	3.363874462	0.034772129	1	89	106	86	140	98	274	203	253	162	201
ENSMUSG00000035397	chr10	Klf16	1.22334985	4.21226E-07	1.61734E-06	2.779565	0.057044952	1	52	54	54	75	65	263	143	116	148	108
ENSMUSG00000036745	chr3	Ttll7	-1.0892291	4.21191E-07	1.61734E-06	5.448957607	0.052736988	-1	952	711	780	973	981	251	569	386	501	551
ENSMUSG00000062960	chr5	Kdr	-1.0954267	4.2123E-07	1.61734E-06	5.68984277	0.053565669	-1	746	935	896	2073	765	467	526	593	424	660
ENSMUSG00000023904	chr17	Hcfc1r1	0.91209363	4.22972E-07	1.62358E-06	7.07500499	0.037852012	1	1813	1346	1169	1545	1103	4104	2197	2727	2576	2848
ENSMUSG00000026024	chr1	Als2	-0.7601514	4.2369E-07	1.62589E-06	4.531057137	0.023957749	-1	470	412	365	527	389	256	300	221	284	335
ENSMUSG00000029474	chr5	Rnf34	-0.7537985	4.26213E-07	1.6349E-06	4.440119999	0.02333482	-1	417	383	373	449	391	233	268	247	247	315
ENSMUSG00000031722	chr8	Hp	2.89559923	4.26272E-07	1.6349E-06	4.168443583	0.329689637	1	7	157	35	16	83	584	351	800	353	449
ENSMUSG00000026361	chr1	Cdc73	-0.8142542	4.28582E-07	1.64331E-06	4.82965494	0.028388165	-1	523	467	466	710	539	288	369	335	259	424
ENSMUSG00000040026	chr7	Saa3	3.97685533	4.32786E-07	1.65897E-06	1.352589697	0.516333825	1	1	4	1	14	2	281	17	29	33	25
ENSMUSG00000034371	chr19	Dak	1.19131134	4.3548E-07	1.66884E-06	2.119980565	0.047570991	1	38	34	34	48	37	100	69	100	85	123
ENSMUSG00000051306	chr5	Usp42	-0.9587704	4.37584E-07	1.67644E-06	2.719861582	0.032108576	-1	133	109	111	166	122	84	68	60	62	87
ENSMUSG00000024424	chr18	Ttc39c	1.46294799	4.37895E-07	1.67718E-06	1.542182525	0.068752678	1	19	17	23	25	25	80	89	47	73	44
ENSMUSG00000024238	chr18	Zeb1	-0.7457848	4.40443E-07	1.68647E-06	5.349936067	0.02426873	-1	735	658	653	980	785	491	518	469	421	584
ENSMUSG00000038489	chr7	Polr2l	0.75365285	4.41105E-07	1.68855E-06	5.279732444	0.02467791	1	463	405	405	491	381	1089	754	703	734	712
ENSMUSG00000023336	chr8	Wfdc1	-0.7530705	4.43087E-07	1.69567E-06	6.432835441	0.025625685	-1	1675	1455	1475	1915	1549	1028	1110	909	1136	1055
ENSMUSG00000024712	chr19	Rfk	-0.7706434	4.4437E-07	1.70011E-06	6.158208445	0.026697483	-1	1437	1269	1190	1729	1118	780	973	723	905	916
ENSMUSG00000055435	chr8	Maf	-0.922799	4.45336E-07	1.70334E-06	7.236571497	0.038957484	-1	3043	2682	2518	3505	2958	1282	1937	1349	1566	2368
ENSMUSG00000030609	chr7	Aen	-0.8728305	4.47639E-07	1.71168E-06	4.681256437	0.032741069	-1	429	437	475	673	463	237	394	240	319	279
ENSMUSG00000037253	chr18	Mex3c	-0.9420171	4.49183E-07	1.71712E-06	3.760395216	0.036006442	-1	227	269	266	341	219	186	192	101	162	115
ENSMUSG00000029461	chr7	Fam168a	-0.8082975	4.49858E-07	1.71923E-06	5.459728404	0.028884501	-1	734	694	744	1257	790	499	552	420	515	624
ENSMUSG00000044350	chr14	Lacc1	1.40914582	4.50277E-07	1.72036E-06	1.95079163	0.068930835	1	27	41	29	29	24	115	80	59	64	129
ENSMUSG00000029472	chr5	Anapc5	-0.8296248	4.52714E-07	1.7292E-06	8.616446074	0.031823497	-1	7888	6472	5921	8899	8238	5231	4931	3672	4973	4322
ENSMUSG00000021051	chr12	Ppp2r5e	-0.7258016	4.54236E-07	1.73453E-06	5.02673298	0.022554941	-1	612	552	504	744	611	360	416	358	404	457
ENSMUSG00000018669	chr11	Cdk5rap3	0.72032197	4.55092E-07	1.737E-06	4.765910838	0.021741984	1	324	288	272	343	293	550	538	493	604	559
ENSMUSG00000059890	chr9	Ube4a	-0.7250986	4.5513E-07	1.737E-06	5.203740912	0.022790308	-1	766	666	588	715	660	490	505	381	413	480
ENSMUSG00000031078	chr7	Cttn	0.75167354	4.58507E-07	1.74941E-06	5.441453766	0.024828701	1	473	495	425	590	427	968	918	959	748	837
ENSMUSG00000027375	chr2	Mal	-1.4055893	4.71721E-07	1.79934E-06	2.197537145	0.073963987	-1	47	90	123	129	95	35	48	39	35	43
ENSMUSG00000038268	chr11	Ovca2	0.86705827	4.7503E-07	1.81147E-06	3.264766584	0.027689685	1	114	89	91	117	89	188	200	202	209	195
ENSMUSG00000025487	chr7	Psmd13	0.7799403	4.76156E-07	1.81526E-06	6.726016433	0.027809596	1	1262	1162	1030	1449	925	2457	2151	2071	2353	1857
ENSMUSG00000071847	chr18	Apcdd1	-1.3323078	4.76823E-07	1.81731E-06	2.029920347	0.06339727	-1	73	106	71	67	100	40	32	30	38	45
ENSMUSG00000012443	chr19	Kif11	1.69935863	4.77031E-07	1.81761E-06	2.297697262	0.112165349	1	45	27	31	41	24	112	204	109	124	44
ENSMUSG00000054418	chr11	2900041M22Rik	1.96462697	4.79842E-07	1.82782E-06	0.112260551	0.083365646	1	11	6	4	3	4	33	24	19	24	23
ENSMUSG00000086564	chr3	Cd101	-2.0167388	4.8135E-07	1.83306E-06	0.180272536	0.101407481	-1	36	29	18	21	18	10	10	3	6	4
ENSMUSG00000040006	chr10	Ginm1	-0.773949	4.86034E-07	1.8504E-06	5.731251192	0.026819563	-1	934	1017	839	1304	918	614	678	480	671	758
ENSMUSG00000025374	chr10	Nabp2	0.68544015	4.8915E-07	1.86175E-06	5.239712116	0.020351036	1	441	383	366	586	393	796	778	717	727	771
ENSMUSG00000054545	chr1	Ugt1a6a	1.89862101	4.94445E-07	1.8814E-06	2.903787265	0.146600685	1	38	80	43	22	40	413	165	96	166	129
ENSMUSG00000073491	chr1	Pydc4	3.70923594	4.94607E-07	1.8815E-06	-0.628390428	0.29582547	1	0	1	1	3	0	1	31	14	12	19
ENSMUSG00000022464	chr15	Slc38a4	-1.0568075	4.96429E-07	1.88792E-06	6.485764036	0.051058374	-1	1588	1694	1434	2011	2223	650	878	801	1005	1392
ENSMUSG00000073902	chr7	Gm1966	4.15914565	4.9882E-07	1.89649E-06	-0.514320657	0.394425638	1	0	1	1	2	0	0	22	8	37	19
ENSMUSG00000021660	chr13	Btf3	0.78498712	5.0059E-07	1.9027E-06	7.266969434	0.028474987	1	1786	1634	1364	2144	1540	4142	3407	2751	2999	2687
ENSMUSG00000046591	chr7	Ticrr	2.64367479	5.04707E-07	1.91783E-06	-0.240529331	0.16013545	1	4	6	1	2	1	28	31	19	15	7
ENSMUSG00000028403	chr4	Zdhhc21	-0.7797005	5.05088E-07	1.91876E-06	4.279982576	0.025171722	-1	319	316	343	475	371	266	264	209	232	191
ENSMUSG00000034108	chr19	Ccs	0.80835972	5.0526E-07	1.91889E-06	4.131500811	0.026807519	1	195	194	146	221	186	380	314	303	350	465
ENSMUSG00000040848	chr1	Sft2d2	0.857948	5.12822E-07	1.94708E-06	4.687388735	0.031885857	1	272	274	267	307	234	393	553	536	528	669
ENSMUSG00000020868	chr11	Xylt2	0.92653903	5.14322E-07	1.95119E-06	3.505192358	0.033960004	1	114	136	112	125	87	317	199	205	202	286
ENSMUSG00000021009	chr12	Ptpn21	-0.7906189	5.14114E-07	1.95119E-06	4.944165278	0.027236258	-1	573	457	467	769	646	395	368	390	295	386
ENSMUSG00000098652	chr16	Gm27671	-2.1560363	5.14302E-07	1.95119E-06	-0.208482821	0.092691331	-1	22	10	16	30	15	3	5	4	3	7
ENSMUSG00000003062	chr13	Stard3nl	1.08031024	5.15462E-07	1.95498E-06	2.730432892	0.043132841	1	63	72	56	74	46	179	146	89	153	159
ENSMUSG00000018417	chr1	Myo1b	-0.7185827	5.1587E-07	1.956E-06	4.213440493	0.020821286	-1	328	324	303	447	316	254	219	203	199	267
ENSMUSG00000063320	chr10	1190007I07Rik	1.4948851	5.18013E-07	1.96359E-06	2.629495217	0.088786814	1	46	52	55	57	26	65	186	154	152	162
ENSMUSG00000046731	chr11	Kctd11	1.12861423	5.18942E-07	1.96658E-06	2.906768444	0.049617328	1	62	67	56	94	67	195	187	204	121	115
ENSMUSG00000052934	chr8	Fbxo31	-0.7604546	5.19129E-07	1.96675E-06	6.730083759	0.026617354	-1	1987	1823	1603	2577	1999	1581	1171	1065	1210	1439
ENSMUSG00000004070	chr16	Hmox2	0.72400607	5.23435E-07	1.98253E-06	5.436498196	0.023189623	1	488	465	422	617	444	1058	825	704	901	923
ENSMUSG00000021577	chr13	Sdha	-0.8495313	5.27188E-07	1.9962E-06	9.947796344	0.033841101	-1	16261	18894	18983	26931	14506	11060	10489	10551	12094	13217
ENSMUSG00000029671	chr6	Wnt16	-3.4954605	5.28153E-07	1.99931E-06	-0.286656944	0.32746203	-1	0	26	18	31	23	2	4	0	1	2
ENSMUSG00000031453	chr8	Rasa3	0.71349221	5.28445E-07	1.99988E-06	4.786986965	0.021616208	1	342	303	294	374	242	693	576	454	504	578
ENSMUSG00000091736	chrX	Yy2	-1.7228215	5.28992E-07	2.00141E-06	0.993824503	0.093928198	-1	50	32	25	57	53	8	22	9	16	16
ENSMUSG00000064147	chr17	Rab44	1.65614502	5.33738E-07	2.01881E-06	0.676722797	0.071014321	1	9	14	9	12	8	40	25	39	43	33
ENSMUSG00000103847	chr16	RP23-123L9.5	3.4454205	5.36926E-07	2.03032E-06	-0.057371931	0.322084403	1	2	1	0	6	1	37	30	3	8	47
ENSMUSG00000000028	chr16	Cdc45	1.30503946	5.38196E-07	2.03458E-06	2.226375175	0.062107806	1	36	36	37	45	40	110	131	122	101	60
ENSMUSG00000035181	chr12	Heatr5a	-0.8612596	5.38542E-07	2.03533E-06	4.511475441	0.032035123	-1	371	373	428	646	388	242	295	181	276	326

ENSMUSG00000050989	chr4	Sepn1	0.7901695	5.41431E-07	2.0457E-06	4.582816778	0.026617074	1	233	235	277	315	239	700	465	423	416	483
ENSMUSG00000036473	chr17	Tbc1d24	-1.0188079	5.42363E-07	2.04867E-06	3.243511875	0.040979647	-1	131	180	175	287	172	81	100	95	103	124
ENSMUSG00000038774	chr10	Ascc3	-0.920464	5.51437E-07	2.08238E-06	3.858610533	0.035194594	-1	287	231	237	390	272	179	210	100	182	146
ENSMUSG00000038352	chr11	Arl5c	1.49099299	5.51796E-07	2.08317E-06	1.239071637	0.069252113	1	15	19	15	25	13	86	60	43	42	39
ENSMUSG00000030427	chr7	Lilra6	3.28177039	5.53976E-07	2.09083E-06	1.431367795	0.378831175	1	7	4	5	7	11	229	57	4	58	44
ENSMUSG00000044296	chr11	Zfp879	-1.4484711	5.55086E-07	2.0939E-06	1.006946439	0.059499024	-1	42	44	41	46	34	13	16	13	15	26
ENSMUSG00000055991	chr5	Zkscan5	-0.8151443	5.55075E-07	2.0939E-06	3.409361521	0.024937347	-1	216	173	173	264	180	125	129	122	108	138
ENSMUSG00000029086	chr5	Prom1	-1.9463713	5.55988E-07	2.09673E-06	2.668347299	0.156041466	-1	103	170	154	218	103	118	24	19	31	26
ENSMUSG00000013584	chr9	Aldh1a2	2.80864839	5.57409E-07	2.10152E-06	2.16135607	0.302862223	1	19	8	27	21	5	323	55	100	130	21
ENSMUSG00000023143	chr16	Nagpa	0.91710321	5.61146E-07	2.11504E-06	3.463218196	0.033222653	1	113	107	96	157	94	337	259	182	174	225
ENSMUSG00000005611	chr7	Mrvi1	-1.0887805	5.66674E-07	2.13473E-06	2.666063896	0.044494288	-1	106	127	95	171	137	94	54	61	50	69
ENSMUSG00000025001	chr19	Hells	1.7849253	5.66597E-07	2.13473E-06	1.419220819	0.110492212	1	18	20	17	17	12	62	106	43	78	31
ENSMUSG00000019731	chr8	Slc35e1	-0.7372943	5.67639E-07	2.13779E-06	5.731914444	0.024574441	-1	881	917	851	1282	1025	769	668	516	645	665
ENSMUSG00000071456	chr12	1110002L01Rik	-1.0081285	5.7084E-07	2.14926E-06	2.812788114	0.037638083	-1	142	105	134	160	146	63	83	68	75	85
ENSMUSG00000019210	chr6	Atp6v1e1	0.76195064	5.72606E-07	2.15533E-06	6.923841883	0.026987507	1	1506	1303	1121	1628	1171	3301	2521	2094	2085	2565
ENSMUSG00000022204	chr14	Ngdn	0.83366313	5.73604E-07	2.15851E-06	4.018217477	0.028619842	1	168	181	154	232	132	440	348	313	320	265
ENSMUSG00000036636	chr17	Clcn7	0.79369753	5.75204E-07	2.16394E-06	4.622802822	0.02708434	1	234	264	270	311	252	511	531	397	438	673
ENSMUSG00000071711	chr15	Mpst	-0.8129875	5.85941E-07	2.20374E-06	5.577846456	0.030000382	-1	1092	933	798	915	766	542	608	477	484	720
ENSMUSG00000028898	chr4	Trnau1ap	0.95021213	5.86761E-07	2.20624E-06	3.714967457	0.037157438	1	136	113	113	175	127	427	263	206	298	217
ENSMUSG00000019173	chr11	Rab5c	0.75526266	5.86964E-07	2.2064E-06	5.829399421	0.025916913	1	647	598	593	714	585	1524	1223	855	1161	1101
ENSMUSG00000028837	chr4	Psmb2	0.74422904	5.88797E-07	2.21262E-06	6.114047112	0.025399654	1	781	768	647	1033	654	1714	1460	1274	1406	1230
ENSMUSG00000029452	chr5	Tmem116	1.88974376	5.88935E-07	2.21262E-06	0.399048017	0.092591576	1	9	10	6	8	4	24	21	34	27	45
ENSMUSG00000037197	chr2	Rbm17	0.72519606	5.9021E-07	2.21682E-06	5.168468246	0.023221482	1	420	385	300	544	381	876	734	710	647	686
ENSMUSG00000020390	chr11	Ube2b	-0.7606559	5.92323E-07	2.22415E-06	8.122527838	0.027282183	-1	5668	5174	4366	6716	4366	3793	3533	2648	3449	3528
ENSMUSG00000026749	chr2	Nek6	1.07723224	5.93607E-07	2.22838E-06	4.238457397	0.050960213	1	180	152	142	236	192	482	461	246	593	297
ENSMUSG00000026339	chr1	Ccdc93	-0.8663036	5.97385E-07	2.24196E-06	4.160077962	0.031928038	-1	305	319	334	450	309	259	167	155	260	189
ENSMUSG00000057234	chr2	Mettl15	-1.1237952	6.02051E-07	2.25882E-06	2.040560497	0.041892983	-1	85	88	68	107	64	43	40	30	44	49
ENSMUSG00000076372	chr16	Mir568	-1.7858296	6.02201E-07	2.25882E-06	0.65377355	0.090046949	-1	34	29	33	50	25	3	14	11	8	17
ENSMUSG00000027304	chr2	Rtf1	-0.7073478	6.0522E-07	2.26953E-06	5.377076927	0.022291404	-1	709	711	655	1063	725	541	507	485	472	567
ENSMUSG00000039748	chr1	Exo1	2.23940039	6.06925E-07	2.27532E-06	0.065626498	0.122348921	1	8	2	4	3	6	20	41	20	26	15
ENSMUSG00000057716	chr6	Tmem178b	-1.5338356	6.08708E-07	2.28139E-06	1.538343796	0.081795108	-1	52	63	58	95	46	18	27	25	10	37
ENSMUSG00000027368	chr2	Dusp2	1.9540207	6.11607E-07	2.29164E-06	0.980929749	0.122991875	1	15	9	10	4	16	82	53	40	35	30
ENSMUSG00000021636	chr13	Marveld2	1.90107487	6.13212E-07	2.29704E-06	0.278229663	0.089338481	1	10	4	6	12	2	27	25	34	21	31
ENSMUSG00000042742	chr6	B630005N14Rik	-1.1145245	6.14445E-07	2.30104E-06	3.120523955	0.050520168	-1	190	142	181	195	165	74	102	58	71	141
ENSMUSG00000051351	chr4	Zfp46	-1.0561308	6.15025E-07	2.3026E-06	4.574540406	0.049984988	-1	412	424	526	624	408	453	218	202	151	259
ENSMUSG00000020576	chr12	Nbas	-0.7284586	6.16693E-07	2.30822E-06	4.377626705	0.022173942	-1	416	336	294	509	381	271	274	224	250	253
ENSMUSG00000050010	chr5	Shisa3	-1.4997567	6.17175E-07	2.30941E-06	1.317725568	0.074466901	-1	50	50	60	44	55	18	27	10	24	23
ENSMUSG00000027951	chr3	Adar	0.94380453	6.18405E-07	2.31339E-06	3.297544244	0.035129817	1	97	81	103	139	78	258	235	144	167	249
ENSMUSG00000036748	chr19	Cuedc2	0.68765496	6.20037E-07	2.31888E-06	5.761039894	0.021387923	1	598	609	566	761	559	1319	1087	953	1011	1103
ENSMUSG00000042608	chr4	Stk40	-1.0961023	6.21761E-07	2.3247E-06	6.330266216	0.05579216	-1	1356	1186	1330	2498	1891	1271	933	580	889	554
ENSMUSG00000005779	chr3	Psmb4	0.76339682	6.39518E-07	2.39045E-06	7.152031038	0.027406626	1	1664	1598	1457	1846	1291	3630	2862	2658	2949	2533
ENSMUSG00000007080	chr5	Pole	1.50773702	6.43812E-07	2.40586E-06	1.494150453	0.076394081	1	16	32	17	22	16	54	82	61	76	48
ENSMUSG00000062257	chr9	Opcml	-1.3580623	6.45874E-07	2.41292E-06	1.504011525	0.060411223	-1	50	50	51	80	63	19	28	17	23	38
ENSMUSG00000049327	chr5	Setd8	-0.7889538	6.47217E-07	2.41729E-06	6.359385324	0.028976458	-1	1587	1540	1366	1838	1413	852	1171	808	1048	1020
ENSMUSG00000045777	chr7	Ifitm10	2.02476368	6.47668E-07	2.41833E-06	2.312284002	0.165481613	1	35	30	27	25	23	37	79	130	117	262
ENSMUSG00000037896	chr12	Rcor1	-0.8213449	6.49801E-07	2.42564E-06	3.960606273	0.027912312	-1	295	241	261	412	276	164	213	142	174	221
ENSMUSG00000002844	chr16	Adprh	0.70353406	6.50591E-07	2.42795E-06	5.605192604	0.022398208	1	574	525	494	684	484	1026	973	1018	882	1002
ENSMUSG00000027195	chr2	Hsd17b12	0.97673009	6.55503E-07	2.44562E-06	4.094857434	0.041205074	1	155	181	155	207	153	411	527	230	393	285
ENSMUSG00000026761	chr2	Orc4	-0.8347839	6.55907E-07	2.44648E-06	3.836924987	0.028665539	-1	285	264	247	324	236	165	200	115	193	160
ENSMUSG00000024384	chr18	Iws1	-0.7158026	6.60889E-07	2.4644E-06	4.767398163	0.022217453	-1	488	442	468	617	499	344	409	305	295	325
ENSMUSG00000042797	chr7	Aqp11	2.25122976	6.6284E-07	2.47102E-06	0.158418555	0.137595508	1	6	2	3	7	7	13	19	28	25	46
ENSMUSG00000048368	chr13	Omd	-1.910315	6.6739E-07	2.48732E-06	0.43349519	0.108195076	-1	37	32	33	23	20	18	6	6	4	9
ENSMUSG00000065126	chr11	Snord104	1.97490082	6.67808E-07	2.48821E-06	0.508220832	0.113300474	1	8	10	7	7	6	59	22	22	43	22
ENSMUSG00000036968	chr5	Cnpy4	1.09185738	6.72273E-07	2.50418E-06	3.120913218	0.047922741	1	80	78	58	98	93	292	218	164	147	140
ENSMUSG00000079487	chrX	Med12	-0.8189865	6.78602E-07	2.52708E-06	4.315657098	0.028949292	-1	360	323	328	462	411	253	224	194	185	321
ENSMUSG00000067058	chr5	Rps15a-ps5	1.3478936	6.80683E-07	2.53416E-06	1.756200225	0.06155834	1	21	34	30	29	21	62	84	86	79	65
ENSMUSG00000028977	chr4	Casz1	-1.0197184	6.88247E-07	2.56163E-06	5.060720843	0.047507351	-1	537	517	465	1161	719	287	355	418	295	426
ENSMUSG00000040123	chr14	Zmym5	-0.7318015	6.95827E-07	2.58916E-06	4.247118352	0.022380895	-1	373	369	274	436	312	244	248	186	226	258
ENSMUSG00000034981	chr5	Parm1	-1.0703962	6.97068E-07	2.59309E-06	5.248347343	0.052772278	-1	832	699	600	864	824	250	416	268	511	543
ENSMUSG00000001666	chr10	Ddt	0.77082819	7.04484E-07	2.61928E-06	4.343972254	0.025307172	1	227	253	218	246	164	462	388	426	372	427
ENSMUSG00000024273	chr18	2700062C07Rik	1.11378476	7.04401E-07	2.61928E-06	1.912029575	0.039765386	1	30	32	29	51	30	98	78	72	77	81
ENSMUSG00000037622	chr4	Wdtc1	-0.7633	7.08989E-07	2.63533E-06	6.704215401	0.02747438	-1	1860	1730	1724	2502	1982	1444	1157	1181	1032	1517
ENSMUSG00000036242	chr14	3632451O06Rik	1.04986432	7.10005E-07	2.6384E-06	3.175852743	0.04440471	1	102	87	74	81	84	166	149	214	222	219
ENSMUSG00000074151	chr8	Nlrc5	1.65841542	7.10506E-07	2.63956E-06	1.181049009	0.089209223	1	10	26	13	8	17	66	53	42	44	60
ENSMUSG00000050761	chr16	Gp1bb	1.52496726	7.11753E-07	2.64349E-06	1.810061813	0.085869287	1	25	29	19	36	21	123	83	97	65	40

ENSMUSG00000098543	chr19	Gm27533	1.26173677	7.13386E-07	2.64885E-06	4.129107368	0.070736244	1	168	188	118	129	148	216	343	344	541	532
ENSMUSG00000098530	chr12	Gm28051	-1.4475185	7.19624E-07	2.67131E-06	1.687658031	0.076411686	-1	73	57	66	85	60	49	23	12	19	36
ENSMUSG00000008682	chrX	Rpl10	0.8185042	7.2144E-07	2.67733E-06	8.177933711	0.032060932	1	3297	2732	2329	4288	3119	7857	6688	4908	5503	5434
ENSMUSG00000019362	chr8	D8Ertd738e	0.76612288	7.24099E-07	2.68578E-06	6.493252154	0.027614916	1	1092	941	833	1232	887	2247	1733	1797	1921	1547
ENSMUSG00000021608	chr13	Lpcat1	0.95610342	7.24099E-07	2.68578E-06	3.387101892	0.036970647	1	110	92	105	133	85	306	282	151	183	204
ENSMUSG00000080935	chr5	Got2-ps1	-1.1730231	7.24576E-07	2.68683E-06	3.577064416	0.059275583	-1	145	229	272	387	203	77	124	108	120	161
ENSMUSG00000005583	chr13	Mef2c	-0.7723397	7.31462E-07	2.71165E-06	8.628407318	0.028658675	-1	8192	6560	6870	9169	6524	4465	4754	4338	4678	5589
ENSMUSG00000015143	chr12	Actn1	1.1019139	7.41887E-07	2.74957E-06	4.577450772	0.055209013	1	214	174	161	344	247	796	612	414	269	601
ENSMUSG00000049804	chrX	Armcx4	-1.0211195	7.42088E-07	2.74958E-06	5.386404376	0.04833172	-1	669	565	808	1361	832	318	517	489	478	421
ENSMUSG00000033715	chr13	Akr1c14	-2.140877	7.60664E-07	2.81766E-06	0.687922479	0.14969959	-1	54	40	34	36	19	3	7	4	11	20
ENSMUSG00000033658	chr8	Ddx19b	-0.7532653	7.66601E-07	2.8389E-06	4.717929628	0.025039612	-1	510	463	432	566	477	269	386	277	317	341
ENSMUSG00000033671	chr1	Cep350	-0.7967697	7.67043E-07	2.83978E-06	5.050010287	0.028766867	-1	551	500	590	836	658	331	396	346	424	466
ENSMUSG00000019866	chr10	Aim1	1.28066355	7.67824E-07	2.84192E-06	2.673225957	0.065990305	1	48	59	46	59	57	187	198	70	158	116
ENSMUSG00000019590	chr11	Cyb561	1.13089754	7.69704E-07	2.84813E-06	2.914149426	0.051019435	1	41	65	70	83	84	235	152	129	168	151
ENSMUSG00000030522	chr7	Mtmr10	-0.8274099	7.70233E-07	2.84933E-06	4.271849169	0.029787575	-1	385	336	397	397	307	198	251	168	242	272
ENSMUSG00000036667	chr6	Fam115a	0.91259246	7.72419E-07	2.85666E-06	4.225530742	0.036670036	1	204	190	164	237	168	309	342	487	338	485
ENSMUSG00000032691	chr11	Nlrp3	2.87848037	7.74886E-07	2.86503E-06	0.177655833	0.24566088	1	2	4	1	5	5	63	37	5	26	14
ENSMUSG00000045128	chr8	Rpl18a	0.80973698	7.76545E-07	2.8704E-06	8.360177182	0.031584104	1	3942	3498	3288	3703	3248	9315	6581	6158	6351	5941
ENSMUSG00000048234	chr1	Rnf149	1.15667162	7.81588E-07	2.88828E-06	3.718163023	0.058367633	1	111	125	110	165	94	483	303	155	189	373
ENSMUSG00000002058	chr11	Unc119	0.93466688	7.82626E-07	2.89135E-06	3.646010967	0.036369441	1	160	134	114	114	106	257	251	223	239	360
ENSMUSG00000020358	chr11	Hnrnpab	0.82951095	7.83772E-07	2.89482E-06	7.184193475	0.032911537	1	1516	1345	1250	2119	1624	3719	3756	2672	2652	2457
ENSMUSG00000046345	chr16	Smco1	-1.0015543	7.89382E-07	2.91477E-06	5.403852319	0.04678659	-1	869	884	836	922	672	284	573	348	472	614
ENSMUSG00000037761	chr2	Actr5	1.20934639	7.91707E-07	2.92258E-06	1.858358451	0.049179237	1	40	27	25	32	32	79	96	81	62	79
ENSMUSG00000031328	chrX	Flna	1.01253924	7.97499E-07	2.94241E-06	7.376845896	0.04901875	1	1276	1392	1256	2390	1958	5623	3975	2422	3226	3168
ENSMUSG00000078348	chr10	Sf3b5	0.86304855	7.97294E-07	2.94241E-06	4.788580835	0.033652407	1	317	261	286	322	263	893	578	512	515	425
ENSMUSG00000044340	chr1	Phlpp1	-0.9436899	7.98439E-07	2.9451E-06	3.438852669	0.036783526	-1	177	192	191	293	207	151	110	91	87	167
ENSMUSG00000079003	chr8	Samd1	0.91036056	7.99175E-07	2.94704E-06	4.212480745	0.036519647	1	160	181	185	263	169	626	381	319	356	301
ENSMUSG00000071267	chr17	Zfp942	-1.2255965	8.00553E-07	2.95134E-06	2.597008862	0.059928604	-1	137	103	110	160	114	39	72	33	76	70
ENSMUSG00000040423	chr1	Rc3h1	-0.80541	8.01114E-07	2.95263E-06	4.790839649	0.029258361	-1	428	502	450	708	539	448	358	238	259	356
ENSMUSG00000101645	chr2	Gm28635	-0.7262943	8.02714E-07	2.95775E-06	5.891059169	0.024605488	-1	1042	972	991	1509	1030	709	760	716	631	825
ENSMUSG00000034738	chr2	Nostrin	1.38698644	8.03645E-07	2.9604E-06	1.135281145	0.056741471	1	19	17	13	23	13	54	66	42	36	46
ENSMUSG00000022504	chr16	Ciita	2.48858787	8.03895E-07	2.96054E-06	0.111165429	0.163030203	1	2	3	9	0	6	31	20	37	13	29
ENSMUSG00000021798	chr14	Ldb3	-0.8717955	8.04183E-07	2.96082E-06	10.9537244	0.036836291	-1	34410	30095	33168	54522	40625	19996	25745	18514	24512	25519
ENSMUSG00000020635	chr12	Fkbp1b	1.58494246	8.05694E-07	2.9656E-06	1.158339886	0.079545573	1	14	18	14	16	15	77	30	35	56	60
ENSMUSG00000027009	chr2	Itga4	-0.919353	8.07776E-07	2.97248E-06	4.378102724	0.037894559	-1	481	323	315	428	461	252	307	164	180	276
ENSMUSG00000021576	chr13	Pdcd6	0.71641159	8.08081E-07	2.97282E-06	4.345547795	0.021782906	1	252	191	202	294	206	498	442	323	382	418
ENSMUSG00000036022	chrX	Fam122b	-1.2465118	8.09071E-07	2.97568E-06	1.439996523	0.047325942	-1	59	44	57	69	45	25	26	23	20	32
ENSMUSG00000079737	chr16	3110001I22Rik	-1.1911299	8.1635E-07	3.00166E-06	1.675025773	0.045606779	-1	68	62	57	75	58	33	35	18	31	37
ENSMUSG00000033016	chr18	Nfatc1	-0.6912188	8.17274E-07	3.00427E-06	5.264291144	0.021657233	-1	721	592	613	977	657	545	484	409	440	525
ENSMUSG00000047368	chr19	Abhd17b	-0.8278989	8.19077E-07	3.0101E-06	3.922741883	0.028855311	-1	310	243	243	398	256	152	200	145	161	229
ENSMUSG00000068614	chr2	Actc1	1.98347757	8.21365E-07	3.01772E-06	11.89056513	0.179213209	1	28921	22673	20013	17837	22873	15389	117011	113107	78286	163323
ENSMUSG00000074165	chr7	Zfp788	-1.1723807	8.25943E-07	3.03374E-06	2.75015336	0.055297865	-1	128	135	129	188	109	45	73	42	88	83
ENSMUSG00000041203	chr8	2310036O22Rik	0.79665141	8.27527E-07	3.03876E-06	5.539497731	0.029494917	1	493	429	481	629	496	1389	910	760	957	831
ENSMUSG00000040359	chr4	Ufl1	-0.8701068	8.32107E-07	3.05477E-06	4.649009828	0.034215643	-1	495	438	455	583	438	224	317	198	340	362
ENSMUSG00000022682	chr16	Rrn3	-0.7199438	8.36462E-07	3.06996E-06	5.457386575	0.023883505	-1	846	830	704	1016	686	616	636	477	456	530
ENSMUSG00000032249	chr9	Anp32a	0.76192493	8.37765E-07	3.07321E-06	5.935570414	0.027285871	1	635	658	579	885	636	1571	1312	1174	1238	989
ENSMUSG00000065979	chr16	Cpped1	-0.6979299	8.37789E-07	3.07321E-06	5.641433071	0.022534583	-1	965	904	838	1083	804	622	633	587	594	662
ENSMUSG00000050967	chr1	Creg2	2.96959017	8.40963E-07	3.08405E-06	-0.151727971	0.236241213	1	2	0	3	2	5	55	11	18	8	20
ENSMUSG00000033618	chr16	Map3k13	-2.2362821	8.41424E-07	3.08454E-06	-0.31892891	0.096338796	-1	12	16	18	23	16	0	3	5	7	4
ENSMUSG00000068854	chr3	Hist2h2be	-0.9197563	8.4154E-07	3.08454E-06	3.394791436	0.034864895	-1	230	205	186	225	168	127	138	79	93	156
ENSMUSG00000028476	chr4	Reck	-0.9374466	8.43355E-07	3.08992E-06	2.943827205	0.033595384	-1	160	137	118	170	157	92	83	61	94	96
ENSMUSG00000035437	chr2	Rabgap1	-0.7699533	8.4345E-07	3.08992E-06	5.172348429	0.027150875	-1	689	620	680	851	549	363	491	357	437	520
ENSMUSG00000002658	chr17	Gtf2f1	0.73742961	8.44522E-07	3.09304E-06	4.810084743	0.024262937	1	294	273	247	421	334	624	618	499	598	511
ENSMUSG00000014074	chr16	Rnf168	-0.7831048	8.58603E-07	3.14379E-06	3.996118773	0.025864767	-1	294	284	289	360	267	177	192	152	226	202
ENSMUSG00000026482	chr1	Rgl1	0.94315749	8.61607E-07	3.15396E-06	4.688870212	0.040578337	1	238	277	304	278	201	648	694	311	566	564
ENSMUSG00000049091	chr7	Sephs2	-0.8314237	8.65947E-07	3.16902E-06	4.197418543	0.030173368	-1	365	336	290	440	317	168	262	165	238	236
ENSMUSG00000028538	chr4	St3gal3	-0.7531531	8.71227E-07	3.18751E-06	6.159878189	0.026891062	-1	1193	1180	1091	1874	1395	919	847	830	785	962
ENSMUSG00000029468	chr5	P2rx7	1.52698147	8.76761E-07	3.20625E-06	2.747992275	0.098592216	1	53	65	46	63	26	313	103	102	103	195
ENSMUSG00000073437	chr17	D330041H03Rik	-1.8979182	8.76809E-07	3.20625E-06	1.358463878	0.135578594	-1	64	73	58	52	40	39	7	10	9	22
ENSMUSG00000034723	chr2	Tmx4	-0.8282917	8.8028E-07	3.2181E-06	3.906280666	0.029051846	-1	279	280	246	371	251	143	169	151	177	234
ENSMUSG00000039377	chr1	Hlx	1.13449988	8.81504E-07	3.22173E-06	3.214753826	0.054559654	1	93	84	80	107	64	291	165	250	114	210
ENSMUSG00000029723	chr5	Tsc22d4	0.7721919	8.88531E-07	3.24656E-06	6.318322785	0.028424722	1	919	789	901	1055	724	1730	1473	1725	1371	1898
ENSMUSG00000021987	chr14	Mtmr6	-0.855412	8.9435E-07	3.26697E-06	5.621399803	0.03449105	-1	1038	926	844	1133	786	484	649	383	692	646
ENSMUSG00000015747	chr3	Vps45	0.7525664	8.95347E-07	3.26976E-06	3.599590134	0.022042749	1	143	122	119	151	129	274	256	223	239	237
ENSMUSG00000079478	chr19	Sssca1	0.7250829	8.95865E-07	3.2708E-06	5.732857136	0.024594995	1	607	552	561	712	548	1341	937	1065	921	1150

ENSMUSG00000038545	chr17	Cul7	0.92305505	8.96749E-07	3.27317E-06	4.56885945	0.038795702	1	224	194	248	324	229	693	406	605	352	471
ENSMUSG00000028229	chr4	Rmdn1	-0.9133425	8.98838E-07	3.27994E-06	4.376773473	0.037552885	-1	365	456	407	545	255	233	198	196	300	239
ENSMUSG00000050578	chr9	Mmp13	2.50929585	8.9922E-07	3.28048E-06	0.65852868	0.210438235	1	7	5	6	7	6	114	24	17	24	26
ENSMUSG00000060510	chr9	Zfp266	-0.7963091	9.01432E-07	3.28769E-06	3.889359514	0.026562088	-1	278	284	248	353	234	144	203	155	168	206
ENSMUSG00000031352	chrX	Hccs	-0.8498071	9.01703E-07	3.28782E-06	4.737406804	0.032871139	-1	403	473	523	800	386	294	365	303	311	269
ENSMUSG00000008384	chr7	Sertad1	0.99742624	9.03763E-07	3.29447E-06	4.016575298	0.04410491	1	179	181	155	180	103	558	326	281	332	267
ENSMUSG00000095990	chr17	Zfp97	-1.7327386	9.07389E-07	3.30682E-06	0.918602877	0.09774223	-1	52	39	48	26	36	12	17	10	19	9
ENSMUSG00000021583	chr13	Erap1	-0.8219386	9.09302E-07	3.31207E-06	4.299228836	0.029811637	-1	351	358	351	462	344	211	257	165	293	227
ENSMUSG00000062328	chr18	Rpl17	0.80942888	9.09293E-07	3.31207E-06	7.638456658	0.031827049	1	2470	2222	1960	2281	1808	5695	4030	3363	4040	3730
ENSMUSG00000033491	chr9	Prss35	2.10144539	9.09683E-07	3.31259E-06	0.220576016	0.11930103	1	6	5	7	4	6	27	27	15	17	51
ENSMUSG00000040738	chr4	Ints8	-0.9319733	9.10781E-07	3.31573E-06	4.023950385	0.038211208	-1	344	298	267	327	334	163	219	124	232	168
ENSMUSG00000019214	chr17	Chtf18	1.86310562	9.11379E-07	3.31704E-06	0.907309151	0.111891628	1	14	7	15	5	13	48	67	41	39	27
ENSMUSG00000068856	chr3	Sf3b4	0.88421709	9.17048E-07	3.3368E-06	3.560253361	0.032349566	1	89	115	112	174	124	297	305	206	208	226
ENSMUSG00000040472	chr14	Rabggta	0.77464125	9.17947E-07	3.33921E-06	3.856746955	0.024817262	1	167	152	131	190	150	338	289	302	226	327
ENSMUSG00000030315	chr6	Vgll4	-0.8431083	9.19826E-07	3.34517E-06	3.727893798	0.029736048	-1	259	236	252	272	232	135	139	137	149	207
ENSMUSG00000003929	chr17	Zfp81	-1.239297	9.25068E-07	3.36336E-06	1.996499991	0.056035147	-1	76	58	94	90	86	36	44	31	46	31
ENSMUSG00000021264	chr12	Yy1	-0.7302133	9.38974E-07	3.41303E-06	4.213254021	0.022809292	-1	307	286	328	463	339	245	252	193	203	243
ENSMUSG00000055660	chr17	Mettl4	-1.1983112	9.39607E-07	3.41444E-06	1.976116115	0.050701383	-1	80	80	82	111	48	39	38	33	44	35
ENSMUSG00000104372	chr11	AL663030.1	-1.0004125	9.46174E-07	3.43741E-06	2.613359834	0.037263734	-1	125	110	120	140	102	57	68	53	78	70
ENSMUSG00000039615	chr17	Stub1	0.71174117	9.55799E-07	3.47148E-06	6.715020182	0.024425161	1	1215	1088	1030	1524	1100	2607	2073	2009	1951	2027
ENSMUSG00000004451	chr1	Ralb	0.93952369	9.56338E-07	3.47253E-06	4.550829279	0.040443163	1	233	275	260	291	134	656	566	407	493	393
ENSMUSG00000028668	chr4	Tceb3	-0.7582206	9.61973E-07	3.49209E-06	5.992435961	0.027390889	-1	1315	1116	1004	1376	1141	797	832	556	829	855
ENSMUSG00000034780	chr2	B3galt1	-1.4272424	9.64306E-07	3.49965E-06	1.569275292	0.072259488	-1	44	70	53	79	65	19	35	16	34	22
ENSMUSG00000034640	chr3	Tiparp	-0.7968191	9.79164E-07	3.55265E-06	3.882892433	0.026821315	-1	265	259	278	355	233	170	216	127	164	200
ENSMUSG00000033965	chrX	Slc16a2	0.95995802	9.8008E-07	3.55505E-06	3.481852643	0.038949099	1	87	121	86	157	111	333	220	236	163	247
ENSMUSG00000015880	chr5	Ncapg	2.32225065	9.82682E-07	3.56356E-06	1.503657184	0.207896472	1	13	28	14	7	3	63	126	63	82	30
ENSMUSG00000024140	chr17	Epas1	-0.8553409	9.84797E-07	3.57031E-06	6.72733475	0.035475187	-1	1402	1759	1917	3131	2067	1397	1226	1169	1037	1341
ENSMUSG00000030513	chr7	Pcsk6	-0.8277426	1.00437E-06	3.64031E-06	4.563571732	0.031074769	-1	335	450	428	568	461	282	291	322	237	246
ENSMUSG00000020608	chr12	Smc6	-0.7787772	1.00906E-06	3.65542E-06	5.248543151	0.028331852	-1	659	730	635	933	630	398	496	339	518	527
ENSMUSG00000046711	chr17	Hmga1	1.90484563	1.00903E-06	3.65542E-06	4.027816547	0.163902116	1	110	87	78	142	96	68	732	322	481	453
ENSMUSG00000074899	chr2	Sptbn5	-1.8376549	1.01805E-06	3.68703E-06	0.133133242	0.081452615	-1	18	26	28	22	20	7	11	4	6	7
ENSMUSG00000041426	chr1	Hibch	-0.8565231	1.02158E-06	3.69887E-06	5.305166124	0.034610902	-1	764	825	748	947	518	376	468	383	554	498
ENSMUSG00000035296	chr14	Sgcg	-0.7816791	1.02236E-06	3.70072E-06	6.825586291	0.029727485	-1	1960	2067	2060	2706	1909	1154	1336	1242	1492	1548
ENSMUSG00000085457	chr13	1110046J04Rik	2.01008434	1.02518E-06	3.70996E-06	0.375198968	0.115961331	1	12	7	4	7	4	27	15	28	34	47
ENSMUSG00000044068	chr11	Zrsr1	-0.9530082	1.03291E-06	3.73699E-06	2.940918564	0.035907431	-1	144	148	134	194	128	87	97	57	70	113
ENSMUSG00000026960	chr2	Arl6ip6	-0.994697	1.04261E-06	3.7711E-06	2.839073741	0.038794603	-1	117	112	131	203	142	67	82	68	86	80
ENSMUSG00000029075	chr4	Tnfrsf4	2.08503565	1.05961E-06	3.8316E-06	-0.109498568	0.101197196	1	8	2	1	4	7	17	26	20	22	19
ENSMUSG00000036860	chr11	Mrpl55	0.86241038	1.062E-06	3.83926E-06	4.526997809	0.0340663	1	212	228	229	335	216	354	511	560	475	487
ENSMUSG00000046876	chr13	Atxn1	-0.7279139	1.06513E-06	3.84956E-06	4.704016724	0.023902624	-1	410	478	411	682	452	313	341	264	311	369
ENSMUSG00000008429	chr9	Herpud2	-0.8175473	1.06825E-06	3.85983E-06	5.165227677	0.031437386	-1	776	622	591	817	605	388	450	335	341	611
ENSMUSG00000048249	chr17	Crebrf	-0.8874363	1.07912E-06	3.8981E-06	3.912162786	0.034739737	-1	271	315	270	324	261	226	133	152	123	230
ENSMUSG00000039943	chr2	Plcb4	-0.8574328	1.08387E-06	3.91425E-06	4.010733643	0.032297262	-1	310	325	283	367	254	152	183	146	231	214
ENSMUSG00000001918	chr7	Slc1a5	1.0976656	1.0936E-06	3.94736E-06	4.996163515	0.057121872	1	228	484	205	258	308	874	731	726	529	688
ENSMUSG00000069601	chr10	Ank3	-0.8631136	1.09337E-06	3.94736E-06	6.053514183	0.036058977	-1	1052	1053	1165	1757	1382	640	746	683	736	1030
ENSMUSG00000037872	chr1	Ackr1	1.27595186	1.09704E-06	3.95874E-06	2.136852468	0.062141789	1	36	31	21	45	52	128	94	103	91	76
ENSMUSG00000049881	chr1	2810025M15Rik	1.12897424	1.09805E-06	3.96035E-06	3.251009037	0.054996055	1	80	102	93	91	69	347	193	215	132	175
ENSMUSG00000100235	chr13	Gm28557	-1.2943762	1.09778E-06	3.96035E-06	1.648318239	0.059083696	-1	70	56	67	77	51	23	41	17	33	29
ENSMUSG00000045071	chr4	E130308A19Rik	-1.131016	1.10169E-06	3.97246E-06	2.679560718	0.052273211	-1	122	137	133	125	121	50	67	46	62	98
ENSMUSG00000068329	chr6	Htra2	0.77451467	1.10954E-06	3.99973E-06	4.615460609	0.027185485	1	316	256	275	286	203	649	551	398	464	468
ENSMUSG00000067148	chr17	Polr1c	0.77893208	1.11062E-06	4.0026E-06	3.765762233	0.025068354	1	154	139	157	154	130	349	281	256	246	262
ENSMUSG00000060032	chr6	H2afj	1.06386691	1.11716E-06	4.02511E-06	3.75267653	0.050756748	1	149	105	106	175	114	535	271	205	262	226
ENSMUSG00000033739	chr17	Fkbpl	1.08379998	1.11761E-06	4.0257E-06	2.249298171	0.042854233	1	51	32	32	61	46	116	99	101	84	113
ENSMUSG00000045036	chr17	Tmem232	-3.4932559	1.11839E-06	4.02748E-06	1.88627673	0.472241211	-1	116	91	97	121	71	43	5	0	2	1
ENSMUSG00000058258	chr13	Idi1	-1.4009095	1.12127E-06	4.03682E-06	1.554154229	0.070292667	-1	70	44	73	77	43	17	35	21	29	24
ENSMUSG00000020831	chr11	0610010K14Rik	0.76460553	1.12222E-06	4.03848E-06	4.364983019	0.025966341	1	232	199	208	274	218	603	385	379	382	369
ENSMUSG00000066148	chr4	Prpf4	-0.6927697	1.12231E-06	4.03848E-06	4.887543944	0.021826274	-1	474	507	470	769	519	365	404	334	353	384
ENSMUSG00000021552	chr13	Gkap1	-0.7673257	1.12294E-06	4.03969E-06	3.685332849	0.02423813	-1	231	222	216	313	221	157	160	120	175	159
ENSMUSG00000021662	chr13	Arhgef28	-1.2170292	1.12674E-06	4.05233E-06	1.902934788	0.053294735	-1	64	73	78	100	65	48	30	22	31	49
ENSMUSG00000035189	chr10	Ano4	-1.9864789	1.12899E-06	4.05937E-06	-0.277631109	0.072404548	-1	15	15	17	22	16	7	4	6	3	3
ENSMUSG00000034612	chr10	Chst11	1.61626079	1.1426E-06	4.10724E-06	2.549867826	0.11164046	1	38	45	44	49	32	269	201	69	64	120
ENSMUSG00000024617	chr18	Camk2a	-0.9880035	1.14312E-06	4.10805E-06	8.716298678	0.048321516	-1	9150	7168	7127	8704	9223	2969	5439	4128	4447	5915
ENSMUSG00000027347	chr2	Rasgrp1	1.79525921	1.14687E-06	4.12047E-06	0.115515301	0.071475171	1	5	10	5	6	5	28	19	23	22	28
ENSMUSG00000022674	chr16	Ube2v2	-1.0268871	1.15265E-06	4.14017E-06	3.396265816	0.045567667	-1	231	184	161	288	189	86	111	75	153	133
ENSMUSG00000025780	chr2	Itih5	-0.9796487	1.15668E-06	4.15357E-06	6.318234574	0.046909445	-1	1525	1533	1452	1575	1710	697	863	902	604	1308
ENSMUSG00000048387	chr12	Osr1	1.30444922	1.1609E-06	4.16768E-06	1.688942724	0.060295647	1	21	16	25	40	31	99	75	67	62	57

ENSMUSG00000023892	chr17	Zfp51	-1.6158313	1.16144E-06	4.16852E-06	2.297140557	0.110096713	-1	103	103	78	161	103	23	35	14	68	52
ENSMUSG00000089945	chr4	Palm2Akap2	-0.7823244	1.16301E-06	4.1731E-06	5.407177583	0.029135281	-1	648	765	727	1169	722	570	464	519	396	597
ENSMUSG00000012117	chr4	Dhdds	0.86379961	1.16571E-06	4.18172E-06	4.168490864	0.033548608	1	211	196	170	211	154	496	389	410	316	271
ENSMUSG00000051747	chr2	Ttn	-1.0982025	1.16765E-06	4.18761E-06	12.48226083	0.059691873	-1	96114	84997	89345	152146	158954	46822	63313	54341	46439	86658
ENSMUSG00000090145	chr1	Ugt1a6b	1.89545673	1.1721E-06	4.20249E-06	2.892157351	0.157330421	1	36	82	42	20	41	412	163	93	166	127
ENSMUSG00000017404	chr11	Rpl19	0.73522402	1.17491E-06	4.21147E-06	8.024154529	0.026905402	1	3242	2802	2575	3387	2556	6443	5489	4754	5101	4836
ENSMUSG00000055407	chr7	Map6	1.2906392	1.17766E-06	4.22024E-06	2.198590628	0.065082005	1	31	43	33	53	33	184	94	84	77	84
ENSMUSG00000058927	chr19	Gm10053	-0.8661818	1.19422E-06	4.27851E-06	4.29602267	0.034160515	-1	343	376	404	451	304	169	216	207	275	254
ENSMUSG00000021981	chr14	Cab39l	-0.7142673	1.19581E-06	4.2831E-06	4.40972808	0.022658497	-1	437	366	397	424	327	306	274	217	256	259
ENSMUSG00000020654	chr12	Adcy3	1.04993135	1.19839E-06	4.29125E-06	2.723941107	0.043928079	1	53	70	44	74	72	156	131	145	109	172
ENSMUSG00000041570	chr1	Camsap2	-0.7994017	1.20125E-06	4.30038E-06	3.799711601	0.02726996	-1	218	241	253	333	264	200	190	117	146	177
ENSMUSG00000028049	chr3	Scamp3	0.74813876	1.20337E-06	4.30687E-06	5.469707521	0.02667666	1	538	433	382	627	490	1195	870	838	811	830
ENSMUSG00000042632	chr15	Pla2g6	-0.8368678	1.20581E-06	4.31448E-06	4.29502441	0.031869904	-1	331	303	321	476	436	325	228	210	192	197
ENSMUSG00000026111	chr1	Unc50	0.76388782	1.20754E-06	4.31956E-06	4.067009981	0.025264986	1	186	193	184	198	153	435	372	287	310	314
ENSMUSG00000025134	chr11	Alyref	0.84057352	1.21822E-06	4.35666E-06	4.308308389	0.032128997	1	217	173	211	276	179	494	514	359	410	289
ENSMUSG00000020087	chr10	Tysnd1	0.80996272	1.22585E-06	4.38284E-06	3.874681289	0.028353382	1	141	153	122	217	159	398	260	305	260	293
ENSMUSG00000022634	chr15	Yaf2	-0.8713494	1.23297E-06	4.40715E-06	3.581606938	0.032429277	-1	208	199	238	283	215	108	155	112	133	176
ENSMUSG00000060730	chr5	Gm10086	2.14502458	1.24656E-06	4.4546E-06	-0.313464379	0.091822202	1	6	5	2	4	1	21	11	18	19	20
ENSMUSG00000040044	chr4	Orc3	-0.9123005	1.24744E-06	4.45661E-06	4.638973392	0.039098835	-1	565	472	385	539	452	230	317	198	385	269
ENSMUSG00000042700	chr12	Sipa1l1	-0.861825	1.24971E-06	4.46357E-06	4.253418978	0.033878332	-1	364	263	336	450	410	179	252	218	184	263
ENSMUSG00000026447	chr1	Pik3c2b	-0.8050236	1.25157E-06	4.46907E-06	5.297451969	0.030982958	-1	845	662	718	831	654	443	372	471	424	616
ENSMUSG00000063894	chr13	Zkscan8	-1.1478641	1.25488E-06	4.47975E-06	2.817958206	0.055521283	-1	153	147	118	163	132	42	86	57	62	105
ENSMUSG00000069895	chr8	Atxn1l	-0.7178796	1.25615E-06	4.48312E-06	4.433258256	0.023019306	-1	354	357	348	574	379	290	298	247	215	281
ENSMUSG00000040829	chr11	Zmynd15	1.95930228	1.26044E-06	4.49731E-06	0.470505787	0.113382424	1	6	9	8	6	8	58	20	36	18	31
ENSMUSG00000022092	chr14	Ppp3cc	-0.9150422	1.26529E-06	4.51345E-06	3.529799479	0.036058259	-1	176	238	205	294	205	106	162	98	148	132
ENSMUSG00000021461	chr13	Fancc	1.32910553	1.27508E-06	4.54721E-06	1.843950573	0.064528188	1	21	23	38	28	34	70	69	82	90	89
ENSMUSG00000037343	chr15	Taf2	-0.795864	1.2771E-06	4.55325E-06	3.821629708	0.02714729	-1	249	239	241	343	259	139	192	140	181	183
ENSMUSG00000093803	chr9	Ppp2r3d	0.87915525	1.27898E-06	4.5588E-06	3.231148441	0.031545644	1	113	99	72	121	83	219	169	214	172	203
ENSMUSG00000029158	chr5	Yipf7	-0.8109437	1.27942E-06	4.55918E-06	6.297261807	0.032345736	-1	1377	1275	1518	2069	1274	928	1128	883	970	731
ENSMUSG00000057657	chr8	Rps18-ps3	2.23508514	1.29717E-06	4.62128E-06	-0.17136102	0.120928619	1	3	5	2	4	5	40	17	17	16	12
ENSMUSG00000024056	chr17	Ndc80	1.88398567	1.29779E-06	4.6223E-06	1.032394498	0.123266256	1	12	14	18	8	7	46	78	36	58	26
ENSMUSG00000027398	chr2	Il1b	3.45468899	1.31362E-06	4.6775E-06	0.737745114	0.431139707	1	1	1	1	11	5	142	49	16	18	10
ENSMUSG00000003949	chr11	Hlf	-1.3077997	1.31956E-06	4.69743E-06	3.499337232	0.078094847	-1	284	284	280	146	168	64	140	96	109	114
ENSMUSG00000092218	chr9	Gm20529	1.69967727	1.3289E-06	4.72949E-06	0.933499805	0.094335897	1	14	11	11	11	14	82	35	36	41	29
ENSMUSG00000054582	chr2	Pabpc1l	2.24144726	1.33029E-06	4.73322E-06	-0.455554918	0.095159051	1	4	5	1	3	2	22	10	18	16	14
ENSMUSG00000036006	chr13	Fam65b	-1.45448	1.3341E-06	4.7456E-06	3.178104832	0.095737377	-1	255	174	163	134	232	39	79	59	76	137
ENSMUSG00000020827	chr11	Mink1	-0.6981808	1.33964E-06	4.76221E-06	5.078214823	0.022877925	-1	595	562	542	772	638	433	424	330	395	523
ENSMUSG00000024959	chr19	Bad	0.76320109	1.33944E-06	4.76221E-06	4.007037292	0.025388958	1	193	168	160	210	151	425	287	329	292	309
ENSMUSG00000046753	chr14	Ccdc66	-1.1104634	1.3398E-06	4.76221E-06	2.747267777	0.050780647	-1	141	120	120	189	110	50	70	46	92	82
ENSMUSG00000026278	chr1	Bok	1.16066809	1.34663E-06	4.78406E-06	2.613008234	0.055110128	1	67	56	51	47	51	158	135	170	108	100
ENSMUSG00000029705	chr5	Cux1	-0.7104275	1.34638E-06	4.78406E-06	6.265682977	0.024829358	-1	1420	1284	1264	1827	1343	1091	1092	819	775	1009
ENSMUSG00000037795	chr5	N4bp2	-0.8042415	1.34765E-06	4.78646E-06	3.361452462	0.026187843	-1	197	181	168	243	178	112	125	102	114	152
ENSMUSG00000040312	chr17	Cchcr1	1.27700964	1.34993E-06	4.79336E-06	1.653473527	0.056341034	1	33	25	26	26	20	96	67	71	63	51
ENSMUSG00000038608	chr1	Dock10	1.10314528	1.35151E-06	4.79773E-06	3.14539536	0.052664843	1	88	87	81	87	67	147	291	127	201	205
ENSMUSG00000051373	chr2	Ppapdc3	-0.8058422	1.35268E-06	4.80068E-06	7.202421035	0.032480145	-1	3066	2548	2685	3123	2496	1396	1773	1746	1668	2115
ENSMUSG00000030815	chr7	Phkg2	0.8775544	1.35839E-06	4.8197E-06	3.514312915	0.032953184	1	135	132	91	138	98	340	203	222	210	226
ENSMUSG00000025321	chr12	Itgb8	-1.9249988	1.36365E-06	4.83714E-06	0.192329415	0.107374846	-1	14	15	34	34	25	8	9	3	6	9
ENSMUSG00000042208	chr11	0610010F05Rik	-0.8629544	1.36429E-06	4.83818E-06	4.01250802	0.03343856	-1	263	270	275	442	305	192	221	128	222	167
ENSMUSG00000041949	chr8	Tango6	-0.9549423	1.36489E-06	4.8391E-06	2.929419239	0.036833331	-1	116	139	124	191	169	85	89	80	88	74
ENSMUSG00000002781	chr7	Tmem143	-0.7009804	1.36568E-06	4.84067E-06	5.723918853	0.023782755	-1	948	952	954	1238	793	656	635	610	611	768
ENSMUSG00000011752	chr19	Pgam1	1.15790736	1.37858E-06	4.88514E-06	3.682275323	0.061519291	1	71	134	118	161	103	315	443	155	280	252
ENSMUSG00000023018	chr15	Smarcd1	0.79805109	1.38917E-06	4.92143E-06	3.74028461	0.027181197	1	155	159	123	179	107	313	264	272	214	312
ENSMUSG00000002297	chr5	Dbf4	1.61182824	1.39605E-06	4.94455E-06	1.46476203	0.096252753	1	21	27	17	17	13	82	94	54	61	32
ENSMUSG00000039831	chr3	Arhgap29	-0.7971967	1.40158E-06	4.96287E-06	4.307331782	0.028947231	-1	346	375	296	556	316	192	258	208	239	274
ENSMUSG00000021243	chr12	Fcf1	0.81845896	1.40399E-06	4.97015E-06	3.757855073	0.028833466	1	151	138	126	166	140	366	303	222	292	219
ENSMUSG00000004099	chr9	Dnmt1	0.77387632	1.40595E-06	4.97583E-06	4.212711078	0.026887251	1	185	184	169	258	218	390	459	301	404	344
ENSMUSG00000021326	chr13	Trim27	0.71803497	1.40777E-06	4.98101E-06	4.798870596	0.023908762	1	285	323	269	392	295	744	534	529	530	486
ENSMUSG00000039765	chr5	Cc2d2a	-0.7784497	1.41714E-06	5.01289E-06	3.548160398	0.0249808	-1	204	225	178	288	202	133	148	119	149	147
ENSMUSG00000101111	chr1	Gm28437	-0.9364885	1.41947E-06	5.01988E-06	3.719180216	0.03901787	-1	246	247	263	347	185	103	139	150	176	156
ENSMUSG00000058291	chr5	Zfp68	-0.8258733	1.42773E-06	5.04781E-06	4.297612047	0.03138851	-1	348	382	370	436	324	187	253	167	258	286
ENSMUSG00000067925	chrX	Cxx1a	0.80451553	1.42894E-06	5.05081E-06	4.357973322	0.029697971	1	247	191	213	262	193	537	364	475	308	435
ENSMUSG00000018428	chr11	Akap1	-0.9756425	1.4333E-06	5.06493E-06	6.052745429	0.047162305	-1	843	1138	1236	2223	1231	608	727	861	656	763
ENSMUSG00000090516	chr9	Rps11-ps1	1.85748694	1.43547E-06	5.0713E-06	0.777401585	0.114706351	1	4	10	13	13	10	71	34	44	21	33
ENSMUSG00000062694	chr6	Cav3	0.74284967	1.44058E-06	5.08809E-06	6.860956582	0.027618212	1	1399	1206	1160	1536	1177	2615	2171	2503	2472	2053
ENSMUSG00000034998	chr17	Foxn2	-0.9042376	1.45025E-06	5.12095E-06	3.559919421	0.035762875	-1	212	203	180	339	216	126	155	84	155	146

ENSMUSG00000042045	chr9	Sln	4.05826913	1.46071E-06	5.15609E-06	4.488052081	0.642411015	1	5	15	8	191	2	1869	235	441	324	700
ENSMUSG00000079484	chr2	Phyhd1	1.20217719	1.46094E-06	5.15609E-06	3.40388878	0.066072863	1	82	81	105	164	50	332	159	237	275	185
ENSMUSG00000031843	chr8	Mphosph6	1.09525838	1.47155E-06	5.19221E-06	2.561998082	0.048245504	1	63	63	44	58	45	180	156	96	113	102
ENSMUSG00000074873	chr19	AI606181	1.32175349	1.47397E-06	5.19943E-06	1.979061374	0.067676948	1	31	37	23	46	26	116	90	88	44	109
ENSMUSG00000026484	chr1	Rnf2	-0.7721254	1.47991E-06	5.21907E-06	3.839337415	0.025716549	-1	238	231	252	357	263	171	168	153	150	216
ENSMUSG00000001630	chr6	Stk38l	-0.7597591	1.48239E-06	5.2265E-06	3.491600203	0.023540214	-1	194	210	196	275	174	139	142	117	130	148
ENSMUSG00000031442	chr8	Mcf2l	-0.9658314	1.48369E-06	5.22979E-06	3.694810316	0.042216027	-1	212	187	207	322	337	199	135	112	120	151
ENSMUSG00000007458	chr6	M6pr	0.8608831	1.48745E-06	5.24038E-06	5.711365085	0.036514503	1	562	539	484	670	514	1244	1500	634	1102	1076
ENSMUSG00000070284	chr9	Gmppb	0.95456839	1.48718E-06	5.24038E-06	3.411085181	0.039747965	1	102	102	100	132	97	342	241	171	228	159
ENSMUSG00000025439	chr7	Clns1a	0.78127504	1.51271E-06	5.32803E-06	4.801330363	0.028894583	1	275	332	263	388	268	447	639	506	602	658
ENSMUSG00000038776	chr1	Ephx1	1.07020897	1.51947E-06	5.35049E-06	4.443368057	0.054937352	1	227	217	174	271	158	808	470	334	251	583
ENSMUSG00000037016	chr3	Frem2	-1.5209062	1.52367E-06	5.36393E-06	3.100299592	0.106201346	-1	197	130	186	245	183	158	60	62	23	64
ENSMUSG00000068745	chr3	Mybphl	3.38279698	1.53556E-06	5.40443E-06	0.170356162	0.351097516	1	3	1	2	0	6	5	29	57	11	42
ENSMUSG00000040661	chr9	Rad54l2	-0.7654395	1.53627E-06	5.40557E-06	3.67848704	0.024809303	-1	208	214	219	301	250	164	177	141	131	156
ENSMUSG00000060743	chr1	H3f3a	-0.8411611	1.53819E-06	5.41095E-06	6.685267732	0.03558142	-1	2083	1852	1865	2330	1708	950	1319	885	1324	1531
ENSMUSG00000032548	chr9	Slco2a1	1.47693475	1.5391E-06	5.41281E-06	2.003244614	0.088923122	1	23	27	23	40	39	155	72	107	78	54
ENSMUSG00000038900	chr2	Rpl12	0.77816912	1.54438E-06	5.43001E-06	7.46369964	0.030695444	1	2048	1928	1733	2280	1699	4300	4236	2679	3935	3128
ENSMUSG00000035151	chr8	Elmod2	-0.9045315	1.57162E-06	5.52439E-06	3.308166136	0.034781819	-1	239	194	143	204	171	104	136	85	108	125
ENSMUSG00000027884	chr3	Clcc1	-0.7160456	1.57852E-06	5.54724E-06	4.77503919	0.024049634	-1	500	487	455	630	461	335	428	249	328	351
ENSMUSG00000041298	chr5	Katnal1	-0.9499536	1.58851E-06	5.58095E-06	2.896933195	0.036565426	-1	166	151	136	163	105	73	90	74	92	78
ENSMUSG00000016946	chr17	Kctd5	0.72296841	1.593E-06	5.5953E-06	4.050813924	0.022928324	1	193	161	170	233	170	338	375	323	281	355
ENSMUSG00000032400	chr9	Zwilch	2.18400943	1.5955E-06	5.60268E-06	0.393531738	0.152270455	1	10	4	8	6	3	27	59	18	37	16
ENSMUSG00000030649	chr7	Anapc15	0.87839121	1.59895E-06	5.61341E-06	3.881916052	0.03481061	1	198	159	136	154	117	393	326	270	324	235
ENSMUSG00000008373	chr7	Prpf31	0.76037075	1.60278E-06	5.62544E-06	4.662889387	0.027192184	1	329	233	247	358	236	501	644	436	540	464
ENSMUSG00000083757	chr4	Rps15a-ps4	2.09324747	1.61661E-06	5.67256E-06	0.133463611	0.116768527	1	4	4	6	1	11	18	27	27	25	29
ENSMUSG00000004267	chr6	Eno2	1.69352193	1.61924E-06	5.67893E-06	1.679993371	0.114960351	1	25	22	18	25	17	160	69	34	46	83
ENSMUSG00000058546	chr11	Rpl23a	0.76226962	1.6192E-06	5.67893E-06	7.659330554	0.029622829	1	2403	2142	1831	2728	2096	5613	4328	3612	3798	3538
ENSMUSG00000032352	chr9	Lrrc1	1.47069949	1.62078E-06	5.68239E-06	1.055449854	0.069566648	1	16	16	15	22	8	45	36	60	43	47
ENSMUSG00000073702	chr1	Rpl31	0.80205243	1.62104E-06	5.68239E-06	7.424709037	0.032722015	1	2220	1795	1704	1934	1630	4748	3608	2897	3674	2991
ENSMUSG00000067369	chrX	Trmt2b	-0.7967451	1.6247E-06	5.69378E-06	4.382405532	0.029508834	-1	347	371	427	501	320	244	250	210	307	222
ENSMUSG00000050122	chr1	Vwa3b	-1.3677884	1.62715E-06	5.70094E-06	1.421046908	0.065427925	-1	56	56	66	69	30	30	19	25	20	23
ENSMUSG00000024646	chr18	Cyb5a	0.7592813	1.6402E-06	5.74522E-06	4.873698244	0.027446936	1	353	397	265	340	255	697	585	509	640	569
ENSMUSG00000029189	chr5	Sel1l3	-0.7978319	1.65448E-06	5.79379E-06	6.399880105	0.032056011	-1	1321	1214	1531	2342	1645	1021	1160	916	883	1055
ENSMUSG00000019699	chr1	Akt3	-0.8206456	1.66259E-06	5.82072E-06	3.508592991	0.028762123	-1	191	242	215	247	175	145	129	102	142	149
ENSMUSG00000041935	chr15	AW549877	-0.8288996	1.6634E-06	5.8221E-06	4.073384618	0.031542611	-1	332	365	290	330	269	172	197	168	182	265
ENSMUSG00000048520	chr5	Fbxl13	2.36928925	1.67136E-06	5.84852E-06	-0.512752196	0.098997767	1	3	3	4	0	3	17	13	15	21	11
ENSMUSG00000038729	chr4	Akap2	-0.7673531	1.67471E-06	5.85876E-06	5.398904394	0.028879445	-1	643	755	724	1152	717	570	467	520	395	596
ENSMUSG00000025613	chr16	Cct8	0.74933541	1.67773E-06	5.86785E-06	7.402705846	0.028654714	1	1981	1677	1679	2415	1696	3839	3865	3404	3393	2783
ENSMUSG00000030605	chr7	Mfge8	1.987483	1.6791E-06	5.87118E-06	6.923156018	0.190052437	1	649	641	601	1092	703	2514	2061	1492	973	9147
ENSMUSG00000032123	chr9	Dpagt1	0.70349762	1.68848E-06	5.90251E-06	4.29596546	0.022255729	1	233	207	199	281	191	518	415	316	355	385
ENSMUSG00000056880	chr9	Gadl1	-0.8089736	1.73963E-06	6.0798E-06	4.171842934	0.030144732	-1	375	314	310	409	295	172	179	221	227	256
ENSMUSG00000025609	chr6	Mkln1	-0.691089	1.74324E-06	6.09088E-06	6.117662746	0.023880929	-1	1354	1142	1074	1678	1177	905	955	829	780	861
ENSMUSG00000040883	chr9	Tmem205	0.95244473	1.7473E-06	6.10355E-06	3.648796908	0.040978623	1	177	128	104	120	98	383	220	256	232	252
ENSMUSG00000026064	chr1	Ptp4a1	-0.7380289	1.76032E-06	6.1475E-06	4.367706142	0.025067571	-1	352	366	335	578	310	232	287	230	232	275
ENSMUSG00000031647	chr8	Mfap3l	-1.1317452	1.76082E-06	6.14768E-06	3.024951016	0.056642301	-1	160	138	181	217	130	45	85	73	89	116
ENSMUSG00000019929	chr10	Dcn	-0.8899072	1.76997E-06	6.1781E-06	8.762206287	0.040789815	-1	9411	9299	8460	7424	6884	4375	5477	4339	4278	6403
ENSMUSG00000021843	chr14	Ktn1	-0.981071	1.78012E-06	6.21195E-06	7.095179136	0.049108673	-1	2397	2331	2334	3893	2695	958	1501	1216	1661	2129
ENSMUSG00000028035	chr3	Dnajb4	-0.8111399	1.7809E-06	6.21195E-06	5.455873398	0.032632368	-1	633	736	815	1384	669	565	544	454	472	568
ENSMUSG00000037646	chr15	Vps13b	-0.8047827	1.781E-06	6.21195E-06	3.528860111	0.027610187	-1	199	216	171	286	217	122	158	114	138	147
ENSMUSG00000029313	chr5	Aff1	-0.7270279	1.78643E-06	6.22933E-06	5.288842306	0.025855464	-1	671	605	691	923	738	497	525	408	392	586
ENSMUSG00000039356	chr2	Exosc2	0.87090025	1.79325E-06	6.25156E-06	3.456279916	0.033060139	1	125	109	89	151	101	263	284	215	215	168
ENSMUSG00000030086	chr6	Chchd6	1.46504553	1.81785E-06	6.33573E-06	1.877681076	0.085928354	1	30	44	18	21	25	65	85	106	90	72
ENSMUSG00000044496	chr4	2510039O18Rik	0.6916903	1.81987E-06	6.34119E-06	4.979825136	0.022825083	1	384	354	325	414	313	855	593	579	529	634
ENSMUSG00000039841	chr6	Zfp800	-1.7370217	1.8246E-06	6.3561E-06	1.389089358	0.120938052	-1	51	65	43	62	66	17	25	3	30	20
ENSMUSG00000038780	chr5	Smurf1	-0.8027316	1.82608E-06	6.35964E-06	4.552914562	0.030694283	-1	334	374	403	701	433	307	254	273	238	320
ENSMUSG00000021733	chr14	Slc4a7	-1.0922964	1.82851E-06	6.36651E-06	3.261024524	0.053800593	-1	165	161	169	346	146	68	116	84	89	136
ENSMUSG00000044792	chr13	Isca1	-0.7420303	1.84208E-06	6.41218E-06	7.348410825	0.028303603	-1	2873	2956	2860	4123	2495	1810	1960	1836	2053	2261
ENSMUSG00000038949	chr1	Cnst	-0.7920183	1.84298E-06	6.41373E-06	5.451218108	0.031130409	-1	800	800	701	1153	711	404	546	469	528	652
ENSMUSG00000020792	chr11	Exoc7	-0.8402926	1.84891E-06	6.43274E-06	6.843315634	0.036133442	-1	2951	1944	1635	2087	2279	1328	1413	1333	1258	1365
ENSMUSG00000024371	chr17	C2	1.45871501	1.85421E-06	6.44958E-06	2.598231423	0.0947502	1	25	44	44	58	62	216	96	142	72	190
ENSMUSG00000066315	chr4	Gm12918	1.00654701	1.86452E-06	6.48384E-06	3.0221291	0.04311055	1	81	81	72	70	86	251	184	158	124	161
ENSMUSG00000046603	chr9	Tcaim	-0.7444111	1.8655E-06	6.48563E-06	5.393626847	0.027339697	-1	694	715	798	1127	619	462	553	487	494	556
ENSMUSG00000034055	chrX	Phka1	-1.0095565	1.86658E-06	6.48777E-06	9.084018762	0.052540205	-1	12130	9171	8673	14049	10391	3827	5803	4481	6572	8619
ENSMUSG00000028914	chr4	Casp9	0.99731867	1.87852E-06	6.52764E-06	2.877796485	0.041653682	1	67	78	69	84	60	125	187	118	175	178
ENSMUSG00000043602	chr11	Zfp3	-0.9126933	1.8798E-06	6.53046E-06	3.674461459	0.037692936	-1	253	209	257	296	217	95	149	131	160	177

ENSMUSG00000025986	chr1	Slc39a10	-1.0365733	1.88148E-06	6.5347E-06	3.189555628	0.048070294	-1	143	174	163	255	175	103	131	56	71	127
ENSMUSG00000100370	chr7	Gm4790	-0.9368978	1.89121E-06	6.56686E-06	2.819917655	0.035685849	-1	128	132	117	179	128	71	102	58	77	82
ENSMUSG00000045691	chr14	Thtpa	-0.7081211	1.8918E-06	6.56726E-06	4.3773853	0.023034804	-1	381	379	347	502	314	239	252	220	285	283
ENSMUSG00000043903	chr8	Gm22	1.28300176	1.90159E-06	6.59962E-06	2.014278542	0.065090074	1	32	26	39	43	29	111	113	91	46	93
ENSMUSG00000059714	chr17	Flot1	0.91020507	1.90885E-06	6.62315E-06	6.187063543	0.042152555	1	820	742	668	894	646	1581	1497	1250	2238	1136
ENSMUSG00000047090	chr10	Tmem198b	0.91593912	1.91034E-06	6.62668E-06	3.209914221	0.035836362	1	102	92	97	99	78	256	161	191	146	224
ENSMUSG00000038372	chr13	Gmds	1.29123367	1.91173E-06	6.62984E-06	1.304687276	0.054738064	1	21	14	17	28	21	61	64	38	60	48
ENSMUSG00000025997	chr1	Ikzf2	-1.2142813	1.92112E-06	6.66077E-06	2.621845802	0.063778971	-1	113	127	117	149	123	29	64	49	72	81
ENSMUSG00000020275	chr11	Rel	-1.7530403	1.92724E-06	6.68034E-06	0.597668595	0.09994289	-1	40	18	33	46	26	11	10	4	18	9
ENSMUSG00000052133	chr16	Sema5b	-2.0696758	1.92908E-06	6.68505E-06	-0.121403729	0.114253228	-1	24	18	7	26	23	8	2	3	6	6
ENSMUSG00000020377	chr11	Ltc4s	2.26495015	1.93812E-06	6.71472E-06	1.284652281	0.205367375	1	15	12	11	8	11	168	32	54	32	31
ENSMUSG00000044258	chr13	Ctla2a	1.28000182	1.95611E-06	6.77536E-06	3.582476798	0.077542574	1	123	107	99	123	64	554	204	173	277	188
ENSMUSG00000032724	chr2	Abtb2	-1.0968048	1.96445E-06	6.80258E-06	3.714467309	0.056659556	-1	149	225	286	405	268	111	133	155	101	174
ENSMUSG00000021823	chr14	Vcl	-0.7669211	1.96603E-06	6.80636E-06	7.023567414	0.030314554	-1	2222	2043	2061	3197	2720	1605	1615	1407	1331	1921
ENSMUSG00000065887	chr4	n-R5s185	-1.3420201	1.97953E-06	6.8514E-06	1.075651104	0.056383048	-1	46	40	36	57	36	15	21	11	22	23
ENSMUSG00000060206	chr4	Zfp462	-1.0138133	1.98876E-06	6.88162E-06	3.224807876	0.045769691	-1	161	157	161	219	220	70	97	117	92	119
ENSMUSG00000026516	chr1	Nvl	-0.682407	1.99976E-06	6.91797E-06	4.223137159	0.020983994	-1	301	327	313	431	335	257	239	226	213	229
ENSMUSG00000003476	chr6	Crhr2	-0.8494592	2.00531E-06	6.93545E-06	5.003811119	0.035641513	-1	442	590	649	874	530	315	340	406	417	367
ENSMUSG00000032411	chr9	Tfdp2	-0.7345633	2.017E-06	6.97417E-06	4.947871814	0.026220169	-1	523	542	529	731	545	314	376	330	381	480
ENSMUSG00000026790	chr2	Odf2	0.82413666	2.01799E-06	6.97587E-06	3.711192279	0.030323415	1	127	143	118	195	120	383	287	213	255	226
ENSMUSG00000064264	chr7	Zfp428	1.14777596	2.03333E-06	7.02715E-06	2.103858096	0.051221742	1	33	35	46	51	28	91	71	93	101	110
ENSMUSG00000029466	chr5	Anapc7	0.67727484	2.03973E-06	7.04752E-06	4.741388858	0.021716469	1	312	288	280	392	261	626	501	555	503	486
ENSMUSG00000083087	chr4	Gm11249	2.46367302	2.04376E-06	7.05927E-06	-0.457180933	0.141261564	1	3	4	2	1	3	11	19	20	24	7
ENSMUSG00000097974	chr7	Gm10605	1.31240542	2.04414E-06	7.05927E-06	3.382751732	0.081532036	1	97	62	63	139	87	114	207	210	316	336
ENSMUSG00000030124	chr6	Lag3	2.17444102	2.04838E-06	7.07089E-06	1.489517142	0.194130102	1	21	14	13	10	12	159	45	45	19	98
ENSMUSG00000033871	chr18	Ppargc1b	-1.1367008	2.04851E-06	7.07089E-06	3.127713231	0.058738225	-1	110	154	196	285	151	65	83	102	77	110
ENSMUSG00000033762	chr15	Recql4	2.06273666	2.06384E-06	7.12201E-06	0.220449303	0.125381796	1	12	6	4	4	3	26	44	24	26	15
ENSMUSG00000082454	chr11	Gm12183	-1.2319086	2.08076E-06	7.17864E-06	2.151190927	0.061943807	-1	90	109	80	85	85	34	58	24	44	52
ENSMUSG00000031262	chrX	Cenpi	1.83713955	2.08302E-06	7.18467E-06	0.334193069	0.098864809	1	4	10	9	8	5	32	37	22	36	16
ENSMUSG00000037095	chr17	Lrg1	1.30558572	2.08869E-06	7.20244E-06	3.682750968	0.082093527	1	64	89	106	184	110	566	257	252	256	167
ENSMUSG00000052429	chr7	Prmt1	0.73715168	2.09133E-06	7.20979E-06	6.671192256	0.028011879	1	1038	1039	945	1642	1086	2299	2062	2070	2104	1829
ENSMUSG00000034118	chr5	Tpst1	0.77086991	2.10726E-06	7.26289E-06	4.175791225	0.027516992	1	186	219	189	216	173	412	344	345	285	468
ENSMUSG00000002068	chr7	Ccne1	1.99702146	2.11084E-06	7.27345E-06	1.869837538	0.17077048	1	19	31	24	4	22	90	145	76	102	44
ENSMUSG00000024687	chr19	Osbp	-0.6955976	2.11465E-06	7.28476E-06	7.004409316	0.025064543	-1	2395	2197	2174	2807	2243	1912	1458	1415	1423	1827
ENSMUSG00000104344	chr9	RP23-444I6.3	-1.4802104	2.11554E-06	7.28603E-06	0.945439613	0.071800218	-1	48	30	35	38	47	13	23	12	16	14
ENSMUSG00000029720	chr5	Gm20605	0.66765808	2.12672E-06	7.32275E-06	4.993399876	0.021480263	1	373	312	344	451	349	800	573	558	580	684
ENSMUSG00000047407	chr17	Tgif1	1.15738975	2.1508E-06	7.40383E-06	3.108215241	0.060891107	1	108	79	72	70	59	286	252	154	121	156
ENSMUSG00000038546	chr13	Ranbp9	-0.7295964	2.15528E-06	7.41745E-06	5.17680038	0.026319102	-1	728	606	580	841	612	378	463	362	462	548
ENSMUSG00000041762	chr2	Gpr155	-0.8770922	2.15808E-06	7.42524E-06	3.989867762	0.036033297	-1	371	297	262	360	238	127	192	172	206	204
ENSMUSG00000037652	chr3	Phc3	-0.7224769	2.15998E-06	7.42995E-06	4.096547134	0.02380747	-1	280	322	257	436	295	258	226	172	194	203
ENSMUSG00000031706	chr8	Rfx1	0.92204329	2.1758E-06	7.48252E-06	3.02792661	0.036099096	1	80	83	51	119	84	218	172	161	143	167
ENSMUSG00000071266	chr17	Zfp946	-1.4010572	2.1817E-06	7.50097E-06	1.855967696	0.080210158	-1	92	75	53	112	54	20	43	22	45	26
ENSMUSG00000028199	chr3	Cryz	-0.8151959	2.18567E-06	7.51093E-06	3.672303242	0.029681566	-1	229	267	251	272	179	169	162	154	136	126
ENSMUSG00000036368	chr17	Rmdn2	-1.0227424	2.18518E-06	7.51093E-06	2.493186387	0.041768291	-1	88	113	97	167	93	54	65	56	65	56
ENSMUSG00000032059	chr9	Alg9	0.78783722	2.19685E-06	7.54749E-06	3.615023633	0.027113818	1	140	114	114	162	133	236	290	234	266	222
ENSMUSG00000024960	chr19	Plcb3	0.68512861	2.20463E-06	7.57237E-06	4.266324852	0.021407616	1	207	206	201	270	209	487	375	356	358	354
ENSMUSG00000023348	chr5	Trip6	0.98467084	2.20959E-06	7.58752E-06	3.419046436	0.04408535	1	94	97	101	119	114	380	222	199	177	181
ENSMUSG00000006456	chr19	Rbm14	0.86962714	2.22861E-06	7.65097E-06	3.692001598	0.034483388	1	130	123	95	190	142	387	290	223	241	220
ENSMUSG00000075707	chr12	Dio3	3.24512631	2.23736E-06	7.67912E-06	0.599474325	0.377686714	1	3	2	8	1	4	120	30	36	14	7
ENSMUSG00000030587	chr7	2200002D01Rik	2.17308184	2.24583E-06	7.70628E-06	0.545773277	0.164201734	1	3	6	10	10	6	81	16	25	30	27
ENSMUSG00000026311	chr1	Asb1	-0.6954915	2.25946E-06	7.75117E-06	4.109983426	0.021863496	-1	293	294	288	401	308	206	218	198	221	224
ENSMUSG00000025512	chr7	Chid1	0.807337	2.26894E-06	7.78178E-06	3.845161322	0.029682833	1	165	135	148	186	138	364	299	311	286	217
ENSMUSG00000028838	chr4	Extl1	-0.7113834	2.27761E-06	7.80958E-06	5.912069955	0.02578673	-1	1131	940	1038	1491	1000	761	645	762	768	770
ENSMUSG00000033174	chr6	Mgll	-0.8383031	2.30217E-06	7.89186E-06	6.198721062	0.036330225	-1	1161	1344	1234	1952	1369	1011	630	913	680	1069
ENSMUSG00000032405	chr9	Pias1	-0.8400539	2.30432E-06	7.89731E-06	3.709622083	0.032236574	-1	211	239	263	342	194	181	151	103	138	193
ENSMUSG00000090639	chr9	Gm20425	1.07834931	2.30637E-06	7.90237E-06	5.794125315	0.059732214	1	418	703	402	540	561	1390	936	1199	753	1898
ENSMUSG00000051674	chr5	Dcun1d4	-0.8518662	2.31369E-06	7.92551E-06	3.195564517	0.03095197	-1	180	151	158	232	153	99	137	84	108	99
ENSMUSG00000029071	chr4	Dvl1	-0.7416143	2.31635E-06	7.93268E-06	7.02345604	0.028737021	-1	2332	2243	2253	3047	2275	1482	1576	1305	1878	1681
ENSMUSG00000001034	chr11	Mapk7	0.90289649	2.33928E-06	8.00925E-06	3.219380832	0.035589023	1	81	68	86	135	109	231	221	181	158	189
ENSMUSG00000068130	chr2	Zfp442	-2.0891819	2.36213E-06	8.08464E-06	-0.318168962	0.106861394	-1	11	14	15	27	17	2	7	1	3	8
ENSMUSG00000091264	chr13	Smim13	-0.7077338	2.36246E-06	8.08464E-06	6.09946808	0.025744911	-1	1209	1157	1146	1652	1193	819	780	757	897	985
ENSMUSG00000099227	chr1	Mir8114	-1.2937221	2.37408E-06	8.12242E-06	3.623807485	0.081538155	-1	244	291	203	162	358	148	84	88	82	184
ENSMUSG00000002831	chr17	Plin4	-0.8782244	2.38458E-06	8.15638E-06	7.296951417	0.040501189	-1	2766	2936	2197	4026	3326	1935	1626	1172	2188	2156
ENSMUSG00000045799	chr14	Gm9800	1.33467467	2.38536E-06	8.15705E-06	1.783778981	0.07011549	1	35	22	26	30	26	84	125	60	60	59
ENSMUSG00000035596	chr7	Mboat7	0.72548199	2.38657E-06	8.15917E-06	4.054348743	0.024058411	1	159	193	154	247	177	404	344	273	301	365

ENSMUSG00000005148	chr14	Klf5	-1.1458512	2.38891E-06	8.16518E-06	1.739263567	0.04767155	-1	66	66	63	80	57	46	33	32	20	34
ENSMUSG00000031309	chrX	Rps6ka3	-0.8851686	2.40012E-06	8.2015E-06	6.348489286	0.04077189	-1	1544	1131	1317	2124	1797	772	1088	682	988	1140
ENSMUSG00000018821	chr19	Avpi1	0.87268331	2.40945E-06	8.23137E-06	3.913759908	0.03564975	1	199	186	132	138	124	301	296	328	303	342
ENSMUSG00000016477	chr13	E2f3	-0.7445551	2.42952E-06	8.2979E-06	4.133872455	0.02578715	-1	334	271	271	472	300	189	232	195	204	243
ENSMUSG00000024985	chr19	Tcf7l2	0.93611383	2.4363E-06	8.31901E-06	3.08045676	0.037896067	1	90	101	73	95	66	215	154	167	134	227
ENSMUSG00000032293	chr9	Ireb2	-0.7572339	2.44009E-06	8.32991E-06	5.387571943	0.029029437	-1	854	744	729	948	645	422	636	428	535	506
ENSMUSG00000037062	chr3	Sh3glb1	-0.7384408	2.45479E-06	8.37806E-06	7.701921869	0.028826329	-1	3596	3741	3484	5669	3152	2586	2681	2423	2151	2907
ENSMUSG00000073616	chr1	Myeov2	0.79855727	2.45969E-06	8.39272E-06	5.781921794	0.032769167	1	696	672	565	568	461	1486	1123	1041	1107	953
ENSMUSG00000035726	chr14	Supt16	0.76729533	2.46526E-06	8.40761E-06	4.809382631	0.029067879	1	309	293	284	392	267	804	640	507	517	421
ENSMUSG00000037824	chr14	Tspan14	0.75822153	2.46476E-06	8.40761E-06	4.946925665	0.02846351	1	290	338	381	366	311	846	636	583	484	625
ENSMUSG00000049922	chr2	Slc35c1	0.80914149	2.46588E-06	8.40768E-06	3.513399446	0.02888311	1	131	106	102	154	120	321	259	179	205	220
ENSMUSG00000040209	chr3	Zfp704	-0.806536	2.46934E-06	8.41742E-06	3.741204812	0.029733262	-1	237	215	228	286	286	174	148	120	146	204
ENSMUSG00000050105	chr4	Grrp1	1.43983834	2.51762E-06	8.57993E-06	2.138864475	0.090281109	1	41	22	22	57	32	198	79	81	75	84
ENSMUSG00000049907	chr5	Rasl11b	1.42013653	2.53113E-06	8.62387E-06	2.065277171	0.08752955	1	19	34	30	56	27	169	63	81	98	74
ENSMUSG00000037236	chr18	Matr3	-0.7867	2.55489E-06	8.7027E-06	5.852369503	0.031991254	-1	1123	1037	978	1403	930	526	728	608	661	924
ENSMUSG00000044345	chr19	Marveld1	0.74303708	2.56189E-06	8.72442E-06	4.457292012	0.02653368	1	258	199	243	292	225	616	375	409	377	470
ENSMUSG00000028134	chr3	Ptbp2	-0.8517841	2.56485E-06	8.73236E-06	3.562793914	0.032870242	-1	240	235	208	252	186	109	165	109	159	137
ENSMUSG00000020241	chr10	Col6a2	0.95650455	2.58192E-06	8.78833E-06	8.560020042	0.048532843	1	3856	3210	3388	4490	4138	8662	7375	10169	4682	9704
ENSMUSG00000092812	chr4	Gm23634	1.77903109	2.58288E-06	8.78948E-06	0.453171489	0.098988265	1	10	9	6	9	7	31	47	37	23	17
ENSMUSG00000055027	chr6	Smyd1	-0.8311036	2.59957E-06	8.8441E-06	8.920455858	0.036841693	-1	9068	8200	8288	11908	8938	4159	6277	5219	6292	6315
ENSMUSG00000027194	chr2	Ttc17	-0.7063608	2.60579E-06	8.86312E-06	4.589295884	0.024125749	-1	451	350	414	518	476	311	284	275	272	346
ENSMUSG00000008333	chr2	Snrpb2	0.79139733	2.63321E-06	8.95419E-06	4.115337755	0.029844144	1	193	195	136	252	170	364	402	299	416	295
ENSMUSG00000020778	chr11	Ten1	0.76314671	2.63766E-06	8.96715E-06	4.332898193	0.027920291	1	260	197	227	237	181	518	385	360	448	349
ENSMUSG00000005417	chr11	Mprip	-0.7076787	2.64532E-06	8.99099E-06	6.725370856	0.026351674	-1	1683	1767	1770	2589	1998	1431	1352	1211	1125	1453
ENSMUSG00000031974	chr8	Abcb10	-0.6735347	2.64648E-06	8.99276E-06	4.833132473	0.022094387	-1	501	481	483	707	448	351	351	364	376	336
ENSMUSG00000013155	chr8	Enkd1	1.6350556	2.65583E-06	9.02233E-06	0.584320032	0.083017432	1	9	12	5	12	11	51	39	31	26	22
ENSMUSG00000062647	chr2	Rpl7a	0.73308492	2.66364E-06	9.04668E-06	8.282432124	0.028717789	1	3592	3121	2875	4475	3444	8076	6610	5662	5932	5592
ENSMUSG00000031782	chr8	Coq9	-0.8252515	2.66434E-06	9.04684E-06	8.45631177	0.036357866	-1	6409	6704	6950	8476	5028	3583	3748	3536	4829	4904
ENSMUSG00000032977	chr10	Fam207a	0.77873774	2.68578E-06	9.11745E-06	3.719217812	0.027440441	1	133	123	136	189	137	362	276	206	271	239
ENSMUSG00000038069	chr8	Cdkn2aip	-0.9882135	2.69494E-06	9.1463E-06	2.59889138	0.040603353	-1	114	115	113	165	88	58	82	55	53	78
ENSMUSG00000026792	chr2	Lrsam1	-0.7419023	2.7112E-06	9.19478E-06	3.885813617	0.025079304	-1	289	285	236	335	228	217	164	141	202	175
ENSMUSG00000028522	chr4	Mier1	-0.7249722	2.71068E-06	9.19478E-06	4.098343191	0.0245455	-1	287	312	274	460	266	244	210	169	183	248
ENSMUSG00000074570	chr2	Cass4	2.14155545	2.71117E-06	9.19478E-06	0.644356741	0.165627194	1	6	5	15	7	5	59	43	12	52	25
ENSMUSG00000030515	chr7	Tarsl2	-1.1954631	2.71614E-06	9.20931E-06	5.652762191	0.074260276	-1	1153	991	957	1243	875	204	619	376	548	728
ENSMUSG00000017499	chr11	Cdc6	1.85512159	2.76016E-06	9.35629E-06	1.334179397	0.141160969	1	20	22	14	9	10	75	92	39	74	25
ENSMUSG00000024357	chr18	Sil1	0.77990771	2.76469E-06	9.36938E-06	4.175470597	0.029076535	1	208	189	133	233	221	423	338	359	308	427
ENSMUSG00000042766	chr3	Trim46	1.93476583	2.78147E-06	9.42167E-06	0.030977065	0.101584075	1	6	8	2	7	4	35	23	26	12	19
ENSMUSG00000044162	chr6	Tnip3	2.68045788	2.78107E-06	9.42167E-06	-0.260168523	0.214350116	1	3	1	0	8	2	21	41	8	19	10
ENSMUSG00000017686	chr11	Rhot1	-0.675619	2.7904E-06	9.44963E-06	5.32917341	0.023090527	-1	715	722	714	880	643	487	552	416	531	534
ENSMUSG00000027709	chr3	Mccc1	-0.6931512	2.79669E-06	9.46863E-06	5.235833558	0.024254571	-1	615	784	651	866	552	453	476	443	459	509
ENSMUSG00000024420	chr18	Zfp521	-0.7874724	2.81189E-06	9.51781E-06	3.944726573	0.029009032	-1	279	281	252	372	265	149	206	144	179	238
ENSMUSG00000023473	chr9	Celsr3	2.86664015	2.82014E-06	9.54342E-06	-0.585196947	0.196959399	1	4	1	1	1	2	18	24	23	6	5
ENSMUSG00000013483	chr11	Card14	2.06236086	2.82807E-06	9.56609E-06	0.949069911	0.165180885	1	6	11	15	8	10	87	19	64	36	30
ENSMUSG00000021645	chr13	Smn1	0.77721984	2.82821E-06	9.56609E-06	3.344889891	0.025804273	1	121	104	95	131	100	252	184	186	217	196
ENSMUSG00000044927	chr6	H1fx	1.77881685	2.83569E-06	9.58906E-06	1.2432857	0.127411484	1	21	15	10	13	15	69	40	90	23	58
ENSMUSG00000051329	chr2	Nup160	-1.0132346	2.86836E-06	9.69721E-06	2.858954147	0.045662195	-1	122	136	158	167	127	75	98	45	88	82
ENSMUSG00000041235	chr4	Chd7	-0.7433275	2.89475E-06	9.78404E-06	4.290346966	0.026566065	-1	317	323	319	501	367	230	226	242	197	292
ENSMUSG00000026788	chr2	Zbtb43	-0.7099391	2.89611E-06	9.78629E-06	3.876247048	0.022782611	-1	271	253	279	322	223	186	190	166	157	205
ENSMUSG00000015092	chr2	Edf1	0.70325922	2.89847E-06	9.79189E-06	6.569495931	0.026151534	1	1125	972	879	1368	1058	2373	1860	1888	1728	1765
ENSMUSG00000092360	chr10	Gm20441	0.72691139	2.9012E-06	9.79875E-06	4.183410437	0.024939535	1	201	223	204	225	156	379	344	373	336	400
ENSMUSG00000036890	chr2	Gtdc1	-0.7926309	2.90865E-06	9.82153E-06	3.707572689	0.028681824	-1	253	241	206	321	211	134	134	142	172	189
ENSMUSG00000039463	chr2	Slc9a8	-0.6571135	2.91493E-06	9.84037E-06	5.183326104	0.021710367	-1	649	583	600	775	690	516	482	373	457	475
ENSMUSG00000022940	chr16	Pigp	-0.7422768	2.92209E-06	9.86213E-06	5.751414495	0.028665795	-1	1111	1020	875	1153	857	568	672	542	756	736
ENSMUSG00000035629	chr16	1700021K19Rik	-0.6670137	2.94189E-06	9.92656E-06	5.216711966	0.022462209	-1	687	617	589	768	718	474	482	397	473	515
ENSMUSG00000015714	chr3	Cers2	0.82885418	2.95639E-06	9.97068E-06	5.287038402	0.035491396	1	408	380	377	559	378	1191	932	529	812	651
ENSMUSG00000044949	chr11	Ubtd2	-1.2176098	2.95592E-06	9.97068E-06	2.082811148	0.061473544	-1	74	78	86	92	97	28	61	40	31	42
ENSMUSG00000021932	chr14	Rnaseh2b	0.98774364	2.9941E-06	1.00954E-05	2.892977188	0.043052455	1	83	72	66	88	56	180	168	143	190	108
ENSMUSG00000042485	chr14	Mustn1	1.40945909	2.99694E-06	1.01026E-05	7.023346153	0.104190727	1	1158	678	1802	958	612	4290	2788	3513	3256	1515
ENSMUSG00000071708	chrX	Sms	-0.73498	3.00721E-06	1.01347E-05	6.919340515	0.028849386	-1	2553	1999	1850	2497	2331	1376	1688	1308	1401	1636
ENSMUSG00000003559	chr19	As3mt	-0.7403418	3.01381E-06	1.01545E-05	5.350793978	0.028245042	-1	690	759	702	962	691	716	468	482	397	443
ENSMUSG00000021866	chr14	Anxa11	-0.9541933	3.04262E-06	1.02483E-05	5.645551879	0.047842938	-1	905	850	794	1288	1092	334	574	497	604	747
ENSMUSG00000027457	chr2	Snph	-1.7260303	3.04311E-06	1.02483E-05	0.497528454	0.097684834	-1	36	17	20	40	37	9	11	4	14	11
ENSMUSG00000015357	chr9	Clpx	-0.7443738	3.06316E-06	1.03133E-05	6.005706499	0.029157693	-1	1098	1127	1034	1768	1038	725	811	620	816	946
ENSMUSG00000024411	chr18	Aqp4	-1.6769051	3.07609E-06	1.03544E-05	4.92945174	0.143901823	-1	481	603	808	1083	519	54	268	146	318	384
ENSMUSG00000044244	chr9	Il20rb	1.72792396	3.07972E-06	1.03641E-05	1.87469776	0.131584643	1	38	26	19	14	22	82	81	52	54	178

ENSMUSG00000028541	chr4	B4galt2	0.92312083	3.08138E-06	1.03672E-05	3.135992516	0.037886375	1	100	83	79	94	87	234	185	211	130	166
ENSMUSG00000044098	chr3	Rsbn1	-1.0649969	3.08391E-06	1.03732E-05	2.762077408	0.050699925	-1	135	112	117	204	115	59	84	53	52	106
ENSMUSG00000030339	chr6	Ltbr	0.64745538	3.08811E-06	1.03849E-05	5.055095596	0.020916333	1	398	399	358	466	306	796	663	548	662	644
ENSMUSG00000033306	chr16	Lpp	-0.767057	3.09156E-06	1.0394E-05	5.15633761	0.030191182	-1	644	551	576	927	667	359	491	432	343	519
ENSMUSG00000039629	chr6	Strip2	-1.6984851	3.09515E-06	1.04035E-05	0.686627839	0.102366722	-1	48	30	31	24	36	12	12	9	5	20
ENSMUSG00000006281	chr14	Tep1	0.66485172	3.10019E-06	1.0418E-05	4.60089603	0.021411609	1	283	243	229	343	295	511	497	420	466	526
ENSMUSG00000081788	chr7	Gm5898	-1.3425381	3.10219E-06	1.04222E-05	1.974992103	0.076835992	-1	67	79	78	89	93	17	39	41	28	50
ENSMUSG00000039844	chr2	Rapgef1	-0.786497	3.10639E-06	1.04338E-05	7.170896685	0.033228719	-1	2405	2151	2356	4100	2748	1554	1693	1621	1669	2071
ENSMUSG00000101188	chr1	Eif4a-ps4	0.97430178	3.11419E-06	1.04575E-05	3.96836722	0.046903385	1	170	129	155	211	121	364	466	215	400	239
ENSMUSG00000031983	chr8	2310022B05Rik	0.86388033	3.12677E-06	1.04972E-05	5.026950232	0.038521892	1	386	307	299	427	304	833	567	894	445	674
ENSMUSG00000048874	chr1	Phf3	-0.7046545	3.13036E-06	1.05067E-05	4.850577911	0.024915173	-1	467	478	464	659	586	393	378	268	333	423
ENSMUSG00000020978	chr12	Klhdc2	-0.8879658	3.13488E-06	1.05194E-05	6.822821738	0.04223641	-1	2541	2174	1967	2507	1764	1010	1333	894	1628	1598
ENSMUSG00000035960	chr14	Apex1	0.70653307	3.14093E-06	1.05371E-05	4.945671954	0.02510538	1	410	336	314	375	298	693	654	635	605	512
ENSMUSG00000027809	chr3	Etfdh	-0.8271883	3.14882E-06	1.05607E-05	6.927578062	0.036706053	-1	1771	2465	2268	3567	1691	1336	1369	1357	1582	1480
ENSMUSG00000028675	chr4	Pnrc2	-0.7189654	3.15007E-06	1.05607E-05	5.353269042	0.02664834	-1	842	779	646	954	583	468	552	428	452	620
ENSMUSG00000073639	chr18	Rab18	-0.7733383	3.15021E-06	1.05607E-05	6.333259195	0.031813256	-1	1602	1365	1334	1990	1333	800	1092	795	910	1258
ENSMUSG00000046139	chr19	Patl1	-0.6936604	3.15487E-06	1.05737E-05	4.697325507	0.023820129	-1	400	431	431	677	460	379	306	273	288	374
ENSMUSG00000058351	chr14	Smim4	0.92442209	3.15685E-06	1.05778E-05	2.822328104	0.036576525	1	75	72	66	100	47	195	143	139	130	138
ENSMUSG00000004951	chr5	Hspb1	1.30813393	3.16432E-06	1.06003E-05	7.247719939	0.090746147	1	1128	954	952	2189	1424	7379	2939	3406	1948	2366
ENSMUSG00000014846	chr8	Tppp3	0.88629823	3.16652E-06	1.06051E-05	6.166532487	0.041763961	1	744	602	781	912	710	1432	1121	1921	1226	1838
ENSMUSG00000009075	chr11	Cabp7	-2.0092035	3.1739E-06	1.06273E-05	0.218233174	0.130298468	-1	8	24	26	36	32	9	8	3	9	5
ENSMUSG00000030268	chr6	Bcat1	1.49904272	3.19446E-06	1.06936E-05	2.542459437	0.105114955	1	80	36	37	29	36	187	198	107	124	74
ENSMUSG00000034158	chr16	Lrrc58	-0.8342135	3.21657E-06	1.0765E-05	4.872635237	0.035725465	-1	486	532	492	777	522	272	475	271	275	424
ENSMUSG00000029551	chr5	Psmg3	0.92125128	3.2418E-06	1.08469E-05	3.53889286	0.040315322	1	133	111	99	161	93	330	284	212	251	155
ENSMUSG00000037977	chr9	6430571L13Rik	-0.8337606	3.24584E-06	1.08578E-05	5.930555564	0.036858263	-1	1136	1186	1258	1202	982	527	881	643	772	728
ENSMUSG00000021218	chr13	Gdi2	0.68968774	3.24745E-06	1.08606E-05	7.016295088	0.025584269	1	1494	1453	1295	1945	1241	3094	2743	2097	2678	2476
ENSMUSG00000027397	chr2	Slc20a1	1.08647363	3.25051E-06	1.08682E-05	3.531098775	0.057364694	1	112	118	100	113	98	477	257	163	202	195
ENSMUSG00000048799	chr18	Cep120	-0.6773987	3.25519E-06	1.08813E-05	4.048041808	0.021234339	-1	290	294	274	372	279	233	225	180	202	194
ENSMUSG00000026655	chr2	Fam107b	1.11475724	3.26254E-06	1.09032E-05	2.933615937	0.057329722	1	57	83	68	84	60	245	188	84	180	152
ENSMUSG00000005566	chr7	Trim28	0.76867813	3.26621E-06	1.09129E-05	6.132604048	0.031407207	1	767	713	579	1044	787	1918	1508	1432	1162	1219
ENSMUSG00000040205	chr7	Cuzd1	-1.7919191	3.28776E-06	1.09823E-05	0.397345202	0.107014631	-1	36	31	20	25	27	10	14	3	13	4
ENSMUSG00000032388	chr9	Spg21	1.00185285	3.298E-06	1.10112E-05	4.67120742	0.051743867	1	387	260	226	175	191	508	644	540	458	606
ENSMUSG00000033253	chr4	Szt2	-0.7557053	3.29777E-06	1.10112E-05	3.670269491	0.026020903	-1	230	214	237	256	237	170	159	152	117	170
ENSMUSG00000038388	chr6	Mpp6	-0.6758908	3.3E-06	1.10152E-05	6.031812433	0.024102181	-1	1175	1124	1072	1507	1126	840	773	704	867	922
ENSMUSG00000035248	chr13	Zcchc6	-0.6609778	3.3018E-06	1.10186E-05	5.085507196	0.022104267	-1	587	524	581	808	602	467	398	345	441	496
ENSMUSG00000098973	chr9	Mir6236	1.41439726	3.3081E-06	1.1037E-05	6.627981435	0.105659312	1	977	432	414	868	1301	4060	2757	1939	1436	1752
ENSMUSG00000083012	chr5	Fam220a	-0.7621383	3.3215E-06	1.10791E-05	5.67434999	0.030544464	-1	801	836	786	1579	872	671	593	556	654	611
ENSMUSG00000043008	chr16	Klhl6	1.49824749	3.32718E-06	1.10953E-05	1.988996107	0.098122689	1	24	30	43	35	16	164	95	87	60	61
ENSMUSG00000074825	chr2	Itpripl1	1.33119562	3.33502E-06	1.11188E-05	2.74864884	0.08383592	1	48	65	44	80	44	303	124	83	157	117
ENSMUSG00000078190	chr1	Dnm3os	1.65037892	3.37887E-06	1.12624E-05	1.363344484	0.109521555	1	27	18	21	12	8	95	54	42	71	41
ENSMUSG00000026574	chr1	Dpt	0.82049423	3.38337E-06	1.12747E-05	6.600897375	0.036187974	1	1056	1184	898	998	1030	1763	1870	2049	1789	2601
ENSMUSG00000050891	chr15	Tatdn1	-0.7465458	3.39649E-06	1.13157E-05	3.810247918	0.025702285	-1	283	255	250	307	206	167	166	149	199	165
ENSMUSG00000079019	chr8	Insl3	2.31682728	3.4161E-06	1.13783E-05	-0.027949671	0.161112887	1	7	3	5	1	4	45	11	18	13	29
ENSMUSG00000039646	chr16	Vasn	0.99619266	3.41752E-06	1.13803E-05	3.891811348	0.049298307	1	140	155	100	169	166	510	355	290	193	273
ENSMUSG00000075706	chr10	Gpx4	0.73069618	3.42285E-06	1.13954E-05	7.9063136	0.029106431	1	2872	2795	2520	3127	2129	6021	4491	4542	4969	4443
ENSMUSG00000045374	chr11	Wdr81	0.77202044	3.43205E-06	1.14233E-05	3.804335444	0.027735985	1	138	172	124	181	146	392	276	226	245	299
ENSMUSG00000052192	chr16	Gm5963	1.53937512	3.43977E-06	1.14462E-05	0.757248489	0.075185864	1	11	14	13	9	11	59	38	33	25	35
ENSMUSG00000042918	chr7	Mamstr	0.9880082	3.44159E-06	1.14468E-05	6.17167287	0.052326346	1	919	540	571	928	667	965	1406	1816	1664	1846
ENSMUSG00000098666	chr14	Mir6950	-1.1273684	3.44124E-06	1.14468E-05	1.525706017	0.044420446	-1	55	53	59	72	45	29	36	25	23	29
ENSMUSG00000032596	chr9	Uba7	0.91911337	3.4469E-06	1.14618E-05	2.860620808	0.036276313	1	68	71	77	80	69	161	146	130	124	203
ENSMUSG00000048138	chr19	Dmrt2	-1.265284	3.45251E-06	1.14777E-05	2.299589784	0.071082577	-1	88	102	107	98	106	24	59	54	36	56
ENSMUSG00000059475	chr9	Zfp426	-0.8354525	3.48443E-06	1.15811E-05	3.291099486	0.031302757	-1	182	164	165	238	179	101	130	83	109	146
ENSMUSG00000038116	chr2	Phf20	-0.7500121	3.48994E-06	1.15966E-05	4.289092998	0.027609567	-1	385	327	324	438	345	188	287	197	242	267
ENSMUSG00000051378	chr11	Kif18b	1.9446642	3.4913E-06	1.15984E-05	0.818259323	0.139088646	1	12	11	11	3	11	45	77	36	26	27
ENSMUSG00000030452	chr7	Nipa2	-0.6665548	3.50453E-06	1.16396E-05	5.018830795	0.022553515	-1	616	531	546	701	560	396	496	322	389	441
ENSMUSG00000028696	chr4	Ipp	-0.8824018	3.51608E-06	1.16752E-05	3.216026408	0.035148379	-1	180	178	179	213	138	78	111	104	108	123
ENSMUSG00000010358	chr11	Ifi35	0.77098745	3.53147E-06	1.17235E-05	4.138709034	0.028965325	1	209	197	194	229	135	464	305	350	358	325
ENSMUSG00000031791	chr8	Tmem38a	-0.8425333	3.53663E-06	1.17378E-05	10.32370416	0.038977847	-1	26486	23229	21205	27998	23530	11676	15621	11585	17676	18098
ENSMUSG00000078812	chr11	Eif5a	0.7043722	3.54022E-06	1.1747E-05	9.0094898	0.027280701	1	6178	5563	5040	6857	5566	12432	10994	9322	10064	9466
ENSMUSG00000027330	chr2	Cdc25b	0.98974335	3.54292E-06	1.17531E-05	3.266464021	0.04586983	1	131	79	60	93	108	250	238	197	169	179
ENSMUSG00000020812	chr11	1810032O08Rik	1.40880538	3.56203E-06	1.18137E-05	1.105105082	0.068215427	1	18	17	19	15	12	71	47	35	51	36
ENSMUSG00000033434	chr5	Gtpbp6	0.82915849	3.60074E-06	1.19392E-05	3.285202002	0.030675974	1	111	86	89	133	99	260	176	200	200	169
ENSMUSG00000092686	chr10	Gm25745	-1.3982766	3.60322E-06	1.19446E-05	2.334418456	0.089630713	-1	81	92	87	165	115	27	65	21	61	47
ENSMUSG00000026103	chr1	Gls	-0.7156476	3.61936E-06	1.19953E-05	5.66155423	0.027041881	-1	911	789	907	1330	790	622	709	489	665	640
ENSMUSG00000050550	chr4	Gm11868	-2.3750348	3.62084E-06	1.19974E-05	1.39123787	0.250281867	-1	49	58	52	103	58	46	3	5	6	9

ENSMUSG00000027206	chr2	Cops2	-0.8430734	3.62687E-06	1.20119E-05	6.113219052	0.038203315	-1	1520	1215	1093	1648	1173	565	843	681	895	1035
ENSMUSG00000037525	chr15	Bcdin3d	1.05102731	3.62694E-06	1.20119E-05	2.171159406	0.044624218	1	42	36	49	54	31	107	88	106	93	85
ENSMUSG00000020182	chr11	Ddc	1.39246448	3.62967E-06	1.20181E-05	2.51359759	0.090025732	1	71	41	41	34	39	120	82	195	106	147
ENSMUSG00000017677	chr11	Wsb1	0.7657475	3.63953E-06	1.20479E-05	3.968309742	0.027893316	1	168	155	172	202	158	410	359	224	328	286
ENSMUSG00000000600	chr5	Krit1	-0.8347789	3.7069E-06	1.22651E-05	3.77634127	0.033461839	-1	274	248	247	309	221	119	164	129	197	184
ENSMUSG00000024998	chr19	Plce1	-0.862064	3.70665E-06	1.22651E-05	3.688172552	0.035672497	-1	199	207	229	380	230	196	136	157	103	152
ENSMUSG00000026433	chr1	Rab29	1.05410477	3.72338E-06	1.23167E-05	3.108040785	0.052364775	1	85	95	80	88	61	294	204	110	186	154
ENSMUSG00000037526	chr14	Atg14	-0.822529	3.73628E-06	1.23564E-05	3.157617719	0.029833391	-1	175	180	163	173	143	99	107	101	93	119
ENSMUSG00000029553	chr6	Tfec	2.0233174	3.73954E-06	1.23643E-05	-0.167886861	0.102927478	1	8	2	2	7	3	26	23	15	23	12
ENSMUSG00000063558	chr1	Aox1	-0.9826921	3.7417E-06	1.23685E-05	3.327651906	0.045927254	-1	173	226	183	262	145	109	66	115	130	121
ENSMUSG00000028059	chr3	Arhgef2	0.71422219	3.76022E-06	1.24268E-05	5.212908845	0.026545553	1	457	391	422	515	308	816	749	823	599	757
ENSMUSG00000035078	chr14	Mtmr9	-0.8140917	3.77145E-06	1.2461E-05	3.111908262	0.028824094	-1	147	154	152	233	133	109	101	83	93	121
ENSMUSG00000004085	chr2	Zak	-0.7146376	3.77535E-06	1.24709E-05	7.909547036	0.028101462	-1	4894	4214	4203	5278	3699	3850	3003	2507	2854	2731
ENSMUSG00000018476	chr11	Kdm6b	-0.834574	3.78088E-06	1.24862E-05	5.283863062	0.036888467	-1	608	706	760	986	663	580	428	465	270	553
ENSMUSG00000049764	chr10	Zfp280b	-0.8305003	3.7834E-06	1.24916E-05	3.962227334	0.033734327	-1	339	306	251	303	270	137	187	166	181	235
ENSMUSG00000092827	chr2	Mir3091	1.98716842	3.79475E-06	1.25261E-05	0.094193108	0.115563707	1	7	4	11	3	2	37	29	19	19	18
ENSMUSG00000025212	chr19	Sfxn3	0.75944936	3.81424E-06	1.25874E-05	5.126695627	0.030061277	1	492	336	314	376	395	690	712	594	705	875
ENSMUSG00000029614	chr5	Rpl6	0.68902517	3.81859E-06	1.25988E-05	7.735218925	0.026109607	1	2660	2281	1995	3035	2234	5193	4560	3793	3811	4205
ENSMUSG00000024883	chr19	Rin1	1.83665454	3.82878E-06	1.26295E-05	1.317519238	0.144453347	1	15	10	16	29	8	92	84	63	41	21
ENSMUSG00000008318	chr7	Relt	-0.7846379	3.83808E-06	1.26572E-05	4.516017818	0.031250339	-1	356	371	494	582	353	299	257	312	246	246
ENSMUSG00000037344	chr5	Slc12a9	1.10480623	3.86614E-06	1.27467E-05	2.873312247	0.056887313	1	62	66	82	72	55	248	117	157	106	181
ENSMUSG00000003500	chr6	Impdh1	0.71182641	3.86819E-06	1.27504E-05	4.777823968	0.025757969	1	297	358	277	350	257	633	546	602	489	492
ENSMUSG00000022641	chr16	Bbx	-0.7811028	3.8827E-06	1.27952E-05	3.390518579	0.027324917	-1	181	174	168	263	197	130	148	120	100	126
ENSMUSG00000035274	chr9	Tpbg	1.4693626	3.9047E-06	1.28647E-05	1.338334635	0.085826626	1	23	10	24	23	14	95	65	44	40	46
ENSMUSG00000038387	chr7	Rras	0.9310456	3.90652E-06	1.28677E-05	5.174719995	0.046050347	1	461	350	333	417	286	1358	579	665	589	723
ENSMUSG00000032860	chr7	P2ry2	-0.7800681	3.93111E-06	1.29456E-05	5.580469741	0.032481102	-1	728	698	940	1312	857	633	629	590	426	596
ENSMUSG00000019806	chr10	Aig1	0.84253603	3.94027E-06	1.29636E-05	3.787505012	0.034519657	1	140	136	122	218	123	402	273	266	186	321
ENSMUSG00000024544	chr18	Ldlrad4	-1.013079	3.93923E-06	1.29636E-05	2.631701924	0.045111914	-1	120	122	120	162	87	82	45	75	57	70
ENSMUSG00000035268	chr2	Pkig	0.76979262	3.93846E-06	1.29636E-05	6.035448081	0.031996305	1	745	665	609	1010	617	1644	1058	1551	1179	1291
ENSMUSG00000041471	chr14	Fam35a	-0.9426579	3.9394E-06	1.29636E-05	2.728162763	0.038673071	-1	121	142	112	173	96	80	66	53	82	84
ENSMUSG00000010376	chr14	Nedd8	0.72241047	3.94207E-06	1.29664E-05	6.380261327	0.028278872	1	1070	953	862	977	794	2100	1634	1455	1746	1547
ENSMUSG00000097296	chr8	Gm26532	1.91877631	3.94827E-06	1.29838E-05	1.627240119	0.16174692	1	17	14	27	14	17	187	66	51	45	41
ENSMUSG00000040410	chr4	Fbxl4	-0.8602191	3.94947E-06	1.29847E-05	3.814593134	0.0363403	-1	317	315	210	257	234	142	184	126	154	205
ENSMUSG00000069769	chr11	Msi2	-0.8331233	3.97109E-06	1.30527E-05	6.710345441	0.03792994	-1	2060	1868	1924	2459	1698	824	1306	1278	1228	1448
ENSMUSG00000028126	chr3	Pip5k1a	-0.6572068	3.99575E-06	1.31307E-05	4.89086103	0.021983449	-1	534	476	554	672	465	437	405	343	292	405
ENSMUSG00000026858	chr2	Fam73b	-0.7480468	4.00184E-06	1.31476E-05	4.03732429	0.027155552	-1	292	278	261	417	287	167	208	173	200	244
ENSMUSG00000035199	chr6	Arl6ip5	0.71396578	4.01129E-06	1.31755E-05	7.675575768	0.02814955	1	2531	2032	2014	2934	2083	4722	3775	4446	3602	4159
ENSMUSG00000022477	chr15	Aco2	-0.7562709	4.01317E-06	1.31786E-05	10.59787278	0.031859081	-1	23822	28130	28137	42007	24446	20505	16586	17576	18845	20577
ENSMUSG00000022201	chr15	Zfr	-0.7652769	4.01875E-06	1.31938E-05	5.417974867	0.031112418	-1	750	684	723	1083	786	420	522	419	558	655
ENSMUSG00000051627	chr13	Hist1h1e	-1.6577432	4.04311E-06	1.32707E-05	1.19596928	0.112831363	-1	49	46	46	57	49	3	23	13	18	28
ENSMUSG00000028701	chr4	Lurap1	-0.9287279	4.08529E-06	1.3406E-05	3.399552744	0.041209957	-1	188	183	218	262	172	98	93	96	156	141
ENSMUSG00000038535	chr9	Zfp280d	-0.841853	4.08864E-06	1.34138E-05	3.30969082	0.032388965	-1	174	165	169	265	173	90	112	110	125	133
ENSMUSG00000031659	chr8	Adcy7	0.81035714	4.09572E-06	1.34339E-05	4.471411644	0.033582281	1	252	217	208	298	222	613	602	283	390	436
ENSMUSG00000079111	chr5	Kdelr2	0.67214296	4.1215E-06	1.35153E-05	5.280690037	0.023611615	1	447	401	392	559	433	940	911	690	686	676
ENSMUSG00000031788	chr8	Kifc3	0.71233947	4.12573E-06	1.3526E-05	3.761747547	0.023412482	1	175	123	137	192	135	311	304	234	244	274
ENSMUSG00000034906	chr2	Ncaph	1.23907417	4.15801E-06	1.36286E-05	2.285675016	0.06797925	1	37	46	52	34	37	120	152	81	116	75
ENSMUSG00000051786	chr15	Tubgcp6	-0.7040439	4.16469E-06	1.36473E-05	3.911320503	0.023428549	-1	245	269	240	350	278	211	181	144	191	204
ENSMUSG00000036376	chr13	Abt1	0.75487403	4.17029E-06	1.36624E-05	3.631747049	0.026346385	1	141	119	117	181	126	337	215	224	221	268
ENSMUSG00000020009	chr10	Ifngr1	0.66640723	4.18482E-06	1.37068E-05	5.076814994	0.022922477	1	341	383	392	464	353	839	645	518	689	696
ENSMUSG00000041763	chr1	Tpp2	-0.7947813	4.19767E-06	1.37457E-05	5.263792346	0.033604807	-1	685	637	610	1081	659	362	532	341	491	560
ENSMUSG00000074457	chr3	S100a16	0.77705255	4.20639E-06	1.3771E-05	6.273732772	0.032928085	1	943	913	764	928	685	2110	1274	1592	1601	1396
ENSMUSG00000074794	chr13	Arrdc3	-0.960677	4.2111E-06	1.37832E-05	5.094937206	0.049506165	-1	660	685	691	642	636	597	314	284	222	508
ENSMUSG00000044948	chr19	Cfap43	1.72468682	4.21298E-06	1.37862E-05	1.902445587	0.135251942	1	14	26	41	26	15	187	93	58	52	71
ENSMUSG00000072720	chr5	Myo18b	-0.8655349	4.22955E-06	1.38371E-05	8.670103403	0.041656874	-1	6955	5821	6083	11630	9138	4333	4665	4815	3938	5765
ENSMUSG00000024824	chr19	Rad9a	1.02105266	4.24667E-06	1.38899E-05	2.697479855	0.046637253	1	73	63	67	66	42	203	146	105	125	122
ENSMUSG00000024165	chr17	Hn1l	1.03541661	4.25582E-06	1.39165E-05	3.336391037	0.05249885	1	102	86	84	118	97	180	321	160	270	158
ENSMUSG00000057835	chr17	Zfp119a	-1.5633472	4.26328E-06	1.39377E-05	1.159769014	0.09714615	-1	59	59	32	50	37	10	12	13	24	28
ENSMUSG00000031402	chrX	Mpp1	0.94758714	4.2815E-06	1.3994E-05	5.418521461	0.048394368	1	591	470	398	354	331	770	1011	646	1094	1058
ENSMUSG00000033701	chr1	Acbd6	0.70431363	4.29356E-06	1.40301E-05	4.706987054	0.025345901	1	278	235	268	392	306	652	516	538	457	470
ENSMUSG00000096942	chr12	Rps19-ps6	0.95158698	4.29719E-06	1.40387E-05	3.029247712	0.041961187	1	78	80	71	119	64	242	178	132	190	127
ENSMUSG00000024143	chr17	Rhoq	-0.9232722	4.30598E-06	1.40641E-05	7.833820739	0.047261105	-1	4624	4079	3992	5704	3966	1669	2687	2713	2057	3652
ENSMUSG00000034252	chr9	Senp6	-0.619762	4.30895E-06	1.40705E-05	5.110152097	0.019771172	-1	643	558	556	809	560	517	455	361	441	451
ENSMUSG00000098090	chr17	2700099C18Rik	2.49932574	4.36702E-06	1.42568E-05	-0.432143843	0.164806724	1	1	3	4	3	2	17	31	9	21	6
ENSMUSG00000098302	chr5	Gm28039	-1.7037305	4.37464E-06	1.42784E-05	0.39859317	0.094896012	-1	26	27	17	40	29	7	8	3	12	16
ENSMUSG00000030805	chr7	Stx4a	0.70183188	4.37672E-06	1.42818E-05	5.86976664	0.026593536	1	770	662	580	734	561	1349	1193	1016	1305	1038

ENSMUSG00000030214	chr6	Plbd1	1.20624766	4.41497E-06	1.44033E-05	3.979746203	0.075889297	1	90	166	115	252	99	275	388	365	504	222
ENSMUSG00000021708	chr13	Rasgrf2	-1.2999873	4.42462E-06	1.44314E-05	2.164839199	0.077144098	-1	65	108	68	143	86	65	32	23	53	35
ENSMUSG00000047123	chr17	Ticam1	0.9330759	4.44249E-06	1.44829E-05	3.087661402	0.04047437	1	59	78	78	121	94	243	157	136	178	189
ENSMUSG00000069237	chr13	C78339	-0.6899905	4.44207E-06	1.44829E-05	5.146432175	0.025044575	-1	738	655	568	757	536	569	494	398	347	413
ENSMUSG00000037331	chr11	Larp1	-0.7414887	4.4511E-06	1.45076E-05	6.913212301	0.030429109	-1	2124	1769	1846	3028	2525	1566	1618	1400	1207	1583
ENSMUSG00000072623	chr6	Zfp9	-0.7980302	4.45551E-06	1.45186E-05	3.416064248	0.029397447	-1	177	186	181	295	172	115	150	103	125	137
ENSMUSG00000046096	chr7	BC030336	-0.7922614	4.46917E-06	1.45597E-05	3.77028277	0.030311994	-1	265	259	272	304	180	152	204	140	140	174
ENSMUSG00000039414	chr17	Heatr5b	-0.8175472	4.50253E-06	1.4665E-05	3.165077782	0.029904339	-1	155	160	144	216	170	112	102	79	99	134
ENSMUSG00000028261	chr4	Ndufaf4	-0.7031198	4.5916E-06	1.49516E-05	4.955271799	0.025812617	-1	563	476	550	848	456	360	460	357	350	392
ENSMUSG00000039209	chr16	Rpl39l	2.01803439	4.59388E-06	1.49555E-05	-0.072749037	0.124005568	1	7	3	2	9	3	34	25	21	18	9
ENSMUSG00000055053	chr10	Nfic	-0.8789219	4.60058E-06	1.49737E-05	8.313587171	0.043224964	-1	5651	5132	5794	7618	6501	2838	3813	3525	2839	5257
ENSMUSG00000080268	chr19	Brms1	0.72775205	4.60162E-06	1.49737E-05	4.049222361	0.02588402	1	200	176	173	226	149	423	349	242	346	323
ENSMUSG00000021824	chr14	Ap3m1	-0.6657449	4.65367E-06	1.51396E-05	4.98070028	0.02303095	-1	562	587	523	728	487	391	472	353	415	352
ENSMUSG00000026219	chr1	Trip12	-0.7085421	4.65671E-06	1.51398E-05	7.131611839	0.02795998	-1	2484	2242	2294	3447	2560	1636	1928	1524	1547	2061
ENSMUSG00000029672	chr6	Fam3c	0.687514	4.65698E-06	1.51398E-05	3.862674181	0.022024153	1	149	165	156	215	141	342	307	251	250	309
ENSMUSG00000063273	chr3	Naa15	-0.7734154	4.65695E-06	1.51398E-05	5.993272285	0.032762364	-1	1252	1043	1058	1450	1183	588	915	630	793	897
ENSMUSG00000020747	chr11	2310067B10Rik	-0.7078275	4.66316E-06	1.51563E-05	6.051893884	0.027377531	-1	1093	1035	1163	1647	1214	789	867	834	699	911
ENSMUSG00000052316	chr16	Lrrc15	2.26399555	4.67348E-06	1.51864E-05	1.849404693	0.240050056	1	16	12	13	26	22	126	37	151	14	139
ENSMUSG00000037174	chr3	Elf2	-0.6661859	4.68549E-06	1.52219E-05	5.396606225	0.023628276	-1	760	737	709	1019	642	532	614	420	507	587
ENSMUSG00000024098	chr17	Twsg1	-0.7039633	4.6889E-06	1.52294E-05	4.987152933	0.026049052	-1	536	517	549	780	552	412	478	268	393	423
ENSMUSG00000024245	chr17	Tmem178	3.04961047	4.71148E-06	1.52992E-05	1.338185852	0.400005246	1	9	10	4	12	3	139	57	12	6	145
ENSMUSG00000084349	chrX	Rpl3-ps1	0.95783764	4.8106E-06	1.56174E-05	3.852060669	0.046605669	1	168	159	107	157	132	534	297	238	256	240
ENSMUSG00000078794	chr7	Dact3	1.00943814	4.88183E-06	1.5845E-05	2.880690098	0.047596676	1	93	67	57	82	59	223	145	169	102	154
ENSMUSG00000002395	chr8	Use1	0.69373031	4.8862E-06	1.58555E-05	5.462301028	0.025903942	1	509	498	456	649	405	846	813	918	931	901
ENSMUSG00000031312	chrX	Itgb1bp2	0.77972079	4.90815E-06	1.59193E-05	8.37793453	0.034311816	1	3916	3234	3120	4691	3384	6061	5801	7540	6382	8311
ENSMUSG00000033033	chr19	Calhm2	1.1754948	4.90789E-06	1.59193E-05	2.274640341	0.061413476	1	34	55	41	50	34	156	112	108	63	97
ENSMUSG00000044788	chr11	Fads6	-1.3179981	4.92996E-06	1.59863E-05	3.263543637	0.088353013	-1	101	241	214	340	132	71	73	92	132	69
ENSMUSG00000036721	chr13	Zscan12	-1.0025991	4.95282E-06	1.60568E-05	2.429498111	0.04388652	-1	112	109	99	113	90	50	53	46	56	82
ENSMUSG00000030607	chr7	Acan	2.10525747	4.97147E-06	1.61135E-05	1.100509615	0.190865059	1	22	4	10	8	11	107	64	38	41	19
ENSMUSG00000040229	chrX	Gpr34	1.69461043	4.97333E-06	1.61158E-05	0.978661757	0.113916386	1	22	12	9	12	9	24	43	44	42	74
ENSMUSG00000007721	chr8	Ccdc124	0.70031167	4.99154E-06	1.6171E-05	5.592042914	0.026608892	1	533	433	427	782	584	1043	956	882	965	1018
ENSMUSG00000028057	chr3	Rit1	0.70242671	5.00811E-06	1.62172E-05	4.642316822	0.025414597	1	251	326	277	323	228	570	496	417	549	483
ENSMUSG00000074824	chr13	Rslcan18	-1.8473478	5.00747E-06	1.62172E-05	-0.092559728	0.092460294	-1	16	13	23	29	16	8	10	4	4	3
ENSMUSG00000033577	chr9	Myo6	-0.7759808	5.01279E-06	1.62286E-05	3.467220834	0.028181195	-1	192	234	185	243	176	164	127	128	100	143
ENSMUSG00000021996	chr14	Esd	0.74384757	5.07084E-06	1.64127E-05	6.273836981	0.030673821	1	980	915	749	984	680	1905	1794	1205	1669	1361
ENSMUSG00000028651	chr4	Ppie	0.7596466	5.10704E-06	1.6526E-05	4.151361319	0.029153088	1	200	160	200	254	166	469	362	326	381	276
ENSMUSG00000038252	chr6	Ncapd2	0.89151405	5.16207E-06	1.67002E-05	4.025340364	0.04089654	1	189	141	153	228	139	283	453	346	370	247
ENSMUSG00000042473	chrX	Tbc1d8b	-1.241846	5.16937E-06	1.672E-05	2.239392145	0.071380254	-1	85	83	89	136	94	33	57	20	59	55
ENSMUSG00000051184	chr7	Zfp524	0.83412105	5.17928E-06	1.67482E-05	3.201619394	0.032069688	1	99	85	98	125	80	241	163	202	175	167
ENSMUSG00000027932	chr3	Slc27a3	1.24212282	5.19787E-06	1.68005E-05	1.510586204	0.058290501	1	30	24	20	23	22	96	65	50	48	55
ENSMUSG00000098789	chr2	Jmjd7	1.08624613	5.19711E-06	1.68005E-05	1.768887335	0.044837656	1	31	28	30	39	28	75	67	79	77	63
ENSMUSG00000034023	chr6	Fancd2	2.0571088	5.20046E-06	1.6805E-05	0.278082357	0.141586795	1	8	10	5	2	5	24	38	14	44	21
ENSMUSG00000079334	chr9	Nat6	0.70536689	5.21508E-06	1.68483E-05	4.464876905	0.025475957	1	240	229	211	337	235	587	372	422	360	494
ENSMUSG00000034311	chrX	Kif4	1.48376541	5.21968E-06	1.68593E-05	1.192024645	0.086203163	1	18	15	18	15	17	41	78	37	64	37
ENSMUSG00000041488	chr19	Stx3	1.29569864	5.22146E-06	1.68612E-05	2.279141964	0.077865676	1	43	49	36	43	31	179	119	48	112	98
ENSMUSG00000027506	chr3	Tpd52	0.81542235	5.22621E-06	1.68726E-05	5.315862876	0.036222993	1	511	362	353	508	414	1015	984	492	914	764
ENSMUSG00000066235	chr9	Pomgnt2	-0.7415899	5.23331E-06	1.68916E-05	3.552160804	0.025567168	-1	254	212	200	234	181	138	144	140	139	147
ENSMUSG00000009471	chr7	Myod1	1.16345945	5.26525E-06	1.69908E-05	5.153516093	0.074077638	1	278	300	329	301	394	1103	867	1059	343	641
ENSMUSG00000031617	chr8	Tmem184c	-1.3367681	5.28321E-06	1.70448E-05	3.288730533	0.092051902	-1	238	194	158	249	197	44	96	40	133	133
ENSMUSG00000026185	chr1	Igfbp5	-1.1720585	5.30697E-06	1.71136E-05	9.827404299	0.077156755	-1	20637	18723	13875	17997	21585	5402	7993	9582	6621	15779
ENSMUSG00000057863	chr17	Rpl36	0.68647774	5.30644E-06	1.71136E-05	7.020576128	0.026510628	1	1566	1364	1373	1816	1307	3283	2848	2310	2443	2235
ENSMUSG00000019883	chr10	Echdc1	-0.8824585	5.31095E-06	1.71224E-05	3.969685681	0.039836815	-1	266	321	274	401	250	113	179	184	187	222
ENSMUSG00000038102	chr8	Trappc11	-0.7026362	5.32553E-06	1.71655E-05	4.741186489	0.025871432	-1	562	435	427	568	467	308	351	250	343	406
ENSMUSG00000040029	chr6	Ipo8	-0.6292301	5.34158E-06	1.72133E-05	4.933685555	0.02064427	-1	600	537	462	621	532	441	431	349	337	401
ENSMUSG00000028096	chr3	Gpr89	-0.7107931	5.34336E-06	1.7215E-05	4.33090451	0.025732748	-1	410	361	277	400	397	274	281	219	240	227
ENSMUSG00000028106	chr3	Rprd2	-0.7077249	5.40387E-06	1.7406E-05	4.349160124	0.025550358	-1	351	336	306	492	397	280	226	237	205	313
ENSMUSG00000028330	chr4	Ncbp1	0.66665264	5.40853E-06	1.74129E-05	4.736615995	0.023056848	1	318	290	273	386	267	653	604	510	437	463
ENSMUSG00000086266	chr7	Igf2os	2.16844649	5.4077E-06	1.74129E-05	-0.313653833	0.136347675	1	4	2	2	7	3	11	10	19	16	33
ENSMUSG00000035790	chr16	Cep19	1.08237708	5.41734E-06	1.74373E-05	3.143959101	0.057916559	1	94	77	78	93	73	110	165	202	221	255
ENSMUSG00000035623	chr7	Rsf1	-0.7221739	5.43298E-06	1.74836E-05	4.102888337	0.026109655	-1	343	271	248	437	301	208	215	169	200	263
ENSMUSG00000040354	chr10	Mars	-0.703838	5.44024E-06	1.75029E-05	5.762727101	0.027255307	-1	1086	753	877	1197	1090	744	698	586	701	639
ENSMUSG00000092412	chr17	Gm20507	1.11272527	5.44195E-06	1.75044E-05	2.508406181	0.05702407	1	72	32	40	67	52	182	135	105	103	100
ENSMUSG00000037851	chr13	Iars	-0.7759361	5.47074E-06	1.7593E-05	6.004721151	0.033492273	-1	1162	958	980	1616	1348	643	918	666	768	856
ENSMUSG00000031137	chrX	Fgf13	-0.8567637	5.47794E-06	1.76121E-05	4.601668968	0.039220574	-1	502	415	410	612	399	196	262	264	254	423
ENSMUSG00000020086	chr10	H2afy2	1.36043229	5.51829E-06	1.77377E-05	1.519401712	0.077537953	1	20	17	29	37	12	95	65	64	51	47

ENSMUSG00000061353	chr6	Cxcl12	-0.7716473	5.54456E-06	1.78181E-05	6.441676105	0.033449362	-1	1380	1477	1406	2406	1583	1201	983	834	855	1406
ENSMUSG00000037855	chr10	Zfp365	2.63831729	5.55494E-06	1.78473E-05	1.087210564	0.304329092	1	10	8	8	5	9	20	39	151	17	42
ENSMUSG00000020246	chr10	Hcfc2	-0.6585724	5.56692E-06	1.78817E-05	4.566848169	0.022194882	-1	456	409	345	556	399	278	331	270	302	310
ENSMUSG00000002580	chr11	Mien1	0.75298428	5.57731E-06	1.7911E-05	4.884864719	0.030315828	1	389	328	284	364	267	828	606	504	632	459
ENSMUSG00000085289	chr18	Gm15337	-1.2955267	5.60765E-06	1.80042E-05	2.458728587	0.081248451	-1	160	109	75	110	115	87	31	49	31	60
ENSMUSG00000028475	chr4	5430416O09Rik	-1.5071678	5.61319E-06	1.80179E-05	1.283540777	0.096293867	-1	41	55	60	60	40	34	8	15	14	29
ENSMUSG00000086567	chr13	Gm2830	0.71373098	5.62141E-06	1.80401E-05	4.832205205	0.027047381	1	318	295	304	436	260	714	536	509	659	459
ENSMUSG00000071662	chr19	Polr2g	0.71210325	5.64356E-06	1.81071E-05	4.9133133	0.027003649	1	353	376	319	397	251	735	677	576	575	483
ENSMUSG00000003418	chr2	St8sia6	-1.6568223	5.66188E-06	1.81575E-05	-0.021266397	0.067203999	-1	20	16	22	25	16	9	5	5	7	8
ENSMUSG00000069682	chr10	Gm10275	0.77656094	5.66077E-06	1.81575E-05	4.627644452	0.03190309	1	308	245	256	278	255	646	576	387	554	383
ENSMUSG00000051427	chr11	Ccdc157	-0.8921298	5.6733E-06	1.81899E-05	2.891770594	0.036562539	-1	151	123	139	166	129	121	65	81	74	79
ENSMUSG00000063714	chr2	Sp3os	1.42282537	5.67986E-06	1.82068E-05	1.170791378	0.077923505	1	12	25	14	26	9	68	35	47	47	55
ENSMUSG00000041977	chr3	Arhgef11	-0.6073141	5.72395E-06	1.83439E-05	5.058198684	0.019384667	-1	579	558	575	759	526	491	400	409	393	459
ENSMUSG00000038370	chr1	Pcp4l1	1.26425369	5.74098E-06	1.83943E-05	2.972488689	0.081169669	1	45	65	51	108	73	89	218	177	230	161
ENSMUSG00000071324	chr10	Armc2	2.22056606	5.74414E-06	1.84002E-05	-0.337480164	0.14294568	1	3	3	0	7	4	31	13	16	7	22
ENSMUSG00000044092	chr5	C130050O18Rik	2.11873697	5.775E-06	1.84948E-05	0.079558679	0.143333994	1	2	2	10	7	4	40	30	12	26	15
ENSMUSG00000022512	chr16	Cldn1	-1.3243603	5.78164E-06	1.85076E-05	2.290444556	0.08411646	-1	53	110	118	159	75	64	59	38	28	36
ENSMUSG00000042331	chr11	Specc1	1.04335025	5.78095E-06	1.85076E-05	2.714419908	0.050861808	1	75	51	54	70	62	165	193	81	121	154
ENSMUSG00000041112	chr13	Elmo1	0.80745012	5.78912E-06	1.85273E-05	3.563671912	0.031509648	1	149	117	131	143	93	333	258	183	205	248
ENSMUSG00000041528	chr9	Rnf123	-0.8559017	5.79407E-06	1.85389E-05	7.163246116	0.041647168	-1	2768	2278	2280	3331	3090	1291	1707	1619	1340	2350
ENSMUSG00000036315	chr17	Znrd1	0.88316279	5.7975E-06	1.85456E-05	3.946618113	0.040271846	1	165	143	148	198	148	514	303	275	326	213
ENSMUSG00000028466	chr4	Creb3	0.62812662	5.80909E-06	1.85785E-05	5.047242193	0.020840839	1	388	366	332	469	375	768	605	665	607	619
ENSMUSG00000068686	chr2	Cd59b	-1.1685489	5.87634E-06	1.87892E-05	2.427255884	0.0647416	-1	138	113	94	122	78	92	39	55	41	40
ENSMUSG00000022484	chr15	Hoxc10	-0.6675243	5.87917E-06	1.8794E-05	6.12885672	0.024877416	-1	1332	1146	1071	1690	1196	960	902	835	717	1006
ENSMUSG00000050288	chr11	Fzd2	1.03775095	5.91333E-06	1.88989E-05	3.04891394	0.052685131	1	67	79	73	104	75	262	138	209	108	181
ENSMUSG00000003573	chr8	Homer3	0.79756812	5.93134E-06	1.89488E-05	3.191960634	0.029001476	1	110	98	94	113	75	235	172	176	156	198
ENSMUSG00000041688	chrX	Amot	-0.8347582	5.93168E-06	1.89488E-05	7.127076964	0.039699908	-1	2568	2088	2140	3659	2978	1400	1838	1174	1944	1829
ENSMUSG00000087380	chr6	2210408F21Rik	-0.777235	5.93738E-06	1.89627E-05	4.434201982	0.031857687	-1	466	415	394	470	283	312	294	237	266	186
ENSMUSG00000046157	chr12	Tmem229b	0.87327224	5.94422E-06	1.89802E-05	3.559539631	0.037847783	1	108	156	108	141	99	372	217	217	196	241
ENSMUSG00000031958	chr8	Ldhd	-0.8433675	5.9662E-06	1.9046E-05	5.595466682	0.039615664	-1	780	1006	1017	1167	655	456	534	540	710	552
ENSMUSG00000027475	chr2	Kif3b	0.74436494	5.99149E-06	1.91224E-05	3.49984601	0.02582858	1	128	132	106	152	106	286	232	190	235	204
ENSMUSG00000021494	chr13	Ddx41	0.83346854	6.0064E-06	1.91656E-05	3.743778516	0.034898848	1	175	136	119	170	113	328	345	217	296	205
ENSMUSG00000027203	chr2	Dut	0.91892244	6.09089E-06	1.94308E-05	3.380131624	0.041687783	1	104	127	96	117	84	223	309	187	217	161
ENSMUSG00000030884	chr7	Uqcrc2	-0.7758141	6.14245E-06	1.95908E-05	9.076149955	0.034762073	-1	9165	10534	10369	13834	7266	5960	6144	5887	6772	7643
ENSMUSG00000052468	chr3	Pmp2	-1.8153698	6.16871E-06	1.96701E-05	1.183864908	0.144588325	-1	18	48	80	73	33	25	20	9	13	12
ENSMUSG00000024201	chr17	Kdm4b	-0.6544698	6.20973E-06	1.97964E-05	4.71292253	0.022457225	-1	442	453	414	589	484	379	297	332	280	371
ENSMUSG00000027799	chr3	Nbea	-1.094997	6.24661E-06	1.99048E-05	2.314171065	0.054144326	-1	89	98	102	108	94	41	34	60	52	64
ENSMUSG00000059474	chr11	Mbtd1	-0.7976112	6.24631E-06	1.99048E-05	3.352367157	0.030264627	-1	210	200	163	235	152	111	138	91	114	150
ENSMUSG00000027303	chr2	Ptpra	0.72632819	6.26098E-06	1.99461E-05	4.880409589	0.028346565	1	337	336	359	355	251	760	671	420	574	585
ENSMUSG00000060096	chr18	Amd-ps3	-1.989955	6.27153E-06	1.99751E-05	0.198449648	0.138157283	-1	40	21	26	20	16	5	15	3	3	8
ENSMUSG00000078695	chr11	Cisd3	0.67390941	6.3724E-06	2.02918E-05	5.510296691	0.025052968	1	521	495	427	670	508	1024	809	947	767	1016
ENSMUSG00000037815	chr18	Ctnna1	0.65613284	6.3956E-06	2.0361E-05	6.272912943	0.024302313	1	891	813	769	1224	808	1711	1535	1542	1344	1583
ENSMUSG00000027318	chr2	Adam33	1.40132989	6.40554E-06	2.0388E-05	1.563419255	0.083447042	1	37	12	25	15	24	86	67	62	50	70
ENSMUSG00000006010	chr1	BC003331	-0.7182146	6.42778E-06	2.04542E-05	4.349496437	0.02683201	-1	386	367	353	482	301	219	270	191	288	282
ENSMUSG00000020668	chr12	Kif3c	-0.724595	6.44696E-06	2.05092E-05	4.55816667	0.027813211	-1	414	370	414	536	443	276	250	306	244	364
ENSMUSG00000026554	chr1	Dcaf8	-0.6972128	6.44802E-06	2.05092E-05	7.961407537	0.028118068	-1	4605	4554	3784	5612	4453	3421	2993	2520	2843	3822
ENSMUSG00000060548	chr14	Tnfrsf19	-0.9784427	6.4662E-06	2.05624E-05	3.473940215	0.048821313	-1	142	221	196	359	188	91	113	136	122	137
ENSMUSG00000062604	chr5	Srpk2	-0.7301624	6.47601E-06	2.05889E-05	4.901715181	0.028925181	-1	619	535	536	658	427	322	414	281	337	480
ENSMUSG00000017721	chr2	Pigt	0.73400878	6.5133E-06	2.0698E-05	5.990530457	0.030392617	1	723	673	575	882	707	1819	1164	1298	1024	1204
ENSMUSG00000021908	chr12	Gm6768	-1.5052659	6.51235E-06	2.0698E-05	0.895691879	0.086534996	-1	39	33	35	51	36	6	18	9	16	25
ENSMUSG00000051343	chr6	Rab11fip5	0.71107824	6.55253E-06	2.08179E-05	5.243334825	0.027853523	1	389	366	372	664	376	957	687	727	612	864
ENSMUSG00000025237	chr9	Parp6	-0.6268299	6.56485E-06	2.08524E-05	4.459592861	0.020086891	-1	408	355	373	467	376	323	295	227	279	286
ENSMUSG00000002881	chr1	Nab1	-0.7265526	6.58047E-06	2.08961E-05	4.017699462	0.026763572	-1	299	276	293	385	248	179	221	152	220	217
ENSMUSG00000032965	chr16	Ift57	0.98577454	6.5816E-06	2.08961E-05	2.266698804	0.04155264	1	42	46	46	65	36	91	112	85	113	105
ENSMUSG00000031803	chr8	B3gnt3	1.68787485	6.59578E-06	2.09363E-05	1.610784973	0.132231153	1	15	25	12	38	15	28	80	68	66	118
ENSMUSG00000020974	chr12	Pole2	1.814852	6.61154E-06	2.09816E-05	1.026294727	0.140467384	1	17	12	5	18	11	50	74	41	59	16
ENSMUSG00000021936	chr14	Mapk8	-0.656996	6.62631E-06	2.10237E-05	5.093114572	0.023331172	-1	587	554	598	836	547	392	478	403	460	414
ENSMUSG00000051185	chr1	Fam174a	-0.7354111	6.63814E-06	2.10564E-05	5.379005199	0.030041522	-1	756	663	646	1143	709	460	586	411	439	655
ENSMUSG00000025185	chr19	Loxl4	-1.4773744	6.69058E-06	2.12131E-05	1.737132335	0.101607139	-1	101	56	55	98	49	40	37	12	36	15
ENSMUSG00000064289	chr2	Tank	-0.8521943	6.69052E-06	2.12131E-05	3.46964749	0.03618673	-1	223	201	179	262	191	112	170	80	128	151
ENSMUSG00000027656	chr2	Wisp2	1.8957008	6.71007E-06	2.12701E-05	1.936441162	0.173843095	1	28	26	22	24	15	202	138	50	67	28
ENSMUSG00000063253	chr8	Scoc	1.18798837	6.73029E-06	2.13294E-05	3.764138871	0.075856476	1	144	116	91	150	113	120	390	308	360	324
ENSMUSG00000050900	chrX	Gm7327	-1.3876119	6.73436E-06	2.13374E-05	1.029872586	0.073223488	-1	45	45	33	45	40	12	16	10	21	28
ENSMUSG00000001415	chr3	Smg5	-0.6862571	6.75453E-06	2.13965E-05	6.20969891	0.026735257	-1	1304	1225	1278	1650	1334	1012	916	788	1065	840
ENSMUSG00000033088	chr15	Triobp	-0.8084873	6.78372E-06	2.14841E-05	5.335761098	0.036594238	-1	766	619	669	847	898	474	389	373	498	662

ENSMUSG00000097006	chr17	9530082P21Rik	-1.0911566	6.80716E-06	2.15534E-05	2.56617494	0.056942035	-1	115	118	110	158	93	78	43	32	69	84
ENSMUSG00000030284	chr6	Creld1	0.74768194	6.82695E-06	2.16112E-05	5.533963722	0.031334597	1	604	507	415	603	447	783	987	1085	877	954
ENSMUSG00000042557	chr9	Sin3a	-0.633399	6.84364E-06	2.16591E-05	4.496835211	0.020681273	-1	391	376	368	562	356	303	320	252	263	303
ENSMUSG00000001151	chr10	Pcnt	-0.8184245	6.86324E-06	2.17163E-05	5.949757658	0.038106571	-1	939	930	1004	1802	1267	677	692	565	760	957
ENSMUSG00000028080	chr3	Lrba	-0.6934697	6.86924E-06	2.17303E-05	4.834828139	0.025998115	-1	428	465	490	689	552	433	327	273	335	418
ENSMUSG00000040663	chr19	Clcf1	1.53565086	6.87128E-06	2.17318E-05	0.967687621	0.092372822	1	14	14	11	23	8	81	38	33	40	31
ENSMUSG00000007038	chr17	Neu1	0.76085886	6.89191E-06	2.17922E-05	4.558552689	0.031084378	1	302	254	229	310	205	687	532	333	460	421
ENSMUSG00000029502	chr5	Golga3	-0.6748571	6.89965E-06	2.18117E-05	5.488289078	0.025294399	-1	782	664	699	1187	816	569	587	524	545	589
ENSMUSG00000048371	chr8	Pdp2	-1.3594717	6.95822E-06	2.19919E-05	1.549921118	0.080437021	-1	69	82	36	62	53	18	35	21	20	35
ENSMUSG00000050107	chr11	Gsg2	1.90350181	6.96121E-06	2.19964E-05	-0.189106071	0.093998326	1	5	4	3	7	4	24	27	10	21	14
ENSMUSG00000020227	chr10	Irak3	1.03186263	6.9734E-06	2.20299E-05	2.256141478	0.046798866	1	41	55	45	60	27	124	93	102	94	96
ENSMUSG00000033237	chr15	Arid2	-0.7165797	6.98538E-06	2.20627E-05	4.272134657	0.026769578	-1	312	295	388	430	350	225	241	242	207	269
ENSMUSG00000031993	chr9	Snx19	-0.6690867	6.99197E-06	2.20786E-05	5.270478218	0.024638942	-1	698	615	632	895	692	425	545	418	518	514
ENSMUSG00000014418	chr7	Hps5	-0.747916	7.0078E-06	2.21208E-05	4.330658461	0.029599865	-1	385	321	383	412	359	195	275	204	237	307
ENSMUSG00000040760	chr14	Appl1	-0.6480642	7.0085E-06	2.21208E-05	4.996352606	0.022694586	-1	596	506	572	740	492	413	476	325	418	394
ENSMUSG00000058756	chr11	Thra	-0.7031279	7.03568E-06	2.22015E-05	6.435970439	0.028329743	-1	1358	1572	1404	2168	1529	1127	912	1036	1054	1238
ENSMUSG00000024530	chr18	Slmo1	2.09944274	7.03825E-06	2.22046E-05	-0.327720684	0.108746993	1	5	6	5	1	1	15	21	19	20	12
ENSMUSG00000027868	chr3	Tbx15	-0.896429	7.06264E-06	2.22766E-05	8.043937408	0.046731387	-1	6404	4923	5007	4393	4520	2325	2997	2905	2634	4147
ENSMUSG00000054619	chr15	Mettl7a1	-0.8066084	7.07061E-06	2.22967E-05	4.711139406	0.035630769	-1	489	578	441	554	406	222	312	285	309	414
ENSMUSG00000018500	chr11	Adora2b	2.0941228	7.08879E-06	2.23489E-05	1.270769799	0.197763306	1	5	14	11	16	17	137	60	31	59	19
ENSMUSG00000025762	chr3	Larp1b	-0.8264415	7.09549E-06	2.23622E-05	5.787909932	0.038836766	-1	1117	988	959	1254	942	414	665	601	729	810
ENSMUSG00000032966	chr2	Fkbp1a	0.70228366	7.0962E-06	2.23622E-05	7.355922736	0.02863743	1	1956	1828	1612	2186	1707	4414	3379	3162	2783	2903
ENSMUSG00000028062	chr3	Lamtor2	0.68689489	7.13518E-06	2.248E-05	5.30988926	0.026145901	1	481	427	379	567	413	1070	750	747	769	660
ENSMUSG00000029640	chr5	Usp12	-0.6800697	7.15483E-06	2.25368E-05	4.484586645	0.024316869	-1	364	340	406	592	362	270	304	258	251	315
ENSMUSG00000051220	chrX	Ercc6l	1.49074713	7.17359E-06	2.25908E-05	0.610112896	0.072089719	1	15	9	7	12	11	38	37	28	41	23
ENSMUSG00000055214	chr1	Pld5	-1.6361664	7.19396E-06	2.26499E-05	1.362479174	0.120630884	-1	57	46	60	51	61	9	17	16	13	43
ENSMUSG00000022490	chr15	Ppp1r1a	-1.0530555	7.25314E-06	2.28268E-05	5.179172711	0.062798946	-1	504	648	570	1224	757	690	369	326	319	242
ENSMUSG00000064158	chr7	Izumo1	-1.568163	7.25343E-06	2.28268E-05	0.220519603	0.072678635	-1	24	24	15	31	24	7	12	8	5	11
ENSMUSG00000026196	chr1	Bard1	1.79669219	7.28249E-06	2.29131E-05	0.346360601	0.106311429	1	5	11	7	7	7	38	38	20	34	14
ENSMUSG00000015733	chr6	Capza2	-0.7899286	7.3355E-06	2.30747E-05	8.277443516	0.036547155	-1	6748	5557	5226	6621	5122	3065	4180	2739	4004	4572
ENSMUSG00000039450	chr11	Dcxr	0.94077052	7.35293E-06	2.31243E-05	2.865137515	0.041645476	1	87	78	56	69	72	211	164	138	116	144
ENSMUSG00000021451	chr13	Sema4d	-0.8268611	7.3979E-06	2.32602E-05	5.839444904	0.039134761	-1	1043	924	907	1327	1243	597	773	451	607	957
ENSMUSG00000037960	chr13	1110007C09Rik	0.68877269	7.39945E-06	2.32602E-05	5.565288686	0.026698546	1	485	500	483	791	467	1168	948	865	987	797
ENSMUSG00000030486	chr7	Zfp108	-1.6054638	7.409E-06	2.3281E-05	0.4231185	0.084888302	-1	27	24	24	33	30	3	12	7	14	13
ENSMUSG00000031631	chr8	Cfap97	-0.7501021	7.40942E-06	2.3281E-05	3.819394447	0.028297751	-1	272	257	228	344	217	136	177	161	162	214
ENSMUSG00000056418	chr9	BC043934	1.95604438	7.42407E-06	2.33218E-05	0.083971678	0.128027396	1	9	5	6	7	1	18	18	34	15	34
ENSMUSG00000041238	chr18	Rbbp8	1.14452257	7.46507E-06	2.34454E-05	2.151545227	0.059102725	1	37	37	46	47	32	105	135	66	108	71
ENSMUSG00000026407	chr1	Cacna1s	-0.8419203	7.4758E-06	2.34738E-05	9.4381058	0.041656539	-1	11868	11574	10837	17025	15167	6492	8399	7837	6782	10962
ENSMUSG00000027381	chr2	Bcl2l11	1.10057325	7.49328E-06	2.35193E-05	3.353598187	0.063142962	1	86	115	112	91	68	199	213	207	141	367
ENSMUSG00000032116	chr9	Stt3a	0.73143699	7.49366E-06	2.35193E-05	5.642841909	0.030286456	1	582	532	521	657	499	1330	1279	749	893	877
ENSMUSG00000021951	chr14	N6amt2	0.77811648	7.50979E-06	2.35646E-05	4.000959778	0.031618147	1	213	178	145	200	137	291	346	314	382	293
ENSMUSG00000064030	chr10	Wibg	0.75641545	7.51408E-06	2.35728E-05	3.58524172	0.028032837	1	147	107	120	170	117	339	232	210	228	216
ENSMUSG00000069633	chr8	Pex11g	1.13044755	7.5665E-06	2.37319E-05	2.356076917	0.059350659	1	59	46	36	44	46	88	84	117	118	147
ENSMUSG00000078495	chr4	Gm13157	3.02192645	7.5906E-06	2.38022E-05	0.508261402	0.371199327	1	4	6	4	2	4	0	59	28	44	53
ENSMUSG00000028068	chr3	Iqgap3	1.47143399	7.60036E-06	2.38274E-05	1.808950541	0.101031525	1	34	32	24	16	24	99	97	105	56	45
ENSMUSG00000099081	chr11	Gm27624	-1.3196857	7.60581E-06	2.38391E-05	1.224257865	0.067400376	-1	42	46	49	58	42	17	19	16	34	17
ENSMUSG00000067344	chr6	Rps25-ps1	1.20152102	7.62917E-06	2.3907E-05	1.952298816	0.064616325	1	45	36	19	30	37	115	69	82	87	72
ENSMUSG00000038301	chr6	Snx10	1.20156594	7.64062E-06	2.39375E-05	2.752336202	0.072804469	1	95	59	51	47	43	129	199	90	162	173
ENSMUSG00000060703	chr2	Cd302	0.95200112	7.70364E-06	2.41295E-05	3.366379495	0.045912005	1	99	130	97	84	98	221	252	137	238	252
ENSMUSG00000038037	chr16	Socs1	2.09774973	7.71734E-06	2.4167E-05	2.18758898	0.221418203	1	54	28	12	22	9	55	95	62	245	117
ENSMUSG00000087259	chr11	2610035D17Rik	2.36470974	7.76518E-06	2.43114E-05	0.954427554	0.252309749	1	22	4	4	10	4	16	70	67	62	25
ENSMUSG00000005107	chr5	Slc2a9	1.70846671	7.80523E-06	2.44313E-05	0.613519898	0.10567571	1	9	14	12	4	8	38	30	23	28	56
ENSMUSG00000040782	chr1	Rfwd2	-0.7558692	7.85297E-06	2.45753E-05	6.115359255	0.032953505	-1	1293	1095	1169	1782	1195	652	951	693	932	960
ENSMUSG00000015461	chr17	Atf6b	0.84074981	7.89343E-06	2.46964E-05	3.938808907	0.037425713	1	158	153	165	240	106	392	357	207	361	286
ENSMUSG00000057069	chr13	Ero1lb	1.39356267	7.92447E-06	2.47879E-05	1.909138515	0.090626784	1	26	28	28	28	36	139	115	39	73	69
ENSMUSG00000039787	chr2	Cercam	0.98863116	7.98152E-06	2.49608E-05	3.724886823	0.051950725	1	149	145	107	113	131	318	230	324	169	382
ENSMUSG00000020308	chr10	Tpgs1	0.69718598	7.98926E-06	2.49794E-05	3.992596599	0.02468525	1	210	149	167	198	171	359	320	311	262	345
ENSMUSG00000051721	chr12	BC068281	-1.2615682	8.01734E-06	2.50616E-05	1.573146508	0.067070794	-1	67	53	47	72	63	15	29	23	28	42
ENSMUSG00000020463	chr11	Smek2	-0.7775833	8.05467E-06	2.51726E-05	4.389618044	0.032869902	-1	351	385	346	557	343	258	278	148	266	313
ENSMUSG00000032097	chr9	Ddx6	-0.6610098	8.07069E-06	2.52171E-05	6.748199731	0.025478822	-1	1916	1912	1874	2340	1759	1334	1461	1222	1192	1594
ENSMUSG00000063358	chr16	Mapk1	-0.6588137	8.07571E-06	2.52271E-05	6.845814809	0.025347245	-1	2041	2017	1918	2572	1950	1382	1605	1208	1418	1671
ENSMUSG00000022617	chr15	Chkb	-0.7043462	8.12554E-06	2.53771E-05	8.072138074	0.029349552	-1	4169	4818	4248	7415	4514	3676	3214	3119	3338	3357
ENSMUSG00000047819	chr3	Tigd4	-1.0156243	8.12807E-06	2.53793E-05	3.615079504	0.055187787	-1	319	227	214	296	164	158	215	91	97	102
ENSMUSG00000028973	chr5	Abcb8	-0.6244284	8.19295E-06	2.55762E-05	5.548614029	0.021945934	-1	821	888	765	1010	739	713	577	559	557	601
ENSMUSG00000026840	chr2	Lamc3	-2.0054298	8.20437E-06	2.56061E-05	0.453196272	0.168211865	-1	30	32	35	14	36	14	13	1	4	10

ENSMUSG00000035621	chr10	Midn	1.00024113	8.20883E-06	2.56143E-05	5.535725729	0.057661808	1	346	418	490	702	369	1426	971	1296	602	747
ENSMUSG00000103436	chrX	RP23-135F22.6	0.63987022	8.27749E-06	2.58228E-05	4.448605026	0.021508942	1	251	231	206	341	244	504	411	360	455	434
ENSMUSG00000006169	chr11	Clint1	-0.7813411	8.30443E-06	2.59011E-05	5.125054816	0.034504006	-1	594	520	529	910	747	329	479	359	398	521
ENSMUSG00000057506	chr19	Bloc1s2	0.84108917	8.31777E-06	2.59369E-05	3.555943996	0.03620535	1	170	103	112	137	99	323	270	198	239	195
ENSMUSG00000050530	chr2	Fam171a1	0.76418471	8.32959E-06	2.5968E-05	3.454988761	0.028507822	1	118	126	111	133	108	253	191	222	181	268
ENSMUSG00000044499	chr10	Hs3st5	-1.4551035	8.36014E-06	2.60574E-05	1.372528709	0.093626671	-1	33	58	63	75	43	24	28	13	31	12
ENSMUSG00000031388	chrX	Naa10	0.62111779	8.3964E-06	2.61646E-05	5.085343585	0.021224345	1	375	356	343	556	373	812	675	646	580	643
ENSMUSG00000026634	chr1	Angel2	-0.6581897	8.4055E-06	2.61871E-05	4.843760237	0.023687887	-1	565	513	501	514	493	350	375	330	382	370
ENSMUSG00000006299	chr1	Aamp	0.66429701	8.41418E-06	2.62083E-05	6.9596966	0.025917004	1	1447	1296	1204	1861	1398	3086	2268	2431	2238	2457
ENSMUSG00000039427	chr16	Alg1	0.67179829	8.44938E-06	2.63121E-05	3.941282659	0.022647079	1	171	174	151	213	167	401	312	254	273	298
ENSMUSG00000020482	chr11	Ccdc117	-0.6948651	8.45548E-06	2.63252E-05	4.524228977	0.026073258	-1	351	374	376	595	429	302	278	221	309	321
ENSMUSG00000028382	chr4	Ptbp3	0.69583253	8.4618E-06	2.6339E-05	4.602031914	0.026336549	1	260	252	246	413	222	576	579	352	447	504
ENSMUSG00000027684	chr3	Mecom	-1.1320658	8.47211E-06	2.63652E-05	2.238572427	0.060297414	-1	91	89	77	136	84	28	63	43	37	64
ENSMUSG00000069744	chr11	Psmb3	0.65957835	8.48869E-06	2.64109E-05	6.619779212	0.025424275	1	1195	1073	1035	1397	990	2390	1926	1897	1888	1730
ENSMUSG00000032265	chr9	Fam46a	0.97256125	8.50856E-06	2.64669E-05	3.433358074	0.049128173	1	118	87	116	114	98	384	251	143	179	218
ENSMUSG00000050860	chr11	Phospho1	-0.7033478	8.51645E-06	2.64855E-05	7.196266467	0.029199766	-1	2602	2252	2300	3542	2891	1932	1832	1825	1472	2052
ENSMUSG00000028398	chr4	Tmem261	0.67961647	8.51963E-06	2.64895E-05	5.117911702	0.025782814	1	420	444	376	472	274	848	725	597	682	638
ENSMUSG00000060427	chr8	Zfp868	-0.9340209	8.5524E-06	2.65855E-05	2.640747854	0.041027522	-1	123	115	113	156	96	101	69	61	45	71
ENSMUSG00000021646	chr13	Mccc2	-0.7089495	8.6108E-06	2.67611E-05	4.90295771	0.027930107	-1	497	594	509	651	501	288	416	328	382	426
ENSMUSG00000085385	chr2	9430008C03Rik	1.17966105	8.64041E-06	2.68471E-05	1.916984299	0.060021477	1	33	34	37	21	37	106	89	64	78	77
ENSMUSG00000021725	chr13	Parp8	-0.7553907	8.64384E-06	2.68518E-05	4.058576088	0.030202471	-1	316	265	304	420	256	192	167	166	221	259
ENSMUSG00000010064	chr9	Slc38a3	-1.0174237	8.65603E-06	2.68837E-05	4.890834509	0.059116459	-1	332	617	713	971	363	332	297	377	289	291
ENSMUSG00000015112	chr6	Slc25a13	1.55909963	8.66465E-06	2.69045E-05	0.991329077	0.103461684	1	9	13	8	34	8	61	53	29	44	40
ENSMUSG00000021282	chr12	Eif5	-0.8006122	8.7463E-06	2.7152E-05	7.097535201	0.037902832	-1	2443	2055	2560	3550	2435	1382	1878	1168	2000	1705
ENSMUSG00000046314	chr12	Stxbp6	-0.9414329	8.76531E-06	2.7205E-05	2.865101708	0.043177325	-1	125	158	159	138	116	88	88	66	93	66
ENSMUSG00000023266	chr17	Frs3	-0.9735307	8.81898E-06	2.73655E-05	2.07280123	0.040031358	-1	80	79	77	98	71	47	45	31	52	51
ENSMUSG00000020114	chr10	Cand1	0.70779849	8.82195E-06	2.73686E-05	4.780139615	0.027696347	1	272	279	298	425	283	757	648	456	453	481
ENSMUSG00000002996	chr12	Hbp1	-0.6918096	8.83065E-06	2.73895E-05	6.272657205	0.027954204	-1	1581	1445	1303	1613	1162	982	920	831	866	1235
ENSMUSG00000032560	chr9	Dnajc13	-0.6189865	8.83743E-06	2.74045E-05	5.088489865	0.02120048	-1	594	552	556	735	622	455	504	354	416	461
ENSMUSG00000046111	chr9	Cep295	-0.9248115	8.84443E-06	2.74201E-05	2.902342543	0.041615396	-1	167	111	134	192	121	78	98	56	101	82
ENSMUSG00000021252	chr12	0610007P14Rik	0.99939365	8.92683E-06	2.76633E-05	2.901547454	0.04951797	1	84	93	64	61	58	213	163	132	170	123
ENSMUSG00000071451	chr13	Psmg4	0.90943225	8.92541E-06	2.76633E-05	2.811324857	0.039014436	1	74	64	75	80	62	197	149	122	155	113
ENSMUSG00000060860	chr7	Ube2s	0.64375328	9.02484E-06	2.79608E-05	5.189818372	0.023171791	1	423	397	372	495	425	869	801	685	658	615
ENSMUSG00000021279	chr12	Cdc42bpb	-0.6270363	9.07139E-06	2.80988E-05	5.066637169	0.021841709	-1	546	569	523	807	593	494	477	338	370	479
ENSMUSG00000096956	chr15	Snhg18	0.81168475	9.08948E-06	2.81486E-05	3.1370593	0.03151743	1	94	100	95	109	70	234	163	171	173	162
ENSMUSG00000029992	chr6	Gfpt1	-0.7382633	9.09619E-06	2.81631E-05	5.407910573	0.031308883	-1	805	693	645	955	850	473	574	370	520	663
ENSMUSG00000020181	chr10	Nav3	-1.5394536	9.11781E-06	2.82238E-05	1.585258267	0.111254262	-1	67	82	50	71	51	13	31	8	31	38
ENSMUSG00000006423	chrX	C330007P06Rik	-0.9000368	9.15368E-06	2.83286E-05	3.712473181	0.043249414	-1	235	230	265	327	209	114	178	89	177	183
ENSMUSG00000038888	chr7	Ctu1	1.21138174	9.18948E-06	2.84331E-05	1.7756406	0.064915494	1	41	16	20	42	30	79	95	72	59	70
ENSMUSG00000061032	chr10	Rrp1	0.62688094	9.19548E-06	2.84453E-05	6.1808551	0.022867815	1	851	757	747	1077	824	1591	1417	1328	1370	1478
ENSMUSG00000017466	chr11	Timp2	0.7702987	9.20049E-06	2.84482E-05	7.716435067	0.035421292	1	2406	2218	2049	2558	2300	5648	4184	4353	2797	4814
ENSMUSG00000039086	chr2	Ss18l1	-1.0678054	9.19949E-06	2.84482E-05	1.985881894	0.050526311	-1	62	66	70	119	76	59	34	34	40	37
ENSMUSG00000018401	chr11	Mtmr4	-0.6723287	9.20303E-06	2.84498E-05	3.82580752	0.022571304	-1	269	250	233	321	220	203	200	138	179	169
ENSMUSG00000024730	chr19	Ms4a8a	2.31690839	9.20837E-06	2.846E-05	0.080751446	0.194251758	1	3	2	6	4	7	52	18	16	32	8
ENSMUSG00000024302	chr18	Dtna	-0.8346894	9.26659E-06	2.86336E-05	6.406778004	0.041116984	-1	1687	1336	1660	1957	1455	702	1001	809	1232	1194
ENSMUSG00000022214	chr14	Dcaf11	-0.6894085	9.33849E-06	2.88494E-05	7.114604256	0.02827729	-1	2516	2450	2326	3247	2251	1752	1617	1352	1993	1943
ENSMUSG00000021594	chr13	Srd5a1	1.47494315	9.37647E-06	2.89603E-05	0.474897375	0.066614589	1	13	11	9	10	6	29	31	35	23	32
ENSMUSG00000030421	chr7	Uri1	-0.6305634	9.42955E-06	2.91179E-05	4.642816367	0.021460597	-1	476	396	395	625	383	333	302	284	314	362
ENSMUSG00000024921	chr19	Smarca2	-0.6427558	9.43651E-06	2.91329E-05	5.13055622	0.02320658	-1	643	621	593	792	534	479	420	342	430	566
ENSMUSG00000017299	chr2	Dnttip1	0.66613578	9.44844E-06	2.91633E-05	4.309893251	0.023556356	1	248	212	199	286	195	506	369	390	368	344
ENSMUSG00000028944	chr5	Prkag2	0.7171629	9.45441E-06	2.91753E-05	4.087898438	0.027208688	1	187	189	155	237	185	324	391	294	395	303
ENSMUSG00000006412	chr1	Pfdn2	0.6525223	9.47121E-06	2.92207E-05	5.657744345	0.024516596	1	615	546	522	748	502	1226	965	895	1059	888
ENSMUSG00000024989	chr19	Cep55	1.82093531	9.48614E-06	2.92603E-05	0.861033001	0.138402441	1	16	12	14	2	9	44	72	34	31	33
ENSMUSG00000028228	chr4	Cpne3	-0.7080338	9.58388E-06	2.95552E-05	4.063429687	0.026574734	-1	297	300	280	362	295	239	238	135	197	229
ENSMUSG00000079427	chr9	Mthfsl	0.97139073	9.58875E-06	2.95637E-05	2.220312993	0.040980158	1	54	41	38	50	44	131	90	83	98	89
ENSMUSG00000030493	chr7	C230052I12Rik	1.33774017	9.64809E-06	2.97401E-05	0.946373639	0.064893218	1	19	11	14	22	10	49	45	41	45	29
ENSMUSG00000038379	chr9	Ttk	1.90316439	9.68524E-06	2.9848E-05	0.22565271	0.12658946	1	5	8	2	8	9	33	39	21	29	11
ENSMUSG00000026827	chr2	Gpd2	-1.1055207	9.71729E-06	2.99402E-05	7.517642332	0.07263792	-1	3548	3123	2758	4985	4325	991	2298	1416	1702	3073
ENSMUSG00000028863	chr4	Meaf6	0.83371106	9.72178E-06	2.99474E-05	3.459024399	0.035830395	1	115	99	108	161	103	326	231	233	165	188
ENSMUSG00000027610	chr2	Gss	0.79998048	9.74886E-06	3.00243E-05	3.222030341	0.031063789	1	98	124	92	108	76	203	195	186	185	183
ENSMUSG00000049233	chr13	Apoo-ps	-0.9198081	9.77091E-06	3.00855E-05	2.689498988	0.040442977	-1	136	113	117	138	113	57	84	55	70	92
ENSMUSG00000027957	chr3	Slc35a3	-0.8321892	9.78167E-06	3.0112E-05	3.297561867	0.034988708	-1	199	178	177	245	136	113	141	73	113	134
ENSMUSG00000020116	chr11	Pno1	-0.8636501	9.81638E-06	3.02122E-05	4.970949226	0.042936015	-1	597	536	519	761	602	237	431	256	466	410
ENSMUSG00000051726	chr12	Kcnf1	-1.1053626	9.8197E-06	3.02158E-05	2.651198605	0.062032601	-1	144	99	127	111	139	71	64	40	92	53
ENSMUSG00000046516	chr16	Cox17	0.74382647	9.89836E-06	3.04511E-05	5.990926075	0.032557621	1	756	679	653	895	571	1858	1274	1197	1229	966

ENSMUSG00000036986	chr9	Pml	0.82529568	9.90541E-06	3.04661E-05	3.124048561	0.03324947	1	98	96	64	115	90	208	189	160	132	212
ENSMUSG00000052837	chr8	Junb	1.69030229	9.90774E-06	3.04666E-05	5.003995014	0.162907047	1	223	209	394	169	103	1792	1028	452	423	421
ENSMUSG00000003948	chr11	Mmd	-0.7304223	9.91101E-06	3.04699E-05	4.773744982	0.030120912	-1	543	551	439	518	467	430	395	271	230	365
ENSMUSG00000046185	chr7	Zfp84	-0.9789723	9.97773E-06	3.06683E-05	2.69317564	0.04684321	-1	112	123	138	160	97	49	86	59	73	81
ENSMUSG00000032397	chr9	Tipin	0.89746516	1.00369E-05	3.08435E-05	3.212572806	0.040992409	1	107	91	86	113	79	151	233	171	239	169
ENSMUSG00000031539	chr8	Ap3m2	0.90993373	1.00437E-05	3.08575E-05	2.973877787	0.040792408	1	77	93	82	70	72	160	156	163	134	209
ENSMUSG00000097908	chr5	4933404O12Rik	-1.3639297	1.00505E-05	3.08716E-05	2.086465404	0.093501711	-1	104	81	76	98	85	86	32	22	24	30
ENSMUSG00000026475	chr1	Rgs16	1.39835336	1.00872E-05	3.09774E-05	2.333119488	0.099440382	1	55	52	42	35	15	123	175	103	67	115
ENSMUSG00000022901	chr16	Cd86	1.48978198	1.00915E-05	3.09838E-05	2.044101695	0.110170349	1	18	44	33	30	28	171	112	45	94	66
ENSMUSG00000001962	chrX	Fam50a	0.65162428	1.01326E-05	3.11031E-05	4.41626143	0.022815116	1	222	240	218	335	223	550	425	332	409	416
ENSMUSG00000018861	chr11	Fdxr	0.98105166	1.0139E-05	3.1116E-05	2.633157654	0.046852137	1	60	80	44	80	42	158	123	144	112	120
ENSMUSG00000074211	chr7	Sdhaf1	0.74191627	1.01505E-05	3.11445E-05	4.238511666	0.029992277	1	204	220	215	265	145	491	346	381	383	315
ENSMUSG00000029490	chr5	Mfsd7a	1.18424667	1.01697E-05	3.11965E-05	1.980387134	0.064186301	1	37	29	33	36	37	97	59	70	123	81
ENSMUSG00000020621	chr12	Rdh14	-0.7552853	1.02E-05	3.12827E-05	5.043930823	0.03272665	-1	706	594	556	719	507	304	427	306	445	511
ENSMUSG00000041319	chr17	Thoc6	0.73957229	1.02148E-05	3.13213E-05	3.841924995	0.028342217	1	173	127	161	156	168	315	279	281	299	273
ENSMUSG00000023087	chr3	Ccrn4l	0.79660932	1.02341E-05	3.13735E-05	4.144736411	0.034815283	1	147	125	202	277	210	431	380	319	341	354
ENSMUSG00000028347	chr4	Tmeff1	1.84018626	1.02538E-05	3.14271E-05	0.272469156	0.116846717	1	5	11	6	5	7	29	36	38	15	18
ENSMUSG00000038279	chr6	Nop2	0.70654241	1.02639E-05	3.1451E-05	4.454537545	0.027422041	1	216	200	242	326	253	479	497	462	401	362
ENSMUSG00000058093	chr13	AA987161	-1.1177994	1.03051E-05	3.15704E-05	1.733660776	0.054633616	-1	75	67	55	82	51	38	43	18	27	41
ENSMUSG00000026867	chr2	Gapvd1	-0.6209449	1.03253E-05	3.16254E-05	5.129675864	0.021746776	-1	610	581	555	834	590	484	453	340	452	526
ENSMUSG00000027360	chr2	Hdc	2.17788623	1.03949E-05	3.18315E-05	0.161173743	0.180089121	1	1	7	2	9	7	59	22	21	13	18
ENSMUSG00000042359	chr2	Osbpl6	-1.0952513	1.04003E-05	3.18412E-05	4.754745479	0.069619192	-1	553	465	483	670	562	110	378	276	327	288
ENSMUSG00000017631	chr11	Abr	0.68615514	1.04419E-05	3.19613E-05	4.425392905	0.025863911	1	238	207	185	394	219	455	463	404	405	424
ENSMUSG00000027076	chr2	Timm10	0.77650401	1.04472E-05	3.19708E-05	4.267070289	0.033378935	1	230	210	195	275	148	427	422	453	371	287
ENSMUSG00000030304	chr6	Ergic2	-0.6856883	1.04552E-05	3.1988E-05	5.442864619	0.027238812	-1	849	732	765	942	700	505	599	450	635	519
ENSMUSG00000039239	chr1	Tgfb2	-0.703764	1.04619E-05	3.20018E-05	4.675599568	0.027765911	-1	538	407	414	524	462	346	361	290	219	373
ENSMUSG00000021706	chr13	Zfyve16	-0.8857299	1.05004E-05	3.21123E-05	3.417113591	0.041101368	-1	200	173	197	272	186	99	147	75	151	134
ENSMUSG00000034247	chr11	Plekhm1	0.67165295	1.05285E-05	3.21914E-05	4.730303571	0.02506644	1	280	283	251	369	334	602	604	388	493	580
ENSMUSG00000031204	chrX	Asb12	-0.6368022	1.05334E-05	3.21993E-05	5.098368623	0.02294323	-1	561	613	557	769	600	456	370	389	454	513
ENSMUSG00000044252	chr18	Osbpl1a	-0.7347078	1.05578E-05	3.22667E-05	5.502711526	0.031530238	-1	700	797	786	1226	745	457	604	456	596	653
ENSMUSG00000018481	chr11	Appbp2	-0.622602	1.05704E-05	3.22983E-05	4.492994636	0.020903835	-1	388	373	348	517	405	325	316	239	259	308
ENSMUSG00000010406	chr14	Mrpl52	0.73729931	1.05728E-05	3.22985E-05	5.002479618	0.031135173	1	402	309	348	425	302	939	687	560	616	479
ENSMUSG00000025724	chr7	Sec11a	0.72968847	1.06067E-05	3.23951E-05	4.708498038	0.029975122	1	319	266	234	344	296	753	615	398	457	456
ENSMUSG00000023009	chr15	Nckap5l	0.94482091	1.06462E-05	3.25084E-05	3.311298585	0.046917241	1	104	83	106	118	87	273	192	231	114	248
ENSMUSG00000024283	chr18	Wac	-0.6060662	1.06559E-05	3.25239E-05	4.879585357	0.0203406	-1	529	473	479	702	472	401	418	300	383	402
ENSMUSG00000053173	chr6	Rpl18-ps2	1.27125963	1.06537E-05	3.25239E-05	1.747391969	0.074761096	1	24	29	18	50	22	125	74	56	63	58
ENSMUSG00000006373	chrX	Pgrmc1	0.71092221	1.0712E-05	3.26878E-05	4.11865421	0.027065583	1	167	179	190	252	188	460	410	276	299	317
ENSMUSG00000048720	chr19	Tbc1d12	-1.0956431	1.07143E-05	3.26878E-05	1.962176529	0.055185362	-1	81	75	75	91	63	45	44	19	36	55
ENSMUSG00000030101	chr6	Sumf1	0.70077565	1.07225E-05	3.27058E-05	4.264346467	0.026582421	1	223	189	195	271	208	529	445	295	314	367
ENSMUSG00000100347	chr1	Gm7895	-1.4161733	1.07354E-05	3.2738E-05	0.983434312	0.081791939	-1	28	30	44	56	45	13	16	13	13	28
ENSMUSG00000071074	chr17	Yipf3	0.75842743	1.08348E-05	3.30338E-05	5.432420332	0.033670809	1	463	458	367	600	502	1274	796	870	622	894
ENSMUSG00000029146	chr5	Snx17	0.6073719	1.08813E-05	3.31683E-05	5.824649336	0.021527831	1	721	636	594	782	607	1251	1093	1070	1030	1134
ENSMUSG00000024118	chr17	1600002H07Rik	1.03289191	1.09314E-05	3.33104E-05	1.782336916	0.042997477	1	35	38	30	35	23	82	75	61	69	76
ENSMUSG00000091449	chr18	Gm10269	0.97010631	1.09326E-05	3.33104E-05	2.191104437	0.040618314	1	44	45	46	44	42	103	94	105	87	88
ENSMUSG00000002489	chr16	Tiam1	-1.0523893	1.10563E-05	3.36797E-05	3.555101097	0.061580639	-1	296	216	224	192	227	171	183	62	103	110
ENSMUSG00000030917	chr7	Tmem159	0.79371743	1.12188E-05	3.41674E-05	3.057283807	0.030061148	1	88	87	94	106	71	164	182	144	155	204
ENSMUSG00000066842	chr1	Hmcn1	-1.186143	1.12247E-05	3.41777E-05	2.344743967	0.071162331	-1	116	73	103	122	101	63	36	25	46	81
ENSMUSG00000034160	chrX	Ogt	-0.681041	1.12314E-05	3.41908E-05	6.504796401	0.027867938	-1	1822	1699	1503	1692	1551	1260	1048	916	1195	1286
ENSMUSG00000036639	chr5	Nudt1	0.87153041	1.13094E-05	3.44209E-05	2.785271301	0.036181394	1	88	63	67	77	60	146	149	108	159	152
ENSMUSG00000018796	chr8	Acsl1	-0.983624	1.13236E-05	3.44565E-05	7.618597607	0.05864513	-1	2467	3584	3053	7030	3798	1576	1986	2178	2117	2840
ENSMUSG00000044447	chr14	Dock5	1.39900673	1.1363E-05	3.45689E-05	1.482866791	0.087484756	1	15	15	28	28	22	108	65	57	38	50
ENSMUSG00000028098	chr3	Rnf115	-0.7659798	1.14287E-05	3.47612E-05	6.039833177	0.035098537	-1	1272	1015	1226	1770	956	662	972	620	888	821
ENSMUSG00000039789	chr16	Zfp597	-0.9425578	1.14658E-05	3.48663E-05	2.82447716	0.044745403	-1	129	104	165	167	118	75	81	54	92	88
ENSMUSG00000021464	chr13	Ror2	1.23057979	1.14691E-05	3.4869E-05	1.381282737	0.061366006	1	19	25	22	24	19	68	59	54	32	71
ENSMUSG00000030116	chr6	Mfap5	0.93272088	1.15133E-05	3.49956E-05	5.828819285	0.052044359	1	562	526	628	685	498	1924	1028	1443	688	1038
ENSMUSG00000038954	chr17	Supt3	0.86051819	1.15439E-05	3.50809E-05	2.809299085	0.035452288	1	80	70	60	82	71	144	132	137	171	136
ENSMUSG00000047592	chr5	Nxpe5	1.82284797	1.16515E-05	3.54004E-05	1.722462221	0.167308445	1	22	20	20	20	20	190	53	83	56	26
ENSMUSG00000028156	chr3	Eif4e	-0.7313549	1.1695E-05	3.55248E-05	6.411351657	0.032252918	-1	1627	1406	1626	1991	1283	875	1141	857	1212	1113
ENSMUSG00000067629	chr17	Syngap1	1.1727144	1.16993E-05	3.55302E-05	2.048127225	0.065549905	1	46	25	42	39	30	121	94	100	52	87
ENSMUSG00000048644	chr8	Ctxn1	1.72937213	1.17277E-05	3.56084E-05	0.261321026	0.103142397	1	5	4	9	8	10	34	26	36	14	23
ENSMUSG00000035783	chr19	Acta2	0.98847034	1.17921E-05	3.57963E-05	7.574076868	0.059444763	1	2167	1642	1500	2141	2043	4256	3260	6272	2573	4092
ENSMUSG00000022526	chr15	Zfp251	-0.799943	1.18063E-05	3.58317E-05	3.359723508	0.032600166	-1	195	195	167	242	166	90	143	103	124	143
ENSMUSG00000021903	chr14	Galnt15	-0.92615	1.18093E-05	3.58331E-05	4.563370563	0.049916618	-1	601	589	356	372	355	259	253	184	284	350
ENSMUSG00000024222	chr17	Fkbp5	1.0675899	1.18188E-05	3.5854E-05	3.838889207	0.064339265	1	125	128	149	178	104	593	289	160	303	256
ENSMUSG00000029175	chr5	Slc35f6	0.71942432	1.18283E-05	3.5875E-05	4.387983535	0.028726068	1	237	238	227	259	206	538	512	286	411	385

ENSMUSG00000047603	chr7	Zfp235	-1.3686359	1.18754E-05	3.60102E-05	1.450457888	0.085781514	-1	57	78	44	67	37	19	28	12	23	38
ENSMUSG00000027411	chr2	Vps16	0.71333561	1.18905E-05	3.60481E-05	3.99418863	0.027430394	1	185	183	136	251	147	342	342	259	366	294
ENSMUSG00000035212	chr4	Leprot	0.67740804	1.19698E-05	3.62805E-05	4.834072378	0.026054179	1	331	354	325	357	255	741	580	418	574	561
ENSMUSG00000033124	chr1	Atg9a	-0.7130161	1.20552E-05	3.65315E-05	7.297259031	0.031095381	-1	2850	2533	2304	3563	3305	1850	1962	1760	1791	2363
ENSMUSG00000012519	chr8	Mlkl	1.35738621	1.20624E-05	3.65424E-05	1.469755678	0.082228603	1	17	9	33	32	19	80	61	48	66	55
ENSMUSG00000036181	chr13	Hist1h1c	0.90874707	1.2064E-05	3.65424E-05	7.065517755	0.05033462	1	1515	1337	1115	1789	1223	1933	2858	2481	2355	4621
ENSMUSG00000001240	chr11	Ramp2	0.69600952	1.20878E-05	3.66064E-05	6.209411614	0.02914058	1	883	877	779	970	691	2064	1312	1422	1320	1380
ENSMUSG00000079550	chr1	Mpp4	1.03862702	1.21594E-05	3.68153E-05	2.080570193	0.048303454	1	46	50	29	42	32	117	92	66	91	86
ENSMUSG00000032536	chr9	Trak1	-0.9566524	1.22693E-05	3.71401E-05	7.099922215	0.055817913	-1	2204	2339	2468	4053	2580	868	1627	1538	1354	2166
ENSMUSG00000052632	chr12	Asap2	-0.8598659	1.23113E-05	3.72592E-05	3.320835154	0.03856066	-1	199	203	174	250	131	124	124	138	78	108
ENSMUSG00000036992	chr2	Nxt1	0.9102474	1.23196E-05	3.72763E-05	2.535849002	0.03883113	1	51	58	50	83	53	159	126	102	121	98
ENSMUSG00000040690	chr4	Col16a1	0.86354138	1.23602E-05	3.73909E-05	5.839679249	0.044901897	1	772	510	568	646	517	1646	1162	1332	666	1256
ENSMUSG00000024666	chr19	Tmem138	1.35233199	1.23692E-05	3.74102E-05	1.376900189	0.07973239	1	33	12	19	18	20	81	69	51	46	43
ENSMUSG00000020003	chr10	Pex7	-0.8318962	1.24112E-05	3.75291E-05	4.003988076	0.038521356	-1	278	292	262	442	264	133	201	154	241	200
ENSMUSG00000026437	chr1	Cdk18	1.56002121	1.24175E-05	3.75398E-05	2.92902371	0.134982682	1	39	42	66	93	45	330	165	79	72	294
ENSMUSG00000043670	chr10	Diras1	3.12209425	1.24999E-05	3.77808E-05	-0.862077971	0.287178128	1	1	0	2	2	1	1	5	21	15	18
ENSMUSG00000031740	chr8	Mmp2	0.9159201	1.25394E-05	3.78844E-05	7.598599851	0.051461786	1	1938	1982	1661	2273	2111	5816	3244	3398	2476	6062
ENSMUSG00000039109	chr13	F13a1	1.39852376	1.25396E-05	3.78844E-05	5.688884093	0.116520407	1	385	413	451	378	444	2270	1385	520	1555	475
ENSMUSG00000025278	chr14	Flnb	-0.7120101	1.26003E-05	3.80596E-05	4.686839887	0.029085957	-1	376	416	445	646	500	387	350	251	243	371
ENSMUSG00000063684	chr2	Gm13910	-0.7428266	1.26042E-05	3.80632E-05	4.760654104	0.031840753	-1	401	534	516	718	372	344	289	312	387	310
ENSMUSG00000060212	chr8	Pcnxl2	-1.8911246	1.26379E-05	3.81568E-05	-0.330589521	0.094115758	-1	11	16	17	20	16	3	4	5	9	2
ENSMUSG00000029910	chr6	Mad2l1	1.39222272	1.26596E-05	3.82141E-05	2.069804741	0.098675819	1	37	32	38	32	26	92	152	61	125	49
ENSMUSG00000025348	chr10	Itga7	0.77627181	1.26684E-05	3.82322E-05	6.992577187	0.036948463	1	1493	1106	1293	1922	1240	2426	2609	3034	2864	2036
ENSMUSG00000057880	chr16	Abat	-1.0616023	1.27026E-05	3.83272E-05	2.137006801	0.053193259	-1	94	84	67	117	74	53	28	56	37	52
ENSMUSG00000046822	chr10	Slc39a3	-0.6409221	1.27069E-05	3.83319E-05	4.618719786	0.022983449	-1	404	418	448	528	418	291	342	264	322	340
ENSMUSG00000015165	chr7	Hnrnpl	0.67308555	1.2759E-05	3.84807E-05	6.580952157	0.027587404	1	1159	1023	944	1392	999	2206	2157	1831	1870	1529
ENSMUSG00000029128	chr5	Rab28	-0.6804945	1.28214E-05	3.86605E-05	5.953146677	0.02782904	-1	1194	1046	1061	1438	962	657	786	701	864	853
ENSMUSG00000099329	chr17	Gm28052	-2.001585	1.28779E-05	3.88225E-05	1.47819081	0.202878599	-1	68	65	58	67	61	0	12	13	27	34
ENSMUSG00000103212	chr1	AC132393.1	0.85648243	1.29025E-05	3.88883E-05	3.075173507	0.037219608	1	71	92	79	117	82	238	190	138	123	193
ENSMUSG00000066979	chr7	Bub3	0.6257784	1.29463E-05	3.9012E-05	5.41040995	0.022940251	1	488	473	459	615	454	1015	892	733	839	733
ENSMUSG00000030555	chr7	Ttc23	-0.7515753	1.30033E-05	3.91754E-05	3.402088765	0.028899026	-1	219	174	174	235	178	157	96	128	120	136
ENSMUSG00000020744	chr11	Slc25a19	-0.6792809	1.30078E-05	3.91803E-05	5.443051865	0.027302573	-1	705	786	787	1047	673	484	558	580	527	558
ENSMUSG00000045107	chr14	Saysd1	0.87568126	1.30884E-05	3.94148E-05	2.833480207	0.037638426	1	83	75	62	87	61	215	131	136	124	138
ENSMUSG00000022884	chr16	Eif4a2	-0.6692835	1.31625E-05	3.96292E-05	8.242044521	0.027832922	-1	6447	5501	4764	6605	4473	4153	3979	3150	3731	4126
ENSMUSG00000098098	chr18	Gm20748	1.5832822	1.32781E-05	3.99688E-05	1.522576679	0.120638732	1	36	19	22	16	8	83	56	94	56	43
ENSMUSG00000053801	chr7	Grwd1	0.73245352	1.32813E-05	3.99698E-05	4.155785946	0.029767154	1	181	176	156	248	230	436	422	336	319	295
ENSMUSG00000028890	chr4	Mtf1	-0.6824863	1.3326E-05	4.00956E-05	4.066867234	0.025216085	-1	307	262	286	372	302	194	195	188	233	230
ENSMUSG00000073771	chr4	Btbd19	1.34241198	1.33774E-05	4.02415E-05	1.427216042	0.080644216	1	22	17	18	26	24	96	72	54	45	34
ENSMUSG00000073676	chr1	Hspe1	0.72577762	1.34089E-05	4.03276E-05	5.975957861	0.031934484	1	727	631	576	919	694	1596	1556	1173	1148	941
ENSMUSG00000034731	chr14	Dgkh	-1.7177634	1.34481E-05	4.0437E-05	0.56227111	0.123666316	-1	27	35	28	47	21	13	21	3	11	4
ENSMUSG00000047423	chr19	AI837181	0.66051295	1.34695E-05	4.04926E-05	5.374662192	0.025782855	1	514	441	429	583	427	828	819	788	654	1055
ENSMUSG00000028017	chr3	Egf	-1.0480241	1.34749E-05	4.05E-05	5.530394207	0.066511223	-1	1103	744	712	1026	1037	309	544	276	683	634
ENSMUSG00000021877	chr14	Arf4	0.66702985	1.34808E-05	4.05089E-05	5.825264391	0.026749792	1	716	595	617	792	546	1298	1317	1056	814	1213
ENSMUSG00000026579	chr1	F5	2.09830226	1.36706E-05	4.10704E-05	-0.061845955	0.151310344	1	1	5	6	2	8	42	14	14	16	24
ENSMUSG00000051934	chr15	Spats2	0.84640021	1.36776E-05	4.10827E-05	3.388264578	0.038118311	1	114	118	84	136	100	215	235	269	153	207
ENSMUSG00000034471	chr11	Caskin2	-0.6541146	1.36986E-05	4.1137E-05	4.42027876	0.023872625	-1	318	350	372	524	385	338	252	248	240	279
ENSMUSG00000001366	chr9	Fbxo9	-0.7351099	1.37769E-05	4.13633E-05	5.707627832	0.032671263	-1	965	770	917	1215	995	554	641	527	591	887
ENSMUSG00000069008	chr3	Gm5537	1.47209702	1.38625E-05	4.16112E-05	0.652277385	0.080999236	1	13	9	10	11	13	30	23	31	48	39
ENSMUSG00000028820	chr4	Sfpq	0.76121469	1.3882E-05	4.16608E-05	5.942285857	0.03530337	1	560	604	527	1001	737	1512	1553	1006	1239	1021
ENSMUSG00000026825	chr2	Dnm1	0.85301686	1.39639E-05	4.18978E-05	3.906191043	0.040863915	1	173	137	137	195	149	442	219	323	211	378
ENSMUSG00000036707	chr1	Cab39	-0.6840616	1.39673E-05	4.18989E-05	7.093561466	0.028974315	-1	2321	2184	2138	3827	2259	1612	1882	1545	1630	1873
ENSMUSG00000021501	chr13	Caml	0.76828654	1.40583E-05	4.2163E-05	3.163794194	0.029482814	1	112	88	72	119	97	214	187	141	184	186
ENSMUSG00000028847	chr4	Trappc3	0.6232239	1.40944E-05	4.22621E-05	4.426033286	0.021436333	1	265	269	217	309	198	472	467	384	369	429
ENSMUSG00000033478	chr19	Fam160b1	-0.7311221	1.41834E-05	4.25198E-05	3.71573238	0.028688315	-1	207	215	268	293	226	184	165	129	129	198
ENSMUSG00000027133	chr2	Nop10	0.65330546	1.42769E-05	4.2791E-05	5.293886533	0.025238348	1	525	456	429	489	360	882	799	699	818	705
ENSMUSG00000071654	chr19	Uqcc3	0.64600003	1.42939E-05	4.28327E-05	5.416138565	0.024823375	1	543	472	422	612	434	984	747	915	745	845
ENSMUSG00000021596	chr13	Mctp1	2.19020037	1.43652E-05	4.3037E-05	0.426914615	0.207993642	1	6	7	6	10	3	43	46	3	42	29
ENSMUSG00000017817	chr2	Jph2	-0.769048	1.43892E-05	4.30998E-05	9.866730766	0.03717435	-1	18307	14858	14320	20331	19685	9164	11429	10211	11889	13430
ENSMUSG00000070526	chr7	Peg12	1.30010608	1.44174E-05	4.31749E-05	0.907756969	0.062983607	1	16	13	15	21	10	38	57	37	32	38
ENSMUSG00000039542	chr9	Ncam1	1.11832818	1.4462E-05	4.32993E-05	4.387908976	0.074326798	1	197	170	188	200	213	493	385	757	215	451
ENSMUSG00000032557	chr9	Uba5	0.68175255	1.44932E-05	4.33833E-05	4.584968268	0.02659709	1	289	267	245	337	232	625	520	424	478	362
ENSMUSG00000015879	chr5	Fam184b	-2.7431897	1.45516E-05	4.35487E-05	0.387314909	0.342287288	-1	28	35	13	55	28	20	4	0	2	0
ENSMUSG00000027253	chr2	Lrp4	-0.8891141	1.45578E-05	4.35581E-05	4.135127921	0.045902957	-1	230	268	314	566	341	229	174	181	145	277
ENSMUSG00000030074	chr6	Gxylt2	1.43663135	1.45991E-05	4.36724E-05	1.200789879	0.089987786	1	20	10	21	13	21	72	31	55	43	57
ENSMUSG00000025026	chr19	Add3	-0.6074319	1.46632E-05	4.38547E-05	5.195539691	0.021614853	-1	622	620	572	826	654	467	514	399	455	532

ENSMUSG00000022401	chr15	Xpnpep3	-1.0060462	1.47324E-05	4.40522E-05	2.74092134	0.05286557	-1	148	121	110	153	123	45	96	65	56	94
ENSMUSG00000098579	chr12	Mir6937	-1.788241	1.47589E-05	4.4122E-05	-0.263529312	0.092974377	-1	13	17	15	19	19	4	3	2	8	9
ENSMUSG00000064340	chrMT	mt-Tl1	-0.9958192	1.47673E-05	4.41311E-05	5.186332738	0.060166035	-1	736	657	710	1102	462	279	244	409	501	522
ENSMUSG00000103124	chr3	RP24-137C19.6	-1.7843901	1.47682E-05	4.41311E-05	1.104932049	0.153416196	-1	17	45	78	65	31	25	20	8	12	11
ENSMUSG00000033721	chr3	Vav3	1.07207425	1.47901E-05	4.41869E-05	2.459806959	0.058250362	1	46	63	51	65	33	141	152	67	127	111
ENSMUSG00000011382	chr7	Dhdh	-0.7515715	1.48311E-05	4.42998E-05	4.550501651	0.032883215	-1	488	397	321	506	469	227	301	241	278	370
ENSMUSG00000017652	chr2	Cd40	1.33547712	1.49003E-05	4.44906E-05	0.846105822	0.066383962	1	12	12	9	25	13	44	41	45	29	35
ENSMUSG00000045962	chr6	Wnk1	-0.6670433	1.49013E-05	4.44906E-05	8.067667031	0.027967061	-1	4823	4211	4229	6330	5026	3234	3653	3182	3235	3589
ENSMUSG00000016554	chr15	Eif3d	0.6524783	1.49459E-05	4.46142E-05	6.02368375	0.025986035	1	720	659	667	929	789	1519	1265	1339	1141	1216
ENSMUSG00000003153	chr6	Slc2a3	1.38144077	1.50692E-05	4.49668E-05	1.499161654	0.087511191	1	23	24	23	17	22	66	74	34	93	50
ENSMUSG00000021770	chr14	Samd8	-0.714273	1.50704E-05	4.49668E-05	5.671751522	0.031049546	-1	852	886	754	1180	1043	542	763	569	553	716
ENSMUSG00000026933	chr2	Camsap1	-0.70702	1.50761E-05	4.49741E-05	4.772715229	0.029267483	-1	454	403	404	706	568	388	290	304	376	330
ENSMUSG00000084106	chr1	Gm6136	0.69682964	1.50959E-05	4.50234E-05	4.018613065	0.026621399	1	198	195	156	214	152	431	360	261	264	322
ENSMUSG00000029330	chr5	Cds1	1.73186895	1.51034E-05	4.50362E-05	0.704693396	0.127979009	1	11	7	7	20	7	71	47	19	30	23
ENSMUSG00000020993	chr12	Trappc6b	-0.6417138	1.51666E-05	4.52152E-05	4.466893299	0.023206639	-1	391	369	338	548	369	284	330	212	289	292
ENSMUSG00000009927	chr9	Rps25	0.71424767	1.51835E-05	4.52558E-05	7.980934427	0.032096941	1	3286	2737	2343	3379	2543	7019	5542	4176	4783	4302
ENSMUSG00000070056	chr8	Mfhas1	1.00002773	1.52304E-05	4.53861E-05	3.208474092	0.055028305	1	48	77	99	134	96	207	263	138	181	208
ENSMUSG00000098992	chr11	Gm27597	0.64692038	1.52538E-05	4.54459E-05	7.147351585	0.02614257	1	1882	1550	1488	1865	1437	3274	3072	2474	2744	2585
ENSMUSG00000049717	chr8	Lig4	-0.9273574	1.52724E-05	4.54916E-05	2.687225312	0.043231912	-1	132	111	113	135	125	58	83	49	82	84
ENSMUSG00000024404	chr18	Riok3	-0.7072946	1.5313E-05	4.55933E-05	6.908099894	0.031225664	-1	2510	2120	1908	2588	1977	1344	1530	1112	1603	1861
ENSMUSG00000081051	chr1	Gm15427	0.65790146	1.53106E-05	4.55933E-05	4.208049492	0.023868756	1	249	199	180	234	197	444	347	319	387	340
ENSMUSG00000090733	chr3	Rps27	0.90469026	1.53534E-05	4.57038E-05	7.573779233	0.051260509	1	2142	2084	1806	2177	1646	7096	3677	3053	3995	2733
ENSMUSG00000035000	chr2	Dpp4	-0.8894361	1.54165E-05	4.58819E-05	2.72483076	0.039337006	-1	135	116	103	168	112	98	63	72	82	57
ENSMUSG00000015478	chr17	Rnf5	0.6151204	1.54412E-05	4.59457E-05	4.502301408	0.021186047	1	278	254	250	332	217	547	420	424	401	440
ENSMUSG00000033054	chr9	Npat	-1.1285669	1.54686E-05	4.60172E-05	2.408221903	0.066059251	-1	103	108	103	149	74	29	57	46	52	81
ENSMUSG00000027883	chr3	Gpsm2	0.83609267	1.54732E-05	4.60212E-05	3.339119195	0.037329658	1	158	95	87	115	80	218	239	199	173	217
ENSMUSG00000029673	chr5	Auts2	-1.0906443	1.54934E-05	4.60715E-05	4.249459413	0.070945914	-1	295	245	291	592	516	169	173	247	120	273
ENSMUSG00000017548	chr11	Suz12	-0.6601923	1.55005E-05	4.60826E-05	4.264681061	0.024353462	-1	374	340	332	436	270	241	284	183	239	266
ENSMUSG00000028070	chr3	Apoa1bp	0.59063979	1.55085E-05	4.60967E-05	5.039948205	0.020264804	1	396	355	310	516	384	735	619	587	596	686
ENSMUSG00000043207	chr4	Zmpste24	-0.6153263	1.5564E-05	4.62518E-05	4.909542018	0.021978616	-1	555	487	492	644	522	403	429	305	422	374
ENSMUSG00000038141	chr17	Tmem181a	1.32171168	1.55741E-05	4.62721E-05	1.719071129	0.083846257	1	25	25	30	28	25	39	85	54	95	92
ENSMUSG00000089911	chr3	Hiat1	-0.6746199	1.55885E-05	4.63051E-05	4.106119042	0.025209855	-1	309	311	297	402	256	224	239	150	221	247
ENSMUSG00000070871	chr1	Ccnyl1	-0.6441143	1.56278E-05	4.64118E-05	4.264541793	0.023065912	-1	354	359	349	385	284	251	242	200	250	276
ENSMUSG00000034071	chr7	Zfp551	-2.4248666	1.5679E-05	4.65541E-05	-0.421425002	0.20450393	-1	21	18	17	10	13	2	11	0	3	0
ENSMUSG00000086859	chr11	2810008D09Rik	1.37904007	1.57681E-05	4.68086E-05	2.044382432	0.098469126	1	45	28	35	25	29	172	68	66	108	61
ENSMUSG00000020594	chr12	Pum2	-0.6249164	1.58025E-05	4.68908E-05	6.320498606	0.024133219	-1	1436	1296	1287	1912	1330	1189	1076	824	943	1124
ENSMUSG00000078915	chr13	Hsp25-ps1	1.2840308	1.5801E-05	4.68908E-05	3.212654722	0.094902252	1	51	71	58	154	73	417	180	204	119	155
ENSMUSG00000058838	chr9	Rps27a-ps2	0.79674941	1.60263E-05	4.75448E-05	3.889109745	0.035828005	1	162	171	138	216	119	349	379	228	344	225
ENSMUSG00000066113	chr4	Adamtsl1	-0.9107544	1.60392E-05	4.75729E-05	4.074190016	0.048716298	-1	363	295	274	262	405	178	191	174	137	272
ENSMUSG00000079509	chrX	Zfx	-0.6512156	1.60492E-05	4.75925E-05	4.056901181	0.02315106	-1	278	290	280	418	252	218	238	177	192	228
ENSMUSG00000024935	chr19	Slc1a1	-1.6491006	1.60944E-05	4.77165E-05	0.866388142	0.123794741	-1	32	28	26	61	49	22	23	11	6	6
ENSMUSG00000005505	chr2	Kbtbd4	-0.7473943	1.61392E-05	4.7839E-05	3.923298518	0.03106921	-1	278	266	252	339	272	140	188	159	179	250
ENSMUSG00000057522	chr11	Spop	-0.6633833	1.617E-05	4.79203E-05	8.18428589	0.02791397	-1	5418	5112	4646	6503	4938	3393	3599	3342	3756	4244
ENSMUSG00000007777	chr11	0610009B22Rik	-0.6981394	1.62141E-05	4.80409E-05	3.953017886	0.026884308	-1	322	296	219	337	248	185	211	147	209	206
ENSMUSG00000048668	chr6	Rhno1	0.84147732	1.62247E-05	4.80621E-05	3.079182794	0.036484754	1	83	93	83	113	73	259	175	158	135	152
ENSMUSG00000031382	chrX	Asb11	-0.8429776	1.62298E-05	4.80669E-05	6.239869113	0.044325027	-1	1161	1225	1190	2394	1394	1226	924	578	996	727
ENSMUSG00000057411	chr17	Fam173a	0.62933359	1.62575E-05	4.81386E-05	4.85333654	0.023023631	1	391	341	297	357	292	660	498	554	541	602
ENSMUSG00000030652	chr7	Coq7	0.66100529	1.62709E-05	4.81682E-05	5.696320073	0.026707832	1	589	587	558	796	477	943	1049	1059	1099	989
ENSMUSG00000031295	chrX	Phka2	0.84176082	1.6286E-05	4.82026E-05	3.117753011	0.036680589	1	99	113	79	94	69	240	155	152	175	178
ENSMUSG00000005103	chr5	Wdr1	0.7252135	1.62944E-05	4.82098E-05	6.915788127	0.033058865	1	1260	1085	1263	2100	1175	3358	2615	2153	2145	2090
ENSMUSG00000029265	chr5	Dr1	-0.8556209	1.62953E-05	4.82098E-05	4.158419982	0.042863445	-1	333	256	318	509	310	160	243	152	174	306
ENSMUSG00000030591	chr7	Psmd8	0.67102732	1.63226E-05	4.82721E-05	7.419037608	0.028417984	1	2362	1856	1845	2061	1669	4071	3396	2978	3441	3313
ENSMUSG00000042419	chr17	Nfkbil1	0.89475824	1.63233E-05	4.82721E-05	3.053182611	0.042425947	1	89	88	62	116	74	245	145	189	122	170
ENSMUSG00000009654	chr10	Oit3	2.60244248	1.63586E-05	4.83665E-05	-0.265293751	0.244800757	1	5	3	3	3	0	29	33	3	8	26
ENSMUSG00000042109	chr15	Csdc2	1.24582692	1.64207E-05	4.85293E-05	2.068213452	0.078122399	1	47	39	31	29	31	95	65	125	62	116
ENSMUSG00000059493	chrX	Nhs	-1.8161572	1.64203E-05	4.85293E-05	0.814586627	0.15334739	-1	54	37	25	35	40	3	16	15	4	21
ENSMUSG00000001755	chr11	Coasy	0.77033215	1.65305E-05	4.88438E-05	3.734499948	0.032731439	1	125	178	141	185	99	301	261	295	230	267
ENSMUSG00000052419	chr6	2610001J05Rik	0.62955972	1.65452E-05	4.88768E-05	5.0330086	0.02340057	1	387	373	339	485	332	825	689	515	674	547
ENSMUSG00000085492	chr17	Trmt61b	2.00250698	1.65511E-05	4.88837E-05	0.299466626	0.171869922	1	4	4	7	14	4	9	47	28	35	22
ENSMUSG00000026946	chr2	Nmi	1.02192433	1.66432E-05	4.91454E-05	2.636854512	0.054035928	1	70	71	56	62	39	124	128	105	181	124
ENSMUSG00000026854	chr2	Usp20	0.72993852	1.66539E-05	4.91667E-05	4.71815744	0.031599353	1	353	258	221	362	281	560	416	590	453	642
ENSMUSG00000038555	chr18	Reep2	1.69539799	1.6692E-05	4.92686E-05	0.563204367	0.11852538	1	10	12	4	12	9	39	23	54	18	32
ENSMUSG00000026495	chr1	Efcab2	-0.699722	1.67242E-05	4.93534E-05	3.636339144	0.025810078	-1	237	200	195	329	190	157	145	138	140	188
ENSMUSG00000035202	chr9	Lars2	1.14375931	1.6754E-05	4.94308E-05	9.415780457	0.082244945	1	7358	3382	4050	7276	9538	21249	20471	12936	9800	13279
ENSMUSG00000031774	chr8	Fam192a	0.64188705	1.67953E-05	4.95423E-05	4.823085107	0.024138494	1	400	263	252	411	323	629	561	507	498	617

ENSMUSG00000031538	chr8	Plat	0.87629512	1.68538E-05	4.97042E-05	3.422620233	0.042334818	1	106	104	92	135	119	230	215	264	135	274
ENSMUSG00000034424	chr8	Gcsh	-0.7931572	1.68656E-05	4.97287E-05	5.365578432	0.038706953	-1	884	790	668	940	620	835	460	373	397	432
ENSMUSG00000029126	chr5	Nsg1	1.15866042	1.70278E-05	5.01964E-05	2.200873496	0.068028469	1	25	52	44	43	39	165	85	87	80	91
ENSMUSG00000084145	chr11	Gm12263	-1.8566753	1.70352E-05	5.02074E-05	-0.112132725	0.108309177	-1	23	19	18	28	8	2	6	4	9	7
ENSMUSG00000026842	chr2	Abl1	-0.6146788	1.70679E-05	5.02933E-05	5.458792049	0.022847953	-1	831	780	754	891	690	585	556	505	546	640
ENSMUSG00000064090	chr11	Vrk2	1.11786445	1.70921E-05	5.03539E-05	2.727008021	0.068118438	1	67	84	41	69	44	135	135	100	217	134
ENSMUSG00000036167	chr15	Pphln1	-0.6622877	1.72221E-05	5.07262E-05	3.779697008	0.023448983	-1	256	230	232	315	216	172	199	132	165	196
ENSMUSG00000034265	chr17	Zdhhc14	1.03876886	1.72551E-05	5.08127E-05	2.450862737	0.055264779	1	50	41	49	71	50	182	96	84	85	147
ENSMUSG00000020707	chr11	Rnf135	1.10622102	1.7404E-05	5.12406E-05	2.062198631	0.059125795	1	33	45	37	34	39	136	67	78	73	100
ENSMUSG00000007279	chr7	Scube2	-1.1829103	1.745E-05	5.13651E-05	1.933860357	0.070112895	-1	87	57	90	103	50	43	35	24	27	58
ENSMUSG00000002500	chr17	Rpl3l	-0.7141727	1.74877E-05	5.14651E-05	8.767707846	0.032674408	-1	7960	7395	7422	10411	7340	4566	5291	4529	5907	6580
ENSMUSG00000021993	chr14	Mipep	-0.6082065	1.76015E-05	5.17783E-05	5.467935718	0.02241328	-1	814	767	757	948	689	573	605	511	583	581
ENSMUSG00000079641	chrX	Rpl39	0.74786359	1.75996E-05	5.17783E-05	6.724612089	0.035342027	1	1335	1288	1134	1282	827	2710	2391	1746	2274	1734
ENSMUSG00000006763	chr7	Saal1	0.83502225	1.76342E-05	5.18545E-05	2.531260967	0.032374242	1	59	64	50	72	57	127	127	100	121	116
ENSMUSG00000093264	chr11	Gm23419	0.69900352	1.76348E-05	5.18545E-05	5.685831248	0.030196586	1	628	533	528	748	496	1249	1345	715	962	963
ENSMUSG00000003617	chr3	Cp	-0.8820718	1.76701E-05	5.19472E-05	3.979227023	0.045639094	-1	268	356	311	281	277	305	161	147	135	165
ENSMUSG00000041360	chr19	D19Bwg1357e	0.72162391	1.77848E-05	5.22735E-05	4.337385903	0.030279033	1	253	189	176	287	230	498	494	362	389	304
ENSMUSG00000041440	chr9	Gk5	-1.4331865	1.78245E-05	5.2379E-05	1.192715459	0.094641414	-1	58	55	50	41	31	12	23	17	12	32
ENSMUSG00000030598	chr7	Fbxo17	0.96911265	1.78648E-05	5.24866E-05	2.750929067	0.048814332	1	93	66	49	56	65	144	129	159	132	145
ENSMUSG00000086316	chrX	2210013O21Rik	0.80491144	1.78869E-05	5.25403E-05	3.457299768	0.035289549	1	134	104	80	148	125	277	196	246	174	235
ENSMUSG00000040865	chr1	Ino80d	-0.6640447	1.78942E-05	5.25509E-05	4.028743282	0.024530161	-1	318	265	279	363	260	241	235	183	153	218
ENSMUSG00000022957	chr16	Itsn1	-0.6924343	1.79005E-05	5.25584E-05	6.259508199	0.030116763	-1	1254	1221	1144	1998	1489	1234	949	791	779	1065
ENSMUSG00000024483	chr18	Ankhd1	-0.581266	1.79189E-05	5.26013E-05	4.997115131	0.019850662	-1	575	505	517	753	511	500	447	356	375	414
ENSMUSG00000026925	chr2	Inpp5e	-0.7017177	1.8062E-05	5.30101E-05	3.604892542	0.026222346	-1	215	234	183	275	208	172	121	157	148	150
ENSMUSG00000029507	chr5	Pus1	0.7579947	1.81218E-05	5.31746E-05	3.740108411	0.032115613	1	129	141	109	235	131	357	274	269	225	238
ENSMUSG00000024217	chr17	Snrpc	0.57802324	1.81736E-05	5.33153E-05	5.052728518	0.019660336	1	414	392	344	462	364	724	661	591	655	602
ENSMUSG00000029405	chr5	G3bp2	-0.7506316	1.81861E-05	5.33409E-05	6.519309214	0.035642309	-1	1737	1506	1356	2292	1735	847	1247	1000	1022	1448
ENSMUSG00000019791	chr10	Hint3	-0.7308711	1.82002E-05	5.33709E-05	4.329492487	0.031182055	-1	409	390	379	427	255	264	232	226	294	207
ENSMUSG00000033454	chr12	Zbtb1	-0.7463724	1.8256E-05	5.35233E-05	3.634818388	0.030574497	-1	226	226	229	317	162	144	163	111	161	173
ENSMUSG00000040565	chr19	Btaf1	-0.9399179	1.82649E-05	5.35382E-05	3.52796445	0.050749106	-1	226	177	188	270	258	137	187	71	145	103
ENSMUSG00000071796	chr8	6820431F20Rik	-1.6322132	1.83437E-05	5.37578E-05	0.436754554	0.104513793	-1	33	36	28	17	24	8	11	9	15	6
ENSMUSG00000039637	chr16	Coro7	0.63710931	1.83807E-05	5.3855E-05	4.099772896	0.022357712	1	198	169	184	236	204	392	327	302	295	381
ENSMUSG00000091086	chr10	Gm5428	0.77166082	1.84073E-05	5.39217E-05	4.074339142	0.034602334	1	186	180	133	273	161	480	390	294	313	256
ENSMUSG00000000532	chr15	Acvr1b	-0.7805703	1.84597E-05	5.4054E-05	5.907956342	0.038270219	-1	1327	1263	999	1016	981	676	801	695	514	922
ENSMUSG00000037940	chr8	Inpp4b	-1.9183048	1.84602E-05	5.4054E-05	1.844267747	0.200273367	-1	27	53	71	215	66	10	28	19	39	20
ENSMUSG00000024501	chr18	Dpysl3	0.80895999	1.8611E-05	5.44841E-05	5.180921033	0.040376597	1	436	394	381	429	312	1084	785	838	501	568
ENSMUSG00000038910	chr17	Plcl2	-0.6506534	1.86275E-05	5.45211E-05	6.021714138	0.026464881	-1	1192	1100	1044	1503	1090	760	790	727	805	1037
ENSMUSG00000057894	chr7	Zfp329	-1.0918415	1.86876E-05	5.46856E-05	2.429341229	0.062399841	-1	105	97	92	153	94	31	62	39	63	79
ENSMUSG00000048379	chr14	Socs4	-0.7467483	1.88433E-05	5.51296E-05	3.170712992	0.028489806	-1	154	173	149	223	137	115	128	89	110	101
ENSMUSG00000007613	chr4	Tgfbr1	-0.7418925	1.88893E-05	5.52527E-05	4.851366019	0.033456946	-1	528	447	442	746	543	362	421	239	274	478
ENSMUSG00000029174	chr5	Tbc1d1	-0.7608183	1.89538E-05	5.54297E-05	5.233660519	0.03576959	-1	624	778	747	957	438	493	555	430	333	471
ENSMUSG00000028370	chr4	Pappa	-1.7509361	1.89608E-05	5.54384E-05	0.168852996	0.119264129	-1	17	17	24	21	36	10	7	7	2	12
ENSMUSG00000078656	chr11	Vps25	0.67668355	1.91305E-05	5.5923E-05	5.489375675	0.028270062	1	612	530	483	541	395	1153	869	760	899	839
ENSMUSG00000015189	chr6	Casd1	-0.6345265	1.91352E-05	5.59249E-05	4.681181879	0.023674501	-1	438	417	404	592	471	334	358	307	255	384
ENSMUSG00000086324	chr16	Gm15564	1.32241263	1.91816E-05	5.6049E-05	4.334499777	0.106870933	1	243	88	85	139	284	659	597	412	286	410
ENSMUSG00000074480	chr3	Mex3a	1.35790466	1.93276E-05	5.64639E-05	1.336414248	0.083559702	1	26	18	23	14	17	72	53	72	34	49
ENSMUSG00000071035	chr17	Gm5499	-1.6426633	1.93414E-05	5.64923E-05	-0.019084763	0.083086904	-1	18	26	17	25	13	4	6	6	10	8
ENSMUSG00000049090	chr18	Zadh2	-0.6531174	1.95003E-05	5.69445E-05	5.524445547	0.026382918	-1	812	874	828	984	682	512	633	510	610	642
ENSMUSG00000020024	chr10	Cep83	-0.9296486	1.95464E-05	5.7067E-05	3.50941826	0.049558144	-1	202	199	221	303	185	96	153	94	184	102
ENSMUSG00000049878	chr4	Rlf	-0.6267972	1.95607E-05	5.70952E-05	4.034197101	0.021698334	-1	289	304	253	353	274	241	225	175	186	222
ENSMUSG00000064280	chr5	Ccdc146	-1.3641091	1.95642E-05	5.70952E-05	2.228230314	0.101613649	-1	118	86	97	112	79	24	54	22	75	32
ENSMUSG00000020219	chr10	Timm13	0.66811609	1.96356E-05	5.72798E-05	6.022313773	0.02808278	1	829	711	729	837	621	1601	1231	1219	1368	1084
ENSMUSG00000025227	chr19	Tmem180	1.55749749	1.9633E-05	5.72798E-05	1.199881898	0.115529766	1	24	17	14	12	13	69	53	20	41	84
ENSMUSG00000055240	chr17	Zfp101	-1.0799526	1.964E-05	5.72805E-05	1.788646407	0.054702823	-1	69	66	70	68	63	27	43	24	42	39
ENSMUSG00000055489	chr7	Ano5	-0.993091	1.96578E-05	5.73207E-05	7.347818622	0.063148948	-1	3364	3158	3079	3393	3047	874	2091	1475	2342	2000
ENSMUSG00000087269	chr2	D330023K18Rik	1.13312579	1.98144E-05	5.77652E-05	1.644362011	0.058244959	1	32	25	25	31	26	46	66	77	65	78
ENSMUSG00000080875	chr5	Gm7332	1.00367016	1.98282E-05	5.77934E-05	2.113476955	0.048137128	1	45	46	32	45	39	111	111	87	82	66
ENSMUSG00000040054	chr10	Baz2a	-0.6261366	2.00242E-05	5.83524E-05	4.794956371	0.023315777	-1	446	465	482	648	467	382	319	288	349	443
ENSMUSG00000052974	chr7	Cyp2f2	1.73594752	2.00794E-05	5.85012E-05	0.690704136	0.136459135	1	13	13	2	15	8	36	24	30	26	70
ENSMUSG00000087366	chr4	Junos	-1.5262132	2.01653E-05	5.87392E-05	1.438258094	0.119416014	-1	42	72	60	85	32	42	16	27	12	13
ENSMUSG00000061878	chr11	Sphk1	2.26952002	2.0181E-05	5.87725E-05	2.103623603	0.285488679	1	16	19	18	37	17	360	110	27	35	57
ENSMUSG00000094439	chr4	Gm21969	-1.1336385	2.02071E-05	5.88363E-05	4.974874244	0.080372707	-1	607	660	584	752	601	125	354	218	449	440
ENSMUSG00000062234	chr5	Gak	0.6576696	2.02684E-05	5.90025E-05	4.517378746	0.025389197	1	264	239	230	343	247	612	507	345	363	474
ENSMUSG00000061136	chr2	Prpf40a	-0.6874512	2.02928E-05	5.90613E-05	4.755081167	0.02845849	-1	460	469	422	664	473	278	419	263	359	361
ENSMUSG00000027111	chr2	Itga6	-0.696408	2.03428E-05	5.91944E-05	5.168537408	0.029920036	-1	505	634	684	994	526	570	461	354	431	433

ENSMUSG00000031781	chr8	Ciapin1	0.69064918	2.04096E-05	5.93764E-05	5.175295408	0.029434833	1	349	400	367	609	352	853	755	795	643	577
ENSMUSG00000058881	chr18	Zfp516	-0.6313035	2.04877E-05	5.95911E-05	4.430014639	0.023166329	-1	366	353	338	485	403	323	267	220	236	337
ENSMUSG00000029598	chr5	Plbd2	0.64181521	2.05743E-05	5.98307E-05	5.481490232	0.025508478	1	527	505	482	585	486	952	863	934	692	992
ENSMUSG00000031591	chr8	Asah1	0.77586945	2.06349E-05	5.99946E-05	4.888042058	0.03706667	1	280	319	328	420	277	510	733	378	688	736
ENSMUSG00000030316	chr6	Tamm41	0.91413161	2.06818E-05	6.01182E-05	2.740069632	0.043909666	1	52	79	61	94	54	175	142	142	134	105
ENSMUSG00000014426	chr17	Map3k4	-0.6351298	2.07727E-05	6.037E-05	4.882963107	0.024226541	-1	491	437	494	728	531	387	337	403	346	401
ENSMUSG00000030527	chr7	Crtc3	-0.6639571	2.07909E-05	6.04102E-05	4.269507537	0.025570018	-1	298	323	338	443	351	259	235	218	195	309
ENSMUSG00000028362	chr4	Tnfsf8	2.89684975	2.08017E-05	6.04291E-05	0.09048548	0.366736447	1	0	3	4	8	1	46	36	4	5	45
ENSMUSG00000025025	chr19	Mxi1	-0.6804554	2.08554E-05	6.05726E-05	5.196405694	0.028620449	-1	617	604	578	977	618	546	404	373	376	613
ENSMUSG00000034274	chr11	Thoc5	0.63509981	2.09389E-05	6.08023E-05	4.15167822	0.022834637	1	214	200	161	270	191	360	368	332	366	322
ENSMUSG00000061477	chr12	Rps7	0.69843945	2.10492E-05	6.111E-05	7.469843403	0.031640935	1	2340	2045	1970	2080	1582	3826	3858	2972	3975	3265
ENSMUSG00000049336	chr11	Tenm2	-1.8819297	2.13202E-05	6.1884E-05	-0.101603095	0.120111155	-1	11	13	26	25	21	2	10	7	4	5
ENSMUSG00000026971	chr2	Itgb6	-0.7561243	2.13581E-05	6.19812E-05	5.216967202	0.035692313	-1	745	648	705	767	594	379	524	550	422	352
ENSMUSG00000027217	chr2	Tspan18	-1.0670015	2.14001E-05	6.209E-05	2.665824443	0.06243378	-1	97	120	132	163	118	61	42	67	51	108
ENSMUSG00000001119	chr10	Col6a1	0.80505313	2.15688E-05	6.25536E-05	8.325006698	0.04229035	1	3260	2923	3182	4250	3759	7237	6249	7880	4135	7780
ENSMUSG00000092137	chr9	Gcom1	-0.6535544	2.15667E-05	6.25536E-05	5.790705592	0.026950926	-1	974	868	896	1419	926	616	769	584	717	817
ENSMUSG00000017376	chr11	Nlk	-0.6984189	2.1592E-05	6.26077E-05	3.399459616	0.025761987	-1	209	200	170	209	172	157	143	118	114	120
ENSMUSG00000034681	chr17	Rnps1	1.07181371	2.16167E-05	6.26665E-05	4.821578191	0.072187073	1	239	272	228	380	245	241	758	703	631	730
ENSMUSG00000026012	chr1	Cd28	-1.2299274	2.18096E-05	6.32125E-05	3.094793639	0.088881482	-1	216	129	154	207	177	34	118	53	81	125
ENSMUSG00000030717	chr7	Nupr1	1.027415	2.18376E-05	6.32806E-05	3.828524338	0.063434331	1	180	168	121	109	103	537	291	283	206	246
ENSMUSG00000067017	chr1	Gm3608	-1.6347692	2.18567E-05	6.33227E-05	-0.111573441	0.077252384	-1	17	16	14	25	20	11	3	6	6	6
ENSMUSG00000006205	chr7	Htra1	0.65924957	2.18705E-05	6.33496E-05	5.76578377	0.02741776	1	726	646	504	620	618	1201	1078	984	922	1260
ENSMUSG00000026208	chr1	Des	0.78276053	2.19181E-05	6.34744E-05	11.70823046	0.040261061	1	32571	28620	29148	58084	38003	75736	55866	77171	63691	71747
ENSMUSG00000040653	chr10	Ppp1r14c	-0.7575118	2.20156E-05	6.37333E-05	7.278673005	0.037349908	-1	3317	2996	2600	2845	2656	1467	2055	1887	1627	2342
ENSMUSG00000074277	chr7	Phldb3	1.53077617	2.20166E-05	6.37333E-05	0.1154699	0.069345003	1	6	4	9	10	7	28	22	25	18	22
ENSMUSG00000044700	chr4	Tmem201	-0.6743748	2.20875E-05	6.39251E-05	5.586861874	0.028652399	-1	779	739	775	1190	933	589	592	623	491	718
ENSMUSG00000045251	chr7	Zfp688	1.36907397	2.21126E-05	6.39797E-05	1.400746533	0.089769269	1	24	35	11	18	15	66	67	62	36	64
ENSMUSG00000064262	chr6	Gimap8	-1.0147158	2.21155E-05	6.39797E-05	2.178651085	0.052068176	-1	87	96	87	114	59	71	40	31	48	51
ENSMUSG00000027384	chr2	Ndufaf5	-0.6834939	2.21697E-05	6.41234E-05	5.214259584	0.029050209	-1	734	654	666	798	549	391	469	391	567	489
ENSMUSG00000039753	chr5	Fbxl5	-0.646713	2.23513E-05	6.46351E-05	5.001788774	0.02562244	-1	570	567	466	762	556	388	391	313	432	511
ENSMUSG00000059895	chr15	Ptp4a3	-0.6944455	2.24083E-05	6.47867E-05	8.733105796	0.031718981	-1	6746	7087	6799	11666	7378	6658	4978	4294	5544	5185
ENSMUSG00000022999	chr15	Lmbr1l	0.88491094	2.24725E-05	6.49586E-05	2.633382474	0.039992101	1	64	70	57	77	50	149	108	133	98	156
ENSMUSG00000031198	chrX	Fundc2	-0.6369345	2.26072E-05	6.53348E-05	7.057821059	0.026386629	-1	2361	2175	2252	3301	2085	1739	1737	1439	1880	1706
ENSMUSG00000031197	chrX	Vbp1	-0.7592011	2.26355E-05	6.5403E-05	5.048840842	0.036057389	-1	677	587	556	756	525	288	566	309	385	451
ENSMUSG00000059005	chr2	Hnrnpa3	0.70792718	2.27169E-05	6.56245E-05	6.765182119	0.032553045	1	1154	1052	1073	1727	1197	2231	2991	1788	2050	1972
ENSMUSG00000026357	chr1	Rgs18	2.10666971	2.28726E-05	6.60606E-05	0.244895022	0.191384778	1	2	10	6	9	2	50	26	9	39	16
ENSMUSG00000073700	chr4	Klhl21	-0.6605312	2.2939E-05	6.62389E-05	6.844618642	0.028368676	-1	1905	2329	1892	2754	1664	1739	1426	1453	1154	1516
ENSMUSG00000019055	chr4	Plod1	0.64213553	2.2944E-05	6.62396E-05	6.171901897	0.026442574	1	745	769	767	1131	800	1848	1404	1305	1158	1495
ENSMUSG00000009566	chr2	Fpgs	0.70638207	2.29865E-05	6.63485E-05	3.574845157	0.027266139	1	146	114	126	170	114	324	221	193	242	220
ENSMUSG00000100009	chr1	Gm7967	-2.2016084	2.29929E-05	6.63532E-05	-0.381388704	0.176319445	-1	21	19	10	22	9	13	2	1	2	1
ENSMUSG00000086825	chr1	Gm15675	1.34652899	2.30572E-05	6.6525E-05	2.278174066	0.100695918	1	35	52	42	34	32	98	50	94	158	148
ENSMUSG00000023411	chr14	Nfatc4	0.89469179	2.30861E-05	6.65946E-05	3.227309894	0.045103354	1	102	98	98	109	73	315	185	188	136	166
ENSMUSG00000036526	chr5	Card11	1.26860305	2.31597E-05	6.67933E-05	1.248357783	0.071638505	1	31	23	15	16	12	55	49	55	40	59
ENSMUSG00000063694	chr6	Cycs	-0.72874	2.31703E-05	6.68099E-05	8.183709314	0.034952882	-1	5233	5523	5424	7033	3957	2895	3763	3258	3888	3961
ENSMUSG00000020818	chr11	Mfsd11	0.62236763	2.3223E-05	6.69482E-05	4.896152063	0.023520369	1	338	386	291	447	287	743	573	447	560	634
ENSMUSG00000094410	chr1	Zbed6	-0.713392	2.33034E-05	6.7166E-05	7.145939499	0.033295852	-1	2608	2259	2278	3069	2858	1546	1967	1510	1480	2266
ENSMUSG00000074088	chr4	Snrnp40	0.64163497	2.3363E-05	6.7324E-05	4.022765108	0.023330291	1	211	191	151	242	150	363	348	277	302	319
ENSMUSG00000008575	chr4	Nfib	-0.6208775	2.34E-05	6.74168E-05	6.909702589	0.025102717	-1	2130	1939	2093	2664	2031	1590	1551	1593	1346	1637
ENSMUSG00000019373	chr11	Cops3	-0.6722803	2.34489E-05	6.75437E-05	6.033311357	0.029022766	-1	1233	1104	1054	1499	1117	750	886	647	990	833
ENSMUSG00000022443	chr15	Myh9	0.81157265	2.35759E-05	6.78955E-05	6.898538369	0.043042358	1	1056	1032	992	2001	1455	3392	2671	2277	1626	2559
ENSMUSG00000042628	chr12	Zfyve1	-0.7380865	2.36981E-05	6.82335E-05	4.400737508	0.033036891	-1	368	381	348	468	391	226	206	246	234	372
ENSMUSG00000032625	chr6	Thsd7a	-1.3732461	2.37885E-05	6.84795E-05	1.262573261	0.090815961	-1	29	57	48	77	38	29	17	9	21	29
ENSMUSG00000040287	chr10	Stac3	-0.7445872	2.38501E-05	6.86427E-05	8.108367726	0.036583336	-1	6319	4996	4449	5297	4577	2637	3644	3080	3490	3903
ENSMUSG00000042793	chr1	Lgr6	-2.8287377	2.39248E-05	6.88436E-05	1.203866913	0.421405144	-1	17	68	59	100	48	32	8	5	0	1
ENSMUSG00000025404	chr10	R3hdm2	-0.7523962	2.39577E-05	6.89239E-05	6.614267692	0.036937555	-1	1448	1538	1582	2712	1964	1176	1072	1085	1021	1610
ENSMUSG00000073987	chr4	Ggh	0.78409574	2.39844E-05	6.89866E-05	3.427237462	0.034082145	1	133	123	118	121	84	227	244	153	233	244
ENSMUSG00000026443	chr1	Lrrn2	1.42972116	2.4003E-05	6.90258E-05	1.463277915	0.103188498	1	18	20	21	31	16	99	59	75	23	58
ENSMUSG00000029823	chr6	Luc7l2	-0.6200644	2.40993E-05	6.92887E-05	6.472135159	0.024928062	-1	1651	1528	1441	1892	1493	1117	1211	1055	1018	1308
ENSMUSG00000050447	chr2	Lypd6	-1.150241	2.41463E-05	6.94095E-05	1.695987352	0.064718427	-1	69	78	56	78	42	29	28	27	24	51
ENSMUSG00000027219	chr2	Slc28a2	-0.9090825	2.41914E-05	6.95248E-05	3.174832086	0.046961041	-1	135	134	150	302	165	104	118	69	118	98
ENSMUSG00000030811	chr7	Fbxl19	0.9880128	2.42435E-05	6.96601E-05	2.200446297	0.048901903	1	39	43	43	63	36	136	105	75	99	72
ENSMUSG00000022698	chr16	Naa50	-0.6979183	2.43434E-05	6.99192E-05	8.089114487	0.032231951	-1	5495	4120	4454	6533	4654	3066	3745	2598	3483	4081
ENSMUSG00000026610	chr1	Esrrg	-1.7535221	2.43437E-05	6.99192E-05	3.174405158	0.184828671	-1	86	144	186	578	102	32	85	93	72	42
ENSMUSG00000023795	chr17	Pisd-ps2	-1.6200692	2.44261E-05	7.01417E-05	1.775707956	0.146669454	-1	69	87	49	105	67	72	16	16	13	20
ENSMUSG00000037568	chr1	Vash2	1.33745583	2.44484E-05	7.01913E-05	3.16108687	0.107192006	1	125	62	68	48	63	158	170	328	118	241

ENSMUSG00000029636	chr5	Wasf3	-1.7108004	2.46514E-05	7.07596E-05	0.051676726	0.104804082	-1	20	20	15	28	23	4	8	6	2	15
ENSMUSG00000046201	chr17	Scaf8	-0.6392877	2.47861E-05	7.11315E-05	4.437535387	0.024283737	-1	402	331	381	524	332	259	264	230	288	335
ENSMUSG00000032220	chr9	Myo1e	1.03798104	2.48491E-05	7.12978E-05	4.771135129	0.068577223	1	293	243	214	358	230	1021	522	405	271	841
ENSMUSG00000091985	chr4	Gm17354	-1.2636435	2.48945E-05	7.14132E-05	1.441263288	0.076210628	-1	54	59	46	53	60	19	37	27	27	14
ENSMUSG00000066415	chr9	Msl2	-0.6020928	2.49844E-05	7.16563E-05	4.624763558	0.021671985	-1	431	392	400	615	389	379	322	253	288	361
ENSMUSG00000027935	chr3	Rab13	0.81417263	2.50661E-05	7.1876E-05	3.676233783	0.038544814	1	184	154	108	125	108	325	225	272	216	281
ENSMUSG00000032374	chr9	Plod2	0.96619059	2.51015E-05	7.19627E-05	3.48838702	0.055488588	1	136	106	90	138	92	354	305	241	130	179
ENSMUSG00000034863	chr8	Ano8	-0.6240813	2.52057E-05	7.22467E-05	4.343639206	0.022809882	-1	368	358	306	462	338	236	265	274	235	282
ENSMUSG00000092595	chr17	Gm20427	0.64564156	2.53057E-05	7.25184E-05	6.832015406	0.027367244	1	1226	1257	1220	1730	1210	3020	2248	2022	2115	1992
ENSMUSG00000089942	chr7	Pira2	2.3443046	2.53849E-05	7.27306E-05	-0.009998171	0.219349655	1	3	2	6	4	5	45	20	3	16	35
ENSMUSG00000074227	chr7	Spint2	1.0591466	2.55441E-05	7.31716E-05	2.158644477	0.058016795	1	36	34	32	59	49	137	63	94	91	94
ENSMUSG00000071335	chr10	G630090E17Rik	-1.1836763	2.56223E-05	7.33807E-05	1.162931214	0.058679352	-1	39	42	53	42	42	19	24	16	24	23
ENSMUSG00000025537	chr5	Phkg1	-0.7724843	2.56877E-05	7.35528E-05	8.961495806	0.039778764	-1	10357	8996	8125	10553	8750	4399	6560	4809	6703	7468
ENSMUSG00000070544	chr2	Top1	-0.7174036	2.57046E-05	7.3586E-05	5.227063317	0.032721794	-1	679	628	583	934	662	351	592	397	394	571
ENSMUSG00000034422	chr16	Parp14	0.68070715	2.57165E-05	7.36052E-05	4.003646773	0.026904257	1	169	172	167	241	166	351	367	231	272	391
ENSMUSG00000039182	chr13	AW209491	-0.9173124	2.58436E-05	7.39538E-05	3.337207392	0.049016747	-1	221	171	189	221	171	62	133	107	134	123
ENSMUSG00000063334	chr10	Krr1	-0.6216554	2.58503E-05	7.39578E-05	4.750834505	0.02353585	-1	509	440	472	578	424	315	423	303	342	339
ENSMUSG00000019787	chr10	Trdn	-0.6539812	2.59477E-05	7.42212E-05	10.32121153	0.028696002	-1	25990	21402	20862	26251	21862	16937	15279	14401	17340	17144
ENSMUSG00000001783	chr10	Rtcb	0.61560616	2.60474E-05	7.44913E-05	6.113900969	0.024541901	1	840	821	760	939	704	1569	1372	1233	1427	1231
ENSMUSG00000027654	chr2	Fam83d	1.95012651	2.60661E-05	7.45293E-05	0.649161479	0.178212621	1	15	5	12	7	4	14	53	27	28	63
ENSMUSG00000019432	chr17	Ddx39b	0.6472147	2.60866E-05	7.45727E-05	6.590302919	0.027484912	1	1147	962	943	1403	1149	2406	2085	1694	1788	1658
ENSMUSG00000024986	chr19	Hhex	1.32297869	2.62407E-05	7.4998E-05	2.001184641	0.094443931	1	34	44	47	23	13	89	109	69	81	104
ENSMUSG00000008540	chr6	Mgst1	1.15915887	2.62603E-05	7.50385E-05	3.838081528	0.083014249	1	66	215	124	99	132	256	320	290	280	449
ENSMUSG00000003665	chr17	Has1	2.92422988	2.63351E-05	7.5237E-05	0.957051355	0.426875568	1	4	5	6	8	7	199	23	23	16	9
ENSMUSG00000029649	chr5	Pomp	0.69696948	2.64146E-05	7.54487E-05	6.601656752	0.031982791	1	1321	1118	1015	1240	824	2321	2001	1742	2139	1594
ENSMUSG00000060429	chr15	Sntb1	-1.8139354	2.6479E-05	7.56171E-05	2.048980941	0.189023826	-1	56	59	90	180	95	4	27	23	42	47
ENSMUSG00000020457	chr11	Drg1	0.61978989	2.64885E-05	7.56218E-05	5.682576093	0.024629292	1	621	523	565	797	523	1075	1044	891	1116	935
ENSMUSG00000062175	chr2	Tgif2	1.34772973	2.64914E-05	7.56218E-05	1.278555915	0.085324812	1	19	20	20	13	22	48	61	59	29	71
ENSMUSG00000048000	chr1	Gigyf2	-0.6965366	2.65147E-05	7.56727E-05	5.030785768	0.030599575	-1	556	520	527	818	601	321	420	400	346	537
ENSMUSG00000057895	chr9	Zfp105	1.38357096	2.66199E-05	7.59575E-05	0.850129077	0.07904046	1	13	22	8	13	12	38	37	29	37	56
ENSMUSG00000062312	chr11	Erbb2	0.96141599	2.66266E-05	7.59612E-05	3.166132609	0.053983092	1	77	85	81	126	81	285	150	234	119	169
ENSMUSG00000056692	chr17	D17Wsu92e	-0.6394777	2.66456E-05	7.59847E-05	8.153045756	0.027345701	-1	4757	4519	4541	7275	4970	3979	3465	3316	3390	4047
ENSMUSG00000091625	chr6	Lsm5	1.08074222	2.66458E-05	7.59847E-05	2.1117344	0.06037973	1	46	47	32	45	30	101	114	75	113	60
ENSMUSG00000039285	chr9	Azi2	-0.5848371	2.66746E-05	7.60513E-05	5.033889102	0.021078854	-1	585	535	532	793	498	421	431	355	450	476
ENSMUSG00000052276	chr16	Ostn	-1.6439441	2.67646E-05	7.62924E-05	0.425286649	0.112218611	-1	35	27	32	35	11	4	15	10	9	10
ENSMUSG00000022507	chr16	1810013L24Rik	-0.5925199	2.69969E-05	7.6939E-05	5.306360413	0.022105957	-1	687	708	712	812	608	553	555	457	452	559
ENSMUSG00000032841	chr2	Prr5l	1.42376632	2.70536E-05	7.70849E-05	0.503730456	0.073924942	1	17	9	8	7	10	38	33	27	22	33
ENSMUSG00000042524	chr15	Sun2	-0.6268874	2.70762E-05	7.71335E-05	7.16229655	0.026102479	-1	2603	2477	2339	3196	2361	1884	1796	1643	1612	2273
ENSMUSG00000014606	chr11	Slc25a11	-0.6650411	2.7098E-05	7.71798E-05	8.503706279	0.02967687	-1	6086	6712	6459	8815	5293	5741	4013	4155	4527	4552
ENSMUSG00000027534	chr3	Snx16	-0.9391685	2.71256E-05	7.72428E-05	2.405876805	0.045748422	-1	112	102	109	102	80	45	61	55	60	68
ENSMUSG00000019932	chr10	Kera	-1.2049053	2.7137E-05	7.72437E-05	5.463364887	0.094431485	-1	1635	793	917	716	482	698	520	219	351	435
ENSMUSG00000027004	chr2	Frzb	-0.8390473	2.71317E-05	7.72437E-05	5.104780735	0.045351301	-1	457	650	782	944	470	450	305	369	332	561
ENSMUSG00000022758	chr16	P2rx6	-0.7747512	2.72604E-05	7.75791E-05	4.069466174	0.036385952	-1	334	310	262	343	314	142	183	196	218	258
ENSMUSG00000022462	chr15	Slc38a2	-0.7956419	2.7642E-05	7.8633E-05	6.193328513	0.041746769	-1	969	1012	1245	2196	1577	979	898	661	927	913
ENSMUSG00000042104	chr14	Uggt2	-0.8613589	2.76404E-05	7.8633E-05	2.738874233	0.039394656	-1	130	117	119	145	119	63	106	65	71	75
ENSMUSG00000020864	chr11	Ankrd40	-0.6394357	2.76821E-05	7.87311E-05	7.640485503	0.027353318	-1	3371	3180	3314	5011	3370	2450	2672	2508	2331	2744
ENSMUSG00000008301	chr18	Phax	0.63800553	2.80119E-05	7.9653E-05	4.270131602	0.024101967	1	270	212	171	250	214	473	382	340	343	375
ENSMUSG00000030062	chr6	Rpn1	0.70099929	2.85592E-05	8.11928E-05	6.441902198	0.032555173	1	1053	856	890	1221	921	2153	2104	1329	1868	1364
ENSMUSG00000058163	chr11	Gm5431	1.6220639	2.86059E-05	8.13088E-05	0.116408017	0.089049061	1	11	6	9	5	3	22	24	20	18	33
ENSMUSG00000024101	chr17	Wash	0.64761427	2.86326E-05	8.13684E-05	4.511141968	0.025568128	1	292	261	239	314	213	586	363	436	434	446
ENSMUSG00000019944	chr10	Rhobtb1	-0.7522466	2.86833E-05	8.14957E-05	3.997378418	0.034219432	-1	368	351	220	307	235	183	206	159	185	233
ENSMUSG00000021696	chr13	Elovl7	-1.5659673	2.87157E-05	8.15712E-05	0.063328763	0.08035102	-1	18	22	26	26	12	10	6	9	7	6
ENSMUSG00000007987	chr5	Ift22	0.99438643	2.87864E-05	8.17555E-05	2.108467134	0.049826828	1	56	42	43	41	25	96	89	84	96	88
ENSMUSG00000040522	chrX	Tlr8	2.18427709	2.88968E-05	8.20524E-05	0.656534226	0.234216828	1	5	14	8	4	6	30	45	6	39	74
ENSMUSG00000092329	chr8	Gm20388	-0.6249077	2.89059E-05	8.20614E-05	6.001503638	0.025565727	-1	1047	1052	1001	1525	1182	930	905	644	827	819
ENSMUSG00000032870	chr4	Smap2	0.58678899	2.90092E-05	8.23381E-05	4.897493706	0.021228476	1	345	335	300	448	345	713	584	547	463	616
ENSMUSG00000030782	chr7	Tgfb1i1	0.85136646	2.91246E-05	8.26487E-05	3.84827329	0.044045559	1	130	134	145	208	145	448	245	325	180	313
ENSMUSG00000017390	chr11	Aldoc	1.70077769	2.91421E-05	8.26816E-05	-0.013917607	0.090428467	1	4	6	5	3	11	24	22	17	17	27
ENSMUSG00000022747	chr16	St3gal6	-0.992659	2.92308E-05	8.29165E-05	6.282277186	0.065375856	-1	1573	1377	1300	1988	1509	399	907	670	1079	1148
ENSMUSG00000049285	chr5	Mblac1	1.2683058	2.93966E-05	8.33699E-05	0.765240497	0.061348297	1	19	9	15	15	10	36	33	32	40	39
ENSMUSG00000054452	chr10	Aes	-0.6312915	2.947E-05	8.35611E-05	9.313093421	0.027072903	-1	11524	10471	10146	14641	11027	9182	7447	7640	8168	8311
ENSMUSG00000006673	chr9	Qrich1	-0.6003655	2.95458E-05	8.37577E-05	5.136713705	0.02273899	-1	626	578	576	807	575	419	494	397	408	560
ENSMUSG00000040723	chr1	Rcsd1	-0.7224538	2.95601E-05	8.37577E-05	7.066009407	0.035011437	-1	2809	2385	2341	2682	2163	1349	1545	1484	1612	2240
ENSMUSG00000075225	chr10	Ccdc162	1.5347272	2.95633E-05	8.37577E-05	0.318498679	0.088441836	1	10	11	8	8	5	25	23	38	18	30
ENSMUSG00000085322	chr2	Gm14261	-1.2545674	2.95615E-05	8.37577E-05	1.540740214	0.078788324	-1	46	57	68	83	42	14	30	21	32	37

ENSMUSG00000037887	chr7	Dusp8	-1.0598571	2.9578E-05	8.37824E-05	5.131372614	0.073589703	-1	484	447	711	981	902	649	440	288	271	234
ENSMUSG00000033184	chr18	Tmed7	-0.6298614	2.96292E-05	8.39105E-05	5.023978512	0.025069575	-1	585	531	473	805	567	420	475	298	400	496
ENSMUSG00000022707	chr16	Gbe1	-0.9239003	2.97127E-05	8.41297E-05	5.564744156	0.056222608	-1	818	945	929	1383	601	338	558	400	741	601
ENSMUSG00000039601	chr17	Rcan2	-0.9841406	2.97238E-05	8.41441E-05	5.056236635	0.063178563	-1	426	619	658	1188	475	397	295	468	401	235
ENSMUSG00000006818	chr17	Sod2	-0.6541994	2.9862E-05	8.45184E-05	7.836818566	0.028915586	-1	3513	4080	3933	6051	3474	3129	2932	2820	2795	2807
ENSMUSG00000024145	chr17	Pigf	1.10582359	2.98702E-05	8.45245E-05	1.335989127	0.053837441	1	17	24	15	37	21	58	64	43	49	53
ENSMUSG00000050910	chr11	Cdr2l	0.87368443	2.99194E-05	8.46465E-05	2.915017001	0.042182331	1	79	81	71	81	75	224	170	153	106	135
ENSMUSG00000027792	chr3	Bche	-0.9559447	3.00382E-05	8.49655E-05	2.924351959	0.052065673	-1	168	138	115	203	120	48	85	94	92	91
ENSMUSG00000034621	chr11	Gpatch8	-0.6752433	3.00461E-05	8.49704E-05	4.952943058	0.028991976	-1	558	532	453	667	615	346	403	386	306	498
ENSMUSG00000062510	chr1	Nsl1	2.07109905	3.01022E-05	8.5112E-05	0.389683134	0.196261815	1	8	8	13	1	2	27	60	23	19	26
ENSMUSG00000074743	chr2	Thbd	-0.6745174	3.01249E-05	8.51589E-05	5.037825701	0.029097338	-1	607	492	526	701	667	526	380	304	475	384
ENSMUSG00000032745	chr13	Gpbp1	-0.6051184	3.01466E-05	8.5203E-05	5.727852401	0.023793141	-1	968	901	806	1252	860	685	739	605	742	648
ENSMUSG00000057329	chr1	Bcl2	-0.8600958	3.03363E-05	8.57219E-05	2.694186026	0.03975549	-1	142	110	110	146	105	96	92	49	69	66
ENSMUSG00000026234	chr1	Ncl	0.66201154	3.04079E-05	8.58893E-05	7.76763033	0.029658394	1	2748	2410	2102	3185	2196	4765	5356	3737	4277	3692
ENSMUSG00000102101	chr16	2310061J03Rik	1.22190098	3.04064E-05	8.58893E-05	1.251297826	0.068498989	1	18	19	14	31	19	81	34	45	49	49
ENSMUSG00000040537	chr5	Adam22	-1.2364083	3.04191E-05	8.59037E-05	1.140865738	0.06883079	-1	40	46	31	67	38	19	19	15	15	34
ENSMUSG00000028882	chr4	Ppp1r8	0.58714473	3.05017E-05	8.61196E-05	4.41131998	0.020555963	1	251	238	228	342	210	480	430	384	398	384
ENSMUSG00000013076	chr9	Amotl1	-0.8240595	3.05908E-05	8.63538E-05	8.359331612	0.045993785	-1	5057	4623	4968	9566	7431	3434	3313	3970	3755	4783
ENSMUSG00000040270	chr4	Bach2	-1.0238306	3.06225E-05	8.64257E-05	1.721509625	0.050021381	-1	69	49	62	83	57	49	25	29	37	32
ENSMUSG00000097145	chr5	9230114K14Rik	-1.4602441	3.07108E-05	8.66574E-05	0.398056009	0.079092052	-1	29	19	31	26	26	6	14	8	13	11
ENSMUSG00000046295	chr8	Ankle1	2.33637792	3.07379E-05	8.67163E-05	-0.147949941	0.211345409	1	5	2	9	2	0	33	31	13	20	8
ENSMUSG00000003779	chr18	Kif20a	1.29606546	3.07903E-05	8.68466E-05	2.4072647	0.097046534	1	59	49	38	37	37	140	203	105	97	56
ENSMUSG00000032118	chr9	Fez1	0.98690682	3.07985E-05	8.68521E-05	2.232362803	0.050588924	1	54	38	37	59	41	151	80	89	96	82
ENSMUSG00000038564	chr5	Ift172	-0.6477026	3.08436E-05	8.69619E-05	4.303989507	0.025388751	-1	315	322	282	498	383	247	282	215	235	272
ENSMUSG00000047181	chr11	Samd14	1.03607655	3.08664E-05	8.70087E-05	1.966274636	0.052842828	1	37	27	36	41	42	102	81	88	54	90
ENSMUSG00000081094	chr8	Rpl19-ps11	0.6105559	3.09227E-05	8.71498E-05	4.318775856	0.022173282	1	250	212	227	271	208	483	406	327	395	352
ENSMUSG00000074513	chr3	Arfip1	0.59885275	3.0962E-05	8.72428E-05	4.394515808	0.0214908	1	245	242	222	335	204	456	478	359	368	401
ENSMUSG00000032199	chr9	Polr2m	-0.6410007	3.10511E-05	8.74763E-05	7.488072997	0.027800472	-1	3170	2926	2865	4517	2963	2092	2438	2127	2129	2645
ENSMUSG00000038393	chr3	Txnip	-0.9498839	3.11076E-05	8.76178E-05	9.173776327	0.061073513	-1	13047	13363	12001	7742	9282	5794	7157	6951	4256	7975
ENSMUSG00000023942	chr17	Slc29a1	0.66448538	3.1173E-05	8.77842E-05	6.154821403	0.029297194	1	836	863	777	861	737	1839	1348	1362	1065	1553
ENSMUSG00000020455	chr11	Trim11	0.64960605	3.12782E-05	8.80628E-05	3.6926484	0.023541294	1	141	135	138	185	144	270	222	246	257	279
ENSMUSG00000025786	chr9	Zdhhc3	-0.646478	3.12895E-05	8.80771E-05	6.180758105	0.027767648	-1	1289	1162	1070	1730	1370	905	968	726	996	1019
ENSMUSG00000051615	chr14	Rap2a	0.68680777	3.13173E-05	8.81374E-05	4.064339111	0.028333389	1	175	183	178	254	163	404	374	226	363	315
ENSMUSG00000042426	chr13	Dhx29	-0.6752475	3.14305E-05	8.84381E-05	4.258227102	0.027792566	-1	378	265	288	459	364	215	271	200	248	261
ENSMUSG00000061838	chr6	Suclg2	-0.6260466	3.14575E-05	8.84963E-05	5.699415423	0.025643524	-1	833	909	898	1343	755	686	727	572	694	650
ENSMUSG00000036078	chr4	Sigmar1	0.80899133	3.14959E-05	8.85867E-05	3.737473747	0.039276297	1	127	143	148	177	120	413	315	171	261	231
ENSMUSG00000053877	chr7	Srcap	-0.6455363	3.15885E-05	8.88291E-05	5.839538025	0.027492135	-1	873	915	971	1422	1043	878	710	671	560	842
ENSMUSG00000035279	chr7	Ssc5d	0.8313075	3.17015E-05	8.9129E-05	5.991266583	0.046113744	1	782	610	584	762	660	1815	1131	1385	716	1651
ENSMUSG00000027088	chr2	Phospho2	-0.6543464	3.18973E-05	8.96614E-05	4.074443554	0.025458271	-1	349	281	257	362	279	185	217	193	225	238
ENSMUSG00000038876	chr10	Rnf146	-0.6013124	3.19543E-05	8.98037E-05	5.258084478	0.023182272	-1	700	641	646	887	572	534	457	469	416	605
ENSMUSG00000025198	chr19	Erlin1	0.89891593	3.20246E-05	8.9983E-05	3.363841117	0.048499589	1	107	112	74	149	92	315	217	136	258	163
ENSMUSG00000028680	chr4	Plk3	1.78777062	3.21389E-05	9.0286E-05	2.197805705	0.187902969	1	24	42	33	24	22	264	145	48	84	38
ENSMUSG00000035674	chr7	Ndufa3	0.65859796	3.21989E-05	9.04364E-05	7.392328009	0.029451703	1	1799	1974	1734	2628	1641	4291	3055	3124	3450	2892
ENSMUSG00000021357	chr13	Exoc2	-0.6387394	3.23533E-05	9.08519E-05	4.225812507	0.024625252	-1	342	297	311	390	344	235	260	176	254	265
ENSMUSG00000039163	chr9	Cmc1	0.68423882	3.23992E-05	9.09624E-05	3.597561594	0.026567061	1	150	138	109	170	120	298	222	236	244	205
ENSMUSG00000023994	chr17	Nfya	0.73309282	3.25808E-05	9.14357E-05	3.700820722	0.031457234	1	127	135	118	182	159	365	279	184	241	257
ENSMUSG00000097207	chr5	6030443J06Rik	-2.1106648	3.2575E-05	9.14357E-05	-0.028488878	0.192035724	-1	21	28	19	14	22	1	0	5	12	8
ENSMUSG00000053617	chr19	Sh3pxd2a	-0.6932232	3.27759E-05	9.19648E-05	6.607921494	0.032415298	-1	1746	1620	1619	2123	1849	1122	1136	1281	961	1568
ENSMUSG00000023393	chr2	Slc17a9	1.95922063	3.28775E-05	9.22312E-05	-0.037356624	0.151643507	1	10	2	3	5	5	46	14	15	21	14
ENSMUSG00000026955	chr2	Sapcd2	1.88787191	3.30129E-05	9.25806E-05	-0.044689228	0.137505073	1	9	5	5	5	2	25	33	27	11	11
ENSMUSG00000085241	chr4	Snhg3	1.05669227	3.30153E-05	9.25806E-05	2.621090325	0.063910042	1	71	67	52	65	36	139	169	71	163	124
ENSMUSG00000028603	chr4	Scp2	-0.6132732	3.31268E-05	9.28746E-05	6.814590063	0.025406335	-1	2046	2077	1811	2603	1654	1474	1530	1220	1488	1552
ENSMUSG00000063108	chr9	Zfp26	-0.8169869	3.31672E-05	9.29693E-05	3.11242048	0.038016405	-1	178	155	139	201	142	93	125	61	105	123
ENSMUSG00000025793	chr11	Hgs	0.61757712	3.32837E-05	9.32772E-05	4.639820519	0.023744716	1	295	246	242	405	283	618	448	481	418	495
ENSMUSG00000070576	chr5	Mn1	-0.8926165	3.33237E-05	9.33706E-05	5.576720367	0.053228778	-1	585	785	768	1435	1090	818	535	516	343	542
ENSMUSG00000022098	chr14	Bmp1	0.71812665	3.33392E-05	9.33952E-05	5.690931621	0.034201151	1	613	589	536	565	571	1345	989	1123	701	1098
ENSMUSG00000031095	chrX	Cul4b	-0.7161441	3.3359E-05	9.34319E-05	3.571806341	0.029527036	-1	219	220	178	302	183	130	159	108	161	170
ENSMUSG00000021193	chr13	Pitrm1	-0.6473088	3.34856E-05	9.37678E-05	5.186196713	0.02712812	-1	589	641	620	862	602	415	486	378	560	462
ENSMUSG00000011263	chr7	Exoc3l2	1.38767684	3.36604E-05	9.42385E-05	0.479049384	0.071029273	1	8	5	8	18	13	35	34	26	25	29
ENSMUSG00000098923	chr1	Tmem185b	0.79920791	3.36932E-05	9.43113E-05	3.122146232	0.035869969	1	79	93	84	125	87	241	195	139	125	199
ENSMUSG00000083061	chr11	Gm12191	1.0712713	3.37936E-05	9.45733E-05	1.932762712	0.058406114	1	44	44	26	30	31	103	83	64	92	66
ENSMUSG00000031851	chr8	Ntpcr	0.68125807	3.39807E-05	9.50778E-05	3.873926851	0.027297056	1	205	146	165	160	149	351	300	273	265	275
ENSMUSG00000060657	chr16	Marf1	-0.5620041	3.41998E-05	9.56719E-05	5.024577873	0.019938817	-1	519	563	539	726	540	499	399	383	392	473
ENSMUSG00000032777	chr7	Gtf3c1	-0.6664765	3.42746E-05	9.58618E-05	5.631624975	0.029430357	-1	841	815	721	1129	1021	594	617	629	537	740
ENSMUSG00000025507	chr7	Pidd1	1.48988092	3.42862E-05	9.58751E-05	0.366298774	0.082079352	1	8	10	10	13	4	28	39	18	31	23

ENSMUSG00000033444	chr10	Specc1l	-0.6011726	3.43795E-05	9.61167E-05	5.747841798	0.023875067	-1	880	897	834	1232	986	838	647	661	609	735
ENSMUSG00000029003	chr4	Mad2l2	0.75477626	3.44584E-05	9.6318E-05	3.118155462	0.031336808	1	110	89	76	118	83	222	150	146	191	170
ENSMUSG00000036437	chr8	Npy1r	-1.6359339	3.45506E-05	9.65567E-05	1.02788459	0.138430983	-1	22	39	33	76	51	31	14	4	13	16
ENSMUSG00000006457	chr19	Actn3	-0.7765496	3.47141E-05	9.69942E-05	12.70452272	0.041661014	-1	141314	105517	90049	146181	144895	68872	84786	66372	75959	106013
ENSMUSG00000038515	chr8	Grtp1	-1.1335002	3.49907E-05	9.77475E-05	1.925102963	0.068117716	-1	51	94	64	110	62	58	28	39	34	30
ENSMUSG00000027603	chr2	Ggt7	1.6543333	3.50111E-05	9.77848E-05	0.121193256	0.098602825	1	10	7	5	8	4	13	23	21	32	28
ENSMUSG00000026315	chr1	Serpinb8	1.2617296	3.50762E-05	9.79471E-05	1.961821726	0.089236221	1	27	17	46	57	20	120	100	59	89	68
ENSMUSG00000021510	chr13	A530054K11Rik	-1.1885201	3.50966E-05	9.79845E-05	2.188790461	0.080720071	-1	85	98	89	105	83	92	29	26	41	38
ENSMUSG00000022358	chr15	Fbxo32	-0.9424706	3.52304E-05	9.83384E-05	5.985283719	0.060036519	-1	1006	1622	1020	1587	990	590	453	656	675	1154
ENSMUSG00000018378	chr11	Cuedc1	-0.6265499	3.53824E-05	9.87429E-05	6.8902686	0.026763321	-1	1848	2120	1853	2860	2092	1792	1317	1443	1445	1623
ENSMUSG00000047554	chr7	Tmem41b	-0.6738211	3.54306E-05	9.88578E-05	4.015711527	0.027515984	-1	295	271	265	358	284	194	248	142	216	213
ENSMUSG00000031370	chrX	Zrsr2	0.64320807	3.54891E-05	9.9001E-05	3.707632669	0.023673065	1	163	131	125	207	133	324	258	233	232	246
ENSMUSG00000036698	chr15	Ago2	-0.7791335	3.55891E-05	9.92604E-05	6.556466236	0.041360929	-1	1618	1337	1465	2453	2038	1115	1205	1213	740	1383
ENSMUSG00000030447	chr7	Cyfip1	0.69052736	3.57833E-05	9.97819E-05	5.189198203	0.031338054	1	386	390	346	564	401	824	942	472	774	677
ENSMUSG00000085795	chr8	Zfp703	0.96787768	3.58064E-05	9.98264E-05	5.049928354	0.062408391	1	197	349	330	435	350	834	606	1012	403	692
ENSMUSG00000065228	chr1	Gm25789	2.17073471	3.58923E-05	0.000100046	-0.125128157	0.201593166	1	8	3	1	7	2	40	24	14	22	5
ENSMUSG00000029312	chr5	Klhl8	-0.6964857	3.59564E-05	0.000100205	5.093991407	0.031803987	-1	711	577	463	728	660	338	451	361	425	542
ENSMUSG00000027540	chr2	Ptpn1	0.72211119	3.61778E-05	0.000100802	4.734286667	0.033705536	1	276	269	274	377	296	822	617	366	460	467
ENSMUSG00000028691	chr4	Prdx1	0.80791551	3.62208E-05	0.000100901	8.105402742	0.045022104	1	3284	3186	2792	3494	2185	7921	6732	3723	6285	4221
ENSMUSG00000060261	chr5	Gtf2i	-0.6935465	3.64633E-05	0.000101557	6.840826323	0.032939953	-1	1998	1969	1811	2760	2059	1247	1469	1360	1124	1947
ENSMUSG00000029817	chr6	Tra2a	0.74388258	3.65246E-05	0.000101707	4.518594122	0.035618554	1	234	226	225	360	236	625	551	363	490	314
ENSMUSG00000041372	chr6	B4galnt3	-1.6642288	3.6571E-05	0.000101816	0.217320817	0.116624733	-1	13	22	32	31	21	10	3	4	11	13
ENSMUSG00000020441	chr11	2310033P09Rik	0.95014214	3.67175E-05	0.000102204	2.421256809	0.048875032	1	57	46	40	63	59	169	103	101	104	88
ENSMUSG00000022387	chr15	Brd1	-0.5932938	3.7132E-05	0.000103337	4.782840727	0.02231329	-1	439	464	480	609	466	385	410	284	308	407
ENSMUSG00000020935	chr11	Dcakd	0.79617942	3.71941E-05	0.000103489	4.654447172	0.041465236	1	208	232	287	391	255	719	406	603	367	508
ENSMUSG00000068205	chr2	Macrod2	-0.7568351	3.73528E-05	0.00010391	3.415909646	0.033489377	-1	240	163	181	245	165	152	120	84	142	147
ENSMUSG00000022913	chr16	Psmg1	0.78493611	3.73602E-05	0.00010391	3.316327964	0.035887191	1	130	85	103	130	91	240	206	196	224	147
ENSMUSG00000031629	chr8	Cenpu	2.26868578	3.74355E-05	0.000104099	-0.667595459	0.155925777	1	5	0	6	0	1	16	18	10	16	7
ENSMUSG00000054611	chr19	Kdm2a	-0.5996289	3.75405E-05	0.00010437	5.72161075	0.023970964	-1	810	899	865	1242	928	793	756	620	598	663
ENSMUSG00000030744	chr7	Rps3	0.67208736	3.75743E-05	0.000104443	8.551637076	0.031419596	1	4728	4200	3745	4997	3890	10080	8019	6357	7247	6161
ENSMUSG00000028830	chr4	AU040320	-0.5914757	3.75901E-05	0.000104466	5.317754914	0.022912653	-1	773	631	614	810	728	604	489	444	497	566
ENSMUSG00000031148	chrX	Gpkow	-0.7156578	3.76002E-05	0.000104473	4.042579388	0.031714152	-1	286	268	276	459	249	172	237	153	221	228
ENSMUSG00000053560	chr8	Ier2	1.08178287	3.80263E-05	0.000105636	4.053507553	0.076070775	1	159	160	169	172	123	646	539	208	239	237
ENSMUSG00000015247	chr4	Nipsnap3b	1.06134533	3.80606E-05	0.00010571	2.158278769	0.060399655	1	43	38	47	38	40	109	114	52	114	91
ENSMUSG00000022721	chr16	Trmt2a	0.65329543	3.80858E-05	0.000105759	3.839731235	0.025118453	1	189	155	141	194	144	360	310	235	271	247
ENSMUSG00000022558	chr15	Mroh1	0.60635812	3.83171E-05	0.000106381	4.310485231	0.022534061	1	210	221	195	331	218	415	397	312	403	420
ENSMUSG00000076240	chr5	Mir702	1.10715716	3.84212E-05	0.000106648	1.714092314	0.061775528	1	28	24	30	31	34	98	87	65	45	58
ENSMUSG00000092074	chr17	Dynlt1a	1.60305184	3.87071E-05	0.000107421	0.619226254	0.116600724	1	12	9	6	16	9	13	46	32	41	38
ENSMUSG00000048486	chr2	Fitm2	-0.7173563	3.87255E-05	0.00010745	6.717449534	0.035422119	-1	1516	1847	1834	2910	1746	1056	1287	1351	1350	1396
ENSMUSG00000009030	chr2	Pdcl	-0.7622099	3.8746E-05	0.000107486	3.734519808	0.035506812	-1	249	235	224	325	212	115	173	140	144	226
ENSMUSG00000026029	chr1	Casp8	0.99179851	3.89474E-05	0.000108023	3.070053177	0.059687768	1	98	104	86	78	43	196	232	111	175	190
ENSMUSG00000078713	chr4	Tomm5	0.66562871	3.89867E-05	0.000108111	5.280414348	0.029389901	1	476	457	455	499	340	981	794	745	771	592
ENSMUSG00000036513	chr3	Commd2	0.75473883	3.91424E-05	0.000108521	3.726493029	0.034629111	1	153	134	157	162	118	328	277	243	306	188
ENSMUSG00000033952	chr1	Aspm	1.71335249	3.93456E-05	0.000109063	1.295428952	0.161451376	1	20	19	14	11	15	41	106	52	69	19
ENSMUSG00000020056	chr10	Ccdc53	0.61965454	3.96514E-05	0.000109889	4.592464168	0.024275202	1	316	296	255	314	227	557	470	422	510	415
ENSMUSG00000089704	chr8	Galnt2	-0.6113152	3.99704E-05	0.000110751	5.983692643	0.025345483	-1	1024	1040	990	1501	1159	928	891	644	825	809
ENSMUSG00000047910	chr18	Pcdhb16	-1.3334325	3.99784E-05	0.000110751	0.764424253	0.074310906	-1	21	44	30	46	29	11	18	15	14	15
ENSMUSG00000061479	chr7	Snrpa	0.62887028	4.00087E-05	0.000110813	4.981260849	0.025782354	1	367	299	298	474	409	775	689	537	586	546
ENSMUSG00000036333	chr12	Kidins220	-0.5985286	4.00806E-05	0.00011099	5.365835546	0.023703027	-1	755	745	672	872	648	493	561	482	493	641
ENSMUSG00000014294	chr18	Ndufa2	0.67380637	4.01389E-05	0.000111063	7.582111697	0.031647454	1	2477	2188	2059	2588	1705	4790	3243	3432	4268	3508
ENSMUSG00000033350	chr9	Chst2	0.97813352	4.01302E-05	0.000111063	2.053061212	0.04928901	1	36	36	38	55	37	129	97	72	63	78
ENSMUSG00000038525	chr5	Armc10	0.74621847	4.01226E-05	0.000111063	3.122011358	0.03101671	1	109	104	77	103	83	190	214	140	160	176
ENSMUSG00000044921	chr10	Rassf9	-1.6593216	4.01388E-05	0.000111063	-0.205054669	0.079189101	-1	18	15	13	25	15	6	2	8	6	7
ENSMUSG00000079323	chr9	Gm20661	1.31374526	4.01562E-05	0.000111089	0.809646984	0.072591624	1	13	14	11	19	12	60	32	33	23	42
ENSMUSG00000030839	chr7	Sergef	1.00360611	4.021E-05	0.000111216	2.151535468	0.05368007	1	48	34	35	59	39	123	109	87	92	59
ENSMUSG00000103316	chr11	Coil	-1.184641	4.02684E-05	0.000111356	1.331195744	0.067494844	-1	47	53	42	54	52	15	25	18	35	26
ENSMUSG00000003437	chr7	Paf1	0.58914813	4.02948E-05	0.000111407	5.050090993	0.022545803	1	384	341	329	524	397	746	617	668	535	674
ENSMUSG00000034192	chr6	Lsm3	0.673764	4.05164E-05	0.000111997	4.227471536	0.02840242	1	196	246	188	255	183	494	418	304	360	302
ENSMUSG00000049489	chr11	Fam58b	0.66624776	4.05295E-05	0.000112011	3.607480579	0.025588717	1	148	132	129	153	130	299	222	226	251	210
ENSMUSG00000026383	chr1	Epb4.1l5	-1.059439	4.06911E-05	0.000112426	1.455355567	0.05164014	-1	50	53	49	64	49	18	30	29	31	30
ENSMUSG00000049600	chr7	Zbtb45	0.82292562	4.06956E-05	0.000112426	2.786447422	0.037569346	1	68	62	57	105	75	150	126	157	118	153
ENSMUSG00000013701	chr14	Timm23	-0.6517762	4.07406E-05	0.000112528	6.614786454	0.029327067	-1	1776	1623	1687	2320	1555	1030	1390	1078	1311	1388
ENSMUSG00000042607	chr6	Asb4	-0.9159086	4.09607E-05	0.000113113	3.244596146	0.051126101	-1	165	138	148	265	205	66	125	120	103	110
ENSMUSG00000041035	chr19	Dpcd	0.65797226	4.11174E-05	0.000113524	3.662902893	0.025342191	1	156	122	119	201	133	290	252	251	240	219
ENSMUSG00000015943	chr3	Bola1	0.61900097	4.13219E-05	0.000114066	3.801951387	0.022231434	1	164	166	148	193	141	300	282	238	292	254

ENSMUSG00000037499	chr1	Nenf	0.61298872	4.13473E-05	0.000114113	5.585126886	0.025231707	1	581	550	507	699	492	1228	841	874	966	829
ENSMUSG00000078566	chr7	Bnip3	-0.6251944	4.16221E-05	0.000114849	6.671816324	0.02705203	-1	1797	1839	1591	2570	1509	1339	1325	1040	1344	1508
ENSMUSG00000022893	chr16	Adamts1	-0.8978692	4.16385E-05	0.000114872	5.111266592	0.054781255	-1	510	641	646	1001	582	673	433	205	380	313
ENSMUSG00000086329	chr2	Gm14233	1.06342576	4.1681E-05	0.000114966	1.837806251	0.058388465	1	39	34	35	35	22	105	71	58	88	59
ENSMUSG00000028907	chr4	Utp11l	0.64336436	4.17049E-05	0.000115009	4.247759279	0.025831916	1	225	206	193	277	200	447	371	363	406	288
ENSMUSG00000022607	chr15	Ptk2	-0.5711984	4.2061E-05	0.000115969	4.884364002	0.020953841	-1	513	447	497	671	501	396	411	374	325	428
ENSMUSG00000041084	chr3	Ostc	0.6909927	4.21424E-05	0.00011617	5.15392533	0.031923308	1	447	372	388	479	338	919	790	520	820	545
ENSMUSG00000035299	chrX	Mid1	-1.6898643	4.21925E-05	0.000116285	1.197766445	0.158933851	-1	54	47	24	42	79	6	14	15	16	33
ENSMUSG00000029674	chr5	Limk1	0.8508487	4.22196E-05	0.000116337	2.40349912	0.037087419	1	48	60	51	58	55	120	107	88	115	112
ENSMUSG00000034109	chr3	Golim4	-0.6724562	4.25633E-05	0.000117261	4.446107586	0.029054954	-1	390	327	356	533	392	235	290	209	272	361
ENSMUSG00000031910	chr8	Has3	-1.2837156	4.26052E-05	0.000117353	2.100166988	0.095328318	-1	95	102	91	87	64	21	31	65	30	48
ENSMUSG00000000295	chr10	Hddc2	0.74978554	4.26386E-05	0.000117422	3.305805424	0.032829444	1	115	126	101	120	79	200	176	213	208	196
ENSMUSG00000047412	chr9	Zbtb44	-0.602615	4.27093E-05	0.000117594	5.020932973	0.023774788	-1	531	529	518	875	495	418	469	388	353	473
ENSMUSG00000028465	chr4	Tln1	0.72439401	4.27313E-05	0.000117631	7.298957509	0.03676734	1	1498	1365	1454	2725	1920	4055	3395	2988	2392	3284
ENSMUSG00000037029	chr7	Zfp146	-0.7396306	4.3063E-05	0.000118521	4.080828325	0.034818439	-1	259	321	300	383	302	146	247	179	219	232
ENSMUSG00000061613	chr17	U2af1	0.62330112	4.31676E-05	0.000118785	5.054062859	0.025696612	1	403	313	339	563	347	836	738	576	595	548
ENSMUSG00000028318	chr4	Polr1e	0.97381096	4.33268E-05	0.0001192	1.998036012	0.049055735	1	44	39	26	51	35	96	90	62	99	71
ENSMUSG00000070803	chr4	Cited4	1.2188596	4.33599E-05	0.000119268	4.990245894	0.100959445	1	425	258	238	196	276	288	670	937	660	993
ENSMUSG00000044229	chr9	Nxpe4	2.33002513	4.33982E-05	0.000119349	0.836802467	0.289753847	1	9	4	15	8	4	4	42	46	62	66
ENSMUSG00000044934	chr13	Zfp367	-0.8948188	4.34076E-05	0.000119352	3.938768175	0.051832057	-1	295	242	270	404	276	95	260	152	169	188
ENSMUSG00000021950	chr14	Anxa8	1.88059865	4.34937E-05	0.000119565	1.222649713	0.197984875	1	32	5	11	12	9	107	34	39	26	81
ENSMUSG00000031805	chr8	Jak3	1.02950246	4.35077E-05	0.00011958	2.862718579	0.064092393	1	65	79	66	83	56	288	114	114	111	170
ENSMUSG00000062908	chr3	Acadm	-0.7463511	4.36068E-05	0.000119829	7.87163426	0.039243293	-1	3129	4530	4211	7025	3338	2984	2530	2701	3076	2948
ENSMUSG00000014329	chr10	Bicc1	0.68595582	4.38258E-05	0.000120407	4.682795862	0.030763298	1	303	268	304	305	269	729	512	480	355	521
ENSMUSG00000066068	chr2	Gm13611	1.23283977	4.3917E-05	0.000120634	1.551047383	0.078275802	1	23	28	27	21	23	116	57	51	48	52
ENSMUSG00000021714	chr13	Cenpk	1.56950037	4.43782E-05	0.000121876	0.142518563	0.089430073	1	7	10	6	9	4	33	32	14	23	17
ENSMUSG00000019528	chr3	Gyg	-0.6260292	4.46075E-05	0.000122482	8.079644469	0.027744127	-1	5034	4774	4194	6402	4220	3278	3491	3053	3685	3821
ENSMUSG00000026584	chr1	Scyl3	-0.8924689	4.47567E-05	0.000122868	2.569290271	0.045153673	-1	124	116	106	119	97	59	68	47	63	97
ENSMUSG00000036885	chr3	Arhgef26	-1.2894553	4.49619E-05	0.000123407	0.944912712	0.077233601	-1	42	33	51	45	21	23	17	18	12	16
ENSMUSG00000039942	chr15	Ptger4	1.08438442	4.50458E-05	0.000123613	1.743734939	0.05892634	1	31	42	30	24	24	97	71	60	66	64
ENSMUSG00000028600	chr4	Podn	0.89245295	4.52277E-05	0.000124088	4.203225874	0.052677721	1	202	171	170	212	195	734	357	320	284	280
ENSMUSG00000027596	chr2	a	-0.9907395	4.53854E-05	0.000124496	1.74624113	0.048216397	-1	58	51	64	87	63	32	33	28	39	45
ENSMUSG00000098917	chr8	Mir7654	-1.2205678	4.54789E-05	0.000124728	0.762351524	0.058983826	-1	27	29	28	52	31	13	17	15	17	15
ENSMUSG00000001098	chr5	Kctd10	0.66593881	4.5514E-05	0.0001248	5.003477809	0.02959024	1	303	382	337	465	355	951	637	554	530	559
ENSMUSG00000037936	chr5	Scarb1	0.6583164	4.55366E-05	0.000124837	5.365893129	0.029397165	1	465	471	450	647	363	1026	727	752	614	1020
ENSMUSG00000023868	chr17	Pde10a	-1.0217405	4.56179E-05	0.000125035	2.090639371	0.056787276	-1	86	49	73	137	77	40	45	38	46	54
ENSMUSG00000020067	chr10	Mypn	-0.7234519	4.56311E-05	0.000125047	8.470235441	0.037176729	-1	6434	5433	5045	8859	7349	3971	4380	3999	3713	5789
ENSMUSG00000007411	chr12	Mark3	-0.6042398	4.57605E-05	0.000125377	5.596159543	0.024805448	-1	950	835	740	1014	802	581	683	516	670	674
ENSMUSG00000069899	chr11	Gm12166	1.55263442	4.5857E-05	0.000125617	0.850559162	0.113909695	1	7	21	12	6	15	46	52	28	47	30
ENSMUSG00000091780	chr15	Sco2	0.68714902	4.59344E-05	0.000125804	3.701846541	0.028560274	1	132	151	123	209	127	303	251	291	211	240
ENSMUSG00000031657	chr8	Heatr3	-0.6099556	4.63139E-05	0.000126819	5.300417979	0.025008009	-1	736	647	609	924	644	491	551	413	585	496
ENSMUSG00000020409	chr11	Slu7	-0.6200171	4.66464E-05	0.000127704	5.017109422	0.025573467	-1	638	592	471	717	508	411	405	306	461	498
ENSMUSG00000008136	chr1	Fhl2	1.438816	4.66628E-05	0.000127724	2.129256351	0.128215266	1	28	20	20	88	23	183	73	94	70	91
ENSMUSG00000021311	chr13	Mtr	-0.7914546	4.6767E-05	0.000127984	3.770787535	0.039602768	-1	242	251	192	334	266	107	165	149	176	207
ENSMUSG00000055116	chr7	Arntl	-1.3551354	4.73009E-05	0.00012942	2.84432645	0.117363703	-1	105	99	91	261	216	40	42	70	57	113
ENSMUSG00000058594	chr2	Fbxo18	-0.5815326	4.76705E-05	0.000130406	5.283023714	0.022702394	-1	675	671	695	790	626	509	549	407	511	568
ENSMUSG00000021785	chr14	Ngly1	-0.8196789	4.76944E-05	0.000130446	5.283030473	0.046328331	-1	707	699	645	957	702	281	490	343	507	664
ENSMUSG00000026134	chr1	Prim2	1.28338186	4.77185E-05	0.000130481	1.528612988	0.087421201	1	27	26	22	23	20	67	96	32	78	46
ENSMUSG00000030410	chr7	Dmwd	0.71850177	4.77261E-05	0.000130481	4.787361074	0.034662596	1	301	266	271	403	313	461	607	713	453	528
ENSMUSG00000034187	chr11	Nsf	0.69799026	4.77466E-05	0.000130512	4.368838239	0.031758152	1	234	200	193	313	234	506	573	317	340	355
ENSMUSG00000051705	chr9	Senp8	-0.8284466	4.79298E-05	0.000130987	2.845612277	0.03952105	-1	131	116	159	144	120	75	82	75	77	107
ENSMUSG00000019773	chr10	Fbxo5	1.36853915	4.80046E-05	0.000131166	0.9702997	0.089482736	1	16	12	14	16	17	60	56	37	42	20
ENSMUSG00000068794	chr6	Col28a1	-1.7866511	4.81338E-05	0.000131467	-0.418269157	0.103020049	-1	13	15	16	23	7	8	7	2	2	4
ENSMUSG00000098465	chr8	Mir1668	0.9859816	4.81249E-05	0.000131467	2.518216438	0.057045758	1	44	43	64	90	42	128	145	138	82	113
ENSMUSG00000017765	chr8	Slc12a4	0.69302348	4.82178E-05	0.000131642	4.385356945	0.031353864	1	209	215	222	333	213	633	423	372	332	356
ENSMUSG00000030255	chr6	Sspn	-0.6670078	4.82261E-05	0.000131642	6.841401471	0.031431264	-1	1914	2047	1968	2774	1829	1148	1716	1475	1372	1472
ENSMUSG00000051396	chr2	Hspa14	0.63611946	4.82142E-05	0.000131642	4.110416671	0.025166809	1	188	215	201	219	172	392	387	290	342	295
ENSMUSG00000031504	chr8	Rab20	1.36879008	4.82696E-05	0.000131735	1.864394607	0.109745729	1	40	23	12	37	34	149	88	39	72	72
ENSMUSG00000038349	chr1	Plcl1	-0.8755318	4.8282E-05	0.000131743	2.626099714	0.043567023	-1	113	105	130	142	95	76	69	63	47	96
ENSMUSG00000029772	chr6	Ahcyl2	-0.6733179	4.83049E-05	0.00013178	3.96985351	0.028388821	-1	254	271	290	372	243	173	210	151	221	223
ENSMUSG00000028567	chr4	Txndc12	0.62454005	4.86349E-05	0.000132654	3.646901724	0.022685864	1	144	155	119	182	129	296	242	211	224	260
ENSMUSG00000039771	chr5	Polr2j	0.58425328	4.87014E-05	0.00013281	4.576685928	0.021849869	1	296	275	237	345	265	589	475	440	407	422
ENSMUSG00000030067	chr6	Foxp1	0.76277372	4.88345E-05	0.000133147	3.823718172	0.036652677	1	184	158	146	153	129	429	275	250	197	307
ENSMUSG00000002006	chrX	Pdzd4	1.04439579	4.88633E-05	0.0001332	1.540214843	0.051330639	1	25	31	24	29	25	84	50	61	47	64
ENSMUSG00000038587	chr10	Akap12	-0.7267067	4.90113E-05	0.000133577	4.413293894	0.034935534	-1	331	372	360	501	407	277	240	277	166	347

ENSMUSG00000028609	chr4	Magoh	0.71655366	4.90603E-05	0.000133684	3.870385637	0.032132612	1	170	164	180	180	120	326	346	228	327	246
ENSMUSG00000053553	chr5	3110082I17Rik	0.92869704	4.90825E-05	0.000133719	2.520373489	0.049439362	1	50	62	49	74	53	100	155	106	140	95
ENSMUSG00000021134	chr12	Srsf5	0.62838702	4.93941E-05	0.000134541	6.281183752	0.02768806	1	1072	867	813	1156	671	1865	1480	1466	1303	1613
ENSMUSG00000026873	chr2	Phf19	1.26540761	4.94448E-05	0.000134653	1.547028556	0.084903141	1	18	30	37	17	17	59	65	60	78	57
ENSMUSG00000038884	chr9	A230050P20Rik	1.00841852	4.95078E-05	0.000134799	1.991528731	0.053427051	1	38	44	35	36	35	120	63	67	75	97
ENSMUSG00000032570	chr9	Atp2c1	-0.6319651	4.95335E-05	0.000134842	4.694005972	0.026300245	-1	409	476	381	673	421	304	381	272	308	388
ENSMUSG00000003541	chr17	Ier3	1.37626403	4.98953E-05	0.000135801	3.388440087	0.125197697	1	106	121	55	88	57	553	255	131	194	119
ENSMUSG00000021807	chr14	2700060E02Rik	0.60350664	4.99769E-05	0.000135996	6.517866587	0.025654331	1	1208	1059	940	1339	892	1837	1882	1687	1896	1686
ENSMUSG00000048458	chr3	Fam212b	-0.8240793	5.00497E-05	0.000136168	3.800360338	0.044058861	-1	251	190	276	343	260	212	105	173	121	207
ENSMUSG00000026198	chr1	Abcb6	-0.5694443	5.00876E-05	0.000136244	4.979809105	0.021374275	-1	530	494	507	760	527	402	421	398	430	409
ENSMUSG00000074818	chr19	Pdzd7	-1.2102073	5.02205E-05	0.000136579	3.304968177	0.096220696	-1	278	187	163	157	218	37	101	78	121	140
ENSMUSG00000038793	chr1	Lefty1	1.36850007	5.07034E-05	0.000137866	0.845742891	0.083163118	1	15	11	20	12	10	48	35	32	52	28
ENSMUSG00000022842	chr16	Ece2	0.88483823	5.08904E-05	0.000138347	2.595361826	0.044366961	1	78	71	39	71	51	138	154	106	106	124
ENSMUSG00000016995	chr2	Matn4	1.30975966	5.09456E-05	0.000138444	2.505277825	0.107127938	1	61	39	40	52	44	272	152	61	76	102
ENSMUSG00000040220	chr8	Gas8	0.97878298	5.0938E-05	0.000138444	2.10080862	0.052243298	1	46	29	32	60	43	123	93	92	64	80
ENSMUSG00000026781	chr2	Acbd5	-0.7825396	5.10191E-05	0.00013859	4.494705646	0.041220656	-1	379	401	390	598	366	177	317	232	236	382
ENSMUSG00000043831	chr7	Lysmd4	-0.703144	5.10158E-05	0.00013859	3.707606782	0.030627781	-1	253	237	225	255	220	160	132	127	193	192
ENSMUSG00000026319	chr1	2310035C23Rik	-0.7025238	5.10893E-05	0.000138753	3.111957228	0.027885011	-1	160	145	144	202	140	105	128	91	109	97
ENSMUSG00000040048	chr17	Ndufb10	0.69265748	5.11202E-05	0.00013881	8.120293758	0.034504056	1	2818	2740	2767	4921	2852	6246	5001	6409	4700	5621
ENSMUSG00000032096	chr9	Arcn1	-0.6058943	5.16854E-05	0.000140318	6.551372452	0.025979425	-1	1687	1504	1482	2165	1623	1251	1330	970	1324	1195
ENSMUSG00000079470	chr1	Utp14b	-1.1461258	5.1853E-05	0.000140745	1.630009354	0.070209246	-1	76	61	71	50	45	39	32	16	32	34
ENSMUSG00000089715	chr15	Cbx6	0.61534733	5.22424E-05	0.000141775	5.593824015	0.026160607	1	520	551	486	706	575	1052	895	1016	747	1049
ENSMUSG00000033319	chr18	Fem1c	-0.5891617	5.24014E-05	0.000142179	4.457048988	0.022230019	-1	380	351	376	554	315	277	302	258	277	310
ENSMUSG00000042492	chr7	Tbc1d10b	0.61140045	5.3129E-05	0.000144125	5.640996132	0.025930937	1	632	473	498	769	580	1126	909	976	834	1075
ENSMUSG00000036737	chr9	Oxsr1	-0.6313671	5.31846E-05	0.000144248	6.404126466	0.02825478	-1	1543	1455	1298	1911	1475	933	1110	987	1195	1167
ENSMUSG00000020614	chr11	Fam20a	1.23861716	5.33041E-05	0.000144544	1.799933259	0.086547945	1	37	29	19	33	30	90	64	103	36	90
ENSMUSG00000056076	chr5	Eif3b	0.59455622	5.33395E-05	0.000144612	6.866540291	0.025233845	1	1361	1167	1160	1907	1383	2468	2452	2055	2197	2291
ENSMUSG00000006782	chr11	Cnp	0.58821711	5.33806E-05	0.000144695	4.354140533	0.021917904	1	209	236	260	286	215	451	386	372	369	417
ENSMUSG00000003549	chr7	Ercc1	0.60706767	5.34004E-05	0.000144721	3.930233771	0.022508452	1	177	159	151	227	181	334	306	304	252	294
ENSMUSG00000020541	chr11	Tom1l1	-0.8819255	5.34126E-05	0.000144726	3.400061743	0.049670895	-1	218	204	156	264	175	84	124	76	149	166
ENSMUSG00000039452	chr9	Snx22	1.9856023	5.38503E-05	0.000145883	0.402441344	0.198566969	1	5	5	7	13	6	18	16	67	16	34
ENSMUSG00000025142	chr11	Aspscr1	0.61549821	5.38773E-05	0.000145928	4.821575229	0.025310476	1	377	315	308	402	260	680	518	467	631	489
ENSMUSG00000083621	chrX	Gm14586	0.80072332	5.38973E-05	0.000145954	3.774982893	0.041166761	1	167	170	140	121	128	376	226	251	317	238
ENSMUSG00000022371	chr15	Col14a1	0.82524513	5.40079E-05	0.000146225	6.440755851	0.048606413	1	852	792	816	1177	1030	2356	1437	1887	1031	2416
ENSMUSG00000000266	chrX	Mid2	-0.7857054	5.41315E-05	0.000146531	2.87814044	0.035743395	-1	123	140	123	170	128	125	75	85	75	76
ENSMUSG00000046691	chr8	Chtf8	0.58238976	5.41505E-05	0.000146554	5.10606351	0.022884421	1	389	360	384	560	369	877	707	599	595	600
ENSMUSG00000033149	chr16	Phldb2	-0.6743637	5.42484E-05	0.000146791	3.993450013	0.029074981	-1	254	297	314	327	250	182	211	167	182	254
ENSMUSG00000031258	chrX	Xkrx	1.59654278	5.42856E-05	0.000146846	-0.146683007	0.075737003	1	8	5	4	5	6	15	19	17	21	22
ENSMUSG00000031756	chr8	Cenpn	1.33592435	5.42897E-05	0.000146846	0.699270288	0.075797991	1	17	15	10	10	10	44	48	23	30	30
ENSMUSG00000040950	chr11	Mgl2	2.04386175	5.44689E-05	0.000147302	2.52769403	0.266901977	1	26	36	26	26	46	11	149	218	192	145
ENSMUSG00000003534	chr17	Ddr1	-0.7726862	5.45241E-05	0.000147423	5.152152476	0.041602564	-1	725	699	709	734	458	578	406	488	260	415
ENSMUSG00000044367	chr11	Slc16a13	1.27293226	5.47235E-05	0.000147933	0.853231291	0.071823737	1	20	17	14	12	9	36	47	26	42	42
ENSMUSG00000022421	chr15	Nptxr	1.09971521	5.48259E-05	0.000148182	1.817080494	0.066294254	1	36	20	19	43	43	103	81	68	62	65
ENSMUSG00000051146	chr16	Camk2n2	1.28851473	5.49502E-05	0.000148489	0.766204802	0.073849141	1	14	9	15	21	9	49	24	34	30	45
ENSMUSG00000028654	chr4	Mycl	1.48014192	5.50663E-05	0.000148774	1.1055619	0.115474541	1	22	17	19	12	8	51	46	69	22	53
ENSMUSG00000041684	chr1	Bivm	-0.863657	5.51742E-05	0.000149036	2.643658475	0.043119286	-1	136	133	115	116	87	62	76	62	69	86
ENSMUSG00000059058	chr1	Tma7-ps	-1.8241248	5.53396E-05	0.000149447	2.907992934	0.219367834	-1	208	177	156	183	135	179	33	23	24	21
ENSMUSG00000098794	chr2	Gm28038	1.27094091	5.53475E-05	0.000149447	1.760926409	0.092945612	1	34	26	33	39	11	98	43	76	92	65
ENSMUSG00000075590	chr15	Nrbp2	0.93629448	5.54279E-05	0.000149635	3.293160824	0.056143823	1	86	109	78	112	107	340	144	231	156	172
ENSMUSG00000030726	chr7	Pold3	0.79008809	5.58692E-05	0.000150797	3.252104173	0.038348189	1	92	105	94	140	85	264	226	147	200	141
ENSMUSG00000060733	chr10	Ipmk	-0.5883327	5.59605E-05	0.000151015	4.347538304	0.022184821	-1	356	347	337	462	317	286	296	199	285	258
ENSMUSG00000001604	chr4	Tcea3	-0.6099033	5.61394E-05	0.000151468	7.152730126	0.026830004	-1	2496	2387	2188	3375	2431	1946	1723	1483	2003	2048
ENSMUSG00000060180	chr11	Myh13	-1.792669	5.68368E-05	0.00015332	4.695773036	0.219193768	-1	675	626	652	911	184	139	112	153	47	506
ENSMUSG00000048497	chr11	Mmgt2	0.91187755	5.71505E-05	0.000154137	2.7014739	0.049467522	1	78	42	60	78	71	190	155	99	102	141
ENSMUSG00000095567	chr4	Noc2l	0.65553114	5.72246E-05	0.000154307	5.231007224	0.029792672	1	466	363	360	555	432	836	849	578	879	599
ENSMUSG00000001173	chrX	Ocrl	-0.6768677	5.73196E-05	0.000154533	3.998477707	0.029470736	-1	287	239	247	387	303	205	222	152	238	180
ENSMUSG00000026628	chr1	Atf3	1.63415465	5.74232E-05	0.000154782	4.314681877	0.182675977	1	68	85	313	177	65	724	650	149	439	535
ENSMUSG00000100807	chr9	Gm29521	2.20972535	5.74755E-05	0.000154894	0.011703336	0.227726327	1	1	11	7	1	2	9	22	21	29	35
ENSMUSG00000038406	chr7	Scaf1	-0.6305428	5.76049E-05	0.000155212	5.522401126	0.027802244	-1	838	668	677	1153	853	561	614	524	517	726
ENSMUSG00000044408	chr12	Sptssa	0.59413801	5.79033E-05	0.000155986	4.722619221	0.023495685	1	324	296	289	405	255	548	617	379	513	535
ENSMUSG00000055239	chr6	Kcmf1	-0.6016268	5.81315E-05	0.000156571	7.039131206	0.026166749	-1	2196	2109	2098	3228	2259	1653	1748	1490	1737	1890
ENSMUSG00000036114	chr4	Rpp25l	0.65341506	5.8379E-05	0.000157207	4.918186561	0.029134092	1	399	354	331	349	299	861	605	480	568	517
ENSMUSG00000051517	chr4	Arhgef39	1.71857631	5.87737E-05	0.000158239	0.18446587	0.127414429	1	9	6	6	6	7	43	29	17	28	9
ENSMUSG00000010067	chr9	Rassf1	0.8036485	5.88864E-05	0.000158477	4.410508685	0.044061432	1	204	231	242	251	211	758	405	340	401	320
ENSMUSG00000022422	chr15	Dscc1	2.08349551	5.89045E-05	0.000158477	-0.273855049	0.178461213	1	8	5	3	2	1	22	34	6	18	12

ENSMUSG00000024600	chr18	Slc27a6	1.58271448	5.89072E-05	0.000158477	-0.164043587	0.081983527	1	5	6	6	8	3	19	28	14	16	16
ENSMUSG00000042148	chr11	Cox10	-0.6609857	5.89023E-05	0.000158477	5.376416448	0.030555912	-1	607	665	765	1088	688	512	543	596	477	477
ENSMUSG00000039530	chr8	Tusc3	0.67158073	5.89935E-05	0.000158678	3.174246023	0.025518904	1	97	103	101	123	87	211	186	148	163	188
ENSMUSG00000033365	chr4	Ipo13	-0.6349917	5.90813E-05	0.000158884	7.469353001	0.029375207	-1	2929	3056	2648	4393	3150	3100	2146	1887	2082	2204
ENSMUSG00000040283	chr11	Btnl9	-0.9141336	5.92097E-05	0.000159199	2.585661968	0.04936547	-1	87	123	97	158	112	91	43	62	61	78
ENSMUSG00000020393	chr11	Kremen1	-0.8834188	5.92383E-05	0.000159245	5.992402746	0.05604953	-1	784	947	1080	2433	1100	966	574	603	658	877
ENSMUSG00000042389	chr6	Tsen2	0.7573539	5.93073E-05	0.0001594	3.042919089	0.033438299	1	86	96	85	90	88	156	150	154	185	183
ENSMUSG00000034459	chr19	Ifit1	1.25752325	5.93519E-05	0.000159489	2.232610362	0.097078433	1	44	44	41	51	21	101	145	73	48	164
ENSMUSG00000034789	chr13	Rab24	0.59963988	5.93837E-05	0.000159544	5.167380531	0.024703002	1	453	416	370	498	385	849	582	677	760	651
ENSMUSG00000052253	chr15	Zfp622	0.56398668	5.95426E-05	0.00015994	4.717533234	0.021026279	1	337	290	275	410	272	627	503	492	428	509
ENSMUSG00000020211	chr10	Sf3a2	0.65385917	5.96621E-05	0.00016023	4.750291532	0.029118213	1	271	253	271	461	312	715	570	509	423	473
ENSMUSG00000025239	chr9	Limd1	-0.5944449	6.00729E-05	0.000161302	6.100916804	0.025179754	-1	1320	1188	1026	1520	1113	863	866	770	930	1026
ENSMUSG00000032666	chr1	1700025G04Rik	-0.6944878	6.01427E-05	0.000161459	6.245322941	0.034694671	-1	1193	1086	1395	2070	1309	955	767	876	1105	1002
ENSMUSG00000079480	chrX	Pin4	0.65116704	6.02284E-05	0.000161658	3.722835338	0.026245149	1	187	154	123	177	119	314	270	241	242	240
ENSMUSG00000020741	chr11	Cluh	-0.6607687	6.04469E-05	0.000162213	7.291310047	0.031835214	-1	2328	2536	2758	4147	2654	1952	1966	2177	1687	2084
ENSMUSG00000025287	chrX	Acot9	0.67116914	6.04915E-05	0.000162257	5.159740891	0.031448325	1	424	341	429	551	317	768	656	604	908	625
ENSMUSG00000028389	chr4	Zfp37	-1.5038059	6.0498E-05	0.000162257	0.211399815	0.089480474	-1	32	27	18	22	16	6	7	10	7	14
ENSMUSG00000031842	chr8	Pde4c	-1.0614752	6.04824E-05	0.000162257	1.321546458	0.05263773	-1	48	46	54	54	38	32	25	27	24	18
ENSMUSG00000021408	chr13	Ripk1	0.76538242	6.05575E-05	0.000162385	3.398899738	0.036324862	1	105	123	110	132	103	291	257	133	198	204
ENSMUSG00000056481	chr19	Cd248	0.75029956	6.05754E-05	0.000162402	5.088670541	0.039515756	1	314	288	362	513	413	818	646	791	426	798
ENSMUSG00000037685	chr5	Atp8a1	-0.9114127	6.11285E-05	0.000163853	5.4149108	0.059333771	-1	844	740	778	951	817	236	532	394	531	702
ENSMUSG00000017969	chr2	Ptgis	1.12644259	6.14087E-05	0.000164573	3.234422638	0.084377292	1	118	92	64	93	67	358	268	183	145	98
ENSMUSG00000092416	chr7	Zfp141	-1.0001359	6.1453E-05	0.00016466	2.309185026	0.05848782	-1	119	102	84	111	67	44	46	36	70	67
ENSMUSG00000025486	chr7	Sirt3	-0.7542739	6.14715E-05	0.000164678	4.391093783	0.038707231	-1	339	404	405	552	271	222	200	277	304	252
ENSMUSG00000077220	chr1	Gm23436	1.70775307	6.16586E-05	0.000165148	0.073020473	0.112921773	1	9	5	8	2	7	23	23	17	35	16
ENSMUSG00000052852	chr6	Reep1	-0.6992193	6.16993E-05	0.000165225	7.111178021	0.03569309	-1	2847	2393	2273	2764	2417	1387	1719	1724	1439	2303
ENSMUSG00000021500	chr13	Ddx46	-0.5764269	6.17593E-05	0.000165354	5.166005534	0.022841784	-1	639	562	530	864	622	531	540	399	459	423
ENSMUSG00000002984	chr7	Tomm40	0.60699438	6.17777E-05	0.000165371	5.205762566	0.02559721	1	414	388	370	634	392	858	738	748	679	599
ENSMUSG00000002010	chrX	Idh3g	-0.6293537	6.17937E-05	0.000165383	8.381030544	0.029174319	-1	5633	6017	6043	7867	4755	4553	3801	3842	4474	4690
ENSMUSG00000022686	chr16	B3gnt5	1.83011997	6.19156E-05	0.000165677	-0.266905626	0.116624307	1	2	6	7	2	5	13	14	25	15	21
ENSMUSG00000029203	chr5	Ube2k	0.5677991	6.1983E-05	0.000165826	5.766261895	0.022760512	1	686	570	536	866	625	1128	1074	993	1055	1040
ENSMUSG00000031732	chr8	Phlpp2	-0.8590363	6.22425E-05	0.000166488	2.518505966	0.042779575	-1	102	108	82	130	118	74	79	41	66	68
ENSMUSG00000039105	chr4	Atp6v1g1	0.58584201	6.22616E-05	0.000166508	7.308323866	0.025082758	1	2096	1735	1683	2215	1715	3474	2989	2696	2908	3503
ENSMUSG00000025735	chr17	Rhbdl1	-0.7232524	6.2285E-05	0.000166538	4.554768745	0.035849102	-1	438	392	401	525	416	187	328	251	313	353
ENSMUSG00000040658	chr17	Dnph1	0.91740987	6.23518E-05	0.000166685	2.566873303	0.049689732	1	71	38	51	69	69	130	160	110	117	101
ENSMUSG00000037351	chr1	Actr1b	-0.5876125	6.24222E-05	0.000166809	7.229139559	0.025225559	-1	2448	2466	2462	3716	2432	2128	1944	1775	1948	1991
ENSMUSG00000086742	chr7	Gm16201	1.42452984	6.24198E-05	0.000166809	0.272971954	0.078057542	1	12	3	11	10	7	34	22	24	21	27
ENSMUSG00000029267	chr5	Mtf2	-0.9352744	6.31406E-05	0.000168697	3.251152352	0.056866309	-1	167	148	149	283	187	73	127	79	83	167
ENSMUSG00000028040	chr3	Efna4	1.78652951	6.32412E-05	0.000168933	-0.375796101	0.102442063	1	8	5	2	4	2	11	15	21	15	18
ENSMUSG00000052707	chr7	Tnrc6a	-0.575195	6.3444E-05	0.000169443	4.941349668	0.022543653	-1	521	506	482	721	515	530	436	343	355	357
ENSMUSG00000027502	chr2	Rtfdc1	0.56332535	6.38074E-05	0.000170381	5.803718975	0.022488786	1	696	665	567	865	579	1255	1066	906	1132	1082
ENSMUSG00000046675	chr12	Tmem251	0.82110394	6.44784E-05	0.000172139	2.834337143	0.039802859	1	73	91	73	76	61	166	179	105	143	140
ENSMUSG00000090659	chr13	Zfp493	-1.3940226	6.46069E-05	0.00017245	0.968091992	0.09966287	-1	45	39	39	43	33	7	14	11	29	21
ENSMUSG00000007880	chr4	Arid1a	-0.6559287	6.46292E-05	0.000172476	5.277703379	0.030373007	-1	601	539	623	982	802	524	522	415	410	593
ENSMUSG00000038784	chr6	Cnot4	-0.5965144	6.49171E-05	0.000173211	4.259407193	0.023124371	-1	331	336	271	434	342	240	259	206	242	292
ENSMUSG00000024539	chr18	Ptpn2	0.61739468	6.50054E-05	0.000173414	3.948060429	0.024045028	1	195	175	168	202	158	363	322	281	297	251
ENSMUSG00000028445	chr4	Enho	0.73995551	6.54843E-05	0.000174658	5.482751623	0.039177267	1	580	558	433	411	470	903	750	1062	878	926
ENSMUSG00000070461	chr2	9230112E08Rik	-0.6959069	6.55132E-05	0.000174702	3.075227265	0.02798163	-1	146	138	128	202	156	117	114	95	83	111
ENSMUSG00000039936	chr4	Pik3cd	0.68552224	6.5535E-05	0.000174727	4.357131603	0.031686554	1	230	276	206	261	188	563	455	286	411	354
ENSMUSG00000019920	chr10	Lims1	-0.6722492	6.57579E-05	0.000175288	5.47729147	0.032216174	-1	728	759	808	1270	573	525	629	451	577	617
ENSMUSG00000051323	chrX	Pcdh19	-0.8098726	6.59223E-05	0.000175692	2.843760492	0.038845686	-1	102	141	113	179	138	97	85	92	66	79
ENSMUSG00000039911	chr4	Spsb1	0.73271785	6.60479E-05	0.000175993	3.594879741	0.034209996	1	107	123	126	180	135	347	209	238	180	253
ENSMUSG00000025477	chr7	Inpp5a	-0.5982211	6.63649E-05	0.000176804	6.28828832	0.025955266	-1	1304	1263	1167	1830	1469	1247	1041	925	896	982
ENSMUSG00000039210	chr1	Gpatch2	-0.6865779	6.65051E-05	0.000177144	3.303440051	0.02838082	-1	176	154	161	238	173	122	116	108	106	160
ENSMUSG00000025491	chr7	Ifitm1	2.16433186	6.67852E-05	0.000177856	0.565020582	0.250122957	1	8	9	3	5	10	98	31	20	24	10
ENSMUSG00000102918	chr18	PCDHGB6	0.67368844	6.71835E-05	0.000178883	6.171172329	0.033010239	1	866	792	666	970	836	1697	1406	1575	956	1605
ENSMUSG00000052534	chr1	Pbx1	-0.6300412	6.73845E-05	0.000179384	4.499357359	0.026828243	-1	347	364	346	640	373	361	301	261	234	294
ENSMUSG00000073792	chr4	Alg6	-0.8868381	6.73983E-05	0.000179387	2.449402719	0.045669046	-1	112	96	107	131	74	61	61	40	75	70
ENSMUSG00000078126	chr14	Rpl23a-ps3	1.15501175	6.74839E-05	0.00017958	1.089908889	0.061923124	1	13	23	17	19	19	50	56	31	48	40
ENSMUSG00000026141	chr1	Col19a1	-1.8068181	6.7697E-05	0.000180113	0.245440244	0.158326202	-1	26	15	27	20	35	9	4	1	15	10
ENSMUSG00000026924	chr2	Sec16a	-0.6012321	6.79097E-05	0.000180644	5.406079701	0.025618174	-1	713	736	645	919	785	666	565	494	413	624
ENSMUSG00000032228	chr9	Tcf12	-0.6639082	6.80802E-05	0.000181063	4.938137717	0.030877157	-1	551	531	485	701	531	296	456	306	365	507
ENSMUSG00000021710	chr13	Nln	0.62288834	6.82069E-05	0.000181366	3.529691618	0.023410541	1	128	122	126	187	112	245	243	201	226	216
ENSMUSG00000038280	chr10	Ostm1	-0.6354935	6.82624E-05	0.000181479	5.207468932	0.028556272	-1	744	624	625	748	593	544	605	343	478	398
ENSMUSG00000021671	chr13	Poc5	-0.7595706	6.85922E-05	0.000182321	2.653678525	0.032392838	-1	100	114	104	143	118	74	74	70	76	80

ENSMUSG00000026721	chr1	Rabgap1l	-0.7735508	6.96293E-05	0.000185043	3.295258409	0.037981201	-1	214	165	147	217	172	132	121	71	148	115
ENSMUSG00000046707	chr8	Csnk2a2	0.629531	6.96993E-05	0.000185193	3.831807446	0.024972944	1	170	154	136	216	154	356	298	243	212	301
ENSMUSG00000002147	chr10	Stat6	0.60989347	7.00096E-05	0.000185983	5.148788778	0.026141149	1	392	383	395	565	364	857	763	484	747	659
ENSMUSG00000034164	chr11	Emid1	-0.8772891	7.01462E-05	0.00018631	3.592981592	0.052018897	-1	239	213	206	297	205	257	104	106	134	97
ENSMUSG00000030424	chr7	Zfp939	-1.3858249	7.02779E-05	0.000186624	0.624323458	0.088043969	-1	26	28	21	43	37	10	7	10	18	19
ENSMUSG00000029776	chr6	Hibadh	-0.618815	7.03812E-05	0.000186863	7.046968218	0.028344705	-1	2269	2548	2252	3089	1832	1643	1641	1508	1823	1877
ENSMUSG00000023971	chr17	Rrp36	0.70697324	7.04805E-05	0.000187069	3.703066724	0.032292956	1	162	124	133	182	131	327	242	294	244	195
ENSMUSG00000041219	chr2	Arhgap11a	0.97866177	7.04854E-05	0.000187069	2.194915758	0.05530606	1	55	41	45	52	30	76	129	82	105	87
ENSMUSG00000045302	chr5	Preb	0.57835997	7.0672E-05	0.000187528	5.959870806	0.024162763	1	801	684	616	856	752	1295	1169	1172	1188	1243
ENSMUSG00000059237	chr9	Ppp1r2-ps4	-1.4078914	7.12628E-05	0.00018906	0.291160634	0.074684019	-1	25	18	19	40	20	6	10	9	10	14
ENSMUSG00000027509	chr2	Rae1	0.64076592	7.14793E-05	0.000189598	4.603552896	0.028216784	1	348	255	228	335	247	680	479	430	416	418
ENSMUSG00000028850	chr4	Gpatch3	0.9184846	7.1631E-05	0.000189965	2.141124987	0.046795126	1	55	37	36	54	39	119	69	75	100	95
ENSMUSG00000031696	chr8	Vps35	-0.8225237	7.17007E-05	0.000190114	5.979526615	0.049679167	-1	1223	1186	1099	1478	1027	508	908	459	990	837
ENSMUSG00000087679	chr2	C330006A16Rik	0.67876377	7.18341E-05	0.000190431	4.740162869	0.032266222	1	272	311	279	426	249	757	466	575	395	493
ENSMUSG00000005774	chr3	Rfx5	-0.8080375	7.2637E-05	0.000192523	3.38261914	0.042422822	-1	262	217	185	168	138	117	118	117	122	137
ENSMUSG00000021830	chr14	Txndc16	-0.6599961	7.28266E-05	0.000192989	4.245803567	0.029507681	-1	332	415	318	402	255	260	244	186	205	306
ENSMUSG00000020205	chr10	Phlda1	0.8492699	7.28919E-05	0.000193126	2.964344164	0.044990645	1	76	74	74	102	82	264	166	125	116	146
ENSMUSG00000096056	chrX	Gm21986	1.02084117	7.35208E-05	0.000194755	2.600204905	0.065105611	1	49	44	49	61	85	181	116	137	82	136
ENSMUSG00000048534	chr9	Amica1	2.67698029	7.37278E-05	0.000195266	0.613288011	0.39155656	1	3	9	6	2	6	140	14	16	19	14
ENSMUSG00000033106	chr8	Slc7a6os	0.71362492	7.44959E-05	0.000197263	3.111394131	0.030282741	1	92	79	92	118	99	224	177	161	154	150
ENSMUSG00000035949	chr2	Fbxw2	-0.5827894	7.51093E-05	0.00019885	5.493726745	0.024355768	-1	872	775	722	953	700	560	594	495	583	708
ENSMUSG00000030314	chr6	Atg7	0.69881167	7.51269E-05	0.000198859	3.506753153	0.030705157	1	138	117	113	158	114	307	231	148	209	253
ENSMUSG00000044221	chr5	Grsf1	-0.6196416	7.51767E-05	0.000198953	6.756665229	0.028536589	-1	1820	1843	1841	2740	1603	1267	1379	1232	1410	1655
ENSMUSG00000045875	chr14	Adra1a	-1.4639499	7.5374E-05	0.000199437	0.766322149	0.108605979	-1	38	33	34	34	34	4	9	18	14	23
ENSMUSG00000037071	chr19	Scd1	-1.7521934	7.56553E-05	0.000200143	7.011753679	0.21934249	-1	892	5369	2123	1153	4558	456	1013	1381	970	886
ENSMUSG00000033055	chr15	Ankrd54	0.79627486	7.59842E-05	0.000200976	2.726508659	0.037108687	1	58	72	64	89	70	185	140	115	119	117
ENSMUSG00000008398	chr10	Elk3	0.67844169	7.60038E-05	0.000200989	4.894635456	0.032790538	1	329	357	282	530	231	836	569	556	465	574
ENSMUSG00000091512	chr3	Lamtor3	0.70447887	7.63063E-05	0.000201751	4.856487981	0.035320624	1	312	338	343	376	261	409	737	520	596	640
ENSMUSG00000042569	chr11	Dhrs7b	0.57507102	7.6534E-05	0.000202315	4.645692147	0.022538184	1	310	322	257	349	253	486	483	465	521	469
ENSMUSG00000057858	chr19	Fam204a	-0.7571605	7.69366E-05	0.000203341	3.601989475	0.037806254	-1	214	166	191	332	236	112	155	123	155	183
ENSMUSG00000039156	chr5	Stim2	-0.6155537	7.70888E-05	0.000203705	5.035863746	0.026873574	-1	661	512	479	693	605	413	410	371	355	565
ENSMUSG00000027102	chr2	Hoxd8	-0.687517	7.71565E-05	0.000203806	4.066678657	0.032070979	-1	258	248	278	475	293	283	209	149	189	222
ENSMUSG00000069806	chr7	Cacng7	1.33315725	7.71464E-05	0.000203806	2.107830573	0.11402873	1	34	36	26	54	29	39	124	130	61	127
ENSMUSG00000052062	chr1	Pard3b	-0.9213301	7.73765E-05	0.000204349	2.399094005	0.05056764	-1	72	98	106	140	90	49	55	47	61	79
ENSMUSG00000091337	chr2	Eid1	0.56590996	7.76052E-05	0.000204914	5.255761963	0.022748166	1	488	377	394	630	420	750	774	673	670	848
ENSMUSG00000030055	chr6	Rab43	0.66038615	7.79564E-05	0.000205803	4.027804983	0.029078656	1	188	176	192	235	146	428	275	282	260	386
ENSMUSG00000044177	chr11	Wfikkn2	-0.6914056	7.82433E-05	0.000206521	3.17938032	0.029053332	-1	141	158	159	211	156	129	97	90	120	124
ENSMUSG00000012114	chr16	Med15	0.59245388	7.8593E-05	0.000207393	4.434525803	0.023635858	1	235	254	241	302	243	552	435	336	339	468
ENSMUSG00000025958	chr1	Creb1	-0.5974339	7.86033E-05	0.000207393	4.272661237	0.023916802	-1	303	312	321	444	348	280	305	202	216	252
ENSMUSG00000031644	chr8	Nek1	-0.785026	7.89099E-05	0.000208143	2.749228812	0.036507837	-1	120	133	111	171	94	80	97	59	72	90
ENSMUSG00000048200	chr7	Cracr2b	0.99389892	7.89174E-05	0.000208143	3.157119585	0.066075084	1	80	104	89	108	57	347	132	186	147	154
ENSMUSG00000070348	chr7	Ccnd1	0.72921708	7.90886E-05	0.000208555	5.028870701	0.038492674	1	338	354	338	531	284	800	868	609	629	411
ENSMUSG00000067873	chrX	Htatsf1	-0.6000398	7.92415E-05	0.000208919	6.478983215	0.026783305	-1	1504	1423	1380	2216	1543	1105	1202	994	1198	1279
ENSMUSG00000021916	chr14	Glt8d1	0.7631121	7.93786E-05	0.000209241	4.071192564	0.040258689	1	228	205	166	199	123	503	360	286	320	258
ENSMUSG00000006576	chr1	Slc4a3	0.87490259	7.95906E-05	0.00020976	3.528163359	0.051900236	1	137	101	121	147	95	395	162	246	231	177
ENSMUSG00000027163	chr2	Commd9	0.60369279	7.96455E-05	0.000209865	4.899960818	0.025596518	1	397	356	359	361	275	629	573	560	627	530
ENSMUSG00000059866	chr5	Tnip2	0.95828891	7.99565E-05	0.000210645	2.521322694	0.056111482	1	80	56	47	53	46	188	107	85	114	117
ENSMUSG00000042694	chr19	Obfc1	0.79987802	8.01113E-05	0.000211013	3.146899342	0.040814113	1	107	102	74	116	77	251	129	193	155	179
ENSMUSG00000024592	chr18	C330018D20Rik	-0.665267	8.0205E-05	0.00021122	3.230051101	0.026453014	-1	174	176	149	210	141	124	119	113	123	105
ENSMUSG00000034686	chr13	Prr7	1.81548486	8.02488E-05	0.000211296	-0.018079171	0.133858968	1	2	8	7	3	7	38	24	21	14	12
ENSMUSG00000067261	chr4	Foxd3	-1.524074	8.03091E-05	0.000211414	0.334615261	0.108525046	-1	19	28	16	43	23	5	12	5	8	18
ENSMUSG00000010122	chr11	Slc47a1	-0.8767087	8.0438E-05	0.000211714	4.668791933	0.05566196	-1	298	347	476	996	410	314	324	267	294	258
ENSMUSG00000059291	chr4	Rpl11	0.61805908	8.053E-05	0.000211916	7.232445149	0.028801631	1	1877	1758	1570	2097	1542	3913	3145	2348	2968	2581
ENSMUSG00000024181	chr17	Mrpl28	0.6024418	8.06795E-05	0.00021227	6.008506869	0.026783397	1	800	772	643	944	658	1540	1097	1255	1296	1133
ENSMUSG00000018040	chr15	Rrp7a	0.5701324	8.11249E-05	0.000213399	5.232930876	0.023192444	1	489	420	368	569	413	783	842	606	770	659
ENSMUSG00000036144	chr12	Meox2	-0.7391929	8.11394E-05	0.000213399	4.055104041	0.037706967	-1	360	310	318	397	167	203	197	178	192	241
ENSMUSG00000061665	chr17	Cd2ap	-0.585108	8.11688E-05	0.000213436	4.14785627	0.02256744	-1	294	330	311	390	253	239	243	196	213	262
ENSMUSG00000038764	chr4	Ptpn3	-1.1416478	8.12805E-05	0.00021369	5.389146943	0.09625744	-1	378	943	986	1586	501	712	317	449	339	329
ENSMUSG00000031349	chrX	Nsdhl	-0.8145465	8.13859E-05	0.000213927	3.261242382	0.043213269	-1	211	213	150	170	150	85	139	99	123	112
ENSMUSG00000054814	chr5	Usp46	-0.6911979	8.15203E-05	0.00021424	3.839194272	0.031789238	-1	241	247	196	352	279	165	178	130	194	221
ENSMUSG00000032609	chr9	Klhdc8b	0.83804878	8.16667E-05	0.000214584	2.895532121	0.043911492	1	86	79	62	93	71	146	103	164	165	182
ENSMUSG00000070814	chr7	6330408A02Rik	-0.6209256	8.20888E-05	0.000215653	3.694608288	0.024356594	-1	231	221	193	284	232	196	179	158	126	170
ENSMUSG00000006335	chr7	Tfpt	0.69557934	8.27121E-05	0.00021725	3.31104022	0.030046867	1	127	108	91	128	103	273	180	186	177	177
ENSMUSG00000024507	chr18	Hsd17b4	-0.6715457	8.29835E-05	0.000217921	5.720167083	0.033335071	-1	786	907	837	1431	911	602	692	492	796	727
ENSMUSG00000082145	chr11	Gm12312	-2.4749683	8.30738E-05	0.000218117	-0.419799055	0.295792862	-1	20	16	10	15	19	14	0	0	2	0

ENSMUSG00000026768	chr2	Itga8	-0.9298687	8.31705E-05	0.00021833	2.031198331	0.048112672	-1	65	79	57	121	72	47	36	41	48	51
ENSMUSG00000024925	chr19	Rnaseh2c	0.6177634	8.39205E-05	0.000220258	3.693441494	0.024206251	1	161	136	129	200	132	328	245	214	250	235
ENSMUSG00000031486	chr8	Gpr124	0.67933298	8.40875E-05	0.000220655	3.816678668	0.030574397	1	180	159	131	177	151	317	312	291	185	302
ENSMUSG00000038803	chr5	Ost4	0.62844644	8.41051E-05	0.00022066	5.732256596	0.029110368	1	716	608	615	662	492	1349	1057	908	1082	880
ENSMUSG00000026857	chr2	Ntmt1	0.68907042	8.43467E-05	0.000221252	3.933848139	0.032203848	1	159	159	177	250	128	390	308	329	258	243
ENSMUSG00000039304	chr3	Tnfsf10	-1.3006523	8.43753E-05	0.000221285	2.760729605	0.115264082	-1	140	189	179	120	70	27	64	63	58	100
ENSMUSG00000024764	chr19	Naa40	-0.557925	8.44404E-05	0.000221414	4.215239446	0.020446813	-1	325	302	303	397	312	252	246	218	258	244
ENSMUSG00000066406	chr7	Akap13	-0.6672411	8.44591E-05	0.000221422	6.38493494	0.033468611	-1	1401	1459	1289	2041	1488	1310	939	934	748	1382
ENSMUSG00000040563	chr9	Lppr2	1.21981729	8.46286E-05	0.000221825	0.975151658	0.070356868	1	13	20	12	17	19	61	30	40	33	46
ENSMUSG00000060288	chr4	Ppih	0.83821355	8.46599E-05	0.000221865	2.943011307	0.044454194	1	76	92	81	89	64	193	203	121	164	113
ENSMUSG00000023966	chr17	Rsph9	1.70014063	8.47294E-05	0.000222006	-0.101947869	0.12415493	1	4	1	6	12	5	32	17	22	10	19
ENSMUSG00000036057	chr9	Ptpn23	0.72718684	8.51513E-05	0.000223069	4.19210398	0.036894807	1	189	168	156	261	246	529	335	308	268	429
ENSMUSG00000006517	chr8	Mvd	0.74612529	8.53791E-05	0.000223624	2.965695879	0.033698964	1	90	70	83	102	82	199	158	165	134	130
ENSMUSG00000050270	chr11	Tmem220	1.16080306	8.54315E-05	0.000223719	0.886492264	0.059049416	1	17	18	16	14	13	36	37	45	37	37
ENSMUSG00000061544	chr17	Zfp229	-1.0188196	8.5582E-05	0.000224072	2.078429121	0.061823015	-1	90	81	57	92	90	30	56	31	55	49
ENSMUSG00000031575	chr8	Ash2l	0.55270053	8.58699E-05	0.000224783	4.789800219	0.021278191	1	310	320	303	470	276	584	565	501	532	490
ENSMUSG00000036940	chr4	Kdm1a	0.55952884	8.6499E-05	0.000226388	4.915512714	0.022009983	1	374	391	318	436	295	712	619	541	540	519
ENSMUSG00000003273	chr7	Car11	-1.1144128	8.65911E-05	0.000226584	1.923352535	0.075834976	-1	104	77	62	75	57	65	35	24	42	26
ENSMUSG00000050234	chr4	Gja4	0.81213955	8.66064E-05	0.000226584	2.877126618	0.040732278	1	71	87	75	86	69	121	149	142	136	200
ENSMUSG00000005656	chr12	Snx6	0.54871862	8.67419E-05	0.000226896	4.875488624	0.021039845	1	361	385	289	427	310	623	621	493	563	538
ENSMUSG00000029335	chr5	Bmp3	-1.6015	8.70392E-05	0.00022763	0.150950743	0.112049442	-1	40	20	17	21	14	12	4	10	7	7
ENSMUSG00000049672	chr17	Zbtb14	-0.8694994	8.70553E-05	0.00022763	2.865343805	0.048532498	-1	142	162	120	148	117	82	114	56	59	107
ENSMUSG00000027466	chr2	Rbck1	0.54529599	8.71998E-05	0.000227966	5.486530892	0.021536508	1	547	513	521	647	481	1004	835	812	794	895
ENSMUSG00000037410	chr9	Tbc1d2b	0.65182122	8.72239E-05	0.000227986	4.297026815	0.029258603	1	159	237	254	253	219	446	398	342	355	413
ENSMUSG00000041740	chr5	Rnf10	-0.6099654	8.72508E-05	0.000228014	8.209369731	0.028553064	-1	4998	4568	4617	7401	5276	4154	3631	3381	3482	4533
ENSMUSG00000070427	chr7	Il18bp	1.14890822	8.74742E-05	0.000228555	1.631030343	0.074582113	1	28	32	26	27	23	45	52	87	62	83
ENSMUSG00000010453	chr1	Kansl3	-0.5675738	8.75004E-05	0.000228574	5.338150504	0.02332632	-1	633	615	710	956	690	585	525	455	553	539
ENSMUSG00000081824	chr16	BC002163	0.74143653	8.75141E-05	0.000228574	3.452831081	0.035991873	1	160	122	102	146	77	268	192	221	216	208
ENSMUSG00000002797	chr6	Ggct	0.89330375	8.76432E-05	0.000228825	2.542125136	0.048965464	1	63	67	51	66	49	83	126	115	134	141
ENSMUSG00000017664	chr2	Slc35c2	0.55851927	8.76415E-05	0.000228825	4.723032827	0.02160009	1	343	297	291	355	294	622	538	460	493	449
ENSMUSG00000037784	chr9	Dzip1l	0.9367694	8.78773E-05	0.000229394	1.593521112	0.0430419	1	28	29	26	35	29	62	70	48	55	75
ENSMUSG00000001120	chr10	Pcbp3	1.06720688	8.80243E-05	0.000229734	1.59457173	0.062033597	1	36	31	21	27	23	88	57	58	71	45
ENSMUSG00000084347	chr11	Akt2-ps	-1.0887964	8.82708E-05	0.000230335	1.800208415	0.067982204	-1	73	75	42	83	70	20	37	38	40	39
ENSMUSG00000038146	chr17	Notch3	-0.7212559	8.83154E-05	0.000230408	5.183680839	0.038326344	-1	553	600	580	884	752	437	458	523	283	529
ENSMUSG00000039917	chr5	Rhbdd2	0.70480005	8.83469E-05	0.000230447	3.164255477	0.03058188	1	107	107	76	110	99	214	171	185	153	171
ENSMUSG00000037415	chr8	Ranbp10	-0.5668044	8.87244E-05	0.000231389	5.014327459	0.022924911	-1	554	481	497	739	604	495	403	360	370	503
ENSMUSG00000045294	chr5	Insig1	-0.9474439	8.88739E-05	0.000231735	4.058371225	0.064588766	-1	427	347	359	255	214	135	269	154	207	153
ENSMUSG00000032515	chr9	Csrnp1	1.42564254	8.94485E-05	0.00023319	2.613194448	0.138189818	1	33	46	65	53	41	353	128	79	76	99
ENSMUSG00000064068	chr3	Mtx1	0.65107478	8.95188E-05	0.00023333	4.171019945	0.029124923	1	198	195	226	266	155	478	360	326	339	288
ENSMUSG00000033411	chr2	Ctdspl2	-0.9191821	8.95717E-05	0.000233424	2.341146636	0.050679597	-1	91	104	78	132	82	47	76	42	67	47
ENSMUSG00000040820	chr16	Hlcs	-0.6346559	9.01741E-05	0.00023495	3.463778054	0.025001962	-1	214	194	182	234	167	154	160	123	140	122
ENSMUSG00000022300	chr15	Dcaf13	0.66418747	9.04713E-05	0.000235681	4.156094741	0.030430392	1	239	200	186	238	159	467	390	269	373	283
ENSMUSG00000042447	chr6	Mios	-0.61215	9.09338E-05	0.000236841	3.784369259	0.024194484	-1	246	227	234	319	211	163	193	142	179	206
ENSMUSG00000032527	chr9	Pccb	-0.595733	9.12138E-05	0.000237526	6.479263986	0.026869773	-1	1479	1660	1508	1981	1377	1250	1053	997	1298	1193
ENSMUSG00000032103	chr9	Pus3	-0.701752	9.13774E-05	0.000237908	3.562762311	0.032574319	-1	291	211	188	220	168	181	140	137	140	131
ENSMUSG00000048351	chr4	Coa7	-0.6304649	9.15397E-05	0.000238286	4.412466481	0.027790835	-1	355	371	379	468	345	246	349	222	295	243
ENSMUSG00000071647	chr19	Eml3	0.6740102	9.19045E-05	0.000239191	3.473376826	0.028988715	1	120	120	123	153	114	318	214	171	198	211
ENSMUSG00000031446	chr8	Cul4a	-0.6783699	9.20433E-05	0.000239508	6.656210903	0.03508671	-1	1869	1714	1661	2278	1737	925	1272	1171	1280	1646
ENSMUSG00000038437	chr11	Mllt6	-0.5816136	9.20843E-05	0.00023957	6.14492362	0.025418141	-1	1166	1149	1152	1767	1134	1074	856	840	975	878
ENSMUSG00000047617	chr2	BC029214	0.77120819	9.32838E-05	0.000242646	3.442540695	0.039464085	1	116	121	127	120	102	269	155	258	210	209
ENSMUSG00000003032	chr4	Klf4	-0.9164822	9.33201E-05	0.000242695	4.067018287	0.060907644	-1	194	259	353	399	406	312	194	123	159	170
ENSMUSG00000026181	chr16	Ppm1f	-0.5514906	9.34349E-05	0.000242948	4.805959467	0.021406231	-1	478	495	471	595	430	373	346	314	390	422
ENSMUSG00000028282	chr4	Casp8ap2	-0.9274038	9.36966E-05	0.000243583	2.629543619	0.055084468	-1	122	107	118	151	98	45	95	46	80	75
ENSMUSG00000042079	chr6	Hnrnpf	0.61998899	9.38778E-05	0.000244009	5.199760341	0.028174072	1	414	427	426	556	338	843	924	547	709	619
ENSMUSG00000003420	chr7	Fcgrt	0.7884337	9.39265E-05	0.00024409	6.553886298	0.047496639	1	1075	1155	864	1072	933	3290	1456	1861	1373	1851
ENSMUSG00000098974	chr19	Gm27505	1.03543382	9.3978E-05	0.000244179	3.713976929	0.076678827	1	152	158	105	115	99	149	252	220	388	402
ENSMUSG00000009079	chr11	Ewsr1	0.56941085	9.40411E-05	0.000244297	6.359457325	0.024523508	1	1053	975	818	1180	902	1894	1708	1412	1517	1491
ENSMUSG00000018974	chr5	Sart3	0.69911768	9.43713E-05	0.000245109	3.757708474	0.033092227	1	134	120	130	224	160	349	324	239	230	219
ENSMUSG00000021835	chr14	Bmp4	-0.8062374	9.48803E-05	0.000246385	2.76187544	0.04078466	-1	146	132	127	143	85	111	77	66	71	74
ENSMUSG00000052911	chr9	Lamb2	-0.7036715	9.52304E-05	0.000247249	7.415509631	0.038204871	-1	2485	2471	2705	4897	3407	2048	1993	2237	1824	2467
ENSMUSG00000095115	chr7	Itpripl2	0.56430398	9.54514E-05	0.000247776	5.023404691	0.0228629	1	361	389	391	483	326	753	738	573	514	592
ENSMUSG00000069910	chr11	Spdl1	1.87106621	9.65963E-05	0.000250702	0.554222048	0.197817872	1	13	1	10	9	9	39	41	18	59	13
ENSMUSG00000052504	chr16	Epha3	1.67998442	9.71572E-05	0.000252064	0.322924203	0.139589299	1	2	7	12	12	6	33	26	10	26	45
ENSMUSG00000059447	chr5	Hadhb	-0.6744868	9.71424E-05	0.000252064	8.048069851	0.035330986	-1	3832	5272	4780	7088	3544	3733	3144	3251	3430	3054
ENSMUSG00000026585	chr1	Kifap3	0.59814635	9.72539E-05	0.000252268	4.319563536	0.024758531	1	246	238	176	293	227	362	392	413	376	397

ENSMUSG00000043421	chr6	Hilpda	1.03631518	9.72996E-05	0.00025234	2.718756471	0.071169483	1	53	74	73	67	45	255	154	94	101	117
ENSMUSG00000028957	chr4	Per3	-0.9647942	9.75145E-05	0.00025285	4.684771235	0.06952651	-1	661	641	592	336	247	324	314	237	273	274
ENSMUSG00000095464	chr16	Gm21987	0.63877489	9.78274E-05	0.000253614	6.050444409	0.030973054	1	839	740	695	949	646	1841	1303	1198	1267	1001
ENSMUSG00000004460	chr16	Dnajb11	0.62355208	9.80844E-05	0.000254234	5.830294804	0.029335273	1	662	599	616	867	602	1200	1397	970	1194	857
ENSMUSG00000040824	chr7	Snrpd2	0.63932224	9.84082E-05	0.000255026	5.480371929	0.030547915	1	609	509	480	571	421	1046	929	784	988	678
ENSMUSG00000028889	chr4	Yrdc	0.81504674	9.84273E-05	0.000255028	3.296444496	0.044732175	1	104	113	104	136	69	276	258	172	169	141
ENSMUSG00000020150	chr10	Gamt	1.03809553	9.84968E-05	0.000255113	6.220438507	0.082289458	1	1222	725	551	477	604	1354	1338	2058	1154	2209
ENSMUSG00000044763	chr16	Trmt10c	-0.5972166	9.8493E-05	0.000255113	3.926948219	0.023612475	-1	249	276	253	359	225	187	232	179	188	194
ENSMUSG00000045672	chr4	Col27a1	0.86940241	9.8562E-05	0.000255235	2.787806505	0.048139006	1	75	54	78	66	79	203	146	136	107	127
ENSMUSG00000099364	chr1	5730419F03Rik	1.67314806	9.88029E-05	0.000255811	0.46125621	0.154142128	1	3	11	8	19	4	20	27	27	54	24
ENSMUSG00000031557	chr8	Plekha2	0.63026579	9.8898E-05	0.000255992	4.825638296	0.028761592	1	418	343	241	315	323	575	574	486	558	608
ENSMUSG00000034271	chr12	Jdp2	0.9443914	9.89093E-05	0.000255992	2.994473824	0.060114508	1	82	76	78	83	77	279	160	185	100	125
ENSMUSG00000052214	chr7	Opa3	-0.6520226	9.96052E-05	0.000257745	6.704669397	0.032743203	-1	1953	1644	1868	2335	1705	1069	1340	1096	1442	1651
ENSMUSG00000022639	chr16	5330426P16Rik	0.76857538	9.96719E-05	0.000257822	2.677228801	0.035443333	1	67	60	60	94	66	176	129	107	124	112
ENSMUSG00000032329	chr9	Hmg20a	-0.5613832	9.96597E-05	0.000257822	4.557785552	0.022068981	-1	466	387	395	436	387	340	301	265	293	351
ENSMUSG00000017146	chr11	Brca1	1.44004867	0.000100132	0.000258966	0.997717101	0.116638326	1	21	13	16	9	14	44	65	35	56	21
ENSMUSG00000022126	chr14	Irg1	2.18538263	0.000100475	0.000259805	0.150603533	0.259811093	1	1	2	1	18	5	55	21	17	12	27
ENSMUSG00000087698	chr4	Gm13031	-1.5273272	0.00010124	0.000261733	0.158808326	0.101113039	-1	26	26	20	17	21	13	10	10	7	2
ENSMUSG00000028312	chr4	Smc2	1.03238504	0.000101368	0.000262017	2.538788822	0.070016543	1	42	48	56	71	60	119	192	77	146	89
ENSMUSG00000030967	chr7	Zranb1	-0.5818128	0.000101726	0.000262894	6.431250898	0.025948466	-1	1619	1548	1333	1815	1390	1241	1005	995	1047	1365
ENSMUSG00000026365	chr1	Cfh	-0.844478	0.000101745	0.000262894	3.57178567	0.050454312	-1	183	234	242	217	236	193	119	78	119	190
ENSMUSG00000032047	chr9	Acat1	-0.6592978	0.000102144	0.000263875	7.434879431	0.033840889	-1	2630	3326	3111	4551	2332	2408	2089	2044	2446	1933
ENSMUSG00000046280	chr3	She	-0.7722458	0.000102173	0.000263901	3.167247362	0.038963954	-1	138	182	168	235	118	109	95	117	86	127
ENSMUSG00000029599	chr5	Ddx54	0.59564039	0.00010234	0.000264285	5.094366338	0.026048495	1	404	343	301	531	451	844	729	567	590	635
ENSMUSG00000086938	chr19	4930481A15Rik	2.70857612	0.000102483	0.000264603	0.295321582	0.418945291	1	1	11	1	4	4	1	35	46	29	40
ENSMUSG00000081128	chr2	Gm13328	-1.3378414	0.000102502	0.000264603	1.028771525	0.099897413	-1	36	34	43	61	34	38	12	16	15	9
ENSMUSG00000040374	chr3	Pex2	-0.5675705	0.000102544	0.000264665	4.710573704	0.022931513	-1	475	452	423	541	427	335	367	271	391	350
ENSMUSG00000015889	chr10	Lta4h	0.55739511	0.000102648	0.000264884	4.841069164	0.022263637	1	358	330	282	457	306	564	649	429	552	588
ENSMUSG00000033918	chr16	Parl	0.57117199	0.000102672	0.000264895	5.293884074	0.024114389	1	420	445	409	669	424	942	705	709	753	715
ENSMUSG00000028834	chr4	Trim63	-0.6165513	0.000102814	0.000265213	7.286966792	0.029584691	-1	2814	2993	2261	3655	2446	2673	1763	1664	1784	2261
ENSMUSG00000011831	chr5	Evi5	-0.6372612	0.000103331	0.000266498	3.567381214	0.026343904	-1	202	191	225	264	184	136	175	130	142	167
ENSMUSG00000055670	chr11	Zzef1	-0.5574948	0.000103366	0.000266539	4.594212571	0.021842246	-1	382	385	435	529	402	332	309	321	289	335
ENSMUSG00000041329	chr11	Atp1b2	-0.6942188	0.000103628	0.000267117	9.216983245	0.037867086	-1	11679	9168	8241	12859	12804	7080	7669	6949	6016	9448
ENSMUSG00000070420	chr5	Zscan25	-0.8738893	0.000103613	0.000267117	2.569410583	0.047939881	-1	99	84	122	161	100	66	63	48	65	95
ENSMUSG00000001656	chr15	Hoxc11	0.97705643	0.000103781	0.000267461	2.54215122	0.063225188	1	56	56	43	94	42	83	105	141	116	165
ENSMUSG00000056671	chr18	Prelid2	1.60945407	0.000104414	0.000269042	0.697306246	0.147456186	1	8	5	12	20	10	69	21	45	29	19
ENSMUSG00000089865	chr9	Dyx1c1Ccpg1	-0.5618339	0.000104717	0.000269774	5.95144213	0.023952673	-1	1031	1093	898	1411	1077	991	772	717	756	855
ENSMUSG00000074210	chr7	E130208F15Rik	-1.5115199	0.000104746	0.000269799	0.234718929	0.108855538	-1	23	28	24	24	18	17	2	12	6	8
ENSMUSG00000009614	chr2	Sardh	0.94200009	0.000104875	0.000270082	2.347914775	0.055120086	1	41	46	43	53	67	141	99	106	71	118
ENSMUSG00000020696	chr11	Rffl	-0.7896111	0.000104914	0.000270131	2.964641636	0.040290445	-1	140	157	148	178	105	81	93	67	97	123
ENSMUSG00000032299	chr9	Commd4	0.67445884	0.000106151	0.000273268	4.22529366	0.032310854	1	262	193	203	223	181	492	378	303	412	286
ENSMUSG00000041341	chr12	Atg2b	-0.5594146	0.000106625	0.000274438	4.661270719	0.02224213	-1	425	366	397	586	471	368	333	317	296	351
ENSMUSG00000016495	chr19	Plgrkt	0.67271672	0.000106977	0.000275292	3.763645347	0.030732043	1	161	186	138	174	113	329	299	211	280	236
ENSMUSG00000020847	chr11	Rph3al	-0.9528216	0.000107127	0.000275628	2.643312917	0.059618748	-1	113	105	93	173	125	55	82	49	100	53
ENSMUSG00000002076	chr17	Hsf2bp	1.7724549	0.000107188	0.000275734	-0.277446739	0.121910466	1	6	3	4	6	4	27	8	25	15	12
ENSMUSG00000026743	chr2	Mllt10	-0.6225262	0.00010739	0.000276203	3.764922512	0.025827511	-1	225	231	240	313	213	178	187	139	145	222
ENSMUSG00000035443	chr9	Thyn1	0.61918726	0.000107589	0.000276664	4.004555777	0.026271118	1	191	196	159	231	161	327	349	257	360	280
ENSMUSG00000050796	chr4	B3galt6	0.99389982	0.000107721	0.000276953	1.874342902	0.057046423	1	36	33	38	39	29	54	96	76	64	92
ENSMUSG00000057561	chr18	Eif1a	0.72630926	0.000107812	0.000277083	4.15768412	0.037937492	1	235	193	173	235	161	476	479	241	349	275
ENSMUSG00000062949	chrX	Atp11c	-0.9391241	0.000107811	0.000277083	2.199864758	0.054255711	-1	86	83	72	122	80	41	66	32	42	71
ENSMUSG00000019467	chr10	Arhgef25	0.69453029	0.000108185	0.00027799	4.21561266	0.034529877	1	255	176	190	224	201	525	315	405	303	319
ENSMUSG00000005802	chr2	Slc30a4	-0.6198432	0.000108228	0.000278051	4.610919885	0.027746544	-1	447	402	379	553	422	248	328	273	365	343
ENSMUSG00000028911	chr4	Srsf4	0.55975432	0.000109111	0.000280268	4.941915225	0.022823269	1	354	298	323	521	364	737	558	558	547	587
ENSMUSG00000017188	chr11	Coa3	0.5927733	0.000109298	0.000280645	5.874665719	0.026827645	1	778	656	571	809	666	1210	1185	1200	1164	963
ENSMUSG00000038482	chr8	Tfdp1	-0.7282452	0.000109295	0.000280645	5.073011811	0.04002729	-1	581	570	545	792	637	267	519	318	484	463
ENSMUSG00000039741	chr11	Bahcc1	-0.7636889	0.000109383	0.000280804	3.099533053	0.038280292	-1	114	133	178	211	158	99	114	103	90	105
ENSMUSG00000042508	chr5	Dmtf1	-0.7039065	0.000109417	0.000280804	3.130161927	0.031337685	-1	168	150	129	200	154	103	111	83	130	109
ENSMUSG00000071419	chr6	Rps15-ps2	0.66401841	0.000109421	0.000280804	3.863207783	0.030274113	1	168	189	123	196	156	400	245	251	288	267
ENSMUSG00000017386	chr11	Traf4	0.81261704	0.000109447	0.00028082	3.604277388	0.046492569	1	141	145	111	144	108	236	254	325	147	283
ENSMUSG00000005949	chr11	Ctns	0.69545974	0.000109682	0.000281373	3.323572913	0.031137213	1	109	122	106	112	108	263	172	163	178	228
ENSMUSG00000042073	chr9	Abhd14b	0.91019134	0.000109802	0.000281628	2.501000697	0.052905702	1	76	64	42	71	35	110	108	96	120	155
ENSMUSG00000098178	chr17	Yam1	0.87446839	0.000109873	0.00028176	12.20041007	0.060288655	1	50091	30921	34212	63974	68938	90798	125248	96129	71076	114628
ENSMUSG00000036372	chr19	Tmem258	0.60885819	0.000110022	0.00028209	5.136807396	0.027523691	1	424	429	391	408	397	890	759	584	683	556
ENSMUSG00000037531	chr3	Mrpl47	-0.611503	0.000110608	0.000283541	4.661969838	0.027173972	-1	465	425	482	597	316	405	332	297	320	278
ENSMUSG00000053870	chr3	Fpgt	-0.9375544	0.000111391	0.000285495	2.152104745	0.053699681	-1	82	74	63	137	76	64	58	27	46	50

ENSMUSG00000047514	chr10	Tspyl1	-0.591162	0.000111517	0.000285764	6.008095681	0.026856528	-1	1361	1081	970	1338	1015	792	859	708	842	985
ENSMUSG00000005628	chr3	Tmod4	-0.6866399	0.000111967	0.000286865	8.606494355	0.037354948	-1	8114	7189	6439	7606	6327	4012	4853	3845	5703	5897
ENSMUSG00000009640	chr4	Dmap1	0.60775694	0.000112052	0.00028703	4.042600636	0.025378398	1	231	165	177	220	172	388	327	307	312	279
ENSMUSG00000020014	chr10	Cfap54	-1.3639446	0.000112839	0.000288992	0.303073235	0.079819445	-1	15	32	22	28	23	10	15	9	7	10
ENSMUSG00000027086	chr2	Fastkd1	-0.6120769	0.000113237	0.000289959	3.71159423	0.024762728	-1	197	236	222	327	197	178	191	152	151	168
ENSMUSG00000024614	chr18	Tmx3	-0.6169753	0.000113614	0.000290871	4.48084843	0.027481614	-1	400	329	352	569	375	291	376	209	264	299
ENSMUSG00000037411	chr5	Serpine1	1.80515838	0.000114293	0.000292556	4.230737728	0.23991194	1	156	103	183	110	57	1218	478	240	432	73
ENSMUSG00000005057	chr5	Sh2b2	0.77092237	0.000114376	0.000292716	2.919115269	0.037743739	1	88	86	70	77	84	145	195	123	138	165
ENSMUSG00000025538	chr5	Sumf2	0.84526826	0.0001144	0.000292723	3.241913142	0.049165549	1	100	85	68	105	135	275	162	204	157	184
ENSMUSG00000032589	chr9	Bsn	1.59153511	0.000114602	0.000293141	0.172945478	0.11094235	1	8	6	7	6	9	18	41	16	15	32
ENSMUSG00000034088	chr1	Hdlbp	-0.6007152	0.000114605	0.000293141	8.307862986	0.028671576	-1	5118	4989	4731	7909	5923	4301	4311	3791	3878	4282
ENSMUSG00000020650	chr12	Bcap29	-0.6862966	0.000114763	0.00029349	4.700622336	0.03506388	-1	521	482	420	559	401	243	423	234	336	384
ENSMUSG00000039230	chr11	Tbcd	0.57217511	0.000114917	0.000293831	4.057806931	0.022253031	1	198	188	161	254	193	334	341	318	286	333
ENSMUSG00000033287	chr15	Kctd17	0.65553697	0.0001155	0.000295266	4.034408044	0.030387311	1	182	162	151	278	179	415	302	328	233	354
ENSMUSG00000102040	chr6	Clec7a	2.1449639	0.000115846	0.000296097	0.41675571	0.263182827	1	5	10	5	1	10	27	25	7	29	73
ENSMUSG00000028580	chr4	Pum1	-0.5883596	0.000115871	0.000296109	5.025923382	0.02575962	-1	552	478	519	733	628	451	472	392	316	495
ENSMUSG00000034765	chr19	Dusp5	1.27407403	0.000117046	0.000299055	2.047543311	0.108045001	1	35	30	19	54	38	169	127	63	56	55
ENSMUSG00000019082	chr7	Slc25a22	0.90110332	0.000117114	0.000299174	4.136650647	0.060956716	1	109	156	138	375	161	509	408	353	322	273
ENSMUSG00000051319	chr2	1500011K16Rik	-0.584205	0.000117166	0.000299254	5.487381955	0.025943891	-1	814	759	715	930	777	597	726	491	594	517
ENSMUSG00000031429	chrX	Psmd10	0.67245373	0.000118037	0.000301422	3.524369417	0.03006116	1	159	131	123	144	96	276	205	201	249	211
ENSMUSG00000022948	chr16	Setd4	1.20123557	0.000118218	0.000301829	0.623811638	0.061662173	1	12	16	11	14	10	47	31	25	27	31
ENSMUSG00000027300	chr2	Ubox5	-0.6284447	0.00011849	0.000302424	3.594160158	0.025932559	-1	238	213	185	260	189	133	152	144	165	170
ENSMUSG00000034245	chr6	Hdac11	-0.729312	0.000118494	0.000302424	3.702882637	0.037318411	-1	299	237	213	211	227	138	137	169	172	171
ENSMUSG00000029346	chr5	Srrd	1.05866897	0.000118798	0.000303145	1.812544859	0.066625418	1	49	26	22	30	35	72	90	50	82	79
ENSMUSG00000036959	chrX	Bcorl1	-0.6658943	0.000118843	0.000303205	4.197916096	0.032028678	-1	360	272	300	386	347	220	223	208	176	328
ENSMUSG00000023905	chr17	Tnfrsf12a	1.44513496	0.000119016	0.000303552	4.981662648	0.159491721	1	178	104	225	550	253	1507	994	623	450	262
ENSMUSG00000053886	chr8	Sh2d4a	-0.8122441	0.000119023	0.000303552	3.144342251	0.044988534	-1	150	220	125	209	129	135	73	105	98	107
ENSMUSG00000099689	chr7	Unspecified	-0.9073475	0.00011917	0.000303871	2.661102608	0.054168917	-1	115	134	121	142	92	49	89	48	71	96
ENSMUSG00000073434	chr17	Wdr90	1.17576565	0.000119275	0.000304084	1.267211586	0.07540404	1	19	21	16	23	24	71	59	34	62	32
ENSMUSG00000051695	chr6	Pcbp1	0.56606415	0.000119843	0.000305477	6.900532938	0.025261571	1	1447	1285	1225	1859	1390	2544	2450	2199	1881	2591
ENSMUSG00000076270	chr14	Mir719	-1.1791355	0.000120062	0.000305979	1.015843797	0.071197434	-1	40	36	32	44	45	11	22	13	24	25
ENSMUSG00000073481	chr1	Marc2	0.56195142	0.000120502	0.000307044	5.907829495	0.024324106	1	724	719	634	800	714	1465	1094	1091	1075	1126
ENSMUSG00000002032	chr9	Tmem25	-0.756016	0.000120612	0.000307213	3.781030066	0.040931732	-1	290	280	276	252	170	135	161	140	176	214
ENSMUSG00000036111	chr7	Lmo1	1.01348051	0.000120593	0.000307213	1.490052479	0.056044124	1	26	27	20	39	21	81	48	45	68	51
ENSMUSG00000022216	chr14	Psme1	0.61655085	0.000120849	0.000307724	5.598752173	0.029271372	1	454	589	513	845	476	1275	889	855	884	900
ENSMUSG00000028124	chr3	Gclm	-0.7395195	0.000120857	0.000307724	3.694129036	0.038638071	-1	263	252	231	292	163	135	194	108	145	206
ENSMUSG00000018740	chr11	Slc25a35	-0.9091732	0.000121572	0.000309488	2.883154951	0.056283853	-1	117	167	161	131	121	69	65	106	78	90
ENSMUSG00000037001	chr11	Zfp39	-0.9433944	0.000121921	0.000310319	2.007193079	0.05238619	-1	82	80	73	87	61	28	48	40	46	55
ENSMUSG00000043391	chr16	2510009E07Rik	-0.6072353	0.000121945	0.000310325	5.008011389	0.02768023	-1	505	462	579	870	505	450	401	398	329	503
ENSMUSG00000041842	chr3	Fhdc1	1.69002716	0.000122356	0.000311314	-0.328605378	0.105459809	1	4	2	7	6	4	11	11	17	21	22
ENSMUSG00000097245	chr10	Gm5421	-0.934991	0.000122914	0.000312676	2.021721887	0.052717882	-1	57	78	68	110	76	40	36	42	41	62
ENSMUSG00000028295	chr4	Smim8	0.75390187	0.000122954	0.000312722	3.577149677	0.040040428	1	137	146	111	187	82	206	268	238	282	206
ENSMUSG00000036867	chr9	Smad6	-0.97666	0.000123383	0.000313755	2.191290739	0.060343256	-1	88	85	85	107	76	50	57	61	22	55
ENSMUSG00000021643	chr13	Serf1	0.90103226	0.000123688	0.000314473	2.444305469	0.051824182	1	79	54	33	55	54	132	100	104	96	134
ENSMUSG00000024844	chr19	Banf1	0.61276061	0.000123825	0.000314764	6.484436061	0.029600648	1	1108	1028	847	1356	961	2269	1913	1653	1657	1362
ENSMUSG00000019817	chr10	Plagl1	1.60443504	0.00012413	0.000315483	4.427072626	0.194196529	1	175	151	142	164	151	153	385	661	168	1241
ENSMUSG00000000901	chr10	Mmp11	0.99100084	0.000124197	0.000315595	2.533200364	0.065235636	1	69	69	53	49	39	153	107	138	71	147
ENSMUSG00000055633	chr7	Zfp580	1.17833153	0.000124276	0.000315738	1.749631658	0.086658937	1	20	23	33	40	31	96	55	91	37	87
ENSMUSG00000040078	chr6	Gm9769	-0.9628523	0.000124318	0.000315789	2.476624134	0.061250747	-1	111	111	87	145	88	38	73	41	84	64
ENSMUSG00000025962	chr1	Fastkd2	-0.6603336	0.000124425	0.000316002	4.115079319	0.031302749	-1	331	317	271	436	234	204	219	165	276	223
ENSMUSG00000042807	chr1	Hecw2	-1.1355327	0.000124836	0.00031699	1.529668689	0.07728129	-1	42	41	50	92	63	33	34	15	37	23
ENSMUSG00000022021	chr14	Diap3	1.50029739	0.00012492	0.000317145	0.726152039	0.126055485	1	10	11	15	17	6	29	70	22	38	24
ENSMUSG00000035529	chr10	Prdm4	-0.5362592	0.000125075	0.000317481	4.425866597	0.020284124	-1	369	352	323	470	376	311	300	234	267	318
ENSMUSG00000022407	chr15	Adsl	-0.6803288	0.000125608	0.000318776	6.675707155	0.036726826	-1	1689	1675	1596	2774	1756	967	1337	1088	1401	1587
ENSMUSG00000028959	chr5	Fastk	-0.5623211	0.000125704	0.000318904	7.346575453	0.025226802	-1	2857	2592	2777	3712	2572	2438	2037	2068	2119	2058
ENSMUSG00000036733	chr7	Rbm42	0.5564494	0.000125691	0.000318904	5.198896526	0.023332142	1	467	367	370	612	413	902	676	670	638	685
ENSMUSG00000055200	chr7	Sertad3	0.74018974	0.000125785	0.000319051	3.135607814	0.036286182	1	114	113	84	107	65	216	168	179	142	181
ENSMUSG00000032766	chr6	Gng11	0.70510059	0.000125877	0.000319226	5.060375856	0.038146403	1	426	407	404	448	204	696	561	607	682	817
ENSMUSG00000057751	chr4	Megf6	1.52027399	0.000126517	0.000320792	1.525581417	0.153029146	1	22	16	22	27	18	138	29	62	25	84
ENSMUSG00000043067	chr9	Dpy19l1	0.63747297	0.000126688	0.000321167	3.804792771	0.027976863	1	176	148	171	180	130	329	338	218	254	244
ENSMUSG00000000253	chr13	Gmpr	-0.5694984	0.000126889	0.000321617	7.60551197	0.02598273	-1	3472	3390	2873	4501	3195	2772	2487	2137	2452	2990
ENSMUSG00000024399	chr17	Ltb	2.27847366	0.000127188	0.000322317	0.315597261	0.296205337	1	8	5	5	4	5	90	8	15	29	11
ENSMUSG00000007646	chr11	Rad51c	1.60030453	0.000127965	0.000324227	0.073954262	0.106899351	1	5	7	5	5	11	24	37	19	13	20
ENSMUSG00000042298	chr11	Ttc19	-0.6062042	0.000128298	0.000325013	5.200043801	0.028017513	-1	593	611	587	899	628	386	549	399	470	565
ENSMUSG00000071644	chr19	Eef1g	0.58762732	0.000128432	0.000325292	9.106924223	0.027930108	1	6655	6116	5704	8357	6133	12066	11177	10886	8630	11380

ENSMUSG00000075054	chr13	Yae1d1	-0.7087965	0.000128878	0.000326363	3.2647676	0.033614335	-1	199	151	143	227	164	109	150	82	124	125
ENSMUSG00000006403	chr1	Adamts4	1.86893921	0.000128964	0.000326521	1.71836854	0.236400085	1	29	11	20	14	24	205	70	83	22	33
ENSMUSG00000041974	chr16	Spidr	1.07889085	0.000129321	0.000327367	1.587695515	0.06858007	1	35	29	21	30	22	65	89	33	64	69
ENSMUSG00000032380	chr9	Dapk2	-1.0339488	0.000130289	0.000329758	3.398592456	0.079048211	-1	197	224	193	232	195	230	84	108	50	99
ENSMUSG00000028248	chr4	Pnisr	-0.5956675	0.000130335	0.000329813	4.924365678	0.026755479	-1	619	553	492	519	506	412	377	305	404	475
ENSMUSG00000024772	chr19	Ehd1	0.60468577	0.000130386	0.000329882	5.609221867	0.02837829	1	566	488	498	748	590	1314	927	835	951	794
ENSMUSG00000067608	chr19	Pcna-ps2	1.27879614	0.000130689	0.000330589	0.800191198	0.086668897	1	10	15	7	27	12	41	42	35	43	24
ENSMUSG00000038602	chr10	Slc35f1	-1.2736351	0.000131071	0.000331496	0.379872874	0.072094869	-1	27	24	27	27	20	21	9	9	8	10
ENSMUSG00000060639	chr13	Hist1h4i	0.90567481	0.000131109	0.000331532	4.603291419	0.063287121	1	313	218	229	271	220	249	663	455	663	509
ENSMUSG00000024387	chr17	Csnk2b	0.59045041	0.000131599	0.000332711	6.486318709	0.027677316	1	1019	970	833	1467	1080	2085	1623	1763	1468	1865
ENSMUSG00000000568	chr5	Hnrnpd	0.63116689	0.00013167	0.000332829	5.458925611	0.030930466	1	451	467	436	733	501	997	1142	769	720	742
ENSMUSG00000021361	chr13	Tmem14c	0.59813705	0.00013205	0.00033373	5.956693025	0.028108448	1	768	714	685	986	553	1426	1352	1077	1253	994
ENSMUSG00000086298	chr11	Gm11716	-0.9107286	0.000132083	0.000333754	4.106489679	0.063108827	-1	228	333	306	526	296	348	147	137	217	134
ENSMUSG00000027642	chr2	Rpn2	0.59394127	0.000133053	0.000336144	6.799717995	0.028179657	1	1363	1231	1087	1631	1313	2645	2610	1737	2051	1952
ENSMUSG00000054079	chr11	Utp18	0.75276008	0.000133368	0.000336878	3.294123169	0.038872073	1	119	103	88	134	95	220	263	143	219	149
ENSMUSG00000014905	chr12	Dnajb9	-0.6999498	0.000134157	0.00033881	4.418346018	0.036782545	-1	403	369	331	570	316	208	347	185	248	339
ENSMUSG00000022752	chr16	Tomm70a	-0.6051761	0.000134522	0.000339672	6.178191835	0.028984011	-1	1282	1182	1272	1740	1070	796	1030	827	1029	981
ENSMUSG00000023224	chr2	Serping1	0.68612959	0.000134629	0.000339879	6.558038158	0.037640694	1	1024	1028	913	1350	1072	2904	1607	1624	1308	2167
ENSMUSG00000044268	chr10	Gm4895	-1.6888214	0.000134859	0.000340399	-0.333564641	0.106333748	-1	13	16	15	9	23	6	4	5	6	5
ENSMUSG00000021000	chr12	Ctage5	-0.5558774	0.000135179	0.000341145	5.6708017	0.024019065	-1	856	807	831	1192	846	816	743	528	638	656
ENSMUSG00000017740	chr2	Slc12a5	-1.4150989	0.000136002	0.000343161	0.064299948	0.079388618	-1	20	17	22	31	12	10	7	11	5	8
ENSMUSG00000059408	chr17	Mrgprh	-1.1581726	0.000136067	0.000343262	1.312060676	0.076186107	-1	65	48	37	51	43	24	23	18	38	16
ENSMUSG00000066361	chr12	Serpina3c	-1.3623432	0.000136325	0.00034385	1.48100108	0.120278835	-1	24	68	57	83	57	46	14	24	15	25
ENSMUSG00000024401	chr17	Tnf	1.60386426	0.000137542	0.000346859	0.387086166	0.133972902	1	6	10	11	13	3	44	38	13	34	16
ENSMUSG00000040181	chr1	Fmo1	0.86402095	0.000137833	0.00034753	3.824009456	0.055688464	1	113	164	135	174	152	195	249	393	246	375
ENSMUSG00000002625	chr17	Akap8l	-0.5591619	0.00013813	0.000348214	4.404930609	0.022609473	-1	410	393	319	396	345	320	265	238	260	313
ENSMUSG00000030032	chr6	Wdr54	1.45988059	0.0001382	0.000348329	0.357899201	0.099330264	1	8	3	6	11	17	32	21	26	30	28
ENSMUSG00000026074	chr1	Map4k4	0.57946616	0.000138374	0.000348704	5.730237371	0.026292044	1	640	625	565	797	549	1331	1013	1058	790	1010
ENSMUSG00000058914	chr15	C1qtnf3	1.14945292	0.000138399	0.000348705	4.487727033	0.103004295	1	340	159	180	254	112	552	408	714	187	643
ENSMUSG00000002329	chr14	Mdp1	0.52377544	0.000138481	0.000348848	4.881309379	0.020285692	1	351	340	356	442	307	596	532	557	568	566
ENSMUSG00000048732	chr11	Klhl11	-1.2794678	0.000138529	0.000348907	0.370519019	0.070616516	-1	28	24	30	25	17	11	11	7	13	14
ENSMUSG00000024843	chr19	Chka	1.13474546	0.000138655	0.000349161	1.952015597	0.082885618	1	27	29	39	43	35	143	101	75	48	57
ENSMUSG00000101556	chr17	Gm28869	1.53306888	0.000138709	0.000349233	0.522930133	0.129418775	1	7	10	8	17	8	33	23	11	51	40
ENSMUSG00000038902	chr3	Pogz	-0.6080777	0.000139022	0.000349958	4.333020427	0.027000251	-1	326	338	333	447	360	213	291	268	223	296
ENSMUSG00000022330	chr15	Osr2	1.52899852	0.000139183	0.000350301	1.291046256	0.153564344	1	9	14	20	40	8	92	27	57	35	71
ENSMUSG00000025723	chr7	Nmb	1.39178913	0.000139397	0.000350776	0.747463636	0.103938311	1	8	11	17	12	14	66	40	20	29	30
ENSMUSG00000100017	chr14	2410022M11Rik	1.08688938	0.000140116	0.000352523	1.162262514	0.063348167	1	17	18	19	31	16	38	46	57	36	55
ENSMUSG00000061751	chr16	Kalrn	-0.6292416	0.000140392	0.000353152	3.728246112	0.027286365	-1	220	213	214	312	235	143	188	139	179	192
ENSMUSG00000015354	chr9	Pcolce2	-0.7088306	0.000141295	0.00035536	3.038791238	0.032895164	-1	161	147	139	176	127	107	131	82	101	82
ENSMUSG00000071649	chr19	B3gat3	0.56260963	0.000141933	0.000356902	5.247707401	0.024280754	1	480	436	406	516	435	879	778	644	781	609
ENSMUSG00000022560	chr15	Slc52a2	0.89826234	0.00014206	0.000357156	2.485560986	0.052683949	1	73	74	36	68	35	134	127	106	103	112
ENSMUSG00000021258	chr12	Ccnk	-0.6282286	0.00014238	0.000357896	5.519838636	0.0310063	-1	733	652	639	1176	975	608	633	549	524	624
ENSMUSG00000048661	chr10	Lemd3	-0.6924089	0.000143077	0.000359584	3.603624667	0.033782499	-1	207	206	178	328	204	142	206	122	115	170
ENSMUSG00000019738	chr7	Polr2i	0.55211001	0.000143709	0.000361041	4.538385368	0.022194423	1	288	293	252	301	256	485	469	355	469	470
ENSMUSG00000028840	chr4	Zfp593	0.83588978	0.000143689	0.000361041	2.980014078	0.047753378	1	94	99	79	76	63	220	165	136	177	116
ENSMUSG00000035047	chr9	Kri1	0.66399514	0.000143841	0.00036131	3.35680381	0.029812154	1	113	107	84	177	110	255	222	170	185	186
ENSMUSG00000024043	chr17	Arhgap28	0.89906476	0.000144243	0.000362253	2.575039474	0.05353161	1	58	57	61	66	59	120	98	167	91	138
ENSMUSG00000007564	chr17	Ppp2r1a	0.5462137	0.000144373	0.000362515	7.097832426	0.02414469	1	1645	1588	1405	2035	1630	3007	2787	2437	2414	2648
ENSMUSG00000026411	chr1	Tmem9	0.72322735	0.000144824	0.000363582	3.8966044	0.038186017	1	179	181	158	159	145	373	275	350	193	312
ENSMUSG00000004455	chr5	Ppp1cc	-0.5877118	0.000145158	0.000364356	5.866480978	0.027370434	-1	1036	1015	967	1377	851	710	833	574	849	834
ENSMUSG00000032315	chr9	Cyp1a1	-1.4071768	0.000145495	0.000365134	0.84730323	0.116716645	-1	61	46	25	23	26	20	21	10	12	13
ENSMUSG00000037523	chr2	Mavs	-0.6508169	0.000145875	0.000366023	5.568856803	0.03349267	-1	749	709	666	1528	774	672	553	550	572	667
ENSMUSG00000000416	chr6	Cttnbp2	-1.4032776	0.00014592	0.000366071	0.221464639	0.088530625	-1	20	25	29	28	12	9	9	6	8	15
ENSMUSG00000032288	chr9	Imp3	0.61576187	0.000146448	0.000367328	4.967061383	0.029115844	1	392	407	308	400	321	888	616	558	532	506
ENSMUSG00000025777	chr1	Gdap1	-1.2493995	0.000146525	0.000367456	2.470850711	0.112544492	-1	137	111	89	86	138	20	77	34	58	73
ENSMUSG00000036305	chr15	Rpl39-ps	0.92697213	0.000146717	0.000367871	2.364973245	0.055973252	1	67	58	48	49	34	146	127	70	98	101
ENSMUSG00000026938	chr2	Fcna	1.63122558	0.000146992	0.000368495	2.122132092	0.189987994	1	42	38	25	18	26	280	71	80	44	61
ENSMUSG00000005338	chr1	Cadm3	-0.9731721	0.000148433	0.000372041	3.874596992	0.072731611	-1	286	205	267	384	303	345	120	126	109	121
ENSMUSG00000004071	chr16	Cdip1	-0.5584274	0.000148625	0.000372455	6.693369772	0.025195786	-1	1711	1742	1559	2410	1799	1394	1332	1207	1411	1480
ENSMUSG00000028161	chr3	Ppp3ca	-0.6039266	0.000148803	0.000372834	7.778422488	0.02988793	-1	4245	3572	3237	4857	3874	2900	2938	2508	2308	3621
ENSMUSG00000099913	chr1	Gm28551	-0.5734828	0.000149177	0.000373704	6.07616652	0.026261397	-1	1179	1130	1046	1628	1069	812	1010	737	928	929
ENSMUSG00000040631	chr8	Dok4	-0.6528174	0.000149309	0.000373969	3.729563512	0.030273486	-1	210	231	232	360	181	224	140	144	156	176
ENSMUSG00000020689	chr11	Itgb3	1.27688854	0.00014944	0.00037423	2.711306998	0.119969759	1	46	56	51	70	55	332	83	99	68	181
ENSMUSG00000031023	chr7	Akip1	0.73072996	0.000149518	0.000374359	2.998585209	0.035257025	1	105	89	79	98	69	196	179	141	162	124
ENSMUSG00000020111	chr10	Micu1	0.56546355	0.00014982	0.000375046	6.438026474	0.025758678	1	1012	987	908	1375	952	1828	1477	1733	1586	1797

ENSMUSG00000063564	chr11	Col23a1	1.03756577	0.00014996	0.000375331	2.978052147	0.078522291	1	46	72	67	117	79	281	114	133	103	234
ENSMUSG00000035824	chr8	Tk2	0.80082734	0.000150065	0.000375525	2.93436624	0.043556338	1	108	81	81	84	53	215	145	136	125	164
ENSMUSG00000053931	chr3	Cnn3	0.69209893	0.00015137	0.000378723	5.909918192	0.038512652	1	761	598	647	859	569	1648	1244	1350	730	1112
ENSMUSG00000043059	chr5	Zfp513	0.73194089	0.000151701	0.000379483	3.135620876	0.036485033	1	82	91	71	146	100	219	157	180	137	192
ENSMUSG00000058396	chr10	Gpr182	1.58647248	0.000152556	0.000381554	-0.245020585	0.096994276	1	6	10	2	5	3	20	15	12	22	18
ENSMUSG00000020413	chr11	Hus1	-0.6864826	0.000152797	0.000382088	3.335073564	0.031945351	-1	175	161	173	245	168	98	137	119	144	122
ENSMUSG00000028842	chr4	Ago3	-0.6893828	0.000153485	0.00038374	3.48945707	0.033573797	-1	196	165	211	215	227	166	166	114	104	150
ENSMUSG00000026171	chr1	Rnf25	0.59488668	0.000153964	0.00038487	4.063732268	0.025410562	1	217	167	183	249	173	446	298	280	287	331
ENSMUSG00000031917	chr8	Nip7	0.66791675	0.000154044	0.000384931	3.864209107	0.032366771	1	165	166	161	225	120	396	299	247	294	217
ENSMUSG00000064080	chr6	Fbln2	0.61236581	0.000154021	0.000384931	6.248979297	0.030311895	1	748	719	828	1352	881	1540	1545	1322	1322	1785
ENSMUSG00000094365	chr7	Gm21982	0.54981407	0.000155102	0.000387505	5.330282821	0.023580793	1	513	414	396	678	450	959	765	725	724	729
ENSMUSG00000030275	chr6	Etnk1	-0.5500514	0.000155731	0.000389007	5.114776216	0.023347506	-1	526	578	530	823	617	486	519	380	392	522
ENSMUSG00000020598	chr12	Nrcam	1.51595347	0.000156671	0.000391285	1.221515758	0.146717682	1	17	12	18	17	19	120	60	22	37	33
ENSMUSG00000029385	chr5	Ccng2	-0.7283109	0.000156866	0.000391702	4.197221356	0.040556323	-1	413	410	299	316	245	269	213	180	167	302
ENSMUSG00000041037	chr7	Irgq	-0.5398592	0.000156996	0.000391958	5.095899638	0.022358148	-1	627	506	531	855	525	474	434	468	405	484
ENSMUSG00000028136	chr3	Snx27	-0.5733383	0.000157164	0.000392306	5.704528774	0.026187315	-1	969	850	787	1170	881	773	810	479	672	704
ENSMUSG00000042377	chr11	Fam83g	1.22651017	0.000157591	0.000393302	1.006174524	0.083505147	1	17	19	14	18	15	23	49	40	39	62
ENSMUSG00000005615	chr16	Pcyt1a	-0.5945445	0.000157864	0.000393913	6.988280505	0.028971239	-1	2436	2213	2076	2679	1977	1440	1795	1374	1612	2031
ENSMUSG00000020661	chr12	Dnmt3a	-0.7263516	0.000157892	0.000393914	6.812865274	0.043250266	-1	1650	1825	1838	3138	2103	1227	1462	1186	1021	2042
ENSMUSG00000022452	chr15	Smdt1	0.54973545	0.000158031	0.000394188	6.501847664	0.024514152	1	1103	1071	990	1374	955	2125	1687	1750	1532	1702
ENSMUSG00000020272	chr11	Stk10	0.75765988	0.000158329	0.000394863	3.006226053	0.038810791	1	70	96	95	112	65	209	188	123	130	168
ENSMUSG00000040033	chr10	Stat2	0.62956678	0.000158387	0.000394935	3.331798468	0.026227296	1	112	128	103	137	101	196	222	173	171	225
ENSMUSG00000036459	chr7	Wtip	0.92921557	0.000158689	0.000395618	3.050722658	0.062510706	1	85	87	69	100	77	341	145	117	133	155
ENSMUSG00000087249	chr11	Gm16062	-0.7688604	0.00015927	0.000396996	2.58034684	0.037289519	-1	102	90	109	167	90	69	76	62	73	74
ENSMUSG00000036613	chr12	Tssc1	0.73503202	0.000159373	0.000397182	2.732625051	0.034556981	1	91	71	60	85	58	155	135	116	138	121
ENSMUSG00000001999	chr2	Blvra	0.73670559	0.000159416	0.000397218	4.194651866	0.041361347	1	226	193	185	228	182	520	432	201	411	313
ENSMUSG00000090084	chrX	Srpx	0.69926129	0.000159689	0.000397826	4.010694821	0.036244649	1	177	181	161	153	220	334	330	268	281	408
ENSMUSG00000022044	chr14	Stmn4	-1.2666054	0.000159751	0.000397912	0.800018816	0.086333048	-1	22	24	47	43	35	22	14	16	15	11
ENSMUSG00000035559	chr8	Mpv17l2	0.61992078	0.000160212	0.000398988	3.819825675	0.027318063	1	214	136	132	192	150	337	257	249	274	270
ENSMUSG00000029610	chr5	Aimp2	-0.6756685	0.000160306	0.000399151	7.621427341	0.037743015	-1	4527	3609	3241	3238	3236	2317	2798	2043	2132	3122
ENSMUSG00000019338	chr3	Zfp687	-0.6503262	0.00016085	0.000400435	4.160351148	0.031647168	-1	342	329	275	330	330	196	229	211	186	307
ENSMUSG00000029430	chr5	Ran	0.6412529	0.00016174	0.000402579	6.728800061	0.033742774	1	1296	1208	1047	1557	1089	2395	2668	1755	2211	1527
ENSMUSG00000100551	chr1	Gm19503	-1.2915349	0.000161924	0.000402965	0.809259401	0.091901719	-1	23	36	24	63	31	17	9	12	22	17
ENSMUSG00000028289	chr4	Epha7	-1.1614703	0.000161983	0.00040304	0.823440062	0.06673596	-1	37	25	30	48	32	11	22	12	20	18
ENSMUSG00000045948	chr7	Mrps12	0.58345424	0.000162199	0.000403506	5.223620112	0.026673782	1	504	475	431	450	348	899	674	729	642	709
ENSMUSG00000054612	chr7	Mgmt	0.97593089	0.000162478	0.000404128	1.992702336	0.060103181	1	49	40	41	38	24	82	82	105	70	74
ENSMUSG00000026241	chr1	Nppc	-1.3433003	0.000162931	0.000405183	0.354015019	0.088808529	-1	23	27	24	32	19	15	18	3	10	8
ENSMUSG00000023206	chr2	Il15ra	-0.6568203	0.000163379	0.000406224	3.223185094	0.028794147	-1	165	170	166	195	144	132	105	102	136	109
ENSMUSG00000028821	chr4	Syf2	0.52252521	0.000163837	0.00040729	5.227004665	0.0211642	1	474	476	417	561	362	812	685	641	729	730
ENSMUSG00000031570	chr8	Ppapdc1b	0.81918956	0.000164196	0.00040811	2.985948957	0.046572791	1	100	87	89	87	55	236	172	127	156	127
ENSMUSG00000027668	chr3	Mfn1	-0.6401552	0.000164484	0.000408754	6.966106825	0.033784954	-1	1810	2095	1950	3804	1924	1579	1766	1492	1596	1523
ENSMUSG00000022853	chr16	Ehhadh	-1.1265066	0.000164609	0.000408991	2.254588727	0.088234684	-1	92	97	103	110	74	18	53	49	42	75
ENSMUSG00000085882	chr11	2610507I01Rik	2.46445443	0.000164658	0.000409041	-0.468188361	0.300901515	1	3	4	4	2	0	0	16	19	24	21
ENSMUSG00000024798	chr19	Htr7	-1.3669839	0.000164888	0.000409539	0.402777662	0.090999607	-1	19	22	34	40	16	10	14	8	7	16
ENSMUSG00000024511	chr18	Rab27b	1.47851309	0.000165131	0.000410068	0.963413816	0.136178372	1	25	11	9	14	12	29	38	51	22	77
ENSMUSG00000070733	chr5	Fryl	-0.6118358	0.000166941	0.000414491	4.411667854	0.028425737	-1	320	367	345	460	411	339	244	253	206	334
ENSMUSG00000042790	chr9	Rnf214	-0.5830044	0.00016716	0.000414961	4.050653538	0.024562186	-1	316	268	260	362	269	200	208	182	226	259
ENSMUSG00000024378	chr18	Stard4	-0.847395	0.000167587	0.000415946	3.450319342	0.053878187	-1	287	186	211	197	150	181	149	95	129	82
ENSMUSG00000028167	chr3	Bdh2	1.33194749	0.000168343	0.000417748	1.02308219	0.102843604	1	11	27	13	15	13	74	54	32	33	31
ENSMUSG00000052942	chr19	Glis3	1.64296967	0.000168391	0.000417793	0.393983299	0.14907905	1	4	11	8	12	7	49	31	19	8	41
ENSMUSG00000019710	chr3	Mrpl24	0.52912554	0.000169137	0.000419571	5.413937744	0.022063663	1	519	492	446	676	474	983	811	699	834	785
ENSMUSG00000029478	chr5	Ncor2	-0.6925999	0.00017016	0.000422033	6.055589754	0.03929852	-1	925	921	1025	1918	1405	856	917	811	646	921
ENSMUSG00000025364	chr10	Pa2g4	0.59762215	0.000170483	0.00042276	6.201637834	0.029199049	1	994	796	753	1069	762	1568	1675	1231	1577	1170
ENSMUSG00000026586	chr1	Prrx1	-0.5548955	0.00017127	0.000424635	5.837621655	0.024869297	-1	941	1033	937	1257	902	1027	733	670	657	714
ENSMUSG00000030838	chr7	Ush1c	-1.4586645	0.000171568	0.000425298	-0.085041015	0.090402864	-1	22	11	19	24	15	14	4	5	6	7
ENSMUSG00000026235	chr1	Epha4	-0.9895129	0.000171874	0.000425906	1.753060493	0.060607929	-1	63	46	63	79	72	45	33	21	30	51
ENSMUSG00000032649	chr1	Colgalt2	-0.7911072	0.00017187	0.000425906	2.913120659	0.043348493	-1	136	156	113	186	115	131	68	90	86	70
ENSMUSG00000030559	chr7	Rab38	1.76530194	0.00017264	0.000427696	0.202122283	0.157153963	1	7	9	13	1	3	20	26	36	17	28
ENSMUSG00000069020	chr2	Urm1	0.60626697	0.000172658	0.000427696	4.740333362	0.028532969	1	324	307	331	390	224	641	509	522	533	414
ENSMUSG00000000631	chr11	Myo18a	-0.6563398	0.000172973	0.000428401	7.529337015	0.035954235	-1	3166	2528	2759	4799	3738	2680	2175	2226	1795	2881
ENSMUSG00000042215	chr1	Bag2	-0.6343091	0.000173193	0.00042887	4.677144752	0.031242011	-1	473	400	420	596	430	249	347	342	378	296
ENSMUSG00000028066	chr3	Pmf1	0.58462061	0.000174089	0.000431013	4.036773586	0.024800688	1	209	202	181	234	147	359	379	268	288	307
ENSMUSG00000034259	chr15	Exosc4	0.5302237	0.000174213	0.000431244	4.545190397	0.020882488	1	309	275	246	306	274	484	443	426	416	471
ENSMUSG00000021906	chr14	Oxnad1	-0.6533389	0.000175214	0.000433645	4.748287415	0.033481214	-1	423	442	530	730	344	312	343	388	323	320
ENSMUSG00000019971	chr10	Cep290	-1.0539359	0.000175821	0.000434934	1.171790212	0.058662272	-1	38	45	38	61	35	17	27	16	29	24

ENSMUSG00000025855	chr5	Prkar1b	1.04362074	0.000175828	0.000434934	1.363250441	0.060748611	1	19	22	26	29	22	80	58	39	36	58
ENSMUSG00000032407	chr9	U2surp	-0.5960353	0.000175769	0.000434934	4.635089328	0.027398682	-1	446	426	414	565	377	276	390	238	340	365
ENSMUSG00000060181	chr10	Slc35e3	0.74329972	0.00017587	0.00043496	2.722802109	0.036095561	1	67	79	51	104	63	167	128	113	127	129
ENSMUSG00000030386	chr7	Zfp606	-0.7839671	0.000175975	0.000435144	2.892357911	0.042508338	-1	124	116	147	212	100	90	107	61	93	89
ENSMUSG00000099117	chr2	Gm27404	1.84653208	0.000176418	0.000436162	-0.436520977	0.128977239	1	3	9	4	2	1	17	9	14	22	15
ENSMUSG00000011171	chr12	Vipr2	-1.1479223	0.000176467	0.000436205	1.958079358	0.090898282	-1	127	46	54	75	85	55	38	21	37	43
ENSMUSG00000084215	chr4	Gm11814	-1.1984231	0.000176554	0.000436344	0.716311854	0.072162856	-1	42	31	27	23	34	18	15	12	13	18
ENSMUSG00000004996	chr8	Mri1	0.67753967	0.000177523	0.000438659	3.732898216	0.03358575	1	148	106	133	199	171	258	308	205	297	254
ENSMUSG00000049680	chr11	Urgcp	-0.5495113	0.000177658	0.000438915	5.458331385	0.024133989	-1	739	659	733	1071	711	691	583	527	482	638
ENSMUSG00000017307	chr2	Acot8	0.80701997	0.000177851	0.000439286	2.740189527	0.04474066	1	99	67	55	86	50	146	129	144	143	115
ENSMUSG00000025646	chr9	Atrip	0.51539693	0.000177877	0.000439286	4.812982904	0.020159509	1	369	339	315	390	301	629	535	523	487	517
ENSMUSG00000033313	chr8	Fbxl8	1.18935277	0.000177902	0.000439286	1.063514755	0.078268517	1	22	17	20	12	16	71	39	42	37	34
ENSMUSG00000017737	chr2	Mmp9	2.02306028	0.00018009	0.000444609	2.179814524	0.298536996	1	12	23	20	25	45	375	61	46	81	36
ENSMUSG00000046556	chr8	Zfp319	-0.8153987	0.000180559	0.00044569	2.940192251	0.046973456	-1	121	124	134	178	161	98	75	92	58	126
ENSMUSG00000053134	chr5	Supt7l	-0.6189483	0.000180738	0.000446052	3.588234867	0.026821701	-1	190	199	206	270	211	131	161	144	148	181
ENSMUSG00000031953	chr8	Tmem170	-1.4619704	0.000180775	0.000446066	0.423822343	0.11678635	-1	24	17	26	43	26	11	19	6	14	3
ENSMUSG00000011832	chr8	Evi5l	-0.5400007	0.000181163	0.000446924	4.25227674	0.021327935	-1	348	307	290	402	327	247	280	223	259	250
ENSMUSG00000029380	chr5	Cxcl1	2.15858249	0.000181187	0.000446924	-0.090273699	0.259065549	1	4	5	7	4	1	47	32	5	18	7
ENSMUSG00000010914	chr2	Pdhx	-0.5843646	0.000181311	0.000447151	6.658676305	0.028365401	-1	1743	1796	1878	2333	1317	1306	1296	1204	1363	1413
ENSMUSG00000059316	chr2	Slc27a4	0.54686776	0.000181415	0.000447327	4.32167352	0.022083567	1	221	220	227	309	229	485	397	323	381	348
ENSMUSG00000036282	chr14	Naa30	-0.5815472	0.000181569	0.000447629	4.438379284	0.025713327	-1	388	377	351	470	344	259	371	258	225	299
ENSMUSG00000042328	chr5	Hps4	0.81541731	0.000182223	0.000449161	2.298363328	0.041616478	1	53	50	41	56	57	110	93	74	112	110
ENSMUSG00000019843	chr10	Fyn	0.63723317	0.000182592	0.000449922	4.097028956	0.030571982	1	175	173	204	264	178	417	258	340	276	402
ENSMUSG00000024044	chr17	Epb4.1l3	0.97044005	0.000182596	0.000449922	2.332502609	0.065189703	1	66	52	29	64	38	103	101	123	66	136
ENSMUSG00000002107	chr2	Celf2	-0.6148621	0.000182691	0.000450078	5.968133012	0.031087674	-1	1094	1040	924	1398	1187	725	787	719	707	1096
ENSMUSG00000049106	chr12	Dcaf5	-0.5827406	0.000183305	0.000451512	5.505016753	0.027440422	-1	846	691	706	1078	756	523	617	545	523	752
ENSMUSG00000031796	chr8	Cfap20	0.70575566	0.0001838	0.000452651	3.131432076	0.034054062	1	99	123	85	100	79	223	183	148	145	180
ENSMUSG00000041220	chr3	Elovl6	-1.1016403	0.00018401	0.000453087	2.640587644	0.09017553	-1	92	183	116	77	138	67	83	54	72	42
ENSMUSG00000026980	chr2	Ly75	1.77176792	0.000184543	0.00045432	-0.441441841	0.124421301	1	2	4	4	6	4	8	27	14	9	18
ENSMUSG00000067424	chr17	Zfp563	-1.3057685	0.000184637	0.000454471	0.572382446	0.088791203	-1	21	26	32	44	24	9	12	7	21	15
ENSMUSG00000022235	chr15	Cmbl	-0.7479993	0.000184926	0.000455102	5.790511635	0.046240192	-1	1223	1113	849	1059	895	460	679	573	623	1025
ENSMUSG00000019795	chr10	Pcmt1	-0.5554954	0.000184992	0.000455183	6.863462109	0.025754696	-1	2251	1990	1882	2403	1794	1478	1588	1287	1605	1732
ENSMUSG00000019897	chr10	Ccdc59	0.61169865	0.000185161	0.000455519	3.757806334	0.026929733	1	173	167	137	200	117	307	293	228	274	222
ENSMUSG00000051586	chr6	Mical3	-0.5807984	0.000185861	0.000457161	4.894306328	0.026517974	-1	435	457	463	745	564	380	352	370	381	452
ENSMUSG00000061068	chr14	Mcpt4	1.0235624	0.000186529	0.000458725	3.284824736	0.080175777	1	45	97	88	111	126	364	140	189	187	183
ENSMUSG00000040721	chr14	Zfhx2	-0.9088122	0.000186565	0.000458732	2.403065567	0.056581001	-1	93	69	88	142	115	52	57	56	43	86
ENSMUSG00000098176	chr15	Ccdc166	1.41292816	0.00018661	0.000458762	0.23952953	0.093645491	1	11	8	6	8	9	33	28	32	15	16
ENSMUSG00000028919	chr4	Arhgef19	1.40335919	0.000186662	0.000458809	0.543402216	0.108564987	1	20	5	9	12	8	23	34	44	24	30
ENSMUSG00000029685	chr6	Asb15	-0.9872914	0.000186928	0.000459382	3.041893798	0.073056518	-1	85	171	192	249	116	64	95	106	95	79
ENSMUSG00000031458	chr8	Coprs	0.77026235	0.000187954	0.000461823	3.040103601	0.041683809	1	82	113	89	94	65	172	161	152	201	143
ENSMUSG00000025815	chr2	Dhtkd1	-1.577424	0.000188389	0.000462809	0.177932217	0.126370488	-1	20	26	13	41	16	4	5	5	11	16
ENSMUSG00000021427	chr13	Ssr1	0.61350227	0.000188491	0.000462979	6.132523916	0.031174541	1	861	778	705	1013	778	1712	1798	1172	1173	1103
ENSMUSG00000030127	chr6	Cops7a	-0.5891343	0.000188887	0.00046387	6.785176206	0.02908073	-1	2106	1797	1689	2337	1939	1985	1280	1130	1386	1466
ENSMUSG00000030247	chr6	Kcnj8	-0.7232307	0.000189125	0.000464292	4.000369772	0.040356486	-1	298	321	339	344	173	181	184	190	170	253
ENSMUSG00000032217	chr9	Rnf111	-0.6103076	0.000189107	0.000464292	3.616846785	0.026466631	-1	214	205	197	281	202	189	173	107	170	151
ENSMUSG00000032739	chr17	Pram1	1.94964244	0.000189216	0.000464434	-0.733999224	0.147057407	1	4	4	0	4	2	16	17	4	17	7
ENSMUSG00000055322	chr1	Tns1	-0.6696458	0.000189498	0.000464969	7.878058399	0.037965288	-1	3334	3824	3873	6431	4290	3556	2794	3053	2069	3413
ENSMUSG00000062646	chr2	Ganc	-0.8334877	0.000189501	0.000464969	5.326732126	0.057240091	-1	949	699	694	781	680	268	463	375	498	735
ENSMUSG00000038510	chr10	Rpf2	0.62951206	0.000190014	0.000466148	3.761401747	0.028861332	1	166	147	139	200	137	273	342	208	285	225
ENSMUSG00000030539	chr7	Sema4b	0.8367987	0.000190384	0.000466972	2.214908382	0.043523447	1	50	40	44	54	52	110	110	87	65	102
ENSMUSG00000034832	chr6	Tet3	-0.5938032	0.00019059	0.000467396	5.316625957	0.028538808	-1	555	655	737	973	658	565	573	438	411	614
ENSMUSG00000043881	chr14	Kbtbd7	-0.919492	0.000190836	0.000467917	2.942816445	0.062257016	-1	120	124	144	235	127	51	103	73	71	129
ENSMUSG00000025178	chr19	Pi4k2a	0.56571614	0.000191069	0.000468404	4.780306537	0.024995945	1	360	305	281	437	274	664	572	390	441	626
ENSMUSG00000030588	chr7	Yif1b	0.5257561	0.000191179	0.000468594	4.902019557	0.021502131	1	399	311	301	467	350	645	578	583	497	566
ENSMUSG00000030879	chr7	Mrpl17	0.52385859	0.000191506	0.000469312	5.596375097	0.022163609	1	652	548	536	725	499	1121	895	833	902	909
ENSMUSG00000064341	chrMT	mt-Nd1	-0.7014308	0.000191886	0.00047016	12.71457848	0.041978081	-1	113209	122820	115273	178289	97883	59404	80315	85537	87891	100967
ENSMUSG00000072591	chr5	5930412G12Rik	1.3394027	0.000192776	0.000472259	2.218673101	0.133101396	1	14	41	23	96	26	122	76	136	98	92
ENSMUSG00000038132	chr13	Rbm24	-0.5893502	0.000193695	0.000474428	6.892916639	0.029222494	-1	2359	2077	1762	2573	1893	1326	1670	1435	1404	1893
ENSMUSG00000034435	chr12	Tmem30b	1.44953525	0.000194019	0.000475138	0.46980925	0.111863216	1	11	5	9	16	9	33	37	30	10	40
ENSMUSG00000014303	chr16	Glis2	0.65467528	0.000194616	0.000476515	3.736979337	0.031525615	1	150	132	154	182	145	317	284	284	171	266
ENSMUSG00000003344	chr10	Btbd2	-0.5260196	0.000194839	0.000476978	4.880899079	0.02154937	-1	454	477	467	660	528	454	352	378	371	411
ENSMUSG00000029536	chr5	Gatc	-0.5324737	0.000195463	0.000478423	4.804782965	0.022000554	-1	488	445	429	631	470	361	382	303	410	401
ENSMUSG00000031930	chr8	Wwp2	0.60392175	0.000195574	0.000478611	4.431666955	0.028206782	1	273	236	232	320	213	585	415	353	446	324
ENSMUSG00000045534	chr6	Kcna5	-1.179091	0.000195733	0.000478915	2.762514032	0.106332998	-1	67	93	131	228	179	125	47	64	52	50
ENSMUSG00000048106	chr3	4632415L05Rik	-1.4979897	0.00019609	0.000479706	0.465605507	0.127997146	-1	18	31	23	37	31	5	10	4	12	23

ENSMUSG00000046567	chr10	4930430F08Rik	-0.8641127	0.000196505	0.000480553	2.125621159	0.04716099	-1	78	65	80	101	85	43	54	40	63	45
ENSMUSG00000060450	chr18	Rnf14	-0.5741497	0.000196497	0.000480553	6.461608958	0.027581972	-1	1779	1604	1435	1744	1276	1083	1177	1054	1148	1303
ENSMUSG00000082292	chr11	Gm12250	2.37771087	0.000196654	0.000480833	-0.055349605	0.334952695	1	0	16	0	2	1	23	25	23	15	27
ENSMUSG00000031290	chrX	Lrch2	-1.3189334	0.000197624	0.000483119	0.401979857	0.086830286	-1	29	23	19	32	26	5	20	8	10	13
ENSMUSG00000073423	chr17	Zfp414	0.76328683	0.000197833	0.000483546	3.25650242	0.042242955	1	137	66	93	117	107	264	180	186	149	195
ENSMUSG00000031731	chr8	Ap1g1	-0.5456486	0.000197886	0.000483591	5.6846617	0.02435397	-1	862	788	798	1252	875	711	784	585	607	730
ENSMUSG00000020152	chr11	Actr2	0.68098698	0.000198173	0.000484208	5.983597411	0.038718361	1	699	714	653	954	617	1491	1748	749	1305	1116
ENSMUSG00000029136	chr5	Rbks	1.26609355	0.000198846	0.000485766	0.974976598	0.092127389	1	12	21	19	10	16	51	40	28	58	34
ENSMUSG00000040441	chr10	Slc26a10	-1.2790673	0.000199138	0.000486396	2.452900213	0.124037358	-1	80	112	96	203	89	113	30	49	44	23
ENSMUSG00000032641	chr6	Gpr19	1.29253917	0.000200445	0.000489502	1.200642458	0.103888333	1	27	16	24	19	7	30	49	55	53	61
ENSMUSG00000087006	chr2	Gm13889	1.17169238	0.000200526	0.000489614	2.780442799	0.104880904	1	61	47	44	103	59	334	110	141	84	108
ENSMUSG00000020886	chr11	Dlg4	0.79276995	0.000202503	0.000494308	2.404685653	0.039733558	1	55	56	62	52	53	126	108	104	88	109
ENSMUSG00000097565	chr13	Gm26965	-1.0083212	0.000202519	0.000494308	1.155604608	0.052421813	-1	48	47	37	44	34	20	24	21	27	22
ENSMUSG00000066724	chr7	Gm10175	1.23582184	0.000202751	0.000494787	1.616470136	0.102719254	1	36	22	27	25	19	117	39	64	76	41
ENSMUSG00000022108	chr14	Itm2b	0.6485239	0.000203036	0.000495397	8.282134818	0.036012278	1	3598	3792	3136	4272	3266	6832	5768	5308	4538	8811
ENSMUSG00000025453	chr13	Nnt	-0.7698471	0.000203198	0.000495618	6.140551873	0.049885148	-1	839	1190	1011	2611	1188	914	813	806	889	822
ENSMUSG00000044768	chr1	D1Ertd622e	-0.6354302	0.000203185	0.000495618	4.275344556	0.031498743	-1	406	344	324	363	301	246	290	179	197	328
ENSMUSG00000029048	chr4	Rer1	0.55041817	0.000204676	0.000499137	6.07752826	0.02521085	1	879	795	725	964	717	1396	1479	1124	1373	1169
ENSMUSG00000001166	chr5	Oas1c	1.61459842	0.000205152	0.000500209	-0.246444645	0.109792368	1	6	5	5	9	1	22	18	19	20	8
ENSMUSG00000042938	chr2	Gm14117	-1.3357604	0.000205761	0.000501607	1.008177795	0.108186907	-1	36	37	43	55	33	4	24	13	22	24
ENSMUSG00000055553	chr8	Kxd1	0.553993	0.000206084	0.000502306	7.956610264	0.026293974	1	3178	3088	2721	3499	2512	5589	4643	4637	4354	4934
ENSMUSG00000030330	chr6	Ing4	0.57381174	0.000207284	0.000505144	5.291352219	0.026758335	1	567	484	423	479	375	961	718	688	693	769
ENSMUSG00000051790	chr11	Nlgn2	0.68425933	0.000207524	0.000505642	3.693565795	0.035129863	1	142	141	131	194	128	375	225	258	169	273
ENSMUSG00000054836	chr9	Elp6	0.84343937	0.000207633	0.000505819	2.244059274	0.046235474	1	58	38	52	61	37	100	99	102	102	77
ENSMUSG00000030814	chr7	Bcl7c	0.52997921	0.000207891	0.000506358	4.942312647	0.022153199	1	402	326	338	430	368	726	583	556	575	518
ENSMUSG00000050930	chr8	Map10	-0.933207	0.000207958	0.000506434	1.774872899	0.053755457	-1	67	54	59	88	58	29	32	29	45	50
ENSMUSG00000033916	chr7	Chmp2a	0.55632391	0.000208081	0.000506645	6.072556433	0.025827704	1	860	797	730	981	693	1659	1291	1110	1350	1143
ENSMUSG00000092454	chr15	Gm2991	1.38669037	0.000208443	0.000507438	0.122397312	0.084420085	1	6	6	8	10	9	25	13	28	25	21
ENSMUSG00000018800	chr11	Abca5	-0.7451672	0.000208962	0.000508612	3.185893769	0.040226881	-1	179	179	140	189	151	75	143	105	108	114
ENSMUSG00000020925	chr11	Ccdc43	-0.5746633	0.000209183	0.000509061	6.104678065	0.027661949	-1	1407	1179	1072	1391	1076	815	918	766	970	1029
ENSMUSG00000021044	chr12	Adck1	-0.5853756	0.000209271	0.000509187	4.669118883	0.027079605	-1	347	443	460	652	382	399	318	320	315	304
ENSMUSG00000048154	chr15	Kmt2d	-0.585982	0.00020935	0.00050929	5.584917207	0.028422457	-1	804	765	724	1107	898	810	598	554	459	733
ENSMUSG00000029729	chr5	Zkscan1	-0.5600461	0.000209492	0.000509547	3.868708079	0.022698535	-1	256	252	232	322	229	206	191	181	153	228
ENSMUSG00000024943	chr19	Smc5	-0.5818158	0.000211355	0.000513989	3.77454499	0.024441229	-1	228	239	205	324	224	181	206	144	190	167
ENSMUSG00000035365	chr10	Parpbp	1.98192874	0.000213062	0.000518051	-0.183883371	0.210007798	1	7	2	4	4	5	10	38	27	15	6
ENSMUSG00000091277	chr12	Gm1818	-1.0438625	0.000213832	0.000519831	1.197837731	0.061505783	-1	43	42	54	52	28	34	23	17	21	22
ENSMUSG00000092060	chr5	Bend4	1.69930664	0.000214302	0.000520884	0.520032384	0.175168289	1	8	12	6	7	11	77	32	12	17	28
ENSMUSG00000070802	chr7	Pnmal2	1.38035718	0.000214747	0.000521874	3.861456565	0.154459756	1	189	120	109	79	89	260	257	667	110	369
ENSMUSG00000093445	chr5	Lrch4	0.52425046	0.000215045	0.000522508	4.763658028	0.021488231	1	338	280	308	425	308	623	474	462	459	598
ENSMUSG00000014776	chr8	Nol3	0.56849899	0.000216582	0.000526151	6.260660387	0.027304103	1	1021	878	792	1186	750	1592	1264	1561	1409	1620
ENSMUSG00000053198	chr7	Prx	-0.727349	0.000216759	0.000526491	3.940075784	0.041583002	-1	198	213	325	411	277	225	208	157	131	224
ENSMUSG00000021240	chr12	Abcd4	0.72042312	0.000217445	0.000528064	3.194698571	0.037585596	1	96	80	126	124	81	205	188	200	166	155
ENSMUSG00000034059	chr2	Ypel4	1.52127114	0.000218054	0.000529452	-0.23288073	0.085407097	1	7	5	6	4	5	26	11	16	18	16
ENSMUSG00000101892	chr15	9130401M01Rik	0.59075077	0.000219462	0.000532777	3.697379556	0.025270159	1	171	125	122	212	141	294	275	226	240	228
ENSMUSG00000025921	chr1	Rdh10	1.09348457	0.000219743	0.000533367	2.570065071	0.089982317	1	53	47	57	76	44	277	98	108	84	91
ENSMUSG00000085793	chr12	Lin52	-0.6232869	0.000219811	0.00053344	3.388785533	0.027624228	-1	214	193	168	201	158	149	128	103	139	149
ENSMUSG00000026589	chr1	Sec16b	0.83483599	0.000220119	0.000534094	1.902643513	0.04034902	1	46	38	33	45	31	90	67	67	71	83
ENSMUSG00000029201	chr5	Ugdh	0.6482169	0.000220196	0.000534188	3.937603938	0.0320733	1	162	164	171	210	173	406	340	186	310	288
ENSMUSG00000017119	chr11	Nbr1	-0.5779309	0.000220949	0.000535828	6.430454265	0.028397358	-1	1602	1404	1293	1992	1441	1033	1098	969	1111	1431
ENSMUSG00000046079	chr5	Lrrc8d	0.77163534	0.00022092	0.000535828	2.909762663	0.042369536	1	70	72	74	120	74	131	202	110	141	178
ENSMUSG00000038271	chr6	Iffo1	0.73659571	0.000221039	0.000535954	5.146111268	0.045191615	1	509	339	384	356	363	659	591	932	547	841
ENSMUSG00000004069	chr16	Dnaja3	-0.5811277	0.000221309	0.000536515	6.765429585	0.028880085	-1	1906	1942	1866	2454	1576	1228	1613	1240	1495	1513
ENSMUSG00000071078	chr8	Nr2c2ap	0.90801662	0.000223235	0.000541092	2.890473028	0.061214088	1	62	80	68	95	72	232	175	108	178	88
ENSMUSG00000030353	chr6	Tead4	1.09172877	0.0002235	0.000541641	2.747554356	0.091980749	1	42	46	37	132	67	155	114	203	142	108
ENSMUSG00000051048	chr7	P4ha3	1.08398153	0.000223625	0.000541849	1.546726745	0.076108814	1	37	18	25	37	17	100	60	49	39	65
ENSMUSG00000038695	chr7	Josd2	0.55059993	0.000223671	0.000541867	5.307756115	0.024830286	1	545	445	439	517	433	861	730	787	760	683
ENSMUSG00000028413	chr4	B4galt1	0.58612508	0.000224556	0.000543915	6.312546083	0.029195038	1	824	914	916	1128	934	2149	1539	1380	1238	1539
ENSMUSG00000053769	chr3	Lysmd1	0.96482404	0.000225411	0.000545797	1.888815692	0.059398829	1	38	35	42	33	30	54	91	80	77	80
ENSMUSG00000072214	chr16	Sept5	0.7460684	0.000225406	0.000545797	3.020891804	0.039822748	1	95	74	83	110	83	201	175	175	155	109
ENSMUSG00000028461	chr4	Ccdc107	0.54803831	0.000225833	0.000546724	4.407962246	0.023124362	1	296	254	233	273	217	465	425	375	413	368
ENSMUSG00000025040	chrX	Fundc1	-0.636679	0.000227143	0.000549802	4.186217857	0.031793314	-1	352	334	263	447	262	187	265	182	222	301
ENSMUSG00000019487	chr17	Trip10	-0.5420563	0.000227558	0.000550709	6.668084126	0.025145972	-1	1929	1712	1623	2226	1520	1688	1390	1192	1277	1235
ENSMUSG00000022711	chr16	Pmm2	0.54471457	0.000228362	0.00055256	4.343668865	0.022805206	1	215	226	224	343	224	501	376	364	354	367
ENSMUSG00000028657	chr4	Ppt1	0.59279014	0.000228499	0.0005527	5.204963859	0.028980059	1	523	451	355	493	364	1018	757	574	658	635
ENSMUSG00000051335	chr13	Gfod1	-0.7681111	0.000228464	0.0005527	2.838512553	0.041447661	-1	92	138	110	208	122	90	92	84	76	83

ENSMUSG00000060938	chr11	Rpl26	0.56492535	0.000228565	0.000552765	7.957959507	0.027739509	1	3275	2923	2671	3408	2650	5157	5059	4354	5228	4380
ENSMUSG00000045007	chr11	Tubg2	1.25056819	0.000228887	0.000553446	0.719942695	0.083796043	1	15	11	15	13	12	28	21	41	42	40
ENSMUSG00000063888	chr17	Rpl7l1	0.53084405	0.000228948	0.000553498	5.63207385	0.023389753	1	566	580	602	714	548	1053	1057	794	946	935
ENSMUSG00000041633	chrX	Kctd12b	-0.7823351	0.000229277	0.000554198	3.094122408	0.045565344	-1	133	173	178	202	110	94	113	84	76	141
ENSMUSG00000024846	chr19	Cst6	0.71856675	0.000230303	0.000556583	3.3908482	0.038693088	1	146	99	90	152	101	268	213	195	230	146
ENSMUSG00000053453	chr14	Thoc7	-0.553453	0.000231575	0.00055956	5.890802313	0.025825014	-1	1106	1005	931	1323	908	718	920	624	809	849
ENSMUSG00000036775	chr17	Decr2	0.77899204	0.000231982	0.000560447	2.866459194	0.043493724	1	101	84	67	100	44	147	137	138	152	163
ENSMUSG00000034120	chr11	Srsf2	0.62768363	0.000232442	0.000561461	6.203329409	0.033694734	1	886	754	693	1120	877	1762	1773	1169	1530	1083
ENSMUSG00000032006	chr9	Pdgfd	-0.9847409	0.000232675	0.000561925	1.846186236	0.063537562	-1	76	71	76	60	58	26	39	40	33	52
ENSMUSG00000074746	chr19	Pdzd8	-0.63316	0.00023332	0.000563387	3.781612393	0.030259201	-1	188	243	250	340	221	159	196	138	173	208
ENSMUSG00000023020	chr15	Cox14	0.56592798	0.000233378	0.000563429	6.793989638	0.027591026	1	1533	1324	1211	1544	1057	2294	1932	2203	2101	2244
ENSMUSG00000029463	chr5	Fam216a	0.83508324	0.000233771	0.00056428	2.107364105	0.04436626	1	46	56	34	55	33	108	80	85	72	93
ENSMUSG00000052406	chr2	Rexo4	0.60320835	0.000233876	0.000564435	4.054415252	0.02814304	1	187	166	173	294	168	294	368	286	355	315
ENSMUSG00000037110	chr2	Ralgapa2	-0.6608559	0.000233981	0.000564591	3.307522639	0.0315287	-1	170	197	143	197	183	109	141	104	119	146
ENSMUSG00000061859	chr4	Inadl	1.50274278	0.000234621	0.000566038	1.45159205	0.161868247	1	16	17	14	41	16	50	65	123	28	41
ENSMUSG00000027199	chr2	Gatm	0.76104901	0.000235234	0.00056742	5.279212105	0.048900598	1	556	387	348	345	472	869	687	970	537	902
ENSMUSG00000023886	chr17	Smoc2	-0.6081303	0.000235568	0.000568126	7.308783449	0.032145613	-1	2760	3095	2586	2711	2929	2364	2266	2034	1801	1792
ENSMUSG00000070942	chr1	Il1rl2	0.86494337	0.000235685	0.000568312	2.472000336	0.051768685	1	61	81	50	46	44	122	109	98	112	130
ENSMUSG00000072115	chr14	Ang	0.80967155	0.000236497	0.000570172	2.384683435	0.043427811	1	57	63	47	58	49	98	106	86	130	107
ENSMUSG00000030641	chr7	Ddias	1.63948614	0.000236712	0.00057059	-0.51962273	0.09448294	1	3	3	6	5	3	20	17	10	15	8
ENSMUSG00000031577	chr8	Tti2	0.66739581	0.000236899	0.000570944	3.014414991	0.030576697	1	83	98	82	123	74	147	163	162	155	166
ENSMUSG00000018012	chr11	Rac3	1.31222952	0.000237255	0.000571702	0.603767655	0.091248791	1	7	10	14	11	16	50	34	24	33	21
ENSMUSG00000056679	chrX	Gpr173	1.27514666	0.000237549	0.000572311	0.169574763	0.065005492	1	8	10	6	12	7	27	28	17	18	25
ENSMUSG00000092781	chr10	Mir3057	-0.9023293	0.000238352	0.000574148	2.600044729	0.059269505	-1	88	97	97	193	113	49	95	56	74	63
ENSMUSG00000011427	chr7	Zfp790	-0.6395032	0.000238665	0.000574803	3.108534218	0.028484402	-1	168	143	143	185	135	147	101	87	102	110
ENSMUSG00000057363	chr1	Uxs1	-0.560126	0.000238903	0.000575277	4.334573402	0.024465484	-1	393	325	336	392	330	256	320	207	276	266
ENSMUSG00000023027	chr15	Atf1	-0.5646477	0.000239133	0.000575731	5.140521352	0.026279001	-1	635	505	513	900	610	446	552	377	413	535
ENSMUSG00000032513	chr9	Gorasp1	-0.5766309	0.000240084	0.000577923	4.331744272	0.026068669	-1	397	352	296	409	332	256	261	207	319	267
ENSMUSG00000022914	chr16	Brwd1	-0.5099691	0.000241378	0.000580937	5.273707743	0.021309087	-1	693	577	582	901	647	548	499	487	491	574
ENSMUSG00000056999	chr19	Ide	-0.5957372	0.000242222	0.000582869	6.676502781	0.030720545	-1	1765	1492	1543	2565	1880	1203	1367	1207	1212	1652
ENSMUSG00000018199	chr1	Trove2	-0.728991	0.000242337	0.000582943	2.839188263	0.036799858	-1	120	111	120	190	120	75	97	93	86	79
ENSMUSG00000025930	chr1	Msc	1.29378561	0.000242299	0.000582943	2.291602309	0.127101916	1	54	39	51	18	37	114	105	167	50	112
ENSMUSG00000000753	chr11	Serpinf1	0.65887242	0.000242928	0.000584264	7.654130349	0.037975891	1	2821	2221	2072	2450	2030	6096	3974	3696	3002	3573
ENSMUSG00000035258	chr16	Abi3bp	-0.6983347	0.000243238	0.00058491	5.298787029	0.041369298	-1	870	652	676	788	626	499	594	256	554	559
ENSMUSG00000023088	chr16	Abcc1	-0.5408866	0.000243407	0.000585216	5.145340824	0.02408173	-1	582	554	562	820	612	517	522	331	496	492
ENSMUSG00000038683	chr13	Pak1ip1	0.52082347	0.000243462	0.000585247	5.284446535	0.02237179	1	490	427	385	652	445	875	779	626	761	708
ENSMUSG00000036036	chr17	Zfp57	1.33753221	0.000243941	0.000586299	-0.014607739	0.066725509	1	5	6	8	11	6	21	19	22	17	21
ENSMUSG00000027495	chr2	Fam210b	-0.5797205	0.000245566	0.000590101	3.47536367	0.023824859	-1	202	190	184	223	182	167	144	121	124	168
ENSMUSG00000057335	chr1	Cep170	-0.5912814	0.000247766	0.000595286	3.686696717	0.025877665	-1	258	206	186	287	212	163	186	127	160	198
ENSMUSG00000020850	chr11	Prpf8	-0.5761362	0.00024809	0.000595961	6.965900315	0.028924193	-1	2072	1839	1847	2981	2458	1580	1724	1495	1595	1785
ENSMUSG00000022391	chr15	Rangap1	0.59059623	0.000249064	0.000598199	5.480576365	0.029448213	1	484	453	444	665	603	1013	1013	833	789	726
ENSMUSG00000010936	chr8	Vac14	0.55165084	0.00025006	0.000600487	4.822324763	0.024702695	1	340	275	282	444	368	598	626	452	564	498
ENSMUSG00000074141	chr7	Il4i1	-1.0245027	0.00025092	0.00060245	2.590016539	0.079865423	-1	182	124	92	95	93	46	65	90	50	63
ENSMUSG00000027752	chr3	Exosc8	0.84409301	0.000251417	0.000603513	3.252948921	0.055387838	1	82	79	98	139	105	250	233	130	250	126
ENSMUSG00000068196	chr16	Col8a1	0.86504961	0.00025145	0.000603513	4.644893651	0.063222385	1	246	252	270	363	194	647	593	745	301	324
ENSMUSG00000027364	chr2	Usp50	1.0982439	0.000251568	0.00060359	1.75649139	0.082256909	1	37	39	32	21	22	102	46	70	80	63
ENSMUSG00000033361	chrX	Prrg3	-0.7294192	0.000251547	0.00060359	3.390782213	0.040688505	-1	190	230	202	220	122	166	117	126	92	140
ENSMUSG00000052675	chr7	Zfp112	-0.8544251	0.000251621	0.000603613	2.09574197	0.047602542	-1	73	70	79	101	77	45	49	31	61	56
ENSMUSG00000024795	chr19	Kif20b	1.24947803	0.000251703	0.000603708	0.750604162	0.0835704	1	11	18	13	11	14	39	53	27	35	24
ENSMUSG00000041773	chr13	Enc1	1.10276783	0.000252831	0.00060631	2.923133113	0.095758497	1	43	89	68	75	73	324	198	121	94	111
ENSMUSG00000045210	chr1	Vcpip1	-0.6062256	0.000253266	0.000607246	3.858297067	0.027949138	-1	255	250	224	324	245	175	214	157	145	244
ENSMUSG00000037608	chr10	Bclaf1	-0.5189748	0.000253639	0.000608038	5.380617071	0.02244996	-1	788	703	662	871	629	617	655	456	525	546
ENSMUSG00000045362	chr7	Tnfrsf26	1.77376428	0.000254023	0.000608853	0.096986491	0.179368622	1	8	8	5	8	2	48	17	5	23	27
ENSMUSG00000038260	chr7	Trpm4	-0.5368003	0.00025551	0.000612314	4.225308831	0.022145782	-1	302	283	303	450	313	271	224	229	236	280
ENSMUSG00000004667	chr10	Polr2e	0.52901241	0.000256347	0.000614214	5.33572001	0.02334425	1	496	478	397	640	459	994	780	712	716	696
ENSMUSG00000027007	chr2	Ssfa2	-0.6327456	0.000256763	0.000615104	4.005689917	0.031571693	-1	240	279	259	409	270	220	235	129	221	222
ENSMUSG00000089872	chr1	Rps6kc1	-0.5714449	0.000257048	0.000615682	4.652798494	0.026488041	-1	461	405	338	551	481	315	349	261	368	351
ENSMUSG00000052631	chr6	Sh2d6	-1.1775846	0.00025792	0.000617665	1.706888582	0.098881334	-1	86	51	68	48	68	63	23	20	26	29
ENSMUSG00000070572	chr4	Trmt112-ps2	1.3417975	0.000258902	0.00061991	0.032633749	0.071818045	1	10	7	8	7	5	22	22	15	26	19
ENSMUSG00000092534	chr7	Pagr1b	0.58192442	0.000259057	0.000620176	3.943595313	0.026024712	1	180	170	154	268	150	378	290	257	314	259
ENSMUSG00000018845	chr11	Unc45b	-0.6269153	0.000259646	0.000621479	7.991576727	0.034782707	-1	5036	4150	3666	5424	4748	2587	3270	3377	3269	3703
ENSMUSG00000022053	chr14	Ebf2	-0.8666271	0.000261015	0.000624649	2.990831689	0.05733947	-1	123	177	156	174	122	70	75	106	66	134
ENSMUSG00000042625	chr17	Safb2	0.55993295	0.000261306	0.000625239	4.544625059	0.025101812	1	283	265	229	322	296	618	417	398	410	429
ENSMUSG00000043017	chr7	Ptgir	0.89861766	0.000261695	0.000626062	1.948342617	0.052795656	1	41	40	40	48	25	85	109	55	69	80
ENSMUSG00000002660	chr17	Clpp	0.53440142	0.000262476	0.000627822	4.677376604	0.023048637	1	346	288	276	410	242	499	480	489	511	471

ENSMUSG00000028150	chr3	Rorc	-0.8372097	0.000263363	0.000629836	4.424737619	0.058977667	-1	247	365	364	762	358	231	271	192	348	203
ENSMUSG00000072572	chr14	Slc39a2	2.31194007	0.000263479	0.000630005	0.08898725	0.322199219	1	9	0	4	3	6	69	22	14	5	19
ENSMUSG00000026712	chr2	Mrc1	0.85320213	0.000264721	0.000632867	5.637252111	0.0631721	1	511	527	493	570	518	1682	1012	557	1362	668
ENSMUSG00000020628	chr12	Trappc12	-0.5953421	0.000265395	0.000634371	4.148183881	0.028071162	-1	273	300	279	452	291	328	198	193	199	238
ENSMUSG00000042541	chr6	Shfm1	0.5871091	0.000265524	0.000634569	6.414496812	0.030098434	1	1142	951	853	1280	876	2068	1755	1410	1814	1322
ENSMUSG00000025041	chr19	Nt5c2	0.71859948	0.000265574	0.00063458	3.877536784	0.041530137	1	128	131	150	246	173	372	273	358	247	225
ENSMUSG00000026031	chr1	Cflar	-0.5113371	0.000266575	0.000636864	5.098554978	0.021608353	-1	588	565	555	764	531	602	495	365	397	460
ENSMUSG00000095440	chr15	Fignl2	1.06275114	0.000267422	0.000638779	0.941301656	0.059331667	1	22	17	12	20	15	44	29	40	36	48
ENSMUSG00000039357	chr14	Fut11	0.69081485	0.000267783	0.00063953	2.787500877	0.032434704	1	79	74	81	88	63	144	149	106	128	158
ENSMUSG00000027637	chr2	1110008F13Rik	0.52254144	0.000267869	0.000639628	5.428969712	0.023013838	1	557	475	448	703	465	919	906	711	851	753
ENSMUSG00000006932	chr9	Ctnnb1	-0.5428841	0.000268549	0.000641048	8.020776023	0.026220689	-1	4600	4320	4068	5764	4264	3774	3619	2827	3082	4039
ENSMUSG00000028224	chr4	Nbn	-0.6024783	0.000268607	0.000641048	3.962480155	0.028240421	-1	233	304	234	376	252	180	212	165	219	226
ENSMUSG00000051344	chr1	Plekhm3	0.80181772	0.00026858	0.000641048	2.832465948	0.0467441	1	62	70	70	95	82	182	179	85	121	167
ENSMUSG00000056121	chr17	Fez2	-0.5963556	0.000268648	0.000641048	6.210509099	0.031009868	-1	1582	1365	1258	1258	1113	940	984	836	1056	981
ENSMUSG00000026837	chr2	Col5a1	0.77451576	0.000269008	0.000641798	7.871618214	0.053205813	1	2255	2156	2339	3202	2905	5030	4459	5945	2601	6070
ENSMUSG00000092232	chr14	Gm20521	0.51668348	0.000269706	0.000643355	5.170632659	0.022169128	1	490	403	397	549	371	853	681	675	594	656
ENSMUSG00000022702	chr16	Hira	-0.5482536	0.000270608	0.000645396	4.515115227	0.024139259	-1	459	353	337	447	413	294	342	262	303	307
ENSMUSG00000024055	chr17	Cyp4f13	0.96669443	0.000270964	0.000646134	2.026265519	0.063904644	1	37	43	38	42	37	146	58	72	71	83
ENSMUSG00000076441	chr2	Ass1	1.62432043	0.000271204	0.000646597	2.032259506	0.205707663	1	18	36	22	46	23	274	84	62	47	36
ENSMUSG00000051235	chr12	Gen1	-1.2180978	0.00027144	0.000647048	0.426752321	0.070675764	-1	27	20	18	35	29	11	18	10	12	9
ENSMUSG00000097184	chr16	4632428C04Rik	-1.1820507	0.000271506	0.000647095	0.927807022	0.081767542	-1	29	46	43	49	19	16	16	18	15	24
ENSMUSG00000035042	chr11	Ccl5	1.77850465	0.000272238	0.00064873	0.52859778	0.206989178	1	6	2	3	22	12	41	17	25	21	62
ENSMUSG00000074846	chr2	Gm10774	1.02517658	0.000272886	0.000650162	1.528162181	0.067003996	1	33	30	28	21	21	81	41	56	67	56
ENSMUSG00000050332	chrX	Amer1	-0.6125082	0.000272974	0.000650262	3.486436721	0.027494571	-1	196	173	191	233	204	131	145	155	129	153
ENSMUSG00000081049	chrX	Rps24-ps3	0.78796371	0.000273898	0.000652352	2.228645955	0.039903502	1	49	54	53	51	40	106	93	77	102	93
ENSMUSG00000036106	chr15	Prr5	0.88678639	0.000274155	0.000652852	2.576506682	0.057292563	1	51	67	60	59	64	175	126	140	79	100
ENSMUSG00000007805	chr1	Twist2	1.23140566	0.000276293	0.000657831	0.440044462	0.070991694	1	13	13	9	12	7	40	24	21	21	35
ENSMUSG00000025140	chr11	Pycr1	0.63331978	0.00027635	0.000657855	3.48929652	0.029949358	1	166	112	107	148	116	271	191	221	212	207
ENSMUSG00000029169	chr5	Dhx15	-0.6303188	0.000276859	0.000658955	5.288938832	0.03405592	-1	703	708	586	874	668	416	680	358	545	499
ENSMUSG00000022604	chr16	Cep97	-0.7759025	0.000277265	0.000659808	2.501307372	0.041285333	-1	98	88	85	137	116	57	82	65	61	68
ENSMUSG00000005360	chr15	Slc1a3	-0.9643976	0.00027797	0.000661374	1.947046954	0.065304748	-1	78	85	63	65	74	49	50	19	46	45
ENSMUSG00000070319	chr9	Eif3g	0.52078752	0.000279218	0.000664231	5.917064298	0.023425872	1	787	674	611	960	682	1319	1101	1110	1168	1101
ENSMUSG00000055485	chr2	Soga1	-1.0186047	0.000279759	0.000665404	2.822418549	0.08169959	-1	120	105	132	181	158	30	90	77	69	106
ENSMUSG00000041135	chr4	Ripk2	0.94266708	0.000280679	0.000667479	1.855819648	0.059160085	1	37	31	42	46	22	98	94	50	72	63
ENSMUSG00000032540	chr9	Abhd5	-0.558914	0.000280901	0.000667893	4.88153919	0.025952041	-1	453	517	517	712	425	349	436	316	423	412
ENSMUSG00000025226	chr19	Fbxl15	0.8482042	0.000282413	0.000671373	1.825332359	0.043387676	1	43	34	33	35	35	83	62	63	74	76
ENSMUSG00000045257	chr17	Morn2	0.94635399	0.000282483	0.000671426	1.973214007	0.062247355	1	57	24	35	48	30	92	66	97	69	82
ENSMUSG00000040447	chr11	Spns2	0.62138893	0.000282758	0.000671851	4.257143511	0.03123224	1	211	213	261	240	182	375	354	290	454	404
ENSMUSG00000043279	chr5	Trim56	-0.5771691	0.000282746	0.000671851	4.039660669	0.026170062	-1	240	304	280	388	252	282	217	181	182	216
ENSMUSG00000078648	chr15	Gm17546	-1.5691203	0.000283123	0.000672603	0.095326909	0.129912817	-1	18	18	25	36	11	15	6	5	11	2
ENSMUSG00000018666	chr11	Cbx1	-0.5542465	0.000283385	0.000673111	4.986833176	0.025711342	-1	641	554	455	635	516	384	515	340	424	427
ENSMUSG00000015957	chr7	Wnt11	0.76704638	0.000284412	0.000675437	3.327277358	0.045588673	1	107	118	103	121	95	212	146	188	159	317
ENSMUSG00000020258	chr9	Glyctk	-1.1385555	0.000285765	0.000678535	0.672508679	0.068431498	-1	34	25	39	31	22	12	18	15	15	15
ENSMUSG00000010175	chr1	Prox1	-0.9953826	0.000286005	0.00067899	2.170834511	0.07225557	-1	86	55	73	171	65	47	46	51	33	62
ENSMUSG00000056579	chr11	Tug1	-0.5091606	0.000286503	0.000680055	5.217591173	0.021763209	-1	658	558	665	779	586	517	537	413	499	538
ENSMUSG00000002908	chr8	Kcnn1	-0.6179081	0.000288263	0.000684116	3.626610004	0.028816061	-1	203	196	200	301	211	146	138	148	190	162
ENSMUSG00000013698	chr1	Pea15a	0.63439066	0.000288662	0.000684948	6.304267384	0.035566112	1	863	919	885	1163	789	2502	1412	1361	1316	1335
ENSMUSG00000033352	chr11	Map2k4	-0.6176187	0.000288845	0.000685264	6.348686282	0.033724817	-1	1487	1360	1309	1758	1430	783	1198	941	993	1312
ENSMUSG00000026565	chr1	Pou2f1	-0.6780896	0.000289593	0.000686924	3.218613458	0.034464499	-1	149	146	152	200	194	152	105	109	87	128
ENSMUSG00000016758	chr15	Bik	1.55237363	0.000289757	0.000687195	0.197361686	0.133555989	1	7	8	12	9	2	19	25	39	13	26
ENSMUSG00000025153	chr11	Fasn	-1.559594	0.000290238	0.00068822	6.289563957	0.209368083	-1	555	3123	1421	657	2512	404	631	1019	402	718
ENSMUSG00000064120	chr17	Mocs1	-0.6936814	0.000290393	0.000688469	3.747274112	0.038455336	-1	226	245	218	304	235	152	125	136	162	257
ENSMUSG00000027324	chr2	Rpusd2	-0.9443326	0.00029052	0.000688655	1.274837513	0.049384025	-1	38	40	43	71	37	29	28	20	23	29
ENSMUSG00000022325	chr15	Pop1	1.10117276	0.000290827	0.000689265	1.61383235	0.08211123	1	40	25	17	28	28	60	99	51	71	44
ENSMUSG00000066568	chr7	Lsm14a	-0.5212779	0.00029106	0.000689701	5.865664376	0.023569229	-1	948	927	929	1422	929	815	864	623	768	844
ENSMUSG00000097769	chr18	Snhg4	0.84427276	0.000291119	0.000689723	2.372045012	0.050837171	1	60	61	33	77	41	139	103	93	112	83
ENSMUSG00000002320	chr14	Tm9sf1	0.54394666	0.000291746	0.000691092	4.761711845	0.024344285	1	325	346	307	363	290	688	529	483	399	534
ENSMUSG00000039662	chr4	Icmt	-0.4992222	0.000291938	0.000691429	5.126126123	0.020816317	-1	552	563	539	786	608	528	489	382	439	528
ENSMUSG00000025083	chr19	Afap1l2	-0.7531278	0.000292495	0.000692632	2.377544308	0.037866553	-1	97	92	77	119	92	65	54	64	50	76
ENSMUSG00000028470	chr4	Hint2	0.66406514	0.000292623	0.000692817	4.422568526	0.036864094	1	240	278	233	314	170	559	335	488	404	343
ENSMUSG00000046562	chr5	Unc119b	-0.529604	0.000295618	0.000699789	4.361167549	0.022293703	-1	350	307	299	490	366	271	281	249	256	309
ENSMUSG00000019054	chr5	Fis1	0.5754254	0.000296591	0.000701973	6.806859361	0.029533874	1	1475	1357	1222	1562	1084	2944	2002	1934	2187	1911
ENSMUSG00000006717	chr13	Acot13	-0.5382892	0.000296808	0.000702369	5.91328893	0.025279584	-1	1011	1050	1023	1426	837	768	829	756	839	800
ENSMUSG00000024830	chr19	Rps6kb2	0.59049904	0.000298297	0.000705654	4.5242898	0.028792819	1	341	249	244	276	244	423	399	480	431	500
ENSMUSG00000031931	chr9	Ankrd49	-0.9284858	0.00029825	0.000705654	2.471066019	0.064600452	-1	112	86	119	127	87	36	88	51	50	80

ENSMUSG00000034974	chr10	Dapk3	0.56411972	0.000299511	0.000708404	4.345597794	0.025730907	1	271	179	209	304	255	463	350	387	377	391
ENSMUSG00000026836	chr2	Acvr1	-0.6350094	0.000301093	0.000711927	3.899996829	0.032369288	-1	212	233	292	360	250	231	230	170	134	189
ENSMUSG00000028394	chr4	Pole3	0.53778028	0.000301102	0.000711927	4.579751463	0.023704593	1	334	264	250	394	219	531	494	422	443	413
ENSMUSG00000063802	chr7	Hspbp1	0.54655175	0.000301869	0.000713499	4.713396076	0.024751576	1	302	281	310	408	285	572	519	514	518	400
ENSMUSG00000067038	chr19	Rps12-ps3	1.25377024	0.000301847	0.000713499	0.67090396	0.089048306	1	15	7	11	17	14	52	34	34	30	18
ENSMUSG00000020134	chr11	Peli1	-0.6358702	0.00030265	0.000715224	3.452022269	0.030564418	-1	197	196	189	248	156	163	127	93	157	156
ENSMUSG00000003380	chr7	Rabac1	0.53866793	0.000304585	0.000719674	6.599156006	0.025835708	1	1228	1153	1069	1374	1057	2462	1770	1605	1809	1770
ENSMUSG00000040018	chr19	Cox15	-0.6741163	0.000306583	0.000724273	5.228226219	0.039628407	-1	628	671	593	886	659	297	517	415	471	639
ENSMUSG00000101939	chr1	Gm28438	-0.931589	0.000306777	0.000724611	2.150293725	0.062230346	-1	72	98	77	115	64	37	40	62	37	65
ENSMUSG00000019763	chr10	Rmnd1	-0.5581302	0.000307387	0.000725805	4.757002061	0.025987229	-1	510	475	449	593	372	330	342	343	418	334
ENSMUSG00000087590	chr18	2410004N09Rik	1.11778316	0.00030735	0.000725805	1.729054831	0.088518175	1	44	28	26	27	23	135	54	52	54	66
ENSMUSG00000011256	chr11	Adam19	0.74043456	0.000307542	0.000726048	4.545887557	0.046936374	1	252	301	245	269	220	421	442	583	285	632
ENSMUSG00000069763	chr11	Tmem100	-1.3330338	0.000308916	0.00072917	3.367053849	0.151183589	-1	190	211	163	336	206	271	59	42	46	77
ENSMUSG00000034768	chr11	Asb16	-0.6934085	0.000309653	0.000730785	6.423493888	0.043088431	-1	1516	1357	1265	2097	1702	728	1165	906	1069	1462
ENSMUSG00000021957	chr14	Tkt	1.16334216	0.000310033	0.000731558	5.58160706	0.119441088	1	171	807	399	312	442	1579	1283	747	1109	729
ENSMUSG00000087412	chr7	Gm15501	0.8483363	0.000310279	0.000732015	3.568327876	0.059334419	1	118	125	103	173	110	463	207	181	241	158
ENSMUSG00000029484	chr5	Anxa3	0.68062408	0.000311651	0.000735128	4.304097348	0.038807209	1	204	240	209	263	205	610	463	251	361	317
ENSMUSG00000033257	chr1	Ttll4	-0.5491967	0.000311748	0.000735234	4.257069246	0.024242859	-1	363	288	298	363	362	253	280	215	255	257
ENSMUSG00000035595	chr10	1600002K03Rik	0.94429531	0.000311867	0.00073539	2.200275481	0.064752222	1	56	45	32	51	43	153	83	68	110	69
ENSMUSG00000029283	chr5	Cdc7	1.18457879	0.000312296	0.000736278	1.061188719	0.08742536	1	11	19	20	15	22	51	60	41	43	26
ENSMUSG00000015653	chr5	Steap2	1.07541688	0.00031289	0.000737554	1.118327316	0.071273942	1	14	14	23	36	12	48	43	34	45	56
ENSMUSG00000022615	chr15	Tymp	0.61128487	0.000313662	0.000739249	3.457245415	0.028097523	1	112	130	106	177	119	241	214	233	186	195
ENSMUSG00000026150	chr1	Mff	-0.5595506	0.000313887	0.000739654	6.66970315	0.02808637	-1	1918	1712	1652	2237	1542	1258	1369	1077	1537	1462
ENSMUSG00000054808	chr7	Actn4	0.57109351	0.00031432	0.000740549	6.288504931	0.02907745	1	787	856	808	1261	988	1930	1576	1407	1199	1552
ENSMUSG00000029414	chr5	Kntc1	1.62346792	0.00031459	0.00074106	0.73299194	0.179911715	1	22	7	10	8	8	20	58	24	62	22
ENSMUSG00000064061	chr16	Dzip3	-0.9449464	0.000315212	0.000742401	1.809270874	0.060357557	-1	59	67	71	82	54	27	44	24	46	48
ENSMUSG00000026274	chr1	Pask	1.62329181	0.000315481	0.000742783	0.334469496	0.157560851	1	15	8	5	3	9	21	46	20	36	15
ENSMUSG00000052821	chrX	Cysltr1	1.01972757	0.00031543	0.000742783	0.815937135	0.052687582	1	15	17	14	21	13	40	37	27	40	34
ENSMUSG00000041417	chr13	Pik3r1	-0.5284982	0.000316452	0.000744943	5.211015122	0.02395568	-1	552	677	551	782	683	606	500	411	450	516
ENSMUSG00000028191	chr3	Bcl10	0.63119165	0.000316766	0.000745558	4.068393186	0.032497574	1	185	200	200	246	145	463	383	286	249	286
ENSMUSG00000019960	chr10	Dusp6	0.56702702	0.000317581	0.000747351	4.88821666	0.027281957	1	353	385	334	437	267	647	731	409	526	582
ENSMUSG00000052310	chr3	Slc39a1	0.54039534	0.000318646	0.00074973	6.329353417	0.026035114	1	1000	956	875	1141	900	2057	1476	1439	1402	1432
ENSMUSG00000028329	chr4	Xpa	0.83049983	0.000318905	0.000750213	2.47879481	0.049550109	1	53	52	62	61	61	167	81	107	108	108
ENSMUSG00000021697	chr13	Depdc1b	1.7124504	0.000319228	0.000750846	-0.216631727	0.15131345	1	8	5	3	6	3	32	18	22	14	5
ENSMUSG00000022010	chr14	Tsc22d1	0.61095433	0.000320151	0.00075289	7.089630551	0.033805494	1	1697	1497	1505	1769	1524	3937	2292	2673	2131	2491
ENSMUSG00000031585	chr8	Gtf2e2	0.59468759	0.000320317	0.000753156	3.69759111	0.027254369	1	171	151	128	186	129	328	268	193	260	220
ENSMUSG00000020646	chr12	Mboat2	1.26190218	0.000320418	0.000753266	1.606724943	0.117661988	1	16	35	30	31	15	72	67	102	29	63
ENSMUSG00000035227	chr7	Spcs2	0.57348214	0.000320524	0.000753388	6.012903474	0.029221039	1	850	673	631	909	798	1406	1470	922	1335	1187
ENSMUSG00000041777	chr2	Cir1	-0.6748241	0.000321247	0.00075496	3.294795486	0.03466317	-1	217	161	169	204	139	105	110	107	136	150
ENSMUSG00000008822	chr12	Acyp1	-0.7803198	0.000322046	0.000756711	3.544364732	0.049839157	-1	296	206	175	225	185	109	146	87	173	179
ENSMUSG00000026701	chr1	Prdx6	0.548265	0.000323992	0.000761156	6.281448326	0.026889084	1	870	898	847	1321	809	1810	1662	1417	1375	1284
ENSMUSG00000022322	chr8	Shcbp1	1.63576462	0.000324135	0.000761363	0.696557233	0.175572994	1	6	19	15	5	7	31	54	30	51	16
ENSMUSG00000043085	chr4	Tmem82	1.51114947	0.000326036	0.000765699	0.024678199	0.117228084	1	3	8	4	12	7	38	20	9	20	21
ENSMUSG00000034674	chr10	Tdg	1.28038357	0.000326275	0.000766133	3.114126955	0.137852239	1	55	79	72	98	67	45	329	175	225	197
ENSMUSG00000085022	chr4	Gm5860	2.12031581	0.000326376	0.000766241	0.362702347	0.30795471	1	9	2	6	9	6	1	48	35	29	37
ENSMUSG00000068749	chr3	Psma5	0.53326222	0.000327658	0.000769121	6.065895629	0.025270748	1	869	865	765	901	662	1513	1357	1179	1231	1189
ENSMUSG00000062488	chr19	I830012O16Rik	1.33702044	0.00032849	0.000770944	1.480639285	0.133083342	1	26	23	13	32	19	34	59	46	40	132
ENSMUSG00000019989	chr10	Enpp3	-0.7991568	0.000328645	0.000771178	2.245728638	0.044064551	-1	106	79	67	97	89	59	59	48	41	70
ENSMUSG00000100153	chr7	Gm5601	-0.8221057	0.00032892	0.000771694	2.22755346	0.046543841	-1	84	85	92	104	70	46	51	46	71	54
ENSMUSG00000034269	chr6	Setd5	-0.5390724	0.000329398	0.000772687	5.302963778	0.025210966	-1	656	625	603	939	675	526	592	466	418	627
ENSMUSG00000025586	chr7	Cpeb1	-0.7138199	0.000331145	0.000776654	4.019436057	0.042810172	-1	334	311	241	306	291	151	171	168	203	301
ENSMUSG00000032179	chr9	Bmp5	-0.8340804	0.000331688	0.000777737	3.908400516	0.058987272	-1	241	373	290	223	267	127	214	219	136	170
ENSMUSG00000073375	chr17	Lrrc30	-0.7532226	0.000331718	0.000777737	5.483519791	0.050706488	-1	1017	664	794	604	1004	460	499	491	594	658
ENSMUSG00000028434	chr4	Epb4.1l4b	-0.9661163	0.000332401	0.000779207	1.954607159	0.067583461	-1	69	68	61	108	69	31	55	21	53	48
ENSMUSG00000025060	chr19	Slk	-0.5489521	0.000333619	0.000781931	5.595133243	0.026542087	-1	823	814	686	1164	817	638	793	509	650	612
ENSMUSG00000023913	chr17	Pla2g7	0.85775862	0.000334043	0.000782794	5.216406423	0.065503019	1	483	380	331	303	431	1308	623	443	589	1025
ENSMUSG00000036596	chr5	Cpz	1.15346141	0.000334856	0.000784567	2.712222213	0.10823643	1	79	51	68	35	56	96	115	123	113	276
ENSMUSG00000021280	chr12	Exoc3l4	1.11247424	0.00033506	0.000784914	4.411320299	0.108838238	1	427	145	175	96	136	382	472	459	478	556
ENSMUSG00000023284	chr5	Zfp605	-1.3539863	0.000335355	0.000785473	0.952810529	0.125671701	-1	51	25	39	41	39	12	11	7	19	35
ENSMUSG00000035632	chr7	Cnot3	0.57306908	0.000336003	0.000786859	4.405985732	0.02735623	1	259	235	185	357	240	546	391	407	325	399
ENSMUSG00000000168	chr9	Dlat	-0.6473519	0.000337208	0.000789472	7.811122771	0.038465742	-1	3641	3879	4324	5687	3058	2240	2766	2818	2781	3600
ENSMUSG00000072969	chrX	Armcx5	-0.8067672	0.000337232	0.000789472	2.111380554	0.044078457	-1	73	69	75	107	77	48	60	35	43	65
ENSMUSG00000015087	chr2	Rabl6	-0.5498458	0.00033737	0.000789663	6.438959601	0.027281788	-1	1579	1478	1317	1851	1457	1110	1123	977	1332	1185
ENSMUSG00000018339	chr11	Gpx3	0.92137526	0.000338296	0.000791699	6.747672921	0.077118183	1	823	1287	963	1317	1118	4481	1474	1909	1271	2608
ENSMUSG00000060950	chr12	Trmt61a	0.83936743	0.00033909	0.000793424	2.415908355	0.051431904	1	55	46	49	65	62	153	95	119	100	78

ENSMUSG00000021356	chr13	Irf4	1.13649266	0.000339907	0.000795202	0.937471935	0.074546631	1	14	24	15	10	18	46	46	38	31	39
ENSMUSG00000089838	chr1	Gm2962	-0.7883617	0.000340402	0.000796228	2.978349654	0.048804335	-1	128	154	153	215	92	131	92	61	102	83
ENSMUSG00000005625	chr3	Psmd4	0.53367286	0.000340654	0.000796685	7.132509904	0.026004046	1	1837	1557	1411	2191	1589	3181	2534	2422	2839	2577
ENSMUSG00000024218	chr17	Taf11	0.55279533	0.000341495	0.000798517	4.055242152	0.024493868	1	206	207	166	270	156	309	360	303	304	323
ENSMUSG00000029528	chr5	Pxn	-0.5880944	0.000341598	0.000798624	6.628196795	0.031475197	-1	1798	1560	1596	2077	1800	1897	1205	1045	1041	1336
ENSMUSG00000017999	chr2	Ddx27	0.6141114	0.000342269	0.00080006	3.551843982	0.029109575	1	126	122	127	170	138	254	292	185	226	191
ENSMUSG00000070577	chr4	Gm572	-1.6795787	0.000342508	0.000800482	2.062991687	0.227809773	-1	114	82	92	106	70	3	33	14	68	37
ENSMUSG00000094686	chr4	Ccl21a	1.01362592	0.000342821	0.000801082	3.963941317	0.089406498	1	213	111	128	211	111	707	242	180	355	244
ENSMUSG00000061666	chr11	Gdpd1	0.79840087	0.000344188	0.000804141	2.458169205	0.045348223	1	54	59	76	55	44	128	104	103	106	115
ENSMUSG00000055762	chr15	Eef1d	0.56555081	0.000344592	0.00080495	7.124494167	0.029283368	1	1645	1589	1419	2240	1544	3483	2571	2877	2269	2409
ENSMUSG00000031790	chr8	Mmp15	-0.6335804	0.000345818	0.000807679	5.490736917	0.035799704	-1	745	696	698	1027	903	515	530	642	433	741
ENSMUSG00000055003	chr6	Lrtm2	1.68728973	0.00034589	0.000807713	0.594632243	0.190915723	1	5	12	12	11	8	8	35	55	24	46
ENSMUSG00000046818	chr3	Ddit4l	-0.8046385	0.000350127	0.00081747	8.396166666	0.059696612	-1	6736	6605	5195	6539	6612	2896	2876	3426	4128	6639
ENSMUSG00000048578	chr5	Mlec	-0.6769663	0.000350306	0.000817751	8.358236208	0.042391739	-1	7253	6143	5324	5381	5635	3258	4284	3455	4154	5424
ENSMUSG00000067780	chr1	Pi15	-0.900892	0.000350953	0.000819125	2.624263904	0.063389575	-1	86	134	106	153	110	95	51	84	38	78
ENSMUSG00000003721	chr1	Insig2	-0.5487232	0.000352114	0.000821694	5.489303193	0.026617224	-1	804	749	703	998	726	517	603	502	675	664
ENSMUSG00000031959	chr8	Wdr59	-0.5796781	0.000352171	0.000821694	3.891629395	0.026763186	-1	266	249	231	342	234	176	164	176	223	221
ENSMUSG00000052825	chr8	Gm9892	-0.8067647	0.00035246	0.000822229	3.060580007	0.052233532	-1	187	136	141	166	148	81	111	54	130	113
ENSMUSG00000026035	chr1	Ppil3	0.69277069	0.00035304	0.000823446	3.332664744	0.037888767	1	128	120	77	154	93	189	204	193	244	166
ENSMUSG00000022110	chr14	Sucla2	-0.6098122	0.000353446	0.000824256	9.216496136	0.034565923	-1	10700	11291	10791	13160	7756	7044	7382	6510	8727	8681
ENSMUSG00000021270	chr12	Hsp90aa1	0.69247687	0.000353904	0.000825185	5.804765667	0.043418747	1	594	545	530	867	662	1328	1592	896	1125	705
ENSMUSG00000037852	chr8	Cpe	-0.6224102	0.000354983	0.000827563	7.978075508	0.035869879	-1	4905	4141	3973	5560	4248	2612	3356	2517	3888	3775
ENSMUSG00000002825	chr9	Qtrt1	0.93201212	0.000356014	0.000829829	2.39934233	0.066057429	1	60	42	51	62	48	188	109	92	102	65
ENSMUSG00000021614	chr13	Vcan	0.6647203	0.000356279	0.000830169	4.776004716	0.038718625	1	309	250	315	412	292	719	748	419	494	372
ENSMUSG00000031273	chrX	Col4a6	-1.4778811	0.000356228	0.000830169	0.220237613	0.12591584	-1	15	22	29	21	27	3	18	8	8	8
ENSMUSG00000029787	chr6	Avl9	-0.8436746	0.000356486	0.000830513	2.308179218	0.05207786	-1	97	84	99	90	89	53	83	45	41	62
ENSMUSG00000057457	chrX	Phex	-1.3759123	0.000358032	0.000833976	0.060611431	0.089915474	-1	22	29	14	15	19	8	8	7	7	12
ENSMUSG00000032905	chr18	Atg12	-0.5436703	0.000359117	0.000836365	5.091651646	0.025785149	-1	697	596	545	596	549	448	490	345	466	514
ENSMUSG00000007833	chr7	Aldh16a1	0.62743312	0.000360705	0.000839922	4.366071225	0.033557865	1	225	221	231	335	198	656	368	317	351	366
ENSMUSG00000056476	chr3	Med12l	-1.4187018	0.000361595	0.000841855	-0.067601384	0.095512497	-1	22	21	17	12	18	5	9	9	4	10
ENSMUSG00000024537	chr18	Psmg2	0.52081587	0.000361901	0.000842426	4.738986243	0.02295289	1	382	325	291	384	249	611	525	474	485	467
ENSMUSG00000033728	chr15	Lrrc14	0.54360494	0.000362363	0.000843362	4.130928524	0.0237976	1	236	226	187	221	180	379	335	336	288	347
ENSMUSG00000075330	chr16	A930003A15Rik	0.65191739	0.000362675	0.000843947	4.40577213	0.036507825	1	272	189	217	263	273	317	426	452	387	504
ENSMUSG00000024286	chr18	Ccny	-0.5174734	0.00036546	0.000850285	6.33237945	0.024340862	-1	1468	1298	1313	1806	1210	1141	1047	948	1008	1272
ENSMUSG00000075266	chr10	Cenpw	1.20338155	0.000365759	0.000850841	0.559700805	0.081768275	1	15	4	10	21	11	32	38	21	28	34
ENSMUSG00000086605	chr2	Gm14290	-0.5801185	0.000368112	0.000856172	3.75600286	0.026519477	-1	253	221	185	289	250	165	200	178	149	183
ENSMUSG00000038079	chr1	Tmem237	0.94200272	0.000368959	0.000857999	1.769086349	0.061163794	1	28	29	23	44	43	63	94	55	75	64
ENSMUSG00000029392	chr5	Rilpl1	-0.5743128	0.000369185	0.00085838	6.162140103	0.030066058	-1	1065	1352	1240	1715	1039	1058	821	752	1050	1019
ENSMUSG00000042606	chr7	Hirip3	0.74200109	0.000369273	0.000858444	2.905827374	0.041970117	1	75	70	71	88	103	136	178	150	152	132
ENSMUSG00000045867	chr10	Cradd	-0.6578549	0.000369625	0.000859119	2.974612158	0.031812672	-1	143	139	131	181	116	95	97	77	93	130
ENSMUSG00000001844	chr5	Zdhhc4	0.5059295	0.000370471	0.000860941	4.461185201	0.021069844	1	262	264	230	347	251	499	397	379	352	481
ENSMUSG00000000094	chr11	Tbx4	1.39134262	0.000372841	0.000866305	1.406072301	0.145869561	1	25	15	19	23	21	16	72	81	47	76
ENSMUSG00000031971	chr8	Ccsap	1.41965624	0.000373346	0.000867335	-0.209240231	0.079403393	1	7	5	9	4	4	20	20	17	13	17
ENSMUSG00000021102	chr12	Glrx5	0.56306539	0.000373956	0.000868607	6.181717621	0.028946448	1	854	849	805	1161	720	1829	1250	1493	1252	1240
ENSMUSG00000020402	chr11	Vdac1	-0.5475594	0.000375387	0.000871785	10.02198176	0.028193614	-1	17266	18246	16630	24776	15746	14192	13468	12616	12606	16158
ENSMUSG00000069539	chr10	Scyl2	-0.6678919	0.000375709	0.00087239	3.727972543	0.036769785	-1	237	214	247	276	224	118	214	130	168	197
ENSMUSG00000034647	chr17	Ankrd12	-0.6417224	0.000380191	0.000882589	3.423895404	0.032579303	-1	193	162	189	227	192	171	143	91	155	121
ENSMUSG00000042532	chr19	Golga7b	1.3629888	0.000380228	0.000882589	3.333912681	0.161798041	1	123	86	64	69	69	48	208	205	280	412
ENSMUSG00000003154	chr6	Foxj2	-0.4878113	0.000380538	0.000883162	5.006270678	0.02046054	-1	503	522	484	741	550	487	429	397	384	486
ENSMUSG00000030188	chr6	Magohb	0.97875906	0.000380616	0.000883197	1.961583009	0.071228779	1	42	40	20	52	36	129	92	74	57	59
ENSMUSG00000050188	chr4	Lsm10	0.80954696	0.000381448	0.00088498	2.489923164	0.04859027	1	69	59	44	74	52	137	104	73	145	113
ENSMUSG00000072872	chr6	Rybp	-0.9850374	0.000381943	0.00088598	1.638188288	0.067465241	-1	53	62	62	71	49	26	45	16	35	43
ENSMUSG00000078684	chr3	5830417I10Rik	1.78406172	0.000382268	0.000886587	1.948810746	0.258117622	1	26	22	22	23	30	6	120	95	124	116
ENSMUSG00000084786	chr9	Ubl5	0.58764674	0.000382623	0.000887264	6.22189385	0.0316937	1	1036	871	800	976	747	2004	1347	1353	1453	1176
ENSMUSG00000022389	chr15	Tef	-0.6618232	0.000384562	0.000891613	8.130420585	0.041057922	-1	6194	5537	5122	4507	3927	3324	3595	2703	3903	4200
ENSMUSG00000024853	chr19	Sf3b2	0.52098283	0.000384796	0.000892008	6.778015793	0.025101834	1	1332	1175	1109	1887	1275	2325	2235	1904	1986	2116
ENSMUSG00000045092	chr3	S1pr1	-0.6703523	0.00038561	0.000893745	4.673812991	0.039857448	-1	354	384	529	595	461	481	260	305	233	338
ENSMUSG00000028284	chr4	Map3k7	-0.5026194	0.000386416	0.000895464	5.866744882	0.022807212	-1	997	941	952	1338	889	790	846	660	768	877
ENSMUSG00000010047	chr9	Hyal2	0.60345453	0.000386748	0.000896085	3.944951216	0.029951261	1	191	182	147	206	176	432	309	281	223	271
ENSMUSG00000037318	chr1	Traf3ip3	1.08557576	0.00038793	0.000898528	2.225079687	0.09233096	1	58	46	35	35	40	87	95	151	51	115
ENSMUSG00000060594	chr9	Layn	1.33441913	0.000387915	0.000898528	1.194699777	0.128770798	1	25	23	16	22	5	83	66	26	30	51
ENSMUSG00000037419	chr9	Endod1	0.63569442	0.000388788	0.000900365	3.491307734	0.032097735	1	130	117	121	163	119	329	229	194	167	196
ENSMUSG00000039997	chr1	Ifi203	0.84357661	0.000389541	0.000901959	3.266856481	0.059106336	1	73	115	116	121	79	148	229	148	163	310
ENSMUSG00000041961	chr11	Znrf3	-0.9590231	0.000390069	0.000903031	2.111018914	0.069252765	-1	76	83	73	117	69	27	53	39	37	77
ENSMUSG00000065460	chr2	Mir133a-2	1.23999847	0.000390627	0.000904175	2.272018874	0.124524983	1	69	51	37	22	25	139	63	108	149	76

ENSMUSG00000032036	chr9	Kirrel3	-1.6419165	0.00039156	0.000906184	0.186252728	0.16773952	-1	25	18	25	35	14	21	10	6	2	2
ENSMUSG00000018322	chr2	Tomm34	0.66396828	0.000392094	0.000907269	3.821882396	0.036638095	1	180	137	137	187	166	430	271	272	224	216
ENSMUSG00000003660	chr2	Snrnp200	-0.5550779	0.00039235	0.000907712	5.765808627	0.028017001	-1	895	819	774	1284	1067	760	803	549	752	737
ENSMUSG00000032806	chrX	Slc10a3	0.71721633	0.00039308	0.000909249	2.320996703	0.034799072	1	57	55	52	70	41	104	107	85	99	99
ENSMUSG00000057667	chr7	Bloc1s3	0.74974731	0.000393335	0.000909689	2.611533933	0.04167226	1	85	62	60	78	48	113	129	137	105	125
ENSMUSG00000004264	chr6	Phb2	0.53158688	0.000393766	0.000910535	6.868732421	0.026277813	1	1380	1336	1239	1985	1244	2768	2146	2282	1985	2104
ENSMUSG00000032855	chr17	Pkd1	-0.5337272	0.000394076	0.000911033	5.514414774	0.025645771	-1	718	721	811	972	790	714	594	546	483	722
ENSMUSG00000051579	chrX	Tceal8	0.52330445	0.000394112	0.000911033	4.568851454	0.023318164	1	302	248	260	410	239	442	475	460	450	437
ENSMUSG00000020493	chr11	Prr11	1.45214028	0.000395455	0.000913987	1.094613146	0.154674906	1	17	12	12	18	20	49	97	44	33	16
ENSMUSG00000056209	chr19	Npm3	0.71462284	0.000396012	0.000915122	3.850657543	0.043493956	1	158	133	155	209	154	344	372	256	312	166
ENSMUSG00000079084	chr9	Ccdc82	-1.1578956	0.000396983	0.000917216	0.776807103	0.082658388	-1	27	34	36	42	26	24	12	8	24	13
ENSMUSG00000037993	chr8	Dhx38	0.5340101	0.000398287	0.000920076	4.284649653	0.023626839	1	243	196	219	286	235	469	427	320	318	347
ENSMUSG00000027583	chr2	Zbtb46	-0.6653515	0.000398519	0.00092046	2.755251108	0.03143952	-1	111	122	100	166	112	86	96	79	77	81
ENSMUSG00000041143	chr4	Tmco4	0.73807526	0.000400089	0.000923829	2.965287606	0.042930473	1	77	66	72	146	76	192	145	106	168	178
ENSMUSG00000066705	chr9	Fxyd6	0.8712449	0.00040011	0.000923829	5.972530163	0.070372777	1	464	721	669	1024	469	2382	872	1433	973	1025
ENSMUSG00000040687	chr2	Madd	0.56492414	0.000400385	0.000924311	3.762474613	0.025274182	1	168	157	149	200	136	357	240	233	249	237
ENSMUSG00000026526	chr1	Fh1	-0.5826198	0.000400883	0.000925309	8.148028847	0.032035502	-1	4897	5075	5044	6707	3784	3440	3462	3395	4199	3959
ENSMUSG00000027165	chr2	B230118H07Rik	-0.5460528	0.000401203	0.000925893	5.550484831	0.026973809	-1	855	850	788	973	671	620	649	473	728	633
ENSMUSG00000029014	chr5	Dnajc2	0.64762808	0.000401649	0.000926771	4.220408393	0.036227081	1	194	177	194	288	226	374	418	280	479	289
ENSMUSG00000038332	chr10	Sesn1	-0.5996712	0.000402009	0.000927447	5.216643509	0.032451834	-1	763	729	502	732	600	470	512	351	426	662
ENSMUSG00000087497	chr11	2810001G20Rik	0.91130585	0.000402526	0.000928488	1.44463256	0.050667323	1	35	26	25	26	21	57	64	53	42	60
ENSMUSG00000040621	chrX	Gemin8	1.0831484	0.000402849	0.000929079	0.682467513	0.062902645	1	17	14	8	16	15	38	31	37	24	33
ENSMUSG00000040188	chr9	Scamp2	0.5068961	0.000403107	0.000929521	5.99857929	0.023449625	1	836	784	635	938	741	1457	1212	1068	1138	1265
ENSMUSG00000052962	chr6	Mrpl35	0.55883936	0.000403445	0.000930147	4.791227427	0.027369857	1	319	326	276	427	319	416	576	533	558	578
ENSMUSG00000066880	chr8	Zfp617	-0.8836384	0.000404546	0.00093253	3.217728935	0.06563846	-1	174	165	172	228	153	50	129	80	146	117
ENSMUSG00000006850	chr18	Tmco6	0.81951239	0.000405609	0.000934827	2.518987376	0.05106045	1	88	55	38	70	52	127	109	102	139	105
ENSMUSG00000039989	chr11	Cbx4	0.7794342	0.000407013	0.000937907	2.575533009	0.045542558	1	56	71	53	76	63	137	127	126	74	139
ENSMUSG00000007033	chr17	Hspa1l	-0.8181506	0.000408039	0.000940118	4.136239491	0.059558726	-1	257	264	291	575	311	349	210	201	158	125
ENSMUSG00000024038	chr17	Ndufv3	0.55438225	0.000408613	0.000941285	6.919021727	0.028788202	1	1326	1362	1246	2023	1400	2742	1967	2515	2115	2391
ENSMUSG00000025503	chr7	Taldo1	0.52209784	0.000412165	0.000949312	6.676772655	0.025404778	1	1389	1296	1076	1368	1107	2176	2133	1788	1856	1896
ENSMUSG00000069874	chr11	Irgm2	-1.3481081	0.000412252	0.000949354	5.0913267	0.165581511	-1	1311	988	711	313	239	175	313	356	259	447
ENSMUSG00000079260	chr9	Tmppe	0.81335191	0.000412488	0.000949742	2.482286558	0.049839728	1	59	50	54	65	65	141	152	107	81	89
ENSMUSG00000027454	chr2	Gins1	1.43450024	0.000412812	0.00095033	1.236160156	0.15117794	1	20	16	24	7	19	61	86	35	60	23
ENSMUSG00000038291	chr8	Snx25	-0.7044149	0.000414361	0.000953739	2.832527766	0.037551983	-1	111	128	131	171	109	88	89	60	102	97
ENSMUSG00000027775	chr3	Mfsd1	0.70419648	0.000414455	0.000953799	5.24108838	0.04537056	1	509	434	437	434	311	1003	878	452	916	595
ENSMUSG00000019718	chr12	L3hypdh	0.96030102	0.000414651	0.000954093	1.308371073	0.056437355	1	26	32	17	25	18	48	46	44	55	59
ENSMUSG00000026662	chr2	Sephs1	-0.4992682	0.00041603	0.00095711	4.6700914	0.021299943	-1	427	420	403	526	434	351	397	297	343	327
ENSMUSG00000040867	chr12	Begain	1.27493444	0.000416329	0.000957638	0.410523552	0.0837252	1	9	14	10	8	10	35	30	22	15	37
ENSMUSG00000072568	chr15	Fam84b	-0.944783	0.000416405	0.000957655	2.498250523	0.071428463	-1	103	121	89	187	57	42	65	52	72	76
ENSMUSG00000031835	chr8	Mbtps1	-0.4957845	0.000417201	0.000959329	5.600041502	0.022233222	-1	831	821	820	1034	720	764	689	553	566	725
ENSMUSG00000018068	chr11	Ints2	-0.9545699	0.000419429	0.000964294	2.22480433	0.070961006	-1	88	69	84	107	100	29	71	36	65	51
ENSMUSG00000082491	chr8	Gm5909	-1.2574664	0.000420688	0.00096703	0.250779079	0.083327014	-1	20	18	19	34	23	19	12	5	9	7
ENSMUSG00000098597	chr5	Mir6418	0.52364652	0.000422	0.000969884	4.136240274	0.022468354	1	206	186	204	273	201	410	374	290	275	342
ENSMUSG00000032577	chr9	Mapkapk3	-0.5172043	0.000422842	0.000971661	5.253969915	0.023949635	-1	687	685	603	752	603	486	551	424	571	519
ENSMUSG00000030802	chr7	Bckdk	-0.5172302	0.000423528	0.000973077	7.324701453	0.025278226	-1	2668	2790	2653	3639	2370	2410	2108	1898	2237	2115
ENSMUSG00000022561	chr15	Gpaa1	0.47815057	0.000424698	0.000975605	5.095305049	0.020048392	1	449	371	348	540	422	736	643	591	601	673
ENSMUSG00000029510	chr5	Gpc2	1.3308734	0.000424992	0.000976119	0.499850099	0.104882078	1	14	11	6	12	11	30	25	49	18	26
ENSMUSG00000045201	chr14	Lrrc3b	-1.0736903	0.000425523	0.000977178	1.279778574	0.079412292	-1	41	34	44	69	48	43	16	22	14	28
ENSMUSG00000026864	chr2	Hspa5	0.68337904	0.000425611	0.00097722	8.133803103	0.04442734	1	2934	2797	2609	4575	3298	6377	7159	3720	6788	4310
ENSMUSG00000022898	chr16	Dscr3	0.55366181	0.000427164	0.000980625	4.640050948	0.0266565	1	338	322	271	291	264	570	439	392	531	482
ENSMUSG00000036023	chr14	Parp2	0.64431483	0.00042787	0.000982085	3.2862587	0.032752438	1	122	126	83	130	99	183	245	161	189	180
ENSMUSG00000002524	chr15	Puf60	0.51984852	0.000428931	0.000984035	6.145326092	0.025065611	1	922	766	730	1103	826	1652	1296	1356	1205	1299
ENSMUSG00000046862	chr4	Pramef8	-0.5721073	0.000428796	0.000984035	3.485088652	0.025310048	-1	212	208	174	246	152	157	138	148	134	150
ENSMUSG00000078974	chr11	Sec61g	0.63073478	0.000428916	0.000984035	5.304188151	0.03642917	1	544	496	428	484	344	904	936	607	885	582
ENSMUSG00000004270	chr6	Lpcat3	0.54024885	0.00042911	0.000984284	4.477869102	0.025113324	1	273	232	209	361	279	452	405	429	351	508
ENSMUSG00000056429	chr6	Tgoln1	-0.5278529	0.000429263	0.000984474	5.765087346	0.025628482	-1	927	997	804	1140	909	857	843	521	685	751
ENSMUSG00000026605	chr1	Cenpf	1.14281352	0.000429376	0.00098457	2.202582071	0.104145023	1	42	41	47	22	49	105	148	114	78	55
ENSMUSG00000047976	chr6	Kcna1	-1.0925799	0.000429666	0.000985074	1.924186983	0.093226222	-1	42	56	59	126	96	48	44	29	21	52
ENSMUSG00000037463	chr7	Fbxo27	1.49360441	0.000429863	0.000985363	-0.097485809	0.105694301	1	4	4	6	9	8	19	9	24	18	26
ENSMUSG00000020277	chr10	Pfkl	0.60223568	0.000430959	0.000987714	4.245020792	0.031232188	1	177	225	201	296	219	533	374	258	317	396
ENSMUSG00000055775	chr11	Myh8	1.34094125	0.00043408	0.000994704	9.553770677	0.167048248	1	6086	6865	2253	4034	11521	23988	14350	21499	6265	22570
ENSMUSG00000097566	chr17	A930024N18Rik	-1.3827851	0.000440234	0.001008641	0.325241953	0.118193908	-1	31	16	15	23	37	19	6	7	8	12
ENSMUSG00000019943	chr10	Atp2b1	-0.6114762	0.000442182	0.001012939	6.015099	0.035036173	-1	996	1003	1048	1661	1158	811	1047	543	856	935
ENSMUSG00000013787	chr17	Ehmt2	0.4911392	0.000442668	0.001013886	5.372322527	0.021680504	1	534	484	462	576	495	955	772	693	704	834
ENSMUSG00000031066	chrX	Usp11	0.94430851	0.000443642	0.001015949	2.452926395	0.071030722	1	58	64	43	45	58	147	97	146	63	121

ENSMUSG00000023940	chr17	Sgol1	1.59249497	0.000443727	0.001015978	0.313325479	0.162328379	1	11	7	8	10	5	20	38	27	42	7
ENSMUSG00000002948	chr8	Map2k7	-0.5126737	0.000443871	0.001016141	6.20502379	0.024531792	-1	1387	1182	1185	1530	1174	1039	915	870	979	1159
ENSMUSG00000034616	chr19	Ssh3	0.79559705	0.000444613	0.001017673	2.488488083	0.047402905	1	63	69	52	68	46	155	98	73	113	134
ENSMUSG00000037316	chr8	Bag4	-0.7503974	0.00044471	0.001017728	2.62726667	0.042876188	-1	95	110	92	159	115	58	74	67	74	95
ENSMUSG00000048922	chr14	Cdca2	1.26582448	0.000445564	0.001019517	0.872359813	0.1075744	1	19	11	16	13	14	45	72	24	27	29
ENSMUSG00000021048	chr12	Mthfd1	-0.516147	0.000448772	0.001026688	5.389522757	0.024216549	-1	730	664	560	985	754	585	625	519	523	558
ENSMUSG00000038872	chr8	Zfhx3	-0.6630656	0.000449143	0.001027368	3.530027859	0.036544351	-1	203	180	187	259	217	178	165	162	88	132
ENSMUSG00000041598	chr11	Cdc42ep4	0.61960413	0.000451746	0.001033153	4.171471201	0.033259559	1	215	172	198	243	220	458	331	285	248	467
ENSMUSG00000062729	chr1	Ppox	0.67950913	0.000451937	0.001033421	3.520110485	0.038283375	1	181	115	123	116	109	220	202	205	244	266
ENSMUSG00000031563	chr8	Wwc2	-0.5638838	0.000452726	0.001035056	3.93677421	0.026532604	-1	215	265	251	376	253	221	241	159	172	214
ENSMUSG00000024370	chr18	Cdc23	-0.5260539	0.000453051	0.001035631	4.557831805	0.024097266	-1	364	414	442	484	352	348	367	273	261	326
ENSMUSG00000055305	chr7	Zfp93	-0.7684764	0.000453694	0.00103693	2.295724557	0.043111869	-1	100	92	88	100	70	60	57	45	49	80
ENSMUSG00000097243	chr14	Gm26908	-1.6795312	0.000453865	0.001037152	-0.229221011	0.150962991	-1	27	18	12	23	5	3	9	8	2	6
ENSMUSG00000033420	chr6	Antxr1	0.60689835	0.000455242	0.001040128	5.477842871	0.034167039	1	651	477	456	614	434	927	905	884	575	1104
ENSMUSG00000022623	chr15	Shank3	-0.6677564	0.000455349	0.001040202	4.061106054	0.039224043	-1	242	233	262	451	343	301	183	178	160	235
ENSMUSG00000037295	chr4	Ldlrap1	0.63296425	0.000456645	0.001042994	3.808947158	0.033825092	1	181	144	155	189	142	426	260	211	205	296
ENSMUSG00000052428	chr1	Tmco1	-0.5211331	0.00045813	0.001046213	5.141322609	0.024544385	-1	667	611	565	743	511	493	572	338	482	484
ENSMUSG00000027834	chr3	Serpini1	-1.4046293	0.000459252	0.001048604	0.149856027	0.109867777	-1	17	20	19	35	18	7	3	5	14	15
ENSMUSG00000022836	chr16	Mylk	-0.6723941	0.00046202	0.001054751	4.451838316	0.040829244	-1	311	313	303	633	463	367	263	221	203	332
ENSMUSG00000025246	chrX	Tbl1x	-0.4928208	0.000462679	0.001056084	4.324430922	0.020364137	-1	370	321	323	394	324	278	276	235	279	283
ENSMUSG00000030722	chr7	Nfatc2ip	-0.7961899	0.000463118	0.001056913	1.97164702	0.04285969	-1	78	80	57	90	57	43	56	41	42	45
ENSMUSG00000078963	chr18	Hsbp1l1	-0.9244214	0.000465798	0.001062855	1.821151056	0.061868549	-1	74	78	63	79	41	49	43	44	24	33
ENSMUSG00000006476	chr2	Nsmf	0.54919069	0.000466994	0.001065412	4.07972799	0.025411974	1	238	204	159	237	179	401	307	319	310	292
ENSMUSG00000048330	chr7	Ric3	-1.3275656	0.000467618	0.00106666	0.610417621	0.115288035	-1	21	37	23	33	36	10	17	3	16	20
ENSMUSG00000001416	chr3	Cct3	0.51627906	0.000468775	0.001069126	6.922109304	0.025453381	1	1589	1370	1275	1913	1326	2423	2555	2137	2407	2102
ENSMUSG00000017724	chr11	Etv4	0.746076	0.000472243	0.001076859	2.925873319	0.044460565	1	62	83	82	123	69	215	142	101	136	179
ENSMUSG00000021222	chr12	Dcaf4	-0.5260763	0.000473326	0.001079153	4.71691061	0.024537596	-1	448	448	397	537	469	375	300	322	311	448
ENSMUSG00000022562	chr15	Oplah	-0.519338	0.000473879	0.001080236	5.203722202	0.024545929	-1	562	657	573	851	597	607	404	468	493	497
ENSMUSG00000057778	chr11	Cyb5d2	-0.5593646	0.000474089	0.00108054	4.114441074	0.026773321	-1	364	312	257	336	258	268	208	170	243	252
ENSMUSG00000038028	chr6	9630033F20Rik	-0.7729039	0.000474558	0.001081433	5.83612565	0.056702008	-1	1189	992	996	1373	845	412	949	480	922	648
ENSMUSG00000102340	chr9	RP24-496O17.2	-1.2200204	0.000474813	0.001081837	0.261048902	0.077150024	-1	16	19	18	29	31	12	12	10	7	12
ENSMUSG00000029686	chr6	Cul1	-0.4999254	0.000476543	0.001085601	6.210464435	0.02354523	-1	1309	1166	1130	1658	1221	1035	975	898	1022	1069
ENSMUSG00000040859	chr4	Bsdc1	-0.5203774	0.000476909	0.001086258	5.360457681	0.024887725	-1	822	718	656	817	585	667	503	448	583	557
ENSMUSG00000047534	chr12	Mis18bp1	1.4484276	0.000479776	0.001092611	0.408359078	0.13105844	1	11	11	13	9	3	16	50	20	28	28
ENSMUSG00000024901	chr19	Peli3	-1.1701679	0.000482158	0.001097856	0.452855376	0.077028775	-1	41	21	21	29	18	17	14	9	12	11
ENSMUSG00000069114	chr3	Zbtb10	-0.7493881	0.000485519	0.00110533	2.683657412	0.044182682	-1	98	107	119	166	104	116	73	75	59	64
ENSMUSG00000076060	chr6	Mir704	1.11711658	0.00048596	0.001106154	1.130149381	0.085402275	1	24	15	18	27	13	49	71	22	46	43
ENSMUSG00000039068	chr3	Zzz3	-0.5044854	0.000488128	0.001110907	4.425305233	0.021900602	-1	363	336	326	508	349	288	325	237	264	333
ENSMUSG00000029605	chr5	Oas1b	1.38166723	0.00048826	0.001111026	0.169763229	0.100500867	1	13	7	8	5	7	33	20	13	18	34
ENSMUSG00000025915	chr1	Sgk3	0.8429114	0.000489031	0.001112599	2.751768995	0.058636176	1	57	53	78	106	61	169	186	82	150	110
ENSMUSG00000026429	chr1	Ube2t	0.83585714	0.000490409	0.001115554	1.937394189	0.048758053	1	34	31	40	53	40	78	81	60	96	71
ENSMUSG00000014039	chr16	Prdm15	-0.7412476	0.000490623	0.001115859	2.590881575	0.042486869	-1	110	83	98	138	123	79	87	53	80	63
ENSMUSG00000079363	chr5	Gbp4	-0.8824394	0.000492859	0.00112076	1.941804626	0.057835894	-1	81	82	73	69	53	41	41	32	37	64
ENSMUSG00000020917	chr11	Acly	-0.8645036	0.000492971	0.001120833	5.395220643	0.071060089	-1	446	1205	738	582	951	566	539	410	492	430
ENSMUSG00000053475	chr2	Tnfaip6	1.3928377	0.00049344	0.001121718	1.870168155	0.161374116	1	38	32	21	29	23	216	74	36	47	57
ENSMUSG00000048807	chr11	Slc35e4	0.51513949	0.000493906	0.001122593	5.129799051	0.024095056	1	431	364	409	463	459	832	630	604	565	738
ENSMUSG00000014554	chr6	Dguok	0.59991848	0.000494632	0.001124062	3.87252212	0.030634432	1	154	209	132	235	137	365	248	247	295	278
ENSMUSG00000033170	chr15	Card10	-0.6869944	0.000496754	0.0011287	3.332090013	0.039382092	-1	178	146	189	236	169	94	122	133	103	168
ENSMUSG00000039148	chr19	Sart1	0.53342723	0.000497478	0.00113016	5.015313736	0.025980028	1	359	314	318	581	412	773	631	589	542	587
ENSMUSG00000027314	chr2	Dll4	-0.7433636	0.000497662	0.001130396	3.421346963	0.047642792	-1	170	190	197	290	153	128	119	152	75	173
ENSMUSG00000050079	chr8	Rspry1	-0.6025072	0.000498066	0.001131128	3.304756986	0.02859842	-1	189	176	127	217	172	127	133	105	139	129
ENSMUSG00000005667	chr6	Mthfd2	1.0210365	0.000498462	0.001131845	3.358337685	0.093793893	1	144	69	89	106	89	307	280	163	278	82
ENSMUSG00000054723	chr17	Vmac	0.85573583	0.000498585	0.00113194	2.459933086	0.057686698	1	62	47	62	57	54	161	78	123	79	126
ENSMUSG00000021236	chr12	Entpd5	-0.5803094	0.000499844	0.001134614	4.036516798	0.029111161	-1	246	320	277	343	266	193	248	164	211	252
ENSMUSG00000029250	chr5	Polr2b	-0.5345485	0.000500365	0.001135613	5.436338572	0.026591475	-1	733	725	695	1010	668	528	617	449	638	647
ENSMUSG00000029924	chr6	Slc37a3	-0.5094421	0.000501564	0.001138148	4.005405696	0.02154062	-1	280	281	257	314	260	241	229	180	199	229
ENSMUSG00000020431	chr11	Adcy1	-1.037751	0.000501703	0.001138279	1.623744237	0.079783265	-1	33	54	46	96	72	23	36	30	29	40
ENSMUSG00000026496	chr1	Parp1	-0.5322418	0.000502157	0.001139124	6.021055147	0.026889873	-1	1133	982	1018	1365	1208	797	1001	765	830	931
ENSMUSG00000103480	chr3	Bdh2	1.27654712	0.000502919	0.001140668	0.881609345	0.108213847	1	10	27	11	13	12	61	51	31	28	28
ENSMUSG00000040987	chr7	Mill2	-1.0995825	0.000503243	0.001141218	0.984577515	0.081932336	-1	38	38	35	41	37	39	12	14	18	15
ENSMUSG00000051989	chr16	Smim11	0.50655907	0.000504288	0.001143402	5.016930695	0.023262772	1	398	371	348	499	375	716	602	573	685	510
ENSMUSG00000034064	chr16	Poglut1	0.54727179	0.000506042	0.001147193	3.825783262	0.024776394	1	177	199	138	201	137	322	294	237	248	266
ENSMUSG00000001768	chr2	Rin2	0.6419809	0.000507381	0.001150041	4.737004207	0.037980605	1	389	311	294	340	211	555	647	319	521	620
ENSMUSG00000025010	chr19	Ccnj	-0.7381635	0.000509148	0.001153853	2.469267656	0.040696366	-1	83	120	94	112	94	64	81	58	61	68
ENSMUSG00000028328	chr4	Tmod1	-0.6879659	0.000509227	0.001153853	8.302021073	0.04629432	-1	6518	5253	5055	6558	5586	2520	4301	3825	3568	5402

ENSMUSG00000015542	chr11	Nat9	0.55335085	0.00051072	0.001157046	3.521775705	0.024334098	1	153	129	120	156	127	264	199	199	225	217
ENSMUSG00000020694	chr11	Tlk2	-0.4901376	0.000510886	0.001157236	5.461875502	0.022247237	-1	761	719	672	1014	686	625	585	519	589	671
ENSMUSG00000042446	chr4	Zmym4	-0.5145586	0.000512456	0.001160604	4.162393741	0.022438097	-1	281	303	253	440	297	253	243	209	233	260
ENSMUSG00000021518	chr13	Ptdss1	0.47879662	0.000514906	0.001165963	5.027101577	0.020684692	1	391	362	335	548	400	688	627	577	525	679
ENSMUSG00000049999	chr2	Ppp1r3d	-0.8717052	0.000515774	0.00116774	2.454007854	0.06210028	-1	120	89	75	104	126	90	46	64	40	72
ENSMUSG00000002733	chr2	Plekha3	-0.7020275	0.00051595	0.001167949	3.146046657	0.040630798	-1	172	150	129	207	153	107	150	74	124	89
ENSMUSG00000040225	chr1	Prrc2c	-0.5254392	0.00051665	0.001169345	5.598817533	0.025969136	-1	757	780	736	1163	844	690	747	581	505	727
ENSMUSG00000059970	chr12	Hspa2	0.86913484	0.000518021	0.001172257	2.810367216	0.064243406	1	76	72	68	105	46	134	126	177	84	203
ENSMUSG00000058355	chr8	Abce1	-0.6070621	0.000518553	0.001173271	5.985848144	0.035363099	-1	1069	943	1010	1518	1180	769	1025	565	962	776
ENSMUSG00000015980	chr7	Lrrc27	1.13939563	0.00052	0.001176356	1.053885356	0.089204669	1	13	20	15	23	19	23	54	35	43	62
ENSMUSG00000020841	chr11	Cpd	-0.4990529	0.000522268	0.001181295	6.697625596	0.024070486	-1	1817	1689	1609	2308	1664	1544	1311	1211	1388	1577
ENSMUSG00000047379	chr19	B3gnt1	0.52001643	0.000526003	0.00118955	4.868858159	0.024538497	1	355	379	277	420	350	599	531	592	450	625
ENSMUSG00000000392	chr2	Fap	0.57875683	0.000526676	0.001190855	4.619016079	0.030405225	1	358	309	285	282	217	505	432	515	432	499
ENSMUSG00000031976	chr8	Urb2	-0.6633757	0.00052675	0.001190855	3.344037904	0.036774667	-1	197	157	148	212	202	99	142	108	152	130
ENSMUSG00000000441	chr6	Raf1	-0.5070894	0.00052696	0.001191135	7.117577473	0.025063211	-1	2415	2162	2329	2924	2306	1934	1875	1597	1956	1999
ENSMUSG00000027524	chr2	Edn3	-1.0090754	0.000529887	0.001197559	1.718542472	0.076740112	-1	63	70	67	66	49	16	38	33	34	50
ENSMUSG00000020376	chr11	Rnf130	0.53774512	0.000530065	0.001197768	5.222153003	0.026916354	1	424	456	403	578	408	905	804	497	768	648
ENSMUSG00000022203	chr14	Efs	0.68393568	0.000532006	0.001201958	2.944466503	0.037204475	1	94	80	69	109	82	173	135	168	107	179
ENSMUSG00000021635	chr13	Rad17	-0.5605364	0.000532165	0.001202125	3.852697833	0.026575631	-1	286	209	270	306	204	196	216	150	187	199
ENSMUSG00000028617	chr4	Lrrc42	0.61078925	0.000532699	0.001203135	3.546458176	0.030929587	1	149	128	121	154	128	335	204	216	184	209
ENSMUSG00000062797	chr7	Il7Rn6	-0.5394964	0.000534171	0.001206265	5.108426724	0.027006929	-1	675	554	515	725	572	378	541	372	485	508
ENSMUSG00000076617	chr12	Ighm	-0.7876944	0.000534971	0.001207876	5.570315241	0.059750264	-1	713	1111	941	1131	588	398	610	794	428	568
ENSMUSG00000017756	chr13	Slc12a7	0.72387185	0.000536784	0.001211729	3.691626976	0.04650717	1	97	112	125	233	161	385	276	207	226	220
ENSMUSG00000034317	chr3	Trim59	0.99013818	0.000536851	0.001211729	1.655786536	0.070735143	1	27	29	38	31	24	61	93	74	50	48
ENSMUSG00000061286	chr7	Exosc5	0.60891021	0.00053739	0.00121275	3.96808877	0.032406915	1	201	183	149	192	186	401	326	277	310	220
ENSMUSG00000027618	chr2	Nfs1	-0.5531032	0.000537568	0.001212956	6.625614997	0.029757592	-1	1795	1685	1709	2169	1410	1129	1297	1135	1470	1471
ENSMUSG00000027660	chr3	Skil	-0.6661456	0.000537775	0.001213228	3.862066978	0.039509152	-1	220	220	314	363	209	250	216	151	122	182
ENSMUSG00000063317	chr7	Usp31	-0.5699843	0.000541084	0.001220495	3.573013778	0.026743543	-1	189	166	225	286	189	163	175	138	139	161
ENSMUSG00000032737	chr7	Inppl1	-0.5505867	0.00054187	0.001222071	7.079023432	0.02970096	-1	2312	2261	2328	2963	2119	1582	1701	1975	1629	2007
ENSMUSG00000035064	chr7	Eef2k	-0.5470444	0.000546207	0.001231654	5.841425363	0.028703285	-1	1103	926	890	1156	981	685	696	650	762	1002
ENSMUSG00000017176	chr11	Nt5c3b	0.66807147	0.000546683	0.001232529	3.329633118	0.03747685	1	82	121	102	160	109	253	185	176	224	157
ENSMUSG00000024968	chr19	Rcor2	-1.0661276	0.000546774	0.001232535	2.856816997	0.102313636	-1	137	124	103	194	166	174	45	54	43	71
ENSMUSG00000062075	chr10	Lmnb2	0.77212678	0.000547618	0.001234238	3.877733103	0.054243612	1	223	147	128	140	156	297	392	364	194	247
ENSMUSG00000098387	chr2	Pet117	-0.9717069	0.000547805	0.001234459	1.362591799	0.062707992	-1	48	36	50	71	40	24	33	32	16	30
ENSMUSG00000027710	chr3	Acad9	-0.5166419	0.000548805	0.001236515	5.275638198	0.024924338	-1	628	721	638	889	531	476	545	478	547	540
ENSMUSG00000058799	chr10	Nap1l1	0.60332538	0.000549947	0.001238888	6.176230373	0.035369851	1	921	830	671	1050	813	1676	1841	1190	1422	999
ENSMUSG00000075053	chr13	Vdac3-ps1	-1.0395274	0.000551428	0.001242024	5.035546634	0.103831337	-1	396	361	903	1399	343	409	309	454	288	275
ENSMUSG00000029642	chr5	Polr1d	0.52329295	0.000552746	0.001244792	6.024374191	0.026356801	1	882	767	744	927	655	1451	1339	1139	1282	1047
ENSMUSG00000022992	chr15	Kansl2	-0.4970772	0.000552932	0.001245011	5.404443015	0.023149798	-1	757	648	729	927	635	541	597	527	569	621
ENSMUSG00000024231	chr18	Cul2	-0.5390562	0.000553569	0.001246245	5.508364408	0.02756958	-1	840	772	677	1007	729	490	660	540	648	671
ENSMUSG00000081665	chr7	Gm15922	2.24423631	0.000554322	0.001247738	-0.07913813	0.34785025	1	2	8	1	4	5	46	20	2	6	38
ENSMUSG00000020491	chr11	2810021J22Rik	-1.0362471	0.000554705	0.001248399	1.11568305	0.072595243	-1	33	47	44	46	35	18	26	21	12	33
ENSMUSG00000039396	chr8	Neil3	1.51091224	0.000554999	0.001248859	-0.234000623	0.111902556	1	2	6	10	4	5	12	15	17	23	19
ENSMUSG00000021327	chr13	Zkscan3	-0.5842205	0.000555811	0.001250485	3.88479397	0.029658114	-1	265	253	266	301	223	196	215	131	231	186
ENSMUSG00000034401	chr4	Spata6	0.75881555	0.000555972	0.001250647	2.656572971	0.045629154	1	86	80	58	76	42	147	152	97	112	129
ENSMUSG00000056917	chr19	Sipa1	0.52590246	0.000557105	0.001252993	4.213524123	0.024046477	1	225	190	223	285	205	434	369	333	265	384
ENSMUSG00000028793	chr4	Rnf19b	0.48304549	0.000559361	0.001257865	4.827899644	0.021021591	1	352	334	294	431	349	638	621	445	475	527
ENSMUSG00000032420	chr9	Nt5e	-0.9765819	0.000560948	0.001261231	1.966228442	0.076131551	-1	79	70	70	87	69	74	36	18	49	35
ENSMUSG00000020184	chr10	Mdm2	-0.5058745	0.000561742	0.001262812	5.555665339	0.024310587	-1	877	742	768	1006	721	771	671	469	560	723
ENSMUSG00000027698	chr3	Nceh1	0.78960065	0.000563527	0.001266623	4.908276534	0.05989899	1	184	332	305	620	238	720	719	380	714	579
ENSMUSG00000083567	chr2	Gm11451	-0.7689676	0.000567523	0.001275397	3.616344776	0.053189693	-1	311	231	193	198	198	95	150	137	142	206
ENSMUSG00000008763	chr3	Man1a2	-0.5378725	0.000568386	0.001277133	4.280448362	0.025741567	-1	303	294	311	457	348	309	286	190	216	297
ENSMUSG00000038733	chr1	Wdr26	-0.5148786	0.000569386	0.001279173	7.127179317	0.026164251	-1	2305	2243	2154	3250	2362	1774	1979	1688	1830	2111
ENSMUSG00000038403	chr3	Hfe2	-0.6040388	0.000569722	0.001279722	9.238831543	0.036469083	-1	12295	10291	9079	12545	10116	6186	7782	6740	8605	9665
ENSMUSG00000030629	chr7	Zfand6	-0.5746114	0.000573821	0.001288722	6.276961923	0.032311459	-1	1472	1410	1278	1652	1106	823	1113	866	959	1314
ENSMUSG00000026159	chr1	Agfg1	-0.4765804	0.000574408	0.001289833	5.08201269	0.020972108	-1	603	528	538	696	562	536	513	354	462	451
ENSMUSG00000042605	chr5	Atxn2	-0.6079804	0.000576089	0.001293401	5.339696584	0.035454078	-1	566	597	651	1067	785	472	576	559	399	600
ENSMUSG00000070583	chr4	Fv1	-1.1786885	0.000577461	0.001296272	1.024072497	0.100983247	-1	42	46	28	57	28	22	16	8	14	37
ENSMUSG00000006527	chr14	Sfmbt1	-0.5570045	0.000579208	0.001299986	3.632458614	0.025699298	-1	191	179	200	307	221	181	173	155	143	161
ENSMUSG00000090381	chr14	Gm6158	1.29245715	0.000580252	0.00130212	0.262665563	0.093998826	1	8	9	8	14	7	43	18	25	23	15
ENSMUSG00000059975	chr7	Zfp74	-0.7760046	0.000581639	0.001305022	2.235151653	0.045436674	-1	85	77	95	94	79	43	61	50	64	57
ENSMUSG00000042594	chr5	Sh2b3	0.61112736	0.000582672	0.00130713	5.087362017	0.035583837	1	402	393	393	472	336	467	864	578	599	826
ENSMUSG00000020265	chr10	Sumo3	0.49564121	0.000584511	0.001311046	5.976019654	0.023727911	1	786	718	694	939	750	1476	1209	997	1201	1144
ENSMUSG00000043629	chr1	1700019D03Rik	-1.1195093	0.000584608	0.001311052	0.665567988	0.075195956	-1	32	25	37	28	27	12	10	18	18	17
ENSMUSG00000051550	chr7	Zfp579	0.70569703	0.000587043	0.001316303	3.358389752	0.043562977	1	105	110	83	157	122	202	160	272	176	205

ENSMUSG00000022792	chr16	Yars2	-0.5837161	0.000587232	0.001316515	3.735428868	0.029087687	-1	236	211	207	356	188	159	206	141	188	168
ENSMUSG00000052337	chr6	Immt	-0.5731405	0.000587616	0.001317164	8.320231217	0.032911936	-1	5214	5564	5615	7803	4506	3790	3979	3635	4848	4639
ENSMUSG00000043872	chr4	Zmym1	-0.8092242	0.000591023	0.001324588	2.300976974	0.052108436	-1	79	90	80	117	92	79	67	33	64	45
ENSMUSG00000031099	chrX	Smarca1	-0.9786363	0.000591872	0.001326279	2.086208024	0.078129041	-1	108	78	66	106	55	21	47	51	50	55
ENSMUSG00000031633	chr8	Slc25a4	-0.544498	0.000592142	0.001326672	11.845999	0.029937021	-1	59816	64510	63863	86055	53031	45710	48853	45284	49977	54013
ENSMUSG00000040187	chr6	Arntl2	1.3302781	0.00059334	0.001329143	-0.149353761	0.077632428	1	6	6	9	6	5	26	18	17	15	14
ENSMUSG00000050315	chr3	Synpo2	-0.5531871	0.000593592	0.001329495	9.320161134	0.030819995	-1	10301	9173	10484	16290	10955	9960	8569	8307	6978	8600
ENSMUSG00000067719	chr5	Gm10221	0.50693431	0.000593989	0.001330169	4.810085694	0.023603254	1	365	315	371	403	264	614	526	514	532	489
ENSMUSG00000037994	chr3	Slc9b2	2.01940236	0.000595317	0.001332931	0.126606936	0.282573261	1	4	6	5	6	6	69	22	4	7	27
ENSMUSG00000067150	chr17	Xpo5	-0.6144503	0.00059768	0.001338006	3.538323112	0.032400385	-1	208	177	172	266	218	140	190	101	148	166
ENSMUSG00000005699	chr8	Pard6a	0.67445506	0.000598948	0.00134063	2.577719331	0.033944093	1	71	69	67	74	53	127	105	116	113	124
ENSMUSG00000031918	chr9	Mtmr2	-0.4916468	0.000599486	0.00134162	4.355716101	0.021288656	-1	329	328	339	489	302	314	294	217	270	293
ENSMUSG00000003190	chr7	Bcl2l12	0.75991424	0.000599867	0.001342259	2.88453426	0.048357377	1	70	89	71	98	73	197	120	162	162	101
ENSMUSG00000024474	chr18	Ik	0.52585025	0.000601267	0.001345174	6.128378494	0.027099608	1	898	732	635	1204	845	1436	1317	1321	1211	1443
ENSMUSG00000101655	chr6	2310040G24Rik	-0.5398403	0.000602363	0.001347412	6.102251553	0.028564258	-1	1339	1156	1169	1350	1029	780	1012	801	896	1067
ENSMUSG00000020312	chr10	Shc2	0.88883299	0.000603682	0.001350145	1.976552054	0.061026311	1	46	39	32	49	33	121	59	73	53	101
ENSMUSG00000083337	chr11	Gm11539	1.33726271	0.000603905	0.001350428	0.446862789	0.111942924	1	13	4	6	10	18	39	36	18	20	32
ENSMUSG00000008435	chr7	Rdh13	-0.516758	0.000604789	0.001352188	4.386020416	0.024008978	-1	335	348	321	488	343	335	318	213	227	316
ENSMUSG00000097412	chr10	1810014B01Rik	-0.6913635	0.000606497	0.00135579	2.980958375	0.039270848	-1	134	134	121	191	140	94	85	124	74	106
ENSMUSG00000022564	chr15	Grina	0.55810231	0.000606609	0.001355824	6.906560919	0.031010119	1	1518	1327	1237	1667	1464	2854	2055	2233	1719	2864
ENSMUSG00000039873	chr2	Neurl2	0.50262671	0.000607008	0.001356499	4.798596334	0.023256064	1	347	304	289	438	337	615	466	502	441	637
ENSMUSG00000042462	chr7	Dctpp1	0.56332238	0.000607858	0.001358181	3.960725201	0.027982517	1	194	176	157	255	155	357	322	266	329	230
ENSMUSG00000042834	chr18	Nrep	-0.8052796	0.000608566	0.001359547	8.389730884	0.065034709	-1	6884	7690	6586	5617	4604	2477	4148	4891	3064	5128
ENSMUSG00000025272	chrX	Tro	1.30183087	0.000608741	0.001359719	0.541396612	0.110597078	1	10	8	14	18	7	34	30	43	12	34
ENSMUSG00000002983	chr7	Relb	0.69471272	0.000609511	0.001361198	3.508892578	0.042325919	1	132	110	125	158	116	391	210	170	187	195
ENSMUSG00000040717	chr14	Il17rd	-0.6763435	0.000609598	0.001361198	2.762730804	0.036093145	-1	124	106	117	169	101	93	91	69	62	107
ENSMUSG00000030098	chr6	Grip2	-0.751481	0.000610094	0.001362088	3.18295232	0.049133095	-1	113	127	163	252	190	117	90	130	97	109
ENSMUSG00000034620	chr10	Tmem5	-0.5586778	0.000613751	0.001370028	4.454286313	0.028649848	-1	386	413	356	468	316	278	301	217	366	275
ENSMUSG00000052957	chr13	Gas1	0.57821086	0.000613846	0.001370028	5.51153062	0.032475578	1	641	524	460	686	427	1253	948	749	611	942
ENSMUSG00000037548	chr17	H2-DMb2	1.51765606	0.000616373	0.001375447	0.618363426	0.165961069	1	11	10	9	12	11	88	19	19	26	21
ENSMUSG00000006676	chr9	Usp19	-0.5431054	0.000618422	0.001379801	7.455919734	0.029632002	-1	2913	2746	2735	4094	3094	2679	2074	2432	1849	2644
ENSMUSG00000063903	chr7	Klk1	-1.787044	0.000618825	0.001380478	-0.251650297	0.198572295	-1	15	16	23	14	15	17	0	4	3	3
ENSMUSG00000068959	chr7	Zfp619	-1.2531216	0.00062074	0.00138453	0.368800653	0.098429933	-1	22	31	20	25	25	11	20	3	12	11
ENSMUSG00000020973	chr12	Dnaaf2	0.84043938	0.000620886	0.001384634	2.01286733	0.05244904	1	32	41	45	43	45	84	106	62	86	71
ENSMUSG00000024862	chr19	Klc2	-0.5401541	0.000622514	0.001388043	6.030449861	0.028678464	-1	1152	990	956	1582	1131	754	845	829	869	1028
ENSMUSG00000032350	chr9	Gclc	-0.6706857	0.000626525	0.001396763	2.887361697	0.036829086	-1	156	121	135	147	107	118	103	61	86	95
ENSMUSG00000024163	chr17	Mapk8ip3	-0.5659112	0.000627002	0.001397605	4.88565383	0.030464269	-1	554	467	500	606	489	600	307	341	356	352
ENSMUSG00000045333	chr8	Zfp423	-0.5994897	0.000627451	0.001398243	3.268854432	0.02967042	-1	141	165	167	226	159	154	116	121	94	136
ENSMUSG00000068566	chr7	Myadm	0.60027157	0.000627489	0.001398243	6.792711143	0.036086468	1	1209	1250	1242	1817	1097	2855	2249	2264	1356	2245
ENSMUSG00000035413	chr11	Tmem98	0.79374422	0.00062866	0.001400631	2.199221613	0.047996625	1	57	42	48	62	35	115	81	90	64	114
ENSMUSG00000041852	chr15	Tcf20	-0.5660797	0.000631263	0.001406206	3.781476605	0.027622389	-1	248	223	193	358	208	160	217	152	169	200
ENSMUSG00000020330	chr11	Hmmr	1.3688712	0.000631812	0.001407204	0.890940584	0.138592267	1	14	14	19	6	16	40	67	31	45	19
ENSMUSG00000038622	chr15	Med30	0.64125418	0.000632008	0.001407416	3.168351506	0.034360584	1	89	114	96	137	82	206	205	144	187	141
ENSMUSG00000090137	chr8	Uba52	0.51420691	0.000633514	0.001410545	7.684122763	0.026695154	1	2689	2611	2327	2878	2099	4748	3712	3751	3538	4046
ENSMUSG00000032998	chr4	Foxj3	-0.4881242	0.000635149	0.00141396	5.065841185	0.022428088	-1	507	531	506	747	619	488	494	404	384	506
ENSMUSG00000020109	chr10	Dnajb12	-0.4976809	0.000635589	0.001414714	5.566613844	0.023963521	-1	830	809	642	1014	839	695	663	547	560	749
ENSMUSG00000026436	chr1	Elk4	0.54680812	0.000636857	0.001417311	5.057043119	0.028532569	1	419	394	352	495	354	946	616	629	484	565
ENSMUSG00000020908	chr11	Myh3	1.62538511	0.00063896	0.001421741	8.460469475	0.255483104	1	2752	2422	345	2255	4870	8042	5514	15554	3358	10293
ENSMUSG00000060935	chr10	Tmem263	0.50677586	0.000639051	0.001421741	4.111689669	0.022428334	1	224	174	186	269	207	351	381	293	300	322
ENSMUSG00000074918	chr2	Inafm2	0.70667059	0.00064094	0.001425717	2.515320556	0.038104409	1	53	66	64	74	58	147	124	93	107	97
ENSMUSG00000016194	chr1	Hsd11b1	-1.0015875	0.00064368	0.001431584	1.92402172	0.083379396	-1	59	87	104	61	49	54	48	27	41	32
ENSMUSG00000006019	chr7	Dhx34	0.64814008	0.000645338	0.001435042	2.858495633	0.033041596	1	84	92	73	91	72	184	143	127	111	149
ENSMUSG00000022972	chr16	1110004E09Rik	-0.4869186	0.000649071	0.001443114	4.328320422	0.021104338	-1	341	351	290	416	340	334	254	245	240	291
ENSMUSG00000027879	chr3	Sec22b	0.49232979	0.000649805	0.001444517	5.18236908	0.023019237	1	448	432	420	518	418	807	705	614	743	585
ENSMUSG00000022807	chr16	Osbpl11	-0.5491493	0.000650678	0.001446226	4.183240801	0.027318258	-1	297	286	283	447	299	243	259	175	212	315
ENSMUSG00000026020	chr1	Nop58	0.6048249	0.000651216	0.001447008	4.440353915	0.034342983	1	273	251	220	307	227	510	537	305	480	302
ENSMUSG00000033809	chr16	Alg3	0.63362651	0.000651236	0.001447008	3.928444271	0.036637332	1	163	142	123	227	228	315	343	310	237	293
ENSMUSG00000098754	chr2	Gm28045	-1.0064115	0.000653904	0.001452703	4.220250377	0.098477508	-1	468	464	377	286	224	102	211	269	120	292
ENSMUSG00000021832	chr14	Psmc6	-0.5953046	0.000655868	0.001456836	6.656908503	0.035677864	-1	2013	1794	1679	2169	1410	1159	1433	946	1650	1353
ENSMUSG00000018347	chr11	Zkscan6	0.84848146	0.00065758	0.001460406	1.901886521	0.053665007	1	49	33	37	36	35	106	86	53	61	76
ENSMUSG00000042046	chr1	Dstyk	-0.4677179	0.000658043	0.001461203	4.482325908	0.019576898	-1	359	366	361	499	346	326	324	256	288	334
ENSMUSG00000063531	chr5	Sema3e	-1.2637043	0.00066065	0.001466758	0.112409956	0.08317236	-1	22	10	25	27	18	9	11	7	11	8
ENSMUSG00000021962	chr14	Dcp1a	-0.661996	0.000661692	0.001468839	3.312182282	0.038446167	-1	133	198	174	206	181	156	150	87	126	106
ENSMUSG00000024529	chr18	Lox	0.80359057	0.000662497	0.001470392	5.670917041	0.06451264	1	725	512	463	633	434	1935	1256	739	808	644
ENSMUSG00000020456	chr11	Ogdh	-0.5848468	0.000662611	0.001470412	9.834481546	0.03506905	-1	13343	14507	14120	24855	15890	13245	10581	12219	9878	13758

ENSMUSG00000026604	chr1	Ptpn14	-0.5411581	0.000664583	0.001474554	4.389650655	0.02696361	-1	324	305	325	580	337	328	290	251	220	305
ENSMUSG00000038831	chr2	Ralgps1	-0.9126534	0.000665912	0.001477268	1.771023424	0.064535665	-1	44	76	64	89	50	42	32	29	29	56
ENSMUSG00000024259	chr18	Slc25a46	-0.5477296	0.000669012	0.00148391	5.654140079	0.029545394	-1	850	775	854	1238	768	534	720	649	671	740
ENSMUSG00000034175	chr11	Rhbdd3	0.55823514	0.00067201	0.001490322	4.497180911	0.029225255	1	275	260	236	354	236	355	399	417	520	475
ENSMUSG00000031386	chrX	Hcfc1	-0.5219456	0.000672362	0.001490867	6.21793885	0.027219328	-1	1221	1097	1146	1688	1396	1089	1086	976	807	1033
ENSMUSG00000059325	chr5	Hopx	0.7163202	0.000672608	0.001491174	3.016394394	0.043550328	1	105	73	96	89	82	225	182	104	158	147
ENSMUSG00000027309	chr2	4930402H24Rik	-0.5728013	0.000674972	0.001496178	3.400241535	0.02754948	-1	175	193	171	199	187	163	127	129	111	158
ENSMUSG00000028729	chr4	Ebna1bp2	0.54308073	0.000675285	0.001496635	4.997497722	0.028347489	1	391	331	329	515	376	805	708	483	626	477
ENSMUSG00000090394	chr1	4930523C07Rik	-0.7034105	0.000676428	0.001498932	2.845146257	0.041189103	-1	91	118	115	209	129	102	91	71	85	92
ENSMUSG00000030351	chr6	Tspan11	0.71277057	0.000680795	0.00150837	2.716530737	0.041263334	1	62	72	70	75	81	153	151	134	96	120
ENSMUSG00000041498	chr1	Kif14	1.70804956	0.00068099	0.001508562	0.247633667	0.208344961	1	4	7	10	8	7	26	53	32	14	6
ENSMUSG00000074656	chr2	Eif2s2	-0.5851504	0.000681937	0.001510419	7.080954756	0.034847203	-1	2708	2244	2104	2862	2197	1587	2024	1335	2225	1636
ENSMUSG00000025979	chr1	Mob4	-0.4974966	0.000682743	0.001511965	5.509985399	0.024132042	-1	868	722	695	967	724	587	680	594	630	575
ENSMUSG00000060044	chr10	Tmem26	1.32921078	0.000683473	0.001513343	0.128628467	0.091207418	1	9	5	9	8	9	36	22	11	24	20
ENSMUSG00000003308	chr9	Keap1	-0.5052843	0.000683694	0.001513591	6.418502195	0.025652241	-1	1547	1332	1303	1924	1401	1297	1177	898	1243	1168
ENSMUSG00000016356	chr2	Col20a1	-0.8964181	0.000683802	0.001513591	2.794291523	0.072526921	-1	93	98	139	173	158	111	85	58	38	104
ENSMUSG00000015002	chr15	Efr3a	-0.5230749	0.000689073	0.001525016	5.271019887	0.026604051	-1	594	599	616	946	654	457	547	452	482	641
ENSMUSG00000038816	chr4	Ctnnal1	-0.6888048	0.000689239	0.001525143	3.309706266	0.041935166	-1	146	162	183	264	155	154	107	124	142	84
ENSMUSG00000008090	chr5	Fgfrl1	0.74336501	0.000690466	0.001527616	5.451313486	0.055274999	1	339	497	519	632	444	1434	595	759	612	1129
ENSMUSG00000002565	chr12	Scin	1.3233472	0.000690933	0.001528408	0.709723256	0.128538814	1	16	9	12	17	10	12	52	29	46	34
ENSMUSG00000025401	chr10	Myo1a	-1.5495846	0.000692489	0.001531607	0.519304157	0.181512457	-1	52	25	23	11	33	21	7	4	11	13
ENSMUSG00000020053	chr10	Igf1	0.6076645	0.000693862	0.0015344	5.995920199	0.03711229	1	652	784	737	854	715	1203	1222	1229	867	1774
ENSMUSG00000020900	chr11	Myh10	-0.6350448	0.000694982	0.001536634	4.533653443	0.038718086	-1	288	330	389	713	409	273	305	312	266	312
ENSMUSG00000030446	chr13	Zfp273	-1.2641455	0.000697013	0.001540881	0.443027584	0.10099953	-1	27	36	28	22	17	7	8	13	17	14
ENSMUSG00000097195	chr9	Snhg5	0.71916434	0.000697677	0.001542105	3.213115591	0.045656291	1	120	132	75	105	81	192	231	173	192	138
ENSMUSG00000070493	chr5	Chchd2	0.56322356	0.000700327	0.001547719	8.352131634	0.032698646	1	4521	3978	3736	4487	2940	7693	5766	5834	6953	5565
ENSMUSG00000023828	chr17	Slc22a3	-1.4604463	0.000700815	0.001548552	1.097385468	0.175808942	-1	21	44	33	86	43	23	14	15	3	34
ENSMUSG00000032624	chr17	Eml4	0.70503637	0.000706668	0.001561237	2.78919694	0.041866391	1	90	64	57	121	59	167	164	123	117	118
ENSMUSG00000031511	chr8	Arhgef7	-0.5615483	0.000708143	0.00156425	6.14962163	0.03182341	-1	1014	1024	1093	1907	1333	1047	1010	867	922	830
ENSMUSG00000019647	chr18	Sema6a	-0.6772032	0.000708732	0.001565304	3.817193122	0.042766971	-1	242	288	294	263	185	215	127	186	133	220
ENSMUSG00000031365	chrX	Zfp275	-0.5729002	0.000711856	0.001571954	3.931350663	0.02988632	-1	289	288	237	263	261	201	248	180	149	219
ENSMUSG00000034345	chr17	Gtf2h5	0.51020059	0.000712984	0.001574198	5.506547756	0.025658644	1	652	553	460	668	464	1034	921	793	864	743
ENSMUSG00000040651	chr14	Fam208a	-0.631352	0.000713797	0.001575513	3.1703644	0.034155672	-1	176	154	160	202	117	144	122	74	116	118
ENSMUSG00000095403	chr8	Gm21092	-0.739064	0.000713806	0.001575513	2.426227262	0.043910877	-1	106	110	89	100	83	86	72	45	66	55
ENSMUSG00000026926	chr2	Pmpca	-0.49389	0.00071807	0.001584674	7.583734828	0.025104429	-1	3412	3300	3093	4002	2916	2680	2612	2361	2700	2631
ENSMUSG00000026463	chr1	Atp2b4	-0.5361607	0.000719963	0.001588601	4.523840895	0.027102284	-1	403	347	350	516	410	342	324	322	209	332
ENSMUSG00000035597	chr12	Prpf39	-0.5688414	0.000720169	0.001588804	3.624514008	0.028210518	-1	208	212	165	259	243	163	166	127	175	173
ENSMUSG00000034648	chr6	Lrrn1	1.23107625	0.000721548	0.001591596	3.123555084	0.145829554	1	19	78	72	190	42	163	173	248	171	216
ENSMUSG00000038213	chr6	Tapbpl	0.69574506	0.000722	0.001592342	2.39016247	0.036244773	1	52	55	65	65	52	113	106	85	97	116
ENSMUSG00000019975	chr10	Ikbip	0.56491677	0.000723028	0.001594357	4.031351588	0.029085264	1	214	179	188	224	169	430	339	304	262	253
ENSMUSG00000031562	chr8	Dctd	0.99228458	0.000724452	0.001597247	1.056046742	0.065846873	1	26	12	15	24	20	48	48	37	48	30
ENSMUSG00000025085	chr19	Ablim1	-0.530781	0.000729258	0.001607589	5.248530962	0.027703199	-1	582	670	603	999	530	678	466	470	420	514
ENSMUSG00000038522	chr10	AI317395	-1.0335709	0.00073126	0.001611748	1.580106435	0.083568149	-1	34	57	74	80	44	21	41	27	37	27
ENSMUSG00000061518	chr1	Cox5b	0.54009016	0.000732242	0.001613656	8.573311541	0.030323925	1	4449	4491	4392	6228	3738	7798	6537	8109	6740	7515
ENSMUSG00000009076	chr11	Zmat5	0.53952182	0.000733981	0.001617235	4.061696174	0.026360882	1	217	215	175	226	172	387	292	260	361	306
ENSMUSG00000031962	chr8	Cdh15	0.82682745	0.000736814	0.001622965	4.98401413	0.068807489	1	363	243	241	498	371	505	681	1054	425	568
ENSMUSG00000037594	chr12	BC022687	1.39287996	0.000736698	0.001622965	0.134021778	0.116634202	1	11	2	6	15	6	30	29	26	13	16
ENSMUSG00000025465	chr7	Echs1	-0.5569756	0.000737111	0.001623364	6.843092011	0.031882172	-1	1733	2249	1902	2759	1605	2086	1336	1298	1498	1408
ENSMUSG00000027716	chr3	Trpc3	-0.7684942	0.000737754	0.001624524	2.175948805	0.045607715	-1	88	71	84	113	61	41	62	50	51	61
ENSMUSG00000020895	chr11	Tmem107	0.93546223	0.0007401	0.001629432	1.555922889	0.06693549	1	32	24	33	43	13	77	58	54	65	47
ENSMUSG00000024290	chr18	Rock1	-0.5478066	0.000740875	0.001630881	3.919579564	0.02700417	-1	244	249	229	378	242	187	247	150	202	212
ENSMUSG00000035069	chr4	Oma1	-0.4995584	0.000742785	0.001634829	4.687103226	0.023554532	-1	440	453	417	555	379	322	364	310	396	336
ENSMUSG00000027488	chr2	Snta1	0.55762983	0.000744997	0.001639439	7.369882468	0.032191273	1	1828	1739	1765	2830	1898	2916	2849	3276	2969	4002
ENSMUSG00000022594	chr15	Lynx1	-0.6836785	0.000745268	0.001639778	7.405141606	0.048379747	-1	2361	2931	3078	4887	2537	1499	1861	2427	2192	2505
ENSMUSG00000001380	chr18	Hars	0.48034549	0.000745463	0.001639947	5.412807326	0.022667073	1	545	463	481	662	499	820	920	707	809	783
ENSMUSG00000022451	chr15	Twf1	0.5898347	0.000747188	0.001643484	3.981271765	0.032231449	1	217	173	168	239	141	380	356	231	337	239
ENSMUSG00000041775	chr7	Mapk1ip1	-0.5699542	0.000750136	0.001649708	3.839312319	0.029398563	-1	247	307	208	298	206	219	179	160	149	232
ENSMUSG00000031548	chr8	Sfrp1	0.92618575	0.000750525	0.001650305	3.095783215	0.07942877	1	83	84	86	73	98	307	171	120	86	237
ENSMUSG00000003808	chr8	Farsa	0.54622326	0.000751738	0.001652712	4.982875677	0.029209086	1	434	309	318	499	361	898	628	508	511	539
ENSMUSG00000027599	chr3	Armc1	-0.5351251	0.000753099	0.001655444	4.666467761	0.027439982	-1	421	422	461	565	366	285	392	273	368	364
ENSMUSG00000074813	chr2	Gm14005	0.90525391	0.000756831	0.001663387	1.167037394	0.050029808	1	23	17	24	25	20	57	47	43	41	37
ENSMUSG00000021792	chr14	Fam213a	-0.6616025	0.000759958	0.001669995	3.763996369	0.040566072	-1	229	297	213	301	193	122	158	155	210	200
ENSMUSG00000008892	chr8	Vdac3	-0.5361323	0.000760525	0.001670978	8.219029776	0.030014864	-1	5228	5411	4458	6507	4746	3478	4354	3371	4219	4385
ENSMUSG00000021319	chr13	Sfrp4	1.08727364	0.000761011	0.001671784	3.522801049	0.115105467	1	60	150	91	86	141	288	165	394	122	283
ENSMUSG00000015095	chr2	Fbxw5	-0.5403699	0.000761401	0.001672378	6.028329291	0.029699589	-1	1224	1055	1044	1329	1095	713	872	766	889	1082

ENSMUSG00000025876	chr13	Unc5a	1.21728363	0.000761612	0.001672579	2.97100355	0.141626679	1	56	71	60	78	78	35	215	182	189	244
ENSMUSG00000056493	chr5	Foxk1	-0.5956015	0.000769597	0.00168985	4.512664157	0.034441163	-1	357	398	352	538	401	309	266	299	195	413
ENSMUSG00000086968	chr3	4933431E20Rik	-0.8529715	0.000772155	0.0016952	1.952840469	0.057416041	-1	81	74	54	79	72	29	48	38	41	62
ENSMUSG00000029993	chr6	Nfu1	0.47727565	0.000773004	0.00169653	5.318741793	0.022386277	1	544	479	470	569	415	775	773	747	736	740
ENSMUSG00000038398	chr8	Upf3a	0.55539509	0.000772904	0.00169653	3.647185147	0.027111543	1	139	142	118	183	166	308	233	228	221	218
ENSMUSG00000000126	chr11	Wnt9a	-0.5763759	0.000773386	0.001696836	4.062607863	0.030977261	-1	278	248	308	428	234	251	195	236	164	243
ENSMUSG00000026856	chr2	Dolpp1	0.6110374	0.000773267	0.001696836	3.210795501	0.031774634	1	99	105	86	136	113	239	191	152	174	149
ENSMUSG00000031864	chr8	Ints10	-0.5393125	0.000773729	0.001697321	3.843676207	0.025915795	-1	241	245	208	351	224	168	211	168	206	192
ENSMUSG00000014769	chr17	Psmb1	0.55155156	0.000777901	0.001706206	7.052150892	0.03159966	1	1887	1626	1478	1772	1245	3248	2410	2186	2827	2231
ENSMUSG00000028149	chr3	Rap1gds1	-0.4937058	0.000778323	0.001706865	6.24575407	0.024905691	-1	1222	1148	1213	1777	1281	1178	1011	835	1010	1126
ENSMUSG00000004661	chr9	Arid3b	-0.8846494	0.000778589	0.001707178	1.728561337	0.061827116	-1	66	58	64	46	70	39	31	29	39	46
ENSMUSG00000025337	chr5	Sbds	0.47950504	0.000779255	0.001708372	4.624627706	0.021641696	1	290	314	266	406	261	585	471	428	428	430
ENSMUSG00000045624	chr2	Esf1	-0.57568	0.000779974	0.001709679	3.975405312	0.030710994	-1	293	268	287	332	214	178	256	162	227	199
ENSMUSG00000024664	chr19	Fads3	0.80979612	0.000780102	0.001709693	3.495253361	0.062298694	1	117	149	109	128	97	278	255	324	134	162
ENSMUSG00000058729	chr1	Lin9	-0.8023157	0.000783028	0.001715835	2.234044666	0.052568822	-1	67	99	87	108	74	47	75	39	48	65
ENSMUSG00000049321	chr11	Zfp2	-0.7726495	0.000783904	0.001717486	1.929421777	0.044771526	-1	65	82	60	89	53	49	52	35	47	40
ENSMUSG00000028788	chr4	Ptp4a2	-0.6358133	0.000784405	0.001718315	9.569822972	0.042532053	-1	15042	12425	12245	16712	12637	6790	10209	7784	11304	12253
ENSMUSG00000009731	chrX	Kcnd1	1.18175413	0.000790348	0.001731061	0.556774134	0.086181282	1	11	11	12	12	14	53	29	27	17	27
ENSMUSG00000050621	chr9	Rps27rt	0.71209354	0.000791077	0.001732388	3.64061394	0.047527343	1	146	140	138	144	124	424	231	176	256	180
ENSMUSG00000098986	chr19	Gm28006	0.97286484	0.000791281	0.001732562	3.898168559	0.093740359	1	200	180	130	117	107	137	297	264	422	459
ENSMUSG00000031826	chr8	Usp10	-0.542197	0.000792895	0.001735823	5.045256745	0.029131516	-1	570	441	473	732	695	447	506	363	452	421
ENSMUSG00000023075	chr4	Akirin1	-0.5494578	0.000793814	0.001737564	5.065265031	0.030035625	-1	628	527	596	616	566	413	547	307	494	454
ENSMUSG00000061079	chr7	Zfp143	-0.5823262	0.000794241	0.001738226	3.126858151	0.028114731	-1	159	142	126	202	146	122	125	82	114	123
ENSMUSG00000006005	chr1	Tpr	-0.5116231	0.000794634	0.001738813	6.432169693	0.026986818	-1	1388	1296	1352	2065	1503	1172	1258	939	1203	1241
ENSMUSG00000048826	chr17	Dact2	-1.318379	0.00079644	0.001742494	0.379500332	0.11396236	-1	13	22	30	26	34	9	10	17	6	13
ENSMUSG00000021711	chr13	Trappc13	-0.5474961	0.000797183	0.001743845	4.696058925	0.029171357	-1	489	447	429	549	374	273	397	275	391	370
ENSMUSG00000074417	chr7	Gm14548	1.7289853	0.00079744	0.001744134	0.206737241	0.210539825	1	5	5	12	6	6	39	39	5	34	12
ENSMUSG00000091957	chr18	Rps2-ps10	0.75253637	0.000799172	0.00174765	2.198996313	0.043983475	1	48	40	49	60	50	80	87	104	80	103
ENSMUSG00000020739	chr11	Nup85	0.51436406	0.000805372	0.001760932	4.69674634	0.02557724	1	317	301	267	429	282	602	564	410	516	394
ENSMUSG00000026923	chr2	Notch1	-0.6278587	0.000805618	0.001761194	4.480111705	0.038783681	-1	276	344	369	587	447	371	293	306	210	249
ENSMUSG00000021265	chr12	Slc25a29	-0.696418	0.000807067	0.001764087	3.256816171	0.044105769	-1	152	160	204	206	146	151	74	122	101	142
ENSMUSG00000028467	chr4	Gba2	-0.5747328	0.000807633	0.001765048	3.422356399	0.028849187	-1	179	203	181	238	148	176	157	105	136	126
ENSMUSG00000074247	chr8	Dda1	0.45010425	0.00081359	0.001777789	5.036615707	0.019517339	1	417	400	356	465	415	688	601	561	591	645
ENSMUSG00000018648	chr11	Dusp14	0.73689594	0.000821922	0.001795433	3.262211551	0.050837304	1	129	98	100	146	62	155	166	236	164	236
ENSMUSG00000100594	chr1	2810414N06Rik	1.22918845	0.000821919	0.001795433	0.559944653	0.099618206	1	11	17	14	11	6	18	36	27	40	31
ENSMUSG00000043964	chr7	Orai3	0.57222334	0.00082206	0.001795455	4.03305183	0.030664291	1	180	185	174	242	193	474	305	290	245	286
ENSMUSG00000033256	chr2	Shf	0.89735071	0.000823109	0.001797464	1.722385392	0.062093521	1	37	38	25	45	21	94	48	67	51	78
ENSMUSG00000022574	chr15	Naprt	0.70712675	0.000823855	0.001798813	2.829634822	0.043271818	1	63	72	73	107	81	184	122	134	159	107
ENSMUSG00000030610	chr7	Det1	-0.5622172	0.00082402	0.001798892	3.552522446	0.027942361	-1	189	162	214	253	213	163	167	130	164	142
ENSMUSG00000039084	chr11	Chad	1.27690349	0.000824931	0.001800599	4.39514611	0.165210505	1	281	131	128	294	102	1235	520	225	331	195
ENSMUSG00000033862	chr8	Cdk10	0.64874968	0.000829177	0.001809585	3.434543325	0.038288696	1	140	88	126	141	123	302	213	189	206	160
ENSMUSG00000035351	chr10	Nup37	0.78833812	0.000829587	0.001810051	2.237962391	0.051235431	1	47	41	52	66	45	97	119	92	101	63
ENSMUSG00000092417	chr17	Gpank1	0.58063815	0.00082965	0.001810051	3.22834025	0.028725127	1	109	128	89	135	92	207	183	185	159	170
ENSMUSG00000063388	chr18	BC023105	-1.5528053	0.000829913	0.001810342	5.04129897	0.242593716	-1	1476	888	599	257	350	83	229	133	435	471
ENSMUSG00000033377	chr3	Palmd	-0.5773862	0.000833854	0.001818087	4.698599726	0.032908379	-1	406	448	427	680	374	289	297	382	292	424
ENSMUSG00000064254	chr7	Ethe1	0.50213101	0.000833668	0.001818087	4.431300059	0.023939412	1	225	259	242	373	234	448	376	417	427	378
ENSMUSG00000089782	chr1	Gm3531	0.72223242	0.000833745	0.001818087	2.909607459	0.045749492	1	85	74	85	96	74	247	131	136	119	125
ENSMUSG00000083836	chr4	Ldha-ps2	-0.9948275	0.000836376	0.001823302	2.560812467	0.091607606	-1	98	108	89	140	139	36	54	52	49	125
ENSMUSG00000020334	chr11	Slc22a4	0.86206459	0.000836558	0.001823415	2.165816753	0.063858179	1	42	47	37	85	25	97	97	61	90	116
ENSMUSG00000085666	chr10	Gm9855	-2.8029384	0.00083697	0.001824028	1.624488265	0.688948823	-1	62	65	86	99	77	60	1	1	0	4
ENSMUSG00000002014	chrX	Ssr4	0.56989069	0.000837797	0.001825546	5.634602427	0.033297584	1	679	635	486	617	542	1165	1071	698	1106	814
ENSMUSG00000032816	chr9	Igdcc4	-0.5205486	0.000841018	0.001832278	5.866607823	0.027845795	-1	893	930	974	1374	968	794	640	776	747	942
ENSMUSG00000025858	chr5	Get4	0.4611418	0.00084284	0.001835962	5.310317628	0.021111441	1	520	475	469	596	423	793	748	660	769	771
ENSMUSG00000021432	chr13	Slc35b3	0.95806703	0.000844137	0.001838501	1.949045956	0.077023454	1	45	35	42	28	35	125	96	43	65	79
ENSMUSG00000075307	chr2	Klhl41	-0.5245684	0.00084439	0.001838765	9.253969078	0.029351995	-1	11154	10232	9407	14396	8942	9558	7415	8500	6927	8508
ENSMUSG00000035642	chr7	Aamdc	0.6338395	0.000846386	0.001842825	6.785896048	0.042278623	1	1610	1263	1109	1247	1164	1595	2016	2392	2375	2440
ENSMUSG00000042684	chr1	Npl	1.35900684	0.000851841	0.001854412	2.341602557	0.175015035	1	39	40	32	47	46	321	94	41	84	61
ENSMUSG00000056870	chr1	Gulp1	-0.8423981	0.00085218	0.001854862	1.730007307	0.053225588	-1	69	56	46	87	52	34	45	40	24	44
ENSMUSG00000042249	chr5	Adrbk2	-0.7348294	0.000852811	0.001855945	2.929255344	0.04883434	-1	122	136	134	152	150	137	89	49	85	107
ENSMUSG00000050144	chr3	Slc25a44	-0.4728947	0.00085921	0.001869582	4.807714992	0.021734944	-1	459	460	430	550	508	402	430	328	335	418
ENSMUSG00000048174	chr1	Tmem81	0.88374255	0.000859939	0.001870876	1.196529392	0.050572198	1	24	23	19	28	19	67	43	37	41	42
ENSMUSG00000031523	chr8	Dlc1	-0.5778509	0.000860382	0.001871549	4.753718427	0.033366764	-1	314	425	499	734	450	431	355	314	301	368
ENSMUSG00000081895	chr7	Rpl17-ps10	0.76368072	0.000863702	0.001878478	2.549594744	0.050638884	1	90	58	41	86	45	143	142	93	108	105
ENSMUSG00000093273	chr11	Mir3064	-0.5214669	0.000864142	0.001879143	4.192914476	0.025633513	-1	358	310	297	356	273	241	281	181	269	248
ENSMUSG00000050471	chr9	Fam118b	-0.5202889	0.000867798	0.001886799	4.487184605	0.026204649	-1	386	389	360	454	367	280	304	218	316	382

ENSMUSG00000057286	chr11	St6galnac2	-0.7779826	0.000868428	0.001887876	2.011114708	0.047375536	-1	84	68	73	85	59	71	45	43	40	38
ENSMUSG00000071054	chr17	Safb	0.5709696	0.000869132	0.001889113	5.506589383	0.033561311	1	494	465	429	755	595	1287	883	812	722	757
ENSMUSG00000060397	chr7	Zfp128	-0.8923322	0.000871092	0.001893078	1.152557719	0.052801236	-1	37	40	43	43	40	20	26	20	29	25
ENSMUSG00000038524	chr18	Fchsd1	0.99511186	0.000873967	0.00189903	1.276854131	0.073211093	1	32	19	20	21	21	63	33	48	63	41
ENSMUSG00000026478	chr1	Lamc1	-0.5915682	0.000882651	0.001917602	7.727559052	0.037364728	-1	3267	3418	3488	4805	4009	2897	2815	2994	1803	3308
ENSMUSG00000045316	chr17	Fahd1	-0.502502	0.000882991	0.001918042	5.424589474	0.025722472	-1	763	795	747	896	547	685	561	567	485	604
ENSMUSG00000030177	chr6	Ccdc77	-0.864433	0.000884203	0.001920377	2.225363869	0.064226299	-1	75	101	72	128	68	35	67	42	70	48
ENSMUSG00000025813	chr7	Homer2	-0.950738	0.000885728	0.00192339	4.533668738	0.093032763	-1	194	385	446	1067	282	255	264	282	257	216
ENSMUSG00000039157	chr2	Fam102a	0.62309982	0.000888122	0.001928289	2.857566073	0.032083014	1	80	86	80	108	65	168	167	119	119	135
ENSMUSG00000021678	chr13	F2rl1	1.56575519	0.000888699	0.001929243	0.279094606	0.1853197	1	7	10	4	16	4	55	29	27	9	13
ENSMUSG00000033389	chr11	Arhgap44	-0.707335	0.000906135	0.001966788	2.775058192	0.04391436	-1	102	94	108	202	126	114	74	72	75	85
ENSMUSG00000030942	chr7	Thumpd1	0.4986217	0.000907067	0.0019682	4.749825887	0.024441161	1	388	312	291	357	301	520	580	487	522	444
ENSMUSG00000047003	chr15	Zfp41	-0.7302013	0.000907021	0.0019682	2.370544672	0.044002822	-1	114	103	63	101	89	63	66	56	53	73
ENSMUSG00000033610	chr19	Pank1	-0.7446111	0.000907989	0.001969894	3.503118363	0.053396681	-1	123	192	201	393	166	136	147	135	145	119
ENSMUSG00000006638	chr5	Abhd1	1.41297068	0.000914372	0.001983434	0.301469968	0.145608675	1	9	6	7	14	9	16	22	51	14	25
ENSMUSG00000003352	chr15	Cacnb3	0.70468406	0.000915167	0.00198485	2.705915422	0.042792426	1	97	61	59	75	69	133	132	112	103	169
ENSMUSG00000018411	chr11	Mapt	-0.5636451	0.000917831	0.001990319	5.827865823	0.033250251	-1	974	732	762	1564	1088	781	679	731	778	756
ENSMUSG00000008140	chr7	Emc10	0.48993307	0.000918534	0.001991535	6.139017906	0.025142157	1	847	772	811	1108	834	1580	1304	1384	1209	1231
ENSMUSG00000044646	chr18	Zbtb7c	1.04597803	0.00091986	0.001994099	1.685725753	0.093779803	1	25	33	28	39	25	87	53	106	35	56
ENSMUSG00000031355	chrX	Arhgap6	-0.8232477	0.000924578	0.002004018	2.2387467	0.057980844	-1	75	78	85	120	83	38	57	36	66	74
ENSMUSG00000053716	chr9	Dusp7	-0.7283402	0.000926277	0.002007389	4.192197454	0.053808993	-1	191	389	397	318	361	247	261	152	245	217
ENSMUSG00000034771	chr10	Tle2	-0.745194	0.000927034	0.002008716	2.331333515	0.046485758	-1	103	89	87	90	87	83	50	46	48	76
ENSMUSG00000028990	chr4	Lzic	0.52586639	0.000927312	0.002009009	3.717247759	0.025033557	1	152	166	137	203	140	258	254	268	247	222
ENSMUSG00000039774	chr4	Galnt12	1.25861524	0.000930325	0.002015224	0.103361289	0.087963929	1	3	12	7	11	8	19	30	21	20	18
ENSMUSG00000015776	chr2	Med22	0.47462438	0.000930886	0.002015814	4.67513025	0.021834994	1	294	312	309	353	309	577	483	417	490	452
ENSMUSG00000068523	chr3	Gng5	-0.4765599	0.000930856	0.002015814	6.658018318	0.024095101	-1	1823	1715	1600	2111	1513	1448	1524	1263	1203	1462
ENSMUSG00000063060	chr14	Sox7	-0.758861	0.000931467	0.002016759	3.121804965	0.054315458	-1	151	184	153	207	114	88	91	109	69	164
ENSMUSG00000038172	chr4	Ttc39b	0.74998405	0.000934799	0.00202366	2.581992765	0.049739321	1	59	69	60	106	37	109	140	120	104	125
ENSMUSG00000019124	chr6	Scrn1	0.79975004	0.000936335	0.002026672	2.569671815	0.05683866	1	43	64	62	81	65	93	148	140	87	130
ENSMUSG00000055681	chr8	Cope	0.48308266	0.000936728	0.002027208	6.294197167	0.024589695	1	1068	888	840	1115	953	1560	1608	1294	1500	1500
ENSMUSG00000070423	chr7	Olfr558	-0.8549623	0.000938721	0.002031207	2.09843963	0.06247376	-1	70	51	73	138	76	40	52	45	39	66
ENSMUSG00000024293	chr18	Esco1	-0.5141849	0.000940502	0.002034746	3.876061713	0.024285679	-1	265	230	240	332	217	208	182	153	220	218
ENSMUSG00000059119	chr7	Nap1l4	-0.4804964	0.000942983	0.002039798	7.650250977	0.024877646	-1	3486	3278	3035	4448	3256	2786	2804	2574	2578	2939
ENSMUSG00000029621	chr5	Arpc1a	0.46209605	0.000943583	0.002040779	5.154632906	0.021489891	1	460	401	372	599	410	824	640	596	665	643
ENSMUSG00000007682	chr12	Dio2	0.92962828	0.000943812	0.002040958	2.290213989	0.078601875	1	49	52	54	68	23	139	104	127	69	70
ENSMUSG00000097287	chr5	D130017N08Rik	-0.8153351	0.000946187	0.002045778	2.301601074	0.0579005	-1	111	95	82	88	79	54	50	63	36	82
ENSMUSG00000021668	chr13	Polk	-0.7491579	0.000951699	0.002057377	2.49300973	0.047928795	-1	117	82	91	123	103	51	59	59	81	84
ENSMUSG00000082127	chr2	Gm13577	1.03144089	0.000957668	0.002069961	1.345751799	0.083553714	1	24	39	15	23	16	57	59	35	66	47
ENSMUSG00000022390	chr15	Zc3h7b	-0.4962817	0.000959498	0.002073597	5.545452728	0.025537768	-1	740	683	782	1060	810	641	619	634	530	731
ENSMUSG00000047547	chr13	Cltb	0.51263971	0.000960216	0.002074826	6.362221287	0.027960877	1	1052	882	915	1325	902	1787	1632	1362	1778	1323
ENSMUSG00000015305	chr10	Sash1	-0.5151915	0.000960693	0.002075537	4.731726037	0.026609988	-1	481	443	419	513	455	362	332	310	293	488
ENSMUSG00000074793	chr2	Hspa12b	-0.6448507	0.00096643	0.002087609	3.897735371	0.040822445	-1	226	236	234	385	275	282	119	162	179	208
ENSMUSG00000024952	chr19	Rps6ka4	0.5788102	0.000968372	0.002091157	4.092634347	0.032663289	1	177	199	177	264	198	472	337	241	355	264
ENSMUSG00000070570	chr7	Slc17a7	-0.9248366	0.000968294	0.002091157	2.306501401	0.077797372	-1	108	83	55	108	118	36	43	63	49	79
ENSMUSG00000030495	chr7	Slc7a10	1.85150934	0.000978739	0.002113218	0.577179217	0.286731037	1	6	15	5	3	13	8	28	40	20	76
ENSMUSG00000034463	chr14	Scara3	0.58257649	0.000980929	0.002117619	4.130649524	0.033267578	1	204	212	190	246	185	401	292	266	262	497
ENSMUSG00000010608	chr12	Rbm25	-0.4905688	0.000985882	0.002127983	5.59144325	0.025067693	-1	840	806	718	1091	757	594	640	569	728	725
ENSMUSG00000036966	chr15	Spryd3	0.49390133	0.000992705	0.002142379	4.008086651	0.022595949	1	207	190	184	222	182	330	338	251	313	294
ENSMUSG00000034161	chr15	Scx	1.14272034	0.000994225	0.002145328	3.645534525	0.134795143	1	106	89	70	212	114	672	240	230	172	113
ENSMUSG00000001150	chr10	Mcm3ap	-0.4962534	0.001001106	0.002159843	4.382783335	0.023894295	-1	356	347	285	489	346	270	260	255	304	313
ENSMUSG00000020224	chr10	Llph	0.65981631	0.001006887	0.002171979	3.287399209	0.040730264	1	125	101	107	133	91	207	253	132	224	149
ENSMUSG00000053334	chr5	Ficd	-0.598933	0.001007746	0.002173496	3.145134238	0.032067246	-1	157	142	111	209	170	129	120	86	107	128
ENSMUSG00000033752	chr3	Mnd1	1.49396078	0.001007905	0.002173503	1.129018411	0.193529249	1	13	20	29	8	7	102	40	52	30	26
ENSMUSG00000064358	chrMT	mt-Co3	-0.834376	0.001008234	0.002173878	3.782412408	0.070751968	-1	192	260	262	404	203	85	116	160	212	216
ENSMUSG00000035575	chr11	Utp6	-0.5138962	0.00101108	0.002179678	5.473528804	0.027651913	-1	870	749	652	864	742	514	646	514	649	648
ENSMUSG00000024953	chr19	Prdx5	0.50737695	0.001014247	0.002186168	7.425075006	0.028058079	1	1915	2021	2038	2870	1797	3956	2920	3255	3247	3083
ENSMUSG00000029408	chr5	Abcb9	-0.6145682	0.001015353	0.002188099	3.260259752	0.034496269	-1	147	172	137	238	166	129	136	142	94	108
ENSMUSG00000029821	chr6	Dfna5	1.38495501	0.001015505	0.002188099	0.174955622	0.125713547	1	4	3	5	14	15	18	20	20	26	33
ENSMUSG00000088609	chr13	Gm24187	0.99326182	0.001015612	0.002188099	3.592330825	0.100958535	1	124	54	61	144	209	327	367	204	192	218
ENSMUSG00000039410	chr4	Prdm16	-0.8248774	0.001018492	0.002193964	1.746270083	0.053872317	-1	52	67	61	86	45	36	35	27	43	50
ENSMUSG00000086219	chr5	Srrm4os	1.35985588	0.001020338	0.002197602	2.145751853	0.179645569	1	65	61	19	15	16	82	98	116	135	65
ENSMUSG00000087260	chr3	Lamtor5	0.48865916	0.001021057	0.002198813	5.1548223	0.024566398	1	475	436	412	565	327	803	749	532	692	623
ENSMUSG00000020458	chr11	Rtn4	-0.680321	0.001022226	0.00220099	9.693553521	0.050856556	-1	17885	15743	13655	16034	12419	6552	11516	8490	11152	13987
ENSMUSG00000026356	chr1	Dars	-0.5450293	0.001025899	0.002208559	5.835284763	0.031671295	-1	1025	900	856	1331	959	615	930	579	849	803
ENSMUSG00000021759	chr13	Ppap2a	0.5275514	0.001029243	0.002215417	5.682191407	0.029570244	1	722	532	528	869	513	861	970	1039	985	1050

ENSMUSG00000076281	chr9	Gm24270	1.07000943	0.001029412	0.002215438	4.023231578	0.119433229	1	184	74	71	205	245	458	580	319	191	253
ENSMUSG00000020372	chr11	Gnb2l1	0.50651247	0.001031692	0.002220004	8.600612512	0.028252406	1	4877	4756	4297	5616	4340	9351	7682	6424	7397	6481
ENSMUSG00000025701	chr6	Alox5	1.0962557	0.001036083	0.002229111	1.237742167	0.096995335	1	25	21	17	18	23	80	55	35	55	24
ENSMUSG00000039901	chr19	9130011E15Rik	-0.5571999	0.001036439	0.002229532	3.819781839	0.029503059	-1	246	240	189	351	230	148	211	166	192	205
ENSMUSG00000032086	chr9	Bace1	-0.5247046	0.001037901	0.002231991	5.724228601	0.029265769	-1	1065	712	796	1084	980	645	758	607	722	796
ENSMUSG00000078851	chr11	Hist3h2a	0.58984522	0.001037834	0.002231991	3.734169376	0.033471212	1	179	154	139	193	122	208	292	270	204	314
ENSMUSG00000042428	chr15	Mgat3	-0.9492399	0.001039796	0.002235722	1.542510342	0.073049072	-1	40	52	47	90	50	42	31	39	16	28
ENSMUSG00000100455	chr1	Gm29170	-0.7843732	0.001041191	0.002238376	1.98245346	0.050042026	-1	90	68	64	71	67	38	54	42	38	58
ENSMUSG00000061787	chr7	Rps17	0.54253694	0.001045268	0.002246796	7.701021624	0.032333694	1	2668	2548	2317	3053	2061	5231	4075	3198	4457	3261
ENSMUSG00000027452	chr2	Acss1	-0.7188015	0.001045707	0.002247393	4.707827889	0.054455718	-1	287	491	382	888	428	476	290	259	335	258
ENSMUSG00000018381	chr11	Abi3	0.99438069	0.001046378	0.002248491	2.380703001	0.094229839	1	43	34	25	91	65	144	99	137	61	111
ENSMUSG00000029676	chr6	Pot1a	-0.5623209	0.001048566	0.002252846	3.451209365	0.028883049	-1	182	218	164	225	172	130	160	128	157	136
ENSMUSG00000021392	chr13	Nol8	-0.5895189	0.001049788	0.002255124	2.978816316	0.030351279	-1	151	126	119	168	133	112	118	71	100	108
ENSMUSG00000021794	chr14	Glud1	-0.5185232	0.001050561	0.002256438	7.142618488	0.029414607	-1	2328	2518	2291	3202	2109	2351	1928	1365	2083	1807
ENSMUSG00000002602	chr7	Axl	0.50126451	0.001051723	0.002258546	6.113069206	0.026952113	1	756	811	782	1019	885	1381	1507	1312	1064	1351
ENSMUSG00000051502	chr5	Ufsp1	0.64666614	0.001051866	0.002258546	4.703889571	0.04359994	1	338	283	310	277	280	343	670	450	469	643
ENSMUSG00000029020	chr4	Mfn2	-0.5325987	0.001054345	0.002263522	9.013004367	0.03139591	-1	8048	8031	8070	13214	8642	6612	6678	6711	6182	8250
ENSMUSG00000028517	chr4	Ppap2b	-0.6238303	0.001057284	0.002269371	6.118901254	0.042189784	-1	979	1159	1072	1954	1199	740	857	647	1000	1215
ENSMUSG00000097350	chr17	4732491K20Rik	1.05040738	0.001057395	0.002269371	1.051873793	0.084507172	1	16	13	23	25	17	24	48	43	54	42
ENSMUSG00000071723	chrX	Gspt2	1.32460638	0.001059063	0.002272602	-0.003207906	0.099319166	1	5	6	13	6	6	14	23	24	21	18
ENSMUSG00000038446	chr10	Cdc40	-0.553992	0.001059401	0.002272979	3.411805738	0.027618455	-1	182	190	165	254	150	135	150	107	141	165
ENSMUSG00000041881	chr17	Ndufa7	0.48596908	0.001060562	0.002275122	6.937286931	0.025763451	1	1638	1479	1315	1883	1316	2971	2111	2167	2223	2230
ENSMUSG00000026664	chr2	Phyh	-0.6109904	0.001060952	0.002275608	7.49328244	0.041063638	-1	2390	3497	3460	4878	2194	2640	2149	2397	2347	2070
ENSMUSG00000020175	chr10	Rab36	1.29377453	0.00106309	0.002279845	0.016406939	0.095178378	1	8	7	12	4	6	18	20	26	21	16
ENSMUSG00000038456	chr6	Dennd2a	0.54395125	0.001063285	0.002279914	3.571224621	0.026991898	1	143	130	136	169	134	237	272	226	168	237
ENSMUSG00000094989	chr13	Rpl9-ps4	1.25147448	0.001063596	0.002280229	0.267496537	0.103441676	1	8	12	7	12	8	24	16	21	42	19
ENSMUSG00000037375	chr1	Hhat	1.18326648	0.001069093	0.002291664	0.877406599	0.106318952	1	18	19	15	17	8	59	35	36	15	50
ENSMUSG00000039661	chr8	Dusp26	0.68365532	0.001071556	0.00229659	4.560590189	0.049092868	1	211	236	280	430	206	562	642	377	496	291
ENSMUSG00000031434	chrX	Morc4	0.5413343	0.001075748	0.002305221	3.584622189	0.026919465	1	142	153	128	158	136	209	231	249	222	230
ENSMUSG00000020982	chr12	Nemf	-0.6478474	0.001080683	0.002315441	4.274848112	0.043191314	-1	353	331	320	399	343	180	244	168	350	275
ENSMUSG00000071533	chr16	Pcnp	-0.5066576	0.001082889	0.002319812	4.808147008	0.026310894	-1	565	446	462	591	385	350	485	313	350	386
ENSMUSG00000003644	chr4	Rps6ka1	0.6625481	0.001083623	0.002321029	3.899374942	0.043754461	1	137	184	183	168	170	439	283	184	241	357
ENSMUSG00000086845	chr4	Gm13010	-2.0637186	0.001087285	0.002328517	3.221622979	0.426634239	-1	208	230	161	247	259	250	14	18	20	10
ENSMUSG00000071076	chr8	Jund	0.76884465	0.001088735	0.002331263	6.197421956	0.064647428	1	639	651	801	1280	727	2970	1171	1140	1043	1388
ENSMUSG00000034006	chr18	Pqlc1	0.56429906	0.001090268	0.002334189	4.827718819	0.033261026	1	358	319	259	501	288	859	512	420	438	565
ENSMUSG00000028636	chr4	Ppcs	0.65940841	0.00109152	0.002336511	2.716339909	0.037320546	1	73	86	66	88	59	161	123	107	143	111
ENSMUSG00000026014	chr1	Raph1	-0.5143294	0.00109213	0.002337459	4.701616214	0.027021839	-1	424	343	462	655	409	369	312	317	321	426
ENSMUSG00000093071	chr4	Gm25951	0.99685149	0.001093417	0.002339856	0.982295428	0.072396833	1	19	12	21	27	13	50	42	24	50	35
ENSMUSG00000020303	chr11	Stc2	-0.7649799	0.001094357	0.002341509	3.133183753	0.057225563	-1	154	172	121	129	221	129	109	104	69	116
ENSMUSG00000036822	chr4	Topors	-0.5720667	0.001095061	0.002342656	3.415162019	0.030379781	-1	185	176	149	270	171	129	165	114	117	170
ENSMUSG00000040599	chr11	Mis12	0.5986064	0.001097862	0.002348289	3.253641017	0.032412049	1	120	112	94	115	113	201	213	148	207	156
ENSMUSG00000020610	chr11	Amz2	-0.4680107	0.00109991	0.002352234	6.26941144	0.02370516	-1	1345	1305	1178	1651	1202	1181	985	917	1111	1089
ENSMUSG00000031256	chrX	Cstf2	-0.5191772	0.001100043	0.002352234	3.519856944	0.024406181	-1	194	181	201	259	166	152	174	134	150	152
ENSMUSG00000083773	chr2	Gm13394	-4.0027486	0.001100416	0.002352672	9.154834838	1.337084517	-1	15682	13454	13038	21198	17026	5986	29	16	8	19
ENSMUSG00000041308	chr8	Sntb2	-0.7122279	0.001101169	0.002353922	2.64057672	0.04504074	-1	119	107	101	148	95	61	85	57	101	73
ENSMUSG00000045094	chr18	Arhgef37	-1.395798	0.001102911	0.002357285	1.669029538	0.183957809	-1	79	57	65	61	67	6	20	13	45	53
ENSMUSG00000042772	chr1	Smg7	-0.4704706	0.001104191	0.002359659	5.640497532	0.023511748	-1	827	770	769	1074	874	679	737	617	631	744
ENSMUSG00000030337	chr6	Vamp1	-0.6629989	0.001104631	0.002360238	4.838738805	0.046663546	-1	557	527	446	574	492	209	358	303	454	461
ENSMUSG00000091228	chr11	Gm20390	0.53281473	0.001105235	0.002361169	8.483041499	0.031624679	1	4468	4539	4133	5397	3329	8022	7172	6608	7165	5533
ENSMUSG00000096929	chr1	A330023F24Rik	-1.0689517	0.001108392	0.002367551	1.684290489	0.10473427	-1	67	90	71	39	40	53	35	19	31	28
ENSMUSG00000047030	chr2	Spata2	-0.5117576	0.001116361	0.002384208	4.46153434	0.026382518	-1	361	352	375	439	385	240	330	279	280	341
ENSMUSG00000074358	chr7	Ccdc61	0.66485551	0.001117233	0.002385706	2.481464779	0.036220434	1	64	61	59	65	63	134	100	112	96	104
ENSMUSG00000036644	chr11	Tbc1d9b	-0.4688973	0.001121544	0.002394545	5.286366842	0.023064982	-1	660	667	620	779	634	648	451	489	527	556
ENSMUSG00000015961	chr1	Adss	0.62899299	0.001122005	0.002395163	3.804464865	0.039336431	1	190	129	139	185	166	307	349	197	320	202
ENSMUSG00000038534	chr11	Osbpl7	0.72625745	0.001122793	0.002396482	2.549988268	0.046473352	1	77	76	50	56	59	148	107	118	91	120
ENSMUSG00000029624	chr5	Ptcd1	-0.5267104	0.001124244	0.002399211	3.821237969	0.026435642	-1	235	254	231	318	201	209	154	179	163	235
ENSMUSG00000020745	chr11	Pafah1b1	-0.4789891	0.001134809	0.002421388	7.082730658	0.025372658	-1	2369	2089	2102	3017	2226	1891	2057	1542	1905	1851
ENSMUSG00000027981	chr3	Rnpc3	-0.712678	0.001135985	0.002423528	2.433858493	0.044382267	-1	102	107	95	105	79	76	84	41	58	71
ENSMUSG00000043065	chr16	Spice1	-0.885516	0.001137457	0.002426296	1.819247661	0.067584088	-1	56	70	71	65	65	51	39	17	44	47
ENSMUSG00000005803	chr2	Sqrdl	-0.4808088	0.001138763	0.002428713	4.924750657	0.023904567	-1	490	520	445	714	478	497	449	311	443	372
ENSMUSG00000068747	chr3	Sort1	-0.6681278	0.001139998	0.002430975	6.890933293	0.049522838	-1	2398	2070	1666	2080	2518	1017	1562	1354	1383	2135
ENSMUSG00000039367	chr14	Sec24c	-0.4653007	0.001140493	0.00243166	6.393614613	0.023656925	-1	1398	1401	1266	1789	1413	1314	1176	972	1135	1180
ENSMUSG00000074577	chr2	Fam65c	1.15956969	0.00114447	0.002439768	0.58366795	0.095203893	1	23	6	8	16	10	46	27	26	22	34
ENSMUSG00000017288	chr11	Vps53	0.47033447	0.001147855	0.002446609	4.564625943	0.022217325	1	281	253	243	405	299	469	445	382	456	482
ENSMUSG00000001313	chr11	Rnd2	0.84415831	0.001151254	0.002453481	1.842606203	0.059438277	1	25	34	48	45	31	105	69	62	55	74

ENSMUSG00000032492	chr9	Pth1r	1.05305481	0.001155403	0.002461947	2.061493407	0.102860681	1	35	56	31	27	42	164	78	81	47	82
ENSMUSG00000037239	chr7	Spred3	0.96745757	0.001162221	0.002475742	0.752359061	0.05759667	1	20	13	16	18	11	36	34	37	31	29
ENSMUSG00000049299	chr11	Trappc1	0.5451803	0.001162231	0.002475742	5.404283269	0.031971896	1	635	550	431	523	411	1052	827	747	820	655
ENSMUSG00000061758	chr6	Akr1b10	-0.5736252	0.001163845	0.002478801	5.725622186	0.035890303	-1	971	1095	971	1016	637	568	707	665	689	820
ENSMUSG00000037570	chr15	Mcrs1	0.47688511	0.001165	0.002480883	4.804491495	0.023406324	1	364	354	282	448	296	657	498	538	487	465
ENSMUSG00000047719	chr4	Ubiad1	-0.6475297	0.001165347	0.002481245	3.947948297	0.042912861	-1	230	225	292	474	202	272	197	197	138	177
ENSMUSG00000033931	chr8	Rbm34	0.68657002	0.001174013	0.002499316	2.642301514	0.042301806	1	80	75	58	89	49	115	158	123	105	113
ENSMUSG00000029291	chr5	Rufy3	-0.8170002	0.001180794	0.002513369	2.365499204	0.061745844	-1	94	68	88	135	98	42	53	44	71	87
ENSMUSG00000022765	chr16	Snap29	-0.5100942	0.001184003	0.002519815	4.429059047	0.026453367	-1	420	326	317	468	353	333	286	209	346	273
ENSMUSG00000020604	chr11	Arsg	0.96861025	0.001184926	0.002521395	1.609555756	0.078770325	1	26	35	26	32	27	45	55	54	52	109
ENSMUSG00000038323	chr1	1700066M21Rik	-0.8368215	0.001185908	0.0025231	1.53803388	0.053488617	-1	65	50	40	71	43	39	30	20	39	36
ENSMUSG00000028060	chr3	2810403A07Rik	-0.4867863	0.001187145	0.002525348	4.537854936	0.024126049	-1	402	416	377	418	383	325	363	248	329	309
ENSMUSG00000031077	chr7	Fadd	0.56670301	0.001189028	0.002528968	3.127229845	0.028587084	1	124	101	89	126	79	191	187	144	160	159
ENSMUSG00000028664	chr4	Ephb2	1.13055593	0.001190881	0.00253214	1.966236677	0.12308408	1	28	26	23	48	51	123	65	91	29	119
ENSMUSG00000048924	chr13	Ccdc125	1.18491202	0.001190793	0.00253214	0.449313237	0.097774015	1	17	11	9	13	6	18	32	18	38	33
ENSMUSG00000087367	chr19	Gm15491	-0.8491453	0.001192487	0.002535168	1.393478625	0.053586111	-1	41	48	43	50	57	24	35	27	28	32
ENSMUSG00000038095	chr5	Sbno1	-0.4764984	0.001192781	0.002535407	5.025895303	0.023793867	-1	570	547	537	637	516	390	541	394	405	485
ENSMUSG00000038065	chr6	Mturn	-0.6365147	0.001193953	0.002537513	3.401871411	0.039595378	-1	198	218	183	154	180	155	104	138	124	147
ENSMUSG00000040774	chr3	Cept1	-0.5361598	0.001194202	0.002537658	4.444595601	0.029695694	-1	388	356	305	448	412	326	347	182	299	300
ENSMUSG00000075000	chr10	Nrbf2	-0.6300457	0.001195177	0.002539342	3.165743235	0.037554168	-1	140	167	153	212	134	105	119	76	116	154
ENSMUSG00000092659	chr7	Mir3100	-1.0112821	0.001196659	0.002542105	1.261912498	0.082756746	-1	43	33	51	53	47	13	26	17	32	35
ENSMUSG00000015932	chr2	Dstn	0.48362899	0.00119817	0.002544928	5.105607591	0.024757793	1	398	389	354	636	383	606	779	577	610	693
ENSMUSG00000040007	chr2	Bahd1	0.5269439	0.001198657	0.002545575	3.644286995	0.026134506	1	139	145	117	209	151	298	264	198	199	242
ENSMUSG00000024219	chr17	Anks1	-0.5563845	0.001198914	0.002545733	4.332058716	0.031873576	-1	232	345	361	525	328	325	270	235	243	256
ENSMUSG00000041390	chr6	Mdfic	0.54580747	0.001199906	0.002547454	4.248049532	0.030256367	1	272	218	212	257	184	346	459	259	340	433
ENSMUSG00000039384	chr1	Dusp10	-0.7699293	0.001203908	0.002555562	5.797848617	0.065664811	-1	1179	1308	997	1092	627	404	1011	717	585	602
ENSMUSG00000027997	chr3	Casp6	0.79327908	0.001204324	0.002556057	2.121769998	0.054448152	1	34	56	48	59	33	112	89	64	66	110
ENSMUSG00000032523	chr9	Hhatl	-0.5640612	0.001208024	0.00256352	7.636497419	0.035846484	-1	3640	3272	2741	3972	3993	2424	2475	2446	2240	3523
ENSMUSG00000029998	chr6	Pcyox1	-0.5953363	0.001209794	0.002566886	6.269040443	0.039415266	-1	1464	1332	1292	1538	1259	716	1132	814	935	1407
ENSMUSG00000021488	chr13	Nsd1	-0.4726014	0.001211326	0.002569748	6.220623713	0.024579111	-1	1307	1087	1181	1657	1243	1075	1066	997	872	1085
ENSMUSG00000059273	chr7	Zc3h4	-0.4726495	0.001216486	0.002580302	4.876703362	0.023246219	-1	467	418	459	683	521	439	430	380	320	438
ENSMUSG00000038020	chr11	Rapgefl1	1.10326539	0.001218976	0.00258519	0.769808733	0.088011581	1	13	17	6	18	20	35	36	38	21	45
ENSMUSG00000019189	chr11	Rnf145	0.53629576	0.001220903	0.002588885	4.27364816	0.029228548	1	270	255	208	255	179	503	354	328	280	408
ENSMUSG00000045629	chr18	Sh3tc2	-0.8951037	0.001224176	0.002595432	1.243887231	0.060134964	-1	29	44	43	59	44	33	26	27	16	27
ENSMUSG00000033581	chr16	Igf2bp2	0.97121276	0.00122761	0.002602317	2.436750643	0.09222512	1	33	34	35	86	80	128	174	82	87	104
ENSMUSG00000038725	chr15	Pkhd1l1	-1.2804975	0.001231473	0.00261011	-0.059983657	0.099320105	-1	25	9	14	26	16	14	6	5	9	6
ENSMUSG00000027208	chr2	Fgf7	-0.8861493	0.001233446	0.002613499	1.367538081	0.060163319	-1	59	45	46	60	30	22	32	21	31	35
ENSMUSG00000049532	chr14	Sall2	0.84637133	0.001233278	0.002613499	1.894228295	0.061436978	1	52	37	30	43	29	79	67	84	48	98
ENSMUSG00000030207	chr6	8430419L09Rik	0.65209139	0.001243004	0.002632999	2.516175344	0.036141811	1	59	72	59	75	58	123	123	116	94	101
ENSMUSG00000059713	chr4	Rcan3	0.60426387	0.001243026	0.002632999	3.118304208	0.033797551	1	101	105	83	135	85	248	150	147	148	156
ENSMUSG00000044501	chr17	Zfp758	-1.1608431	0.001247459	0.002641989	2.020907621	0.130711855	-1	63	86	79	120	63	9	63	30	46	49
ENSMUSG00000032314	chr9	Etfa	-0.5541823	0.001248718	0.002644255	7.252571111	0.034685276	-1	2218	2757	2561	4206	1988	1926	1929	1875	2213	2098
ENSMUSG00000054939	chr16	Zfp174	-0.7900234	0.001251841	0.002650467	1.617974117	0.047677527	-1	66	55	52	57	48	34	34	27	35	47
ENSMUSG00000064317	chr10	Gm10146	0.86407118	0.001253205	0.002652952	1.49064214	0.057851763	1	29	40	22	31	19	77	54	51	52	49
ENSMUSG00000043419	chr11	Chd3os	1.25557784	0.001254184	0.002654623	-0.170241681	0.074257572	1	8	8	3	8	6	16	22	15	15	19
ENSMUSG00000059851	chr7	Suv420h2	0.58381521	0.001255233	0.002656441	3.936113085	0.034483958	1	183	185	174	202	158	431	244	326	241	249
ENSMUSG00000046351	chr13	Zfp322a	-0.5107062	0.001256012	0.002657687	3.923128218	0.025490465	-1	297	231	240	293	254	189	238	183	212	189
ENSMUSG00000030674	chr7	Qprt	1.07125198	0.001258771	0.002663122	1.223069635	0.093950651	1	15	18	16	21	34	59	38	53	29	65
ENSMUSG00000001729	chr12	Akt1	0.49926253	0.001259265	0.002663763	6.408457515	0.027836047	1	888	962	894	1545	1008	1775	1772	1508	1362	1716
ENSMUSG00000034412	chr11	Tbc1d10a	0.87431814	0.001261904	0.002668942	2.771104613	0.076123808	1	62	66	61	86	76	285	120	121	92	102
ENSMUSG00000084843	chr2	B230312C02Rik	-0.8390536	0.00126352	0.002671956	6.860064201	0.079322113	-1	3059	1669	1613	2405	2346	616	1933	1123	1370	1706
ENSMUSG00000033207	chr19	Mamdc2	1.67519173	0.001267696	0.002680381	2.743329189	0.290558026	1	45	47	28	65	49	111	102	69	28	523
ENSMUSG00000025034	chr19	Trim8	0.50919585	0.001271683	0.002688405	5.08253569	0.027773477	1	374	367	379	525	433	893	689	589	462	634
ENSMUSG00000036180	chr8	Gatad2a	0.44556623	0.001272534	0.002689796	4.984084589	0.020767474	1	395	362	363	509	367	572	665	566	572	586
ENSMUSG00000059323	chr15	Tonsl	0.46880579	0.001274094	0.002692686	5.765666613	0.024048356	1	758	688	595	775	577	1241	1054	879	1049	937
ENSMUSG00000021496	chr13	Pcbd2	0.68362486	0.001276711	0.00269781	2.551136856	0.041320496	1	58	65	66	84	55	145	102	94	138	98
ENSMUSG00000020903	chr11	Stx8	0.47864371	0.001277423	0.002698906	4.373835886	0.02321032	1	292	256	233	326	184	405	418	348	399	388
ENSMUSG00000005986	chr19	Ankrd13d	1.26486878	0.001290791	0.002726738	0.215464647	0.113164648	1	7	11	8	14	5	44	16	25	20	14
ENSMUSG00000095325	chr17	Zfp870	-0.6436507	0.001292114	0.002729119	2.78324303	0.037909458	-1	133	117	112	138	114	84	75	65	106	101
ENSMUSG00000091345	chr9	Col6a5	1.57777182	0.001292487	0.002729495	1.448397682	0.239770093	1	20	16	8	18	33	36	38	45	29	171
ENSMUSG00000029587	chr5	Zfp12	-0.5440357	0.001295879	0.002736245	3.292315488	0.027238705	-1	164	149	156	226	165	145	119	98	141	142
ENSMUSG00000031938	chr9	4931406C07Rik	0.67373848	0.001297165	0.002738547	3.708321497	0.046616029	1	151	193	135	157	104	218	251	280	189	357
ENSMUSG00000034211	chr5	Mrps17	0.45572633	0.001297902	0.002739689	5.119872195	0.022061176	1	493	451	370	509	358	771	697	618	592	600
ENSMUSG00000079317	chrX	Trappc2	-0.5634623	0.00130097	0.00274575	3.562289479	0.030827526	-1	168	220	204	264	185	130	166	130	154	190
ENSMUSG00000060803	chr19	Gstp1	0.48440941	0.001302835	0.002749271	6.135987747	0.026159949	1	967	754	692	1095	872	1436	1331	1199	1433	1279

ENSMUSG00000038425	chr18	Poli	0.98902335	0.001304381	0.002752119	0.962232019	0.073635449	1	23	11	13	25	19	43	25	43	44	41
ENSMUSG00000045114	chr7	Prrt2	0.61020523	0.001304889	0.002752774	2.851036037	0.032927718	1	93	82	86	89	66	156	141	142	114	146
ENSMUSG00000018677	chr11	Slc25a39	0.476381	0.001305828	0.002753923	5.951412296	0.025155179	1	732	715	691	1024	709	1355	1305	1170	952	1096
ENSMUSG00000067942	chr17	Zfp160	-0.817665	0.00130569	0.002753923	2.130062982	0.06035898	-1	68	70	73	127	73	58	45	31	73	45
ENSMUSG00000020121	chr10	Srgap1	0.99780699	0.001306577	0.002755087	1.651070091	0.089369005	1	20	28	30	34	36	86	41	85	38	77
ENSMUSG00000058402	chr7	Zfp420	-0.9465831	0.0013081	0.002757882	1.117699993	0.066942772	-1	39	37	35	55	37	16	27	14	33	24
ENSMUSG00000028608	chr4	0610037L13Rik	0.49195624	0.00130881	0.002758964	4.982179625	0.025826902	1	461	372	360	431	323	706	587	522	677	512
ENSMUSG00000044433	chr8	Camsap3	1.1447915	0.001311309	0.002763815	0.35791903	0.081374249	1	10	6	13	14	10	29	19	30	17	34
ENSMUSG00000042962	chr12	Gm5436	0.56759491	0.001313211	0.002767406	3.437171209	0.030750002	1	118	146	96	174	113	248	169	203	191	234
ENSMUSG00000028848	chr4	Gpn2	0.65810512	0.001314754	0.002770239	2.773265539	0.03924609	1	83	62	85	96	62	175	149	112	130	107
ENSMUSG00000000881	chrX	Dlg3	0.87403665	0.001315302	0.002770977	2.165234222	0.070260301	1	32	52	53	52	38	140	76	72	57	121
ENSMUSG00000023852	chr17	Chd1	-0.4968259	0.001318008	0.002776259	4.105338296	0.024713575	-1	292	291	271	372	269	233	275	171	251	230
ENSMUSG00000029434	chr5	Vps33a	-0.4849923	0.001318618	0.002777126	5.402112402	0.025693859	-1	800	726	635	827	673	657	610	407	621	589
ENSMUSG00000040128	chr4	Pnrc1	-0.5876448	0.001319978	0.002779571	5.37417505	0.03831915	-1	795	781	639	856	632	696	494	493	317	728
ENSMUSG00000047284	chr11	Neurl4	-0.4513286	0.001321951	0.002783305	4.880961829	0.021322384	-1	497	480	470	614	467	367	404	382	410	455
ENSMUSG00000040712	chr11	Camta2	-0.5648443	0.001323858	0.002786901	5.598241521	0.035526008	-1	663	683	742	1269	979	817	628	568	480	716
ENSMUSG00000056260	chr3	Lrif1	-0.8149209	0.001329201	0.002797729	2.685742168	0.064902714	-1	124	116	91	172	105	44	95	51	71	113
ENSMUSG00000020424	chr11	Gatsl3	0.96021501	0.001333425	0.002806195	1.976493197	0.084570478	1	34	50	36	38	32	158	74	49	63	74
ENSMUSG00000055912	chr6	Tmem150a	-0.5353069	0.001334425	0.002807878	4.412549747	0.030245209	-1	364	392	324	418	364	436	266	216	230	283
ENSMUSG00000027222	chr2	Pex16	0.52202968	0.001337497	0.002813919	4.115164884	0.027777178	1	194	222	181	271	188	299	292	364	306	385
ENSMUSG00000021203	chr12	Otub2	-0.7566264	0.001340641	0.002820107	2.300744454	0.051584811	-1	102	104	81	97	66	44	55	53	61	78
ENSMUSG00000033047	chr15	Eif3l	0.45892914	0.001344407	0.002827179	6.006318757	0.023426775	1	820	816	668	963	763	1356	1209	1124	1053	1338
ENSMUSG00000050628	chr11	Ubald2	-0.5169511	0.001344322	0.002827179	4.641560674	0.028482154	-1	445	435	389	490	415	471	363	284	229	341
ENSMUSG00000040688	chr17	Tbl3	0.54920114	0.001350394	0.002839342	4.425562421	0.031976118	1	219	210	197	394	288	451	486	374	413	348
ENSMUSG00000058331	chr13	Zfp85	-0.9866677	0.001353314	0.002845054	0.987210292	0.073847293	-1	58	35	29	36	27	19	21	15	25	22
ENSMUSG00000022814	chr16	Umps	0.70041346	0.001355842	0.00284994	3.227408953	0.048831316	1	102	85	94	117	123	248	244	109	188	154
ENSMUSG00000024150	chr17	Mcfd2	0.54176669	0.001358538	0.002855176	5.480323041	0.032570098	1	541	556	491	642	472	1076	1059	599	921	682
ENSMUSG00000081603	chrX	Gm14681	1.03313503	0.001359649	0.002857083	1.179969367	0.087600763	1	28	31	10	21	14	48	60	47	44	34
ENSMUSG00000014602	chr1	Kif1a	-1.2666899	0.001361965	0.002861518	0.93596853	0.142400239	-1	20	21	40	61	49	36	17	8	11	16
ENSMUSG00000050912	chr9	Tmem123	-0.4772065	0.001364632	0.002866691	5.055060649	0.024585847	-1	557	575	563	701	481	480	508	354	364	571
ENSMUSG00000037353	chr15	Letmd1	0.5288559	0.001365325	0.002867717	3.647346324	0.026963882	1	161	176	138	158	120	271	221	223	213	270
ENSMUSG00000030232	chr6	Aebp2	-0.4423993	0.00136638	0.0028695	5.00654636	0.020762365	-1	520	490	490	767	507	528	450	360	443	446
ENSMUSG00000044854	chr1	1700056E22Rik	1.14969441	0.001366765	0.002869878	0.136661718	0.07327917	1	10	10	9	7	8	32	17	22	18	20
ENSMUSG00000039221	chr3	Rpl22l1	0.55821936	0.001369622	0.002875013	6.007761887	0.035175984	1	864	824	696	841	636	1507	1511	1010	1338	896
ENSMUSG00000055692	chr16	Tmem191c	1.25309298	0.001369434	0.002875013	0.113194266	0.095235776	1	11	8	8	6	8	27	13	27	14	28
ENSMUSG00000028936	chr4	Rpl22	0.52760688	0.001372993	0.002881655	6.85509992	0.031827696	1	1538	1498	1185	1593	1239	2915	2311	1889	2366	1709
ENSMUSG00000021476	chr13	Habp4	-0.474294	0.001381628	0.002899345	5.332913884	0.024568515	-1	767	598	631	858	639	509	572	584	524	543
ENSMUSG00000074582	chr2	Arfgef2	-0.4985542	0.001388191	0.002912679	4.899996515	0.026728083	-1	448	425	481	770	500	367	384	379	419	457
ENSMUSG00000027332	chr2	Ivd	-0.5403111	0.001391942	0.002920111	7.12192263	0.033586517	-1	2435	2812	2171	2716	2117	1476	2017	1649	1877	2208
ENSMUSG00000016128	chr5	Stard13	-0.5969317	0.001394556	0.002925156	3.436656695	0.035005721	-1	175	187	175	255	174	132	149	160	91	163
ENSMUSG00000028468	chr4	Rgp1	-0.4467839	0.001396423	0.002928633	5.469755703	0.02186697	-1	793	719	658	1001	656	671	631	544	540	678
ENSMUSG00000030397	chr7	Mark4	-0.6761251	0.001397364	0.002930166	3.260285101	0.046030047	-1	149	128	130	272	201	108	116	125	93	152
ENSMUSG00000016664	chr15	Pacsin2	-0.4977134	0.001400113	0.002935489	5.84676041	0.027796757	-1	863	1009	939	1362	870	757	787	640	927	768
ENSMUSG00000057003	chr11	Myh4	-0.7887735	0.001402877	0.002940845	15.29771741	0.0720954	-1	732534	568974	517385	990306	1004683	311374	496885	397769	407111	798040
ENSMUSG00000093577	chr3	Gm20632	1.38083929	0.001406312	0.002947604	-0.001935074	0.127870549	1	11	9	4	5	6	23	28	13	8	31
ENSMUSG00000042642	chr3	Flad1	-0.4572146	0.001406782	0.002948145	5.216659233	0.022693767	-1	589	602	584	844	593	562	467	531	428	563
ENSMUSG00000038467	chr2	Chmp4b	0.46359516	0.001407245	0.002948674	7.119017286	0.02469741	1	1825	1725	1494	2108	1567	3009	2769	2327	2629	2432
ENSMUSG00000061882	chr5	Ccdc62	0.66942892	0.00140839	0.002950631	2.459217027	0.039103172	1	62	68	50	70	58	139	103	94	114	89
ENSMUSG00000045667	chr11	Smtnl2	0.7126632	0.001409928	0.002953224	7.152859321	0.058618162	1	1402	1332	1404	2314	1653	1556	2792	2649	3549	3701
ENSMUSG00000073968	chr7	Trim68	-0.6993324	0.00141005	0.002953224	2.669122877	0.045937824	-1	137	115	104	123	96	100	52	63	75	101
ENSMUSG00000045211	chr14	Nudt18	0.58691076	0.001411323	0.002955446	3.534223858	0.033947701	1	137	164	135	136	105	261	216	209	167	275
ENSMUSG00000021022	chr12	Ppp2r3c	-0.5092195	0.001411714	0.002955822	4.090920821	0.026486432	-1	331	309	261	322	255	213	265	177	241	245
ENSMUSG00000028086	chr3	Fbxw7	-0.5070542	0.001419287	0.002971233	5.106966691	0.028170096	-1	572	583	527	767	566	369	447	411	487	594
ENSMUSG00000074219	chr8	Gm10644	-1.233166	0.001419883	0.002972036	-0.213268227	0.077078669	-1	19	9	16	18	16	6	9	6	7	8
ENSMUSG00000001948	chr9	Spa17	1.01555572	0.001421164	0.002973828	1.139824231	0.086213842	1	35	11	22	22	12	44	53	49	41	38
ENSMUSG00000031928	chr9	Mre11a	-0.5465382	0.001421138	0.002973828	3.688027616	0.029949333	-1	243	199	195	261	231	203	215	120	167	148
ENSMUSG00000039686	chr2	Zer1	-0.4529457	0.00142289	0.002976993	5.194803181	0.02229889	-1	649	614	568	709	596	524	458	465	464	608
ENSMUSG00000028032	chr3	Papss1	0.49208309	0.001429601	0.002990587	3.581612382	0.022696712	1	128	145	133	189	140	243	239	190	213	248
ENSMUSG00000057637	chr4	Prdm2	-0.5483624	0.00143073	0.0029925	4.862044992	0.032986207	-1	464	377	478	673	578	513	329	410	305	370
ENSMUSG00000070426	chr7	Rnf121	-0.4818323	0.001435766	0.003002583	5.204115814	0.025524143	-1	729	618	613	713	515	647	501	410	516	442
ENSMUSG00000087381	chr4	Gm16008	-1.014908	0.001436753	0.003004197	1.013548043	0.080654743	-1	48	48	26	29	37	23	14	17	23	26
ENSMUSG00000022841	chr16	Ap2m1	0.51571168	0.001438311	0.003007006	6.715156582	0.03061238	1	1255	1067	1158	1770	1237	2376	2255	1612	2213	1652
ENSMUSG00000064225	chr9	Paqr9	-1.094741	0.001439009	0.003008015	2.527926487	0.124494263	-1	41	98	108	243	103	35	53	69	73	59
ENSMUSG00000020262	chr10	Adarb1	-0.5583304	0.001446812	0.003023874	3.386962987	0.030215578	-1	175	184	180	222	158	169	146	102	103	170
ENSMUSG00000048939	chr16	Atp13a5	-1.1459533	0.001452319	0.00303493	0.852556351	0.108059622	-1	50	44	29	24	25	9	22	19	20	15

ENSMUSG00000019861	chr10	Gopc	-0.5761194	0.001456137	0.003042453	3.992750246	0.034798431	-1	297	246	261	387	232	180	274	137	227	220
ENSMUSG00000026718	chr2	Stam	-0.5298495	0.001459146	0.003048285	3.939571456	0.028770399	-1	272	230	253	327	260	188	228	172	160	273
ENSMUSG00000040797	chr6	Iqsec3	1.02090674	0.001460043	0.003049702	2.499630101	0.107081931	1	65	46	42	56	61	89	156	197	55	98
ENSMUSG00000044043	chr18	Pcdhb14	-1.0107437	0.001462857	0.003055125	0.89446208	0.076088181	-1	34	29	24	43	44	18	26	23	12	15
ENSMUSG00000019132	chr13	BC005537	0.52079302	0.001464028	0.003057112	6.578110967	0.03124406	1	1112	1162	1135	1434	1004	2169	2127	1213	1996	1738
ENSMUSG00000028709	chr4	Mob3c	0.7259388	0.001465071	0.003058833	2.502184538	0.048490267	1	68	78	61	63	39	154	100	99	101	112
ENSMUSG00000096544	chr3	Gm4617	1.31919632	0.001468998	0.003066574	-0.165691682	0.099692685	1	3	10	3	8	8	18	18	17	23	12
ENSMUSG00000023055	chr15	Calcoco1	-0.4744139	0.001469589	0.003067173	6.46519561	0.025821417	-1	1574	1447	1304	1923	1428	1307	1156	1150	996	1436
ENSMUSG00000029464	chr5	Gpn3	-0.541258	0.001469724	0.003067173	3.619684127	0.028962679	-1	231	238	174	242	190	167	160	116	179	190
ENSMUSG00000050368	chr2	Hoxd10	-1.3200235	0.001470289	0.003067896	-0.227509372	0.099386616	-1	11	17	20	23	8	6	4	6	8	10
ENSMUSG00000035236	chr2	Scai	-0.8007708	0.001473982	0.003074683	1.606882649	0.050868412	-1	57	37	53	75	57	37	31	31	42	33
ENSMUSG00000057098	chr11	Ebf1	-0.5076144	0.001473959	0.003074683	3.753561346	0.025387496	-1	225	219	221	320	194	190	154	162	171	226
ENSMUSG00000066151	chr4	Fkbp15	0.46198634	0.001475593	0.003077583	4.454345647	0.022130149	1	272	261	263	335	237	503	400	321	445	401
ENSMUSG00000034563	chr9	Ccpg1	-0.4685859	0.001479026	0.003084283	6.022329886	0.024946969	-1	1054	1129	911	1442	1100	1118	825	788	822	913
ENSMUSG00000031729	chr8	Ist1	0.47840569	0.001490066	0.003106842	5.359384691	0.025456834	1	478	504	436	675	470	1067	778	701	677	693
ENSMUSG00000038668	chr4	Lpar1	0.48032548	0.001490409	0.003107095	4.449061205	0.024197286	1	311	231	279	317	214	516	406	393	350	408
ENSMUSG00000007029	chr17	Vars	0.54469541	0.001490871	0.003107594	5.355458482	0.033461986	1	471	358	395	742	539	922	932	767	624	721
ENSMUSG00000044197	chr5	Gpr146	-0.4864809	0.001491605	0.003108659	5.433815939	0.026469878	-1	695	605	695	939	816	652	535	527	629	588
ENSMUSG00000044950	chr11	Pwwp2a	-0.6374924	0.001495893	0.003117132	2.422484444	0.034735844	-1	86	91	95	126	80	69	70	57	72	67
ENSMUSG00000075701	chr7	Vimp	0.48805689	0.001496613	0.003118166	5.037517008	0.02611122	1	475	388	366	447	350	830	671	483	623	533
ENSMUSG00000043702	chr14	Pde12	-0.6687334	0.00149825	0.003121113	2.95358152	0.043944873	-1	132	115	162	150	134	72	121	81	96	110
ENSMUSG00000099492	chr1	Gm5525	0.97154065	0.001504884	0.003134465	1.216373786	0.077822093	1	26	15	14	32	24	32	65	44	38	57
ENSMUSG00000017679	chr2	Ttpal	0.55910078	0.001507308	0.003139046	3.283173274	0.029945931	1	118	96	111	142	112	265	179	160	153	185
ENSMUSG00000029428	chr5	Stx2	0.55877766	0.00150825	0.00314054	3.501817737	0.030808598	1	130	160	124	143	114	223	207	179	257	221
ENSMUSG00000022536	chr16	Glyr1	-0.4759539	0.001517788	0.00315993	5.790648987	0.025699258	-1	980	840	893	1224	872	734	831	570	839	802
ENSMUSG00000098457	chr15	Mir8097	1.0537251	0.001523125	0.003170568	0.890548369	0.089253713	1	17	18	10	26	13	68	30	37	28	28
ENSMUSG00000096780	chr17	Tmem181b-ps	-0.9626978	0.001532367	0.003189332	1.772805288	0.0881727	-1	67	72	43	77	67	63	49	17	33	24
ENSMUSG00000049124	chr17	Gm8186	0.8561335	0.00153289	0.003189946	2.202695526	0.070813685	1	64	42	30	53	48	122	109	70	114	56
ENSMUSG00000035245	chr6	Eogt	-0.5996149	0.001535899	0.00319573	2.735091381	0.032481196	-1	133	107	105	150	96	99	99	70	70	89
ENSMUSG00000021846	chr14	Peli2	-0.6637896	0.001536506	0.003196519	3.314456875	0.04555892	-1	174	183	148	215	179	204	97	79	104	148
ENSMUSG00000037706	chr7	Cd81	0.48969211	0.001538585	0.003199858	7.042456563	0.028026783	1	1659	1558	1438	2000	1524	2842	2521	2746	1917	2534
ENSMUSG00000063362	chr8	Alg11	-0.5978513	0.001538672	0.003199858	2.843221953	0.033085071	-1	115	124	114	134	142	107	92	77	89	95
ENSMUSG00000081485	chr11	Gm12338	0.55569869	0.001538798	0.003199858	5.988439373	0.035607057	1	857	814	795	820	525	1463	1134	1036	1465	1059
ENSMUSG00000042589	chr5	Cux2	-1.3048048	0.001547144	0.003216734	0.534818419	0.141498646	-1	10	30	38	46	19	12	14	11	19	6
ENSMUSG00000033737	chrX	Fndc3c1	-0.9693159	0.001548677	0.003219442	1.544957551	0.085623839	-1	72	62	52	59	32	16	39	37	28	33
ENSMUSG00000030245	chr6	Golt1b	0.52207224	0.001549452	0.003220574	4.443678535	0.02926961	1	283	252	228	293	263	521	503	324	427	317
ENSMUSG00000026032	chr1	Ndufb3	0.53056441	0.001555156	0.00323195	6.868112942	0.032963708	1	1375	1538	1362	1861	1024	2801	1984	2187	2427	1852
ENSMUSG00000006235	chr9	Epor	1.37810009	0.001555842	0.003232855	0.465213939	0.15439279	1	9	20	7	5	9	55	18	33	18	24
ENSMUSG00000096370	chr19	Gm21992	0.48866314	0.001556054	0.003232855	3.783633829	0.023682192	1	180	163	148	216	143	325	260	253	240	225
ENSMUSG00000057777	chr3	Mab21l2	1.45369444	0.001566062	0.003253162	-0.125578344	0.152917444	1	9	7	7	7	1	7	21	13	26	26
ENSMUSG00000029389	chr5	Ddx55	0.70257351	0.001568245	0.003257215	2.158915349	0.043400042	1	41	47	43	74	43	108	81	64	98	89
ENSMUSG00000047414	chr12	Flrt2	-0.5259482	0.001569703	0.003259758	3.76698646	0.028098881	-1	226	243	254	295	172	216	212	151	147	183
ENSMUSG00000033216	chr6	Eefsec	0.61160753	0.00157638	0.003273138	2.824402921	0.03474984	1	102	68	64	99	78	170	147	119	111	143
ENSMUSG00000084910	chr4	C630043F03Rik	-0.9815187	0.001578607	0.003277274	1.330962541	0.083222223	-1	38	39	52	72	39	40	18	12	32	31
ENSMUSG00000028980	chr4	H6pd	-0.4699768	0.00158658	0.00329285	5.787367572	0.025250363	-1	1027	892	858	1066	914	701	758	640	776	896
ENSMUSG00000031543	chr8	Ank1	-0.6633812	0.001586581	0.00329285	9.30287387	0.052285283	-1	11961	9772	8907	13791	13244	5073	7927	7172	8365	11117
ENSMUSG00000025484	chr7	Bet1l	0.48249292	0.001587657	0.003294595	3.88648122	0.023237108	1	181	187	181	215	147	348	295	243	257	258
ENSMUSG00000041079	chr16	Rwdd2b	0.67095009	0.001588484	0.003295331	2.183955262	0.03806807	1	49	57	40	68	41	94	104	78	81	86
ENSMUSG00000055980	chr1	Irs1	-0.7135492	0.001588252	0.003295331	6.879685772	0.059940375	-1	2536	2207	1815	2189	2076	720	1871	1397	1501	1712
ENSMUSG00000070923	chr4	Klhl9	-0.5085674	0.001590682	0.003299402	5.489069021	0.029475708	-1	930	728	657	990	643	575	660	436	622	736
ENSMUSG00000061130	chr17	Ppm1b	-0.5004816	0.001591626	0.003300871	6.851164425	0.029390233	-1	1748	1688	1782	3131	1877	1563	1581	1586	1440	1610
ENSMUSG00000054408	chr8	Spcs3	0.53413413	0.001594182	0.003305681	5.382018681	0.0325504	1	551	451	443	677	430	938	959	574	929	629
ENSMUSG00000046791	chr12	2410016O06Rik	0.83735605	0.001594512	0.003305874	2.30493424	0.068405663	1	50	43	38	83	47	122	153	83	55	95
ENSMUSG00000022620	chr15	Arsa	0.63708746	0.001595517	0.003307468	3.899468008	0.04380939	1	146	193	167	226	134	494	228	228	231	312
ENSMUSG00000052566	chr8	Hook2	0.73358518	0.001595952	0.003307879	2.178362093	0.048008323	1	55	58	41	57	35	127	72	81	85	85
ENSMUSG00000087365	chrX	C430049B03Rik	1.2295475	0.001596991	0.003309541	0.4567561	0.112255295	1	5	13	12	10	14	41	29	36	14	22
ENSMUSG00000078789	chr11	Dph1	0.57549313	0.001597501	0.003310108	3.108634674	0.031518747	1	115	95	99	117	82	147	159	168	175	176
ENSMUSG00000039473	chr16	Ubn1	-0.4448068	0.001597909	0.003310462	5.594351014	0.02237398	-1	869	715	727	1033	809	775	643	620	580	726
ENSMUSG00000003072	chr10	Atp5d	0.54889725	0.001600579	0.003315503	8.768123745	0.03590478	1	4601	4863	4971	7458	4714	10616	7164	9550	6455	8533
ENSMUSG00000036893	chr2	Ehmt1	-0.4889799	0.001607129	0.003328577	4.406677534	0.025515214	-1	355	323	303	488	377	260	300	261	256	356
ENSMUSG00000006463	chr19	Zdhhc24	0.72419664	0.001608514	0.003330952	2.525536359	0.050067562	1	79	61	55	62	57	169	101	89	83	137
ENSMUSG00000013622	chr5	Atraid	0.45774576	0.001617898	0.003349888	5.722639649	0.023894123	1	705	679	619	737	560	1157	877	927	948	1077
ENSMUSG00000030714	chr7	Ccdc101	0.52520748	0.001619057	0.003351792	3.617220633	0.027714849	1	137	127	114	211	159	296	221	194	213	253
ENSMUSG00000034152	chr13	Exoc3	-0.4676211	0.001623999	0.003361524	5.516382693	0.02481317	-1	792	708	663	1002	797	595	677	599	659	586
ENSMUSG00000029142	chr5	Mrpl33	0.51106429	0.001626221	0.003365624	6.265945089	0.030502146	1	1013	965	937	1088	717	1856	1427	1290	1599	1214

ENSMUSG00000020929	chr11	Eftud2	0.48710067	0.001627048	0.003366838	5.11369055	0.026625366	1	415	338	325	594	485	723	730	565	630	647
ENSMUSG00000022544	chr16	Fam86	0.55828581	0.001628916	0.003370203	3.661442842	0.031695381	1	173	176	138	148	115	285	232	209	271	221
ENSMUSG00000029070	chr4	Mxra8	0.54262972	0.001629847	0.003371631	6.480548523	0.034576243	1	1402	1088	919	959	987	1871	1731	1628	1440	1984
ENSMUSG00000008734	chr7	Gprc5b	-0.5366302	0.001630599	0.003372349	5.745152777	0.033367584	-1	889	798	846	1266	949	814	546	651	586	987
ENSMUSG00000036099	chr10	Vezt	-0.4648814	0.001630676	0.003372349	4.66101076	0.023354905	-1	461	382	399	527	410	370	312	306	403	333
ENSMUSG00000021277	chr12	Traf3	-0.451255	0.00163175	0.00337407	4.814869432	0.022170995	-1	459	386	467	649	465	454	386	365	326	409
ENSMUSG00000038014	chr13	Fam120a	-0.4782438	0.001633318	0.003376813	6.870520408	0.026959695	-1	1922	1687	1732	2812	2070	1710	1855	1359	1438	1641
ENSMUSG00000034243	chr16	Golgb1	-0.4400406	0.001637654	0.003385276	5.028146213	0.021354298	-1	552	513	479	653	588	561	441	381	439	441
ENSMUSG00000034903	chr2	Cobll1	-0.7739143	0.001638171	0.003385845	2.091578026	0.053970378	-1	64	82	77	110	60	40	46	62	54	45
ENSMUSG00000047686	chrX	Zcchc5	0.74808498	0.001639102	0.003387267	2.644757932	0.055074273	1	90	64	65	60	58	140	90	130	98	169
ENSMUSG00000030079	chr6	Ruvbl1	0.48409767	0.001640507	0.003389671	4.366307608	0.025005576	1	304	233	212	308	221	380	481	343	385	361
ENSMUSG00000026966	chr2	Ssna1	0.46263086	0.00164753	0.003403677	4.541315929	0.022861357	1	313	314	273	316	231	515	450	372	438	422
ENSMUSG00000104011	chr1	RP24-272N10.3	1.11158679	0.001660161	0.003429266	0.635370078	0.097995411	1	8	18	9	25	8	33	26	40	35	23
ENSMUSG00000029231	chr5	Pdgfra	0.4652369	0.001662905	0.003434426	5.426317113	0.024519078	1	568	531	486	542	535	913	780	796	697	879
ENSMUSG00000022610	chr15	Mapk12	-0.48147	0.001667352	0.003443101	7.209175433	0.027552335	-1	2717	2482	2253	3159	2269	2190	1901	1651	2341	1992
ENSMUSG00000003316	chr8	Glg1	-0.4685729	0.001677722	0.003464004	6.077016972	0.025576604	-1	1218	1025	998	1463	1146	865	1023	791	889	1050
ENSMUSG00000016940	chr11	Kctd2	0.47778379	0.001680526	0.00346928	4.267370482	0.024192565	1	259	233	183	308	216	410	326	295	404	386
ENSMUSG00000020328	chr11	Nudcd2	0.51063075	0.001682322	0.003472476	3.813683362	0.026730727	1	181	179	142	211	146	264	337	219	273	244
ENSMUSG00000045180	chrX	Shroom2	-0.9077827	0.001684703	0.003476876	0.931399847	0.061613703	-1	34	27	32	41	40	26	26	14	21	15
ENSMUSG00000020280	chr11	Pus10	-0.7265491	0.001687232	0.00348146	3.217020617	0.055797782	-1	171	169	159	213	144	79	150	61	141	134
ENSMUSG00000030096	chr6	Slc6a6	-0.5811203	0.001687422	0.00348146	6.503825704	0.040057028	-1	1738	1476	1667	1796	1391	1011	1287	764	1236	1655
ENSMUSG00000033852	chr2	Gm28042	0.67900305	0.001688556	0.003483286	2.32460164	0.041128016	1	60	54	54	55	54	96	89	101	109	92
ENSMUSG00000050229	chr1	Pigm	0.57623704	0.001691583	0.003489015	3.257022944	0.032862097	1	129	99	100	157	85	235	191	163	131	209
ENSMUSG00000012535	chr6	Tnpo3	-0.4676082	0.001692205	0.003489267	5.61746195	0.025144868	-1	837	718	723	1096	879	715	747	544	713	642
ENSMUSG00000035399	chr2	Oser1	-0.5239234	0.001692138	0.003489267	3.337167764	0.026459803	-1	197	159	139	206	178	150	135	106	139	141
ENSMUSG00000009549	chr2	Srp14	0.45437612	0.001695615	0.003494752	6.405000679	0.024246497	1	1184	1010	907	1277	955	1839	1541	1534	1450	1635
ENSMUSG00000020716	chr11	Nf1	-0.4648241	0.001695509	0.003494752	4.447803933	0.023171443	-1	365	305	340	539	347	363	289	239	273	335
ENSMUSG00000022425	chr15	Enpp2	-0.625075	0.001695255	0.003494752	3.642106502	0.041986093	-1	191	267	183	219	246	132	169	138	136	220
ENSMUSG00000023345	chr9	Poc1a	0.90583966	0.001698633	0.003500456	1.174090027	0.066331663	1	21	20	19	34	17	64	51	48	28	36
ENSMUSG00000029407	chr5	Uso1	-0.515484	0.001705147	0.003513363	6.662773241	0.031540484	-1	1930	1610	1501	2139	1711	1179	1561	1102	1591	1346
ENSMUSG00000020719	chr11	Ddx5	-0.478265	0.001706094	0.003514795	8.159048445	0.027523801	-1	5421	4734	4404	5819	4429	4325	4461	3016	3883	3896
ENSMUSG00000074505	chr9	Fat3	-1.2441769	0.001710326	0.003522995	0.141545816	0.110574245	-1	24	14	16	27	23	20	5	11	4	8
ENSMUSG00000033669	chr15	Zfp7	1.18834812	0.001712999	0.00352798	0.203354313	0.095407009	1	12	9	12	11	2	32	28	18	21	17
ENSMUSG00000035314	chr7	Gdpd5	-0.659626	0.00171405	0.003529624	3.104077403	0.04510006	-1	199	133	126	177	141	171	89	89	78	117
ENSMUSG00000047242	chrX	Taf9b	-0.5855804	0.001714785	0.003530618	3.093485538	0.033461874	-1	162	138	140	176	137	94	107	87	123	138
ENSMUSG00000026921	chr2	Egfl7	0.54572817	0.001722756	0.003545984	5.557533496	0.034679949	1	596	641	600	629	373	1230	765	881	794	903
ENSMUSG00000044813	chr4	Shb	0.73765544	0.001722604	0.003545984	2.883323086	0.055891424	1	77	74	58	101	95	178	138	197	94	130
ENSMUSG00000091754	chr14	Gm3636	0.96332085	0.001727088	0.003554379	1.307531702	0.079230246	1	29	17	27	22	22	39	40	40	70	62
ENSMUSG00000007610	chr8	Gtpbp3	-0.5237769	0.001734988	0.003569584	3.726499741	0.028507392	-1	261	224	229	241	193	219	203	156	162	142
ENSMUSG00000049232	chr6	Tigd2	-0.612537	0.001734771	0.003569584	3.488244423	0.039277304	-1	203	208	201	268	129	114	174	112	142	175
ENSMUSG00000041117	chr7	Ccdc8	0.59460646	0.001737011	0.003573222	3.250377428	0.035672719	1	124	102	107	130	94	174	179	228	142	193
ENSMUSG00000019158	chr7	Tmem160	0.51138298	0.001738865	0.003576509	4.685104722	0.02918299	1	329	309	283	379	275	700	421	437	516	393
ENSMUSG00000076258	chr16	Gm23935	1.11691451	0.001741258	0.003580904	8.352134427	0.14786912	1	3002	1116	1515	4395	5435	11823	8716	7252	3323	5947
ENSMUSG00000068580	chr2	Zfyve19	0.59423651	0.001742089	0.003582085	3.237489061	0.035285351	1	102	96	110	124	117	162	173	168	226	178
ENSMUSG00000041912	chr3	Tdrkh	0.96631217	0.001744158	0.003585812	0.895645832	0.070605936	1	14	19	14	17	22	35	39	24	37	52
ENSMUSG00000034714	chr11	Ttyh2	-0.5897757	0.001745748	0.003588553	5.712002692	0.04103164	-1	986	814	837	1021	1001	833	536	631	452	987
ENSMUSG00000041168	chr17	Lonp1	-0.4659169	0.001749242	0.003595207	6.552623821	0.025744242	-1	1494	1471	1461	2330	1437	1360	1199	1225	1315	1320
ENSMUSG00000006542	chr1	Prkag3	-0.7477451	0.001749979	0.003596193	7.563893172	0.067224323	-1	4946	3002	3107	2846	3519	1368	2072	2182	2599	3193
ENSMUSG00000022565	chr15	Plec	-0.6057103	0.001753849	0.003603616	9.263331137	0.044475132	-1	8748	8562	10021	16650	11876	10438	7940	8760	5588	7198
ENSMUSG00000039178	chr5	Tbc1d19	-0.5600591	0.001754327	0.003604068	3.867430467	0.033599726	-1	315	222	234	270	240	156	211	147	213	227
ENSMUSG00000020553	chr11	Pctp	0.6233861	0.001757052	0.003609136	2.78104784	0.036989594	1	84	69	61	93	88	155	135	119	147	111
ENSMUSG00000055817	chr17	Mta3	0.55914984	0.001759805	0.003614259	2.958059437	0.029391884	1	79	95	75	127	87	150	157	139	136	161
ENSMUSG00000027284	chr2	Cdan1	-0.5432933	0.001769537	0.003633714	3.460299	0.02975329	-1	158	162	190	243	209	159	155	115	155	141
ENSMUSG00000033763	chr8	Mtss1l	-0.7473611	0.001771797	0.003637819	6.157172803	0.066742361	-1	992	989	891	2190	1706	1161	627	910	556	1121
ENSMUSG00000035829	chr2	Ppp1r26	-0.9007988	0.001772897	0.003639542	1.344877087	0.0687735	-1	48	33	38	60	57	28	20	28	38	23
ENSMUSG00000001524	chr17	Gtf2h4	0.54874402	0.001775862	0.003645011	3.519011553	0.030872709	1	146	116	127	170	128	183	252	206	248	203
ENSMUSG00000025608	chr6	Podxl	-0.5884123	0.001776092	0.003645011	5.515735753	0.040683884	-1	645	622	661	1422	828	631	596	684	467	590
ENSMUSG00000034839	chr9	Larp6	0.98178285	0.001776343	0.003645011	0.890443794	0.074358796	1	15	24	14	21	12	37	36	45	23	45
ENSMUSG00000046207	chr11	Pik3r6	0.88062433	0.001788385	0.003669183	1.982863976	0.0765513	1	34	44	37	64	24	131	48	69	81	78
ENSMUSG00000033276	chr1	Stk36	1.09947654	0.001809351	0.003711652	1.039884751	0.105425979	1	22	17	22	10	18	36	27	56	53	39
ENSMUSG00000030407	chr7	Qpctl	0.73488063	0.001813364	0.00371934	2.221860728	0.050756352	1	46	68	29	63	48	105	95	74	86	104
ENSMUSG00000029458	chr5	Brap	-0.4192655	0.001819146	0.003730651	5.053385028	0.019656498	-1	552	521	553	690	508	515	475	405	399	527
ENSMUSG00000033938	chr8	Ndufb7	0.50849707	0.001825374	0.003742874	7.760993335	0.031437833	1	2725	2645	2527	3305	2176	5698	3478	4040	3907	3743
ENSMUSG00000019297	chr14	Nop9	0.48448623	0.001830104	0.003752021	4.114759105	0.025032881	1	207	192	173	289	214	391	364	309	305	271
ENSMUSG00000006307	chr7	Kmt2b	-0.475011	0.001832089	0.003755541	4.725902467	0.025324354	-1	390	391	457	566	477	453	407	296	307	350

ENSMUSG00000101104	chr1	Gm29247	0.73766369	0.001833588	0.003758062	1.985857191	0.048313748	1	57	43	31	53	31	94	90	65	61	83
ENSMUSG00000031767	chr8	Nudt7	0.71390382	0.001839384	0.003769389	4.126256134	0.058556606	1	118	251	177	307	139	250	391	370	405	321
ENSMUSG00000043424	chr18	Eif3j2	-2.0643822	0.001844435	0.003779185	4.62522194	0.473962819	-1	608	568	540	744	508	700	34	26	44	35
ENSMUSG00000028782	chr4	Bai2	-1.0625053	0.001851373	0.003792846	0.434985862	0.07831888	-1	28	20	29	25	22	18	7	16	14	10
ENSMUSG00000018126	chr15	Baiap2l2	1.09470043	0.001852344	0.003794278	0.985220695	0.103510411	1	22	19	15	16	15	23	29	59	40	51
ENSMUSG00000005983	chr16	1700037C18Rik	0.9044676	0.001853285	0.00379565	1.139917259	0.062871683	1	17	24	25	20	20	42	34	43	53	47
ENSMUSG00000022756	chr16	Slc7a4	1.40183669	0.001856366	0.003800845	0.018010877	0.138046334	1	6	6	10	5	8	28	7	28	14	27
ENSMUSG00000033544	chr1	Angptl1	-0.6886425	0.001856154	0.003800845	4.899476482	0.055877442	-1	689	590	466	455	500	313	295	377	268	606
ENSMUSG00000032598	chr9	Nckipsd	0.61752199	0.001860002	0.003807732	3.091484327	0.038921999	1	80	76	102	127	108	170	138	188	157	172
ENSMUSG00000016763	chr15	Scube1	-1.3275907	0.001860932	0.003809077	0.319550526	0.151345376	-1	15	32	35	31	8	18	14	9	6	6
ENSMUSG00000028949	chr5	Smarcd3	-0.4584345	0.001861992	0.003810691	7.041992833	0.025423568	-1	2444	2028	1996	2764	2149	1800	1711	1746	1812	1965
ENSMUSG00000017478	chr8	Zc3h18	-0.4400699	0.001869869	0.003826251	4.624715929	0.021214095	-1	420	353	370	588	395	400	344	319	303	340
ENSMUSG00000022890	chr16	Atp5j	-0.505942	0.001870508	0.003826997	8.49738678	0.031389387	-1	6272	6517	5970	8179	4842	4668	4594	4152	5566	5338
ENSMUSG00000024773	chr19	Atg2a	-0.5021898	0.00187465	0.003834911	4.690438847	0.028588355	-1	433	347	378	604	496	465	309	324	287	363
ENSMUSG00000032743	chr7	D430042O09Rik	-0.6691812	0.001880129	0.003845557	2.52759745	0.04322994	-1	94	96	104	113	107	68	65	52	75	97
ENSMUSG00000025950	chr1	Idh1	0.57181268	0.001891969	0.003869153	5.596310866	0.038891291	1	479	757	642	598	391	1188	943	762	880	968
ENSMUSG00000040929	chr19	Rfx3	-0.8034417	0.00189222	0.003869153	1.484349956	0.052565929	-1	53	51	54	63	34	27	40	27	35	30
ENSMUSG00000039081	chr14	Zfp503	-0.5742902	0.001893088	0.003870363	4.001655377	0.036490057	-1	207	320	231	406	266	187	218	194	170	275
ENSMUSG00000015766	chr6	Eps8	0.72074093	0.001899403	0.003882706	3.125402331	0.055673673	1	84	80	100	117	101	151	239	95	213	177
ENSMUSG00000026563	chr1	Tada1	0.6022643	0.001905031	0.00389364	2.942308544	0.035755356	1	75	93	80	125	77	133	192	131	138	149
ENSMUSG00000045576	chr3	St7l	-0.5811114	0.001909783	0.003902783	3.368766611	0.03517435	-1	173	162	168	213	194	103	175	112	129	148
ENSMUSG00000042595	chrX	Fam199x	-0.719809	0.001911957	0.003906653	2.166543673	0.048671555	-1	76	66	83	115	69	43	66	42	49	70
ENSMUSG00000018326	chr2	Ywhab	0.46474713	0.001916451	0.003915263	6.538494558	0.026068435	1	1051	1199	1013	1455	1105	2139	1955	1602	1537	1592
ENSMUSG00000024878	chr19	Cbwd1	-0.6074813	0.001919939	0.003921816	3.559652073	0.039857558	-1	229	205	173	285	169	106	198	116	168	165
ENSMUSG00000043445	chr17	Pgp	-0.4534851	0.001922389	0.003926247	5.114861573	0.023586118	-1	534	538	581	848	502	521	411	432	489	528
ENSMUSG00000070808	chr7	Gltscr1	-0.6129636	0.001930595	0.003942431	3.184801187	0.038800476	-1	130	147	167	226	144	104	123	113	85	155
ENSMUSG00000037022	chr8	Mmaa	-0.5035829	0.001932725	0.003946205	3.880447914	0.026784434	-1	256	233	254	356	190	201	190	193	218	181
ENSMUSG00000024735	chr19	Prpf19	-0.4636066	0.00193324	0.003946678	7.662923417	0.026375751	-1	3694	3316	3076	4407	3083	2644	2752	2584	2814	3076
ENSMUSG00000031537	chr8	Ikbkb	0.46051934	0.001934714	0.003949112	4.400677492	0.023158838	1	275	263	207	326	250	480	421	294	392	411
ENSMUSG00000021967	chr14	Mrpl57	0.44812634	0.001935174	0.003949473	4.559902362	0.022077289	1	330	275	293	336	243	502	426	363	456	469
ENSMUSG00000000085	chr4	Scmh1	-0.4329164	0.0019371	0.003952827	4.902796098	0.021102323	-1	475	477	442	716	465	514	387	368	371	441
ENSMUSG00000015668	chrX	Pdzd11	0.56923162	0.001941855	0.003961952	4.115393591	0.036227434	1	277	234	174	195	147	337	364	306	363	303
ENSMUSG00000075376	chr2	Rc3h2	-0.4880673	0.001943137	0.003963989	5.240856791	0.02784437	-1	693	582	591	820	605	415	601	426	485	634
ENSMUSG00000082100	chr11	Glns-ps1	-2.4153493	0.001946032	0.003969314	1.746335948	0.618634998	-1	63	93	79	58	106	81	3	2	3	2
ENSMUSG00000026170	chr1	Cyp27a1	-0.4493145	0.001949437	0.00397568	4.719346651	0.022713585	-1	446	446	434	477	438	464	328	314	335	379
ENSMUSG00000020755	chr11	Sap30bp	0.44821128	0.001954114	0.003984635	4.257175474	0.021517245	1	224	219	237	306	214	425	360	348	335	323
ENSMUSG00000023991	chr17	Foxp4	0.55603144	0.001956084	0.00398749	3.53884472	0.032419716	1	149	115	104	186	144	275	200	242	167	235
ENSMUSG00000034639	chr6	Setmar	-0.6269646	0.001955998	0.00398749	2.286001163	0.034877625	-1	83	82	90	100	75	64	64	53	56	69
ENSMUSG00000037455	chr10	Slc18b1	-0.7111358	0.001958342	0.003991511	2.327040994	0.048856176	-1	110	87	87	80	85	49	74	52	60	68
ENSMUSG00000045008	chr10	9030612E09Rik	-0.8663972	0.001960032	0.003994372	1.406817053	0.066136824	-1	61	49	55	42	35	29	27	20	33	38
ENSMUSG00000031176	chrX	Dynlt3	-0.4733818	0.001974798	0.004023877	5.623615606	0.026616287	-1	970	784	803	1012	701	654	694	513	702	807
ENSMUSG00000056131	chr9	Pgm3	0.74269679	0.001975196	0.004024102	2.13073806	0.052281819	1	46	31	50	67	44	82	111	72	96	72
ENSMUSG00000042354	chr14	Gnl3	0.52417447	0.001979678	0.004032646	4.429620182	0.03116948	1	297	243	208	341	230	467	527	295	450	332
ENSMUSG00000035615	chr4	Frmpd1	1.42158631	0.001988732	0.004050497	0.908282741	0.195969744	1	19	13	18	14	6	32	32	70	10	61
ENSMUSG00000010517	chr4	Faf1	-0.4705564	0.001989823	0.004051938	5.697059848	0.026365308	-1	883	782	721	1234	899	737	724	576	799	707
ENSMUSG00000021376	chr13	Tpmt	-0.79769	0.001990206	0.004051938	1.628024318	0.0558991	-1	81	52	48	60	41	38	43	25	35	37
ENSMUSG00000062563	chr12	Cys1	0.86942809	0.001990309	0.004051938	1.728179252	0.070150586	1	50	41	23	27	25	93	73	50	60	62
ENSMUSG00000035473	chr17	Galm	0.94311907	0.001991012	0.00405278	1.588881357	0.08408743	1	36	31	33	26	19	39	61	64	50	93
ENSMUSG00000054893	chr7	Zfp667	-0.6711037	0.001993559	0.004057372	2.372484692	0.042573677	-1	113	86	70	119	79	63	78	63	62	52
ENSMUSG00000054752	chr4	Fsd1l	-0.7541199	0.00199621	0.004062177	4.348467551	0.06703535	-1	325	344	341	547	357	117	217	248	234	404
ENSMUSG00000042523	chr12	Dnal1	-0.6085268	0.002001421	0.004072187	2.847256985	0.036548823	-1	142	131	105	152	109	89	92	95	67	115
ENSMUSG00000033732	chr8	Sf3b3	0.47360607	0.002004466	0.004077197	5.483290238	0.02655622	1	518	545	478	720	533	1079	976	777	678	749
ENSMUSG00000074738	chr4	B930041F14Rik	0.77653473	0.002004407	0.004077197	1.87168186	0.054825874	1	34	44	35	50	31	95	52	73	55	90
ENSMUSG00000018446	chr11	C1qbp	0.5046723	0.002017512	0.004103136	6.193942637	0.031010864	1	792	806	758	1421	803	1597	1532	1444	1224	1200
ENSMUSG00000051768	chr7	Xrcc1	0.44555023	0.00202186	0.00411138	4.16957954	0.021109998	1	237	206	207	262	214	372	312	327	302	370
ENSMUSG00000015522	chr3	Arnt	-0.4618436	0.002024491	0.004116131	5.420147203	0.025193814	-1	733	662	581	1019	726	603	642	486	513	701
ENSMUSG00000038527	chr6	C1rl	1.13279923	0.002038336	0.004143678	0.674293895	0.101867748	1	13	22	10	10	12	41	35	41	16	31
ENSMUSG00000050856	chr5	Atp5k	0.49687522	0.002045836	0.00415832	8.194000331	0.030767813	1	3432	3652	3141	5172	2913	6913	4899	5701	5241	5236
ENSMUSG00000015291	chrX	Gdi1	0.45429439	0.002047041	0.004160164	5.714985393	0.024626819	1	671	700	581	741	594	1282	894	861	939	996
ENSMUSG00000082192	chrX	Gm14719	-1.6694555	0.002055542	0.004176832	-0.212747553	0.236710306	-1	30	12	16	11	15	19	4	2	1	4
ENSMUSG00000097994	chr6	Gm26982	0.93844967	0.002057818	0.00418085	0.851034556	0.066891287	1	14	20	11	27	14	52	33	29	37	29
ENSMUSG00000020802	chr11	Ube2o	-0.4916753	0.002067024	0.004198942	4.930757264	0.02819632	-1	565	434	409	715	545	367	419	341	416	519
ENSMUSG00000039621	chr2	Prex1	0.51002712	0.002070209	0.004204802	4.458847598	0.029695786	1	215	203	270	407	263	511	427	327	373	475
ENSMUSG00000029208	chr5	Guf1	-0.4876012	0.002073682	0.004211243	4.488534272	0.02691048	-1	418	385	392	464	287	286	312	258	360	297
ENSMUSG00000022960	chr16	Donson	1.03965485	0.0020765	0.004216353	0.912340479	0.09161743	1	20	16	9	20	20	42	54	26	47	23

ENSMUSG00000058183	chr4	Mmel1	2.04696234	0.002077928	0.00421864	0.135687152	0.391697593	1	8	13	5	1	0	32	9	55	9	20
ENSMUSG00000097404	chr19	Gm10814	-1.0707527	0.002082907	0.004228135	0.726828711	0.096487964	-1	41	38	21	23	31	12	14	11	19	25
ENSMUSG00000039824	chr10	Myl6b	2.02292042	0.002084029	0.004229797	4.81952736	0.467804574	1	62	54	60	685	79	1690	240	1301	262	203
ENSMUSG00000033706	chr6	Smyd5	0.53649456	0.002085007	0.004230553	3.48585875	0.030163934	1	128	124	131	176	117	258	258	147	220	194
ENSMUSG00000038696	chr2	Mapkap1	-0.4461747	0.002084997	0.004230553	5.221749912	0.023266929	-1	605	581	581	878	577	467	532	505	534	521
ENSMUSG00000044534	chr9	Ackr2	-1.0713431	0.002086962	0.004233907	0.240432645	0.074572477	-1	13	19	25	31	20	15	13	9	10	9
ENSMUSG00000042111	chr1	Ccdc115	0.49893294	0.002090074	0.004239605	4.23607589	0.027775874	1	247	222	194	284	212	422	396	238	406	337
ENSMUSG00000042271	chrX	Nxt2	-0.9311466	0.002094458	0.00424788	1.530631167	0.082632338	-1	66	51	45	63	47	18	48	17	31	42
ENSMUSG00000028639	chr4	Ybx1	-0.4626167	0.002107848	0.004274416	8.624178958	0.026874567	-1	7158	6113	5812	8709	6444	6185	5985	4401	5230	5403
ENSMUSG00000033405	chr14	Nudt15	-0.902292	0.002110114	0.004278392	1.202601902	0.069257467	-1	44	33	47	49	39	15	31	17	29	32
ENSMUSG00000020166	chr10	Cnot2	-0.4554018	0.002112922	0.004283464	4.655850954	0.023580431	-1	373	405	425	569	398	330	356	286	350	407
ENSMUSG00000041718	chrX	Alg13	-0.7242566	0.002116614	0.004290326	2.086267347	0.05013284	-1	79	63	73	84	83	72	48	30	51	56
ENSMUSG00000029366	chr5	Dck	0.70456519	0.002117845	0.0042922	2.502149741	0.049832829	1	61	69	66	73	44	98	146	82	128	105
ENSMUSG00000030105	chr6	Arl8b	-0.4855656	0.002119455	0.004294839	6.611981999	0.029131107	-1	1842	1703	1519	1984	1452	1240	1616	1015	1371	1414
ENSMUSG00000071650	chr19	Ganab	0.47704055	0.002127465	0.004310446	5.560333153	0.027347064	1	488	556	504	742	643	1082	1036	765	787	825
ENSMUSG00000029376	chr5	Mthfd2l	-0.7519176	0.002129194	0.004313323	1.913119609	0.052295562	-1	70	88	57	65	59	39	52	40	39	52
ENSMUSG00000031710	chr8	Ucp1	-3.1591918	0.002130109	0.004314551	2.297399878	1.005755512	-1	11	339	189	10	65	1	13	52	0	9
ENSMUSG00000051736	chr10	Fam229b	0.96846569	0.002130923	0.004315574	0.918462758	0.07736146	1	21	11	14	25	18	34	26	50	37	41
ENSMUSG00000028456	chr4	Unc13b	-0.6825267	0.002131307	0.004315727	2.238540982	0.044260086	-1	81	77	84	112	71	69	47	39	64	71
ENSMUSG00000007216	chr6	Zfp775	-0.5855571	0.00213312	0.004318772	2.965445317	0.034311869	-1	143	104	116	213	123	102	101	103	99	96
ENSMUSG00000034543	chr11	Morc2a	-0.4407456	0.002134116	0.004320163	4.445585632	0.021600767	-1	343	338	323	493	372	336	308	263	252	349
ENSMUSG00000031227	chrX	Magee1	0.77636107	0.002149578	0.004350833	2.098741949	0.060186611	1	51	47	30	68	35	94	102	91	48	94
ENSMUSG00000005981	chr16	Trap1	-0.4571761	0.002151874	0.00435485	7.126969016	0.026040064	-1	2285	2457	2284	3045	2011	2072	2028	1731	2019	1754
ENSMUSG00000022994	chr15	Adcy6	-0.4939218	0.002152656	0.004355801	5.194579229	0.029117241	-1	461	655	596	903	589	594	487	490	389	524
ENSMUSG00000029913	chr6	Prdm5	0.91779924	0.002154775	0.004359458	1.273262136	0.072330064	1	27	19	23	19	28	35	49	59	51	47
ENSMUSG00000097277	chr7	2900076A07Rik	-0.8017312	0.002155319	0.004359928	1.641415721	0.05690201	-1	60	41	49	85	53	41	28	46	28	35
ENSMUSG00000019917	chr10	Sept10	-0.5929625	0.002157659	0.00436403	3.301301569	0.037445365	-1	182	172	189	192	135	94	129	119	142	146
ENSMUSG00000004642	chr5	Slbp	0.59378218	0.002160055	0.004368244	3.516847128	0.038471711	1	150	122	134	157	109	293	289	170	209	158
ENSMUSG00000019906	chr10	Lin7a	-0.95099	0.002163963	0.004375513	1.194622948	0.08076978	-1	37	42	21	54	60	31	22	26	20	22
ENSMUSG00000028629	chr4	Exo5	0.81052664	0.002165345	0.004377674	1.555266759	0.056590543	1	34	31	31	32	23	51	81	41	58	61
ENSMUSG00000042423	chr7	Fbrs	0.51093625	0.002165661	0.004377679	4.45552411	0.030049234	1	237	203	248	376	285	580	402	382	323	423
ENSMUSG00000090222	chr1	Gm16340	-1.1180257	0.002167635	0.004381036	0.689683207	0.109029334	-1	20	39	37	38	19	9	10	22	15	20
ENSMUSG00000026641	chr1	Usf1	0.43099652	0.002169642	0.004384459	4.533458798	0.020716336	1	303	272	256	357	276	522	393	418	394	436
ENSMUSG00000026377	chr1	Nifk	0.45271554	0.002176295	0.004397268	4.546422455	0.023237414	1	324	283	250	366	246	534	422	431	431	375
ENSMUSG00000032215	chr9	Rsl24d1	0.45126198	0.002180241	0.004404605	5.202306378	0.024051912	1	526	447	446	498	385	800	713	643	704	600
ENSMUSG00000023019	chr15	Gpd1	-0.7076628	0.002180724	0.004404942	9.854881559	0.063148593	-1	17996	16190	15407	18360	17152	6072	11427	10314	11395	17825
ENSMUSG00000020335	chr11	Zfp354b	-1.0065861	0.002187379	0.004417747	0.923694803	0.085928467	-1	37	36	25	44	36	9	19	14	24	30
ENSMUSG00000081855	chr5	Rpl17-ps5	1.50706766	0.002188152	0.00441867	-0.33145534	0.150807904	1	6	3	6	4	6	22	16	7	28	7
ENSMUSG00000024740	chr19	Ddb1	0.4677814	0.002193402	0.004428632	7.987946845	0.027600366	1	3146	2847	2672	4217	3089	5270	4454	4939	4201	5172
ENSMUSG00000039985	chr6	Fam60a	1.0597994	0.002194487	0.004430181	0.880972452	0.096252628	1	17	18	22	13	11	43	61	32	28	25
ENSMUSG00000043943	chr9	Naalad2	-0.5352687	0.002207801	0.004456417	3.387081764	0.029877462	-1	158	164	205	231	155	156	144	142	127	120
ENSMUSG00000036995	chr4	Asap3	0.60727452	0.002208655	0.004457496	2.8561759	0.036968011	1	91	79	63	91	94	136	126	143	149	143
ENSMUSG00000083344	chr7	Gm7363	1.30161248	0.002209623	0.004458806	-0.04582589	0.125311408	1	8	9	7	11	1	30	17	21	20	9
ENSMUSG00000053080	chr19	2700081O15Rik	-0.5002775	0.002216357	0.004471748	4.030195183	0.027980396	-1	256	312	258	318	267	275	245	197	157	231
ENSMUSG00000000149	chr5	Gna12	0.50113173	0.002217154	0.004472711	5.687188546	0.030670062	1	579	569	700	773	547	1429	912	823	813	993
ENSMUSG00000038241	chr2	Cep250	0.50347192	0.002217752	0.004473271	3.570926417	0.026374498	1	153	144	126	159	140	230	248	170	208	274
ENSMUSG00000079037	chr2	Prnp	-0.4938395	0.002219935	0.004477028	6.931394711	0.030569601	-1	2533	2008	1780	2244	2023	1794	1595	1560	1296	2053
ENSMUSG00000048701	chr10	Ccdc6	-0.5331161	0.002221502	0.004479544	6.167330264	0.035302767	-1	1056	1112	1019	1786	1399	1146	1026	906	645	1098
ENSMUSG00000019872	chr10	Smpdl3a	-0.5602835	0.002223427	0.004482778	5.646693269	0.03868897	-1	993	948	834	889	745	598	733	423	662	900
ENSMUSG00000098381	chr3	Mir7225	-0.4902133	0.002226691	0.004488712	7.808494507	0.030376645	-1	3749	3291	3140	5409	4082	3855	3090	2676	2470	3235
ENSMUSG00000026637	chr1	Traf5	0.69699512	0.002228177	0.004491059	2.181196251	0.044876562	1	60	50	54	51	34	110	86	74	75	102
ENSMUSG00000043079	chr18	Synpo	-0.6101367	0.002231694	0.0044975	6.601160551	0.046669759	-1	1349	1265	1359	2971	1965	1647	1267	1281	1070	1020
ENSMUSG00000038619	chr3	Ensa	-0.4853027	0.002235266	0.004504049	7.349085937	0.029677776	-1	3087	2710	2544	3252	2561	2072	2284	1708	2472	2550
ENSMUSG00000015711	chr3	Prune	-0.4795948	0.002240286	0.004512913	6.523098928	0.028679908	-1	1635	1564	1382	2032	1399	1524	1098	955	1447	1263
ENSMUSG00000084523	chr8	Mir1903	-1.3692539	0.002240311	0.004512913	-0.175416736	0.138948579	-1	6	22	17	17	20	4	11	3	6	11
ENSMUSG00000027404	chr2	Snrpb	0.43998435	0.002244765	0.004520687	7.053200906	0.024273363	1	1649	1591	1547	2159	1482	3047	2448	2231	2388	2400
ENSMUSG00000028397	chr4	Kdm4c	-0.5258345	0.002244817	0.004520687	3.283389762	0.028667413	-1	155	154	171	215	153	143	152	103	100	150
ENSMUSG00000030423	chr7	Pop4	0.55136549	0.002245357	0.004521122	3.637984943	0.033080765	1	167	159	142	167	109	282	283	176	260	199
ENSMUSG00000006699	chr4	Cdc42	0.45028055	0.002246707	0.004522557	8.109548008	0.025703902	1	3790	3368	3067	4206	3003	5864	5448	4407	5218	5157
ENSMUSG00000031029	chr7	Eif3f	0.50088866	0.002246717	0.004522557	7.125279939	0.031589843	1	1644	1494	1349	2367	1821	3609	2563	2501	2108	2661
ENSMUSG00000035376	chr16	Ptplb	0.79419955	0.002247255	0.00452299	2.199985488	0.063784129	1	49	62	40	38	50	102	134	70	68	91
ENSMUSG00000023961	chr17	Enpp4	-0.6009478	0.002248388	0.00452407	5.454581723	0.044448736	-1	797	763	678	999	709	325	678	583	541	684
ENSMUSG00000032714	chr10	Syde1	0.59681476	0.002248439	0.00452407	3.508738207	0.039097368	1	130	141	114	158	124	352	211	210	171	172
ENSMUSG00000019997	chr10	Ctgf	1.65450071	0.002249756	0.004526067	5.504718364	0.327707277	1	270	351	287	531	219	4192	747	278	531	229
ENSMUSG00000015656	chr9	Hspa8	0.51211353	0.002260531	0.004547091	9.56593944	0.033463575	1	10180	8235	6963	12393	9177	13628	17192	14798	13281	13569

ENSMUSG00000005370	chr17	Msh6	0.5990681	0.002262191	0.004549774	2.997074878	0.037489884	1	98	99	74	134	66	197	159	126	166	127
ENSMUSG00000038526	chr3	Car14	-0.540329	0.002263841	0.004551783	5.183884338	0.035450891	-1	526	563	479	1003	678	481	427	381	584	535
ENSMUSG00000097960	chr8	A330074K22Rik	-1.0933946	0.002263672	0.004551783	0.924762382	0.106195632	-1	31	24	37	77	18	17	17	21	14	23
ENSMUSG00000030007	chr6	Cct7	0.44525109	0.002264315	0.004552081	7.136845469	0.024938796	1	1758	1728	1527	2248	1646	2998	2910	2377	2566	2407
ENSMUSG00000004814	chr5	Ccl24	1.49829599	0.002265369	0.004553545	1.89571776	0.250133466	1	25	45	27	17	21	206	125	34	60	20
ENSMUSG00000081752	chrX	Gm14680	-0.5878029	0.002265842	0.00455384	3.113755599	0.035840913	-1	164	142	150	178	130	86	100	113	123	131
ENSMUSG00000018900	chr11	Slc22a5	-0.5352246	0.002282842	0.004587347	3.580153055	0.031005462	-1	170	218	208	250	196	151	184	121	183	150
ENSMUSG00000059049	chr4	Frem1	-0.93702	0.002284105	0.004589225	1.545123265	0.085932867	-1	50	49	60	69	47	37	30	35	10	46
ENSMUSG00000081534	chr15	Slc48a1	0.45317555	0.002295884	0.00461223	5.968003415	0.025335071	1	787	740	642	1057	734	1325	1129	935	1116	1421
ENSMUSG00000039715	chr2	Wdr34	0.72385683	0.002300079	0.004619767	2.509541335	0.054571902	1	93	39	50	66	64	124	116	121	103	100
ENSMUSG00000049744	chr2	Arhgap15	1.07360169	0.002300298	0.004619767	0.352419741	0.074614873	1	13	8	16	9	8	28	31	18	22	28
ENSMUSG00000043015	chr1	Tmem194b	1.01763408	0.002315748	0.004650128	0.751644434	0.083896695	1	15	20	10	11	19	43	33	40	29	24
ENSMUSG00000030842	chr7	Lamtor1	0.44768611	0.00231645	0.00465087	6.87449122	0.025221544	1	1656	1517	1321	1623	1257	2586	2132	1902	2075	2392
ENSMUSG00000030083	chr6	Abtb1	0.4888952	0.002318356	0.004654028	4.807745141	0.028309532	1	432	352	310	360	270	601	430	489	523	618
ENSMUSG00000028322	chr4	Exosc3	0.54272805	0.002320274	0.004657209	3.290457119	0.031020957	1	115	107	102	153	111	233	209	146	202	148
ENSMUSG00000032782	chr11	Cntrob	0.77951257	0.002321782	0.004659568	2.134597944	0.061100763	1	53	36	58	49	36	110	83	109	68	68
ENSMUSG00000022797	chr16	Tfrc	-0.63963	0.002328269	0.004671914	8.202539801	0.052204799	-1	4108	4145	6191	8544	4150	2661	4433	3916	3553	4082
ENSMUSG00000046572	chr5	Zfp518b	-0.6183514	0.00233272	0.004680174	2.385709864	0.035875252	-1	96	78	83	122	85	81	68	58	50	74
ENSMUSG00000041895	chr11	Wipi1	-0.4872661	0.0023405	0.004695111	5.893824917	0.029458318	-1	1001	931	936	1426	913	686	776	755	752	1057
ENSMUSG00000043716	chr1	Rpl7	0.47234894	0.002346029	0.004705526	8.424403809	0.028583859	1	4809	4266	3927	4900	3537	7597	6890	5715	6664	5778
ENSMUSG00000038302	chr10	Lace1	-0.5396774	0.002360803	0.004734478	4.088799975	0.033567818	-1	279	346	307	368	196	200	245	188	250	239
ENSMUSG00000022314	chr15	Rad21	-0.4497236	0.002366824	0.004745872	6.120488734	0.025186885	-1	1179	1128	1028	1659	1041	969	1065	875	806	1089
ENSMUSG00000024969	chr19	Mark2	-0.4499372	0.002377611	0.004766818	5.289192648	0.024536956	-1	594	619	676	907	578	701	534	451	469	556
ENSMUSG00000003526	chr16	Prodh	0.72898407	0.002379163	0.004769245	1.961376173	0.049946342	1	35	46	37	49	43	112	69	55	78	72
ENSMUSG00000038670	chr7	Mybpc2	-0.6165018	0.002384097	0.004778451	12.30991475	0.048969199	-1	115036	80717	71314	95518	93701	45724	69864	55973	63941	90811
ENSMUSG00000035770	chr8	Dync1li2	-0.4293055	0.00238957	0.004788048	6.457481677	0.023132329	-1	1493	1438	1338	1905	1361	1342	1257	1059	1202	1259
ENSMUSG00000057572	chr4	Zbtb8os	0.54799393	0.00238957	0.004788048	3.462128788	0.032784535	1	160	124	100	178	104	208	229	159	246	214
ENSMUSG00000005034	chr3	Prkacb	-0.4364624	0.00239185	0.004791928	5.52239248	0.023259315	-1	736	713	686	1069	753	694	688	519	566	730
ENSMUSG00000056687	chr11	Gm11696	1.25830729	0.002393587	0.004794722	0.195516953	0.131220027	1	12	8	5	17	3	40	18	12	16	32
ENSMUSG00000018921	chr11	Pelp1	0.44943204	0.002394285	0.004794928	4.632136462	0.023511005	1	313	269	274	408	298	518	485	501	372	448
ENSMUSG00000059518	chr5	Znhit1	0.4412701	0.002394376	0.004794928	4.938733352	0.023079912	1	448	369	341	481	302	725	555	504	573	525
ENSMUSG00000001665	chr10	Gstt3	0.71048954	0.002401211	0.004807926	2.468369137	0.052091873	1	49	80	43	69	63	101	94	107	102	142
ENSMUSG00000036934	chr8	4921524J17Rik	-0.5819517	0.002401565	0.004807946	3.265320552	0.036646402	-1	184	159	124	215	171	98	142	99	122	160
ENSMUSG00000019726	chr13	Lyst	-1.0786962	0.002402606	0.004809342	2.056837095	0.129272644	-1	59	90	75	109	78	21	69	13	52	58
ENSMUSG00000063765	chr15	Chadl	0.97409824	0.002404409	0.004812262	0.583469913	0.071564611	1	10	8	13	23	15	36	23	29	24	36
ENSMUSG00000021038	chr12	Vipas39	0.51824014	0.002406164	0.004815085	3.728472942	0.029676249	1	164	177	143	208	117	271	303	175	249	271
ENSMUSG00000025425	chr18	St8sia5	-0.5764481	0.002406714	0.004815495	4.561085468	0.040040266	-1	411	396	321	560	422	193	368	275	310	385
ENSMUSG00000047022	chr12	Mipol1	-0.8034619	0.002412421	0.004826223	1.439060586	0.056250409	-1	49	42	45	54	55	22	37	24	33	38
ENSMUSG00000001383	chr18	Zmat2	0.46883879	0.002423911	0.004848515	6.383923241	0.027725976	1	1238	988	932	1131	912	1860	1581	1398	1664	1410
ENSMUSG00000030730	chr7	Atp2a1	-0.5943518	0.002427815	0.004855631	14.80779139	0.045719842	-1	518484	428238	382546	619754	621197	333354	363614	355946	284706	530543
ENSMUSG00000025078	chr19	Nhlrc2	-0.6363542	0.002442847	0.004883636	2.625760646	0.041443244	-1	96	109	108	124	110	101	87	47	74	82
ENSMUSG00000073557	chr1	Ppp1r12b	-0.6265662	0.002442209	0.004883636	7.896945997	0.050528911	-1	3398	3493	3668	7270	4167	2227	3042	3264	2576	4090
ENSMUSG00000085525	chr4	Gm13166	-1.6197312	0.002442866	0.004883636	-0.235353231	0.227429381	-1	22	15	20	14	11	20	2	3	4	1
ENSMUSG00000021719	chr13	Rgs7bp	-1.1362808	0.002444155	0.004885513	0.265159967	0.100558053	-1	13	19	19	34	27	16	10	15	9	5
ENSMUSG00000028741	chr4	Mrto4	0.4833915	0.00244592	0.004888342	4.645840016	0.027663269	1	288	270	260	384	346	580	542	425	454	376
ENSMUSG00000049047	chrX	Armcx3	-0.463484	0.002451292	0.004898379	4.376621812	0.024680439	-1	361	303	317	450	358	240	311	262	297	302
ENSMUSG00000003531	chr16	Dgcr6	0.42090263	0.002453781	0.004902651	4.87860079	0.020829598	1	368	362	330	486	330	680	488	484	552	542
ENSMUSG00000029726	chr5	Mepce	0.48434597	0.002455359	0.004905102	4.703102542	0.027986857	1	339	278	247	447	315	678	461	445	374	532
ENSMUSG00000025612	chr16	Bach1	-0.4856714	0.002456682	0.004907045	4.210096372	0.027141003	-1	313	320	302	432	245	257	299	179	225	299
ENSMUSG00000054469	chr17	Lclat1	-0.4791741	0.002459878	0.004912725	3.992622539	0.025780772	-1	253	249	223	367	287	273	239	169	202	202
ENSMUSG00000037364	chr5	Srrt	0.48143547	0.002463458	0.004919173	5.204678304	0.028397867	1	423	385	404	648	446	902	752	606	710	539
ENSMUSG00000024993	chr19	Fam45a	-0.5871651	0.002463819	0.00491919	3.12655689	0.037176718	-1	158	165	143	170	133	109	125	70	131	129
ENSMUSG00000029111	chr5	Nelfa	0.49724599	0.00246576	0.00492166	3.474541635	0.026090215	1	138	116	103	178	147	241	215	190	186	221
ENSMUSG00000038371	chr7	Sbf2	-0.4891178	0.002465613	0.00492166	3.989403272	0.0270819	-1	257	261	278	344	235	235	224	152	192	276
ENSMUSG00000021876	chr14	Rnase4	0.48254662	0.002482897	0.004955157	5.506638457	0.028826229	1	579	625	573	571	449	1040	901	672	909	811
ENSMUSG00000031889	chr8	D230025D16Rik	-0.4351047	0.002484704	0.004958057	4.455700009	0.021744364	-1	386	377	326	446	337	316	354	231	295	325
ENSMUSG00000097906	chr13	Gm9625	-1.5420496	0.002487104	0.004962136	4.753966399	0.29197255	-1	688	567	509	638	569	860	87	78	74	99
ENSMUSG00000022367	chr15	Has2	1.04198732	0.00248911	0.00496543	1.214480927	0.104147619	1	10	20	30	25	20	88	45	30	38	43
ENSMUSG00000014592	chr4	Camta1	-0.5605416	0.00249233	0.004971143	4.261739473	0.037374235	-1	239	301	289	596	307	329	242	238	228	226
ENSMUSG00000027968	chr3	Larp7	0.50783794	0.002496994	0.004979736	3.610352219	0.028156354	1	134	155	126	210	125	230	263	230	236	195
ENSMUSG00000020454	chr11	Eif4enif1	-0.441017	0.002498032	0.004981094	4.765659778	0.022962838	-1	454	477	432	579	389	346	433	311	388	397
ENSMUSG00000018398	chr11	Sept8	0.42409993	0.002499736	0.004983782	5.053461995	0.021432132	1	413	381	377	485	443	718	652	493	560	690
ENSMUSG00000071648	chr19	Rom1	0.67253369	0.002502171	0.004987926	3.006662962	0.050164589	1	80	87	78	126	86	113	140	163	138	235
ENSMUSG00000042502	chr7	Cd2bp2	0.42464879	0.002505162	0.004993174	5.384642848	0.021972537	1	596	484	450	617	504	917	762	695	723	813
ENSMUSG00000022412	chr15	Mief1	-0.4335542	0.00251788	0.005017809	4.691716926	0.022048848	-1	403	401	420	621	378	444	372	306	334	340

ENSMUSG00000026489	chr1	Adck3	-0.7295309	0.002518812	0.00501895	9.079806996	0.068943328	-1	5771	10657	9984	17939	7153	9135	4838	7513	6502	5201
ENSMUSG00000079610	chr1	Ankrd39	0.65409	0.002520429	0.005021455	2.649621165	0.043895082	1	71	80	66	63	71	123	111	127	140	108
ENSMUSG00000024758	chr19	Rtn3	0.45614839	0.002525773	0.005031386	6.104937441	0.026253926	1	806	824	745	1066	879	1660	1394	1000	1230	1254
ENSMUSG00000032398	chr9	Snapc5	0.53670686	0.002526185	0.00503149	4.24207274	0.034102232	1	248	254	213	262	166	277	417	320	415	376
ENSMUSG00000023267	chr4	Gabrr2	1.31082283	0.002531329	0.005041016	1.355336293	0.183095714	1	26	18	13	19	26	64	35	13	58	116
ENSMUSG00000067430	chr17	Zfp763	-1.0400651	0.002537866	0.005053314	1.418296632	0.110956246	-1	61	38	63	60	35	10	40	21	26	39
ENSMUSG00000028309	chr4	Rnf20	-0.416846	0.002539987	0.005056818	4.901485712	0.020545656	-1	515	476	453	618	478	399	418	382	445	432
ENSMUSG00000027371	chr2	Fahd2a	-0.4777873	0.002543759	0.005063606	4.378319027	0.026747627	-1	357	398	354	419	266	353	255	239	308	260
ENSMUSG00000024941	chr19	Scyl1	-0.4492072	0.002549814	0.005074935	6.189187987	0.025552996	-1	1254	1101	1183	1688	1087	944	1080	876	1046	1076
ENSMUSG00000054693	chr9	Adam10	-0.4704076	0.002554969	0.005084473	4.992281739	0.02698204	-1	548	552	549	677	426	419	539	323	390	510
ENSMUSG00000005465	chr8	Il27ra	1.20258705	0.002559877	0.005093514	0.387161938	0.121165412	1	10	5	14	17	7	34	28	19	11	43
ENSMUSG00000051147	chr8	Nat2	1.07852765	0.002560611	0.005094248	0.624791066	0.097057662	1	21	13	10	14	9	44	35	13	26	40
ENSMUSG00000056144	chr7	Trim34a	1.18244552	0.002564002	0.005100268	1.472976819	0.149782992	1	33	27	24	15	19	18	70	63	54	91
ENSMUSG00000027832	chr3	Ptx3	0.60899789	0.00256581	0.005103139	4.238262815	0.044739336	1	250	223	248	213	162	581	391	294	341	261
ENSMUSG00000030878	chr7	Cdr2	0.72244624	0.002567075	0.005104929	3.062932251	0.059223927	1	83	103	102	103	69	278	165	112	178	113
ENSMUSG00000068141	chr17	Gm10232	0.85295998	0.002576973	0.005123883	0.966781624	0.054762534	1	20	15	21	27	14	48	39	29	41	35
ENSMUSG00000036528	chr7	Ppfibp2	-0.5394131	0.002587555	0.00514404	3.572341892	0.032578607	-1	180	207	167	346	162	200	164	126	148	151
ENSMUSG00000064370	chrMT	mt-Cytb	-0.5848515	0.002587847	0.00514404	13.24848489	0.044846412	-1	149407	172942	167519	262542	130290	95313	115698	122256	154011	142137
ENSMUSG00000032026	chr9	Rexo2	0.46834785	0.002588297	0.005144204	5.629892185	0.027503462	1	684	606	522	738	545	995	1055	713	1063	861
ENSMUSG00000023912	chr17	Slc25a27	-0.6992316	0.002590676	0.005148199	2.083502623	0.047592939	-1	80	77	86	73	61	47	53	42	60	54
ENSMUSG00000004947	chr5	Dtx2	0.58937665	0.002597545	0.005161116	3.227154272	0.038392617	1	102	90	89	162	112	276	162	146	149	183
ENSMUSG00000024797	chr19	Vps51	0.46159115	0.002603798	0.005172804	4.197636665	0.02435595	1	216	212	196	290	231	457	338	319	269	352
ENSMUSG00000029096	chr5	Htra3	0.5087729	0.002606828	0.005178088	5.75158402	0.032782205	1	660	632	602	749	652	1334	909	1078	679	1184
ENSMUSG00000014551	chr6	Mrps25	0.43233492	0.002610009	0.00518367	4.840089646	0.022373835	1	338	362	336	496	291	620	570	501	524	461
ENSMUSG00000073176	chrX	Zfp449	-0.7166024	0.002617266	0.005197344	2.382113276	0.052996047	-1	80	68	84	146	100	52	57	56	78	70
ENSMUSG00000028851	chr4	Nudc	0.42470843	0.002618767	0.005199582	5.568357957	0.022433889	1	582	554	509	821	568	968	951	788	891	833
ENSMUSG00000039982	chr19	Dtx4	0.50276643	0.002619137	0.005199582	4.32588657	0.029852536	1	182	249	232	301	261	457	361	396	288	410
ENSMUSG00000019864	chr10	Rtn4ip1	-0.4429249	0.002626837	0.005214127	4.987072687	0.023741417	-1	480	539	525	753	438	457	427	465	408	423
ENSMUSG00000024188	chr17	Luc7l	0.52842096	0.002627359	0.005214167	3.948772305	0.032208497	1	180	177	171	201	199	427	288	245	296	230
ENSMUSG00000026255	chr1	Efhd1	-0.7136248	0.002627603	0.005214167	2.344401919	0.052743137	-1	67	79	71	148	101	76	54	67	51	59
ENSMUSG00000038538	chr6	Ubn2	-0.4192534	0.002631245	0.005220653	4.911784545	0.021041149	-1	543	458	446	589	517	470	393	411	369	454
ENSMUSG00000028291	chr4	Akirin2	0.46208352	0.002632688	0.005222775	4.902952183	0.0259886	1	412	325	302	504	341	721	608	544	406	557
ENSMUSG00000054312	chr3	Mrps21	0.43987701	0.002637034	0.005230653	6.028059746	0.024570598	1	896	728	669	1099	761	1439	1179	1186	1148	1176
ENSMUSG00000025784	chr9	Clec3b	0.54290242	0.002642203	0.005240164	6.339011715	0.037997684	1	929	964	823	1037	1110	1768	1250	1737	1162	1912
ENSMUSG00000045671	chr11	Spred2	-0.4847434	0.002642694	0.005240392	3.677846252	0.025667708	-1	218	230	207	288	166	190	188	175	138	173
ENSMUSG00000016833	chr5	Mrps18c	0.46564327	0.002644143	0.005242522	4.672982894	0.026116838	1	357	302	284	424	236	469	549	423	525	432
ENSMUSG00000025938	chr1	Slco5a1	-0.5554917	0.002648066	0.005249556	5.23146462	0.038818062	-1	553	562	715	964	558	373	525	603	433	516
ENSMUSG00000079362	chr5	Gbp6	-0.9584185	0.002655907	0.005264354	1.277313441	0.087928765	-1	39	57	48	47	35	19	17	22	24	46
ENSMUSG00000020079	chr10	Supv3l1	-0.5082803	0.002662133	0.005275946	3.987636219	0.029832631	-1	227	239	283	411	233	191	248	202	189	230
ENSMUSG00000020659	chr12	Cbll1	-0.5954289	0.002674776	0.00530025	3.10262776	0.038774373	-1	125	131	119	239	157	108	130	93	89	133
ENSMUSG00000042029	chr12	Ncapg2	0.85432439	0.002681456	0.005312735	2.110616368	0.078124684	1	46	61	31	55	30	67	135	69	99	68
ENSMUSG00000026791	chr2	Slc2a8	0.57748817	0.002686502	0.005321978	3.510656405	0.038208653	1	114	173	127	172	90	267	177	225	213	219
ENSMUSG00000021975	chr14	Ints9	0.45334732	0.002688547	0.005325273	3.78668853	0.022263515	1	180	164	155	208	154	313	243	253	245	237
ENSMUSG00000029093	chr5	Sorcs2	0.69294634	0.002691241	0.005329854	3.192810747	0.055390493	1	96	100	95	117	103	222	175	196	84	238
ENSMUSG00000025092	chr19	Hspa12a	-0.6596183	0.002708931	0.005364128	3.020278882	0.049002579	-1	110	153	154	160	147	73	89	118	103	118
ENSMUSG00000001249	chr7	Hpn	-0.6134861	0.002711825	0.005369099	3.093630733	0.041918135	-1	136	160	165	209	95	135	85	100	117	107
ENSMUSG00000025008	chr19	Tctn3	0.72901097	0.002712881	0.005370428	1.789027451	0.049386851	1	45	35	33	52	23	88	58	59	61	74
ENSMUSG00000018449	chr11	Rpain	0.64200005	0.002716779	0.005377384	2.820466961	0.043994509	1	95	88	77	71	68	175	135	97	156	130
ENSMUSG00000015759	chr14	Cnih1	0.42789573	0.002717524	0.005378097	5.901900661	0.023213422	1	779	755	648	888	720	1251	1269	1023	952	1110
ENSMUSG00000042784	chr3	Muc1	1.3592102	0.002719073	0.0053804	-0.310426708	0.131063423	1	3	5	7	9	4	26	9	20	17	7
ENSMUSG00000034709	chr17	Ppp1r21	0.57942314	0.002720178	0.005381824	3.375033483	0.037618129	1	111	123	116	146	115	286	221	143	211	149
ENSMUSG00000031508	chr8	Ankrd10	0.47498271	0.002721163	0.005383012	4.851661633	0.027662249	1	360	305	374	442	313	634	489	629	507	459
ENSMUSG00000091580	chr16	Gm6467	0.81081396	0.00272651	0.005392825	1.230617198	0.054195357	1	31	19	22	30	18	63	43	34	39	53
ENSMUSG00000002496	chr17	Tsc2	-0.464834	0.002740172	0.00541908	5.910138857	0.027639565	-1	934	872	936	1360	1101	775	812	818	741	963
ENSMUSG00000026999	chr2	Nup35	-0.6044663	0.002743233	0.005424367	3.524831246	0.042463673	-1	208	174	184	269	195	172	162	98	201	106
ENSMUSG00000026173	chr1	Plcd4	-0.7226051	0.002748912	0.005434826	6.793784852	0.068367679	-1	2639	1998	1824	1811	1901	667	1543	1192	1691	1657
ENSMUSG00000071646	chr19	Mta2	0.4280999	0.002753706	0.005443535	5.518918572	0.022956502	1	592	589	532	695	500	1109	835	758	769	836
ENSMUSG00000025145	chr11	Lrrc45	0.64172075	0.002756341	0.005447751	2.654664505	0.042982633	1	85	74	67	73	58	161	89	109	128	128
ENSMUSG00000038418	chr18	Egr1	1.03368321	0.002756618	0.005447751	4.632314929	0.136371227	1	296	256	268	213	159	664	1183	335	172	407
ENSMUSG00000031862	chr8	Atp13a1	0.46321012	0.002760767	0.005455179	4.467481187	0.025548321	1	260	232	232	361	298	550	435	366	378	364
ENSMUSG00000029838	chr6	Ptn	1.0167405	0.002763364	0.005459538	3.083017734	0.126575351	1	133	72	67	100	43	140	154	130	95	401
ENSMUSG00000024593	chr18	Megf10	-0.8714946	0.002772067	0.005475909	2.750371203	0.089140768	-1	161	140	114	108	108	64	71	107	32	106
ENSMUSG00000027131	chr2	Emc4	-0.5110855	0.002772826	0.005475909	5.248620229	0.03308227	-1	811	653	607	652	575	433	603	384	533	600
ENSMUSG00000055917	chr12	Zfp277	0.79145442	0.002772524	0.005475909	2.731415296	0.072583847	1	57	65	65	108	64	67	144	121	176	157
ENSMUSG00000020956	chr12	Dtd2	0.67414311	0.002776831	0.005483046	2.596654153	0.049083981	1	72	54	64	98	55	122	93	100	103	178

ENSMUSG00000029482	chr5	Aacs	0.57903161	0.002777996	0.005484219	3.359968285	0.037498105	1	114	154	96	105	128	210	208	197	189	185
ENSMUSG00000039286	chr3	Fndc3b	-0.4716152	0.002778211	0.005484219	4.360500037	0.026529893	-1	344	324	338	444	323	289	298	192	259	369
ENSMUSG00000031246	chrX	Sh3bgrl	0.52887572	0.002795397	0.005517365	4.865809001	0.0349695	1	389	327	332	433	295	593	793	351	452	640
ENSMUSG00000032715	chr2	Trib3	0.94684719	0.002802172	0.005529957	0.857366134	0.07576282	1	19	18	11	25	13	50	27	24	47	33
ENSMUSG00000030189	chr6	Ybx3	-0.494263	0.002803369	0.005531539	9.015510815	0.032513781	-1	8281	7462	6920	13081	9844	8213	7296	6195	6172	7360
ENSMUSG00000025384	chr11	2310003H01Rik	-0.4497791	0.002808417	0.005540716	4.146442956	0.023308607	-1	286	294	299	360	273	222	256	208	248	279
ENSMUSG00000024528	chr18	Srfbp1	-0.5318144	0.002813781	0.005550515	2.875604251	0.028189381	-1	131	118	115	171	106	107	94	82	99	101
ENSMUSG00000036777	chr9	Anln	0.94504488	0.002817477	0.005557023	2.375266611	0.102563718	1	61	48	36	45	64	96	197	91	103	55
ENSMUSG00000053898	chr7	Ech1	-0.5515976	0.002825915	0.005572877	7.37780896	0.040245303	-1	2182	3005	2863	4618	2283	2372	1837	1872	2682	2222
ENSMUSG00000004936	chr9	Map2k1	-0.5018449	0.002834173	0.005588374	6.206164827	0.03281779	-1	1444	1296	1133	1457	1106	823	1026	883	899	1348
ENSMUSG00000026785	chr2	Pkn3	0.62654208	0.002842996	0.00560419	2.575672005	0.040761957	1	61	75	58	100	51	160	102	104	103	112
ENSMUSG00000072582	chr11	Ptrh2	0.44051342	0.002842884	0.00560419	4.021427423	0.021914837	1	217	210	177	247	170	325	289	272	304	325
ENSMUSG00000075033	chr16	Nxpe3	1.03868018	0.002850093	0.005617388	0.46056259	0.084383542	1	12	16	12	12	8	42	23	20	33	19
ENSMUSG00000031144	chrX	Syp	0.83036363	0.002850759	0.005617908	1.201381358	0.059951619	1	18	22	19	30	27	40	49	48	32	57
ENSMUSG00000024983	chr19	Vti1a	-0.4704321	0.002851956	0.005618683	4.029851538	0.025625336	-1	277	238	267	346	277	203	244	183	214	267
ENSMUSG00000074733	chr19	5830428H23Rik	0.84464738	0.002851878	0.005618683	2.11876275	0.07690163	1	41	42	36	54	51	61	69	95	134	75
ENSMUSG00000023938	chr17	Aars2	-0.4739112	0.002856713	0.005627262	4.466526922	0.027019091	-1	360	314	347	533	367	263	294	268	352	319
ENSMUSG00000026072	chr1	Il1r1	0.68283227	0.002858267	0.00562953	3.306950153	0.055113984	1	94	114	84	134	131	254	254	114	226	142
ENSMUSG00000024777	chr19	Ppp2r5b	-0.4110188	0.00286008	0.005632305	4.990890198	0.020624684	-1	516	482	491	693	522	462	430	398	412	522
ENSMUSG00000026618	chr1	Iars2	-0.5216047	0.00286269	0.005636652	6.146168027	0.035519495	-1	1217	1229	1149	1621	1031	705	938	802	1046	1229
ENSMUSG00000025162	chr11	Csnk1d	0.45445763	0.002897506	0.005704402	6.132705356	0.026850548	1	790	795	835	1157	843	1758	1277	1240	1109	1266
ENSMUSG00000008305	chr4	Tle1	-0.5194807	0.002897925	0.005704422	3.890794956	0.031816086	-1	213	218	258	381	235	249	158	154	196	237
ENSMUSG00000027074	chr2	Slc43a3	-0.4770805	0.002908676	0.005724779	4.333780357	0.027478765	-1	327	297	294	428	393	372	298	223	227	261
ENSMUSG00000011837	chr8	Snapc2	0.47235661	0.002910981	0.005728509	4.001206839	0.02580758	1	214	189	185	234	170	392	240	282	289	309
ENSMUSG00000023952	chr17	Gtpbp2	-0.4423761	0.00291763	0.005740785	5.845343263	0.025247596	-1	1031	950	954	1116	864	762	762	659	856	931
ENSMUSG00000002105	chr2	Slc39a13	0.4161197	0.002918818	0.005742315	5.049182382	0.021338574	1	488	386	370	476	384	668	601	631	549	626
ENSMUSG00000041936	chr4	Agrn	-0.5895269	0.002928635	0.005760817	4.656451581	0.044177181	-1	405	400	476	570	400	439	218	280	234	484
ENSMUSG00000001576	chr17	Ergic1	0.43612258	0.002930933	0.005764526	5.753696166	0.024454108	1	702	648	595	854	622	1019	1131	1040	811	1049
ENSMUSG00000046318	chr18	Ccbe1	0.90146866	0.0029331	0.005767976	1.690186533	0.08394422	1	42	20	44	31	22	96	72	50	40	75
ENSMUSG00000007812	chr5	Zfp655	-0.4864169	0.002934473	0.005769864	3.544013743	0.025902002	-1	173	217	192	269	159	166	178	136	145	162
ENSMUSG00000037461	chr1	Ints7	0.4852421	0.002941888	0.00578363	3.63046635	0.026129715	1	171	138	119	173	159	247	268	212	225	215
ENSMUSG00000019179	chr5	Mdh2	-0.4779628	0.002946517	0.005791916	9.981751073	0.030783458	-1	15850	16911	16563	25523	13921	14033	12750	13399	13421	15270
ENSMUSG00000021963	chr14	Sap18	0.42062771	0.002950877	0.00579967	5.502466126	0.022473689	1	604	580	497	725	488	959	889	751	850	781
ENSMUSG00000025393	chr10	Atp5b	-0.4939767	0.002976031	0.005848287	11.63912749	0.032985716	-1	47693	54880	54675	78969	44406	40908	39949	40957	42880	51043
ENSMUSG00000041915	chr18	Ammecr1l	-0.4893852	0.002985455	0.005865981	3.903015975	0.028047534	-1	227	247	224	375	233	275	188	146	192	217
ENSMUSG00000025059	chrX	Gyk	1.0854776	0.002985979	0.005866185	1.661690757	0.129403884	1	25	23	29	37	30	85	119	28	76	31
ENSMUSG00000039199	chr8	Zdhhc1	0.60360605	0.002996429	0.005884523	3.579224971	0.043342231	1	139	132	132	164	131	320	138	251	187	272
ENSMUSG00000039480	chr10	Nt5dc1	-0.7877051	0.002996576	0.005884523	2.135013341	0.066596292	-1	84	86	66	103	67	34	58	29	63	72
ENSMUSG00000044556	chr4	Tex38	1.09532595	0.002995974	0.005884523	0.381441178	0.095755592	1	8	16	8	12	11	26	23	31	13	37
ENSMUSG00000035407	chr4	Kank4	-0.8275521	0.002997062	0.005884651	1.190130443	0.059359743	-1	37	42	35	47	45	34	23	27	14	30
ENSMUSG00000026603	chr1	Smyd2	-0.4999809	0.00299805	0.005885763	7.199713652	0.03340544	-1	2182	2329	2092	4113	2344	2673	1775	1749	1863	1936
ENSMUSG00000032648	chr19	Pygm	-0.5631508	0.00300208	0.005892848	12.49044423	0.042881221	-1	96758	87124	78461	135184	116344	62278	74818	65949	68345	107847
ENSMUSG00000060798	chr3	Intu	-0.9749208	0.00300466	0.005897082	1.109310561	0.092200148	-1	39	41	52	38	30	23	23	15	37	14
ENSMUSG00000016921	chr2	Srsf6	0.44648859	0.003019032	0.005924458	6.120109935	0.026131526	1	968	724	771	1150	797	1559	1436	1188	1235	1137
ENSMUSG00000019933	chr10	2310015B20Rik	-0.7959742	0.003021673	0.005928808	5.42132812	0.083684354	-1	953	825	724	777	730	1157	456	320	295	406
ENSMUSG00000034206	chr16	Polq	1.13930454	0.00302219	0.005928991	0.08195432	0.090793517	1	7	7	8	13	8	27	26	16	25	10
ENSMUSG00000003955	chr16	Fam162a	0.41778739	0.003030737	0.00594409	5.390125335	0.022197437	1	528	499	486	723	452	770	787	754	758	827
ENSMUSG00000067365	chr5	Tmem128	0.55450269	0.003030466	0.00594409	3.346354676	0.035072217	1	156	108	100	160	88	250	212	166	196	155
ENSMUSG00000042348	chr13	Arl15	-0.5799863	0.003031664	0.005945074	2.960170612	0.036938036	-1	153	140	140	144	105	110	110	93	70	121
ENSMUSG00000039050	chr2	Osbpl2	-0.4226276	0.003033761	0.005948352	4.524268993	0.021474809	-1	370	379	389	495	327	383	316	259	290	359
ENSMUSG00000027298	chr2	Tyro3	0.76173229	0.003035223	0.005950383	1.499955571	0.051634804	1	30	21	33	38	27	48	54	55	64	54
ENSMUSG00000101320	chr18	Gm28529	-1.2287209	0.003043778	0.005966316	-0.087083161	0.111503222	-1	17	15	15	19	20	2	11	4	8	15
ENSMUSG00000049969	chr4	Plekhf2	0.49058923	0.003066206	0.006009436	3.785545612	0.027653501	1	167	157	169	211	144	272	300	174	265	299
ENSMUSG00000003269	chr7	Cyth2	0.48052295	0.003068613	0.006013311	4.332428971	0.028065279	1	240	250	251	310	197	547	337	365	320	347
ENSMUSG00000038607	chr4	Gng10	0.49517014	0.003072527	0.006020136	3.625264162	0.027901682	1	158	141	137	208	118	329	226	201	208	211
ENSMUSG00000035051	chr17	Dhx57	-0.4702752	0.003077379	0.006028799	3.565928999	0.024488862	-1	205	187	214	234	173	179	143	144	154	184
ENSMUSG00000039361	chr7	Picalm	-0.4990288	0.00308502	0.00604292	6.79865341	0.033360112	-1	2010	1759	1793	2469	1718	2085	1555	949	1550	1475
ENSMUSG00000029110	chr5	Rnf4	0.40961335	0.003086316	0.006044611	4.974519325	0.020798552	1	383	383	374	525	349	656	677	496	559	537
ENSMUSG00000055041	chr15	Commd5	0.58478003	0.00309082	0.006052586	3.289604431	0.039688123	1	142	108	127	133	66	225	176	165	203	177
ENSMUSG00000030752	chr7	Kdm8	-0.5267687	0.003093979	0.006057923	2.976086814	0.029245517	-1	126	145	113	172	128	119	99	82	111	109
ENSMUSG00000103458	chr18	PCDHA4	-0.6638536	0.003104031	0.006076752	2.968978036	0.050804993	-1	142	140	118	171	135	63	95	87	89	152
ENSMUSG00000020290	chr11	Xpo1	-0.5057327	0.0031051	0.006077994	5.070351693	0.032886831	-1	613	512	556	732	524	355	591	331	515	463
ENSMUSG00000027006	chr2	Dnajc10	-0.4589828	0.003107645	0.006082123	5.47636139	0.027321711	-1	804	758	675	961	650	788	660	431	638	560
ENSMUSG00000000355	chrX	Mcts1	0.47664216	0.00311044	0.006086742	4.913987919	0.028810421	1	469	382	347	422	254	604	599	479	631	538
ENSMUSG00000014763	chr17	Fam120b	-0.4773119	0.003123662	0.00611176	4.034972509	0.027042093	-1	308	290	217	361	245	228	199	179	233	274

ENSMUSG00000035310	chr5	Lin54	-0.6859004	0.003131844	0.006126911	2.234311381	0.049291063	-1	80	75	82	103	82	49	74	35	62	68
ENSMUSG00000029038	chr4	Ssu72	0.4488897	0.003140749	0.006143472	5.006534925	0.025455693	1	436	409	396	445	326	765	570	495	663	534
ENSMUSG00000003134	chr1	Tbc1d8	-0.4819745	0.00314281	0.006146643	3.986038188	0.027488452	-1	294	304	208	331	234	204	189	203	220	253
ENSMUSG00000031750	chr8	Il34	0.64237514	0.003144977	0.006150021	2.820294606	0.046204284	1	109	76	52	95	73	159	140	158	115	116
ENSMUSG00000087128	chr4	Gm12655	-0.8823893	0.003154004	0.00616681	0.958213487	0.06544948	-1	26	39	38	41	32	20	20	25	24	15
ENSMUSG00000081810	chr4	Gm11878	0.92106535	0.003183267	0.006223155	1.261636402	0.084020845	1	40	24	14	21	17	74	41	37	42	50
ENSMUSG00000032320	chr9	Rcn2	0.43969425	0.00319102	0.006237439	5.021717442	0.024495837	1	480	385	347	467	368	555	698	559	522	707
ENSMUSG00000021458	chr13	2010111I01Rik	0.50236875	0.003206242	0.006266318	4.993400285	0.032577778	1	396	360	369	549	303	953	593	486	534	507
ENSMUSG00000042660	chr18	Wdr55	0.4942149	0.003212194	0.006277026	3.540546238	0.027771487	1	135	120	120	198	144	250	263	171	219	200
ENSMUSG00000064302	chr1	Clasp1	-0.5175534	0.003212619	0.006277026	5.993622174	0.035735297	-1	1039	939	999	1378	1224	743	742	875	734	1165
ENSMUSG00000038429	chr6	Usp5	0.43232066	0.003217818	0.006286124	6.340210237	0.024922325	1	1094	867	887	1346	970	1786	1501	1402	1482	1427
ENSMUSG00000053253	chr14	Ndfip2	-0.4574737	0.003218175	0.006286124	3.88182755	0.024383836	-1	268	237	238	302	218	214	215	151	181	251
ENSMUSG00000001435	chr10	Col18a1	0.55638228	0.003250178	0.006347749	5.337561749	0.040889437	1	488	459	425	589	472	936	727	931	427	906
ENSMUSG00000040296	chr4	Ddx58	0.52381017	0.003259477	0.00636502	3.141657295	0.030000665	1	113	100	101	141	80	185	182	140	133	202
ENSMUSG00000028188	chr3	Spata1	-0.9170482	0.003261572	0.006368221	0.875564168	0.071332025	-1	28	29	36	39	35	13	15	22	26	20
ENSMUSG00000030982	chr7	9030624J02Rik	0.4122062	0.003272818	0.006389287	4.737311838	0.020999193	1	332	289	292	446	346	556	528	445	481	468
ENSMUSG00000038400	chr2	Pmepa1	0.88338698	0.003278626	0.006399732	4.952276264	0.103991511	1	279	262	256	460	370	1364	487	763	253	456
ENSMUSG00000025894	chr9	Aasdhppt	-0.5177152	0.003281421	0.006404293	4.009275145	0.032769302	-1	286	248	274	349	249	162	222	181	218	288
ENSMUSG00000055994	chr8	Nod2	0.92105588	0.003283054	0.006406585	0.835344233	0.07298245	1	17	19	22	15	11	29	39	39	38	30
ENSMUSG00000022178	chr14	Ajuba	0.64735622	0.003283681	0.006406914	2.64184846	0.046491985	1	65	73	45	102	73	118	121	123	91	156
ENSMUSG00000038085	chr2	Cnbd2	0.8985469	0.003284464	0.006407548	2.011334621	0.091272735	1	57	33	51	27	31	52	78	89	99	91
ENSMUSG00000020514	chr11	Mrpl22	0.45728339	0.003290381	0.006418195	4.400796093	0.025723405	1	291	242	287	306	192	413	400	389	401	375
ENSMUSG00000062683	chr15	Atp5g2	0.44530545	0.00330168	0.006439335	7.131468735	0.026963066	1	1739	1841	1588	2108	1567	3166	2436	2757	2270	2568
ENSMUSG00000004151	chr12	Etv1	-0.9187727	0.003312811	0.006459243	1.305899743	0.086996125	-1	57	50	48	45	29	43	29	21	28	13
ENSMUSG00000063383	chr17	Zfp947	1.53809916	0.003312718	0.006459243	-0.515544591	0.18512181	1	5	2	3	10	2	2	18	16	15	17
ENSMUSG00000021109	chr12	Hif1a	-0.5256584	0.003321875	0.006476011	4.613149579	0.035589573	-1	456	416	433	475	356	308	447	206	283	399
ENSMUSG00000085037	chr4	4933421O10Rik	1.02038976	0.003325152	0.006481495	1.050577675	0.101919028	1	13	12	25	15	28	31	41	34	50	55
ENSMUSG00000031536	chr8	Polb	-0.4419561	0.003333615	0.006497086	5.513982937	0.02563007	-1	721	708	753	1103	664	797	610	539	655	566
ENSMUSG00000031545	chr8	Agpat6	0.42604878	0.00333732	0.0065034	5.935511344	0.024115961	1	713	701	684	1064	749	1331	1154	1056	1134	1048
ENSMUSG00000053137	chr15	Mapk11	0.79453454	0.003342438	0.006512466	1.958405511	0.066831342	1	55	42	36	38	32	96	52	55	80	108
ENSMUSG00000029777	chr6	Gars	0.4727991	0.003348539	0.006523443	6.177895542	0.030110171	1	922	801	733	1198	887	1384	1466	1546	1280	1141
ENSMUSG00000020063	chr10	Sirt1	-0.6813471	0.003365254	0.006555093	2.919591373	0.055087981	-1	105	135	124	215	115	78	114	63	75	140
ENSMUSG00000026500	chr1	Cox20	0.51745538	0.003373096	0.006569414	4.049263073	0.03316267	1	243	227	159	234	147	337	291	357	309	276
ENSMUSG00000097284	chr14	4930480K23Rik	-1.1635054	0.003373546	0.006569414	0.1125884	0.113216641	-1	13	21	22	29	15	18	15	4	7	5
ENSMUSG00000026127	chr1	Imp4	0.48107586	0.003387393	0.006595459	4.074583482	0.028239366	1	213	188	170	294	186	417	378	234	289	287
ENSMUSG00000028173	chr3	Wls	0.46092848	0.003388996	0.00659766	4.811453053	0.027154976	1	360	379	292	425	301	493	557	449	442	710
ENSMUSG00000030956	chr7	Fam53b	-0.4924335	0.003391403	0.006601427	5.139927974	0.031811924	-1	521	627	596	848	493	559	366	496	373	596
ENSMUSG00000022848	chr16	Dirc2	-0.4263627	0.003391901	0.006601478	5.993482115	0.024278423	-1	1102	1045	991	1370	947	922	867	758	807	1090
ENSMUSG00000026705	chr1	Klhl20	-0.5598546	0.003394879	0.006606353	3.508352088	0.037508084	-1	211	184	201	235	169	103	172	133	138	195
ENSMUSG00000058709	chr7	Egln2	-0.4597991	0.00339952	0.006614463	6.81955093	0.028848315	-1	2153	1687	1659	2235	1991	1619	1407	1276	1614	1854
ENSMUSG00000022003	chr14	Slc25a30	-1.1304894	0.003400313	0.006615085	1.457894526	0.147305623	-1	72	67	54	37	36	12	43	11	34	35
ENSMUSG00000071369	chr10	Map3k5	-0.5784509	0.003410456	0.006633817	3.787904451	0.041596308	-1	185	184	222	383	264	242	188	130	196	147
ENSMUSG00000090946	chr12	Ccdc71l	0.54761974	0.003410891	0.006633817	2.958867051	0.032767594	1	87	88	77	110	100	180	159	103	147	157
ENSMUSG00000084020	chr11	Wsb2-ps	-1.6138399	0.003411831	0.006634722	0.683635206	0.297441233	-1	42	27	32	34	32	44	3	3	4	9
ENSMUSG00000028211	chr4	Trp53inp1	-0.7540938	0.003415509	0.006640952	3.794340814	0.073565983	-1	311	300	219	216	226	156	136	185	81	281
ENSMUSG00000042251	chr1	Pm20d1	-1.1399072	0.003417073	0.006643067	1.012419094	0.137116636	-1	30	63	25	59	21	33	7	21	18	18
ENSMUSG00000027018	chr2	Hat1	0.56693788	0.003427851	0.006663094	4.228277345	0.041035468	1	237	232	236	253	158	422	427	289	438	238
ENSMUSG00000060904	chr10	Arl1	-0.4952559	0.003444785	0.00669508	6.326337043	0.033370162	-1	1575	1281	1144	1763	1263	962	1275	788	1283	1117
ENSMUSG00000093185	chr4	Gm25692	0.67991104	0.003454026	0.006712105	2.269853201	0.048664914	1	43	54	59	66	46	87	105	99	66	114
ENSMUSG00000020271	chr11	Fbxw11	-0.4360322	0.003463087	0.006728778	5.986349393	0.025543121	-1	1108	981	963	1297	1074	848	893	805	773	1076
ENSMUSG00000006369	chr15	Fbln1	0.98295112	0.003465265	0.006732075	4.462402309	0.129196981	1	186	196	168	282	265	1229	283	383	196	367
ENSMUSG00000039634	chr4	Zfp189	-0.7384072	0.003466858	0.006734234	1.629261921	0.052381166	-1	49	60	59	69	41	40	45	22	39	37
ENSMUSG00000042410	chr2	Agps	-0.4394783	0.003469111	0.006737673	4.970790842	0.02489853	-1	569	462	495	702	469	468	512	316	473	403
ENSMUSG00000019087	chrX	Atp6ap1	0.43142033	0.003471948	0.006742246	7.552227293	0.025679765	1	2560	2369	2056	2737	2174	4185	3689	2850	3405	3547
ENSMUSG00000002379	chr17	Ndufa11	0.46122158	0.003477513	0.006752115	7.437566091	0.029375378	1	2202	2055	2116	2848	1710	4019	2916	3275	3286	2883
ENSMUSG00000037992	chr11	Rara	0.49518598	0.003499989	0.006794811	4.210277405	0.030684534	1	197	244	200	300	201	487	308	375	279	313
ENSMUSG00000081999	chr2	Gm13461	0.63561636	0.003514412	0.006821864	2.58530057	0.04521554	1	66	64	54	91	69	136	135	96	135	81
ENSMUSG00000026643	chr2	Nmt2	-0.4893259	0.003515096	0.006822245	4.065558608	0.029557543	-1	365	294	241	282	257	218	226	200	245	238
ENSMUSG00000033487	chr14	Fndc3a	-0.5679725	0.003552335	0.006893562	3.30241637	0.038353435	-1	157	159	142	264	158	122	166	82	122	153
ENSMUSG00000020708	chr11	Psmc5	0.42922824	0.003558249	0.006902163	7.51083995	0.02555043	1	2594	2127	2069	2777	2035	3744	3357	3062	3562	3352
ENSMUSG00000027955	chr3	Fam198b	-0.4981998	0.003558128	0.006902163	5.010301172	0.032798497	-1	647	601	525	594	427	404	405	423	342	601
ENSMUSG00000061689	chr2	Dlgap4	0.54879759	0.003557342	0.006902163	6.376899763	0.041417764	1	1092	777	873	1215	1068	1832	1644	1993	1021	1544
ENSMUSG00000001521	chr6	Tulp3	0.50888707	0.003559829	0.00690427	3.549317926	0.030643831	1	182	111	133	165	122	271	217	227	173	225
ENSMUSG00000027230	chr2	Creb3l1	0.68680942	0.003568393	0.006919919	3.871031708	0.061127587	1	136	101	160	236	199	291	291	372	160	342
ENSMUSG00000025228	chr19	Actr1a	0.43699107	0.00359004	0.006960933	6.723333797	0.026288436	1	1285	1226	1115	1852	1264	2358	1903	1946	1632	2103

ENSMUSG00000027447	chr2	Cst3	0.52447625	0.003592637	0.006965001	8.802111899	0.038521038	1	6542	6082	5046	5007	4342	11755	8192	6673	8365	8373
ENSMUSG00000024258	chr18	Polr2d	0.45738005	0.003597528	0.006973516	3.770393103	0.024564547	1	159	170	158	211	152	299	303	214	246	219
ENSMUSG00000024558	chr18	Mapk4	-1.3471053	0.003604369	0.006985807	0.308948674	0.186840372	-1	6	26	19	44	27	22	9	11	4	6
ENSMUSG00000028419	chr4	Chmp5	0.40733352	0.003609905	0.006995568	5.033267275	0.021399418	1	452	449	371	508	317	673	593	552	610	610
ENSMUSG00000031015	chr7	Swap70	0.51753345	0.003614342	0.007003195	3.931759986	0.033149014	1	197	186	158	215	171	424	291	185	303	268
ENSMUSG00000032425	chr9	Zfp949	-0.6626975	0.003615901	0.007005243	3.360455079	0.054948547	-1	209	205	165	188	156	237	93	90	117	116
ENSMUSG00000014158	chr5	Trpv4	1.07427187	0.003619252	0.007010765	1.242340774	0.124225277	1	14	20	16	26	30	102	30	42	45	31
ENSMUSG00000020131	chr10	Pcsk4	0.96183991	0.003639817	0.007049623	0.31988742	0.063969263	1	11	8	12	13	12	23	20	21	29	27
ENSMUSG00000020196	chr10	Cabin1	0.47500003	0.003641182	0.007051289	4.297344955	0.028429615	1	246	210	194	315	258	482	335	377	274	396
ENSMUSG00000060843	chr10	Ctnna3	-0.7983491	0.003643391	0.00705459	2.277515715	0.074227831	-1	121	75	65	92	94	32	62	44	62	81
ENSMUSG00000031967	chr8	Afg3l1	-0.405071	0.003687689	0.007139374	5.923861002	0.022162855	-1	1020	970	928	1353	905	943	862	800	839	813
ENSMUSG00000000301	chr11	Pemt	0.87867986	0.00369467	0.007151899	1.143048371	0.072388317	1	24	33	14	25	13	37	45	47	45	44
ENSMUSG00000009739	chr15	Pou6f1	-0.5044355	0.003696412	0.007153289	3.890935043	0.031465255	-1	229	240	240	340	243	219	189	149	261	175
ENSMUSG00000024665	chr19	Fads2	-0.6932347	0.003696044	0.007153289	2.422026839	0.054961732	-1	75	90	94	123	101	57	63	59	47	102
ENSMUSG00000030754	chr7	Copb1	-0.4462892	0.003702884	0.007164821	5.468134049	0.0267308	-1	804	693	699	946	666	589	668	473	711	608
ENSMUSG00000038462	chr13	Uqcrfs1	-0.4769836	0.003705611	0.007169105	8.920045601	0.032106085	-1	7455	8183	8491	12248	6128	7297	6038	6214	6583	6927
ENSMUSG00000021483	chr13	Cdk20	0.74316366	0.003706264	0.007169377	2.490233938	0.064842443	1	54	78	48	71	54	142	140	58	134	91
ENSMUSG00000018209	chr2	Stk4	0.42684569	0.003712726	0.007180883	4.451636189	0.022731878	1	304	236	248	326	269	511	444	329	391	373
ENSMUSG00000003038	chr4	Hmgn2	0.55208152	0.003713761	0.007180897	3.456438779	0.036543309	1	151	156	102	131	112	172	234	215	197	229
ENSMUSG00000020902	chr11	Ntn1	-0.5896759	0.003713466	0.007180897	3.916892122	0.044914089	-1	263	214	233	324	307	306	241	162	137	144
ENSMUSG00000036534	chr8	Slc38a7	0.53043576	0.003717235	0.007186276	3.442486578	0.033308474	1	140	122	120	172	105	311	206	149	172	212
ENSMUSG00000066036	chr4	Ubr4	-0.4503444	0.003717571	0.007186276	6.907009911	0.028227839	-1	1947	1751	1736	2752	2186	1813	1521	1639	1405	1905
ENSMUSG00000005506	chr2	Celf1	-0.4458191	0.003722141	0.007194114	6.337342652	0.027387936	-1	1292	1196	1237	1818	1423	1026	1269	995	1096	1188
ENSMUSG00000036026	chr17	Tmem63b	-0.4581085	0.003729199	0.00720676	6.034403732	0.028745705	-1	1043	1065	1006	1519	1046	791	807	895	982	997
ENSMUSG00000032449	chr9	Slc25a36	-0.4539011	0.003736306	0.007219496	4.891767632	0.02702995	-1	409	440	436	710	567	453	368	355	392	475
ENSMUSG00000024301	chr17	Kifc5b	1.09870962	0.003738623	0.007222196	0.241148136	0.10265166	1	11	7	8	16	8	27	39	23	13	15
ENSMUSG00000070709	chr7	1700049G17Rik	-0.7226195	0.003738737	0.007222196	1.520303345	0.048493677	-1	60	48	51	55	41	46	35	31	32	26
ENSMUSG00000049832	chr17	Gm9840	0.89110001	0.003741832	0.007227176	1.035760162	0.072560006	1	16	20	23	21	19	58	35	28	52	31
ENSMUSG00000028702	chr4	Rad54l	0.76447517	0.003742822	0.007228089	1.427453563	0.053097892	1	31	32	25	27	25	55	67	39	56	46
ENSMUSG00000022024	chr14	Sugt1	-0.4476924	0.003745226	0.007231732	5.716954698	0.027233987	-1	983	908	754	1105	780	841	674	546	849	725
ENSMUSG00000022621	chr15	Rabl2	0.78193805	0.003750692	0.007240364	1.545597694	0.059518968	1	38	35	21	26	31	80	56	45	45	64
ENSMUSG00000099875	chr1	Gm15453	0.95454283	0.003750732	0.007240364	0.744387846	0.082478939	1	20	14	13	24	8	26	50	24	32	34
ENSMUSG00000082935	chr1	Gm7658	-0.9809094	0.003769265	0.007275133	2.418534113	0.121113404	-1	136	79	79	116	108	141	46	40	30	39
ENSMUSG00000021592	chr13	Arsk	-0.7001141	0.003775667	0.007286484	2.260530941	0.055337075	-1	78	95	84	101	73	66	50	31	67	79
ENSMUSG00000074272	chr7	Ceacam1	-0.6619837	0.003788634	0.0073105	2.352216176	0.048334159	-1	81	67	85	116	107	66	83	52	48	68
ENSMUSG00000024787	chr19	Snx15	0.45105777	0.0037936	0.007319072	3.760915441	0.023972666	1	190	141	172	214	132	292	252	230	225	271
ENSMUSG00000005043	chr11	Sgsh	0.6539602	0.003800706	0.007331768	3.075596306	0.052500107	1	102	81	77	131	93	284	113	147	128	167
ENSMUSG00000038002	chr17	Cramp1l	-0.5121979	0.003809394	0.007347515	3.181903109	0.02987896	-1	123	154	149	199	160	123	125	105	109	142
ENSMUSG00000043962	chr4	Thrap3	-0.4357712	0.00381302	0.007353494	5.898801402	0.025988116	-1	965	955	931	1249	1004	727	887	764	769	979
ENSMUSG00000046470	chr2	Sox18	0.60804015	0.00381708	0.007360309	4.11372359	0.048877301	1	213	173	154	338	160	460	236	386	226	393
ENSMUSG00000033147	chr3	Slc22a15	0.88973394	0.003818918	0.007362835	0.696519807	0.062929731	1	12	17	15	17	16	47	28	22	28	34
ENSMUSG00000021892	chr14	Sh3bp5	-0.4968832	0.003820147	0.00736419	5.136753584	0.033219343	-1	513	531	512	917	622	390	458	430	579	501
ENSMUSG00000028268	chr3	Gbp3	0.96989313	0.003827184	0.007376738	2.455942659	0.118546504	1	56	73	45	51	42	66	97	115	65	235
ENSMUSG00000016018	chr13	Skiv2l2	-0.5359906	0.00383634	0.007393365	4.967441155	0.03874414	-1	555	485	500	730	497	259	512	355	466	471
ENSMUSG00000025781	chr2	Atp5c1	-0.4614861	0.003840425	0.007400218	9.370317158	0.030329088	-1	10640	11601	11184	15610	8573	10023	8839	8019	9692	8888
ENSMUSG00000031754	chr8	Nudt21	0.50965029	0.00384273	0.007403639	3.659467047	0.031603488	1	150	137	151	209	127	315	271	213	232	173
ENSMUSG00000102947	chr2	AL772372.1	0.99434933	0.003850278	0.007417158	1.805449188	0.117059127	1	30	25	21	58	36	154	54	65	38	61
ENSMUSG00000015289	chrX	Lage3	0.45340042	0.003856632	0.007428023	4.480135171	0.026354535	1	350	258	255	303	228	512	429	380	425	351
ENSMUSG00000029790	chr6	Cep41	0.90768448	0.00385698	0.007428023	1.0233257	0.081085797	1	29	12	12	32	15	45	51	37	41	28
ENSMUSG00000042814	chr2	Mcts2	0.58372858	0.003863094	0.00743877	2.778381093	0.03841426	1	103	70	69	84	74	116	155	117	124	146
ENSMUSG00000066839	chr9	Ecsit	-0.4432374	0.003877061	0.007464638	6.291339094	0.027263235	-1	1269	1167	1203	1971	1190	1045	1044	1088	1014	1206
ENSMUSG00000033060	chr14	Lmo7	-0.5053193	0.003878173	0.007465751	6.395491381	0.035697361	-1	1413	1254	1401	2028	1314	888	981	1111	1258	1393
ENSMUSG00000020064	chr10	Herc4	-0.4348497	0.003884073	0.007476078	4.553074601	0.024263642	-1	488	362	319	480	360	334	336	258	337	360
ENSMUSG00000021224	chr12	Numb	-0.5396791	0.003888803	0.007483346	3.782796323	0.036573938	-1	227	224	184	337	244	160	214	124	163	252
ENSMUSG00000071497	chr19	Nutf2-ps1	-0.8787776	0.00388892	0.007483346	0.89155769	0.068457771	-1	44	40	22	35	27	18	27	16	17	22
ENSMUSG00000030034	chr6	Ino80b	0.56845354	0.003900646	0.007504877	3.225435662	0.038738804	1	110	104	105	136	99	266	148	162	123	210
ENSMUSG00000046491	chr11	C1qtnf2	0.61589372	0.003912777	0.007527182	3.605566699	0.048224037	1	191	145	114	124	128	236	226	253	153	323
ENSMUSG00000034757	chr11	Tmub2	0.42070976	0.003914245	0.007528969	4.579083563	0.022585969	1	340	314	267	341	252	487	398	428	408	502
ENSMUSG00000021901	chr14	Bap1	-0.3973108	0.003922115	0.00754203	5.868987705	0.021559131	-1	1011	930	900	1208	901	921	790	733	832	839
ENSMUSG00000073802	chr4	Cdkn2b	-0.8842239	0.003921949	0.00754203	0.688346317	0.063552467	-1	36	22	22	35	30	25	18	13	17	13
ENSMUSG00000035944	chr15	Ttc38	0.8949521	0.003923911	0.007544447	2.184971016	0.097475872	1	33	61	34	62	41	42	87	110	92	131
ENSMUSG00000035757	chr15	Selo	-0.4536304	0.003927172	0.00754864	4.019288634	0.025458462	-1	302	211	262	344	271	248	207	182	232	243
ENSMUSG00000039372	chr1	March4	-1.1609495	0.003926927	0.00754864	-0.03494323	0.101907284	-1	21	9	11	24	24	7	11	5	11	9
ENSMUSG00000021911	chr14	Parg	-0.4411931	0.003937578	0.007567601	4.421514269	0.024794201	-1	395	321	347	447	323	251	349	289	281	300
ENSMUSG00000033021	chr1	Gmppa	0.39832048	0.003942905	0.007576796	5.039028054	0.020806212	1	434	417	343	522	396	688	594	512	660	590

ENSMUSG00000027936	chr3	Crtc2	0.48558549	0.003963137	0.007614627	4.251063881	0.030476569	1	236	187	194	351	222	518	346	333	311	306
ENSMUSG00000032062	chr9	2310030G06Rik	-1.0702601	0.003973779	0.007634025	2.173243324	0.144918224	-1	91	83	88	118	67	121	29	28	41	19
ENSMUSG00000047821	chr11	Trim16	-0.5648605	0.003976476	0.007638158	5.309492882	0.044060644	-1	660	623	712	887	640	308	533	522	522	696
ENSMUSG00000039678	chr2	Tbc1d13	0.41312547	0.003982007	0.007647729	4.731836738	0.022008525	1	315	322	354	396	299	617	479	464	430	485
ENSMUSG00000029664	chr6	Tfpi2	0.99674552	0.004006157	0.007693054	0.563789235	0.08723957	1	11	12	14	13	16	35	28	40	15	28
ENSMUSG00000022895	chr16	Ets2	-0.4368098	0.004009139	0.007697723	5.990674916	0.026518	-1	1051	999	1052	1428	939	1200	868	775	712	886
ENSMUSG00000008167	chr8	Fbxw9	0.60017757	0.004014342	0.007706004	2.374401414	0.037941822	1	61	61	61	70	46	129	90	86	84	111
ENSMUSG00000092327	chr5	Gm20488	-0.5497508	0.004014555	0.007706004	3.146133952	0.035799895	-1	157	182	141	158	131	128	136	88	129	99
ENSMUSG00000078184	chr1	B020018G12Rik	0.97399825	0.004015202	0.007706189	0.563883597	0.07924266	1	13	16	10	14	14	45	26	24	33	18
ENSMUSG00000022816	chr16	Fstl1	0.49113992	0.004017866	0.007710243	8.089433348	0.034528633	1	3594	3400	3480	3703	2632	6753	4765	5364	3809	5412
ENSMUSG00000024271	chr18	Elp2	0.39993628	0.004019605	0.007712521	4.916345136	0.02089262	1	431	386	308	451	358	615	601	504	548	527
ENSMUSG00000030685	chr7	Kctd13	0.85102849	0.004024174	0.007720227	1.724844046	0.08012463	1	34	37	26	39	32	112	59	68	31	67
ENSMUSG00000032802	chr2	Srxn1	0.53488809	0.004035208	0.007740333	4.783302465	0.038764631	1	390	308	340	385	246	670	541	355	677	415
ENSMUSG00000079164	chr1	Tlr5	1.18739531	0.004036151	0.007741079	1.140682617	0.157936935	1	23	15	14	17	24	16	30	44	60	82
ENSMUSG00000029276	chr5	Glmn	-0.6817072	0.004042192	0.007750792	2.65315618	0.055012834	-1	147	100	81	137	105	52	94	59	85	96
ENSMUSG00000029501	chr5	Ankle2	-0.402832	0.004042324	0.007750792	4.733669092	0.021029959	-1	447	440	416	540	406	384	416	303	331	436
ENSMUSG00000046152	chr8	Fut10	0.86935472	0.004051482	0.007767286	2.630853957	0.095784589	1	59	74	51	75	60	48	176	133	105	171
ENSMUSG00000034667	chr10	Xpot	-0.4231938	0.004053498	0.007770084	5.032643367	0.023870712	-1	545	497	489	709	553	430	545	366	490	443
ENSMUSG00000032064	chr9	Dixdc1	-0.8374715	0.004058051	0.007777043	1.597476112	0.076219583	-1	71	67	39	52	48	27	34	22	34	54
ENSMUSG00000068391	chr15	Chrac1	-0.421082	0.004058241	0.007777043	5.543996658	0.024250272	-1	850	721	738	970	701	726	606	510	728	686
ENSMUSG00000021287	chr12	Xrcc3	1.05293745	0.004059353	0.007778107	0.010948882	0.075821834	1	9	6	11	9	7	21	19	21	22	13
ENSMUSG00000037260	chr8	Hgsnat	0.51039905	0.00406291	0.007783856	4.294298696	0.03417622	1	231	243	206	284	233	277	443	289	438	415
ENSMUSG00000063785	chrX	Utp14a	0.52468878	0.004076608	0.007809028	3.7471369	0.034854801	1	135	144	118	271	160	330	269	229	245	213
ENSMUSG00000021900	chr14	Btd	0.47437595	0.004084441	0.00782296	3.584586934	0.026711461	1	169	136	143	166	125	288	207	230	192	212
ENSMUSG00000019194	chr7	Scn1b	-0.4270174	0.004087017	0.007826822	9.130762888	0.026314404	-1	10205	8913	8527	11683	8687	8207	7622	7444	7274	8485
ENSMUSG00000053559	chr15	Smagp	0.84781457	0.004089848	0.007831171	2.214865218	0.086910562	1	47	57	46	63	28	176	53	87	75	88
ENSMUSG00000023191	chr6	Leprel2	0.49063146	0.004097765	0.007845255	4.193915768	0.031077515	1	264	217	204	251	189	446	353	332	222	394
ENSMUSG00000029209	chr5	Gnpda2	-0.7243407	0.004109401	0.007866454	2.319928837	0.061779964	-1	91	119	62	102	79	56	58	41	53	94
ENSMUSG00000002104	chr2	Rapsn	0.43268785	0.004119902	0.007885477	4.876271607	0.024917855	1	354	363	325	459	356	605	489	636	494	506
ENSMUSG00000039682	chr5	Lap3	-0.4188506	0.004132069	0.007907681	5.620105342	0.024135213	-1	789	787	839	1079	705	703	684	574	759	707
ENSMUSG00000033845	chr1	Mrpl15	0.43805618	0.004142996	0.007927507	5.985044934	0.026880523	1	769	714	743	1121	691	1088	1223	1224	1209	1159
ENSMUSG00000030224	chr6	Strap	-0.4539644	0.004150628	0.007941023	6.647678516	0.029296478	-1	1789	1629	1567	2073	1578	1296	1605	1022	1540	1442
ENSMUSG00000103392	chr3	RP23-436F15.5	-0.741252	0.004175831	0.007988148	1.819001792	0.059582279	-1	75	72	57	68	46	40	62	29	42	36
ENSMUSG00000014550	chr6	Zfyve20	-0.4770727	0.004178103	0.007991401	4.422634354	0.029976787	-1	337	295	352	488	384	239	331	240	287	358
ENSMUSG00000054920	chr5	Klhl5	0.48493995	0.004182836	0.007997263	3.394476954	0.027426799	1	114	124	134	160	113	212	209	147	197	228
ENSMUSG00000062704	chr8	9430002A10Rik	1.62288658	0.004182181	0.007997263	-0.210792443	0.265887412	1	1	2	7	12	5	18	18	36	3	14
ENSMUSG00000066553	chr12	Gm6969	-2.2523377	0.004182884	0.007997263	4.517357511	0.654451277	-1	609	597	554	620	423	634	12	19	15	26
ENSMUSG00000023755	chr15	Rhebl1	0.86095655	0.004197059	0.008023266	0.849202666	0.065665594	1	18	16	19	27	9	33	36	31	43	32
ENSMUSG00000037536	chr14	Fbxo34	-0.4698551	0.004233392	0.008091614	3.490363862	0.026118875	-1	216	173	193	216	163	154	155	126	145	183
ENSMUSG00000002319	chr14	Ipo4	0.42841714	0.004242538	0.008107988	5.791045631	0.025603742	1	651	647	599	879	738	1228	1095	1044	818	1003
ENSMUSG00000010110	chr19	Stx5a	0.4142362	0.004254867	0.008130437	4.6000584	0.022277222	1	349	292	275	345	278	571	420	401	441	425
ENSMUSG00000055436	chr3	Srsf11	-0.4333976	0.00426927	0.008156845	5.149818173	0.025588551	-1	651	584	497	749	560	416	569	418	488	564
ENSMUSG00000073725	chr1	Lmbrd1	-0.4657237	0.004273945	0.00816466	5.257206215	0.029966179	-1	686	587	553	873	620	445	585	378	575	633
ENSMUSG00000028417	chr4	Tal2	0.9982901	0.00427929	0.008173753	0.97594143	0.107417223	1	18	9	14	35	17	60	30	51	33	25
ENSMUSG00000027176	chr2	Cstf3	0.51891744	0.004282273	0.008178335	3.190508878	0.031706802	1	122	104	108	128	89	175	203	187	142	156
ENSMUSG00000099858	chr1	Gm6652	-1.0242416	0.004290335	0.008192611	2.217E-05	0.069352715	-1	17	21	17	19	14	6	11	10	10	10
ENSMUSG00000030095	chr6	Tmem43	0.40471162	0.004295625	0.008201593	5.505675762	0.022539135	1	566	550	502	738	559	1029	837	708	844	813
ENSMUSG00000026519	chr1	Tmem63a	0.40242565	0.00429676	0.008202639	4.775662639	0.021223701	1	346	315	308	407	370	614	534	428	471	499
ENSMUSG00000079434	chr1	Neu2	1.02007781	0.004300982	0.008209576	4.122260864	0.144874887	1	255	209	107	147	128	85	435	418	380	539
ENSMUSG00000023034	chr15	Nr4a1	-0.7977615	0.004306466	0.008218922	7.18997313	0.091769706	-1	1215	2362	3935	3887	2395	2934	2007	1019	1512	1404
ENSMUSG00000100215	chr1	Gm8292	1.00389362	0.004310314	0.008225142	0.357172414	0.083107164	1	16	8	8	15	10	36	22	28	24	15
ENSMUSG00000103183	chr4	RP23-118E21.11	1.00281198	0.004330824	0.008263153	1.117625541	0.107871929	1	22	11	19	16	31	36	30	37	52	66
ENSMUSG00000054509	chr14	Parp4	-0.4706089	0.004346369	0.008291681	3.8505297	0.027979211	-1	249	228	195	353	228	269	210	146	164	201
ENSMUSG00000021066	chr12	Atl1	-1.0536734	0.004351257	0.008299312	0.394243599	0.102367628	-1	32	36	15	20	17	8	16	13	14	12
ENSMUSG00000023094	chr2	Msrb2	-0.6091335	0.004351557	0.008299312	3.970151886	0.04981236	-1	221	322	317	329	207	189	187	204	274	141
ENSMUSG00000037813	chr2	D630003M21Rik	-0.7485232	0.004360725	0.008315663	1.745343387	0.059016231	-1	66	66	55	66	49	52	27	50	29	39
ENSMUSG00000037613	chr7	Tnfrsf23	0.60707683	0.004370205	0.008332604	3.777096265	0.048598601	1	202	150	135	146	161	406	168	257	221	297
ENSMUSG00000021536	chr13	Adcy2	-0.4155623	0.00438346	0.008356737	4.998420673	0.023302775	-1	543	507	450	725	507	401	449	388	459	528
ENSMUSG00000051116	chr5	Gm8121	-0.8053319	0.004395988	0.008379478	1.520653992	0.069907125	-1	80	46	41	52	42	45	22	28	37	32
ENSMUSG00000030688	chr7	Stard10	-0.5642834	0.004402944	0.008391592	5.379668207	0.045175204	-1	757	690	657	944	661	913	393	473	590	389
ENSMUSG00000027776	chr3	Il12a	-0.7660614	0.00440968	0.008402139	1.628664396	0.062073973	-1	76	53	41	57	52	29	36	27	36	52
ENSMUSG00000080893	chr5	Gm15920	-1.3094865	0.0044091	0.008402139	4.980297013	0.240987569	-1	608	667	546	890	649	1047	115	158	118	123
ENSMUSG00000020526	chr11	Znhit3	-0.5376699	0.004423972	0.008427938	3.091617857	0.03449129	-1	174	151	132	165	120	136	119	72	118	119
ENSMUSG00000032503	chr9	Arpp21	0.52497212	0.004424426	0.008427938	4.543883278	0.037759983	1	288	261	229	382	268	395	386	582	330	523
ENSMUSG00000083443	chr6	Gm15519	-0.8706259	0.004428158	0.008433897	0.66314931	0.062911917	-1	27	30	30	31	23	20	14	10	17	24

ENSMUSG00000070044	chr8	Fam149a	0.67756599	0.004429416	0.008435144	1.952476091	0.049672188	1	40	42	34	62	38	104	77	74	49	74
ENSMUSG00000009621	chr2	Vav2	0.53554706	0.004439839	0.008453841	3.122294345	0.034696728	1	79	102	101	166	81	194	160	149	144	185
ENSMUSG00000032285	chr9	Dnaja4	-0.5418013	0.004443717	0.008460072	6.087185299	0.042222284	-1	819	1088	1266	1987	943	1125	989	901	767	742
ENSMUSG00000024446	chr17	Rpp21	0.50202866	0.004454896	0.0084802	3.42238757	0.030268679	1	135	142	119	130	122	254	202	168	218	174
ENSMUSG00000054309	chr12	Cpsf3	0.41537249	0.004457582	0.008484158	4.487046572	0.022525314	1	271	264	241	376	279	475	471	332	430	379
ENSMUSG00000005683	chr10	Cs	-0.4630187	0.004458844	0.008484248	9.804914614	0.031581381	-1	13111	15060	14389	21963	13447	12833	11668	12552	10254	14081
ENSMUSG00000040502	chr10	March9	0.81465316	0.004458545	0.008484248	1.43226336	0.07002747	1	32	22	22	37	26	92	46	33	44	56
ENSMUSG00000017615	chr11	Tnfaip1	-0.4334158	0.004462837	0.008489534	6.136554973	0.026814124	-1	1068	1058	1001	1725	1221	1192	951	870	941	942
ENSMUSG00000029404	chr5	Arl6ip4	0.39486216	0.004462362	0.008489534	5.070289925	0.02112449	1	502	390	350	561	369	686	587	554	599	684
ENSMUSG00000034320	chr18	Slc26a2	-0.4584641	0.004463466	0.008489575	3.63947974	0.025705176	-1	234	163	194	278	202	174	196	142	159	180
ENSMUSG00000019986	chr10	Ahi1	0.73918467	0.004464135	0.008489693	1.479409531	0.052725782	1	36	34	26	27	24	69	60	43	55	45
ENSMUSG00000056313	chr8	1810011O10Rik	-0.637902	0.00448697	0.008531958	4.168697026	0.056301515	-1	212	300	351	428	330	411	191	207	161	189
ENSMUSG00000026670	chr1	Uap1	-0.4245267	0.004489882	0.008535471	5.273219395	0.024947753	-1	651	637	556	858	609	583	548	407	636	517
ENSMUSG00000042961	chr15	Egflam	-0.4309289	0.004490039	0.008535471	4.796950512	0.025063386	-1	468	482	441	553	422	338	459	329	422	371
ENSMUSG00000072837	chr10	Mir546	-0.5317385	0.004503691	0.008560259	3.815663399	0.036926182	-1	236	262	221	331	190	184	177	167	130	279
ENSMUSG00000024991	chr19	Eif3a	-0.4989122	0.004513604	0.008577934	6.855321569	0.036234389	-1	1985	1831	1615	2790	1967	1178	1781	1301	1515	2040
ENSMUSG00000051557	chr4	Pusl1	0.56078142	0.004517328	0.008583845	2.738823467	0.036280693	1	62	70	71	125	71	137	136	114	128	122
ENSMUSG00000026558	chr1	Uck2	0.47343093	0.004525928	0.008599017	4.775711159	0.030625325	1	329	324	345	356	333	687	537	500	499	370
ENSMUSG00000085227	chr5	6330418K02Rik	0.96287189	0.004535533	0.008616095	0.624553623	0.08528491	1	22	18	10	14	7	27	34	32	34	24
ENSMUSG00000085408	chr4	C530005A16Rik	-0.8380134	0.004538006	0.008619621	1.172547787	0.069832891	-1	43	30	31	52	49	17	31	21	21	35
ENSMUSG00000030057	chr6	Cnbp	-0.492724	0.004540399	0.008622995	8.762859113	0.035809938	-1	8098	6860	6774	9838	6514	4723	6102	4784	7018	6700
ENSMUSG00000030094	chr6	Xpc	-0.5080581	0.004547526	0.008635357	3.27804221	0.030989036	-1	161	159	134	242	152	121	130	103	154	137
ENSMUSG00000033933	chr6	Vhl	0.45005137	0.004564096	0.008665644	3.456912708	0.023788124	1	143	131	132	151	124	242	203	194	191	194
ENSMUSG00000034285	chr11	Nipsnap1	1.05532853	0.004569455	0.008674248	0.460474845	0.105380668	1	16	3	10	16	15	45	25	25	19	24
ENSMUSG00000051331	chr6	Cacna1c	-0.6753924	0.004569869	0.008674248	1.851482466	0.04756249	-1	52	67	51	88	64	44	49	41	32	54
ENSMUSG00000026986	chr2	Hnmt	-0.7405388	0.004576496	0.008685647	1.573452412	0.056848802	-1	45	73	42	54	51	36	44	31	31	33
ENSMUSG00000097167	chr3	Gm16740	1.01620526	0.004585035	0.008700671	0.592892046	0.100625182	1	21	15	7	17	8	42	25	32	15	37
ENSMUSG00000086782	chr4	E130102H24Rik	-1.3661291	0.004593216	0.008715012	-0.124836688	0.167172058	-1	22	21	12	10	20	1	6	5	14	10
ENSMUSG00000022160	chr14	Mettl3	0.47164616	0.00460119	0.008728957	3.499828192	0.027046129	1	145	122	131	154	143	237	224	202	219	177
ENSMUSG00000086240	chr1	Gm7846	1.24467049	0.004604803	0.008734626	-0.069720952	0.135416846	1	13	8	5	8	2	33	24	12	16	10
ENSMUSG00000038453	chr11	Srcin1	-0.9499576	0.004605971	0.008735657	0.681030577	0.086085024	-1	25	36	22	34	29	13	15	11	13	31
ENSMUSG00000035765	chr18	Dym	-0.4394783	0.004620256	0.00876156	5.706286424	0.027491563	-1	842	733	715	1234	978	839	710	587	746	741
ENSMUSG00000022272	chr15	Myo10	-0.4946276	0.004634432	0.008787251	6.214892756	0.035501354	-1	1417	1177	1033	1517	1323	993	822	1144	786	1267
ENSMUSG00000056569	chr1	Mpz	-0.6605592	0.004648291	0.008812333	6.525686793	0.063934646	-1	817	1345	1988	2561	1739	1341	1393	1061	769	1301
ENSMUSG00000020225	chr10	Tmbim4	0.40272864	0.004651676	0.008817554	5.393227429	0.022575332	1	594	513	491	587	495	926	769	748	696	764
ENSMUSG00000014226	chr1	Cacybp	-0.4532443	0.004662036	0.008835994	5.520929145	0.029196079	-1	922	768	672	922	669	615	755	468	712	609
ENSMUSG00000022225	chr14	Cma1	0.8893452	0.004674078	0.008857615	3.393622964	0.108769833	1	53	94	118	131	140	476	132	172	151	195
ENSMUSG00000025742	chrX	Prps2	0.64620291	0.004689719	0.00888605	2.258410195	0.046910115	1	37	60	54	74	46	112	102	65	95	92
ENSMUSG00000062353	chr5	Gm15772	0.58519426	0.004697091	0.008898814	2.836751004	0.040972217	1	107	76	69	89	76	119	133	152	146	131
ENSMUSG00000050213	chr4	Snip1	0.5578135	0.004706317	0.008915083	3.218998422	0.038697307	1	96	104	109	137	107	271	194	135	161	141
ENSMUSG00000027655	chr2	Dhx35	-0.4456657	0.004710929	0.00892261	3.508037225	0.023675757	-1	208	171	168	262	167	184	168	129	145	156
ENSMUSG00000069208	chr13	Zfp825	-0.7633706	0.004713574	0.008926411	1.915160165	0.068324417	-1	97	64	56	76	51	40	52	23	53	54
ENSMUSG00000098332	chr9	5031420N21Rik	0.67660514	0.004716061	0.008929911	2.463269377	0.055249639	1	81	69	59	59	39	148	104	113	88	89
ENSMUSG00000033760	chr19	Rbm4b	0.68502274	0.004723071	0.008941972	2.143068604	0.0541602	1	45	55	32	61	52	134	81	62	78	81
ENSMUSG00000098950	chr2	Gm28036	-0.4136737	0.00473077	0.008955335	5.430460319	0.02409228	-1	715	679	742	880	644	566	660	518	623	641
ENSMUSG00000071454	chr12	Dtnb	0.78217566	0.004732623	0.008957631	1.139710177	0.05557772	1	24	20	24	20	24	57	35	42	40	40
ENSMUSG00000020485	chr11	Supt4a	0.42469435	0.004749599	0.008988544	4.346154968	0.02367064	1	306	253	245	285	196	432	391	334	321	421
ENSMUSG00000036275	chr11	9530068E07Rik	0.41130558	0.004753984	0.008995624	6.520844132	0.024628269	1	1286	1163	1018	1320	1070	2075	1817	1504	1516	1676
ENSMUSG00000040327	chr17	Cul9	-0.5122468	0.004756371	0.008997764	4.081265172	0.035277326	-1	304	225	241	390	321	237	193	164	284	254
ENSMUSG00000079083	chr9	Jrkl	-0.8668058	0.004756403	0.008997764	1.717594865	0.088227194	-1	64	47	67	70	57	15	39	30	45	53
ENSMUSG00000020949	chr12	Fkbp3	-0.4592513	0.004774458	0.009030698	6.981092838	0.031084558	-1	2264	2198	1957	2772	1758	1438	1761	1577	2011	1837
ENSMUSG00000000759	chr8	Tubgcp3	-0.5388045	0.004777076	0.009033204	3.269166628	0.036530168	-1	157	152	159	223	154	118	157	78	144	139
ENSMUSG00000023885	chr17	Thbs2	0.50290993	0.004776995	0.009033204	5.683829424	0.036528813	1	821	545	562	660	564	1388	903	776	733	1173
ENSMUSG00000027569	chr2	Mrgbp	0.57933129	0.00479165	0.009059538	2.425958628	0.037329443	1	60	54	58	91	53	129	116	79	95	97
ENSMUSG00000021910	chr14	Nisch	0.44920588	0.00479416	0.009062298	6.590302153	0.029608992	1	1097	1066	1023	1656	1260	2119	1658	1864	1429	2020
ENSMUSG00000028184	chr3	Lphn2	-0.4293231	0.00479476	0.009062298	4.215633972	0.024073498	-1	354	330	270	374	255	246	286	242	219	292
ENSMUSG00000032640	chr7	Chsy1	0.60621669	0.004795055	0.009062298	2.977274921	0.045809245	1	66	101	78	98	110	175	195	125	113	160
ENSMUSG00000086741	chr8	Gm15816	1.15025404	0.004803163	0.009076394	3.883273435	0.188034832	1	171	87	75	139	200	75	298	344	217	698
ENSMUSG00000020899	chr11	Pfas	-0.4730424	0.004806843	0.009082119	3.518182024	0.027751816	-1	191	175	154	245	219	174	170	137	158	137
ENSMUSG00000015468	chr17	Notch4	-0.5020804	0.004811393	0.009089488	4.16514702	0.034146481	-1	302	297	309	402	254	351	202	260	167	232
ENSMUSG00000033099	chr15	Nol12	0.45253739	0.004839241	0.009140861	4.619143655	0.028049155	1	360	264	277	369	272	629	457	366	487	381
ENSMUSG00000010362	chr11	Rdm1	-0.4984823	0.004841547	0.009143956	4.269111726	0.034026779	-1	389	369	280	340	287	374	243	182	277	233
ENSMUSG00000033900	chr3	Map9	-0.8661998	0.004842188	0.009143956	1.481801871	0.087235114	-1	82	41	43	33	55	38	28	29	34	26
ENSMUSG00000060512	chr5	0610040J01Rik	1.09159553	0.0048473	0.009152372	0.771448322	0.129416503	1	15	22	17	13	7	15	49	31	44	34
ENSMUSG00000001930	chr6	Vwf	0.61154696	0.004848128	0.0091527	4.705156335	0.053448486	1	207	276	225	449	384	446	508	443	386	787

ENSMUSG00000042293	chr9	Gm5617	0.63889555	0.004851131	0.009157133	2.224992105	0.046004288	1	60	58	39	62	46	103	98	99	62	90
ENSMUSG00000019822	chr10	Smpd2	0.46034699	0.004856498	0.009166025	3.455058791	0.025975619	1	142	138	113	191	103	252	206	182	188	201
ENSMUSG00000036585	chr18	Fgf1	-0.6193694	0.004869613	0.009189537	4.299799871	0.053987605	-1	212	297	373	623	299	288	253	223	312	181
ENSMUSG00000069844	chr11	Sco1	-0.499981	0.004884744	0.009216847	3.347069373	0.030795441	-1	176	177	178	199	146	159	121	143	146	109
ENSMUSG00000042178	chr7	Armc5	0.47883119	0.004889627	0.009224815	4.093916978	0.030677891	1	228	167	154	285	229	377	305	338	247	347
ENSMUSG00000040928	chr4	S100pbp	0.52791956	0.004892927	0.009229795	3.142950576	0.034174753	1	114	115	94	131	79	184	199	154	117	189
ENSMUSG00000017132	chr11	Cyth1	-0.4006149	0.004894159	0.009230468	5.355771183	0.022613556	-1	659	655	653	900	611	613	537	476	597	656
ENSMUSG00000029416	chr5	Slc15a4	0.46751522	0.004894605	0.009230468	4.038813097	0.028708663	1	206	180	181	246	207	450	314	233	263	303
ENSMUSG00000059995	chr11	Atxn7l3	0.40266612	0.004896233	0.009232292	4.89955002	0.022153236	1	351	362	388	438	361	649	521	511	458	635
ENSMUSG00000023092	chrX	Fhl1	-0.9483094	0.004905957	0.00924938	9.788129265	0.133142384	-1	7803	12776	25607	36024	7534	13665	7900	10792	10482	6333
ENSMUSG00000012428	chr5	Steap4	-0.4185772	0.0049162	0.009267442	5.296362673	0.02480272	-1	570	665	635	832	639	547	632	432	558	574
ENSMUSG00000081281	chrX	Gm6274	1.1077537	0.004919922	0.009273207	0.165582669	0.107259317	1	11	9	10	7	9	18	14	36	18	23
ENSMUSG00000024713	chr19	Pcsk5	0.74384503	0.004932745	0.009296122	3.200644983	0.075089738	1	103	94	87	124	97	347	180	144	78	199
ENSMUSG00000049553	chr6	Polr1a	0.53150439	0.00494282	0.009313853	4.972791016	0.040541388	1	356	288	268	546	465	463	655	626	556	699
ENSMUSG00000057229	chr7	Atp5sl	-0.4079535	0.004946226	0.009319016	4.755222364	0.022706406	-1	424	450	449	571	395	442	345	403	330	366
ENSMUSG00000001833	chr9	Sept7	-0.4620327	0.004972029	0.009366219	6.362378467	0.031494447	-1	1459	1226	1231	1984	1269	1052	1394	811	1183	1216
ENSMUSG00000036452	chr18	Arhgap26	-0.5835384	0.00497262	0.009366219	2.803829067	0.041794485	-1	126	131	110	130	114	84	95	66	76	130
ENSMUSG00000035929	chr17	H2-Q4	0.87891333	0.004980417	0.00937964	4.788366018	0.11263152	1	228	333	275	349	255	1450	344	373	281	569
ENSMUSG00000016481	chr1	Cr1l	-0.4033363	0.004984254	0.009385602	5.377353799	0.02311413	-1	732	683	608	862	642	669	633	428	553	651
ENSMUSG00000036916	chrX	Zfp280c	-0.686907	0.00498846	0.009392256	1.884386924	0.052004856	-1	70	58	52	97	56	37	59	36	36	56
ENSMUSG00000084098	chr2	Gm13422	-0.8946137	0.004989522	0.00939299	0.478389905	0.064976263	-1	24	24	15	31	30	18	17	11	12	15
ENSMUSG00000020027	chr10	Socs2	-0.7906421	0.004995845	0.00940236	3.764675147	0.088774753	-1	263	338	363	169	111	191	179	169	136	132
ENSMUSG00000029714	chr5	Gigyf1	-0.4497604	0.004995477	0.00940236	4.691711592	0.028174317	-1	440	434	422	559	367	501	299	296	278	421
ENSMUSG00000026048	chr1	Ercc5	-0.414947	0.004998485	0.009406062	3.783105608	0.021300228	-1	220	217	202	289	236	207	203	170	176	201
ENSMUSG00000006301	chr1	Tmbim1	0.45064945	0.005008376	0.009423406	6.25816459	0.029904268	1	1017	836	845	1168	952	1968	1240	1107	1512	1432
ENSMUSG00000052738	chr6	Suclg1	-0.4325183	0.005009333	0.009423938	8.240945137	0.028159802	-1	4957	5230	5148	6327	4255	3982	4246	4006	4251	4466
ENSMUSG00000044938	chr9	Klhl31	-0.5821536	0.005011349	0.009426461	8.735243655	0.05105169	-1	9755	7149	6479	7961	6628	3558	6184	5293	4966	7718
ENSMUSG00000028019	chr3	Pdgfc	0.89747418	0.005035977	0.009471514	1.212544804	0.086236704	1	11	26	25	29	22	60	28	43	38	64
ENSMUSG00000033044	chr11	Dhrs7c	-0.4974905	0.005046397	0.009489834	8.116284707	0.037309619	-1	4815	4566	4132	5801	4884	2946	3634	3078	4081	4990
ENSMUSG00000024937	chr19	Ehbp1l1	-0.4697719	0.005048436	0.00949239	9.271424405	0.03340004	-1	10590	8602	8847	14499	11310	7709	8279	8416	9057	8590
ENSMUSG00000037621	chr6	Atoh8	0.82423176	0.005063064	0.009518614	2.185426244	0.084911593	1	45	42	38	54	57	173	75	97	57	64
ENSMUSG00000090000	chr18	Ier3ip1	0.39218518	0.005077148	0.009543809	5.503288194	0.021936127	1	610	557	524	706	523	1036	867	739	761	808
ENSMUSG00000078572	chr11	1810043H04Rik	0.49912754	0.005084724	0.009556764	4.067329511	0.03385048	1	234	199	174	251	173	457	250	323	307	258
ENSMUSG00000036225	chr18	Kctd1	0.77990681	0.005085827	0.009557552	1.404995936	0.063100654	1	28	34	21	39	17	67	68	41	44	41
ENSMUSG00000021913	chr14	Ogdhl	1.12432962	0.005086729	0.009557962	0.976517957	0.148144413	1	16	19	14	21	16	25	19	77	29	51
ENSMUSG00000054115	chr15	Skp2	0.92104104	0.005088221	0.00955948	1.641597052	0.103911619	1	48	23	31	30	21	61	114	41	61	43
ENSMUSG00000020676	chr11	Ccl11	-0.4913723	0.005091386	0.009564141	3.690340016	0.031740759	-1	193	237	243	223	206	210	198	160	162	140
ENSMUSG00000067370	chr17	B3galt4	0.72753694	0.00511571	0.009608542	1.219947437	0.047226589	1	26	29	18	28	22	48	53	38	40	45
ENSMUSG00000059486	chr6	Kbtbd2	-0.4006618	0.005118313	0.009612139	4.427246823	0.021418143	-1	350	361	339	449	319	294	348	253	274	340
ENSMUSG00000023939	chr17	Mrpl14	0.45895686	0.00512128	0.00961642	5.441746399	0.030603138	1	534	525	537	736	409	951	726	835	903	666
ENSMUSG00000016253	chr2	Nelfcd	0.42456348	0.005129853	0.009631224	5.065936053	0.025545744	1	413	393	396	554	377	574	623	715	510	684
ENSMUSG00000092544	chr8	Gm20422	-0.930183	0.00513878	0.009646688	1.250773056	0.098329596	-1	39	46	51	56	30	10	26	20	34	36
ENSMUSG00000063952	chr17	Brpf3	-0.518646	0.005142983	0.009653281	3.673336554	0.035663359	-1	189	158	205	295	265	206	164	150	132	202
ENSMUSG00000001436	chr10	Slc19a1	0.51788477	0.005152481	0.009669771	2.920602573	0.031860424	1	88	104	70	104	89	150	153	134	146	131
ENSMUSG00000035863	chr10	Palm	0.45017302	0.005153152	0.009669771	4.083696532	0.026828741	1	206	188	205	255	205	415	298	285	234	367
ENSMUSG00000071252	chr13	2210408I21Rik	-0.798793	0.005174915	0.009709304	0.930851125	0.059182193	-1	27	35	34	34	38	25	22	14	23	23
ENSMUSG00000037638	chr12	Zbtb42	0.65077576	0.005180164	0.009717848	2.102835688	0.047203986	1	43	58	49	57	34	108	93	60	80	77
ENSMUSG00000029475	chr5	Kdm2b	-0.486651	0.00518616	0.009727792	3.35570887	0.029512556	-1	137	170	164	239	174	154	148	101	132	157
ENSMUSG00000020038	chr10	Cry1	-0.6054936	0.005198319	0.00974929	3.1143903	0.04780627	-1	146	126	161	200	138	79	121	75	136	141
ENSMUSG00000089798	chr5	1700028K03Rik	-0.8413378	0.005206369	0.009763077	0.727891304	0.061867691	-1	26	22	29	41	30	21	12	16	17	24
ENSMUSG00000020682	chr11	Mmp28	-0.9466596	0.005232963	0.009811629	0.947442461	0.094444024	-1	44	23	32	46	34	9	17	22	20	32
ENSMUSG00000039483	chr2	Asb6	0.46106295	0.005249943	0.009842147	3.390098288	0.025985511	1	139	127	126	146	110	246	211	153	174	202
ENSMUSG00000040652	chr9	Oaz2	-0.4233528	0.005272464	0.009883041	7.882101025	0.027239642	-1	4496	3885	3790	4596	3355	3332	3170	3011	3188	3743
ENSMUSG00000085455	chr5	1810059H22Rik	1.18923831	0.005274727	0.009885957	-0.285473885	0.099981565	1	5	7	6	8	5	18	23	18	12	7
ENSMUSG00000029403	chr5	Cdkl2	-0.5879426	0.005286031	0.009905815	2.72957399	0.041989118	-1	106	118	106	145	109	77	92	61	112	82
ENSMUSG00000012076	chr12	Brms1l	-0.4406785	0.005298589	0.009926686	4.062811046	0.0258509	-1	311	256	260	305	285	207	242	201	241	256
ENSMUSG00000041231	chr11	Ublcp1	-0.4316661	0.005298583	0.009926686	3.893757707	0.024108701	-1	270	239	255	307	194	202	236	180	202	205
ENSMUSG00000021388	chr13	Aspn	-0.5221262	0.005301015	0.009928829	4.872482559	0.039583764	-1	530	486	563	604	380	386	413	342	248	580
ENSMUSG00000055044	chr19	Pdlim1	1.09868332	0.005301154	0.009928829	5.706774733	0.179499375	1	208	273	323	1581	311	1821	863	1510	871	734
ENSMUSG00000041966	chr2	Dcaf17	-0.6016559	0.005313074	0.009949823	2.433549492	0.042510268	-1	98	92	73	116	97	86	72	43	77	67
ENSMUSG00000005354	chr15	Txn2	0.43119047	0.005319619	0.009960745	8.011820554	0.028347797	1	3197	3262	3242	4192	2552	5282	4359	4820	4849	4827
ENSMUSG00000071855	chr18	Ccdc112	1.15701613	0.00532981	0.009978489	-0.315674323	0.091764739	1	4	8	2	11	6	16	18	12	10	20
ENSMUSG00000066877	chr1	Nck2	-0.5345765	0.005337463	0.009991479	4.427052721	0.040725899	-1	390	374	336	422	359	186	290	228	315	402
ENSMUSG00000054484	chr2	Tmem62	0.63689033	0.005357721	0.010028058	2.415821428	0.048866567	1	75	45	51	73	60	138	90	116	78	96
ENSMUSG00000044791	chr9	Setd2	-0.3805697	0.00537004	0.010049769	5.103235109	0.020441894	-1	541	528	493	755	583	549	495	410	449	537

ENSMUSG00000024065	chr17	Ehd3	0.66693517	0.005371685	0.010051502	1.992162765	0.050194318	1	39	40	35	64	45	68	81	61	69	107
ENSMUSG00000028878	chr4	Fam76a	-0.4765399	0.005375596	0.010057473	4.676490673	0.032419451	-1	497	485	418	505	305	343	404	236	347	417
ENSMUSG00000043131	chr6	Mob1a	0.44023722	0.005385283	0.010073087	5.246652981	0.028099455	1	455	505	418	605	418	901	777	464	748	698
ENSMUSG00000079283	chr1	2310009B15Rik	0.57823168	0.005385382	0.010073087	2.621713492	0.040923276	1	70	75	57	105	57	95	129	105	122	136
ENSMUSG00000024527	chr18	Afg3l2	-0.4630837	0.005389238	0.010078949	6.413233162	0.03224837	-1	1241	1441	1353	2204	1210	1007	1133	1125	1228	1320
ENSMUSG00000092243	chr17	Gm7030	2.09394073	0.005402951	0.010103243	0.986758851	0.552540001	1	8	14	13	4	10	61	36	7	1	146
ENSMUSG00000037376	chr2	Trmt6	0.52976182	0.00540896	0.010113127	3.491700864	0.037060935	1	179	125	121	148	105	225	237	161	262	187
ENSMUSG00000043510	chr5	Hscb	0.57771197	0.005418838	0.010130241	2.570673434	0.039178043	1	73	64	68	77	64	151	112	82	125	101
ENSMUSG00000019564	chr10	Arid3a	0.68384622	0.005419889	0.01013085	2.289990925	0.056888422	1	56	50	54	71	42	106	117	66	60	135
ENSMUSG00000031161	chrX	Hdac6	0.50767169	0.0054322	0.010152504	3.12626993	0.032191743	1	120	102	80	130	99	165	150	143	197	167
ENSMUSG00000041729	chr9	Coro2b	0.51891447	0.005436007	0.010158261	3.240038716	0.034227853	1	89	108	94	152	129	222	162	171	142	203
ENSMUSG00000077450	chr17	Rab11b	0.41200416	0.005439498	0.010163426	6.498718546	0.025508274	1	1171	1070	960	1393	1184	2071	1673	1554	1397	1766
ENSMUSG00000025880	chr18	Smad7	-0.6905221	0.005441301	0.010165436	2.650683435	0.062480851	-1	106	104	141	141	76	123	88	49	51	81
ENSMUSG00000029298	chr5	Gbp9	-0.8778237	0.005456829	0.010193083	1.56715751	0.092533295	-1	48	68	55	60	43	14	35	27	34	53
ENSMUSG00000032468	chr9	Armc8	-0.4893764	0.005463652	0.010204463	5.377609594	0.035387631	-1	782	639	634	847	706	398	601	479	588	739
ENSMUSG00000039623	chr5	Ap5z1	0.64098788	0.005471807	0.010218329	2.549392614	0.050767587	1	66	73	62	70	60	144	133	66	133	97
ENSMUSG00000019804	chr10	Snx3	0.41204601	0.005487	0.010245332	6.865301198	0.025752697	1	1549	1300	1240	1948	1455	2483	2435	1849	2146	1973
ENSMUSG00000022151	chr15	Ttc33	-0.4946882	0.005489002	0.010247701	4.716857255	0.035285466	-1	510	505	424	466	365	268	348	305	410	434
ENSMUSG00000094595	chr4	Fsbp	-0.976661	0.005492483	0.01025283	0.847346251	0.100826939	-1	38	40	21	39	29	8	26	11	24	23
ENSMUSG00000027276	chr2	Jag1	-0.5194998	0.005494928	0.010256025	3.463408612	0.03568844	-1	177	155	160	290	189	203	169	99	127	143
ENSMUSG00000018566	chr11	Slc2a4	-0.4734168	0.005495994	0.010256645	8.274198808	0.034484724	-1	4228	5067	5135	8173	4565	3813	4367	3755	4479	4685
ENSMUSG00000030374	chr7	Strn4	0.43503027	0.005515102	0.010290929	4.708248652	0.02674727	1	325	304	331	405	285	653	454	507	362	477
ENSMUSG00000004837	chr11	Grap	0.64514692	0.00552538	0.010308731	2.965959233	0.055241606	1	81	106	82	123	58	257	121	141	124	130
ENSMUSG00000024304	chr18	Cdh2	0.78007159	0.005536096	0.010327346	1.711431737	0.072593638	1	36	28	32	56	23	68	83	81	41	50
ENSMUSG00000021456	chr13	Fbp2	-0.6157026	0.005553769	0.01035795	5.938662383	0.057529384	-1	777	858	720	1912	1370	1089	729	561	655	967
ENSMUSG00000060981	chr13	Hist1h4h	0.51522176	0.005553984	0.01035795	3.08062817	0.033348923	1	97	105	99	146	69	161	157	131	166	186
ENSMUSG00000020527	chr11	Myo19	-0.7160632	0.005555163	0.010358766	1.742975071	0.05714046	-1	46	65	64	68	55	43	49	42	39	26
ENSMUSG00000024208	chr17	Uqcc2	0.43999363	0.005558797	0.010364161	6.961496937	0.029556067	1	1858	1396	1375	1881	1386	2093	2358	2279	2595	2303
ENSMUSG00000024782	chr19	Ak3	-0.4601547	0.005566625	0.010377371	6.456049325	0.032126931	-1	1419	1546	1389	1887	1342	996	1305	1237	984	1485
ENSMUSG00000028426	chr4	Rad23b	-0.433015	0.005570904	0.010383963	6.658269659	0.028487489	-1	1807	1618	1508	2139	1592	1182	1641	1252	1379	1538
ENSMUSG00000038578	chr4	Susd1	1.13275642	0.005576949	0.010393844	0.665192237	0.139951921	1	14	16	9	9	18	69	16	27	27	26
ENSMUSG00000062116	chr7	Zfp954	0.61021941	0.005580313	0.010398728	2.332074252	0.043558253	1	62	54	54	68	51	147	88	75	91	87
ENSMUSG00000037262	chr2	Kin	0.55690471	0.005581211	0.010399015	2.580841483	0.036659097	1	66	67	60	97	65	145	100	113	114	97
ENSMUSG00000024833	chr19	Pola2	0.40541661	0.005588421	0.01041106	4.18596228	0.021964781	1	209	212	232	314	198	341	361	319	317	342
ENSMUSG00000034724	chr5	Cnot6l	-0.42569	0.005590158	0.010412907	4.640165078	0.025518916	-1	393	384	370	594	398	363	358	333	256	425
ENSMUSG00000020537	chr11	Drg2	0.38497905	0.005605902	0.010439472	4.677492493	0.020378396	1	328	332	303	364	312	549	507	402	427	479
ENSMUSG00000031818	chr8	Cox4i1	0.47103518	0.005605913	0.010439472	9.661439347	0.034439895	1	8948	10198	9455	14533	8003	20028	12824	15691	13765	14674
ENSMUSG00000039117	chr2	Taf4a	-0.475084	0.005621239	0.010466618	3.289904737	0.028375951	-1	160	144	154	206	174	143	163	100	125	132
ENSMUSG00000024875	chr19	Yif1a	0.4053635	0.00562214	0.010466902	5.157006167	0.023731948	1	476	422	412	566	410	888	661	618	586	571
ENSMUSG00000033857	chr11	Engase	0.6287918	0.005623938	0.010468855	3.463251327	0.054279329	1	102	143	105	115	162	203	175	209	173	321
ENSMUSG00000039958	chr6	Mettl20	-0.5671507	0.005626197	0.010471665	3.145973486	0.042260728	-1	173	170	159	157	114	118	96	121	87	153
ENSMUSG00000022676	chr16	Snai2	0.75883307	0.005628287	0.01047416	1.592559515	0.063683002	1	34	24	38	37	26	51	70	58	38	79
ENSMUSG00000021578	chr13	Ccdc127	-0.3805915	0.005654167	0.01052092	5.190747768	0.020805279	-1	634	561	529	808	557	541	590	437	473	549
ENSMUSG00000104357	chr3	TTC14	-0.5931425	0.005656773	0.010524369	2.556419061	0.042917828	-1	112	95	95	117	97	64	79	56	98	77
ENSMUSG00000043587	chr9	Pxylp1	0.71322689	0.005665044	0.010538354	1.899332468	0.058210163	1	46	36	35	38	46	77	93	65	79	50
ENSMUSG00000041263	chr3	Rusc1	0.41886712	0.005666834	0.010540282	3.909480899	0.023038809	1	168	189	181	268	152	312	283	267	254	277
ENSMUSG00000037204	chr15	Atg101	0.40371802	0.00567421	0.010552596	5.207640727	0.023639004	1	503	437	482	562	380	826	581	620	685	720
ENSMUSG00000021255	chr12	Esrrb	-1.3398847	0.005684792	0.010570869	1.724404164	0.247901578	-1	24	39	47	213	43	56	26	31	24	10
ENSMUSG00000043795	chr7	Prr33	-0.4343886	0.005692077	0.010583008	7.362672968	0.029076874	-1	2881	2357	2600	3664	2655	2048	2264	2016	2499	2557
ENSMUSG00000043251	chr8	Exoc3l	0.9384098	0.005700342	0.010596964	2.242560255	0.12053877	1	58	37	42	67	34	106	57	186	53	83
ENSMUSG00000031065	chrX	Cdk16	-0.4076173	0.005706729	0.010607426	7.497274136	0.025628198	-1	2878	2769	2805	4005	2950	2662	2371	2375	2456	2806
ENSMUSG00000019927	chr10	Ube2d1	-0.492409	0.0057264	0.010642576	7.771100573	0.037583212	-1	4201	3707	3059	4417	3644	2266	3000	2618	2860	4030
ENSMUSG00000049624	chr9	Slc17a5	0.60685016	0.005727541	0.01064328	2.844830788	0.047370207	1	89	84	85	100	59	170	154	76	155	146
ENSMUSG00000027677	chr3	Ttc14	-0.4503255	0.005759263	0.010700805	3.622715817	0.026513765	-1	220	209	191	225	200	166	179	134	195	167
ENSMUSG00000004568	chr8	Arhgef18	-0.4606153	0.005786695	0.010750345	3.356518024	0.026805403	-1	160	160	142	235	182	166	139	109	128	158
ENSMUSG00000041189	chr11	Chrnb1	0.44260027	0.005791184	0.010757255	6.393001441	0.029926086	1	1285	1059	938	1119	885	1685	1466	1708	1358	1659
ENSMUSG00000031154	chrX	Otud5	0.40152044	0.005800458	0.01077305	4.476225708	0.02222978	1	304	297	246	324	249	524	374	351	369	451
ENSMUSG00000073680	chr4	Tmem88b	0.82746079	0.005805944	0.010781806	1.155286223	0.074376219	1	30	28	14	22	18	35	43	46	34	60
ENSMUSG00000079677	chr9	Fdx1l	0.42077734	0.005820771	0.010807904	4.812184374	0.0254925	1	321	317	320	503	336	664	499	499	529	426
ENSMUSG00000032119	chr9	Hinfp	-0.8511226	0.005831191	0.010825814	1.392417068	0.083990364	-1	53	56	61	45	24	28	40	25	30	23
ENSMUSG00000040822	chr14	1700123O20Rik	0.49211586	0.005849883	0.010859074	3.397432526	0.03137271	1	162	123	128	141	90	231	206	197	173	187
ENSMUSG00000019428	chr8	Fkbp8	0.41069077	0.005857707	0.01087071	6.959016308	0.02600305	1	1847	1548	1405	1717	1413	2572	2251	1953	2346	2487
ENSMUSG00000046404	chr1	Yod1	-0.5797939	0.005857706	0.01087071	2.339926122	0.039133345	-1	79	82	98	101	80	65	80	55	61	63
ENSMUSG00000100621	chr19	Gm28374	0.60776264	0.00586825	0.010888829	2.352982098	0.043498319	1	46	54	67	77	50	131	89	91	95	86
ENSMUSG00000078570	chr4	1110065P20Rik	0.4242073	0.005886489	0.010921223	3.769182466	0.023426705	1	173	159	165	218	147	285	233	249	264	230

ENSMUSG00000044548	chr12	Dact1	0.53280286	0.005895498	0.010936486	2.854215269	0.035179332	1	90	83	79	119	65	154	132	132	102	168
ENSMUSG00000042677	chr4	Zc3h12a	0.74215365	0.005918994	0.010978615	2.286709104	0.070672241	1	45	39	65	81	37	154	75	70	73	120
ENSMUSG00000036002	chr4	Fam214b	0.39854453	0.005920668	0.010980263	5.29798658	0.023398071	1	528	451	468	666	425	893	666	714	612	768
ENSMUSG00000033446	chr14	Lpar6	0.63733992	0.005929354	0.010994911	2.493671447	0.050509124	1	70	80	60	65	44	122	127	79	84	139
ENSMUSG00000030110	chr6	Ret	-0.659526	0.005934865	0.011003671	3.892812589	0.06362701	-1	220	215	286	278	329	102	217	208	149	249
ENSMUSG00000054708	chr10	Ankrd24	-0.5327691	0.0059432	0.011017664	2.612614677	0.033653856	-1	117	108	89	117	97	101	74	65	81	81
ENSMUSG00000062691	chr17	Cebpzos	0.49597644	0.005960043	0.011047422	3.84206958	0.033983571	1	161	188	184	190	150	205	295	258	305	284
ENSMUSG00000045438	chr5	Cox19	0.38060131	0.005963145	0.011051707	5.011149984	0.020888592	1	399	417	377	554	346	684	591	570	587	534
ENSMUSG00000040694	chr17	Apobec2	-0.472592	0.005972189	0.011067	8.716315489	0.035108292	-1	7043	6644	6787	10011	6247	4750	5280	5270	5836	7521
ENSMUSG00000026889	chr2	Rbm18	-0.3910093	0.005987029	0.01109303	5.463704336	0.022713139	-1	813	738	649	883	645	694	605	563	549	708
ENSMUSG00000067916	chr4	Gm13139	1.20784579	0.005990387	0.011097779	0.165535029	0.154023456	1	10	8	8	9	9	7	39	12	30	24
ENSMUSG00000102426	chrX	RP23-330G24.3	0.94427317	0.006018744	0.011148835	0.325401189	0.078789016	1	12	11	5	22	8	32	21	19	21	28
ENSMUSG00000026657	chr2	Frmd4a	0.4453554	0.00602196	0.011153314	3.497098093	0.025390137	1	155	120	132	182	119	234	246	175	176	225
ENSMUSG00000037070	chr8	Rbmxl1	0.56571161	0.006024405	0.011156365	2.956703906	0.041159267	1	69	93	97	111	87	164	201	118	140	123
ENSMUSG00000024234	chr18	Mtpap	-0.4205763	0.006037027	0.011178258	4.031658087	0.023969402	-1	286	268	268	330	234	221	229	206	199	280
ENSMUSG00000039270	chr4	Megf9	-0.6723225	0.006039908	0.01118211	2.658267716	0.060237747	-1	84	96	110	141	135	72	85	52	112	68
ENSMUSG00000062846	chr2	Gm14176	1.13688801	0.006069367	0.011235161	-0.249063238	0.100701884	1	5	6	4	10	8	17	12	20	21	9
ENSMUSG00000017929	chr2	B4galt5	0.4842921	0.006081939	0.011255453	4.763786303	0.034558227	1	361	319	359	355	276	740	633	369	398	470
ENSMUSG00000070305	chr9	Mpzl3	-0.8141328	0.006081456	0.011255453	1.735479288	0.084466789	-1	64	74	54	48	61	64	32	19	31	48
ENSMUSG00000022723	chr16	Crybg3	-0.5724859	0.00608619	0.011261829	4.535634632	0.048890421	-1	328	340	468	525	394	184	344	288	272	419
ENSMUSG00000003934	chr11	Efnb3	-0.9553788	0.006097036	0.011280405	0.257908696	0.083366332	-1	10	22	21	28	25	14	14	9	9	14
ENSMUSG00000028998	chr5	Tomm7	0.45223074	0.006102108	0.011288293	5.828955829	0.031301616	1	853	741	600	833	553	1405	1078	969	1090	824
ENSMUSG00000086915	chr10	Gm16365	0.85619937	0.006107213	0.011296242	0.612163423	0.065057799	1	14	18	9	19	14	40	24	32	24	27
ENSMUSG00000023707	chr5	Ogfod2	0.48869657	0.00613747	0.011350706	3.809228965	0.032726548	1	174	157	165	161	193	322	260	270	262	208
ENSMUSG00000033114	chr13	Slc35d2	0.8903037	0.006162837	0.011396112	0.636756895	0.073966831	1	17	18	11	17	11	50	28	23	28	23
ENSMUSG00000038086	chr9	Hspb2	0.47515174	0.006173057	0.0114135	6.346234121	0.035100178	1	1268	928	933	1040	874	1375	1287	1621	1643	1731
ENSMUSG00000020381	chr11	3010026O09Rik	0.73617797	0.006174256	0.011414206	1.757841352	0.063355362	1	43	46	30	37	25	51	68	78	69	62
ENSMUSG00000033633	chr8	Clec18a	-1.1415901	0.00618061	0.011424442	-0.045375234	0.115742137	-1	23	26	13	21	5	9	8	7	10	9
ENSMUSG00000019088	chrX	Dnase1l1	-0.5011323	0.006201874	0.011462231	6.814092651	0.039415042	-1	2510	2156	1728	1747	1584	1529	1671	1076	1570	1786
ENSMUSG00000053774	chr16	Ubxn7	-0.401314	0.00621348	0.011482162	4.236485265	0.022279179	-1	294	330	317	379	268	314	269	231	219	292
ENSMUSG00000088559	chr1	Mir1981	0.85578149	0.006229213	0.011509715	0.799754166	0.070456305	1	17	12	21	21	14	44	21	36	33	35
ENSMUSG00000031714	chr8	Gab1	-0.4156358	0.006271574	0.011586454	4.411884763	0.024547742	-1	325	374	319	492	307	345	280	243	251	372
ENSMUSG00000089682	chr14	Bcl2l2	-0.3751733	0.006274551	0.01159042	5.211892307	0.020711546	-1	607	599	555	825	543	515	575	488	501	545
ENSMUSG00000043366	chr7	Olfr78	-1.1211879	0.006279235	0.01159754	0.373653705	0.131216685	-1	15	16	19	35	36	17	5	17	14	7
ENSMUSG00000043770	chr4	Gm12481	0.41038716	0.006281817	0.011600776	5.379034343	0.025348173	1	636	484	515	602	418	852	756	755	781	715
ENSMUSG00000047485	chrX	Klhl34	-1.59469	0.006282926	0.011601292	2.417045851	0.368386191	-1	10	80	96	402	50	64	32	53	46	14
ENSMUSG00000026784	chr2	Pdss1	-0.5432355	0.006307273	0.011644708	3.038822146	0.038480081	-1	135	125	157	184	117	99	130	96	125	86
ENSMUSG00000025878	chr13	Uimc1	0.45917496	0.006331405	0.011687719	3.916563667	0.029156093	1	229	206	161	195	146	338	311	206	279	290
ENSMUSG00000048787	chr7	Dcun1d3	-0.4281697	0.006333278	0.011689633	3.745575277	0.024416871	-1	253	169	220	283	215	208	192	163	172	193
ENSMUSG00000075229	chr16	Ccdc58	0.46198582	0.00634708	0.01171356	3.674258575	0.029011773	1	152	168	139	215	124	261	244	241	257	188
ENSMUSG00000051256	chr6	Jagn1	0.37375187	0.006353809	0.01172443	4.742413661	0.019879502	1	367	334	310	388	326	537	532	441	476	471
ENSMUSG00000024050	chr17	Wiz	-0.4246696	0.006374156	0.011760423	4.388907213	0.025871182	-1	340	309	306	457	373	361	278	247	225	353
ENSMUSG00000032114	chr9	Slc37a4	-0.5007881	0.006376871	0.01176388	7.661584857	0.039879367	-1	3988	3432	3058	3551	3510	2564	2626	2658	1972	3891
ENSMUSG00000025144	chr11	Stra13	0.40977368	0.006379244	0.011766703	4.149087314	0.023078742	1	255	218	203	249	200	376	335	251	343	342
ENSMUSG00000035469	chr14	Rcbtb1	-0.4335536	0.006396523	0.011795462	4.25203807	0.02664316	-1	303	331	284	413	296	218	294	214	283	304
ENSMUSG00000042396	chr9	Rbm7	-0.5033154	0.006395868	0.011795462	3.390187136	0.034291213	-1	184	189	128	228	181	149	139	93	148	175
ENSMUSG00000022247	chr15	Brix1	0.42659354	0.00639934	0.0117991	4.166824708	0.025646529	1	241	211	206	310	176	332	384	298	360	292
ENSMUSG00000059208	chr17	Hnrnpm	0.44246258	0.006416332	0.011828869	6.494619677	0.030735335	1	1088	1112	945	1447	1116	1864	2091	1461	1748	1311
ENSMUSG00000068245	chr14	Phf11d	0.74627213	0.006422471	0.011838625	1.809811958	0.066332153	1	38	52	40	30	25	58	75	67	61	83
ENSMUSG00000031311	chrX	Nono	0.40860076	0.006448588	0.011885199	6.156184464	0.025962098	1	1079	875	775	1071	770	1347	1507	1249	1157	1373
ENSMUSG00000026162	chr1	Nhej1	0.55338593	0.006472285	0.011927147	2.49471341	0.037120632	1	65	58	64	94	54	115	91	94	121	113
ENSMUSG00000036751	chr7	Cox6b1	0.4443508	0.006473055	0.011927147	8.903860009	0.031675664	1	5990	6189	5677	7781	4757	10910	7596	9632	8387	8498
ENSMUSG00000032012	chr9	Pvrl1	0.70603202	0.00648013	0.01193861	2.269757861	0.064780289	1	54	43	39	68	62	147	97	102	59	73
ENSMUSG00000027412	chr2	Lpin3	0.71501478	0.006481533	0.011939472	2.699796168	0.070875578	1	65	75	62	96	63	67	143	175	125	124
ENSMUSG00000035378	chr6	Shq1	0.75520389	0.006482306	0.011939472	1.136190553	0.05867638	1	29	18	16	36	17	45	51	33	45	38
ENSMUSG00000043155	chr4	Hpdl	0.87873553	0.006488861	0.01194997	1.279216893	0.094729005	1	25	24	24	37	12	37	46	76	37	43
ENSMUSG00000024866	chr19	Acy3	0.72634463	0.006496467	0.011962401	2.103432903	0.067656087	1	50	52	41	51	39	76	70	107	51	118
ENSMUSG00000086596	chr9	Susd5	-0.7327058	0.006506016	0.011978406	1.732767577	0.064057065	-1	52	68	50	74	55	42	40	51	40	22
ENSMUSG00000026479	chr1	Lamc2	1.06913521	0.006509978	0.011982543	1.481252	0.151403502	1	18	19	26	33	31	113	58	63	46	16
ENSMUSG00000028212	chr4	Ccne2	-0.720964	0.00650985	0.011982543	1.839182358	0.063169797	-1	63	64	57	75	62	41	68	22	39	45
ENSMUSG00000042616	chr4	Oscp1	0.84950592	0.006521881	0.012002872	0.695306606	0.065418309	1	15	16	15	20	13	22	34	28	40	31
ENSMUSG00000036856	chr4	Wnt4	-0.5824574	0.006534878	0.012024925	4.677792186	0.051949349	-1	466	404	301	518	581	269	355	208	436	396
ENSMUSG00000048186	chr2	Bend7	-0.8473834	0.006535585	0.012024925	0.72276287	0.071891612	-1	25	27	27	48	22	27	20	9	18	16
ENSMUSG00000031520	chr8	Vegfc	-0.736085	0.006546276	0.012043011	1.430280451	0.059511543	-1	50	47	50	60	34	41	33	25	39	20
ENSMUSG00000055839	chr17	Tceb2	0.46456744	0.006552078	0.012052098	7.138583719	0.034364091	1	2238	1685	1565	1766	1518	3710	2535	2311	2547	2313

ENSMUSG00000022338	chr15	Eny2	0.41358428	0.006556014	0.012057751	4.743110131	0.025111706	1	323	320	341	418	302	650	542	468	435	401
ENSMUSG00000032040	chr9	Dcps	0.49630954	0.006560065	0.012063613	3.375627117	0.033263139	1	127	123	110	162	114	290	177	162	199	158
ENSMUSG00000020333	chr11	Acsl6	-0.616876	0.006567879	0.012076394	4.255366001	0.057551312	-1	333	294	285	482	335	140	199	209	279	388
ENSMUSG00000027803	chr3	Wwtr1	-0.4215364	0.006573628	0.012085375	5.120084447	0.026828665	-1	558	593	610	739	464	451	472	456	411	630
ENSMUSG00000061371	chr10	Zfp873	-0.8657045	0.006575933	0.012088024	0.683089453	0.074391919	-1	36	27	23	41	18	21	16	10	24	15
ENSMUSG00000029029	chr4	Wrap73	0.43659032	0.006583257	0.012099894	3.648361486	0.025622942	1	140	163	147	219	123	274	218	204	246	225
ENSMUSG00000039782	chr5	Cpeb2	-0.5842963	0.006597294	0.0121241	3.16831693	0.047391224	-1	171	136	162	206	123	89	109	84	122	176
ENSMUSG00000059412	chr9	Fxyd2	1.11382897	0.006605342	0.012137294	0.860623086	0.146052155	1	11	28	12	10	16	75	26	38	24	27
ENSMUSG00000025470	chr7	Zfp511	0.63802768	0.006614679	0.012152853	2.425677396	0.052039789	1	70	53	51	56	72	141	121	81	101	80
ENSMUSG00000039852	chr4	Rere	-0.4585009	0.006627571	0.012174938	6.487663134	0.03331368	-1	1295	1403	1311	2172	1608	1274	1169	1127	964	1654
ENSMUSG00000034042	chr4	Gpbp1l1	-0.4196082	0.006628971	0.01217591	4.449221661	0.025485546	-1	307	346	329	538	351	332	286	268	258	380
ENSMUSG00000030739	chr7	Myh14	-0.3981991	0.006633469	0.012181322	4.6561899	0.023071995	-1	394	420	343	569	414	444	310	337	330	352
ENSMUSG00000036427	chr7	Gpi1	0.62961082	0.006634473	0.012181322	9.967452741	0.063834225	1	11968	10160	9484	15134	12107	11065	18558	20511	16916	31498
ENSMUSG00000042997	chr3	Nhlrc3	0.53759985	0.006634532	0.012181322	3.076293089	0.038161339	1	96	75	114	128	92	222	159	111	149	170
ENSMUSG00000032422	chr9	Snx14	-0.4309966	0.006642986	0.012195241	4.00938872	0.025930493	-1	268	266	243	356	242	222	215	169	261	245
ENSMUSG00000034795	chr14	Ccdc122	0.91582728	0.00666156	0.012227733	0.416197976	0.071449932	1	14	11	17	9	10	23	25	24	24	32
ENSMUSG00000021811	chr14	Dnajc9	0.42719052	0.006662549	0.012227942	4.231322103	0.02609312	1	257	243	221	300	171	388	401	303	361	295
ENSMUSG00000049939	chr6	Lrrc4	1.24836116	0.006675632	0.012250346	-0.160030252	0.141588311	1	3	9	6	7	8	31	19	21	10	7
ENSMUSG00000040624	chr10	Plekhg1	-0.5455083	0.006684188	0.012264437	2.906849042	0.039204982	-1	107	142	114	178	116	93	112	95	69	122
ENSMUSG00000030946	chr7	Lhpp	-0.4198275	0.006693039	0.012279064	4.339446685	0.025490248	-1	387	333	267	381	346	360	312	222	233	291
ENSMUSG00000015243	chr4	Abca1	0.8943792	0.006703743	0.012293913	4.556683931	0.124734228	1	214	291	257	236	206	630	389	321	151	1053
ENSMUSG00000022760	chr16	Thap7	0.44800749	0.006703771	0.012293913	3.420916327	0.026045104	1	115	135	129	153	132	216	207	195	195	182
ENSMUSG00000025175	chr11	Fn3k	0.48185232	0.006702055	0.012293913	3.870241401	0.033116005	1	165	192	166	222	157	265	228	349	244	281
ENSMUSG00000025403	chr10	Shmt2	0.40118517	0.006714246	0.012311507	5.408409987	0.024647537	1	518	490	483	761	492	997	765	780	662	744
ENSMUSG00000020846	chr11	Fam101b	-0.4677071	0.006757411	0.012389031	5.188194195	0.033739125	-1	707	660	573	737	473	470	458	544	361	654
ENSMUSG00000097080	chr18	1700086O06Rik	0.94228022	0.006779588	0.01242806	0.663751985	0.089612698	1	19	14	19	12	9	44	23	38	21	30
ENSMUSG00000028646	chr4	Rragc	0.41569666	0.006796279	0.012457022	5.081062094	0.026216719	1	438	418	360	588	369	771	708	423	546	734
ENSMUSG00000031502	chr8	Col4a1	-0.4489822	0.006805455	0.012472206	9.166971676	0.032758824	-1	8705	9298	9994	13108	8553	8712	7396	8295	6043	9284
ENSMUSG00000026798	chr2	Coq4	0.51989101	0.006809801	0.012478533	3.094806609	0.036194652	1	86	119	102	144	68	166	159	159	165	158
ENSMUSG00000021290	chr12	2010107E04Rik	0.44966565	0.006830015	0.012513935	7.785160683	0.032698151	1	3002	2936	2842	3165	1937	4640	3625	4085	4316	4074
ENSMUSG00000033032	chr18	Afap1l1	-0.5103311	0.006838378	0.012527615	6.388900153	0.041620689	-1	1411	1412	1342	1861	1326	752	1022	1048	1359	1401
ENSMUSG00000063275	chr2	Ptpla	-0.4412227	0.006853276	0.012553262	7.337366506	0.031395033	-1	3312	2628	2421	2916	2539	1921	2448	2110	2121	2559
ENSMUSG00000036503	chr3	Rnf13	-0.535285	0.006858294	0.012560807	4.91646089	0.044471405	-1	629	506	450	620	454	278	472	256	472	526
ENSMUSG00000012483	chr6	Rpa3	0.64676869	0.00686147	0.012564977	2.641285245	0.056905634	1	77	77	76	75	48	157	146	86	140	82
ENSMUSG00000021111	chr12	Papola	-0.4026534	0.006892756	0.012620616	5.892639124	0.025437746	-1	1034	883	938	1205	971	873	957	672	903	768
ENSMUSG00000027651	chr2	Rprd1b	-0.3819863	0.006912713	0.012655498	5.323148656	0.022258382	-1	629	629	619	869	632	556	594	496	528	659
ENSMUSG00000032387	chr9	Rbpms2	0.75104448	0.006920979	0.012668971	1.964271303	0.072157204	1	27	44	43	54	41	82	71	111	52	67
ENSMUSG00000032258	chr9	Lca5	-0.9005993	0.006931307	0.012686215	0.236430766	0.064372994	-1	23	19	16	24	21	12	13	10	16	9
ENSMUSG00000044702	chr7	Palb2	1.3024054	0.00698058	0.012774726	-0.284534173	0.151141554	1	5	9	6	5	4	16	24	6	26	8
ENSMUSG00000098140	chr5	Gm26938	0.65248868	0.006982607	0.012776763	2.63488394	0.058545505	1	92	62	53	91	57	165	154	94	123	74
ENSMUSG00000070939	chr1	Tgfbrap1	-0.4190751	0.006991462	0.012791292	4.284826858	0.025480176	-1	298	283	330	423	321	364	239	237	270	250
ENSMUSG00000002007	chrX	Srpk3	0.44500038	0.006993724	0.012793754	6.115716133	0.031567921	1	958	676	750	1112	891	1147	1182	1387	1316	1438
ENSMUSG00000023571	chr4	Fam132a	0.47844548	0.00699896	0.012801658	3.428112231	0.03091156	1	132	151	105	146	126	180	248	177	186	219
ENSMUSG00000020738	chr11	Sumo2	-0.4352432	0.007002727	0.012806871	4.42454171	0.028027722	-1	344	337	334	479	344	274	384	208	302	319
ENSMUSG00000054766	chr2	Set	0.42622007	0.007008536	0.012815819	6.467147113	0.029103142	1	1134	1086	909	1452	1067	1965	1997	1391	1593	1356
ENSMUSG00000025757	chr3	Hspa4l	-0.4834057	0.007011034	0.012818708	3.195389532	0.030755515	-1	150	140	153	210	137	126	146	129	113	100
ENSMUSG00000051067	chr10	Lingo3	-0.7582108	0.007020103	0.012833612	4.219634905	0.089734897	-1	305	285	259	423	459	86	280	247	172	327
ENSMUSG00000032366	chr9	Tpm1	-0.4449035	0.007066741	0.012917182	14.45753454	0.032581467	-1	464941	348131	329649	443185	348929	293438	323258	247638	332427	359583
ENSMUSG00000021810	chr14	Ecd	-0.3871303	0.007081601	0.012941296	5.206599532	0.022907724	-1	618	599	531	744	617	492	563	434	558	555
ENSMUSG00000026576	chr1	Atp1b1	-0.7439506	0.007081785	0.012941296	6.966956723	0.089707653	-1	1078	2105	2563	4926	1432	2082	1444	1646	1389	1075
ENSMUSG00000022340	chr15	Sybu	-0.9286675	0.007087775	0.012950548	0.784285856	0.092257344	-1	27	36	12	43	40	20	14	17	19	20
ENSMUSG00000002767	chr17	Mrpl2	0.3899787	0.00709053	0.012953888	6.116184226	0.024144119	1	843	827	837	1205	784	1449	1241	1260	1257	1200
ENSMUSG00000044477	chr17	Zfand3	-0.4006557	0.007101774	0.012972735	6.400632455	0.025698668	-1	1315	1339	1187	1899	1452	1291	1175	1075	1050	1363
ENSMUSG00000064373	chr15	Sepp1	0.50835571	0.007112042	0.012989794	7.90305744	0.042245597	1	2905	3242	2898	3247	2370	5086	3841	4268	3176	6716
ENSMUSG00000020019	chr10	Ntn4	-0.5122708	0.007142392	0.013043521	4.062956267	0.039238057	-1	235	294	287	368	271	320	179	261	165	195
ENSMUSG00000047539	chr1	Fbxo28	-0.3820569	0.007143802	0.013044392	4.524014339	0.021219825	-1	435	323	354	493	336	367	351	298	287	324
ENSMUSG00000025648	chr9	Pfkfb4	-0.5204276	0.007147301	0.013049077	5.624371341	0.043285467	-1	1048	829	819	801	782	545	654	439	808	854
ENSMUSG00000003382	chr3	Etv3	-0.4284513	0.007155395	0.013062147	3.68968038	0.025239361	-1	216	235	169	268	208	192	172	141	177	211
ENSMUSG00000025702	chr6	March8	-0.3868176	0.007163252	0.013074782	5.270135075	0.023023593	-1	693	600	576	829	568	550	544	426	550	660
ENSMUSG00000020075	chr10	Ddx21	-0.4596422	0.007188883	0.013119852	5.443542942	0.033363317	-1	775	613	630	1032	729	571	788	432	651	546
ENSMUSG00000024576	chr18	Csnk1a1	-0.391692	0.007193716	0.013126958	7.564379507	0.025046502	-1	3158	2962	2781	4121	3047	2754	2768	2471	2399	2982
ENSMUSG00000013921	chr7	Clip3	0.63224434	0.007195458	0.013128423	3.256816457	0.058268185	1	124	105	91	120	109	184	179	222	91	260
ENSMUSG00000054150	chr12	Syne3	-0.7215872	0.007206716	0.013147248	2.014105748	0.067125336	-1	76	60	72	100	59	51	77	27	52	36
ENSMUSG00000030741	chr7	Spns1	0.35859634	0.007213743	0.013158349	4.96665785	0.019147381	1	394	415	366	492	368	646	603	527	501	587
ENSMUSG00000059923	chr11	Grb2	0.40469036	0.007215451	0.013159748	6.536567076	0.026396207	1	1303	1172	1050	1341	1071	1664	1613	1552	1799	1980

ENSMUSG00000090386	chr16	Mir99ahg	0.8429099	0.007223229	0.013172214	0.859475888	0.071996463	1	22	20	19	11	16	39	26	33	38	40
ENSMUSG00000038718	chr2	Pbx3	0.61555516	0.007241688	0.013204153	2.147794595	0.046684815	1	50	50	35	76	45	105	107	68	64	84
ENSMUSG00000031479	chr8	Vps36	-0.3936057	0.007246965	0.013212051	5.494359807	0.024180831	-1	821	724	676	920	672	593	680	590	681	617
ENSMUSG00000037553	chr4	Zdhhc18	0.45313689	0.007258046	0.013230528	4.966951947	0.03182294	1	388	325	317	520	420	831	652	390	493	615
ENSMUSG00000062929	chr12	Cfl2	-0.483971	0.00727881	0.013266646	8.614782653	0.038625718	-1	7158	6011	6495	9112	5553	3890	5346	5024	5423	6842
ENSMUSG00000045464	chr2	2810002D19Rik	0.90213572	0.007297904	0.013299714	1.309800654	0.09984614	1	17	30	27	27	20	26	56	47	73	44
ENSMUSG00000044033	chr2	Ccdc141	0.49107134	0.007311446	0.013321359	3.818772609	0.035400945	1	184	146	147	240	157	221	231	325	234	311
ENSMUSG00000061589	chr10	Dot1l	-0.4037743	0.007311687	0.013321359	5.269384556	0.025402364	-1	588	535	637	865	651	663	634	450	470	503
ENSMUSG00000039899	chr5	Fgl2	0.63495762	0.007321005	0.013336596	4.490136418	0.06358806	1	199	202	202	414	305	807	353	357	433	299
ENSMUSG00000048832	chr19	Vps37c	0.37355549	0.007326481	0.013344832	5.131802441	0.021343368	1	421	392	437	629	406	768	608	598	626	625
ENSMUSG00000022557	chr15	Bop1	0.41295919	0.007337048	0.013362337	5.035995131	0.026312708	1	384	328	351	560	475	669	716	528	576	565
ENSMUSG00000031012	chrX	Cask	-0.4553051	0.007343248	0.013371887	3.678967702	0.029149042	-1	221	181	183	269	241	194	185	136	143	222
ENSMUSG00000004221	chrX	Ikbkg	-0.3760973	0.007382118	0.013440917	4.561672574	0.020756069	-1	372	376	385	501	349	348	327	281	340	376
ENSMUSG00000034509	chr17	Mad2l1bp	0.46135706	0.007438064	0.013541016	4.024686691	0.031483573	1	191	186	190	292	164	376	286	321	313	228
ENSMUSG00000085890	chr11	Tnfsf13os	1.27038165	0.00744048	0.01354365	-0.14403597	0.154971382	1	10	7	7	3	6	5	17	20	25	21
ENSMUSG00000027828	chr3	Ssr3	-0.4427685	0.007444162	0.013548589	7.850521185	0.032409107	-1	4419	3914	3454	4387	3593	2942	3707	2335	3408	3601
ENSMUSG00000040356	chr17	Skiv2l	0.37847364	0.007446216	0.013550562	4.96936502	0.021742415	1	425	355	354	471	414	673	506	550	532	623
ENSMUSG00000054676	chr7	1600014C10Rik	-0.3776705	0.007454541	0.013563945	5.205396365	0.021989881	-1	602	607	565	751	574	482	541	527	497	555
ENSMUSG00000058298	chr10	Mcm9	0.71402029	0.007465007	0.01358122	1.145279868	0.04935301	1	22	21	24	28	22	44	53	41	33	40
ENSMUSG00000038871	chr6	Bpgm	-0.5391842	0.007479498	0.013605813	6.460304645	0.047639782	-1	1629	1470	1462	1842	1364	757	1164	883	1343	1684
ENSMUSG00000018509	chr11	Cenpv	0.43102827	0.007488069	0.01361786	3.714371861	0.02587529	1	159	133	143	222	172	294	232	237	238	218
ENSMUSG00000032558	chr9	Nphp3	-0.7093192	0.007487754	0.01361786	1.110243396	0.050175217	-1	32	38	35	47	37	34	23	24	18	28
ENSMUSG00000028884	chr4	Rpa2	0.41334207	0.007510052	0.013656062	4.501588504	0.02551271	1	331	278	251	306	268	505	451	353	444	352
ENSMUSG00000001175	chr12	Calm1	-0.4552682	0.007512677	0.01365728	8.961853474	0.034501735	-1	9302	7381	6630	10476	9262	6833	7833	5035	7540	7161
ENSMUSG00000028841	chr4	Cnksr1	0.62556275	0.007512356	0.01365728	4.625863428	0.062349089	1	282	226	266	433	252	896	417	372	508	273
ENSMUSG00000022175	chr14	Lrp10	0.40167382	0.007517569	0.013664397	5.830741261	0.02581364	1	702	693	624	939	703	1266	1103	1011	763	1164
ENSMUSG00000038459	chr7	Abhd17c	0.49554376	0.007520118	0.013667252	3.328514372	0.0340414	1	112	112	104	164	124	286	191	160	151	169
ENSMUSG00000037408	chr1	Cnnm4	-0.6323408	0.007525019	0.013674381	3.698872181	0.060872639	-1	139	200	211	412	228	168	176	220	129	124
ENSMUSG00000018770	chr2	Atp5g3	0.44555262	0.00753755	0.013695372	9.713256705	0.033130631	1	9764	10566	10336	15059	7818	18213	13551	16309	14074	16878
ENSMUSG00000026289	chr1	Atg16l1	-0.394591	0.007544611	0.013706419	4.587256407	0.023352406	-1	449	369	401	451	350	382	355	269	368	317
ENSMUSG00000043635	chr5	Adamts3	-0.7985773	0.007575758	0.013761216	1.54871767	0.080627822	-1	54	40	42	79	54	54	38	18	39	20
ENSMUSG00000069678	chr6	Pcgf1	0.58528905	0.007579943	0.013767028	2.465055212	0.043739659	1	56	60	68	80	57	155	88	92	104	92
ENSMUSG00000013736	chr6	Trnt1	-0.434932	0.007588514	0.013780804	3.897740236	0.027166144	-1	286	238	243	284	214	180	228	170	231	215
ENSMUSG00000025789	chr7	St8sia2	1.34714866	0.007603714	0.013806614	1.705514479	0.265759859	1	21	24	30	27	28	51	103	164	18	21
ENSMUSG00000062203	chr16	Gspt1	-0.4475879	0.007607514	0.01381172	5.921941552	0.032459901	-1	1038	873	902	1333	1075	665	1010	707	929	851
ENSMUSG00000027699	chr3	Ect2	0.94166685	0.007628994	0.013848918	0.90606025	0.106964763	1	17	17	20	24	11	25	66	28	42	25
ENSMUSG00000026896	chr2	Ifih1	0.72622906	0.007632517	0.013853514	2.219803753	0.071305688	1	41	56	54	55	46	61	108	57	107	127
ENSMUSG00000036390	chr6	Gadd45a	0.45699242	0.007642661	0.013870125	5.180755532	0.033150987	1	612	430	324	454	442	723	641	557	768	726
ENSMUSG00000028926	chr5	Cdk14	0.5689484	0.007681479	0.013938762	3.323078362	0.046864622	1	143	111	127	98	105	244	226	112	172	221
ENSMUSG00000028100	chr3	Nudt17	1.06931536	0.007682779	0.013939312	-0.088431002	0.089751006	1	11	8	7	4	8	27	15	11	18	19
ENSMUSG00000060373	chr14	Hnrnpc	0.41702013	0.007689105	0.013948979	6.387634291	0.02844683	1	1040	1026	1006	1321	952	1886	1878	1378	1433	1259
ENSMUSG00000034544	chr3	Rsrc1	-0.4254608	0.007726955	0.014015824	4.074531175	0.026456839	-1	299	245	242	384	270	213	285	184	235	250
ENSMUSG00000030269	chr6	Mtmr14	-0.42409	0.007734426	0.014027556	4.124089345	0.026631056	-1	338	301	269	305	259	282	255	168	239	272
ENSMUSG00000086583	chr7	Gm15500	0.39984221	0.007735943	0.014028486	4.475593596	0.023912822	1	288	255	242	349	289	445	441	339	466	363
ENSMUSG00000021891	chr14	Mettl6	0.48434821	0.007739162	0.014032503	3.216014189	0.032321386	1	100	86	107	167	114	203	183	157	180	150
ENSMUSG00000004535	chr6	Tax1bp1	-0.4189265	0.00775576	0.014060774	6.248929218	0.028713874	-1	1306	1281	1090	1669	1164	1096	1059	754	1202	1210
ENSMUSG00000002365	chr17	Snx9	-0.4440709	0.00776672	0.014078818	4.527081387	0.030334019	-1	346	397	343	518	375	282	353	218	358	378
ENSMUSG00000071632	chr16	2510002D24Rik	-0.4375088	0.007772747	0.014087915	3.729618181	0.027214511	-1	242	247	216	245	174	175	181	177	197	178
ENSMUSG00000063882	chr4	Uqcrh	0.44984938	0.007781395	0.01410176	8.936411294	0.033984825	1	6140	6482	6085	7796	4488	11131	7958	9358	9605	8043
ENSMUSG00000036377	chr5	C530008M17Rik	-0.8790676	0.007791743	0.014116852	0.534165763	0.078531246	-1	20	18	23	36	32	19	18	7	14	19
ENSMUSG00000043099	chr11	Hic1	0.66588654	0.007791577	0.014116852	3.835677083	0.069298118	1	171	189	141	179	133	216	265	403	141	379
ENSMUSG00000046434	chr15	Hnrnpa1	0.43575898	0.007801597	0.014132873	6.462673249	0.031287424	1	1164	1031	968	1398	1038	1729	2233	1541	1344	1436
ENSMUSG00000035868	chr17	3110052M02Rik	-1.1076799	0.007811471	0.014148926	0.12191492	0.131549345	-1	22	28	12	22	15	21	7	2	9	12
ENSMUSG00000021958	chr14	Pinx1	0.69808477	0.007816584	0.014156353	2.054528699	0.064860054	1	44	37	31	60	57	100	97	60	96	54
ENSMUSG00000065529	chr11	Mir22	-0.8285668	0.007819906	0.014160535	2.029211676	0.096953902	-1	80	83	76	71	65	19	45	42	45	81
ENSMUSG00000047866	chr8	Lonp2	-0.408024	0.007833567	0.014183435	5.552262299	0.026692812	-1	850	751	693	944	743	545	675	605	692	753
ENSMUSG00000032475	chr9	Nck1	-0.381855	0.007839258	0.0141919	4.365431007	0.021449088	-1	333	316	326	466	299	354	271	233	296	306
ENSMUSG00000024134	chr17	Six2	-0.9392233	0.007848565	0.014206909	3.421560913	0.140047671	-1	316	198	180	76	236	90	178	147	53	124
ENSMUSG00000061028	chr7	Clasrp	0.49379194	0.007853306	0.01421365	3.13455872	0.033232486	1	114	106	103	124	88	223	152	174	137	142
ENSMUSG00000028232	chr4	Tmem68	0.57351292	0.007863106	0.014229544	2.526871819	0.04324968	1	60	67	72	78	59	148	136	91	88	91
ENSMUSG00000035505	chr5	Cox18	-0.6200485	0.007864641	0.014230479	3.058648361	0.056553717	-1	123	166	130	190	135	180	107	80	57	115
ENSMUSG00000026723	chr2	Trdmt1	-0.6722933	0.007866793	0.014232531	2.052548562	0.059266796	-1	76	79	68	93	55	64	78	34	42	38
ENSMUSG00000022370	chr15	Mrpl13	0.40637552	0.007869364	0.014233645	5.6055376	0.026576579	1	670	685	569	722	469	953	939	817	983	819
ENSMUSG00000069206	chr13	Zfp874a	-0.6688411	0.007869446	0.014233645	2.317223615	0.060570255	-1	90	93	82	120	64	35	84	55	61	70
ENSMUSG00000022793	chr16	B4galt4	0.60388612	0.007879662	0.014250278	2.312404346	0.047768275	1	60	48	43	98	43	126	87	84	95	86

ENSMUSG00000052512	chr7	Nav2	-0.5612868	0.007891475	0.014269795	4.57312093	0.050208414	-1	303	329	372	720	422	335	256	384	207	377
ENSMUSG00000064346	chrMT	mt-Tw	0.58256523	0.007910325	0.014302031	6.032208207	0.056178421	1	742	819	910	784	603	1027	849	1381	1768	1272
ENSMUSG00000031105	chrX	Slc25a14	0.86067898	0.007912631	0.01430435	1.046993795	0.085672116	1	23	20	21	24	14	67	39	27	48	24
ENSMUSG00000027285	chr2	Haus2	-0.539958	0.0079143	0.014304907	3.416705827	0.042824837	-1	232	177	152	211	162	113	160	92	176	161
ENSMUSG00000048895	chr11	Cdk5r1	1.1265691	0.007914986	0.014304907	1.584794148	0.180887938	1	44	33	23	15	17	26	67	113	38	70
ENSMUSG00000020873	chr11	Slc35b1	0.39853458	0.007927164	0.014325065	5.243847126	0.025151954	1	524	431	372	577	525	748	773	593	728	667
ENSMUSG00000015748	chr3	Prpf3	0.40518176	0.007936891	0.014340787	3.807812802	0.023008531	1	165	151	170	231	175	277	293	217	255	251
ENSMUSG00000032002	chr9	Dcun1d5	-0.4333928	0.007979585	0.014416065	5.164061063	0.029963587	-1	603	588	526	853	521	476	510	372	641	478
ENSMUSG00000025969	chr1	Nrp2	0.47460782	0.007980872	0.014416526	4.89681993	0.035920477	1	354	344	399	513	256	834	619	375	474	557
ENSMUSG00000021012	chr12	Zc3h14	-0.4185642	0.007988562	0.014428553	5.415731918	0.028179325	-1	667	664	666	962	688	500	667	509	554	744
ENSMUSG00000031934	chr9	Panx1	0.70563677	0.008010413	0.01446615	3.783593998	0.078578309	1	154	121	141	210	151	596	242	230	173	171
ENSMUSG00000059461	chrX	Gm7331	1.12851566	0.0080132	0.014469313	-0.11914161	0.107399384	1	9	11	5	4	7	26	20	8	20	15
ENSMUSG00000101102	chr1	Gm28609	1.7319951	0.008016516	0.014473431	-0.454643165	0.32065133	1	6	5	6	2	1	1	7	15	22	29
ENSMUSG00000027274	chr2	Mkks	-0.3890121	0.008035824	0.014506417	5.504785569	0.024295497	-1	839	757	760	909	569	717	651	564	638	637
ENSMUSG00000027611	chr2	Procr	0.56457636	0.008040994	0.014513874	2.835271094	0.043870694	1	82	78	90	98	72	199	125	108	94	165
ENSMUSG00000028655	chr4	Mfsd2a	1.68906611	0.008044005	0.014517435	-0.372192745	0.334568816	1	1	5	7	6	3	26	29	18	7	0
ENSMUSG00000072889	chr5	Nfxl1	0.57127175	0.008078356	0.014577547	2.416982172	0.042723675	1	66	53	52	93	52	130	113	69	105	95
ENSMUSG00000005823	chr17	Gpr108	0.38436087	0.008095745	0.014607041	5.031411027	0.023091008	1	475	437	342	439	403	633	635	536	632	573
ENSMUSG00000005968	chr3	Tuft1	1.01641041	0.00811227	0.014634966	0.625600983	0.120228625	1	17	17	6	21	9	60	20	18	30	28
ENSMUSG00000042380	chr4	Smim12	0.37626652	0.008120682	0.014648252	4.736846942	0.02163871	1	358	323	304	416	322	610	467	469	475	430
ENSMUSG00000049960	chr14	Mrps16	0.41032889	0.008156323	0.014710643	5.349272661	0.027111665	1	562	556	477	607	401	911	716	759	769	627
ENSMUSG00000051107	chr13	Gm15440	0.40356078	0.008161953	0.014718898	5.909369245	0.026723673	1	753	632	604	1036	847	1211	1116	1047	998	1213
ENSMUSG00000089726	chr14	Mir17hg	1.13269894	0.008169635	0.01473085	0.066625114	0.1269274	1	9	8	4	8	13	33	23	15	24	8
ENSMUSG00000095432	chr13	Zfp748	-0.6650182	0.008182633	0.014752384	1.499376591	0.050525653	-1	56	50	44	57	41	35	47	22	30	38
ENSMUSG00000026088	chr1	Mitd1	0.75908266	0.008188614	0.014761263	1.658534881	0.075741323	1	48	33	31	39	17	49	85	51	70	54
ENSMUSG00000015290	chrX	Ubl4	-0.4007598	0.008204412	0.014785953	6.205837519	0.026553395	-1	1333	1202	1103	1629	1027	1014	1064	873	1179	1047
ENSMUSG00000097842	chr7	9330104G04Rik	1.04256572	0.008204426	0.014785953	0.351586851	0.118261213	1	14	9	7	10	15	16	19	16	38	36
ENSMUSG00000030225	chr6	Dera	0.47903691	0.008232204	0.014834101	3.161539459	0.031600327	1	118	92	95	145	102	163	178	140	200	155
ENSMUSG00000059586	chr15	Nsmce2	0.48871956	0.008283989	0.01492549	3.447357396	0.034444069	1	118	167	108	154	120	242	228	205	193	159
ENSMUSG00000026568	chr1	Mpc2	-0.4360244	0.008286196	0.014927542	7.298883204	0.032146441	-1	2434	2928	2735	3590	1885	2193	2152	2096	2347	2091
ENSMUSG00000050240	chr16	Hic2	-0.7297923	0.008302359	0.014954733	1.318990527	0.06147654	-1	35	57	44	42	41	39	26	20	30	32
ENSMUSG00000022554	chr15	Hgh1	0.60162515	0.008324989	0.014993563	1.89715816	0.04264405	1	52	36	34	51	40	76	78	70	68	61
ENSMUSG00000030590	chr7	Fam98c	0.46151162	0.008327871	0.014996821	3.899762498	0.032164511	1	164	184	168	280	144	382	214	271	263	275
ENSMUSG00000036555	chr5	Iqce	0.58948882	0.008335072	0.015007855	2.174372792	0.04308377	1	55	51	46	49	57	84	83	94	76	91
ENSMUSG00000097383	chr10	1500026H17Rik	0.90831645	0.008339369	0.015013658	0.23171886	0.073017778	1	8	10	15	16	5	23	23	20	21	24
ENSMUSG00000022434	chr15	Fam118a	-0.5651214	0.008357393	0.015044168	2.817092813	0.04507521	-1	126	129	116	137	107	151	91	66	73	82
ENSMUSG00000052557	chr8	Gan	-0.8397288	0.008360661	0.015048112	0.396817127	0.061963004	-1	21	21	21	30	22	20	13	15	13	9
ENSMUSG00000037108	chr5	Zcwpw1	1.01626578	0.008387093	0.015093743	-0.007665955	0.083188897	1	5	10	7	9	11	23	15	18	24	14
ENSMUSG00000069372	chr18	Ctxn3	0.61959834	0.008389748	0.015096578	3.646938079	0.06024062	1	192	113	89	219	129	347	179	141	268	306
ENSMUSG00000061601	chr5	Pclo	-1.0208612	0.008399958	0.015113004	0.171912203	0.107912741	-1	22	20	14	24	21	4	10	10	8	22
ENSMUSG00000023341	chr16	Mx2	1.01804925	0.008405208	0.015120503	0.435723996	0.107351432	1	14	18	9	9	9	40	24	18	14	39
ENSMUSG00000022865	chr16	Cxadr	-1.0149939	0.008409516	0.015126307	-0.062683787	0.085284287	-1	10	21	17	23	13	9	12	11	6	7
ENSMUSG00000040606	chr4	Kazn	-0.7699943	0.008415141	0.015134476	1.925431933	0.081657714	-1	60	74	50	102	64	89	32	36	30	39
ENSMUSG00000073627	chr1	C130036L24Rik	0.92870942	0.008421859	0.015144608	0.731573095	0.097686759	1	15	20	11	18	14	22	41	21	25	55
ENSMUSG00000041594	chr14	Tmtc4	-0.6940137	0.008433681	0.015163916	1.59672508	0.058890358	-1	42	39	58	70	59	35	44	23	37	43
ENSMUSG00000037957	chr12	Wdr20	-0.4683436	0.008439105	0.015171718	3.244123667	0.030476984	-1	154	171	148	195	142	121	121	99	145	155
ENSMUSG00000085348	chr11	Gm12300	1.33871244	0.008443812	0.015178228	5.747152467	0.294253158	1	163	262	125	943	840	268	1137	2155	1005	1507
ENSMUSG00000046324	chr19	Ermp1	-0.4174954	0.008448582	0.015184849	3.902970813	0.025477143	-1	264	235	219	288	256	210	212	202	231	178
ENSMUSG00000005397	chr13	Nid1	-0.4838164	0.008453229	0.015191247	7.594934509	0.039932496	-1	2857	3201	3403	3849	3386	2449	2582	2706	1811	3618
ENSMUSG00000020926	chr11	Adam11	0.84392736	0.008470954	0.015221143	0.506871035	0.069898065	1	18	17	8	18	8	32	22	26	29	26
ENSMUSG00000020513	chr11	Tubd1	-0.5680046	0.008529153	0.015323748	2.90180437	0.045943238	-1	147	142	126	127	108	69	118	85	110	99
ENSMUSG00000032512	chr9	Wdr48	-0.4151743	0.008533236	0.015329113	4.01182981	0.02563793	-1	282	267	226	365	235	259	254	162	238	213
ENSMUSG00000045482	chr5	Trrap	-0.3640926	0.008543237	0.015345108	5.095048142	0.021038846	-1	566	521	526	669	570	570	483	454	394	541
ENSMUSG00000030732	chr7	Chrdl2	-1.0026891	0.008563022	0.015378669	0.609867986	0.116410118	-1	12	32	28	36	32	15	21	18	16	6
ENSMUSG00000031153	chrX	Gripap1	0.37046404	0.008574185	0.015396739	4.558427466	0.020997905	1	330	261	252	416	278	501	438	384	416	424
ENSMUSG00000040697	chr4	Dnajc16	-0.4084397	0.008601481	0.015443768	4.417907536	0.025740195	-1	332	313	355	425	376	263	323	300	263	338
ENSMUSG00000019143	chr18	Hars2	-0.4129365	0.008611822	0.015460349	4.258726245	0.025986485	-1	353	344	292	385	249	256	235	245	265	330
ENSMUSG00000000739	chr8	Sult5a1	0.80083812	0.008638323	0.015505935	2.02616939	0.090305902	1	47	42	34	38	50	143	50	71	48	103
ENSMUSG00000029547	chr5	Ints1	-0.4516068	0.008641441	0.01550954	5.41940805	0.033747731	-1	638	565	599	994	893	588	600	580	479	698
ENSMUSG00000039671	chr2	Zmynd8	0.43293543	0.008647608	0.015516622	4.379951525	0.029290727	1	222	229	208	388	279	540	366	342	332	376
ENSMUSG00000058748	chr8	Zfp958	-0.7664385	0.008647459	0.015516622	1.63130402	0.078154343	-1	45	64	59	64	47	44	44	15	27	53
ENSMUSG00000004415	chr5	Col26a1	0.61376047	0.008651082	0.015520863	3.078189051	0.056011257	1	124	110	102	78	69	220	133	173	113	186
ENSMUSG00000006050	chr18	Sra1	0.36918338	0.008678468	0.015567998	5.157130203	0.021784727	1	485	441	406	556	427	713	719	546	697	600
ENSMUSG00000007379	chr3	Dennd2c	-0.5864601	0.008711624	0.015625469	3.101841627	0.051703517	-1	213	132	124	157	131	125	85	85	93	169
ENSMUSG00000027669	chr3	Gnb4	-0.4782891	0.008719184	0.015637022	3.826499145	0.035118348	-1	246	283	234	298	164	273	203	158	139	198

ENSMUSG00000036529	chr15	Sbf1	-0.4000984	0.008725461	0.015646272	5.76053707	0.026630992	-1	806	791	835	1172	988	970	822	676	626	739
ENSMUSG00000022009	chr14	Nufip1	0.49847283	0.008741088	0.015672283	3.001396921	0.034202447	1	93	92	97	125	81	200	176	105	127	153
ENSMUSG00000037089	chr17	Slc35b2	0.38279878	0.008758567	0.015701607	4.983314124	0.023277671	1	472	403	384	414	353	685	648	489	515	589
ENSMUSG00000023909	chr17	Paqr4	0.5115678	0.008766082	0.015713064	3.205810154	0.038155186	1	85	127	111	146	91	166	198	196	155	153
ENSMUSG00000081219	chr2	Bambi-ps1	1.09121988	0.008774407	0.015725969	0.105110138	0.125819222	1	11	9	3	14	8	26	23	10	11	36
ENSMUSG00000092345	chr4	Gm20503	0.4352691	0.008781563	0.015736776	3.680241468	0.027726012	1	170	146	152	220	123	333	231	207	209	220
ENSMUSG00000050663	chr10	Trhde	-0.9818429	0.008787446	0.0157453	-0.117651804	0.083185318	-1	16	15	16	15	17	6	12	6	6	14
ENSMUSG00000093593	chr17	Gm20683	-0.4356078	0.008794653	0.015756194	6.434015778	0.032216415	-1	1298	1379	1408	2082	1295	955	1227	1219	1208	1343
ENSMUSG00000030137	chr6	Tuba8	-0.5915427	0.008839921	0.015835264	7.722741971	0.060375472	-1	3733	2712	3172	5149	4269	1844	3707	2120	3664	2298
ENSMUSG00000057367	chr9	Birc2	-0.376382	0.008846684	0.01584535	4.537492691	0.021914847	-1	401	376	342	454	371	383	311	254	350	350
ENSMUSG00000078784	chr3	1810022K09Rik	0.55956153	0.008856063	0.015860116	3.577916422	0.048550469	1	180	125	121	149	134	213	274	182	314	159
ENSMUSG00000024132	chr17	Eci1	-0.4376068	0.00886307	0.015870631	6.100499021	0.032383032	-1	937	1182	1109	1853	890	1000	874	857	1026	988
ENSMUSG00000040282	chr2	BC052040	-0.7418464	0.008883926	0.015905937	1.855060867	0.075287371	-1	40	50	51	113	78	41	45	35	54	38
ENSMUSG00000030145	chr6	Zfp248	-0.7022876	0.008896748	0.015926855	0.991276725	0.049565455	-1	39	30	31	36	36	25	23	24	21	23
ENSMUSG00000035762	chr13	Tmem161b	-0.5592769	0.008912987	0.015953882	3.075046879	0.045539989	-1	142	144	143	199	115	72	146	114	107	105
ENSMUSG00000049556	chr9	Lingo1	1.07386448	0.008918732	0.015960077	-0.260869693	0.091640233	1	6	5	11	5	6	17	22	14	10	15
ENSMUSG00000051851	chrX	Cxx1c	0.68908818	0.008917775	0.015960077	1.773500052	0.059810093	1	41	29	42	44	31	95	52	60	45	82
ENSMUSG00000060301	chr10	2610008E11Rik	-0.4124236	0.008936784	0.015990332	3.970319368	0.025448042	-1	278	235	279	315	217	207	214	206	198	264
ENSMUSG00000026615	chr1	Eprs	-0.4638417	0.008965956	0.016040476	7.447381812	0.037203942	-1	3021	2653	2410	4222	2919	1794	2423	2154	2832	2677
ENSMUSG00000009376	chr6	Met	-0.4387715	0.008968253	0.016042532	4.385322507	0.030487552	-1	403	384	294	372	322	254	386	252	260	288
ENSMUSG00000039405	chr7	Prss23	-0.4761653	0.008970871	0.016045161	6.626548761	0.038914973	-1	1701	1392	1579	2302	1639	939	1300	1299	1487	1658
ENSMUSG00000057440	chr18	Mpp7	-0.7046826	0.008988043	0.016073818	1.298498636	0.056119656	-1	44	47	34	58	35	40	29	19	35	23
ENSMUSG00000001518	chr6	Itfg2	-0.4479755	0.008989645	0.016074627	3.511895596	0.028984231	-1	189	176	191	236	179	126	185	151	143	172
ENSMUSG00000024942	chr19	Capn1	-0.4033923	0.008999381	0.016089976	6.570234041	0.027823572	-1	1730	1495	1386	1813	1611	1452	1284	1300	1051	1603
ENSMUSG00000035206	chr10	Sppl2b	-0.4599242	0.009001383	0.016091497	4.289863119	0.033550208	-1	270	292	316	438	364	224	249	247	250	364
ENSMUSG00000026553	chr1	Copa	0.39693055	0.00900878	0.016102662	6.916995274	0.027074278	1	1509	1387	1254	2080	1586	2134	2407	1935	2303	2414
ENSMUSG00000022043	chr14	Trim35	-0.4911097	0.009023566	0.016127028	8.189409831	0.041961553	-1	5027	4284	4657	5995	5394	2887	3629	4224	3666	5253
ENSMUSG00000036097	chr19	Fam178a	-0.3765071	0.009045566	0.01616428	4.617306845	0.022160809	-1	375	345	385	527	428	374	373	335	312	342
ENSMUSG00000046897	chr15	Zfp740	-0.3759951	0.009059384	0.016186902	5.312512799	0.023182931	-1	647	680	633	845	543	729	537	496	497	574
ENSMUSG00000032741	chr5	Tpcn1	-0.4193152	0.009078126	0.016218317	6.20787505	0.029968573	-1	1056	1188	1080	1637	1347	1063	992	983	842	1286
ENSMUSG00000018427	chr11	Ypel2	-0.5671462	0.009085697	0.016229768	3.409231434	0.049699023	-1	214	186	153	244	146	134	108	142	90	219
ENSMUSG00000060771	chr1	Tsga10	-0.6105541	0.009099044	0.016251531	1.824114713	0.04511168	-1	51	57	62	90	51	47	52	43	41	38
ENSMUSG00000032058	chr9	Ppp2r1b	0.55738115	0.009101049	0.016253035	2.956186918	0.045179099	1	73	109	67	110	100	196	168	95	143	147
ENSMUSG00000041548	chr5	Hspb8	0.49783732	0.009116772	0.016279035	8.983212778	0.043336618	1	8824	5498	4998	6434	5464	8095	8789	9484	11037	10583
ENSMUSG00000032621	chr13	Srek1	-0.4009956	0.009119681	0.016282149	4.18405651	0.024477376	-1	343	286	273	360	271	221	253	252	266	272
ENSMUSG00000044629	chr11	Cnrip1	0.58877476	0.009127749	0.016294472	2.624768121	0.049177469	1	86	66	79	68	57	155	127	106	75	134
ENSMUSG00000020523	chr11	Fam114a2	-0.3957615	0.009135104	0.016305518	5.809158103	0.026359327	-1	1134	859	816	1098	838	751	850	642	861	839
ENSMUSG00000029426	chr5	Scarb2	-0.3748512	0.009144855	0.016320839	6.384757394	0.023949985	-1	1492	1342	1191	1662	1339	1300	1155	1074	1095	1321
ENSMUSG00000073405	chr17	C920025E04Rik	1.89045288	0.009148026	0.016324414	1.199998333	0.536331338	1	8	11	15	10	21	76	41	2	5	163
ENSMUSG00000026659	chr1	Dusp12	0.61674275	0.009167805	0.016353444	2.599602613	0.054731023	1	73	76	57	92	53	177	111	76	137	90
ENSMUSG00000029454	chr5	Mapkapk5	-0.4112146	0.009167524	0.016353444	5.507390957	0.028273611	-1	701	674	682	1118	726	753	634	524	728	545
ENSMUSG00000068184	chr13	Ndufaf2	0.53093657	0.009165554	0.016353444	3.097031381	0.041500304	1	132	108	74	122	80	154	196	125	189	148
ENSMUSG00000079144	chr1	A130010J15Rik	-0.6335225	0.00917068	0.016356486	2.612598343	0.058123649	-1	112	85	104	128	114	43	90	67	89	92
ENSMUSG00000029253	chr5	Cenpc1	-0.6180286	0.009183781	0.016377763	2.24181683	0.051529587	-1	86	73	81	111	68	40	70	46	68	72
ENSMUSG00000020691	chr11	Mettl2	-0.579437	0.009190668	0.016387953	2.578001411	0.04682326	-1	86	101	121	145	73	74	94	62	83	70
ENSMUSG00000029675	chr5	Eln	0.68540696	0.009200581	0.016403536	6.336990127	0.081229928	1	742	796	682	1239	1167	1741	1200	2284	728	2147
ENSMUSG00000071064	chr8	Zfp827	-0.5399473	0.009206196	0.016411453	3.116008795	0.042798914	-1	119	142	127	262	122	126	104	132	101	104
ENSMUSG00000050627	chr9	Gpd1l	-0.3637997	0.009222822	0.016438995	5.365011042	0.021719936	-1	659	662	621	860	651	622	575	603	539	590
ENSMUSG00000031753	chr8	Cog4	-0.3914364	0.009225276	0.016441271	6.137722012	0.026060164	-1	1341	1116	978	1423	1101	925	1003	1001	943	1075
ENSMUSG00000060601	chr7	Nr1h2	-0.4071052	0.009297603	0.01656806	4.953437304	0.027242706	-1	559	474	475	599	511	592	409	290	444	454
ENSMUSG00000039914	chr10	Coq10a	-0.4299611	0.009302935	0.016575449	8.153494491	0.03241078	-1	4177	4970	4517	7229	3777	3744	3974	3692	4293	4019
ENSMUSG00000040428	chr7	Plekha4	0.60255045	0.00932436	0.016611505	2.34605382	0.049413934	1	57	44	60	69	62	132	87	94	64	114
ENSMUSG00000009013	chr5	Dynll1	0.51851709	0.009372778	0.016695634	5.756173034	0.046243477	1	582	513	520	1014	720	1595	1218	873	820	740
ENSMUSG00000027861	chr3	Casq2	0.85854675	0.009392277	0.016728235	7.506112304	0.128178547	1	860	1595	2017	4466	1147	5443	2484	5601	2658	2837
ENSMUSG00000020889	chr11	Nr1d1	-0.551838	0.009402152	0.01674369	6.684261201	0.053102935	-1	1448	1386	1757	2464	2070	1539	1236	1695	760	1571
ENSMUSG00000003421	chr7	Nosip	0.35286537	0.009429469	0.016790197	5.075514299	0.020169187	1	439	360	420	598	397	668	625	576	581	628
ENSMUSG00000085783	chr16	Gm9816	-0.5933094	0.009433525	0.01679528	2.024137461	0.045226559	-1	69	85	56	86	59	46	54	41	54	62
ENSMUSG00000031701	chr8	Dnaja2	-0.4367732	0.009459823	0.016839955	7.348530676	0.03342856	-1	2965	2709	2416	3315	2568	1771	2598	1909	2181	2823
ENSMUSG00000090086	chr5	AI480526	-0.6340283	0.009465608	0.016848108	2.657615842	0.060122247	-1	141	130	101	96	88	81	57	96	61	100
ENSMUSG00000092192	chr9	Dyx1c1	-0.8617224	0.009493559	0.016895706	0.268465235	0.06982815	-1	28	20	22	19	15	14	12	9	12	16
ENSMUSG00000070867	chr4	Trabd2b	0.59449464	0.009501799	0.016908218	2.389147637	0.048500117	1	44	56	47	79	77	117	110	97	77	102
ENSMUSG00000052369	chr15	Tmem106c	0.48547799	0.009531164	0.016958313	3.442840744	0.035276849	1	161	136	114	148	108	308	193	150	187	197
ENSMUSG00000021040	chr12	Slirp	0.40883103	0.009544285	0.016979497	4.980758468	0.027641726	1	459	434	352	467	305	561	587	544	689	532
ENSMUSG00000038047	chr4	Haus6	-0.5308535	0.009546329	0.016980972	2.711961293	0.039329698	-1	123	102	101	155	91	81	105	61	99	84
ENSMUSG00000022517	chr16	Mgrn1	-0.3825304	0.00955841	0.017000298	5.907988407	0.024931591	-1	906	939	918	1425	912	848	822	758	818	1004

ENSMUSG00000055835	chr8	Zfp1	-0.488026	0.009587754	0.017050318	2.784271468	0.032534815	-1	107	117	107	151	109	94	97	74	80	117
ENSMUSG00000006219	chr4	Fblim1	1.03731642	0.009608905	0.017084495	2.513657573	0.172717438	1	41	55	66	50	54	332	101	50	52	103
ENSMUSG00000029699	chr5	Ssc4d	-0.7309268	0.009609417	0.017084495	1.354359866	0.067190195	-1	54	53	42	39	37	40	22	20	29	40
ENSMUSG00000024913	chr19	Lrp5	-0.4548531	0.009622743	0.01710525	4.900134181	0.034570296	-1	393	442	435	823	511	474	374	418	296	494
ENSMUSG00000053329	chr10	D10Jhu81e	-0.409031	0.009623539	0.01710525	7.565664426	0.029481413	-1	3021	3333	3128	4087	2583	3289	2326	2392	2844	2450
ENSMUSG00000028369	chr4	Svep1	0.43374925	0.009674487	0.017193621	5.032187053	0.031405309	1	356	409	394	465	430	885	511	607	459	619
ENSMUSG00000049940	chr3	Pgrmc2	0.37077478	0.009683508	0.017207464	5.289284563	0.022848829	1	592	503	411	578	451	800	714	679	646	755
ENSMUSG00000025208	chr19	Mrpl43	0.37613652	0.00969677	0.01722716	5.407041635	0.023719004	1	546	508	538	689	470	924	716	810	671	783
ENSMUSG00000044442	chr16	N6amt1	-0.4617651	0.009697057	0.01722716	3.447812359	0.031663383	-1	226	209	152	202	143	150	167	116	150	160
ENSMUSG00000100680	chr6	1810044D09Rik	0.63800126	0.009707059	0.017242737	1.76575747	0.051249479	1	45	46	31	40	28	78	50	61	66	70
ENSMUSG00000072825	chr12	Cep170b	-0.4260365	0.009714346	0.017253488	3.97607146	0.028274256	-1	236	219	232	329	317	243	243	187	184	236
ENSMUSG00000021178	chr12	Psmc1	0.3961113	0.009734972	0.017287924	7.259236386	0.027635028	1	2380	1892	1787	2215	1580	2950	2865	2634	2867	2870
ENSMUSG00000080772	chr4	Gm12543	0.93273554	0.009746603	0.017304182	0.584455443	0.097724484	1	17	12	8	18	15	38	25	13	43	28
ENSMUSG00000087150	chr6	BC064078	1.3767938	0.009746106	0.017304182	0.422920747	0.251430138	1	3	14	9	8	14	78	26	15	16	11
ENSMUSG00000047371	chr7	Zfp768	-0.3736461	0.009759156	0.017324268	5.043245274	0.022933762	-1	553	480	558	717	468	438	438	445	467	543
ENSMUSG00000048222	chr2	Mfap1b	0.48753122	0.009773642	0.01734778	3.547209075	0.036864197	1	150	134	134	195	110	161	289	210	198	239
ENSMUSG00000032264	chr9	Zw10	0.45652315	0.009781893	0.01736022	3.352574371	0.030437599	1	118	130	131	139	112	170	224	178	202	174
ENSMUSG00000041025	chr4	Iffo2	0.47127768	0.009786921	0.017366939	2.961432409	0.031251985	1	93	84	86	143	78	176	158	139	120	136
ENSMUSG00000017428	chr11	Psmd11	-0.3961076	0.009799137	0.017386409	6.609036522	0.027443796	-1	1877	1660	1587	1872	1260	1526	1422	1143	1451	1344
ENSMUSG00000101249	chr1	Gm29216	-0.4913877	0.009810207	0.017403841	3.691788798	0.037629909	-1	188	221	211	342	169	167	139	169	220	168
ENSMUSG00000038305	chr1	Spats2l	0.53484709	0.00981606	0.017409677	3.262454722	0.043475463	1	132	115	102	119	105	162	159	231	134	222
ENSMUSG00000066042	chr4	Med18	0.76430624	0.009815871	0.017409677	0.837707239	0.061893142	1	21	24	15	19	12	32	39	26	37	36
ENSMUSG00000087236	chr1	Gm1305	0.78076771	0.009817234	0.017409677	1.158815854	0.073521928	1	28	23	18	27	19	77	34	33	40	35
ENSMUSG00000039308	chr14	Ndst2	0.48954874	0.009839267	0.017446537	3.440270174	0.036074242	1	114	133	108	145	160	288	202	153	180	210
ENSMUSG00000020515	chr11	Cnot8	0.3623482	0.0098485	0.017460692	5.53236752	0.022129203	1	617	613	567	725	492	887	894	804	756	900
ENSMUSG00000097039	chr15	Pvt1	0.87201478	0.009853377	0.017467123	0.96437581	0.095893752	1	28	14	10	30	15	51	43	17	37	46
ENSMUSG00000028483	chr4	Snapc3	-0.4273646	0.009855182	0.017468106	3.289807577	0.026089541	-1	193	158	143	191	142	166	130	128	116	135
ENSMUSG00000068921	chr3	Dap3	0.44077788	0.009865154	0.017483565	5.645588262	0.033551167	1	655	589	563	835	537	706	969	843	1136	1003
ENSMUSG00000020263	chr10	Appl2	-0.4175991	0.009875695	0.017500028	4.014695364	0.027307173	-1	300	272	234	319	244	275	204	159	215	278
ENSMUSG00000030965	chr7	Fam175b	-0.3541992	0.009923797	0.017583036	4.782288412	0.020142478	-1	499	424	403	573	402	395	423	331	390	427
ENSMUSG00000000530	chr15	Acvrl1	0.50292361	0.009931735	0.017594184	4.211565921	0.041794579	1	185	183	178	360	245	556	340	305	286	294
ENSMUSG00000015451	chr17	C4a	1.43705843	0.009932607	0.017594184	-0.194234949	0.234820729	1	3	8	4	7	7	46	4	14	8	18
ENSMUSG00000024766	chr19	Lipo1	-0.6565147	0.009935192	0.017596534	2.061316043	0.059933732	-1	99	64	50	98	63	39	67	44	42	65
ENSMUSG00000061104	chr8	Gm10094	0.53497061	0.009943682	0.017609339	2.389164885	0.038152455	1	65	64	44	84	56	117	83	95	93	106
ENSMUSG00000029554	chr5	Mad1l1	0.70260589	0.009963515	0.017642226	3.404827334	0.081479127	1	117	84	85	151	157	213	173	351	127	179
ENSMUSG00000031715	chr8	Smarca5	-0.4174198	0.009968242	0.01764836	5.2796256	0.029595368	-1	669	596	593	939	542	503	739	446	523	498
ENSMUSG00000025373	chr10	Rnf41	0.39679662	0.009990381	0.017685315	4.105437609	0.024375951	1	230	221	171	269	211	408	351	259	264	316
ENSMUSG00000005204	chr11	Senp3	0.37380424	0.01004806	0.017785168	4.994379736	0.023116513	1	458	424	387	491	306	698	583	506	598	548
ENSMUSG00000050945	chr18	Zfp438	-0.5773375	0.01006683	0.017816135	1.983783424	0.042128185	-1	82	59	60	80	62	45	49	45	51	61
ENSMUSG00000047126	chr11	Cltc	-0.4120346	0.010083022	0.017842531	7.429071455	0.030271251	-1	2807	2673	2722	3818	2700	2784	2746	1666	2626	2312
ENSMUSG00000021367	chr13	Edn1	0.90380911	0.01008637	0.017846196	0.40923761	0.0816729	1	10	12	8	17	15	21	40	24	20	22
ENSMUSG00000021371	chr13	Mcur1	-0.3864244	0.010093433	0.017856433	5.542675193	0.025551238	-1	645	739	747	1106	719	770	639	624	543	727
ENSMUSG00000038058	chr6	Nod1	-0.4165621	0.010096783	0.017860098	3.971339466	0.02725067	-1	248	286	255	326	214	286	229	154	192	239
ENSMUSG00000031849	chr8	Comp	1.23675874	0.010135305	0.017925971	5.279301332	0.264461749	1	604	249	342	358	171	3033	561	350	438	306
ENSMUSG00000024948	chr19	Map4k2	-0.4637941	0.010138509	0.017927101	3.143397007	0.031406891	-1	141	158	151	179	124	144	104	89	130	134
ENSMUSG00000037373	chr5	Ctbp1	-0.376951	0.010137499	0.017927101	7.28082363	0.025281288	-1	2548	2399	2265	3393	2538	2265	2219	1885	2218	2463
ENSMUSG00000024048	chr17	Myl12a	0.44748047	0.010146517	0.017938992	7.693075818	0.035883243	1	2388	2337	2197	4339	2076	4276	3855	4374	3238	3690
ENSMUSG00000022503	chr16	Nubp1	0.46313441	0.010182457	0.017997979	3.571614885	0.032964293	1	167	129	121	181	141	229	286	153	245	203
ENSMUSG00000065987	chr8	Cd209b	-1.7461358	0.010182024	0.017997979	0.814417848	0.474617345	-1	24	49	39	22	50	53	3	5	2	3
ENSMUSG00000029050	chr4	Ski	-0.4280591	0.010215194	0.01805356	6.292895193	0.032362785	-1	1179	1146	1093	1827	1487	1383	1203	843	861	1218
ENSMUSG00000047250	chr2	Ptgs1	0.62405549	0.010250435	0.018113551	2.185703533	0.053902052	1	44	49	46	61	58	118	59	98	83	79
ENSMUSG00000032115	chr9	Hyou1	0.47805984	0.010253413	0.018116524	5.551689858	0.039928513	1	495	481	497	803	653	1136	1135	641	914	651
ENSMUSG00000075324	chr2	Fign	-0.8952097	0.010282988	0.018166482	1.349458829	0.113700346	-1	43	50	29	66	50	9	26	32	26	44
ENSMUSG00000036299	chr18	BC031181	0.43333259	0.010291923	0.018179968	5.158297321	0.032095086	1	519	432	465	471	358	982	675	588	571	551
ENSMUSG00000039630	chr1	Hnrnpu	0.39664943	0.010301192	0.018194042	7.120163737	0.028112345	1	1633	1641	1506	2628	1646	2968	3015	2120	2425	2428
ENSMUSG00000022840	chr16	Adcy5	-0.8572338	0.010303805	0.018196358	1.846823644	0.111892468	-1	39	74	30	85	106	35	41	42	30	54
ENSMUSG00000029053	chr4	Prkcz	-0.8565093	0.010307253	0.018200147	1.036752467	0.098114264	-1	57	26	36	29	36	39	26	15	17	17
ENSMUSG00000038543	chr3	BC028528	0.77518151	0.010340534	0.018254355	2.555398505	0.094902198	1	71	92	77	45	25	171	108	96	96	127
ENSMUSG00000045039	chr7	Megf8	-0.3737939	0.010340564	0.018254355	5.543613148	0.023970899	-1	794	642	674	989	825	688	660	648	626	683
ENSMUSG00000019470	chr8	Xab2	0.40657636	0.010350414	0.018269435	4.043909604	0.025922741	1	221	195	182	265	190	425	299	277	242	292
ENSMUSG00000001552	chr11	Jup	-0.4833305	0.010362186	0.018287493	6.400994225	0.04162718	-1	1297	1265	1256	1920	1616	1553	937	1281	744	1261
ENSMUSG00000022231	chr15	Sema5a	-0.6034158	0.010363262	0.018287493	3.405086708	0.059215438	-1	173	146	179	261	189	164	107	181	67	160
ENSMUSG00000020715	chr11	Ern1	-0.4406906	0.010372138	0.018300846	3.550901974	0.029605876	-1	177	181	159	297	194	206	154	139	125	186
ENSMUSG00000030089	chr6	Slc41a3	-0.4890894	0.010381389	0.018314857	6.690301956	0.04276508	-1	1550	1665	1491	2326	1967	948	1526	1568	1246	1654
ENSMUSG00000026596	chr1	Abl2	-0.4434936	0.010415811	0.018373264	4.407178154	0.032732586	-1	294	285	357	506	380	387	327	253	206	301

ENSMUSG00000020857	chr11	Nme2	0.41055595	0.010440607	0.018412356	8.297089512	0.030508425	1	4141	4235	3822	4922	3058	6828	5901	5588	6031	4932
ENSMUSG00000034154	chr2	Ino80	-0.417953	0.010440146	0.018412356	4.300488317	0.028528348	-1	337	346	280	409	302	296	362	181	259	281
ENSMUSG00000059751	chr13	Rps3a3	1.00277619	0.010444545	0.018416977	-0.180231867	0.079696086	1	4	10	8	10	5	21	20	15	13	13
ENSMUSG00000005225	chr6	Plekha8	-0.4829764	0.010473857	0.018466333	2.61817824	0.031546187	-1	107	105	92	122	97	88	93	75	81	73
ENSMUSG00000056537	chrX	Rlim	0.37245384	0.010478678	0.018472502	4.893844614	0.023035497	1	392	380	396	468	290	648	627	468	471	527
ENSMUSG00000037366	chr4	Pafah2	0.6098638	0.010493632	0.018496532	1.995098604	0.050568849	1	45	59	31	56	37	71	80	82	76	69
ENSMUSG00000032633	chr11	Flcn	-0.364814	0.010497045	0.018500215	5.510151627	0.022877408	-1	757	708	645	987	735	762	644	509	627	721
ENSMUSG00000040415	chr10	Dtx3	0.42149749	0.010502577	0.018507631	5.051265192	0.030313611	1	467	400	405	451	372	877	475	631	514	606
ENSMUSG00000020089	chr10	Ppa1	0.38609888	0.010523926	0.018542913	5.263656495	0.02553457	1	510	486	442	629	418	696	841	717	684	590
ENSMUSG00000032113	chr9	Chek1	0.99889518	0.010575904	0.018632149	0.094060093	0.104075216	1	5	12	11	11	7	22	32	12	23	13
ENSMUSG00000047649	chr7	Cd3eap	-0.4837029	0.010578176	0.018633803	3.063271786	0.034513603	-1	121	144	140	203	114	104	112	128	101	113
ENSMUSG00000029780	chr6	Nt5c3	-0.4172488	0.01059414	0.018659572	5.673279855	0.030548688	-1	1008	847	878	978	627	687	712	563	737	866
ENSMUSG00000022521	chr16	Crebbp	-0.3873479	0.01060064	0.018668667	4.68820288	0.024946132	-1	373	400	391	551	455	453	396	338	279	360
ENSMUSG00000079418	chrX	Atg4a	-0.4509679	0.01061145	0.01868535	4.390376078	0.033905071	-1	360	384	344	406	297	211	277	255	339	347
ENSMUSG00000032878	chr11	Ccdc85a	-0.7697487	0.010617004	0.018692774	1.66136334	0.083176798	-1	47	50	63	94	37	19	45	33	44	41
ENSMUSG00000031883	chr8	Car7	-0.9674713	0.010619965	0.018695632	0.591453053	0.115296715	-1	20	36	26	32	23	12	6	23	11	24
ENSMUSG00000033105	chr10	Lss	-0.6449054	0.010640951	0.018730217	1.748008031	0.055693223	-1	64	60	57	59	53	39	60	27	43	38
ENSMUSG00000038217	chr11	Tlcd2	0.57220623	0.010656402	0.018752691	3.765783068	0.054501478	1	173	191	148	162	128	151	263	265	252	373
ENSMUSG00000090673	chr19	Gm340	-1.0289663	0.010655994	0.018752691	0.276547207	0.124417029	-1	13	16	31	26	23	7	5	15	14	17
ENSMUSG00000054863	chr15	Fam19a5	0.62797138	0.010659754	0.018756229	1.734223657	0.050654375	1	30	39	35	58	27	70	74	65	48	60
ENSMUSG00000054435	chr6	Gimap4	-0.5167861	0.01066389	0.018761144	3.28282354	0.041692831	-1	172	171	164	245	103	179	99	123	106	143
ENSMUSG00000018893	chr15	Mb	-1.0377991	0.010668276	0.018766498	10.40810147	0.192393629	-1	9602	29552	32682	55964	13055	30670	7237	15528	13841	6226
ENSMUSG00000053626	chr8	Tll1	-0.8046023	0.010677902	0.018781067	0.719271959	0.072099227	-1	24	29	30	36	26	10	18	16	25	21
ENSMUSG00000097467	chr9	Gm26737	1.1875232	0.010697902	0.018813876	-0.351666502	0.13586439	1	3	3	7	6	10	19	19	20	6	10
ENSMUSG00000025407	chr10	Gli1	-0.917938	0.010719897	0.018850186	0.790752805	0.110347684	-1	21	28	39	45	25	30	10	18	8	26
ENSMUSG00000028431	chr4	Ikbkap	-0.374387	0.010764028	0.018925407	5.011914859	0.023636342	-1	532	515	427	710	536	407	509	434	467	460
ENSMUSG00000028430	chr4	Nol6	0.36565816	0.010768008	0.018930023	4.862473606	0.022307776	1	380	351	299	491	375	567	565	500	426	612
ENSMUSG00000038046	chr11	Rnmtl1	0.44137049	0.010777354	0.018944069	3.654826424	0.030503347	1	137	145	158	228	127	226	251	267	205	217
ENSMUSG00000041716	chr12	Gm20604	-0.3968689	0.010796273	0.018974939	3.609688851	0.023428652	-1	214	210	194	251	158	183	170	152	178	169
ENSMUSG00000029386	chr5	Tctn2	0.69750456	0.010803341	0.018984973	1.197425459	0.056740623	1	23	18	24	33	25	49	53	48	34	34
ENSMUSG00000025089	chr19	Gfra1	-0.4589046	0.010831472	0.019032015	3.218476712	0.031868603	-1	148	164	133	161	180	147	125	102	116	145
ENSMUSG00000023439	chr6	Gnb3	0.72609448	0.0108823	0.019116646	1.38312517	0.067744535	1	23	23	21	47	27	34	62	54	48	52
ENSMUSG00000038544	chr4	Inip	0.58568449	0.010882373	0.019116646	2.3790703	0.049376839	1	50	58	57	95	46	136	122	78	83	82
ENSMUSG00000026764	chr2	Kif5c	0.98602674	0.010891438	0.019130167	1.12483325	0.139072454	1	20	13	19	25	25	17	34	49	38	82
ENSMUSG00000034932	chr10	Mrpl54	0.38728777	0.010911905	0.019163707	5.701038816	0.026372437	1	759	639	607	765	580	1205	933	841	1018	816
ENSMUSG00000027550	chr3	Lrrcc1	0.66414977	0.010948214	0.019225058	2.116698359	0.064155777	1	51	60	51	49	30	58	93	81	100	85
ENSMUSG00000040479	chr2	Dgkz	-0.4010995	0.010976127	0.019270093	6.096554177	0.028780139	-1	1295	1254	1060	1142	999	1070	945	773	1052	976
ENSMUSG00000056770	chr12	Setd3	-0.3713969	0.010976618	0.019270093	6.786331922	0.02489522	-1	1910	1681	1659	2359	1699	1523	1575	1414	1561	1770
ENSMUSG00000033596	chr8	Rfwd3	0.53049773	0.011000145	0.019308971	3.330665267	0.044960354	1	107	127	117	139	113	253	246	136	204	125
ENSMUSG00000024335	chr17	Brd2	-0.3816627	0.011025541	0.019351118	6.745920473	0.026363639	-1	1759	1704	1825	2264	1510	1935	1555	1193	1375	1607
ENSMUSG00000045930	chr12	Clec14a	-0.5027726	0.011032025	0.019360068	3.587888871	0.041390197	-1	209	222	220	233	154	244	121	111	149	190
ENSMUSG00000058006	chr4	Mdn1	-0.4836206	0.011057331	0.01940204	3.396649284	0.03669707	-1	161	130	157	259	205	175	167	125	127	118
ENSMUSG00000021731	chr13	Mrps30	0.37136139	0.011066668	0.019415986	5.061988779	0.023600878	1	415	419	397	585	362	753	504	624	591	593
ENSMUSG00000028953	chr5	Abcf2	-0.3887355	0.011081893	0.019440259	7.01472173	0.027478812	-1	2365	1875	1851	2801	2084	1710	1951	1599	1996	1855
ENSMUSG00000020630	chr12	Rnaseh1	0.63081556	0.011085666	0.019444436	2.679083699	0.061489135	1	99	58	61	79	69	211	117	73	110	122
ENSMUSG00000051166	chr12	Eml5	-0.7412457	0.011109689	0.019484128	1.878694406	0.078886472	-1	81	57	50	78	67	22	35	46	52	60
ENSMUSG00000002741	chr11	Ykt6	0.37152618	0.011140183	0.019535157	6.316140538	0.024801139	1	1072	1008	942	1333	844	1717	1421	1328	1507	1361
ENSMUSG00000099681	chr11	1700052K11Rik	-0.5275641	0.011186345	0.019613644	2.607940448	0.04062745	-1	135	93	99	128	74	100	70	78	69	84
ENSMUSG00000028883	chr5	Sema3a	-0.8237335	0.011193054	0.019622946	2.387745429	0.110917666	-1	157	98	86	78	65	60	70	20	83	71
ENSMUSG00000004044	chr11	Ptrf	0.40195359	0.011247133	0.019715281	7.938005938	0.029784715	1	3062	2853	2702	4084	3106	5884	4247	4673	3807	4238
ENSMUSG00000014349	chr11	Ube2z	0.36758232	0.011269246	0.019751566	5.80356844	0.023939226	1	666	753	690	881	637	1240	1057	799	1050	1006
ENSMUSG00000019857	chr10	Asf1a	-0.4380094	0.011279366	0.019766823	3.378961775	0.029114076	-1	179	159	174	174	187	140	154	140	141	136
ENSMUSG00000026203	chr1	Dnajb2	-0.3834592	0.011285221	0.019774605	5.864204817	0.026232046	-1	1056	947	882	1217	822	1018	768	774	881	679
ENSMUSG00000034601	chr12	2700049A03Rik	-0.5223907	0.011311907	0.019818881	2.358713406	0.036580209	-1	94	90	78	109	71	72	82	62	62	58
ENSMUSG00000029066	chr4	Mrpl20	0.3800081	0.011316358	0.019823036	5.11196394	0.02498983	1	458	422	443	561	355	727	715	543	682	517
ENSMUSG00000046836	chr1	Brox	-0.3862209	0.011317115	0.019823036	4.807546163	0.025448115	-1	477	404	422	639	431	472	411	268	435	400
ENSMUSG00000030271	chr6	Ogg1	0.68068548	0.01132843	0.019840368	2.103283696	0.068578742	1	54	43	47	59	36	52	112	57	101	95
ENSMUSG00000020260	chr10	Pofut2	0.36262015	0.011364122	0.019900385	4.952561077	0.022349041	1	367	383	351	515	400	714	611	512	451	562
ENSMUSG00000028339	chr4	Col15a1	-0.5294328	0.011392533	0.019947637	7.312262467	0.051714852	-1	2343	2699	2673	3258	2943	1504	1987	2765	1550	2691
ENSMUSG00000031239	chrX	Itm2a	-0.6300847	0.011397084	0.019953107	8.747363625	0.073470039	-1	9417	7568	6765	8215	6814	3379	4479	4046	5418	10216
ENSMUSG00000041540	chr6	Sox5	-0.9952983	0.011400498	0.019956583	-0.015389319	0.096768969	-1	15	13	18	18	22	9	6	16	6	10
ENSMUSG00000046807	chr10	Lrrc75b	-0.945491	0.011417195	0.019983308	-0.004685236	0.081035619	-1	14	15	12	27	19	14	6	6	10	13
ENSMUSG00000020261	chr11	Slc36a1	0.49181322	0.011418959	0.019983893	3.260895267	0.03735485	1	129	122	92	132	110	263	208	124	159	159
ENSMUSG00000007122	chr1	Casq1	-0.4680853	0.011436135	0.020011447	12.95026798	0.040873753	-1	164299	131225	109798	137699	137392	94080	111383	103736	86184	146843
ENSMUSG00000061723	chr7	Tnnt3	-0.3999751	0.011460505	0.02005158	14.27871713	0.02991604	-1	365514	289840	274793	412149	346690	275143	286610	245690	272121	320122

ENSMUSG00000025271	chrX	Pfkfb1	-0.4906301	0.011466065	0.020056286	4.852541461	0.042515856	-1	379	567	563	658	346	331	401	325	510	374
ENSMUSG00000055538	chr14	Zcchc24	-0.3943342	0.011465166	0.020056286	6.849292991	0.028530277	-1	1994	1922	1514	2225	2074	2084	1477	1382	1437	1805
ENSMUSG00000067567	chrX	Hdac8	0.54150625	0.011470697	0.020061877	2.167301363	0.039019199	1	61	52	39	63	50	81	82	76	91	91
ENSMUSG00000037788	chr6	Vopp1	0.43696423	0.011484824	0.020084071	3.277123216	0.028712003	1	95	137	118	153	103	211	190	155	157	189
ENSMUSG00000041653	chr15	Pnpla3	-1.0374351	0.011503473	0.020114168	2.441877113	0.182836475	-1	31	165	88	97	142	25	54	93	43	64
ENSMUSG00000039236	chr7	Isg20	0.96638393	0.011521016	0.020142321	0.706077021	0.120488529	1	16	20	18	11	9	55	17	21	26	45
ENSMUSG00000071172	chr17	Srsf3	0.48202113	0.011571736	0.020228466	5.969287653	0.042433745	1	774	731	635	1128	671	1450	1531	876	1346	769
ENSMUSG00000004263	chr6	Atn1	0.38130273	0.011590147	0.020258115	6.783388188	0.026681708	1	1336	1251	1254	1922	1403	2562	1825	1775	1993	2052
ENSMUSG00000000317	chr11	Bcl6b	-0.6635047	0.011638283	0.020335545	3.94946683	0.077712171	-1	230	370	389	276	121	239	180	203	127	225
ENSMUSG00000001865	chr3	Cpa3	0.64633595	0.011638268	0.020335545	2.312467208	0.063656489	1	33	55	53	77	63	135	68	106	88	85
ENSMUSG00000036845	chr7	Lin37	0.46442771	0.011638811	0.020335545	3.030798853	0.032052533	1	101	95	84	123	101	187	154	165	119	137
ENSMUSG00000034484	chr18	Snx2	0.49965185	0.011657971	0.020366475	5.148929743	0.04479949	1	455	454	419	469	375	830	769	377	893	531
ENSMUSG00000018931	chr11	Natd1	-0.3852585	0.011663208	0.020373078	4.322501037	0.024622282	-1	340	319	317	356	336	305	232	263	271	338
ENSMUSG00000021273	chr14	Fdft1	-0.4253182	0.011668971	0.020380597	5.629065609	0.032616569	-1	828	972	743	1058	636	806	764	569	773	533
ENSMUSG00000034522	chr14	Zfp395	-0.4678374	0.011678434	0.020394575	4.462224287	0.038115698	-1	346	346	362	473	371	366	202	257	244	445
ENSMUSG00000037971	chr9	1110032A03Rik	0.55093304	0.011739862	0.02049929	2.943745812	0.048265589	1	85	93	84	115	81	91	148	164	156	166
ENSMUSG00000083240	chr2	Gm13453	-0.7522101	0.011747201	0.020509542	2.661700399	0.094633545	-1	118	106	84	168	112	173	56	52	46	61
ENSMUSG00000062300	chr7	Pvrl2	0.52990367	0.011777608	0.020560061	2.967054153	0.043581312	1	93	100	100	108	67	194	104	144	123	180
ENSMUSG00000020994	chr12	Pnn	-0.3452798	0.011780178	0.020561979	4.596953249	0.019765068	-1	416	359	367	477	389	367	353	301	331	383
ENSMUSG00000015981	chr7	Stk32c	1.07342251	0.011784106	0.020566267	-0.093685292	0.110325381	1	8	4	8	7	11	22	10	24	11	22
ENSMUSG00000001127	chrX	Araf	-0.3616824	0.011812983	0.020614091	6.128497107	0.023736404	-1	1203	1146	1020	1489	1024	1081	933	849	1009	1129
ENSMUSG00000006342	chr10	Susd2	0.64034677	0.01181801	0.020620288	2.367124721	0.062150391	1	63	53	51	58	65	164	76	100	65	100
ENSMUSG00000031155	chrX	Pim2	0.87607217	0.011820925	0.020622799	0.734459806	0.094146757	1	21	16	7	16	20	37	27	30	45	22
ENSMUSG00000033705	chr2	Stard9	-0.4911971	0.011827039	0.020630891	3.440710465	0.039440094	-1	176	212	224	170	141	172	148	110	133	171
ENSMUSG00000057176	chr7	Gm166	0.70417181	0.011859444	0.020684836	1.107847745	0.056836711	1	31	22	17	22	22	35	44	41	37	47
ENSMUSG00000029833	chr6	Trim24	-0.4359894	0.011871588	0.020703434	5.018343931	0.033764542	-1	623	502	513	570	541	319	453	426	471	557
ENSMUSG00000074398	chr3	Gm15441	-1.436498	0.011912345	0.020771919	0.217419712	0.306426539	-1	13	22	5	35	40	9	2	11	2	22
ENSMUSG00000028293	chr4	Slc35a1	-0.3697542	0.011926254	0.020793579	4.294424114	0.022516624	-1	316	338	288	384	311	309	243	235	277	329
ENSMUSG00000068134	chr2	Zfp120	-0.4429916	0.011947617	0.020828227	3.451384963	0.030981926	-1	214	199	154	190	168	140	165	116	162	166
ENSMUSG00000013236	chr17	Ptprs	-0.3920997	0.011970665	0.020865803	5.621417377	0.027766676	-1	960	748	860	861	701	724	635	695	604	809
ENSMUSG00000011114	chr9	Tbrg1	0.34758048	0.012017475	0.020944785	5.1316143	0.021023073	1	488	454	391	563	402	667	700	547	677	602
ENSMUSG00000032171	chr9	Pin1	0.36680709	0.012037729	0.020974853	5.566297336	0.024096737	1	644	647	578	692	509	893	909	813	915	805
ENSMUSG00000038679	chr15	Trps1	-0.4740642	0.012036251	0.020974853	3.211333231	0.035642189	-1	165	127	147	192	162	149	123	92	97	170
ENSMUSG00000038930	chr7	Rccd1	-0.5310185	0.012067261	0.02102369	2.698141671	0.04237782	-1	124	78	108	159	98	103	80	95	75	72
ENSMUSG00000025785	chr9	Exosc7	0.41632924	0.01207539	0.02103523	3.803621959	0.028095175	1	205	161	135	215	170	243	299	221	287	238
ENSMUSG00000024807	chr19	Syvn1	0.43558471	0.012079962	0.021039681	4.988648483	0.033818175	1	396	343	293	526	455	855	580	515	419	634
ENSMUSG00000036980	chr5	Taf6	-0.352674	0.012080956	0.021039681	4.849769995	0.021307387	-1	505	458	469	548	416	401	441	360	440	414
ENSMUSG00000078201	chr2	Tmem203	0.47783226	0.012096225	0.021063648	2.978276261	0.034479496	1	119	78	99	112	75	147	132	144	143	169
ENSMUSG00000031201	chrX	Brcc3	-0.4435757	0.012116602	0.021096502	4.062746416	0.033311261	-1	329	292	249	296	253	184	263	176	256	267
ENSMUSG00000078765	chr7	U2af1l4	0.3413289	0.01212012	0.021099999	4.905226247	0.019865884	1	428	356	364	445	365	600	580	467	546	534
ENSMUSG00000027649	chr2	Ctnnbl1	0.40871386	0.01212732	0.021109904	3.62928092	0.026428175	1	155	166	119	224	129	284	213	209	218	220
ENSMUSG00000058317	chr14	Ube2e2	0.6114744	0.012132811	0.021116832	2.369115232	0.056304465	1	54	51	69	67	54	120	99	107	54	119
ENSMUSG00000028886	chr4	Eya3	0.3515964	0.012205449	0.021240612	4.590911585	0.0207333	1	295	298	285	400	296	507	507	375	387	428
ENSMUSG00000004565	chr8	Pnpla6	0.44207705	0.012224323	0.021270809	3.189739368	0.029722018	1	132	102	107	134	94	204	139	162	151	192
ENSMUSG00000073633	chr1	Fbxo36	0.79276421	0.012227549	0.021273774	0.715280613	0.07057629	1	21	18	19	11	12	35	27	28	36	30
ENSMUSG00000017639	chr11	Rab11fip4	0.98599434	0.01223136	0.021277755	0.356855868	0.112394106	1	14	13	13	13	4	43	30	13	23	17
ENSMUSG00000053929	chr15	Cyhr1	-0.3710332	0.012246659	0.021301718	6.489636423	0.025495455	-1	1542	1348	1359	1826	1473	1258	1172	1203	1274	1472
ENSMUSG00000024899	chr19	Papss2	0.49971771	0.012262724	0.021327007	3.364469001	0.04026936	1	118	140	123	147	99	237	279	137	153	176
ENSMUSG00000020017	chr10	Hal	2.18115758	0.012271674	0.021339917	0.390551392	0.714974564	1	6	8	5	6	5	131	16	2	15	0
ENSMUSG00000020564	chr12	Atxn7l1	-0.4018172	0.012289653	0.021365949	3.760406409	0.025742003	-1	208	241	237	248	199	192	203	179	156	216
ENSMUSG00000068882	chr2	Ssb	0.38470767	0.012289701	0.021365949	5.889571461	0.027117706	1	857	772	618	939	655	1107	1258	903	1209	989
ENSMUSG00000020561	chr12	Twistnb	-0.5604737	0.01230161	0.021383993	3.236180841	0.051947085	-1	170	165	140	208	147	77	176	85	142	132
ENSMUSG00000019848	chr10	Popdc3	-0.3792814	0.012311299	0.021398174	4.848047513	0.025005511	-1	494	410	387	732	432	371	437	389	400	433
ENSMUSG00000098802	chr7	Mir7046	0.82666253	0.012320899	0.021412197	1.19033637	0.091536272	1	27	22	30	21	14	81	41	34	39	32
ENSMUSG00000038354	chr3	Ankrd35	0.80889856	0.012322677	0.021412623	1.251531528	0.092004316	1	23	29	17	31	22	42	22	56	45	67
ENSMUSG00000002957	chr7	Ap2a2	0.40657899	0.012334659	0.021428117	6.275030551	0.030666428	1	938	893	825	1249	1059	2043	1346	1209	1378	1275
ENSMUSG00000074280	chr9	Gm6166	1.12706326	0.012333726	0.021428117	2.605998457	0.222648168	1	58	77	57	50	32	379	130	29	80	79
ENSMUSG00000023089	chr6	Ndufa5	0.43474752	0.012362819	0.021471699	7.43154278	0.035691823	1	2167	2380	2106	2791	1547	3891	2873	3058	3729	2607
ENSMUSG00000056836	chr7	Gm6851	1.00303851	0.012361482	0.021471699	-0.052593627	0.114618147	1	12	3	7	16	4	12	25	20	17	16
ENSMUSG00000041815	chr15	Poldip3	0.43250974	0.0123713	0.021483758	4.918293205	0.033363717	1	349	377	369	452	359	917	562	430	469	487
ENSMUSG00000084957	chr19	Bbip1	-0.4395902	0.012409459	0.021547348	4.703253897	0.034229295	-1	545	388	383	522	392	315	362	319	477	310
ENSMUSG00000046413	chr8	Irx3os	-1.7545926	0.012439794	0.021597336	0.180804369	0.466985344	-1	9	21	52	34	2	1	12	15	1	8
ENSMUSG00000030970	chr7	Ctbp2	-0.4746758	0.012456214	0.021623159	3.44153867	0.036590588	-1	156	148	170	298	174	141	169	107	167	151
ENSMUSG00000032342	chr9	Mto1	-0.362291	0.012471728	0.021647401	4.422879323	0.022023042	-1	399	322	303	450	323	316	316	239	324	332
ENSMUSG00000024414	chr11	Mrpl27	0.36131957	0.012525331	0.021737133	5.312834409	0.023357809	1	549	524	503	607	403	771	788	668	732	676

ENSMUSG00000038880	chr17	Mrps34	0.37459961	0.012526536	0.021737133	5.749943035	0.025685234	1	771	610	577	888	657	1206	915	1007	797	1038
ENSMUSG00000022012	chr14	Enox1	0.74074422	0.01253225	0.021744349	0.842997419	0.0610491	1	15	16	12	27	23	40	37	34	26	33
ENSMUSG00000021756	chr13	Il6st	-0.3974867	0.012541749	0.021758129	7.263528121	0.029882084	-1	2364	2175	2201	3481	2848	2665	2326	1840	1772	2296
ENSMUSG00000035382	chr9	Pcsk7	-0.3912863	0.012549535	0.021768934	4.066715736	0.025401316	-1	286	236	236	367	289	262	226	178	247	267
ENSMUSG00000051159	chrX	Cited1	0.81947571	0.012559655	0.021783785	0.948955039	0.08206234	1	28	16	17	12	22	57	35	28	32	37
ENSMUSG00000040549	chr2	Ckap5	-0.3741015	0.012590697	0.021834915	5.370196041	0.0252097	-1	652	650	544	987	673	560	656	550	587	573
ENSMUSG00000055653	chrX	Gpc3	0.57288363	0.01262944	0.021899387	4.547383322	0.059741629	1	216	248	238	341	345	468	322	433	294	766
ENSMUSG00000054720	chr5	Lrrc8c	-0.4463663	0.012631491	0.021900225	3.83792056	0.033764257	-1	232	219	205	308	258	276	246	141	158	171
ENSMUSG00000055368	chr8	Slc6a2	-1.0970397	0.012644465	0.02192	0.306764117	0.167890958	-1	15	21	25	13	37	24	7	14	8	6
ENSMUSG00000099309	chr9	Mir7085	-0.8115315	0.01264924	0.021925558	0.86681391	0.083744626	-1	48	33	23	32	26	18	16	21	14	32
ENSMUSG00000014791	chr8	Elmo3	0.74856397	0.012654115	0.021928569	0.981963804	0.065998348	1	21	17	24	18	21	50	31	26	34	49
ENSMUSG00000035168	chr2	Tanc1	-0.4732567	0.01265324	0.021928569	3.832346134	0.038174312	-1	224	210	210	368	228	247	153	219	128	222
ENSMUSG00000044456	chr12	Rin3	0.64030684	0.012664355	0.021941782	3.615960538	0.072567325	1	115	101	91	217	190	369	204	219	127	305
ENSMUSG00000090019	chr6	Gimap1	0.6336146	0.01266488	0.021941782	1.966678695	0.058256372	1	54	39	44	58	27	105	57	75	56	84
ENSMUSG00000069094	chr3	Pde7a	-0.4411886	0.012671324	0.021950226	4.699333624	0.034783395	-1	474	376	412	579	392	346	318	241	480	405
ENSMUSG00000031461	chr8	Myom2	-0.4598055	0.012706327	0.022008133	10.84321262	0.040604021	-1	30845	24727	25624	44260	34429	20378	24961	22908	24250	33458
ENSMUSG00000026470	chr1	Stx6	0.37820094	0.012742583	0.022065462	3.928091378	0.023094059	1	178	196	178	251	178	353	267	268	226	285
ENSMUSG00000030780	chr7	BC017158	0.51337383	0.012741313	0.022065462	2.36963451	0.036948952	1	62	61	57	78	52	105	102	81	76	122
ENSMUSG00000044231	chr13	Nhlrc1	-0.453926	0.01276259	0.022097368	3.181195318	0.032022013	-1	170	163	115	191	136	154	96	120	118	130
ENSMUSG00000034190	chr14	Chmp7	-0.3894548	0.012764191	0.022097402	5.650816526	0.027880973	-1	947	805	734	1059	713	731	653	595	862	694
ENSMUSG00000075486	chr14	Commd6	0.49994655	0.012787621	0.022135223	2.967698462	0.038989364	1	98	103	99	90	80	201	141	135	144	117
ENSMUSG00000026154	chr1	1110058L19Rik	0.43658718	0.012817198	0.022183673	4.34221858	0.033583697	1	258	298	226	343	163	336	342	388	416	397
ENSMUSG00000039756	chr3	Dnttip2	-0.4176247	0.012823414	0.022191684	4.350785732	0.030365603	-1	393	332	318	434	262	294	353	191	318	267
ENSMUSG00000025224	chr19	Gbf1	-0.4080931	0.012832269	0.022204258	6.171523423	0.03119886	-1	1181	956	994	1643	1376	974	1060	1033	854	1120
ENSMUSG00000003166	chr16	Dgcr2	-0.368212	0.012846057	0.022225365	5.578062904	0.024814788	-1	704	731	685	1063	836	744	682	612	575	796
ENSMUSG00000036941	chr18	Elac1	-0.4652628	0.012873617	0.022270289	3.628703799	0.036306762	-1	230	199	189	250	192	186	129	113	185	232
ENSMUSG00000024190	chr17	Dusp1	-0.8328803	0.012875419	0.02227065	6.040771039	0.131074107	-1	860	1284	1794	1259	977	1610	1117	379	318	576
ENSMUSG00000028974	chr4	Dffa	-0.4111498	0.01289065	0.022294236	5.689499642	0.031294437	-1	783	765	776	1376	754	608	722	723	701	837
ENSMUSG00000026667	chr1	Uhmk1	-0.3808674	0.012908837	0.022322928	4.969263332	0.025989846	-1	485	475	458	733	502	533	532	304	394	472
ENSMUSG00000042705	chr18	Commd10	0.45418672	0.012919288	0.022338237	3.015155028	0.031220335	1	95	97	94	130	86	175	153	110	172	143
ENSMUSG00000003360	chr15	Ddx23	-0.3992989	0.012925721	0.022346594	5.885055623	0.029688453	-1	916	818	802	1426	1084	797	846	687	898	923
ENSMUSG00000022426	chr15	Josd1	-0.3540099	0.012927807	0.022347438	4.8151913	0.021943252	-1	424	494	409	602	424	500	403	315	402	401
ENSMUSG00000029063	chr4	Nadk	0.39760057	0.012941654	0.022368607	4.871501046	0.028207262	1	308	376	335	476	381	749	579	383	510	513
ENSMUSG00000043889	chr13	Gm8399	0.71334514	0.012950414	0.02238098	0.889535953	0.057089147	1	19	20	14	30	15	40	45	29	31	30
ENSMUSG00000027646	chr2	Src	0.5113727	0.01302958	0.022515011	2.98065437	0.041348655	1	102	79	95	106	93	200	116	118	121	197
ENSMUSG00000026626	chr1	Ppp2r5a	-0.3554208	0.013035922	0.022523186	6.600398524	0.023839227	-1	1469	1538	1521	2037	1553	1510	1424	1213	1375	1431
ENSMUSG00000014444	chr8	Piezo1	0.46720515	0.013052427	0.022548915	5.487428949	0.040703407	1	602	462	431	654	646	1322	943	681	625	728
ENSMUSG00000026308	chr1	Klhl30	-0.4531499	0.01305889	0.022557291	6.935314871	0.039225091	-1	1743	1518	1875	2961	2493	1586	1552	1858	1495	1895
ENSMUSG00000037916	chr19	Ndufv1	-0.4192076	0.013065536	0.022565983	8.539205028	0.033900804	-1	5177	6076	6389	9500	4968	5395	4565	5036	5377	5544
ENSMUSG00000070604	chr7	Vsig10l	0.96703784	0.013071533	0.02257355	0.359841951	0.107800476	1	6	15	12	11	13	27	17	20	17	44
ENSMUSG00000041957	chr16	Pkp2	0.7453599	0.013074828	0.022576451	1.339389337	0.075701866	1	26	17	30	32	28	39	34	45	56	70
ENSMUSG00000102976	chr1	Zc3h11a	-0.4124935	0.013090091	0.022600014	6.953021926	0.032493956	-1	2146	1831	1787	2467	2285	1546	1942	1514	1448	2236
ENSMUSG00000001739	chr5	Cldn15	0.62505208	0.013112851	0.022636513	1.825100159	0.054515873	1	32	38	29	57	45	88	58	76	55	61
ENSMUSG00000020287	chr11	Mpg	0.58657947	0.013125866	0.022656181	3.411913052	0.059507539	1	119	130	120	139	115	394	145	159	143	210
ENSMUSG00000029625	chr5	Cpsf4	0.52341549	0.013133932	0.022667304	3.521217767	0.047085453	1	147	128	120	169	131	383	226	164	180	157
ENSMUSG00000032186	chr9	Tmod2	-0.5607514	0.013137557	0.022670761	2.663782881	0.049287458	-1	118	74	123	145	95	61	98	76	88	85
ENSMUSG00000018858	chr11	Ict1	0.32831828	0.013148803	0.022684566	4.915804129	0.018739432	1	417	364	366	478	363	615	553	472	539	559
ENSMUSG00000056501	chr2	Cebpb	0.80236824	0.013147642	0.022684566	4.60308108	0.120430036	1	174	263	262	339	272	1262	429	242	398	266
ENSMUSG00000020385	chr11	Clk4	-0.362596	0.01319096	0.022754487	4.472253239	0.022659844	-1	418	391	322	425	297	391	307	257	302	329
ENSMUSG00000019853	chr10	Hebp2	0.91949954	0.013200863	0.02276876	0.987906585	0.120551164	1	15	16	21	26	17	86	28	35	20	32
ENSMUSG00000050555	chr9	Hyls1	0.79090888	0.013207828	0.022777962	0.620927456	0.070836514	1	13	14	11	16	22	30	33	27	33	22
ENSMUSG00000019790	chr10	Stxbp5	-0.5066228	0.013223364	0.022801941	3.548088056	0.044265437	-1	192	174	201	244	201	200	164	74	157	197
ENSMUSG00000009378	chr19	Slc16a12	-0.8326992	0.013227711	0.022805371	0.388711052	0.073453095	-1	18	22	27	30	17	17	15	7	18	13
ENSMUSG00000061815	chr1	Rufy4	-1.6539432	0.013228616	0.022805371	-0.021675176	0.421992819	-1	4	36	27	12	17	24	7	2	1	2
ENSMUSG00000082516	chr2	Gm13342	-0.941656	0.013235713	0.022814791	0.171811303	0.101256371	-1	14	24	16	25	20	6	15	5	17	13
ENSMUSG00000002504	chr17	Slc9a3r2	-0.4599438	0.013278079	0.022884997	4.853288715	0.038824925	-1	353	417	378	836	547	501	335	343	367	444
ENSMUSG00000007817	chr14	Zmiz1	-0.459009	0.013295697	0.022912536	5.395385511	0.039423178	-1	547	552	619	1206	763	591	648	467	466	731
ENSMUSG00000063406	chr5	Tmed5	-0.5411619	0.013304792	0.022925382	4.278867902	0.053268797	-1	297	261	253	565	362	162	341	204	259	313
ENSMUSG00000027427	chr2	Polr3f	-0.4788872	0.013333623	0.022972228	3.203433042	0.03692471	-1	132	173	165	210	113	109	151	110	125	124
ENSMUSG00000027455	chr2	Nsfl1c	0.35236343	0.013336759	0.022974798	6.180508796	0.023353065	1	1000	869	816	1225	857	1439	1338	1152	1377	1328
ENSMUSG00000054894	chr12	Atp5s	-0.467709	0.013345289	0.022986661	3.195549407	0.035095932	-1	154	160	170	168	126	114	134	99	150	121
ENSMUSG00000058254	chrX	Tspan7	-0.3864717	0.013379591	0.023042904	6.86162463	0.028617447	-1	1821	1865	1579	2635	1973	1734	1575	1529	1341	2068
ENSMUSG00000038347	chr17	Tcte2	1.19002095	0.013397677	0.02307121	-0.133732825	0.187980917	1	12	4	4	12	4	3	19	21	22	22
ENSMUSG00000040268	chr7	Plekha1	-0.3503132	0.013400468	0.023073173	4.911632624	0.021828406	-1	477	502	511	633	389	500	479	363	388	432
ENSMUSG00000017778	chr13	Cox7c	0.41133299	0.013407977	0.023083258	8.046689217	0.032817218	1	3383	3615	3462	4214	2296	5901	4643	4503	5117	4494

ENSMUSG00000026036	chr1	Nif3l1	-0.4257103	0.013409802	0.023083556	3.726105129	0.030304201	-1	223	217	222	257	199	150	239	148	182	194
ENSMUSG00000030683	chr7	Sez6l2	0.85108679	0.013422989	0.023103411	1.421255613	0.1118861	1	21	29	33	44	10	63	33	65	35	71
ENSMUSG00000013846	chr15	St3gal1	0.41598811	0.013466201	0.023172078	4.74185615	0.031187806	1	338	334	282	362	373	685	552	468	356	444
ENSMUSG00000031841	chr8	Cdh13	-0.4154891	0.013465473	0.023172078	7.052102684	0.033270522	-1	2436	2053	1983	2552	2243	1662	1746	2006	1483	2350
ENSMUSG00000036502	chrX	Tmem255a	-1.1900159	0.01347155	0.023178429	-0.093567451	0.1881801	-1	24	17	25	11	7	6	5	5	5	20
ENSMUSG00000030045	chr6	Mrpl19	-0.3557672	0.013487006	0.023202166	4.552056923	0.021885319	-1	377	348	371	521	347	321	384	315	321	328
ENSMUSG00000089889	chr5	0610040B10Rik	0.73523515	0.0135043	0.023229058	0.799013868	0.061883888	1	20	19	17	16	17	27	31	31	40	34
ENSMUSG00000026509	chr1	Capn2	0.37233795	0.013554156	0.023311948	6.376538283	0.026410443	1	1077	934	971	1478	974	1697	1763	1179	1528	1508
ENSMUSG00000024491	chr18	Rbm27	-0.4728892	0.013568659	0.023334019	3.786467628	0.038867326	-1	205	195	233	327	232	179	286	140	167	167
ENSMUSG00000084235	chr5	Gm15421	0.8160508	0.013583054	0.023355901	0.729068046	0.080142059	1	23	19	17	11	11	44	38	25	23	30
ENSMUSG00000022034	chr14	Esco2	1.23921663	0.013593756	0.023371428	-0.054552701	0.204084059	1	11	12	2	9	3	10	32	20	25	7
ENSMUSG00000029168	chr5	Dpysl5	-0.7782343	0.013650095	0.023462518	1.18828245	0.082881467	-1	56	30	36	46	36	17	22	19	39	32
ENSMUSG00000034312	chr6	Iqsec1	-0.4408095	0.013649433	0.023462518	5.558040905	0.036737694	-1	640	711	671	1218	841	733	666	578	442	861
ENSMUSG00000010538	chr3	Tsacc	0.6624867	0.013802079	0.023720837	1.349216238	0.059020477	1	23	30	25	39	23	56	41	42	64	38
ENSMUSG00000028158	chr3	Mttp	-0.6902967	0.013812326	0.02373553	2.193164399	0.078942619	-1	100	76	75	104	58	109	39	41	35	60
ENSMUSG00000013150	chr8	Gfod2	-0.4485146	0.013854043	0.023804291	3.188142333	0.032221643	-1	131	122	142	215	168	126	121	108	119	148
ENSMUSG00000041241	chr4	Mul1	-0.3582559	0.013862492	0.023815881	5.366947749	0.023676632	-1	651	615	624	964	622	573	594	606	540	623
ENSMUSG00000005320	chr13	Fgfr4	0.66507994	0.013864356	0.023816155	3.274585978	0.079532911	1	150	74	82	122	122	175	182	310	116	159
ENSMUSG00000032803	chr9	Cdv3	-0.3672403	0.013870285	0.023823412	7.268032405	0.026205589	-1	2457	2345	2196	3753	2337	2519	2340	2037	2006	2104
ENSMUSG00000042106	chr9	Fam212a	0.56576534	0.013884878	0.023845546	2.015929692	0.044218269	1	43	52	47	57	36	100	69	69	79	65
ENSMUSG00000086013	chr6	Gm15706	0.98245616	0.013901315	0.023870841	-0.012460361	0.100421011	1	17	9	4	9	4	18	21	15	22	17
ENSMUSG00000036960	chr3	Clca5	-1.0918322	0.013947708	0.023945871	-0.314759055	0.138352869	-1	18	21	15	10	5	10	8	3	4	11
ENSMUSG00000083610	chr3	Oaz2-ps	-0.6172553	0.013948436	0.023945871	2.019105946	0.055937297	-1	78	67	64	95	54	33	49	52	48	70
ENSMUSG00000043557	chr17	Mdga1	-0.5922899	0.01395122	0.023947709	5.394193521	0.067345143	-1	810	832	671	620	763	281	594	652	435	737
ENSMUSG00000058809	chr11	Gm12141	-0.5556277	0.013964221	0.023967083	2.204194715	0.044642237	-1	66	74	69	117	76	55	57	59	71	53
ENSMUSG00000000581	chr11	C1d	-0.4153522	0.014022149	0.024063551	4.646586976	0.031409829	-1	496	384	349	534	373	265	417	288	349	422
ENSMUSG00000044030	chr7	Irf2bp1	0.35940658	0.014028433	0.02407138	4.589454407	0.02284107	1	311	269	294	411	286	532	438	455	360	416
ENSMUSG00000066613	chr5	Zfp932	-0.5968006	0.01403327	0.024076722	2.395019989	0.055582261	-1	98	82	72	120	92	63	63	66	94	45
ENSMUSG00000048126	chr1	Col6a3	0.4802521	0.01405664	0.024113858	8.265052052	0.04539279	1	3544	3237	3478	4338	4427	5865	5747	7019	3634	6923
ENSMUSG00000020364	chr11	Zfp354a	-0.6011027	0.014069513	0.024132979	2.041597407	0.054035025	-1	58	74	80	97	52	45	58	37	51	69
ENSMUSG00000000743	chr8	Chmp1a	0.3474629	0.01409085	0.024166612	6.072462123	0.022977663	1	954	838	794	1045	779	1290	1215	1153	1233	1243
ENSMUSG00000039960	chr8	Rhou	-0.4931969	0.014121714	0.024216573	3.505862318	0.042073262	-1	130	191	156	303	211	195	175	142	127	127
ENSMUSG00000021546	chr13	Hnrnpk	0.36092206	0.014133148	0.024233207	7.446488943	0.025502444	1	2291	2232	1957	2949	2009	3550	3712	2779	2955	3052
ENSMUSG00000038822	chr10	Hace1	-0.5771427	0.014146085	0.024252415	2.23824014	0.050532361	-1	103	72	71	93	72	55	72	42	77	55
ENSMUSG00000027465	chr2	Tbc1d20	0.34289708	0.01416567	0.024283013	5.835673127	0.022201598	1	783	725	713	908	622	1247	1017	975	911	1070
ENSMUSG00000024049	chr17	Myom1	-0.4560324	0.014180136	0.02430483	10.00806061	0.041200552	-1	15430	14397	13713	26733	19609	11976	14243	13258	13055	18201
ENSMUSG00000033323	chr18	Ctdp1	0.48297311	0.014203164	0.024341314	3.248749776	0.03903324	1	108	106	93	188	98	260	198	134	157	153
ENSMUSG00000001039	chr11	B9d1	0.70891208	0.014210569	0.024351019	1.3853292	0.068194515	1	39	27	25	19	28	63	50	52	48	38
ENSMUSG00000042675	chr7	Ypel3	0.4543697	0.014212784	0.02435183	5.791546192	0.039713433	1	788	711	602	740	621	1731	789	823	884	1067
ENSMUSG00000020427	chr11	Igfbp3	0.60321454	0.014214709	0.024352141	5.452972097	0.070357513	1	554	378	351	707	615	1081	642	669	493	1481
ENSMUSG00000052748	chr1	Swt1	-0.6213976	0.014243091	0.024397774	2.102381073	0.060118216	-1	90	68	68	106	50	45	77	34	58	55
ENSMUSG00000034853	chr4	Acot11	0.77069057	0.014285046	0.024466642	2.810367876	0.107004407	1	33	115	68	133	38	109	134	145	177	135
ENSMUSG00000024033	chr17	Rsph1	0.80261196	0.014340585	0.024558757	1.783007279	0.103512252	1	34	46	35	26	35	49	48	76	50	119
ENSMUSG00000028121	chr3	Bcar3	0.48276887	0.014352958	0.024576934	3.255851569	0.03870595	1	96	145	112	123	105	183	242	154	159	160
ENSMUSG00000090015	chr5	Gm15446	-0.6002016	0.014358397	0.024583236	1.801325264	0.050314371	-1	52	61	59	72	58	34	52	33	51	48
ENSMUSG00000062580	chr1	Timm17a	-0.3794155	0.014362237	0.024586799	6.651637624	0.028044551	-1	1465	1661	1546	2379	1485	1606	1506	1456	1317	1234
ENSMUSG00000025730	chr17	Rab40c	0.44595194	0.014370493	0.024597919	3.383037623	0.032749148	1	170	115	96	143	126	240	181	152	185	218
ENSMUSG00000020061	chr10	Mybpc1	-0.5366079	0.014372586	0.024598489	10.53668678	0.057183542	-1	14418	25424	27368	42540	23134	24527	20017	22398	14638	17474
ENSMUSG00000036241	chr4	Ube2r2	-0.3623551	0.014389819	0.024624967	7.24639977	0.025785574	-1	2772	2596	2298	2946	2112	2274	2064	2060	2052	2387
ENSMUSG00000021033	chr12	Gstz1	-0.3713067	0.014411709	0.024659408	5.505486912	0.026092479	-1	751	824	725	868	633	810	539	612	628	644
ENSMUSG00000039470	chr8	Zdhhc2	-0.7112826	0.01445232	0.024725869	1.449351944	0.075089841	-1	56	52	43	59	33	59	28	19	32	26
ENSMUSG00000027243	chr2	Harbi1	-0.5386748	0.014463583	0.02474211	2.275045426	0.043571204	-1	93	80	82	87	73	52	65	57	57	83
ENSMUSG00000044562	chr7	Rasip1	0.47165868	0.01448189	0.024770395	4.213457953	0.040783565	1	189	213	230	339	191	531	265	367	250	348
ENSMUSG00000043439	chr11	E130012A19Rik	0.75320694	0.014503475	0.024804279	0.725662144	0.064048838	1	13	20	17	20	14	37	33	23	22	42
ENSMUSG00000020176	chr11	Grb10	0.48079584	0.014524725	0.024837582	7.397657463	0.045759434	1	2043	1865	1615	2555	2406	3498	2553	3950	2124	3869
ENSMUSG00000027593	chr2	Raly	0.34508994	0.01453278	0.024848316	6.169632591	0.022946478	1	996	853	825	1219	851	1388	1346	1141	1300	1398
ENSMUSG00000037772	chr7	Mrpl23	0.34860103	0.014549456	0.024873785	5.196741635	0.022536681	1	515	473	379	585	451	777	665	596	704	603
ENSMUSG00000030259	chr6	Rassf8	-0.4657742	0.014554053	0.024878602	4.066597728	0.039353039	-1	233	200	310	434	276	245	235	208	163	296
ENSMUSG00000039617	chr3	Gm7488	1.02213631	0.01457479	0.024911003	0.201460066	0.131913061	1	8	10	7	15	10	38	23	11	31	9
ENSMUSG00000037058	chr18	Paip2	-0.3770977	0.01458273	0.024921525	6.810843221	0.027904986	-1	2019	1951	1701	2173	1597	1534	1523	1372	1799	1720
ENSMUSG00000049409	chr6	Prokr1	-0.9605063	0.014590454	0.024931677	0.393807175	0.120278796	-1	11	21	34	27	24	8	10	10	17	21
ENSMUSG00000034163	chr10	Zfc3h1	-0.4065682	0.014596284	0.024938591	4.217044853	0.029653484	-1	361	355	283	300	259	325	225	208	266	280
ENSMUSG00000027244	chr2	Atg13	-0.3437044	0.01463935	0.025009113	5.074022521	0.021779904	-1	553	498	526	746	493	594	449	388	435	567
ENSMUSG00000026095	chr1	Asnsd1	-0.3584409	0.014646169	0.025017704	6.312095019	0.024942925	-1	1316	1245	1149	1801	1186	1137	1259	953	1172	1158
ENSMUSG00000020883	chr11	Fbxl20	-0.4094192	0.01465684	0.025032872	4.422444606	0.030647464	-1	362	362	336	444	313	434	257	254	211	358

ENSMUSG00000036323	chr5	Srp72	-0.3571549	0.014693483	0.02509239	5.664872748	0.024346246	-1	874	858	763	950	780	723	818	581	728	780
ENSMUSG00000037664	chr7	Cdkn1c	0.88873516	0.01469935	0.025099342	6.855396931	0.155094026	1	1999	1413	1131	691	700	1731	1605	3514	1018	4297
ENSMUSG00000051650	chr11	B3gnt2	0.51696948	0.014726127	0.025141992	3.324042703	0.045963845	1	107	134	132	140	91	260	251	114	159	179
ENSMUSG00000031669	chr8	Gins3	0.79339236	0.014748909	0.025175794	0.685128745	0.077259722	1	21	18	15	16	10	37	38	22	36	20
ENSMUSG00000072893	chr11	4933439C10Rik	0.72673754	0.014749528	0.025175794	1.429704224	0.076737766	1	36	24	31	25	26	76	35	57	34	60
ENSMUSG00000003585	chr11	Sec14l2	-1.0426869	0.014777453	0.025220379	0.000853641	0.141385167	-1	18	23	21	10	15	22	9	6	5	6
ENSMUSG00000015127	chr17	Unkl	-1.0188187	0.014808848	0.025270873	1.001474217	0.164960911	-1	38	24	41	43	42	2	28	20	28	22
ENSMUSG00000026042	chr1	Col5a2	0.38241685	0.014867043	0.025367085	7.625034886	0.029135488	1	2769	2306	2416	2961	2303	3666	3700	3656	2865	4353
ENSMUSG00000037791	chr11	Phf12	-0.368258	0.014875977	0.025379231	4.163989943	0.023650775	-1	306	262	274	376	282	259	266	220	209	320
ENSMUSG00000092558	chr17	Med20	-0.369992	0.014929903	0.025468123	4.321735599	0.0243447	-1	355	305	315	376	315	338	295	228	316	242
ENSMUSG00000019774	chr10	Mtrf1l	-0.4860741	0.014941619	0.025481888	2.649894673	0.036495157	-1	108	95	111	113	105	78	92	70	94	84
ENSMUSG00000024902	chr19	Mrpl11	0.36401971	0.014941254	0.025481888	5.481441084	0.025255902	1	603	560	588	701	455	937	819	749	868	719
ENSMUSG00000028226	chr4	Mmp16	0.72704808	0.01495367	0.025499327	0.720111352	0.057692943	1	15	17	13	22	18	31	24	31	29	39
ENSMUSG00000020032	chr10	Nuak1	-0.4153181	0.014982739	0.02554578	4.299533783	0.031309322	-1	297	276	270	556	303	345	265	273	210	283
ENSMUSG00000032911	chr9	Cspg4	0.54713625	0.015070392	0.025692095	4.543230925	0.057472942	1	240	248	287	422	224	665	380	600	278	326
ENSMUSG00000022514	chr16	Il1rap	-0.7187108	0.015104111	0.025746142	1.717227186	0.082140366	-1	63	57	71	63	39	34	56	17	42	48
ENSMUSG00000046387	chr18	Pcdhb17	-0.6392105	0.015105779	0.025746142	1.585460617	0.058265964	-1	47	44	47	71	54	24	42	40	30	47
ENSMUSG00000044211	chr6	Gm7887	-0.8992812	0.015127846	0.025780609	0.263898402	0.095934652	-1	17	19	11	38	22	14	11	12	17	7
ENSMUSG00000098798	chr8	Gm27288	0.55712293	0.015156007	0.025825452	2.445137146	0.048976138	1	64	67	68	70	50	85	139	95	108	87
ENSMUSG00000027210	chr2	Meis2	0.88490432	0.015160799	0.02582732	0.20495076	0.090447247	1	11	6	9	19	9	19	20	24	13	32
ENSMUSG00000033653	chr16	Vps8	0.41116985	0.015159285	0.02582732	3.558970772	0.028529568	1	155	108	121	201	165	260	223	184	203	221
ENSMUSG00000030077	chr6	Chl1	1.40412874	0.015178587	0.02585447	0.94225121	0.334706111	1	10	15	22	16	8	132	41	6	26	15
ENSMUSG00000058173	chr9	Smco4	0.36362674	0.015284261	0.026031299	3.733218407	0.021794975	1	192	159	159	198	150	247	248	226	233	255
ENSMUSG00000051169	chr6	Rpusd3	0.56973277	0.015290001	0.026037901	2.964228698	0.056600495	1	86	97	103	89	80	93	139	170	148	190
ENSMUSG00000037750	chr11	Fam222b	0.42026249	0.015356221	0.026147484	3.113478459	0.028020529	1	107	85	94	146	114	185	164	144	142	164
ENSMUSG00000029545	chr5	Acads	-0.3962937	0.015358971	0.026148979	6.933353124	0.031395661	-1	1806	2112	2075	2929	1521	1994	1422	1708	1681	1801
ENSMUSG00000024970	chr19	AI846148	0.44742923	0.015368951	0.026162785	3.221448391	0.032845057	1	103	135	88	136	117	219	159	167	139	186
ENSMUSG00000051675	chr4	Trim32	-0.4380126	0.015380083	0.026178546	3.40138297	0.032272856	-1	170	168	132	247	186	125	176	121	144	158
ENSMUSG00000022498	chr16	Txndc11	0.44574897	0.015384458	0.026182804	3.543091283	0.034531986	1	139	113	119	218	147	263	272	181	204	170
ENSMUSG00000026135	chr1	Zfp142	-0.4626072	0.015388155	0.026185907	3.319820554	0.036605549	-1	140	151	146	257	168	146	104	152	117	157
ENSMUSG00000018286	chr11	Psmb6	0.36076184	0.015416308	0.02623062	7.583807132	0.026179452	1	2823	2391	2225	2891	2185	4056	3638	2882	3599	3483
ENSMUSG00000022070	chr14	Bora	0.74548127	0.015418571	0.026231279	0.892409496	0.071174904	1	30	16	14	21	15	34	48	33	33	28
ENSMUSG00000022808	chr16	Snx4	0.34254082	0.015454047	0.026288432	4.523154029	0.020998284	1	326	275	283	370	253	476	453	330	414	423
ENSMUSG00000000976	chr11	Heatr6	-0.440437	0.015463003	0.026295847	3.37744778	0.032568856	-1	177	160	127	230	192	126	163	129	156	135
ENSMUSG00000042831	chr7	Alkbh6	0.39056677	0.015463744	0.026295847	3.658433602	0.025797013	1	191	149	141	192	135	258	252	199	248	201
ENSMUSG00000052539	chr3	Magi3	-0.4940376	0.01546405	0.026295847	2.598301285	0.038355745	-1	94	103	104	128	89	69	104	75	70	84
ENSMUSG00000020218	chr10	Wif1	-0.7632849	0.015556447	0.026449745	3.103197228	0.109360194	-1	299	107	117	202	84	170	121	50	104	77
ENSMUSG00000068739	chr3	Sars	0.35842696	0.015564294	0.026459868	6.354219551	0.025480412	1	1040	967	860	1517	1009	1693	1430	1444	1413	1517
ENSMUSG00000027810	chr3	Eif2a	-0.3945925	0.015580028	0.026483395	5.183622428	0.02995891	-1	730	602	510	685	539	427	564	400	571	589
ENSMUSG00000024425	chr18	Ndfip1	-0.3676865	0.015610629	0.026532184	5.341640075	0.026011072	-1	753	688	605	846	521	583	591	435	602	680
ENSMUSG00000004054	chr19	Map3k11	0.38994468	0.01562797	0.026558428	4.580931129	0.02815566	1	277	300	324	363	268	629	368	382	374	471
ENSMUSG00000028563	chr4	Tm2d1	-0.359389	0.015661375	0.026608725	4.192100816	0.022771243	-1	342	288	275	342	272	245	294	230	264	264
ENSMUSG00000045730	chr18	Adrb2	-0.4901951	0.015660662	0.026608725	4.05131811	0.045259124	-1	242	323	341	297	217	356	197	157	212	211
ENSMUSG00000025375	chr11	Aatk	-0.4744151	0.015672675	0.026624688	3.306721348	0.039076522	-1	126	141	176	207	194	178	125	131	100	138
ENSMUSG00000002017	chr17	Fam98a	-0.3320623	0.015711489	0.02668738	5.271256995	0.02085797	-1	671	554	574	810	601	563	580	520	559	557
ENSMUSG00000028745	chr4	Capzb	0.3952363	0.015807257	0.026846788	8.42848724	0.031867653	1	4903	4173	3730	5081	4269	5372	6755	5882	6170	7677
ENSMUSG00000029534	chr6	St7	-0.4891084	0.015825894	0.026875175	3.291779817	0.042458176	-1	147	128	174	246	155	194	151	97	122	100
ENSMUSG00000022911	chr16	Arl13b	-0.5764312	0.015829697	0.026878367	2.04468613	0.050650449	-1	70	73	60	100	58	54	63	29	59	59
ENSMUSG00000021318	chr13	Gli3	0.63564025	0.015846639	0.026903866	1.887339538	0.063577881	1	42	45	29	54	39	72	87	77	37	82
ENSMUSG00000031385	chrX	Plxnb3	-0.7720533	0.015859895	0.026919831	1.072626893	0.085321987	-1	18	36	44	52	37	18	29	21	29	22
ENSMUSG00000031879	chr8	Fam96b	0.43061418	0.015859265	0.026919831	4.066202796	0.033986466	1	175	161	204	285	233	414	289	311	294	253
ENSMUSG00000001506	chr11	Col1a1	0.55121938	0.015878179	0.026947593	11.12845041	0.062143632	1	35289	22504	27245	24176	24587	54063	40842	48327	21516	53941
ENSMUSG00000072966	chrX	Gprasp2	-0.877047	0.015889999	0.026961106	0.187912542	0.092647326	-1	26	23	11	17	21	13	14	5	12	15
ENSMUSG00000097640	chr5	Gm20033	1.16087612	0.015888349	0.026961106	0.315990244	0.194302879	1	11	21	4	5	9	34	14	41	12	24
ENSMUSG00000004633	chr6	Chn2	0.7371212	0.015921488	0.027011255	1.743217054	0.086352086	1	52	35	40	27	23	98	80	39	48	68
ENSMUSG00000031380	chrX	Figf	0.58854783	0.015937965	0.027032645	1.783499361	0.048932845	1	36	45	30	53	34	71	50	56	67	81
ENSMUSG00000031403	chrX	Dkc1	-0.4258393	0.015936267	0.027032645	4.611269273	0.034482884	-1	443	382	390	496	369	251	437	257	392	352
ENSMUSG00000102171	chr14	RP23-117H6.2	-0.9735704	0.016030692	0.027186621	0.195989271	0.123500325	-1	18	17	28	15	22	7	7	10	21	11
ENSMUSG00000021506	chr13	Pitx1	1.26494575	0.016035962	0.02719226	-0.048894439	0.235271832	1	11	10	3	8	4	49	5	14	9	21
ENSMUSG00000054099	chr5	Slc25a40	-0.5303928	0.016102279	0.027301401	2.140277192	0.042580527	-1	68	77	76	87	69	70	69	37	51	62
ENSMUSG00000031451	chr8	Gas6	0.40833321	0.016106811	0.027305772	7.143608775	0.033926318	1	1688	1545	1690	2454	1727	4003	2306	2098	2421	2476
ENSMUSG00000022205	chr15	Sub1	0.33198995	0.016120102	0.027324991	5.587326299	0.021376917	1	683	614	558	756	558	972	955	741	815	895
ENSMUSG00000024534	chr18	Sncaip	-0.5879487	0.016143854	0.02736008	1.877430041	0.052669838	-1	67	70	55	71	55	48	38	38	38	71
ENSMUSG00000032602	chr9	Slc25a20	0.41201125	0.016144718	0.02736008	5.91832401	0.033999262	1	551	763	630	1229	746	1152	1049	1166	1042	1202
ENSMUSG00000027544	chr2	Nfatc2	-0.442568	0.016158499	0.027380114	4.094847156	0.036489983	-1	319	263	216	395	278	346	210	249	159	219

ENSMUSG00000021615	chr13	Xrcc4	-0.5233319	0.016176155	0.027406708	2.547458271	0.044549861	-1	107	99	85	137	80	59	85	61	95	82
ENSMUSG00000019278	chr8	Dpep1	0.43199953	0.016197749	0.027439968	3.885261639	0.033673741	1	166	197	202	197	160	359	246	280	190	306
ENSMUSG00000027942	chr3	4933434E20Rik	-0.3479718	0.016209462	0.027456483	5.781483049	0.023850243	-1	1018	889	798	1047	827	800	875	687	830	748
ENSMUSG00000042451	chr1	Mybph	0.56280261	0.016211824	0.027457157	9.274531772	0.065091104	1	9807	4899	5309	8866	8494	7643	12661	10426	12020	17268
ENSMUSG00000067242	chr19	Lgi1	-1.5148008	0.016323078	0.027642232	0.372586041	0.383042412	-1	5	20	23	80	10	16	1	17	10	4
ENSMUSG00000031924	chr8	Cyb5b	-0.3515336	0.016339434	0.027666578	6.118160647	0.024657304	-1	1098	1153	1102	1495	971	980	1052	961	1007	960
ENSMUSG00000058492	chr9	Scp2-ps2	-0.5793938	0.016375813	0.027724816	1.96237026	0.051599755	-1	73	72	53	93	50	55	58	42	31	63
ENSMUSG00000066798	chr2	Zbtb6	-0.4926315	0.016396603	0.027756652	2.394435332	0.036758353	-1	93	82	71	120	85	74	79	61	54	82
ENSMUSG00000025369	chr10	Smarcc2	-0.360659	0.016421809	0.027795956	5.620749723	0.025704472	-1	735	755	713	1066	856	799	685	577	606	864
ENSMUSG00000028689	chr4	Ccdc163	0.69476316	0.016447551	0.027836156	1.55104997	0.074307015	1	36	31	31	32	28	90	60	61	38	35
ENSMUSG00000079055	chr12	Slc8a3	-0.5433313	0.016482445	0.027891834	5.166357663	0.059160564	-1	731	657	550	653	558	248	440	402	607	657
ENSMUSG00000021244	chr12	Ylpm1	-0.3774291	0.016489457	0.027900321	4.22406359	0.026020957	-1	261	269	293	426	322	281	268	262	208	302
ENSMUSG00000049562	chr19	Ap5b1	0.83737481	0.01650921	0.027930362	2.252002834	0.128440862	1	47	46	42	75	40	237	68	49	85	59
ENSMUSG00000085945	chr7	2310014F06Rik	-1.1318539	0.016512813	0.027933077	0.316708752	0.186389249	-1	13	22	26	43	14	8	6	13	25	4
ENSMUSG00000049191	chrX	Rgag4	0.73325007	0.016521903	0.027945071	1.140839197	0.075669211	1	24	20	24	19	27	62	43	22	37	50
ENSMUSG00000018425	chr11	Dhx40	-0.4031776	0.016552826	0.027993985	4.008247364	0.029597418	-1	293	268	246	288	254	178	228	209	231	272
ENSMUSG00000037997	chr6	Parp11	0.46773202	0.016602924	0.028075314	2.637657989	0.034035189	1	72	89	61	86	72	118	120	101	118	120
ENSMUSG00000022433	chr15	Csnk1e	-0.3507305	0.016626956	0.028111985	5.62312071	0.024326718	-1	849	819	757	964	718	748	735	678	548	829
ENSMUSG00000025795	chr10	Rassf3	-0.4059305	0.016628634	0.028111985	6.271396567	0.0334697	-1	1204	1338	1254	1775	1029	1440	842	1114	860	1186
ENSMUSG00000039568	chr16	Ubald1	0.39971946	0.016716055	0.028256359	5.43651662	0.031750775	1	599	512	480	671	518	1148	698	707	574	929
ENSMUSG00000061322	chr4	Dnaic1	1.32614047	0.01672854	0.028274045	-0.021189954	0.262184796	1	6	16	6	6	2	9	8	42	22	16
ENSMUSG00000029290	chr5	Zfp326	-0.4828045	0.016731757	0.028276062	2.935928693	0.0398677	-1	117	105	120	170	144	93	124	80	86	132
ENSMUSG00000030996	chr7	Art1	-0.4029235	0.016820885	0.028423248	8.057020982	0.03370722	-1	4908	5006	4024	5227	3450	5057	3203	3544	3033	4010
ENSMUSG00000050014	chr15	Apol10b	-0.6545383	0.016824447	0.02842583	1.233121568	0.059045822	-1	38	50	31	60	27	30	36	21	25	30
ENSMUSG00000063480	chr15	Nhp2l1	0.37894635	0.016864277	0.028489682	5.58021931	0.028649264	1	623	574	590	740	564	963	1010	724	1015	690
ENSMUSG00000022899	chr16	Slc15a2	-1.2642801	0.016877258	0.028508165	-0.103902461	0.241449809	-1	10	20	20	19	16	25	3	7	1	4
ENSMUSG00000070729	chr4	Gm12966	0.82288141	0.016893155	0.028531569	0.648522923	0.093781421	1	14	19	9	30	7	26	32	35	22	34
ENSMUSG00000024661	chr19	Fth1	0.37406614	0.016913179	0.028561936	10.48802598	0.029286253	1	18675	16396	14931	24426	19302	29377	26189	21718	25627	29973
ENSMUSG00000041378	chr16	Cldn5	0.57745492	0.016929965	0.02858683	4.30028598	0.06607548	1	278	281	230	261	122	390	260	534	265	449
ENSMUSG00000074479	chr3	Gm10704	-0.8431727	0.016933193	0.028588826	2.996728582	0.137870352	-1	173	165	138	181	99	250	58	58	58	52
ENSMUSG00000050697	chr15	Prkaa1	-0.3692366	0.016943216	0.028602293	4.187042583	0.024923741	-1	311	261	271	408	280	258	319	194	239	285
ENSMUSG00000020788	chr11	Atp2a3	0.61148707	0.016956253	0.028620845	4.182592449	0.073937044	1	179	204	190	274	217	756	326	246	189	313
ENSMUSG00000031972	chr8	Acta1	-0.4078663	0.01696055	0.02862464	15.32064488	0.034873842	-1	718554	580687	536595	865529	784024	584198	565630	555588	469315	701044
ENSMUSG00000039953	chr4	Clstn1	-0.3711686	0.016972337	0.028641075	5.537329402	0.02748444	-1	649	724	691	1086	771	825	598	619	527	748
ENSMUSG00000062376	chr19	2010012O05Rik	-0.3839608	0.016994671	0.028675302	3.563349492	0.024955874	-1	204	177	187	230	188	158	162	164	181	160
ENSMUSG00000020781	chr11	Tsen54	0.4342019	0.016997638	0.028676846	3.1782395	0.032138532	1	122	83	88	152	124	187	183	135	164	171
ENSMUSG00000038227	chr6	Hoxa9	-0.4236554	0.017004834	0.028685524	3.406925252	0.030897828	-1	179	173	180	207	155	126	164	150	115	175
ENSMUSG00000039616	chr18	Mocos	0.77293955	0.017026297	0.028718263	2.085901181	0.10588518	1	43	39	52	53	38	112	111	22	96	89
ENSMUSG00000048550	chr2	Thnsl1	-0.5843117	0.017072605	0.028792895	2.370245589	0.057638796	-1	101	76	100	106	69	42	83	60	58	86
ENSMUSG00000079355	chr9	Ackr4	-0.9014701	0.017084198	0.028808971	0.605706281	0.121434088	-1	46	25	22	24	19	25	23	12	5	16
ENSMUSG00000006705	chr17	Pknox1	-0.4130226	0.017110635	0.028850071	3.503161395	0.029799366	-1	190	198	164	254	156	161	210	124	150	143
ENSMUSG00000061118	chr5	Dnajc30	0.34414704	0.017146298	0.028906714	4.48623381	0.021910274	1	282	308	257	344	271	473	367	416	391	386
ENSMUSG00000081792	chr4	Anp32b-ps1	0.88763977	0.017152957	0.028914453	-0.025715945	0.071390058	1	8	8	8	9	11	22	14	18	21	15
ENSMUSG00000049288	chr3	Lix1l	0.39547557	0.01719332	0.028978996	4.064593866	0.028879407	1	210	221	183	276	184	408	287	314	217	323
ENSMUSG00000003581	chr11	Rnf215	0.46051968	0.017198348	0.028983976	2.934699169	0.035462862	1	96	90	79	111	95	200	151	126	125	113
ENSMUSG00000028708	chr4	Mknk1	-0.41924	0.017201876	0.028986426	4.717563736	0.034500537	-1	454	473	444	466	382	298	408	260	374	493
ENSMUSG00000022074	chr14	Tnfrsf10b	0.63946611	0.017217419	0.029009119	1.43247039	0.055676084	1	34	29	33	27	25	62	49	59	39	46
ENSMUSG00000032946	chr19	Rasgrp2	-0.4238873	0.017230887	0.029028312	3.048115568	0.029548435	-1	151	124	124	145	148	120	116	106	101	126
ENSMUSG00000039183	chr17	Nubp2	0.37527852	0.0172355	0.029029085	3.801640792	0.024694011	1	168	160	169	219	180	340	227	225	242	246
ENSMUSG00000042761	chr9	Mrap2	-2.235702	0.01723472	0.029029085	0.079550192	0.850975339	-1	25	12	19	23	36	29	0	0	0	0
ENSMUSG00000099226	chrX	Mir7091	-0.6441848	0.017240771	0.029034464	1.831402502	0.065504021	-1	96	61	55	58	42	43	43	48	46	38
ENSMUSG00000021418	chr13	Rpp40	-0.4522535	0.017247697	0.029042627	3.236319611	0.035704042	-1	196	134	130	188	155	112	157	101	115	158
ENSMUSG00000028927	chr4	Padi2	-0.4229072	0.017255554	0.029052357	7.054899368	0.037161931	-1	2252	1848	1971	2951	2366	1967	2197	2166	1432	1471
ENSMUSG00000029911	chr6	Ssbp1	0.33874302	0.017283322	0.029095605	4.745830701	0.021748732	1	366	368	296	425	306	476	548	447	494	465
ENSMUSG00000034472	chr8	Rasd2	0.72661363	0.017295036	0.029111818	0.933697702	0.072167708	1	14	20	19	28	19	29	46	29	47	29
ENSMUSG00000001588	chr11	Acap1	1.17180041	0.017314771	0.029141527	0.284597931	0.200984606	1	10	15	9	6	8	66	20	11	14	15
ENSMUSG00000025324	chr7	Atp10a	-0.5237084	0.017354256	0.029204465	2.515564039	0.045811666	-1	112	95	83	97	102	80	92	47	68	91
ENSMUSG00000031988	chr9	Vps26b	-0.3416951	0.01736237	0.029214602	5.452868122	0.023195962	-1	743	715	679	864	639	691	670	484	644	669
ENSMUSG00000001016	chr3	Ilf2	0.35496098	0.017376101	0.029234187	5.154433191	0.024761685	1	491	431	402	599	411	772	805	531	606	554
ENSMUSG00000022360	chr15	Atad2	0.65769315	0.017383257	0.029242706	2.430319218	0.07587673	1	55	59	77	63	47	126	147	71	124	59
ENSMUSG00000034308	chr8	Sdr42e1	0.91499094	0.017410388	0.029281298	0.392489798	0.107927627	1	15	19	11	9	6	37	26	12	29	23
ENSMUSG00000091896	chr18	Ube2d2a	0.33036222	0.01740999	0.029281298	5.160976183	0.021267885	1	456	427	436	652	403	728	729	542	615	640
ENSMUSG00000026078	chr1	Pdcl3	0.3751944	0.017471352	0.029380293	5.15919489	0.027991976	1	417	416	408	629	454	552	685	684	711	623
ENSMUSG00000025413	chr4	Ttc4	-0.3300215	0.017501941	0.029428191	5.261315913	0.021303334	-1	630	618	571	810	558	574	564	533	575	513
ENSMUSG00000015023	chr8	Ddx19a	-0.3996152	0.017533099	0.029477036	4.195844142	0.030205009	-1	288	301	273	329	341	214	294	206	272	294

ENSMUSG00000072770	chr6	Acrbp	0.78291009	0.017564134	0.02952566	0.519429027	0.074909426	1	13	10	15	18	15	42	17	23	28	25
ENSMUSG00000032423	chr9	Syncrip	-0.3657345	0.01757097	0.029533599	5.879252588	0.027214611	-1	954	816	839	1476	914	870	1016	691	801	824
ENSMUSG00000015750	chr3	Aph1a	0.34744154	0.017647075	0.029657951	4.820272125	0.023224841	1	350	409	346	444	297	642	518	492	413	518
ENSMUSG00000032481	chr9	Smarcc1	0.34062686	0.01764945	0.029658377	5.048996734	0.022695252	1	438	394	357	601	399	688	704	568	526	529
ENSMUSG00000000561	chr3	Wdr77	0.34543195	0.017687693	0.029711923	5.39816064	0.023815314	1	579	471	442	739	549	872	850	682	731	715
ENSMUSG00000057788	chr8	Ddx49	0.36456133	0.017683985	0.029711923	4.338456984	0.024916049	1	270	249	232	305	252	360	375	353	429	320
ENSMUSG00000063179	chr7	Pstk	-0.3805126	0.017686633	0.029711923	4.299131969	0.027206535	-1	295	318	318	457	274	233	282	248	311	308
ENSMUSG00000037938	chr2	Chchd5	0.49313099	0.017694547	0.029719865	3.473220696	0.045272361	1	163	156	94	135	128	322	166	204	177	186
ENSMUSG00000007476	chr2	Lrrc8a	-0.4177391	0.017703119	0.029730688	4.205449058	0.033611031	-1	257	292	333	368	306	397	225	225	207	241
ENSMUSG00000041629	chr11	Fam104a	0.3666377	0.017763252	0.029828092	5.285700711	0.026920367	1	527	418	424	660	515	673	640	656	733	866
ENSMUSG00000074576	chr2	Mocs3	0.57703925	0.017864888	0.029995156	1.928184335	0.051925654	1	45	45	38	64	30	93	90	65	56	57
ENSMUSG00000013629	chr5	Cad	0.46093132	0.017897059	0.030045562	3.805589875	0.040557128	1	135	148	131	280	188	294	344	230	242	203
ENSMUSG00000026005	chr1	Rpe	-0.4671943	0.017913945	0.030070298	3.146471657	0.038606982	-1	134	155	124	186	157	96	161	99	105	138
ENSMUSG00000022400	chr15	Rbx1	0.34529694	0.017938951	0.030108657	6.272437924	0.024607051	1	1120	925	903	1267	874	1634	1477	1203	1448	1305
ENSMUSG00000030435	chr7	U2af2	0.34998831	0.017955063	0.03013208	5.818714425	0.024986991	1	707	658	652	983	711	1224	1209	912	941	885
ENSMUSG00000097632	chr19	4930552P12Rik	-1.0256137	0.018041308	0.030273181	-0.134742851	0.126492893	-1	12	20	14	24	10	9	9	6	16	2
ENSMUSG00000036112	chr10	Metap2	-0.388534	0.018108853	0.030382873	7.274486802	0.031880433	-1	2812	2526	2537	2968	2208	1822	2477	1834	2096	2706
ENSMUSG00000084838	chr16	Gm10241	-0.8179144	0.01811147	0.030383615	0.370437544	0.077395107	-1	17	28	20	35	13	11	16	11	15	16
ENSMUSG00000039795	chr3	Zfand1	0.79110827	0.018151634	0.030447341	2.408394246	0.118607355	1	62	63	58	62	37	32	103	123	121	147
ENSMUSG00000017667	chr2	Zfp334	-0.5915278	0.018163746	0.030464	2.16191977	0.059440009	-1	61	82	69	91	86	63	61	61	29	71
ENSMUSG00000038126	chr5	Mphosph9	-0.582035	0.018169698	0.030470326	2.077613398	0.055336805	-1	60	77	69	101	62	79	53	58	32	48
ENSMUSG00000079036	chr12	Alkbh1	0.50013187	0.018212062	0.030537706	2.828088573	0.042878833	1	88	71	93	95	81	187	145	130	107	101
ENSMUSG00000028069	chr3	Gpatch4	0.42717188	0.018222719	0.030551911	4.378452143	0.035875995	1	287	184	198	346	306	447	434	337	420	298
ENSMUSG00000000346	chr15	Dazap2	0.35691914	0.018280092	0.030644425	6.381806717	0.026562661	1	1038	1111	1008	1425	890	1895	1612	1223	1532	1413
ENSMUSG00000098915	chr9	Rpl15-ps2	-2.461177	0.018378884	0.030806342	3.093085109	1.105836071	-1	208	200	211	253	191	226	1	3	0	3
ENSMUSG00000019433	chr8	Gipc1	0.33840285	0.018418431	0.030868928	4.653595878	0.021951648	1	333	302	301	418	300	615	442	393	397	453
ENSMUSG00000040147	chrX	Maob	-0.5253202	0.018494096	0.030992024	3.487893207	0.052985856	-1	120	220	189	229	212	106	138	140	155	200
ENSMUSG00000024668	chr19	Sdhaf2	-0.3699185	0.018522844	0.031036478	5.289115493	0.027706258	-1	635	644	597	898	530	465	567	512	627	590
ENSMUSG00000037885	chr2	Stk35	-0.4655758	0.018534074	0.03104785	3.241539391	0.039979452	-1	180	173	171	155	122	172	132	96	95	153
ENSMUSG00000064337	chrMT	mt-Rnr1	0.52010838	0.018532057	0.03104785	8.644917655	0.057954743	1	3351	4150	4613	8518	4403	6225	5554	7626	8987	9778
ENSMUSG00000052656	chr6	Rnf103	-0.363015	0.018552066	0.031074267	4.422802614	0.025285189	-1	327	360	286	465	358	284	336	279	255	371
ENSMUSG00000005469	chr8	Prkaca	0.41422206	0.018695645	0.031311004	7.638597912	0.036739094	1	2565	2413	2290	3158	2330	3218	3130	4334	3081	4692
ENSMUSG00000036840	chr8	Siah1a	-0.3760072	0.018701966	0.031317838	3.280841816	0.02372746	-1	162	147	142	201	158	160	147	115	125	138
ENSMUSG00000039994	chr10	Timeless	0.55887389	0.018751267	0.031396634	2.725186764	0.056482668	1	54	102	77	105	54	165	117	111	143	95
ENSMUSG00000035936	chr13	Aldh5a1	-0.4755329	0.018770259	0.03142467	3.270704798	0.04112591	-1	150	146	160	257	126	132	102	165	121	126
ENSMUSG00000030706	chr7	Mrpl48	0.41958639	0.01878508	0.031445716	5.836476818	0.036940282	1	768	734	642	871	626	727	1108	1148	1216	1059
ENSMUSG00000018340	chr11	Anxa6	0.35606125	0.018796547	0.031461143	8.251518003	0.027259083	1	4091	3600	3433	4964	3881	5326	5659	5436	5388	6039
ENSMUSG00000010751	chr7	Tnfrsf22	0.52950609	0.018801311	0.031465348	2.239869072	0.044678454	1	65	51	46	60	57	114	76	76	69	111
ENSMUSG00000038552	chr5	Fndc4	0.65971352	0.018883216	0.031598639	1.86695038	0.073497462	1	48	29	49	44	32	88	100	54	68	43
ENSMUSG00000102828	chr18	RP23-407E2.30	-0.5480031	0.0189613	0.031725503	3.443782272	0.058376227	-1	194	192	156	229	183	84	146	120	121	242
ENSMUSG00000041439	chr1	Mfsd6	-0.3908227	0.018967439	0.031731976	3.477085217	0.02711638	-1	170	214	146	249	159	169	171	141	151	147
ENSMUSG00000045573	chr4	Penk	0.75105735	0.018978084	0.031745984	3.898013206	0.115690486	1	197	209	135	98	161	664	150	204	217	320
ENSMUSG00000055148	chr8	Klf2	0.79995203	0.019018108	0.031809129	4.570134108	0.133874423	1	133	230	310	279	311	1233	413	322	290	276
ENSMUSG00000074802	chr10	Gas2l3	0.89728198	0.019027017	0.031820221	1.620504528	0.144538949	1	19	13	40	37	42	73	104	23	51	66
ENSMUSG00000030852	chr7	Tacc2	-0.4395856	0.019077542	0.031900901	8.588129132	0.041823842	-1	6065	5725	5385	9197	6902	8659	4493	4574	4361	4924
ENSMUSG00000042190	chr5	Cmklr1	0.45005144	0.019099469	0.031932742	3.761725075	0.039086952	1	121	161	135	253	184	303	318	200	251	200
ENSMUSG00000056735	chr5	A930024E05Rik	0.91227661	0.019101153	0.031932742	-0.195257976	0.083254238	1	8	7	8	8	7	17	13	21	9	19
ENSMUSG00000068740	chr3	Celsr2	-0.6214746	0.019131966	0.031980428	2.65893447	0.07172894	-1	83	83	100	156	140	44	100	86	73	92
ENSMUSG00000007850	chr11	Hnrnph1	-0.3924231	0.019166986	0.032032558	6.38298106	0.032746627	-1	1254	1250	1206	1922	1461	1317	1478	1001	1178	921
ENSMUSG00000025156	chr11	Gps1	-0.3452295	0.019167736	0.032032558	5.490792392	0.024471084	-1	811	676	630	931	706	616	667	569	712	653
ENSMUSG00000005533	chr7	Igf1r	-0.6130344	0.019242118	0.032153019	2.423604652	0.068373823	-1	71	87	70	130	117	85	81	82	41	50
ENSMUSG00000014837	chr8	4931428F04Rik	0.67335928	0.019260416	0.032179745	1.313397843	0.068062219	1	38	24	25	29	19	50	40	62	34	49
ENSMUSG00000023967	chr17	Mrps18a	0.37332249	0.019306916	0.03225358	5.632723952	0.029184832	1	562	593	552	1017	545	1077	913	915	860	795
ENSMUSG00000057672	chr8	Pkn1	-0.3900225	0.019312292	0.032258705	4.96080539	0.031038456	-1	438	439	497	783	495	514	385	326	532	441
ENSMUSG00000001288	chr15	Rarg	0.43898986	0.019334853	0.032292532	4.303544793	0.038443884	1	242	211	253	280	249	489	367	400	208	391
ENSMUSG00000028962	chr5	Slc4a2	0.38450143	0.019340303	0.032297775	4.704606859	0.029713899	1	327	282	334	461	286	719	441	431	379	453
ENSMUSG00000070713	chr8	Gm10282	0.78272982	0.019364367	0.032334096	1.528834699	0.104318705	1	31	44	29	21	23	37	91	43	64	48
ENSMUSG00000038712	chr3	Fam63a	0.33413292	0.019382688	0.032360822	5.048565573	0.022403029	1	440	417	401	574	356	787	587	463	542	650
ENSMUSG00000073471	chr17	Rsph3a	-0.4102216	0.01946309	0.032491178	3.18897375	0.029042125	-1	154	126	138	205	147	122	128	106	145	129
ENSMUSG00000015942	chr5	Gtf2ird2	-0.4439503	0.019473965	0.032505451	2.666958456	0.032738564	-1	98	94	116	130	97	99	94	72	75	93
ENSMUSG00000026525	chr1	Opn3	1.00583541	0.019484804	0.032519658	0.508255774	0.159586395	1	7	21	14	11	10	9	27	40	33	29
ENSMUSG00000030603	chr7	Psmc4	0.33669966	0.01950579	0.032550796	6.656648044	0.024203809	1	1423	1233	1220	1590	1179	2015	1895	1661	1882	1729
ENSMUSG00000001419	chr3	Mef2d	-0.3857048	0.019548626	0.032618385	7.805818907	0.032317552	-1	3561	3191	3068	5289	3938	3104	2968	3305	2684	3741
ENSMUSG00000026380	chr1	Tfcp2l1	-0.7985867	0.019637463	0.032762705	1.244271646	0.106476948	-1	37	50	60	30	32	23	22	17	28	45
ENSMUSG00000004609	chr7	Cd33	0.77437514	0.01964751	0.032775556	1.00560439	0.089485272	1	19	29	21	14	18	43	45	20	49	37

ENSMUSG00000024054	chr17	Smchd1	-0.4337367	0.019659136	0.032791035	4.07875758	0.037196803	-1	248	293	249	394	263	185	327	175	251	226
ENSMUSG00000021540	chr13	Smad5	-0.3228316	0.019665019	0.032796933	5.329969885	0.021304602	-1	648	626	617	821	615	729	588	515	523	569
ENSMUSG00000029822	chr6	Osbpl3	0.50090608	0.019836316	0.033078672	3.044290405	0.046547175	1	88	85	65	140	126	220	150	145	125	142
ENSMUSG00000024805	chr19	Pcgf5	-0.3776403	0.019839836	0.033080595	3.670919203	0.026218389	-1	183	197	185	303	204	237	178	158	164	164
ENSMUSG00000021504	chr13	B4galt7	0.43634494	0.019911922	0.033196829	3.357438743	0.03510024	1	142	136	134	147	82	260	200	154	164	180
ENSMUSG00000002679	chr12	Med6	0.41720936	0.019934038	0.033229738	3.191086158	0.030738352	1	135	115	99	145	84	212	159	146	174	152
ENSMUSG00000050705	chr17	2310061I04Rik	0.35482017	0.0199695	0.033284882	5.959972902	0.026753332	1	722	742	797	1078	741	1164	1053	1224	988	1248
ENSMUSG00000042185	chr9	Nfrkb	-0.3668275	0.019994388	0.033314446	3.68591902	0.024484217	-1	199	226	187	239	215	181	189	166	162	212
ENSMUSG00000049811	chr11	Fam161a	0.79966418	0.01999276	0.033314446	0.614045362	0.08293234	1	13	12	15	15	20	31	27	16	27	45
ENSMUSG00000056947	chr3	Mab21l1	-0.8214258	0.019993538	0.033314446	0.980650819	0.110567149	-1	35	51	26	30	33	13	30	12	19	36
ENSMUSG00000031604	chr8	Msmo1	0.63277642	0.020011474	0.03333894	3.372959995	0.080649171	1	144	116	152	88	86	217	307	128	242	124
ENSMUSG00000000942	chr6	Hoxa4	0.66546682	0.020030858	0.03336347	1.688366535	0.073978549	1	46	37	20	34	40	53	46	66	58	85
ENSMUSG00000027463	chr2	Slc52a3	0.75840681	0.020030973	0.03336347	0.560630569	0.068509462	1	14	10	20	18	12	28	29	27	19	35
ENSMUSG00000070283	chr9	Ndufaf3	0.38595987	0.020038682	0.033372334	4.1693693	0.029089216	1	261	233	238	235	180	314	322	358	337	310
ENSMUSG00000033769	chr6	Exoc6b	-0.356262	0.020044361	0.033377814	3.9892206	0.023959367	-1	250	242	218	317	291	265	230	185	212	242
ENSMUSG00000044937	chr10	BC030307	-0.7264993	0.02006733	0.033412081	0.811894869	0.072001669	-1	36	26	37	28	24	18	16	26	18	22
ENSMUSG00000029049	chr4	Morn1	0.83330604	0.02008771	0.033442029	0.265735881	0.083388689	1	16	8	11	12	10	23	26	26	11	26
ENSMUSG00000033417	chr19	Cacul1	-0.3353859	0.020115652	0.033484559	5.209025386	0.023084409	-1	593	587	541	838	532	507	629	443	501	586
ENSMUSG00000018474	chr11	Chd3	0.42217603	0.020126276	0.033498254	4.56219853	0.036421525	1	286	292	275	337	300	552	436	489	250	480
ENSMUSG00000031703	chr8	Itfg1	-0.367583	0.020137333	0.033512665	5.628915497	0.028566447	-1	887	881	684	965	731	616	833	570	721	778
ENSMUSG00000022337	chr15	Emc2	-0.3749575	0.020140307	0.033513625	6.192254071	0.03018186	-1	1277	1229	1175	1565	930	894	1161	965	1148	993
ENSMUSG00000022849	chr16	Hspbap1	0.57197797	0.020163546	0.033544307	1.981861683	0.053448687	1	56	31	47	60	36	109	71	66	67	62
ENSMUSG00000073478	chr1	D730003I15Rik	0.79845696	0.020162723	0.033544307	0.680241199	0.086089162	1	19	19	15	13	13	25	27	19	44	37
ENSMUSG00000042032	chr11	Mat2b	-0.3655943	0.020186914	0.03357622	5.846962807	0.028422423	-1	978	1022	934	1191	711	712	835	773	892	865
ENSMUSG00000057530	chr4	Ece1	-0.4445138	0.020187534	0.03357622	5.810849793	0.042577535	-1	814	922	919	1304	880	1354	676	665	563	679
ENSMUSG00000020777	chr11	Acox1	-0.3554803	0.020194314	0.0335835	6.517595759	0.027269456	-1	1321	1467	1317	2158	1458	1228	1334	1219	1288	1473
ENSMUSG00000043323	chr5	Fbrsl1	-0.3877212	0.020200958	0.033590551	3.801783039	0.028433291	-1	175	219	219	325	236	210	178	190	172	229
ENSMUSG00000046010	chr11	Zfp830	-0.3753263	0.020221738	0.033621105	3.263170772	0.023867256	-1	159	143	147	205	147	140	137	118	140	139
ENSMUSG00000024168	chr17	Tmem204	-0.5249617	0.020228019	0.033627547	3.856144028	0.056248731	-1	171	235	236	411	230	339	141	161	176	157
ENSMUSG00000024019	chr17	Cmtr1	-0.3506444	0.020237235	0.033634866	5.379043608	0.025688185	-1	716	667	614	787	674	547	580	510	588	753
ENSMUSG00000026309	chr1	Ilkap	0.36677564	0.020235896	0.033634866	5.201503154	0.028026188	1	498	486	397	609	410	921	597	589	724	554
ENSMUSG00000031568	chr8	Rwdd4a	-0.3388155	0.020273131	0.03369052	4.355797886	0.02209411	-1	315	295	321	470	306	281	289	283	293	318
ENSMUSG00000036902	chr8	Neto2	-0.7371519	0.020284571	0.033705524	0.835671848	0.081296301	-1	24	33	29	37	32	23	18	11	15	36
ENSMUSG00000098399	chr7	Gm27995	0.84645268	0.020292316	0.033714386	0.291148754	0.086044442	1	6	19	9	15	9	24	18	27	23	22
ENSMUSG00000096549	chr17	Prickle4	-0.8606669	0.020301045	0.033724879	0.03926376	0.081583442	-1	16	20	16	18	17	6	13	12	14	7
ENSMUSG00000028223	chr4	Decr1	-0.3944493	0.020330377	0.033769592	6.967938199	0.033992206	-1	1654	2197	1934	3246	1708	2065	1552	1620	1956	1625
ENSMUSG00000021684	chr13	Pde8b	-0.6685824	0.02034076	0.033782824	0.918772612	0.05941013	-1	28	40	29	43	23	26	28	20	16	22
ENSMUSG00000052423	chr1	B4galt3	0.45611566	0.020374385	0.033834649	3.444328864	0.039310044	1	129	129	144	157	115	334	186	162	167	180
ENSMUSG00000104279	chr1	RP24-252K15.4	0.71276215	0.020395646	0.033865932	1.135701113	0.08067331	1	20	23	21	43	12	48	38	52	27	44
ENSMUSG00000029073	chr4	Cptp	-0.3914778	0.020423811	0.03390867	4.132828086	0.030231864	-1	361	289	249	300	268	212	239	221	247	309
ENSMUSG00000087165	chr11	2010001A14Rik	0.80252947	0.02043162	0.033917605	0.660286514	0.090666352	1	23	14	12	15	14	54	20	21	27	30
ENSMUSG00000034216	chr2	Vps18	0.34733077	0.020513443	0.034049391	4.265342469	0.023287837	1	241	218	217	311	267	419	327	299	304	407
ENSMUSG00000036432	chr3	Siah2	-0.3903169	0.020533651	0.034078887	3.705035805	0.028897896	-1	215	199	212	289	184	264	193	155	157	152
ENSMUSG00000074102	chr9	Rbm15b	0.39514568	0.020552798	0.034106614	3.798013957	0.029981077	1	161	177	157	250	150	368	236	246	217	219
ENSMUSG00000000738	chr8	Spg7	-0.3566122	0.020590844	0.034165694	6.639373109	0.027687326	-1	1533	1486	1528	2375	1494	1397	1343	1231	1536	1615
ENSMUSG00000015083	chr2	C8g	0.84372442	0.02061445	0.034200801	0.606837967	0.106174366	1	17	16	7	17	17	15	27	26	30	47
ENSMUSG00000020601	chr12	Trib2	-0.3528371	0.020658894	0.034266401	4.865406381	0.025491601	-1	493	548	415	614	370	441	516	383	352	394
ENSMUSG00000068206	chr15	Pick1	-0.3575379	0.020658548	0.034266401	5.193555935	0.026700444	-1	674	647	570	675	482	479	490	461	578	595
ENSMUSG00000039116	chr10	Gpr126	-0.7543299	0.020672797	0.034285393	1.644383031	0.10314093	-1	41	43	51	90	60	59	58	17	27	25
ENSMUSG00000030735	chr8	Gm9755	0.51629958	0.020694045	0.03431656	3.419180066	0.053139174	1	93	119	119	203	122	190	147	281	194	190
ENSMUSG00000090622	chr10	A930033H14Rik	-0.7857484	0.020709625	0.034338322	0.53856788	0.081313586	-1	37	25	24	26	14	16	13	13	14	24
ENSMUSG00000021519	chr13	Mterf3	-0.3659112	0.02075695	0.034408627	3.877180222	0.0252451	-1	238	237	249	294	205	183	208	198	224	222
ENSMUSG00000044155	chr6	Lsm8	0.39348362	0.020754949	0.034408627	3.397167206	0.027939716	1	147	135	120	171	101	216	222	165	197	166
ENSMUSG00000026211	chr1	Obsl1	-0.403736	0.020763225	0.034414947	7.02195148	0.035904605	-1	2424	1775	1974	2580	2260	1614	1604	2055	1527	2279
ENSMUSG00000020235	chr10	Fzr1	0.34621786	0.020781281	0.034437518	4.58407084	0.023989817	1	313	270	292	386	306	536	469	409	419	351
ENSMUSG00000028999	chr5	Rint1	-0.4805334	0.020781771	0.034437518	3.213926787	0.043919279	-1	183	144	123	181	164	86	159	114	140	121
ENSMUSG00000052997	chr7	Uba2	-0.3574638	0.020787846	0.034443501	5.38225573	0.027043044	-1	680	572	702	917	627	694	723	425	544	615
ENSMUSG00000026826	chr2	Nr4a2	-1.3001802	0.020792956	0.034447885	1.267530095	0.332945028	-1	17	32	140	32	14	46	21	13	12	20
ENSMUSG00000025213	chr19	Kazald1	-0.5307614	0.020818858	0.034486138	2.994353869	0.053768723	-1	162	123	109	126	164	88	151	90	108	86
ENSMUSG00000041429	chr17	Nthl1	0.64307342	0.020820981	0.034486138	1.4010665	0.064590345	1	32	38	15	39	23	59	41	52	40	58
ENSMUSG00000007867	chr12	Ift43	0.52514806	0.020840728	0.034514754	2.916842267	0.052281662	1	107	85	71	128	68	228	129	148	109	106
ENSMUSG00000030056	chr6	Isy1	0.37543275	0.020844001	0.034516084	4.148829038	0.027648067	1	219	214	248	272	188	400	367	284	322	255
ENSMUSG00000028028	chr3	Alpk1	0.69303	0.020915376	0.034630173	0.843253766	0.063510745	1	17	24	15	20	18	50	36	24	30	29
ENSMUSG00000047260	chr11	Emc6	0.34232689	0.02094019	0.034667151	6.008742657	0.025305368	1	886	788	681	1200	721	1429	1125	1122	1058	1148
ENSMUSG00000044730	chr4	9930104L06Rik	-0.4225898	0.020992125	0.034749016	3.174586331	0.032545137	-1	169	140	144	173	134	122	158	86	125	133

ENSMUSG00000031825	chr8	Crispld2	-0.4544767	0.02102335	0.034796583	4.163547121	0.042761056	-1	295	284	320	281	331	293	358	177	217	191
ENSMUSG00000056185	chr19	Snx32	0.48981005	0.021055211	0.034845189	3.237286895	0.046173524	1	160	87	100	133	98	142	158	189	159	234
ENSMUSG00000028933	chr5	Xrcc2	-0.5386428	0.021117944	0.034944872	1.91481745	0.04629687	-1	67	71	58	86	43	50	54	36	46	58
ENSMUSG00000014301	chr16	Pam16	0.32695005	0.021176121	0.035036991	4.604027231	0.021328256	1	292	336	289	407	280	511	423	404	451	410
ENSMUSG00000100309	chr1	Gm6644	-0.5627426	0.021180716	0.035040445	2.415875379	0.057143896	-1	95	104	85	90	86	41	72	71	72	85
ENSMUSG00000082908	chr2	Gm13736	-1.2400107	0.021188994	0.035049992	3.597308186	0.326911194	-1	261	275	202	341	189	459	38	36	52	36
ENSMUSG00000043257	chr4	Pigv	-0.3653174	0.021253777	0.035148832	3.861779494	0.025617283	-1	271	216	223	264	232	242	199	150	219	224
ENSMUSG00000083879	chr2	Gm14038	-2.0394354	0.021251865	0.035148832	1.087353014	0.810540226	-1	53	49	44	49	45	65	2	0	0	3
ENSMUSG00000012405	chr14	Rpl15	0.36855636	0.021269689	0.035170986	7.133682077	0.030139019	1	2037	1834	1737	2010	1488	2536	2915	2108	2910	2425
ENSMUSG00000036545	chr11	Adamts2	0.40435758	0.021278544	0.035181465	5.733673997	0.035501942	1	682	623	651	686	728	872	1014	1082	725	1230
ENSMUSG00000032567	chr9	Aste1	0.67902929	0.021289855	0.035196004	1.080796581	0.06587241	1	19	21	24	26	23	34	45	52	28	39
ENSMUSG00000040111	chr9	Gramd1b	0.50219645	0.021300671	0.03520972	4.161202969	0.052848213	1	192	175	151	305	279	330	345	294	219	523
ENSMUSG00000020706	chr11	Ftsj3	0.34583639	0.021333986	0.035260618	5.053896375	0.025024359	1	446	367	352	584	438	595	762	524	578	566
ENSMUSG00000021809	chr14	Nudt13	-0.391074	0.021375714	0.035325408	4.186247935	0.030681451	-1	274	324	314	422	208	279	207	252	269	268
ENSMUSG00000079884	chr9	Gm10698	-0.6617449	0.021380193	0.035328634	2.172641163	0.081552263	-1	73	71	77	98	82	24	78	41	64	69
ENSMUSG00000035293	chr12	G2e3	-0.5221303	0.021403015	0.035362163	1.809367854	0.040584246	-1	57	62	59	63	55	47	43	42	42	53
ENSMUSG00000022704	chr16	Qtrtd1	-0.4725582	0.021414464	0.035372716	2.384345221	0.037019912	-1	84	75	93	108	82	78	85	62	58	67
ENSMUSG00000066637	chr12	Ttc32	-0.4354655	0.021413343	0.035372716	3.090055941	0.034404694	-1	129	125	127	223	126	133	142	84	116	111
ENSMUSG00000031478	chr8	Nek3	0.67357993	0.021445532	0.035419848	1.324402047	0.072445754	1	34	31	24	29	18	32	42	45	60	57
ENSMUSG00000048445	chr11	Ccdc57	0.62178482	0.021455765	0.035432562	1.71873424	0.063704844	1	43	40	32	40	30	47	45	66	71	81
ENSMUSG00000024581	chr18	Napg	-0.343709	0.021475139	0.035460367	4.262338356	0.02329521	-1	329	263	311	379	307	279	303	212	278	304
ENSMUSG00000022855	chr16	Senp2	-0.3287954	0.021545123	0.035571724	5.015055756	0.022516092	-1	606	503	515	538	492	528	500	381	457	474
ENSMUSG00000101878	chr6	Gm8203	0.63505209	0.02158899	0.03563994	1.702254652	0.067795616	1	43	31	29	47	33	57	104	46	51	53
ENSMUSG00000022964	chr16	Tmem50b	-0.3871331	0.02165599	0.035742101	4.366072733	0.030707752	-1	343	368	270	386	359	245	339	223	330	311
ENSMUSG00000078153	chr11	Psme2b	0.67628555	0.021653467	0.035742101	1.568705459	0.076476132	1	38	34	29	35	26	71	78	47	61	28
ENSMUSG00000079022	chr15	Col22a1	-0.4575835	0.021683091	0.035782605	5.64814509	0.046077149	-1	1097	845	739	975	668	838	983	668	435	540
ENSMUSG00000006418	chr2	Rnf114	-0.3472488	0.021692351	0.035793659	5.281586903	0.025643647	-1	606	589	644	909	518	706	506	457	590	540
ENSMUSG00000070697	chr5	Utp3	0.32102793	0.021704836	0.035810033	4.937376051	0.021306168	1	437	361	356	537	346	558	600	522	566	515
ENSMUSG00000001785	chr10	Pwp1	-0.3660123	0.021716216	0.03582458	4.374674059	0.027134532	-1	365	324	295	447	310	295	352	212	343	271
ENSMUSG00000032244	chr9	Fem1b	-0.3460926	0.021754775	0.035883954	5.008666487	0.025149252	-1	533	438	459	689	566	527	534	368	480	404
ENSMUSG00000025279	chr14	Dnase1l3	1.29772152	0.021775064	0.03591318	0.084531884	0.27654278	1	8	5	8	6	12	31	16	45	2	13
ENSMUSG00000031527	chr8	Eri1	0.43276719	0.021826482	0.035993736	3.324559898	0.035552123	1	123	119	100	151	134	225	223	129	204	151
ENSMUSG00000053897	chr3	Slc39a8	0.92211759	0.021870971	0.036062847	-0.090692009	0.10008855	1	9	8	5	8	11	23	20	6	20	18
ENSMUSG00000015597	chr17	Zfp318	-0.3695876	0.021887965	0.03608661	3.707434065	0.025983201	-1	178	240	182	286	206	211	196	149	166	205
ENSMUSG00000018736	chr11	Ndel1	-0.3637765	0.021963087	0.036206192	5.608684586	0.028796152	-1	853	779	761	968	723	645	800	485	774	778
ENSMUSG00000032456	chr9	Nmnat3	-0.4356955	0.021990579	0.036247238	3.622087032	0.037532015	-1	182	218	188	277	185	113	185	154	183	206
ENSMUSG00000070705	chr7	Eid2b	-0.5372503	0.022008354	0.036272259	2.415436969	0.052612732	-1	88	110	91	88	79	54	93	62	74	63
ENSMUSG00000017801	chr11	Mlx	0.37952314	0.022028645	0.036301421	3.824232122	0.028080731	1	163	192	174	246	140	323	295	209	257	218
ENSMUSG00000028807	chr4	Zbtb8a	0.6073684	0.022052001	0.036335624	1.543545808	0.058882376	1	39	23	34	43	26	65	65	59	34	52
ENSMUSG00000040666	chr16	Sh3bgr	-0.4381414	0.022075521	0.036370091	9.333192465	0.043635315	-1	14765	11068	10379	10400	8326	7188	8895	8491	9564	10308
ENSMUSG00000040586	chrX	Ofd1	-0.4549112	0.022143312	0.036477478	2.930983033	0.037688611	-1	131	116	120	151	128	87	91	92	130	114
ENSMUSG00000027624	chr2	Epb4.1l1	0.36414028	0.022155333	0.03649298	3.946723752	0.025664407	1	201	186	186	224	196	363	248	212	268	325
ENSMUSG00000033972	chr17	Zfp944	-0.4923605	0.022171506	0.036515316	2.283080175	0.04000391	-1	89	77	76	98	74	62	60	55	81	63
ENSMUSG00000046329	chr17	Slc25a23	-0.3892786	0.022178879	0.036523155	4.323530751	0.031101588	-1	245	330	292	505	328	306	258	315	258	265
ENSMUSG00000020034	chr10	Tcp11l2	-0.389115	0.022187865	0.036533647	5.530419452	0.033149025	-1	796	771	667	977	700	584	606	558	547	973
ENSMUSG00000031979	chr8	Cog2	-0.338382	0.022203128	0.036550167	4.132336268	0.022317688	-1	273	266	257	416	253	297	258	206	253	247
ENSMUSG00000045288	chr11	Ush1g	-1.221002	0.02220189	0.036550167	-0.366244627	0.215681806	-1	1	19	20	22	7	6	7	6	3	10
ENSMUSG00000066441	chr12	Rdh11	0.50521378	0.022230478	0.03659088	2.452620342	0.04529061	1	77	55	70	81	47	127	126	74	99	89
ENSMUSG00000026483	chr1	Fam129a	-0.3323348	0.022247045	0.036613836	4.783057784	0.022783594	-1	428	447	398	638	388	415	369	399	336	463
ENSMUSG00000034032	chr2	Rpap1	-0.3845352	0.022264358	0.036638015	4.403282303	0.030577468	-1	335	317	316	464	351	234	302	273	275	403
ENSMUSG00000040242	chr6	Fgfr1op2	-0.3464253	0.022273773	0.036649193	5.472016573	0.025966808	-1	773	666	680	938	652	603	745	488	681	668
ENSMUSG00000082016	chr7	Pgam1-ps2	1.04604757	0.022302399	0.036691976	-0.044048363	0.153043057	1	4	7	8	16	6	21	32	4	17	19
ENSMUSG00000037326	chr17	Capn15	-0.5970653	0.022305834	0.036693308	2.031691029	0.064776562	-1	51	60	84	96	66	42	60	38	42	77
ENSMUSG00000006288	chr14	Ttc5	0.36747677	0.022348221	0.036758708	3.488755068	0.024656328	1	145	145	141	162	127	264	205	177	183	197
ENSMUSG00000020882	chr11	Cacnb1	-0.3733387	0.022390385	0.036823726	8.177685211	0.031727666	-1	5147	4228	4317	5760	4884	3658	3866	3722	4100	5204
ENSMUSG00000006215	chr4	Zbtb17	-0.3684078	0.02242216	0.036871645	4.57556354	0.028264991	-1	341	312	329	589	442	379	335	287	353	340
ENSMUSG00000027673	chr3	Ndufb5	-0.3841211	0.02243137	0.036882449	8.400474618	0.033648807	-1	5721	5626	5728	7330	4247	6652	4230	4329	4659	4186
ENSMUSG00000020888	chr11	Dvl2	0.4587177	0.022470035	0.036941678	3.123229373	0.040422391	1	116	88	81	152	107	170	147	206	134	149
ENSMUSG00000010025	chr11	Aldh3a2	-0.3522476	0.022515816	0.037012591	3.990665195	0.024300071	-1	265	279	259	319	199	230	257	191	211	245
ENSMUSG00000020728	chr11	Cep112	0.7985558	0.022540316	0.037048506	0.27634583	0.080981598	1	10	9	15	18	7	16	21	27	23	24
ENSMUSG00000079560	chr6	Hoxa3	-0.6283022	0.022547276	0.03705559	1.412378047	0.062802662	-1	45	54	40	57	35	27	30	33	23	50
ENSMUSG00000030595	chr7	Nfkbib	0.32661833	0.022563095	0.037077227	4.510669047	0.021502226	1	316	259	274	354	295	474	454	328	401	411
ENSMUSG00000020869	chr11	Lrrc59	0.41213377	0.022601988	0.037136772	5.501356244	0.03755076	1	554	480	432	807	640	1054	1074	634	835	641
ENSMUSG00000000435	chr10	Myf5	-0.742474	0.022662954	0.037232567	0.780865112	0.078199644	-1	27	29	27	40	27	25	11	21	11	30
ENSMUSG00000032637	chr7	Atxn2l	0.33012559	0.02267284	0.03724443	5.355178696	0.023439894	1	532	478	471	675	544	947	730	672	611	774

ENSMUSG00000042472	chr12	Zfp410	-0.3701954	0.022767428	0.037395414	4.003921196	0.027360057	-1	252	229	253	385	233	282	248	183	236	190
ENSMUSG00000032305	chr9	Fam219b	0.35095116	0.022832738	0.037497944	3.795021387	0.023448068	1	187	167	150	211	185	284	282	211	255	229
ENSMUSG00000038848	chr2	Ythdf1	-0.3095065	0.022835617	0.037497944	5.274480353	0.020447	-1	658	596	541	770	622	665	585	482	519	575
ENSMUSG00000059920	chr16	4930453N24Rik	-0.3172678	0.0228379	0.037497944	5.357639168	0.021604544	-1	672	613	625	891	599	599	651	552	532	640
ENSMUSG00000050890	chr4	Pdik1l	-0.6243069	0.022841862	0.037500042	1.544070464	0.06298798	-1	55	41	34	84	44	28	47	29	40	35
ENSMUSG00000058446	chr6	Znrf2	-0.3391906	0.022848991	0.037502937	4.850246856	0.024294383	-1	441	477	454	615	413	413	452	311	381	524
ENSMUSG00000083626	chr7	Gm4459	0.51281968	0.022847964	0.037502937	2.334583529	0.046754072	1	69	52	46	77	59	108	88	113	66	96
ENSMUSG00000031169	chrX	Porcn	0.51461554	0.022855119	0.037508589	2.330339839	0.04704374	1	77	46	57	66	54	88	79	105	99	96
ENSMUSG00000022571	chr15	Pycrl	0.3878423	0.022873104	0.037533698	3.561026378	0.028712127	1	171	159	147	160	114	248	200	200	236	195
ENSMUSG00000029033	chr4	Acap3	0.33780589	0.02290076	0.037574667	3.821090453	0.021466922	1	183	187	171	219	162	309	274	220	233	246
ENSMUSG00000040158	chr11	Tax1bp3	0.41245868	0.022979861	0.037700028	2.952247853	0.030283077	1	89	93	89	140	80	165	143	136	112	156
ENSMUSG00000024137	chr17	E4f1	-0.3957275	0.022989595	0.037711571	3.379450571	0.029931152	-1	177	165	148	209	173	211	136	119	115	152
ENSMUSG00000032010	chr9	Usp2	-0.3776894	0.023001091	0.037726001	7.422173022	0.032632748	-1	2601	2676	2896	3534	2718	3627	2343	2001	2000	2346
ENSMUSG00000027634	chr2	Ndrg3	0.31940258	0.0230905	0.037868203	4.894408681	0.021411801	1	404	371	366	504	328	553	552	480	453	654
ENSMUSG00000086725	chr11	A630052C17Rik	-0.8869767	0.02310511	0.037887718	0.124834799	0.105961126	-1	26	18	17	26	8	15	11	4	9	17
ENSMUSG00000071317	chr10	Bves	-0.346214	0.023140149	0.037940723	5.759348907	0.026528574	-1	953	829	805	1127	811	656	775	763	742	934
ENSMUSG00000034203	chr6	Chchd4	0.32774504	0.023150717	0.037953598	4.393417533	0.021621469	1	276	242	294	324	242	445	394	336	362	366
ENSMUSG00000043866	chr7	Taf10	0.34619366	0.023174801	0.037988625	5.08684	0.025799396	1	475	395	377	538	440	852	605	551	601	501
ENSMUSG00000040274	chr5	Cdk6	0.86282922	0.023217607	0.03805071	0.062975083	0.09496691	1	4	10	14	13	7	24	20	22	18	12
ENSMUSG00000091050	chr15	9330020H09Rik	0.93167515	0.023218121	0.03805071	0.367696275	0.130885444	1	21	3	14	12	9	29	14	28	19	34
ENSMUSG00000025745	chr5	Hadha	-0.4165219	0.023222731	0.038053804	8.416314281	0.040022509	-1	4224	5422	4985	9989	5125	5614	4190	4932	4330	4819
ENSMUSG00000018451	chr11	6330403K07Rik	-1.2612717	0.023245954	0.038087392	2.586774011	0.344018363	-1	180	120	83	142	98	214	18	18	11	41
ENSMUSG00000041236	chr13	Vps41	-0.330652	0.023308755	0.038185812	5.72656577	0.024165121	-1	1014	883	767	985	736	761	805	677	763	814
ENSMUSG00000099632	chr2	2900093K20Rik	0.83076919	0.02334214	0.038236022	0.185592923	0.078016376	1	13	11	14	7	8	23	18	17	26	21
ENSMUSG00000002393	chr8	Nr2f6	0.33542672	0.02338244	0.038297548	4.474085054	0.023205665	1	249	259	264	396	295	461	377	407	385	381
ENSMUSG00000042225	chrX	Ammecr1	0.47329683	0.023420034	0.038352053	3.232771893	0.044361028	1	125	107	107	126	111	187	163	220	105	203
ENSMUSG00000066640	chr5	Fbxl18	-0.3630359	0.023421206	0.038352053	4.088019943	0.026763018	-1	254	252	269	324	310	242	227	245	206	285
ENSMUSG00000029101	chr5	Rgs12	0.46394986	0.023440604	0.038379321	2.871614339	0.039635868	1	88	92	95	85	85	157	107	127	119	172
ENSMUSG00000043183	chr13	Simc1	-0.574995	0.023485141	0.038447736	1.631516477	0.05286692	-1	58	41	42	59	65	42	38	35	46	34
ENSMUSG00000029171	chr5	Pgm1	0.59679825	0.023518208	0.038497362	2.343776949	0.069638295	1	48	50	52	102	47	132	122	64	110	61
ENSMUSG00000025428	chr18	Atp5a1	-0.3707336	0.02352361	0.038501695	11.27877953	0.032017062	-1	35467	40761	39593	61982	33646	37702	33525	35962	31372	38217
ENSMUSG00000039108	chr2	Lsm14b	-0.3410479	0.023533718	0.038513729	5.585203026	0.025723648	-1	886	797	640	920	747	669	741	719	573	741
ENSMUSG00000042682	chr14	Selk	0.33562456	0.023607056	0.038629225	5.814096902	0.025137587	1	822	725	635	967	580	1302	1085	857	968	931
ENSMUSG00000053964	chr7	Lgals4	0.67725462	0.023620864	0.038647295	0.902575444	0.070916241	1	22	14	12	33	20	41	25	40	34	34
ENSMUSG00000030357	chr6	Fkbp4	-0.3567367	0.023625435	0.03865025	6.977106098	0.029180555	-1	1898	1789	1808	2844	2250	1897	2034	1695	1797	1577
ENSMUSG00000072946	chr12	Ptgr2	-0.3603316	0.023631821	0.038656172	6.002005911	0.029227428	-1	923	1049	1076	1559	812	896	927	946	866	922
ENSMUSG00000057193	chr9	Slc44a2	-0.3469036	0.023639022	0.038663426	8.113126502	0.027879854	-1	5319	4579	4038	4881	4182	4195	3806	3658	3886	4350
ENSMUSG00000027080	chr2	Med19	0.36405202	0.023664427	0.038700448	3.389062626	0.024392295	1	145	133	110	174	116	193	195	171	196	195
ENSMUSG00000094497	chr1	Gm8210	-2.2840445	0.023667639	0.038701172	2.165607741	1.04691061	-1	125	117	85	100	110	130	2	1	0	1
ENSMUSG00000047330	chr1	Kcne4	0.80960722	0.023712376	0.03876979	1.643012063	0.125234343	1	36	23	37	48	19	132	67	31	34	55
ENSMUSG00000027575	chr2	Arfgap1	0.32024839	0.023719509	0.038776917	5.151864201	0.02212021	1	471	426	410	593	455	733	649	571	691	568
ENSMUSG00000031939	chr9	Taf1d	0.53982717	0.023734923	0.038797577	2.656754662	0.055950037	1	84	86	81	72	49	150	148	79	129	95
ENSMUSG00000030960	chr7	Mettl10	0.47257662	0.023738183	0.038798368	2.357423355	0.038035866	1	71	61	62	64	52	102	100	87	101	83
ENSMUSG00000047669	chr10	Msl3l2	0.85144391	0.023756193	0.038823265	0.203826656	0.098926606	1	13	12	6	19	5	15	32	16	20	24
ENSMUSG00000027605	chr2	Acss2	-0.4269991	0.023759826	0.038824661	4.882875621	0.040143248	-1	336	560	459	750	433	388	371	471	453	343
ENSMUSG00000041798	chr11	Gck	-1.078576	0.023763168	0.038825582	0.355064982	0.199397873	-1	12	6	35	53	15	10	8	14	10	18
ENSMUSG00000091845	chr6	Gm4604	0.89809513	0.023768644	0.03882999	0.376580816	0.115159533	1	11	20	13	5	10	25	37	20	25	17
ENSMUSG00000084168	chr11	Atp5l2-ps	0.56065656	0.0238535	0.038964062	1.822671015	0.051399198	1	40	51	42	38	32	70	59	74	62	65
ENSMUSG00000017692	chr11	Rhbdl3	0.42726957	0.023868848	0.038984577	3.628455225	0.037139911	1	160	147	163	182	125	198	206	177	233	333
ENSMUSG00000068798	chr3	Rap1a	-0.3983163	0.023898485	0.039028421	5.552694956	0.035699692	-1	820	704	701	1048	721	506	737	468	760	823
ENSMUSG00000030532	chr7	Hddc3	-0.9905572	0.023926701	0.039069935	4.305071831	0.221115149	-1	446	356	380	416	342	739	95	98	109	93
ENSMUSG00000025728	chr17	Pigq	0.31320167	0.023936015	0.039080577	5.030197106	0.020916991	1	402	395	435	523	406	677	635	568	486	586
ENSMUSG00000020232	chr10	Hmg20b	0.35897756	0.023944584	0.039090001	3.797000667	0.025422077	1	165	180	163	252	147	317	230	229	207	288
ENSMUSG00000025737	chr17	Wdr24	-0.3641988	0.024033432	0.039230466	3.774492017	0.02607275	-1	247	217	178	282	218	213	160	190	212	191
ENSMUSG00000024639	chr19	Gnaq	-0.3441607	0.024037666	0.039232795	4.354946414	0.024622844	-1	318	321	318	436	309	303	340	202	287	340
ENSMUSG00000080989	chr2	Gm14048	-0.8053969	0.024076279	0.039291229	0.329862912	0.090951486	-1	29	28	21	16	13	16	13	9	11	19
ENSMUSG00000028719	chr4	Cmpk1	0.34227579	0.024120761	0.039359224	5.115383764	0.025627227	1	466	453	420	587	357	654	766	447	650	649
ENSMUSG00000085614	chr4	1700123M08Rik	-0.5492588	0.024136845	0.039380871	2.591655774	0.058850497	-1	140	114	94	95	77	53	81	85	83	86
ENSMUSG00000048232	chr4	Fbxo10	0.50314562	0.024142481	0.039385469	2.957344221	0.05008779	1	106	81	80	103	99	99	143	165	126	192
ENSMUSG00000045538	chr8	Ddx28	0.35177159	0.024200468	0.039475461	3.822120557	0.024358535	1	180	182	164	242	155	332	240	245	204	269
ENSMUSG00000038967	chr11	Pdk2	-0.4090958	0.024208889	0.039484588	8.692281171	0.039200204	-1	5732	6430	5910	10484	7015	6482	4862	5817	4371	7570
ENSMUSG00000036208	chr16	BC027231	-0.6335774	0.024216893	0.039493033	1.829861128	0.074001311	-1	94	60	49	55	52	57	37	36	58	32
ENSMUSG00000083282	chr19	Ctsf	0.35591472	0.02427397	0.039581496	4.932350545	0.027574978	1	427	416	372	440	328	712	456	564	435	632
ENSMUSG00000060862	chr4	Zbtb40	-0.4118079	0.024286386	0.039597122	3.197475978	0.032531244	-1	128	135	125	218	170	159	137	103	119	120
ENSMUSG00000074643	chr2	Cpne1	-0.3403028	0.024297893	0.039611263	4.159713059	0.023656314	-1	288	286	298	337	265	255	300	200	244	284

ENSMUSG00000028631	chr4	Kcnq4	-0.3964976	0.024323803	0.039648877	4.98735472	0.034836758	-1	508	471	389	747	585	463	429	542	318	468
ENSMUSG00000031093	chrX	Dock11	0.44202382	0.024362834	0.039707868	3.075354282	0.037551311	1	91	103	105	129	96	177	176	103	187	140
ENSMUSG00000015804	chr5	Med28	0.35880747	0.024389293	0.039746358	5.23691038	0.028593887	1	509	497	439	610	408	952	695	582	714	523
ENSMUSG00000056820	chr8	Tsnax	-0.3218781	0.024467979	0.03986994	6.581717838	0.023796091	-1	1711	1536	1389	1982	1340	1455	1451	1262	1386	1387
ENSMUSG00000041000	chr4	Trim62	0.68834427	0.024491148	0.039903042	0.905266831	0.072257976	1	15	17	21	31	16	50	22	36	29	39
ENSMUSG00000045319	chr2	Proser2	0.67738985	0.02453851	0.039975547	1.190126996	0.073535135	1	31	23	14	27	28	41	31	51	36	56
ENSMUSG00000040591	chr2	1110051M20Rik	0.38782464	0.024578005	0.040035221	3.594967736	0.029733541	1	189	139	122	171	150	208	203	218	203	272
ENSMUSG00000024052	chr17	Lpin2	0.47287959	0.024620338	0.040099504	2.793830488	0.042728647	1	76	66	83	123	80	182	145	90	123	112
ENSMUSG00000027620	chr2	Rbm39	-0.3405477	0.024631046	0.040112269	6.125978854	0.026526198	-1	1151	1064	1045	1573	1019	1147	1154	748	1048	950
ENSMUSG00000043061	chr12	Tmem18	-0.4398415	0.024719442	0.040251535	3.378363129	0.039529304	-1	167	192	176	197	147	128	172	87	167	160
ENSMUSG00000055884	chr12	Fancm	-0.6600244	0.024751302	0.040298718	1.276772314	0.070095286	-1	38	48	37	68	23	24	31	33	23	34
ENSMUSG00000087589	chr1	D430040D24Rik	-0.7064973	0.024762465	0.040312198	0.542404063	0.063610301	-1	23	29	21	25	25	16	17	16	11	23
ENSMUSG00000024376	chr18	Epb4.1l4a	-0.5928311	0.024798134	0.040365245	2.147199437	0.066772318	-1	61	75	77	122	57	90	48	60	33	52
ENSMUSG00000038777	chr3	Sema6c	-0.4298415	0.024800827	0.040365245	7.133154725	0.043288605	-1	1987	2115	2129	3339	2504	1588	1804	2466	1508	2302
ENSMUSG00000091474	chr7	2610021A01Rik	-0.6565107	0.024807193	0.040370905	1.883465347	0.082773737	-1	61	63	60	93	52	24	59	26	52	65
ENSMUSG00000051041	chr7	Olfml1	-0.5519276	0.024826378	0.040397422	2.387409503	0.058970836	-1	92	104	77	90	87	104	60	36	75	68
ENSMUSG00000024206	chr17	Rfx2	0.59630746	0.024841679	0.040417614	1.998306162	0.06632688	1	48	49	41	58	34	107	40	84	70	79
ENSMUSG00000053411	chr15	Cbx7	-0.3567005	0.024844662	0.040417762	3.627061952	0.024700259	-1	195	209	178	238	202	171	162	170	186	184
ENSMUSG00000053656	chr5	Dancr	0.90691229	0.024860246	0.040438408	0.304071462	0.121088813	1	14	16	13	7	6	39	24	22	22	11
ENSMUSG00000078931	chr8	Pdf	-0.3280172	0.024870848	0.040450945	5.543783155	0.024140765	-1	834	753	714	920	645	630	790	588	657	702
ENSMUSG00000022706	chr16	Mrpl40	0.34796969	0.024899977	0.04049361	4.424083559	0.025642034	1	321	285	242	324	229	433	416	325	444	333
ENSMUSG00000056167	chr9	Cnot10	0.32566719	0.02493869	0.040551847	4.416216603	0.022145794	1	264	281	254	366	245	445	349	375	403	353
ENSMUSG00000073295	chrX	Nudt11	-0.7201693	0.024947259	0.040561063	0.308855164	0.061111422	-1	21	22	19	25	17	17	9	11	15	17
ENSMUSG00000054792	chr9	Klhl18	-0.3597021	0.025060818	0.040740956	3.617288201	0.025434586	-1	193	204	163	253	207	211	177	140	185	159
ENSMUSG00000061306	chr11	Slc38a10	-0.3359756	0.025078078	0.040764273	6.475875613	0.026154502	-1	1305	1431	1389	2134	1214	1446	1278	1135	1196	1380
ENSMUSG00000026958	chr2	Dpp7	0.4912953	0.025104925	0.040803166	4.136786635	0.053302559	1	250	206	179	257	192	614	320	192	311	263
ENSMUSG00000024095	chr17	Hnrnpll	-0.3728654	0.025129996	0.040839166	4.054376164	0.029068122	-1	273	257	234	357	272	225	282	166	269	233
ENSMUSG00000005161	chr8	Prdx2	0.36989768	0.025154111	0.040873602	7.608563501	0.032297896	1	2482	2763	2380	3304	1835	4749	3134	3495	3301	3337
ENSMUSG00000040250	chr6	Asun	-0.3390099	0.025197697	0.040939667	3.736119913	0.022589422	-1	233	210	191	251	213	233	206	155	166	198
ENSMUSG00000028568	chr4	Btf3l4	0.38440087	0.025259286	0.041034962	4.178578005	0.031465156	1	242	239	206	255	216	248	374	289	338	407
ENSMUSG00000031166	chrX	Wdr13	-0.3720577	0.025285252	0.041067598	4.659478872	0.030439594	-1	515	458	398	431	305	381	307	310	369	425
ENSMUSG00000055799	chr6	Tcf7l1	0.49022471	0.025282772	0.041067598	2.961059851	0.048507572	1	74	93	66	141	105	135	148	143	106	199
ENSMUSG00000051098	chr13	Mblac2	-0.7427779	0.025354484	0.041175258	0.497263297	0.076089425	-1	29	22	23	29	18	9	12	19	18	20
ENSMUSG00000039382	chrX	Wdr45	0.3584293	0.025396614	0.041238884	4.498461574	0.027705506	1	300	331	247	345	246	553	322	371	394	432
ENSMUSG00000024997	chr19	Prdx3	-0.3344301	0.025408367	0.04124847	7.455452175	0.026407809	-1	2855	2916	2904	3711	2253	2676	2630	2257	2565	2541
ENSMUSG00000032348	chr9	Gsta4	-0.4058752	0.02540842	0.04124847	3.281917276	0.032408358	-1	157	189	117	224	137	172	142	112	133	119
ENSMUSG00000028256	chr3	Odf2l	-0.5093878	0.025437873	0.041291489	2.38985958	0.048078791	-1	111	82	85	93	76	56	85	55	81	67
ENSMUSG00000010607	chr9	Pigyl	0.35394243	0.025451669	0.041309085	3.819493049	0.02534048	1	193	194	171	237	126	276	245	237	261	262
ENSMUSG00000030672	chr7	Mylpf	-0.4753839	0.025457645	0.041313986	14.30099371	0.053977304	-1	464442	323815	309485	333105	307033	177494	294489	232949	304795	360896
ENSMUSG00000039115	chr9	Itga9	-0.3937725	0.025499506	0.041377115	4.290550926	0.033790243	-1	353	247	247	422	384	344	252	219	225	345
ENSMUSG00000032897	chr4	Nfyc	-0.3038252	0.025519424	0.041402392	5.129447985	0.020262758	-1	566	561	534	655	548	533	476	464	519	556
ENSMUSG00000096054	chr10	Syne1	-0.3760963	0.025521008	0.041402392	5.249834359	0.032106099	-1	580	455	528	934	728	541	539	482	484	654
ENSMUSG00000030611	chr7	Mrps11	0.35730139	0.025557989	0.041457573	4.249361512	0.027050726	1	232	257	250	297	198	377	362	312	397	280
ENSMUSG00000059022	chr6	Kcp	0.53028487	0.025568403	0.041469653	2.938793003	0.057765104	1	84	79	87	96	109	158	98	166	101	204
ENSMUSG00000029343	chr5	Crybb1	0.77414957	0.025593949	0.041506269	1.546692684	0.113114392	1	23	37	46	23	21	50	30	65	65	75
ENSMUSG00000074305	chr9	Peak1	-0.3173017	0.025610251	0.041527888	4.794140771	0.021849447	-1	414	419	432	586	439	508	436	350	328	400
ENSMUSG00000005672	chr5	Kit	-0.5298222	0.025627515	0.041551062	2.009025903	0.050137347	-1	70	58	71	87	59	57	39	58	39	68
ENSMUSG00000073409	chr17	H2-Q6	1.06118759	0.025659014	0.041597306	2.940418883	0.252167464	1	52	92	46	90	82	549	65	93	49	118
ENSMUSG00000033722	chr1	BC034090	0.61158411	0.025688476	0.041640239	1.827362287	0.069924909	1	40	32	33	48	48	72	55	96	44	68
ENSMUSG00000062110	chr5	Scfd2	0.41387676	0.025697439	0.041649938	3.258142837	0.034201358	1	140	100	108	145	111	151	174	203	180	164
ENSMUSG00000051341	chr17	Zfp52	0.74034834	0.025739216	0.041712811	0.892568847	0.090738643	1	22	18	20	27	10	19	41	37	44	33
ENSMUSG00000021079	chr12	Timm9	0.33945444	0.025796428	0.041800681	3.980164457	0.023594347	1	210	206	191	270	159	303	292	289	281	259
ENSMUSG00000045503	chr2	Sys1	0.32694943	0.025808577	0.041815519	4.340379341	0.022395667	1	250	271	226	327	258	428	374	340	375	312
ENSMUSG00000026174	chr1	Rqcd1	0.31241882	0.025915972	0.04198276	4.5653977	0.020710691	1	316	296	292	400	268	491	456	350	438	401
ENSMUSG00000057897	chr11	Camk2b	-0.3957445	0.025917806	0.04198276	7.515800221	0.03734943	-1	3263	2610	2810	4057	2842	2465	2257	2825	1873	3461
ENSMUSG00000009418	chr1	Nav1	0.44766143	0.025928079	0.041994534	4.502710505	0.04493378	1	218	271	287	302	327	625	418	407	247	451
ENSMUSG00000041126	chr11	H2afv	0.30757071	0.025936754	0.042003716	5.23221659	0.021014701	1	528	490	460	572	442	778	616	616	699	676
ENSMUSG00000041479	chr14	Syt15	0.61913076	0.025941168	0.042005998	1.031755295	0.05523385	1	23	24	17	25	23	36	31	33	39	50
ENSMUSG00000020420	chr7	Zfp607	-0.942008	0.025965333	0.042040257	0.226378408	0.133785038	-1	18	12	34	31	9	8	12	10	18	10
ENSMUSG00000013495	chr5	Tmem175	0.47522864	0.026079683	0.042220508	2.85681095	0.044338385	1	110	96	70	95	72	128	158	94	121	178
ENSMUSG00000089824	chr2	Rbm12	-0.3493968	0.026113643	0.042270591	3.501975413	0.023736862	-1	179	186	170	237	167	171	182	127	163	164
ENSMUSG00000061458	chr12	Nol10	0.37686522	0.026129604	0.042291527	3.658107444	0.028745371	1	183	143	123	213	154	258	297	195	192	216
ENSMUSG00000036104	chr1	Rab3gap1	-0.3046906	0.026192549	0.042388498	5.077515215	0.020466149	-1	554	506	483	728	516	475	500	434	481	568
ENSMUSG00000026544	chr1	Dusp23	-0.3835795	0.026256428	0.042486956	5.535537066	0.034167962	-1	956	751	693	789	694	602	562	635	576	900
ENSMUSG00000004098	chr9	Col5a3	0.4507775	0.026269374	0.042502983	7.128349074	0.048616411	1	1328	1539	1319	2396	2248	2959	2529	3054	1726	2916

ENSMUSG00000036975	chr1	Tmem177	-0.3314253	0.02629728	0.042543209	3.867525497	0.021853178	-1	245	229	206	318	212	205	209	193	217	221
ENSMUSG00000055128	chr14	Cgrrf1	-0.3199105	0.026325123	0.042583323	4.926249433	0.022596759	-1	545	497	468	560	431	405	434	404	462	488
ENSMUSG00000024146	chr17	Cript	-0.3115576	0.026378515	0.042659816	4.919043772	0.021372136	-1	554	516	433	569	416	478	433	361	458	470
ENSMUSG00000057614	chr5	Gnai1	-0.5205478	0.026378369	0.042659816	2.11653599	0.04896958	-1	75	78	61	98	61	58	59	64	34	68
ENSMUSG00000064141	chr4	Zfp69	-1.166906	0.026395899	0.042682991	-0.1549846	0.233882149	-1	8	23	14	25	11	25	3	5	3	4
ENSMUSG00000066037	chr4	Hnrnpr	-0.3822735	0.02644843	0.042762987	4.429296172	0.032179732	-1	402	358	296	497	275	232	384	259	302	338
ENSMUSG00000037519	chr7	Ppfia1	-0.3264619	0.026483713	0.04281508	4.515250205	0.023006121	-1	337	326	363	509	361	373	349	250	331	353
ENSMUSG00000020775	chr11	Mrpl38	0.33289784	0.02658629	0.042975942	5.80015793	0.02578775	1	707	701	667	991	628	1267	917	1067	831	988
ENSMUSG00000024191	chr17	Bnip1	0.33417101	0.02659433	0.042983966	4.202662433	0.023460699	1	247	230	209	285	234	398	347	341	299	280
ENSMUSG00000039713	chr4	Plekhg5	0.45339625	0.026599665	0.042987618	3.75643739	0.044580945	1	155	197	153	185	148	339	173	311	185	255
ENSMUSG00000040365	chr11	Trim41	0.32283009	0.026620129	0.043015716	4.78986287	0.02282856	1	375	327	356	411	348	661	447	464	440	499
ENSMUSG00000022750	chr16	Klhl22	0.34155264	0.026635088	0.043034913	4.811097459	0.026004844	1	402	388	271	421	355	476	477	512	481	596
ENSMUSG00000030779	chr7	Rbbp6	-0.3150625	0.026673562	0.043092093	5.00462091	0.022104963	-1	459	465	487	731	518	497	477	401	418	542
ENSMUSG00000037020	chr7	Wdr62	0.69083936	0.026682318	0.043101257	1.526091192	0.08749649	1	35	43	34	18	23	59	62	33	53	72
ENSMUSG00000040302	chr5	Rbm48	-0.6648481	0.026723471	0.043162745	2.064503539	0.090354911	-1	61	68	82	95	66	30	68	33	37	90
ENSMUSG00000044715	chr12	Gskip	0.33985565	0.026745601	0.043193497	3.773464531	0.02298066	1	178	177	177	199	157	299	246	201	252	242
ENSMUSG00000033883	chr3	D3Ertd254e	-0.5268623	0.026818452	0.043306145	1.761870786	0.047640673	-1	54	59	50	64	60	54	40	42	30	54
ENSMUSG00000024193	chr17	Phf1	0.42719614	0.026841168	0.043337819	3.800564474	0.039590677	1	217	156	155	224	132	407	191	225	247	234
ENSMUSG00000059820	chr9	AU019823	-0.3749469	0.026849304	0.043340941	3.371216229	0.027819452	-1	188	155	179	185	150	165	125	126	141	172
ENSMUSG00000087117	chr11	Gm11523	1.1782933	0.026848807	0.043340941	0.079976386	0.251090428	1	19	12	3	5	3	7	27	35	13	21
ENSMUSG00000027546	chr2	Atp9a	0.42487654	0.026857829	0.043349696	5.07257251	0.041992815	1	364	411	407	600	368	990	547	585	633	401
ENSMUSG00000019818	chr10	Cd164	-0.3779576	0.026909288	0.043427738	7.148819111	0.034398534	-1	2662	2164	1956	2839	2339	1609	2283	1951	1687	2514
ENSMUSG00000031785	chr8	Gpr56	0.56956523	0.026914912	0.043431799	4.519084928	0.075934694	1	178	201	191	511	322	721	330	512	302	374
ENSMUSG00000101257	chr1	2310015K22Rik	1.09089336	0.026935308	0.043459693	1.755319396	0.257278196	1	20	34	44	36	19	8	84	51	67	148
ENSMUSG00000037418	chr19	Best1	1.05321919	0.027016077	0.043584981	-0.322410798	0.142626437	1	7	8	3	7	7	24	5	18	7	20
ENSMUSG00000025158	chr11	Rfng	0.34457992	0.027037565	0.043614613	3.994427228	0.024828226	1	202	193	173	268	206	341	234	281	270	320
ENSMUSG00000021918	chr14	Nek4	-0.6970956	0.027046428	0.043623875	1.765984276	0.096937388	-1	58	68	57	53	63	17	41	33	52	60
ENSMUSG00000044600	chr8	Smim7	0.41496564	0.027062674	0.043640758	6.232070996	0.041189187	1	1223	1057	869	989	646	1110	1449	1286	1598	1511
ENSMUSG00000057262	chr15	Gm10020	-1.9998348	0.027063141	0.043640758	3.507594732	0.868341185	-1	307	249	271	299	215	382	5	9	4	4
ENSMUSG00000054293	chrX	A630033H20Rik	0.80776842	0.027084383	0.043669974	0.462273639	0.099872737	1	18	16	12	13	8	21	39	12	26	32
ENSMUSG00000028410	chr4	Dnaja1	0.33302149	0.027132527	0.043742554	5.49293428	0.025675984	1	631	540	477	734	589	969	950	666	800	720
ENSMUSG00000017421	chr11	Zfp207	-0.3118022	0.027150526	0.043762767	5.78139223	0.022648443	-1	944	878	785	1092	838	897	919	654	774	769
ENSMUSG00000032198	chr9	Dock6	-0.3947008	0.027151328	0.043762767	4.038020265	0.034125976	-1	294	248	297	311	227	309	227	249	153	218
ENSMUSG00000070643	chr1	Sox13	-0.4143874	0.02717745	0.04379982	3.086993583	0.033972881	-1	131	118	118	222	135	150	100	115	108	115
ENSMUSG00000059511	chr13	Gm20563	0.643777	0.027337586	0.044052819	0.968365087	0.060735161	1	21	15	18	27	25	48	42	23	35	35
ENSMUSG00000025626	chrX	Phf6	-0.6263443	0.027437532	0.044208779	2.277720155	0.080493501	-1	96	65	79	131	64	50	88	28	81	57
ENSMUSG00000085151	chr2	1110018N20Rik	0.63498989	0.027461651	0.04424254	0.935887282	0.057803274	1	22	17	24	26	15	30	36	34	41	35
ENSMUSG00000051238	chr9	Swsap1	0.54357061	0.027608018	0.044473221	1.90789255	0.051711192	1	41	47	45	36	47	66	69	70	60	85
ENSMUSG00000052298	chr11	Cdc42se2	0.30944223	0.02764457	0.044526969	5.273515097	0.021896764	1	572	456	429	637	482	743	798	577	641	737
ENSMUSG00000071350	chr14	Setdb2	-0.5073588	0.02774623	0.044685562	1.95486233	0.045184393	-1	65	64	72	79	49	46	64	45	50	48
ENSMUSG00000001467	chr5	Cyp51	0.61969315	0.027771559	0.044721201	3.70460662	0.088593867	1	175	137	169	162	112	233	367	180	380	108
ENSMUSG00000020536	chr11	Llgl1	0.31446929	0.027790474	0.044743979	4.48886459	0.021460323	1	296	255	270	388	281	491	374	394	340	428
ENSMUSG00000027479	chr2	Mapre1	0.32048089	0.027792106	0.044743979	6.227001736	0.024484998	1	992	933	930	1229	883	1686	1467	1140	1279	1244
ENSMUSG00000024603	chr18	Dctn4	-0.3081611	0.027818988	0.044782099	5.204600427	0.021702062	-1	575	575	537	822	544	640	528	424	499	608
ENSMUSG00000041477	chr6	Dcp1b	0.53712729	0.027904684	0.044914876	1.766948612	0.04859495	1	45	43	39	36	34	61	62	62	53	78
ENSMUSG00000030433	chr7	Sbk2	0.77631216	0.027939381	0.044965544	4.86598525	0.144579798	1	139	329	354	480	302	303	295	731	420	1215
ENSMUSG00000015176	chr19	Nolc1	0.35648988	0.027990841	0.045043177	4.92846597	0.029326344	1	369	341	308	566	417	630	685	500	532	437
ENSMUSG00000045248	chr8	Med26	-0.6858225	0.028043557	0.045119212	3.735691838	0.110469107	-1	137	168	241	369	306	382	123	103	110	134
ENSMUSG00000080727	chr3	C920021L13Rik	0.77845891	0.028044547	0.045119212	0.195199481	0.078637301	1	9	10	11	11	14	13	23	20	22	26
ENSMUSG00000020801	chr11	Med31	0.47528519	0.028067423	0.045144867	2.584189957	0.043988412	1	95	65	68	87	52	98	116	119	118	102
ENSMUSG00000038235	chr1	F11r	0.40796829	0.028070184	0.045144867	4.054360736	0.037148947	1	177	240	212	280	152	411	243	339	258	286
ENSMUSG00000051149	chr2	Adnp	-0.3360541	0.028066929	0.045144867	5.234786113	0.026224652	-1	541	583	561	823	625	490	578	468	488	688
ENSMUSG00000073542	chr18	Cep76	-0.4054151	0.028092162	0.045175016	3.127798848	0.032690417	-1	153	131	136	177	136	100	125	108	112	160
ENSMUSG00000026102	chr1	Inpp1	-0.4377598	0.0281079	0.045195123	2.563147165	0.035884745	-1	93	98	94	131	83	89	87	75	87	63
ENSMUSG00000027566	chr2	Psma7	0.35816267	0.028145834	0.045250911	6.543547735	0.031105823	1	1292	1277	1129	1458	942	2267	1729	1332	1829	1438
ENSMUSG00000024097	chr17	Srsf7	0.42143879	0.028209373	0.045347849	4.732890962	0.041493795	1	316	323	283	451	323	602	694	380	504	305
ENSMUSG00000045427	chrX	Hnrnph2	-0.3412344	0.028247412	0.045403775	5.460204961	0.027383301	-1	795	724	609	942	612	548	732	532	629	719
ENSMUSG00000023286	chr4	Ube2j2	0.31035783	0.028305914	0.045492577	5.352212417	0.02237928	1	550	503	493	698	478	713	733	714	776	730
ENSMUSG00000033632	chr18	AW554918	-0.4875457	0.028379088	0.045604937	2.246915199	0.044570774	-1	78	66	71	91	95	56	78	57	61	62
ENSMUSG00000067928	chr17	Zfp760	-0.577012	0.028405137	0.045641549	1.693360881	0.060503487	-1	63	72	53	55	34	55	37	34	42	37
ENSMUSG00000020923	chr11	Ubtf	0.31025406	0.028431006	0.045677863	6.025574775	0.022984339	1	894	811	759	1126	762	1362	1241	1045	1142	1100
ENSMUSG00000079659	chr5	Tmem243	-0.4905879	0.028454453	0.045710279	2.113739363	0.043066931	-1	75	73	74	88	57	51	73	43	58	61
ENSMUSG00000022864	chr16	D16Ertd472e	-0.6929272	0.028540647	0.045843476	0.647251083	0.068532321	-1	33	22	31	28	19	15	25	16	18	16
ENSMUSG00000041560	chr7	Gltscr2	0.32124373	0.028563135	0.045874119	6.008391562	0.024721373	1	900	804	727	1060	781	1354	1020	1066	1043	1364
ENSMUSG00000052981	chr13	Ube2ql1	0.85373099	0.028566289	0.045874119	-0.213667039	0.08193153	1	4	8	8	14	5	18	12	12	17	18

ENSMUSG00000032313	chr9	AI118078	-0.8637124	0.028588413	0.045904373	0.016928729	0.097659553	-1	16	23	16	20	11	4	12	14	8	13
ENSMUSG00000033906	chrX	Zdhhc15	0.70258303	0.028603042	0.045917312	0.691635244	0.072463616	1	16	21	21	14	11	26	39	25	27	33
ENSMUSG00000050148	chrX	Ubqln2	-0.3761773	0.028600483	0.045917312	3.89713073	0.030633859	-1	250	226	177	370	239	201	221	186	173	272
ENSMUSG00000015605	chr17	Srf	-0.3336648	0.028609642	0.045922632	6.519721257	0.027072367	-1	1397	1242	1397	2014	1594	1517	1218	1236	1345	1306
ENSMUSG00000024963	chr19	Dnajc4	-0.3313527	0.028650443	0.045982843	4.051780587	0.023530678	-1	289	251	259	308	257	298	212	203	218	266
ENSMUSG00000050908	chr16	Tvp23a	0.80461579	0.028659465	0.045990607	0.452787526	0.102968578	1	18	20	7	14	8	26	22	34	15	31
ENSMUSG00000097530	chr7	Kansl2-ps	-0.5213568	0.028661862	0.045990607	2.136749557	0.051384097	-1	88	53	63	111	66	68	49	57	67	45
ENSMUSG00000039043	chr7	2610034B18Rik	0.45926133	0.028730035	0.046094705	2.80082801	0.042520744	1	78	80	95	115	63	179	130	102	136	103
ENSMUSG00000070953	chr2	Rabepk	0.42663946	0.028748177	0.046118517	2.915930907	0.036493142	1	106	103	75	118	72	162	130	111	165	127
ENSMUSG00000039813	chr4	Tbc1d2	0.72552506	0.028765563	0.046141111	0.795416877	0.086675566	1	18	22	18	16	15	23	45	19	40	36
ENSMUSG00000056938	chr11	Acbd4	-0.3472943	0.028827443	0.046235064	4.151327359	0.026517715	-1	292	288	247	347	298	350	217	244	208	257
ENSMUSG00000046721	chr7	Rpl14-ps1	0.40596275	0.028837312	0.046245584	5.211650858	0.039372603	1	542	460	388	601	392	1125	671	651	492	538
ENSMUSG00000053644	chr18	Aldh7a1	0.32859883	0.028849183	0.046259314	4.781891543	0.02459221	1	380	352	287	433	359	459	525	475	421	608
ENSMUSG00000035329	chr12	Fbxo33	0.58117311	0.028893607	0.046319919	2.161745734	0.068831672	1	54	41	47	81	40	117	96	56	106	52
ENSMUSG00000066607	chr9	6030419C18Rik	-0.4161161	0.028891578	0.046319919	3.201048147	0.035281452	-1	130	143	147	227	134	105	126	140	130	129
ENSMUSG00000020866	chr11	Cacna1g	-0.5166409	0.028934806	0.046380645	2.684119465	0.055805368	-1	123	76	104	160	97	107	77	93	46	103
ENSMUSG00000004393	chr11	Ddx56	0.40409216	0.028948651	0.046397516	4.490057149	0.038015698	1	266	250	242	445	253	558	485	396	383	263
ENSMUSG00000027774	chr3	Gfm1	-0.3411651	0.029045335	0.046547139	6.962944148	0.028670603	-1	1879	2042	1892	3000	1689	2020	1954	1818	1634	1546
ENSMUSG00000032182	chr9	Yipf2	0.48053798	0.029068087	0.04657826	2.817805717	0.04728301	1	96	98	75	82	76	156	93	144	145	117
ENSMUSG00000041264	chr5	Uspl1	-0.3228741	0.029100767	0.04662528	4.919638226	0.024003842	-1	535	440	482	559	473	474	439	358	512	403
ENSMUSG00000079043	chr2	Fastkd5	-0.3811038	0.029138665	0.046680649	3.328061828	0.029733347	-1	196	143	137	177	180	140	138	135	144	145
ENSMUSG00000054027	chr10	Nt5dc3	-0.3394274	0.029190094	0.04675768	6.257954012	0.028102049	-1	1237	1116	1110	1585	1322	990	1171	996	1009	1339
ENSMUSG00000029144	chr5	Gtf3c2	-0.2910901	0.029201592	0.046770736	4.913886599	0.01912902	-1	514	449	456	578	464	475	473	408	418	432
ENSMUSG00000022075	chr14	Rhobtb2	-0.4193734	0.029234483	0.046818051	5.173993478	0.042239755	-1	680	607	492	703	586	321	475	444	578	677
ENSMUSG00000021420	chr13	Fars2	-0.3204401	0.029285874	0.046894979	4.42683475	0.022695635	-1	338	396	322	438	281	319	293	283	318	339
ENSMUSG00000035513	chr2	Ntng2	-0.5377707	0.029295565	0.046905122	3.506023616	0.065788773	-1	199	129	152	414	140	113	138	143	179	169
ENSMUSG00000026872	chr2	Zeb2	-0.4398249	0.029324711	0.04694641	4.479071499	0.045723499	-1	378	350	367	402	392	250	414	171	300	412
ENSMUSG00000033166	chr14	Dis3	-0.486166	0.029413206	0.047082071	3.183364377	0.051280986	-1	141	148	122	209	164	92	155	78	162	121
ENSMUSG00000073910	chr4	Mob3b	0.68829918	0.029416188	0.047082071	0.866123812	0.073318922	1	25	24	21	13	12	42	35	26	34	34
ENSMUSG00000047098	chr14	Rnf31	0.36268469	0.029499612	0.047210189	3.742129813	0.028240519	1	160	142	133	249	188	303	239	234	214	231
ENSMUSG00000025245	chr9	Lztfl1	-0.4334454	0.02952243	0.047241296	3.510057165	0.041408518	-1	232	228	175	186	139	161	180	106	184	154
ENSMUSG00000009470	chr13	Tnpo1	-0.3267837	0.029573871	0.047318194	5.514698063	0.025558225	-1	752	674	636	969	765	719	825	531	568	678
ENSMUSG00000000782	chr11	Tcf7	0.73001303	0.029603978	0.047360943	0.338474452	0.071217085	1	15	13	11	19	6	23	21	28	19	24
ENSMUSG00000042507	chr12	Elmsan1	-0.3654058	0.029784362	0.04764407	3.913731672	0.029293016	-1	216	210	220	331	281	200	214	200	186	267
ENSMUSG00000054091	chr3	1810037I17Rik	0.38521287	0.029854192	0.047750308	5.111916614	0.035676771	1	436	508	430	582	286	795	641	550	728	475
ENSMUSG00000024561	chr18	Mbd1	-0.3432865	0.029858864	0.047752315	3.662286923	0.024758334	-1	212	183	193	233	220	202	207	167	150	179
ENSMUSG00000040857	chr7	Erf	0.36465573	0.029865374	0.047757261	3.560291692	0.027530654	1	154	144	143	172	145	303	212	183	169	215
ENSMUSG00000023046	chr15	Igfbp6	0.47459412	0.030043648	0.048036841	5.674085688	0.05569877	1	725	479	669	786	527	1581	819	1105	553	823
ENSMUSG00000023806	chr17	Rsph3b	0.56615297	0.030080884	0.048090876	2.735822241	0.0711382	1	66	82	68	109	70	62	125	128	164	148
ENSMUSG00000047694	chrX	Yipf6	-0.3224837	0.030176454	0.048238147	4.128132543	0.022576351	-1	286	237	263	374	284	277	274	246	232	231
ENSMUSG00000001964	chrX	Emd	0.32653871	0.030220105	0.048286331	4.74400806	0.024668037	1	373	272	333	460	334	579	528	423	491	407
ENSMUSG00000031700	chr8	Gpt2	-0.4649491	0.030220417	0.048286331	7.265150227	0.054447094	-1	2557	2696	2495	3210	2333	1490	2201	1293	3079	2427
ENSMUSG00000073600	chr18	Prob1	-0.3709172	0.030210754	0.048286331	6.275399964	0.034106935	-1	1252	1102	1062	1927	1245	995	953	1154	971	1415
ENSMUSG00000075279	chr2	Mrpl23-ps1	0.38606954	0.0302193	0.048286331	3.302274065	0.030718716	1	134	105	107	142	139	228	192	149	181	154
ENSMUSG00000103125	chr18	RP23-407E2.6	-0.6679212	0.030235051	0.048304193	1.572856232	0.087747885	-1	54	42	45	70	52	20	33	25	36	66
ENSMUSG00000102836	chr18	RP23-407E2.5	-0.667921	0.030243378	0.048311973	1.572856232	0.087758995	-1	54	42	45	70	52	20	33	25	36	66
ENSMUSG00000020325	chr10	Fstl3	0.71684477	0.030327479	0.048439081	1.154822361	0.094247614	1	27	22	11	29	29	70	46	39	22	38
ENSMUSG00000022223	chr14	Sdr39u1	-0.3040529	0.030329879	0.048439081	5.959459578	0.022513421	-1	1050	960	923	1268	927	991	958	844	894	851
ENSMUSG00000095588	chr4	Gm12350	0.36226394	0.030334573	0.048441042	3.493145557	0.027247994	1	128	139	146	194	122	230	230	197	195	170
ENSMUSG00000052794	chr8	1700030K09Rik	-0.4988718	0.030423736	0.048577874	1.974075019	0.045778529	-1	79	52	66	69	65	60	41	49	50	58
ENSMUSG00000019471	chr9	Cdc37	0.31135755	0.030457376	0.048621219	6.854291138	0.02421398	1	1525	1470	1295	2002	1437	2276	1958	2095	1913	2202
ENSMUSG00000069835	chr11	Sat2	0.64809315	0.03045784	0.048621219	1.956348452	0.087468993	1	65	56	25	54	20	95	58	83	69	68
ENSMUSG00000025810	chr8	Nrp1	-0.3854236	0.030471781	0.048637918	5.984199924	0.036836287	-1	708	1096	938	1755	932	1118	877	777	826	899
ENSMUSG00000005682	chr10	Pan2	-0.4086074	0.030479516	0.048644709	3.345213868	0.035863549	-1	205	187	141	183	137	203	148	124	120	115
ENSMUSG00000068039	chr17	Tcp1	0.321945	0.030489442	0.048654994	7.576160143	0.026159214	1	2569	2305	2056	3406	2398	3831	3772	3317	3069	3330
ENSMUSG00000049307	chr9	Fut4	0.66789521	0.03050847	0.048679802	0.784974876	0.066152366	1	28	13	16	17	17	37	39	25	29	30
ENSMUSG00000017781	chr11	Pitpna	0.32379053	0.030518148	0.048689685	7.570850437	0.026456259	1	2709	2182	2216	3072	2424	3752	3633	2699	3411	3823
ENSMUSG00000035456	chr5	Prdm8	-0.8721627	0.030595069	0.048806835	0.083631182	0.110449302	-1	10	13	25	20	22	14	5	14	11	10
ENSMUSG00000001100	chr11	Poldip2	-0.3313044	0.030653843	0.048895014	6.859257295	0.027517434	-1	1904	1909	1855	2464	1543	1533	1573	1599	1745	1904
ENSMUSG00000073233	chr12	Gm9144	-0.7518869	0.030675669	0.048924243	0.393387424	0.080462757	-1	15	18	21	31	27	16	14	9	11	23
ENSMUSG00000024220	chr17	Zfp523	-0.3414048	0.030686549	0.048933198	3.66597634	0.024656135	-1	213	206	192	250	187	189	157	156	179	226
ENSMUSG00000087331	chr15	1810021B22Rik	0.59847757	0.030688286	0.048933198	1.192274769	0.059395934	1	31	24	25	26	21	43	44	53	29	42
ENSMUSG00000036256	chr5	Igfbp7	0.33429712	0.030713776	0.048968256	6.969668317	0.028097902	1	1697	1693	1627	1943	1296	2542	2349	2284	1751	2503
ENSMUSG00000039231	chrX	Suv39h1	0.44289811	0.030784718	0.049075763	3.075999646	0.042050356	1	112	86	97	137	95	237	177	121	140	114
ENSMUSG00000030020	chr6	Prickle2	-0.5577056	0.030828469	0.049139904	1.89260556	0.060106138	-1	55	68	72	68	54	35	50	47	37	68

ENSMUSG00000027387	chr2	Zc3h8	0.53182067	0.030835819	0.049146015	2.60624259	0.060454811	1	60	78	57	108	64	68	139	103	134	126
ENSMUSG00000031616	chr8	Ednra	0.50344315	0.030847187	0.049158527	2.782652055	0.054268787	1	84	76	75	131	57	206	117	126	85	119
ENSMUSG00000045886	chr10	Gm9803	0.50331213	0.030873664	0.049195112	2.06473371	0.04895883	1	61	31	52	70	38	81	75	67	81	84
ENSMUSG00000033186	chr14	Mzt1	-0.4990994	0.030882667	0.049203848	4.21487855	0.059878648	-1	347	292	286	391	298	116	293	208	262	361
ENSMUSG00000009097	chr16	Tbx1	0.42229685	0.030905187	0.049234115	4.295792896	0.042459448	1	241	201	206	372	239	282	329	458	282	457
ENSMUSG00000004473	chr7	Clec11a	0.62267759	0.030910832	0.049237496	3.198192194	0.090286229	1	163	99	100	98	68	363	174	137	105	137
ENSMUSG00000074886	chr13	Grk6	0.31630801	0.030918531	0.049244146	4.295725221	0.02208119	1	247	256	245	291	251	447	374	298	328	329
ENSMUSG00000011306	chr8	Sugp1	0.3198215	0.030956485	0.049298978	4.318861107	0.022957131	1	297	232	205	328	258	392	326	321	375	384
ENSMUSG00000029390	chr5	Tmed2	0.37260045	0.030964286	0.049305784	6.290522361	0.034807014	1	1028	942	949	1265	905	1133	1771	1205	1705	1344
ENSMUSG00000034889	chr10	Cactin	0.35964119	0.030994686	0.049346886	3.914028222	0.028737168	1	171	179	179	278	177	393	254	211	266	260
ENSMUSG00000074876	chr2	Spata5l1	-0.6262653	0.030997161	0.049346886	1.556230876	0.075436842	-1	51	43	50	74	40	22	36	24	52	46
ENSMUSG00000059142	chr17	Zfp945	-0.5548775	0.031017944	0.049374349	2.624607283	0.067249199	-1	107	99	111	126	93	38	93	68	90	108
ENSMUSG00000021895	chr14	Arhgef3	-0.3410519	0.031047287	0.049409802	3.774736554	0.024858908	-1	202	247	213	302	173	210	185	185	194	203
ENSMUSG00000022023	chr14	Wbp4	-0.3049535	0.031044408	0.049409802	4.882004487	0.021639734	-1	474	420	422	636	479	462	408	355	471	451
ENSMUSG00000000732	chr10	Icosl	0.54525781	0.031061897	0.049427425	1.687498838	0.053866187	1	41	39	39	43	25	71	82	46	50	52
ENSMUSG00000016409	chrX	Nkap	-0.3773426	0.031120904	0.049515682	3.429806114	0.030063237	-1	202	167	141	229	164	151	195	111	144	159
ENSMUSG00000021365	chr13	Nedd9	-0.4731466	0.031144221	0.049547142	3.525449393	0.051364777	-1	108	182	219	308	180	206	156	140	110	174
ENSMUSG00000031422	chrX	Morf4l2	0.31849854	0.031151634	0.049553293	6.911977138	0.025591795	1	1754	1457	1424	1941	1424	2137	2454	1970	2241	2079
ENSMUSG00000002413	chr6	Braf	-0.3886274	0.031188277	0.049605937	3.230776717	0.031523518	-1	135	142	147	207	155	141	158	89	131	140
ENSMUSG00000002250	chr17	Ppard	-0.3300014	0.031196845	0.049613917	4.889568732	0.025803088	-1	424	444	409	662	524	494	362	406	372	508
ENSMUSG00000035305	chr4	Ror1	-0.6595124	0.031216924	0.049640201	1.528006545	0.085410053	-1	39	59	47	45	59	20	52	32	38	32
ENSMUSG00000022094	chr14	Slc39a14	0.61838872	0.031242982	0.049674537	3.857020807	0.09280966	1	163	124	164	249	153	652	222	161	250	174
ENSMUSG00000023460	chr17	Rab12	-0.3243515	0.031245625	0.049674537	7.011900145	0.026630654	-1	2188	2243	2072	2558	1639	2315	1807	1721	1648	1899
ENSMUSG00000024042	chr17	Sik1	0.64694216	0.031283646	0.049729326	4.573804838	0.103797796	1	182	233	436	312	197	953	368	441	218	433
ENSMUSG00000018102	chr13	Hist1h2bc	0.36270096	0.031306096	0.049759353	5.557378165	0.032518173	1	709	553	559	726	521	676	805	849	840	1121
ENSMUSG00000034911	chr8	Ushbp1	-0.3752855	0.031327003	0.049786922	4.145064859	0.032642725	-1	310	289	311	338	229	354	181	215	229	280
ENSMUSG00000101970	chr7	RP23-32A8.1	0.44056009	0.03139494	0.049889219	2.742059427	0.039691107	1	91	74	86	108	58	132	134	116	88	149
ENSMUSG00000035325	chr5	Sec31a	0.34290642	0.031405512	0.049900346	6.043909025	0.029357243	1	836	745	730	1149	890	1405	1207	1193	860	1374
ENSMUSG00000025050	chr19	Pcgf6	-0.4896581	0.031425857	0.049926996	2.038734993	0.044992238	-1	63	59	75	75	73	53	63	54	42	59
ENSMUSG00000029152	chr5	Ociad1	-0.3109026	0.031452267	0.049963274	7.050606468	0.024504671	-1	2291	2163	1861	2700	1952	2347	1976	1783	1696	1889
ENSMUSG00000029594	chr5	Rbm19	-0.4475765	0.031548734	0.05011082	2.970998653	0.042847673	0	114	110	118	172	151	84	137	86	116	109
ENSMUSG00000097375	chr13	6720427I07Rik	0.65942386	0.031593979	0.050176983	1.16052027	0.075857795	0	32	33	19	18	18	53	45	30	48	35
ENSMUSG00000022602	chr15	Arc	0.84273824	0.031616864	0.050207623	0.528074907	0.123992667	0	8	18	22	15	6	34	38	28	13	25
ENSMUSG00000054474	chr6	Thnsl2	0.48166791	0.031625251	0.050215236	2.543147156	0.047904652	0	79	68	61	72	72	75	115	106	115	127
ENSMUSG00000031672	chr8	Got2	-0.3779356	0.031656884	0.050254044	8.714488996	0.036816142	0	5280	6921	6855	11248	5643	5862	5651	5800	6116	6292
ENSMUSG00000037846	chr10	Rtkn2	0.8717489	0.031656242	0.050254044	1.110365979	0.156193479	0	33	28	9	12	23	28	34	68	29	52
ENSMUSG00000055632	chr2	Hmcn2	-0.4525958	0.031700901	0.050318204	6.416521125	0.052173305	0	1044	1264	1505	1875	1641	1350	892	1367	751	1529
ENSMUSG00000000276	chr11	Dgke	-0.4538968	0.031731918	0.050361717	2.655203856	0.042212156	0	104	85	98	159	93	73	97	65	101	89
ENSMUSG00000022965	chr16	Ifngr2	-0.3117691	0.031829118	0.050510248	6.759118605	0.024653468	0	1931	1786	1660	2048	1501	1885	1642	1348	1458	1587
ENSMUSG00000026047	chr1	Kdelc1	0.40382043	0.031879633	0.050584667	2.996408409	0.03360748	0	107	111	99	118	69	155	173	123	143	137
ENSMUSG00000070372	chr3	Capza1	-0.4155576	0.031895598	0.050604254	4.322539114	0.041414062	0	314	291	356	430	306	252	365	166	353	257
ENSMUSG00000024070	chr17	Prkd3	-0.3644992	0.031937413	0.050664845	4.079973191	0.030613374	0	243	315	266	367	224	280	307	172	226	222
ENSMUSG00000000486	chr7	Sept1	0.7167344	0.031976098	0.050720457	1.110742958	0.098588855	0	26	24	18	37	11	73	29	39	25	42
ENSMUSG00000029802	chr6	Abcg2	0.32330755	0.032034089	0.050806675	4.396618146	0.024132559	0	274	293	225	389	220	416	432	309	384	364
ENSMUSG00000005621	chr7	Zfp592	-0.3726992	0.032056576	0.050836571	4.32565221	0.032838555	0	230	289	336	494	340	374	293	225	255	283
ENSMUSG00000029062	chr4	Cdk11b	0.32077509	0.032065039	0.050844223	5.746526146	0.025610503	0	685	610	575	1057	671	1173	971	933	850	944
ENSMUSG00000046191	chr18	Pcdhb20	-0.6533302	0.032114482	0.050916846	0.97150979	0.072150507	0	39	28	20	39	42	34	26	15	19	24
ENSMUSG00000002343	chr8	Armc6	0.34583076	0.03213283	0.050934381	3.652419791	0.025689069	0	191	139	133	202	155	290	235	207	205	205
ENSMUSG00000039201	chrX	Tbc1d25	0.45814403	0.032132215	0.050934381	2.120696743	0.03764517	0	51	48	48	61	56	95	75	62	82	86
ENSMUSG00000030847	chr7	Bag3	0.42623491	0.032211262	0.051052914	6.89364899	0.046754473	0	1232	1191	1239	2669	1412	3317	2004	2278	1681	1921
ENSMUSG00000027326	chr2	Casc5	0.93773875	0.03223002	0.051076852	0.15144184	0.148604792	0	8	10	16	8	7	12	42	12	22	17
ENSMUSG00000001482	chr8	Def8	-0.3736487	0.032308851	0.051195976	5.594414407	0.034973196	0	841	655	705	1043	827	489	718	637	719	844
ENSMUSG00000022483	chr15	Col2a1	0.98887295	0.032316649	0.051202527	3.600552256	0.242841711	0	154	72	113	167	99	772	123	286	61	104
ENSMUSG00000018659	chr11	Pnpo	0.34347434	0.032331938	0.051220943	4.216533062	0.027179039	0	298	229	212	276	199	351	321	288	402	320
ENSMUSG00000004394	chr11	Tmed4	-0.3106141	0.032350729	0.051244904	5.801428151	0.024029166	0	919	834	757	1249	871	1063	783	697	727	814
ENSMUSG00000064037	chr5	Gpn1	0.29668069	0.032373462	0.051275102	4.534561175	0.020105172	0	326	293	273	369	282	442	442	383	417	389
ENSMUSG00000031298	chrX	Gpr64	-0.6758672	0.032411341	0.051329281	0.598800238	0.067649872	0	34	22	27	28	17	25	18	17	12	16
ENSMUSG00000026427	chr1	Eif2d	-0.2971085	0.032420131	0.051337383	4.997291692	0.020964995	0	520	482	482	635	497	473	417	451	474	511
ENSMUSG00000021622	chr13	Ckmt2	-0.4790498	0.032504508	0.051465164	10.39434748	0.059787006	0	15593	25372	26776	36254	14393	20523	15812	20376	20354	14077
ENSMUSG00000018442	chr11	Derl2	0.38846177	0.032549531	0.051530612	4.287359022	0.035900014	0	296	256	197	296	211	514	395	231	377	298
ENSMUSG00000008450	chr8	Nutf2	-0.3235226	0.032555809	0.051534714	5.365524604	0.025748593	0	734	668	613	794	597	544	632	523	690	580
ENSMUSG00000006362	chr8	Cbfa2t3	-0.5230585	0.032657562	0.051689931	4.254763992	0.06753725	0	250	265	292	549	340	201	222	362	143	331
ENSMUSG00000021062	chr12	Rab15	0.79005686	0.032777999	0.051874682	2.870692181	0.152668085	0	39	39	49	246	51	194	120	146	135	148
ENSMUSG00000034333	chr15	Zbed4	-0.41913	0.03278296	0.051876659	2.679048654	0.035112264	0	120	83	101	122	109	98	93	80	91	77
ENSMUSG00000084013	chr2	Gm14270	0.55293197	0.032798971	0.051896119	1.677118683	0.058007625	0	45	26	44	43	27	78	51	44	67	59

ENSMUSG00000034413	chr17	Neurl1b	0.45393599	0.032805284	0.051900233	2.460671671	0.040689364	0	69	54	53	83	79	122	109	101	85	91
ENSMUSG00000065990	chr4	Aurkaip1	0.35296799	0.032834822	0.051941084	6.189016005	0.031768792	0	1016	938	915	1117	782	1971	1206	1213	1208	1122
ENSMUSG00000021275	chr12	Tecpr2	-0.4461552	0.032876949	0.052001838	2.521889753	0.039797357	0	98	87	86	122	92	70	86	59	69	106
ENSMUSG00000038517	chr11	Tbkbp1	0.41013055	0.032931362	0.05208201	3.148888759	0.036285733	0	90	106	117	154	95	230	156	128	165	141
ENSMUSG00000044475	chr10	Ascc1	0.33319821	0.032950742	0.052100868	4.070528986	0.025117735	0	249	213	200	246	190	354	272	284	332	274
ENSMUSG00000058388	chr3	Phtf1	0.43333975	0.03294842	0.052100868	2.973639576	0.040318446	0	106	124	76	115	70	192	138	131	144	122
ENSMUSG00000025722	chr7	Wdr73	0.42664677	0.032980115	0.052141412	2.75110236	0.037499397	0	83	68	82	100	86	176	106	107	115	118
ENSMUSG00000027075	chr2	Slc43a1	-0.4281094	0.032998418	0.052164449	3.430017299	0.041573536	0	210	211	127	195	167	164	157	160	92	171
ENSMUSG00000048388	chr2	Fam171b	0.59859969	0.033032622	0.052212613	1.933624022	0.07336514	0	42	42	42	46	45	37	86	64	78	95
ENSMUSG00000073599	chr18	Ecscr	0.46041461	0.033041376	0.052220544	3.535048852	0.049599924	0	143	144	140	193	104	390	185	186	165	174
ENSMUSG00000032719	chr1	Sbspon	-0.7771691	0.033070646	0.052260894	0.213337422	0.090370482	0	12	20	20	26	20	19	19	9	7	9
ENSMUSG00000042895	chr15	Abra	-0.5124228	0.033079486	0.052268954	7.177132204	0.068371009	0	1805	2257	2232	4666	2067	2561	2066	967	2590	1634
ENSMUSG00000067377	chrX	Tspan6	0.46467015	0.033126323	0.052337043	3.176392396	0.049290658	0	121	103	116	153	70	232	199	175	116	126
ENSMUSG00000058979	chr6	Cecr5	-0.3162663	0.03314728	0.052364235	4.561789694	0.023467044	0	373	411	368	482	313	330	323	305	375	372
ENSMUSG00000054477	chr18	Kcnn2	-0.7404886	0.033217936	0.052469922	1.051245023	0.103893205	0	24	33	54	46	25	14	38	20	23	24
ENSMUSG00000030317	chr6	Timp4	-1.1428961	0.033224161	0.052473824	3.982425486	0.328140043	0	115	206	182	624	520	496	67	27	158	90
ENSMUSG00000041199	chr17	Rpusd1	0.444201	0.03328444	0.052563089	2.443797719	0.038792455	0	71	76	56	67	63	104	120	94	84	98
ENSMUSG00000020910	chr11	Adprm	0.4623466	0.033303173	0.05258673	2.459046578	0.04265947	0	68	75	67	68	56	127	81	91	114	95
ENSMUSG00000027016	chr2	Zfp385b	-0.729474	0.033359277	0.052667777	2.414457852	0.125428427	0	67	112	127	54	109	52	75	97	32	62
ENSMUSG00000079243	chr9	Xirp1	-0.5345263	0.033362037	0.052667777	7.057359917	0.0745754	0	1957	1289	1882	4550	2438	2946	1680	1568	1602	1174
ENSMUSG00000026708	chr1	Cenpl	0.62757553	0.033371687	0.052677062	0.995788433	0.064451447	0	24	25	18	20	21	53	39	23	39	32
ENSMUSG00000057531	chr13	Dtnbp1	0.33665476	0.033391656	0.05270263	5.15273144	0.02815954	0	396	389	418	752	420	809	674	508	629	631
ENSMUSG00000048039	chr3	Isg20l2	0.3292666	0.033443262	0.052778119	3.737868475	0.02359212	0	165	163	174	227	147	274	277	225	207	221
ENSMUSG00000051950	chr5	B3glct	0.39339614	0.033455519	0.052791503	2.970440925	0.031697943	0	91	90	102	125	89	181	153	110	148	126
ENSMUSG00000055850	chr6	Rnf181	0.33799176	0.033464713	0.052800049	5.487755735	0.028610669	0	644	619	571	595	496	1119	790	642	739	827
ENSMUSG00000075284	chr2	Wipf1	0.33559538	0.033510263	0.052865948	4.451458351	0.026728686	0	278	280	232	400	257	484	482	286	319	431
ENSMUSG00000000325	chr16	Arvcf	-0.3903199	0.033661802	0.053099023	4.078615157	0.036406138	0	258	204	245	405	318	343	249	198	210	196
ENSMUSG00000035478	chr10	Mbd3	0.30276134	0.03369433	0.053144336	6.576927054	0.023641554	0	1286	1133	1077	1664	1237	1868	1753	1568	1638	1780
ENSMUSG00000034868	chr17	Myl12b	0.47366257	0.03371404	0.053169423	5.706211891	0.05803345	0	633	635	550	1005	485	1933	841	692	773	816
ENSMUSG00000002546	chr2	Golga2	-0.3124202	0.033762444	0.053239752	6.308732853	0.025087696	0	1357	1159	1069	1624	1343	1325	1081	1010	1116	1250
ENSMUSG00000031671	chr8	Setd6	0.3858651	0.033780838	0.053261217	3.022894425	0.031224091	0	95	101	85	146	94	157	145	152	156	127
ENSMUSG00000053470	chr6	Kdm3a	-0.3300153	0.033783679	0.053261217	3.767355604	0.02389296	0	255	208	196	276	190	194	199	159	209	216
ENSMUSG00000054823	chr8	Whsc1l1	-0.3201284	0.033791005	0.053266759	4.046198729	0.023201785	0	251	236	282	338	251	253	270	200	225	246
ENSMUSG00000029635	chr5	Cdk8	-0.3490526	0.03380093	0.053276395	3.388870663	0.025836083	0	169	148	145	242	168	145	159	142	139	158
ENSMUSG00000097048	chr6	1600020E01Rik	0.50522487	0.033859239	0.053362282	1.68527621	0.04476014	0	42	35	38	45	30	81	59	48	58	51
ENSMUSG00000018999	chr6	Slc35b4	0.3360053	0.03392736	0.053463613	3.618288865	0.02438423	0	161	169	140	190	141	265	249	166	198	237
ENSMUSG00000005609	chr7	Ctr9	-0.3055714	0.033949147	0.053486976	4.750290954	0.022364878	0	449	403	335	557	471	441	423	353	353	392
ENSMUSG00000013646	chr11	Sh3bp5l	-0.2878568	0.033953667	0.053486976	4.959970697	0.019944114	0	506	490	455	617	475	546	412	423	411	495
ENSMUSG00000024926	chr19	Kat5	0.31261417	0.033950869	0.053486976	4.169208789	0.022212079	0	261	226	218	290	196	383	326	251	333	330
ENSMUSG00000079108	chr12	Srp54b	-0.5807082	0.034048171	0.053629802	3.47166329	0.082489422	0	197	262	138	190	186	76	186	88	209	154
ENSMUSG00000026696	chr1	Vamp4	-0.3493487	0.034136745	0.053763257	3.639403434	0.02751511	0	218	207	193	240	173	218	197	127	144	209
ENSMUSG00000031820	chr8	Babam1	0.32635248	0.034207672	0.053868893	5.895838028	0.027271944	0	940	766	688	816	702	1022	1050	1093	1051	1159
ENSMUSG00000080002	chr5	Gm5566	0.70984152	0.034212356	0.053870199	0.245838014	0.059121333	0	11	14	11	11	12	24	24	18	20	21
ENSMUSG00000022369	chr15	Mtbp	0.64180093	0.034273614	0.053960575	1.359051241	0.079581899	0	41	37	23	26	14	55	64	39	42	43
ENSMUSG00000027115	chr2	Kif18a	-0.8397867	0.034404631	0.054160748	0.169697509	0.109206309	0	27	15	19	25	11	6	19	14	12	7
ENSMUSG00000004018	chr11	Fancl	0.50572286	0.034535976	0.054361392	2.149642562	0.051619323	0	65	44	41	65	51	97	99	65	94	58
ENSMUSG00000036560	chr7	Lgi4	-0.4601578	0.034585398	0.054433054	2.673552459	0.045434107	0	113	116	97	123	91	66	89	90	67	117
ENSMUSG00000037206	chr9	Islr	0.43734625	0.034602893	0.054454457	6.336396925	0.050236366	0	960	998	1002	1035	1058	1675	1110	1815	933	2046
ENSMUSG00000022668	chr16	Gtpbp8	-0.3708501	0.034665529	0.054546885	3.310958301	0.029905853	0	165	141	179	216	127	141	150	123	154	129
ENSMUSG00000031134	chrX	Rbmx	0.33763868	0.034673287	0.054551346	4.130947477	0.026717722	0	252	220	194	278	204	342	394	290	309	250
ENSMUSG00000084896	chr11	Gm11632	-0.6624068	0.03467617	0.054551346	1.120191812	0.081955579	0	30	45	42	52	20	33	30	21	14	33
ENSMUSG00000030545	chr7	Pex11a	-0.4445052	0.034701004	0.054584269	3.396960628	0.046007398	0	128	186	162	263	164	121	136	108	196	156
ENSMUSG00000041124	chr9	Msantd4	-0.3079802	0.034736153	0.054633409	5.028111059	0.023293716	0	580	476	449	739	464	419	505	459	461	520
ENSMUSG00000000378	chr11	Ccm2	-0.397117	0.034780125	0.054696414	4.326876018	0.039102004	0	359	325	312	402	294	453	238	171	303	261
ENSMUSG00000058558	chr5	Rpl5	0.34224907	0.034815157	0.054745346	7.820357522	0.03115997	0	3192	2809	2622	3466	2756	4445	4495	3179	4875	3636
ENSMUSG00000045555	chr10	Mettl24	0.82140594	0.034844552	0.054774737	-0.129746884	0.0851824	0	12	6	8	10	6	24	19	12	17	10
ENSMUSG00000046727	chr18	Cystm1	-0.323248	0.034845606	0.054774737	7.018762453	0.027566198	0	2238	1858	1917	2780	1996	1871	1973	1432	2051	2085
ENSMUSG00000047989	chr18	Ino80c	-0.3106213	0.034843393	0.054774737	5.052866733	0.023876962	0	573	510	523	652	473	419	485	418	521	561
ENSMUSG00000033191	chr4	Tie1	-0.3594685	0.034918273	0.054882792	5.447362368	0.033206304	0	662	758	702	966	578	874	470	603	506	681
ENSMUSG00000026200	chr1	Glb1l	0.52024515	0.034964419	0.054947964	1.531097172	0.045728743	0	39	36	30	34	29	65	58	44	54	45
ENSMUSG00000082241	chr16	Gm15776	-0.5674301	0.034967601	0.054947964	1.215796113	0.057986832	0	38	42	38	40	37	46	29	24	26	21
ENSMUSG00000026199	chr1	Ankzf1	0.47812292	0.035050103	0.055071415	2.617596413	0.049305019	0	91	78	65	83	57	110	87	136	94	141
ENSMUSG00000031969	chr9	Acad8	-0.3163289	0.035156435	0.055232277	5.345801396	0.025284683	0	667	716	651	803	518	579	572	588	629	567
ENSMUSG00000078762	chr7	Haus5	0.55991699	0.035161164	0.055233497	2.068077101	0.067767928	0	58	51	28	71	40	75	103	60	99	57
ENSMUSG00000026965	chr2	Anapc2	0.29487279	0.035172512	0.055245114	5.57208329	0.022066051	0	667	567	520	803	631	929	832	792	816	902

ENSMUSG00000018287	chr11	Spag7	0.3144255	0.035259671	0.055375791	6.529345997	0.025970363	0	1426	1149	1055	1415	1088	1598	1712	1507	1663	1858
ENSMUSG00000025229	chr19	Pitx3	0.50404248	0.035280767	0.055402697	2.710883593	0.058478028	0	58	55	64	135	90	114	103	141	108	145
ENSMUSG00000026037	chr1	Orc2	-0.3592518	0.035301223	0.055428591	3.863042492	0.030230325	0	243	231	247	269	214	196	234	147	250	205
ENSMUSG00000028601	chr4	Echdc2	-0.3943269	0.035329368	0.055466553	3.158589632	0.034623738	0	149	135	162	171	127	179	112	99	126	110
ENSMUSG00000037907	chr11	Ankrd13b	-0.376565	0.035337729	0.055473447	3.643403045	0.032836242	0	166	188	170	302	225	197	159	148	151	229
ENSMUSG00000038264	chr9	Sema7a	0.45833966	0.035420822	0.055597643	4.268621698	0.053145496	0	216	207	170	361	263	550	384	405	218	265
ENSMUSG00000058665	chr1	En1	0.6278257	0.035429989	0.055605785	2.544853634	0.092777991	0	41	44	78	89	81	111	83	170	70	126
ENSMUSG00000018583	chr11	G3bp1	-0.3189299	0.035443457	0.055620678	7.209019956	0.027073378	0	2553	2095	1987	3043	2583	2318	2317	1927	1866	2345
ENSMUSG00000061780	chr10	Cfd	1.37983099	0.035483314	0.055676973	6.262266041	0.485786621	0	86	1645	262	215	811	337	868	3077	932	3604
ENSMUSG00000025479	chr7	Cyp2e1	1.57362674	0.035550215	0.055775685	3.596211933	0.616211731	0	12	281	10	37	91	48	144	494	111	634
ENSMUSG00000009681	chr10	Bcr	0.47894393	0.035635098	0.055902586	2.872990746	0.052298215	0	82	79	77	134	81	231	139	109	89	127
ENSMUSG00000039804	chr2	Ncoa5	0.32810412	0.035649127	0.055918317	3.929913195	0.024794028	0	214	169	163	264	195	308	312	219	289	249
ENSMUSG00000013822	chr9	Elof1	0.31279582	0.035659215	0.055927864	4.832025278	0.024133892	0	449	374	318	419	324	551	568	418	557	473
ENSMUSG00000042165	chr3	Gm9774	0.39801852	0.035673976	0.055939448	2.772098517	0.032658493	0	98	85	71	95	81	149	110	121	124	118
ENSMUSG00000068264	chr2	Ap5s1	0.36611592	0.035674607	0.055939448	4.082277281	0.032174583	0	211	203	236	256	186	406	268	347	227	301
ENSMUSG00000096210	chr15	H1f0	0.35616714	0.035703053	0.055977773	7.266274959	0.033951067	0	2363	2130	1725	2208	1621	2588	2692	2802	2354	3649
ENSMUSG00000047370	chr7	Gm7367	-0.6982348	0.035730961	0.056015245	0.474424414	0.074612506	0	17	28	27	28	17	15	14	16	11	23
ENSMUSG00000100410	chr13	2310020H05Rik	0.71239075	0.035744799	0.056030653	1.410997318	0.108990224	0	19	42	23	37	22	66	29	77	44	38
ENSMUSG00000030323	chr6	Ift122	0.51925096	0.035749762	0.056032149	4.664746388	0.070016425	0	468	311	240	252	260	262	472	527	484	653
ENSMUSG00000032333	chr9	Stoml1	0.33693008	0.035766528	0.056052141	3.66428854	0.025390409	0	199	167	129	178	152	259	220	197	227	243
ENSMUSG00000001891	chr11	Ugp2	-0.4147863	0.035795221	0.056090818	8.83458184	0.046463555	0	6868	6755	6638	13319	6246	4694	7229	5594	7555	6635
ENSMUSG00000001349	chr9	Cnn1	-0.7876813	0.035819381	0.056116093	1.318696248	0.13943554	0	15	35	34	58	81	29	35	26	20	33
ENSMUSG00000028633	chr4	Ctps	0.35201663	0.035818034	0.056116093	4.435466072	0.030517876	0	277	216	226	383	315	458	498	337	354	330
ENSMUSG00000023919	chr17	Cenpq	-0.459429	0.035844394	0.056148986	2.012833547	0.039371183	0	62	72	55	86	64	60	53	49	59	48
ENSMUSG00000053477	chr18	Tcf4	-0.3279815	0.03587549	0.056191398	5.792393403	0.027967989	0	858	875	885	1258	748	813	706	904	681	885
ENSMUSG00000031530	chr8	Dusp4	-0.6480169	0.035883564	0.056197747	0.890910789	0.07285626	0	36	43	19	34	26	18	29	19	23	21
ENSMUSG00000030399	chr7	Ckm	-0.3604445	0.035950456	0.056296198	14.59038537	0.035313677	0	449196	341791	330245	499754	448387	316936	353804	301044	346870	444697
ENSMUSG00000102644	chr5	THAP6	0.51484246	0.035960143	0.056305059	1.750600351	0.050319002	0	45	40	38	44	31	52	59	58	57	84
ENSMUSG00000044018	chr4	Mrpl50	-0.3124736	0.036088973	0.056500447	5.649931235	0.025271274	0	879	851	807	907	678	735	732	645	785	746
ENSMUSG00000023259	chr9	Slc26a6	-0.4541024	0.036134354	0.056565158	3.078712593	0.04751368	0	132	128	139	191	131	75	102	116	148	126
ENSMUSG00000023072	chr7	Cep89	0.4244885	0.036187373	0.056641811	2.713475637	0.038229347	0	94	75	74	90	75	105	105	114	127	148
ENSMUSG00000003546	chr17	Klc4	0.32069762	0.03620604	0.056664683	4.492963958	0.024905254	0	320	268	297	326	267	508	337	375	358	461
ENSMUSG00000048040	chrX	Arxes2	0.95887386	0.036210698	0.056665627	0.096204882	0.167340451	0	7	11	11	11	7	13	16	24	6	42
ENSMUSG00000050737	chr2	Ptges	0.45504385	0.036285544	0.056776395	2.608771027	0.04446667	0	61	84	65	79	83	103	108	125	95	130
ENSMUSG00000066595	chr1	Mfsd7b	-0.5075393	0.036328321	0.056836965	3.470232137	0.063115583	0	156	300	142	224	138	104	192	134	166	138
ENSMUSG00000031314	chrX	Taf1	-0.3495455	0.036406732	0.056947211	4.005777513	0.029088338	0	246	268	229	381	222	237	273	163	254	221
ENSMUSG00000044674	chr5	Fzd1	0.48319677	0.036406936	0.056947211	3.010761404	0.05447655	0	98	102	94	119	80	261	167	90	111	141
ENSMUSG00000028964	chr4	Park7	0.33295206	0.03644651	0.057002734	8.871554463	0.030169649	0	7280	5726	5557	7027	5302	8145	8848	7328	9327	8891
ENSMUSG00000074649	chr2	BC029722	0.28896143	0.03647959	0.057048086	5.091415046	0.020884448	0	522	439	377	538	407	715	577	580	586	595
ENSMUSG00000097487	chr11	Ptges3l	0.36262858	0.036571041	0.057184702	6.539938304	0.035247048	0	1572	1179	1013	1218	1052	1449	1916	1796	1647	1669
ENSMUSG00000025872	chr13	Thoc3	0.32186078	0.036612318	0.057242841	4.096292242	0.024458166	0	219	210	203	299	200	365	364	287	271	257
ENSMUSG00000033768	chr19	Nrxn2	-0.7854833	0.036624954	0.057256193	0.255126659	0.102020246	0	14	18	25	18	25	16	19	10	5	15
ENSMUSG00000020658	chr12	Efr3b	-0.5927376	0.03664674	0.057283842	3.41215718	0.088580649	0	115	129	167	423	150	206	116	133	76	162
ENSMUSG00000007837	chr7	Prrg2	0.3513069	0.036729617	0.057406971	3.417779421	0.027356622	0	157	119	130	159	126	250	168	164	177	213
ENSMUSG00000004040	chr11	Stat3	0.38720073	0.036734239	0.057407774	6.510890247	0.040333806	0	1221	973	912	1688	1159	2670	1613	1556	1192	1500
ENSMUSG00000054021	chr13	Sirt5	0.42039589	0.036759997	0.057441606	3.330623986	0.042067429	0	117	109	126	196	94	157	166	234	176	185
ENSMUSG00000046519	chr3	Golph3l	-0.3691352	0.036871607	0.057609567	3.87655699	0.032832728	0	285	278	199	258	201	182	246	163	193	256
ENSMUSG00000025791	chr4	Pgm2	-0.4007411	0.036963227	0.057746262	10.18238389	0.044023733	0	21520	18227	16737	22385	19502	11419	16000	13997	17469	22507
ENSMUSG00000041731	chr19	Pgm5	0.58386433	0.036977844	0.057762641	4.492389922	0.089977424	0	227	297	309	332	171	439	277	784	249	405
ENSMUSG00000026918	chr2	Brd3	-0.3197194	0.03698223	0.057763036	5.275452424	0.026355007	0	610	555	580	815	643	620	508	624	440	610
ENSMUSG00000022860	chr16	Chodl	-0.3449587	0.037017606	0.05781183	3.748760972	0.027771309	0	278	201	203	254	177	217	236	158	166	186
ENSMUSG00000032415	chr9	Ube2cbp	-0.5322865	0.037032918	0.05782928	1.776374536	0.057086111	0	63	51	41	85	55	56	43	30	32	62
ENSMUSG00000040860	chr4	Crocc	0.51267514	0.037173124	0.058041736	1.782456424	0.051542107	0	45	32	40	48	38	59	59	47	81	71
ENSMUSG00000040146	chr9	Rgl3	0.8053268	0.037282527	0.058206054	0.366550965	0.11890508	0	11	20	8	17	7	26	26	33	9	26
ENSMUSG00000087221	chr15	BC037032	-0.7145841	0.037289113	0.058209834	0.247974726	0.06869888	0	18	24	18	17	21	13	17	12	10	14
ENSMUSG00000027358	chr2	Bmp2	-0.5736697	0.037298167	0.058217464	1.205883558	0.058816514	0	30	32	33	55	46	39	24	29	22	30
ENSMUSG00000033629	chr9	Ptplad1	0.32085034	0.037327716	0.058257081	4.140615231	0.024619151	0	206	221	209	319	213	398	345	296	288	266
ENSMUSG00000029402	chr5	Snrnp35	0.30564446	0.037581969	0.058643514	3.882013648	0.021172483	0	198	171	193	230	181	278	278	249	244	270
ENSMUSG00000097320	chr7	C630016N16Rik	0.72548501	0.037583712	0.058643514	1.201331505	0.109839239	0	23	34	22	25	17	26	31	50	36	76
ENSMUSG00000053110	chr9	Yap1	-0.3095168	0.037624671	0.058700871	6.061051467	0.025517689	0	1057	1060	932	1452	1029	1013	929	943	813	1168
ENSMUSG00000026172	chr1	Bcs1l	-0.3012879	0.03763619	0.058712289	4.184829249	0.021319369	0	303	295	254	386	257	293	260	269	251	247
ENSMUSG00000026155	chr1	Smap1	0.30114117	0.037650243	0.058727655	4.243359976	0.021627266	0	237	231	235	348	215	354	369	290	301	387
ENSMUSG00000103565	chr15	Sgsm3	-0.3482698	0.037728255	0.058842774	3.260764481	0.026509183	0	159	137	144	198	154	149	127	106	142	158
ENSMUSG00000040818	chr14	Dennd6a	-0.3237948	0.037777776	0.058913435	3.526288064	0.023376169	0	175	185	180	247	162	189	173	130	156	183
ENSMUSG00000004945	chr17	Tmem242	-0.3064713	0.037820437	0.058973383	5.987718831	0.025001669	0	1074	1038	1023	1262	831	947	952	798	1002	921

ENSMUSG00000000088	chr9	Cox5a	0.33775238	0.037845538	0.05900594	9.214592697	0.031543574	0	7361	7598	7262	10720	6492	13901	9815	11168	9704	9644
ENSMUSG00000026424	chr1	Gpr37l1	-0.667439	0.037878272	0.059050389	0.578225094	0.072413096	0	23	26	23	32	22	23	23	18	7	16
ENSMUSG00000051177	chr2	Plcb1	-0.5877535	0.037913624	0.059098908	1.792020293	0.071460882	0	46	65	43	110	43	33	43	45	51	44
ENSMUSG00000019039	chr9	Dalrd3	0.3946764	0.037932379	0.059121549	3.15281678	0.035215815	0	127	93	120	123	99	218	129	150	165	153
ENSMUSG00000003198	chr17	Zfp959	-0.5537388	0.03798653	0.059199347	1.488187908	0.059894649	0	41	32	60	55	49	33	39	30	31	45
ENSMUSG00000027510	chr2	Rbm38	-0.3592609	0.03801469	0.059236628	7.041664977	0.035335346	0	1817	1759	1930	3346	2307	2436	1712	1952	1621	1716
ENSMUSG00000060244	chr1	Alyref2	0.5232375	0.038027795	0.059250442	1.354900046	0.04715441	0	34	33	23	32	26	49	41	50	44	49
ENSMUSG00000026939	chr2	Tmem141	0.32736054	0.038058584	0.059291803	3.683735411	0.024314588	0	173	190	154	187	135	249	230	213	236	227
ENSMUSG00000039515	chr2	Ppp2r4	0.30796546	0.038128815	0.059394597	6.813248041	0.02580865	0	1505	1369	1293	1865	1467	2494	1860	1854	2050	1909
ENSMUSG00000022661	chr16	Cd200	-0.3743969	0.038235916	0.059553512	4.862673122	0.036710031	0	457	496	532	681	296	504	470	372	279	452
ENSMUSG00000022974	chr16	Paxbp1	0.3489779	0.038239354	0.059553512	3.424062115	0.027285695	0	137	145	133	139	135	198	213	156	197	207
ENSMUSG00000020472	chr11	Zkscan17	-0.3040315	0.038282153	0.059613523	4.440911488	0.022707038	0	367	354	298	435	329	379	271	304	264	366
ENSMUSG00000026421	chr1	Csrp1	0.3970889	0.038291981	0.059622184	5.683634924	0.042529455	0	494	588	630	923	680	1529	842	842	662	950
ENSMUSG00000028189	chr3	Ctbs	-0.4556901	0.038323876	0.059665199	2.48689309	0.044507701	0	110	84	90	117	74	69	103	56	80	70
ENSMUSG00000033565	chr15	Rbfox2	-0.354781	0.038333471	0.05967349	6.591421366	0.034359654	0	1563	1496	1382	2131	1531	1136	1304	1510	1142	1774
ENSMUSG00000003099	chr7	Ppp5c	-0.2933443	0.038341835	0.059679863	5.937288953	0.02291919	0	962	890	954	1272	953	934	931	789	923	910
ENSMUSG00000058076	chr1	Sdhc	-0.3240398	0.038384343	0.059739374	8.277156612	0.029082113	0	4661	4967	4885	7345	4112	4630	4276	4514	4272	4746
ENSMUSG00000032252	chr9	Glce	-0.3326651	0.038513161	0.059933185	3.620350972	0.02550466	0	193	196	186	220	211	198	194	166	136	189
ENSMUSG00000042670	chr2	Immp1l	-0.3189542	0.038565488	0.060007934	5.271573896	0.026702176	0	723	596	550	798	536	677	562	423	649	496
ENSMUSG00000022472	chr15	Desi1	0.32112536	0.038597452	0.060050984	4.166717831	0.025162735	0	218	211	203	335	225	399	354	316	273	280
ENSMUSG00000040520	chr4	Manea	-0.4448069	0.038608784	0.060061929	2.513670147	0.043533833	0	118	86	98	96	80	104	88	64	58	76
ENSMUSG00000068735	chr2	Trp53i11	-0.4608539	0.038755174	0.060282951	4.423668013	0.056053544	0	300	354	433	568	214	401	322	333	181	236
ENSMUSG00000031425	chrX	Plp1	-0.4924227	0.038835454	0.060401102	2.474878606	0.0557434	0	73	76	99	114	110	117	75	59	52	71
ENSMUSG00000070605	chr4	Gm13251	-0.8422613	0.038918033	0.060522803	1.818403824	0.175155346	0	95	53	54	73	52	108	35	12	28	24
ENSMUSG00000027184	chr2	Caprin1	-0.337808	0.038945189	0.060558296	6.464964698	0.031258015	0	1464	1299	1237	1980	1415	1144	1543	952	1234	1507
ENSMUSG00000026388	chr1	3110009E18Rik	-0.6555842	0.038957862	0.060571262	0.737330259	0.07423097	0	32	34	26	30	19	34	17	14	18	16
ENSMUSG00000037325	chr3	Bbs7	-0.4490367	0.038963812	0.060573775	2.701329391	0.04531399	0	91	97	89	155	121	76	102	73	107	81
ENSMUSG00000040385	chr19	Ppp1ca	0.29991669	0.038996751	0.06061824	7.780582406	0.024969522	0	3168	2823	2684	3462	2554	4272	3975	3723	3756	4079
ENSMUSG00000066643	chr12	Wdr35	-0.3909963	0.039013903	0.060638157	3.40482376	0.036149316	0	194	185	166	176	158	110	157	160	143	164
ENSMUSG00000009487	chr7	Otog	1.12251481	0.039019261	0.060639741	0.253714459	0.271399631	0	15	8	13	7	6	28	20	54	4	11
ENSMUSG00000074466	chr3	Gm15417	0.34299901	0.039042638	0.060669325	4.219051918	0.029394289	0	317	241	189	274	197	350	377	259	371	334
ENSMUSG00000043259	chr10	Fam13c	-0.4034104	0.039052362	0.060677689	2.597595368	0.033961216	0	98	105	101	117	82	77	84	82	80	93
ENSMUSG00000042870	chr8	Tom1	-0.3005783	0.039082972	0.060718499	4.764341096	0.022920276	0	471	450	364	527	416	397	360	339	414	470
ENSMUSG00000025602	chr9	Zfp202	-0.5136409	0.039106336	0.060748044	1.628977805	0.051206616	0	72	45	38	62	45	39	43	31	44	43
ENSMUSG00000028901	chr4	Gmeb1	-0.3295663	0.039139438	0.060792708	3.458888523	0.024508936	0	190	170	156	242	152	190	157	129	137	179
ENSMUSG00000098557	chr14	Kctd12	0.39607194	0.039158737	0.060815924	4.810801422	0.041672871	0	373	320	348	512	266	447	649	362	396	757
ENSMUSG00000036570	chr7	Fxyd1	0.31692779	0.039180533	0.060843014	8.259025507	0.028045859	0	4099	3810	3526	4803	4070	6723	5014	5405	5428	5185
ENSMUSG00000042211	chr18	Fbxo38	-0.3075619	0.039284977	0.060998427	4.5625686	0.023847827	0	409	340	343	510	349	392	342	243	344	406
ENSMUSG00000062995	chr6	Ica1	0.58337116	0.039325624	0.061054757	1.187360038	0.06347974	0	27	13	26	44	20	47	39	41	41	42
ENSMUSG00000041975	chr2	Mettl8	0.38569677	0.039459464	0.061255745	2.614515774	0.02980069	0	77	74	71	92	73	115	109	102	110	118
ENSMUSG00000051444	chr3	Bbs12	0.72181513	0.039493519	0.061301802	0.239318707	0.082826538	0	10	13	14	16	6	25	26	12	26	18
ENSMUSG00000026097	chr1	Ormdl1	-0.4168936	0.039514901	0.06132818	3.20697218	0.041630371	0	170	137	145	170	152	107	175	83	132	142
ENSMUSG00000103970	chr9	RP23-250G8.14	-0.6359729	0.039528931	0.061343142	1.459419406	0.086359205	0	52	48	55	51	32	18	51	24	32	43
ENSMUSG00000052609	chr12	Plekhg3	0.34506814	0.039583882	0.061414779	3.51398896	0.027545714	0	132	131	143	183	152	273	182	185	177	221
ENSMUSG00000101304	chr9	Plet1os	-0.3874596	0.039581083	0.061414779	3.612754139	0.03684848	0	216	226	161	241	181	200	179	97	203	184
ENSMUSG00000029191	chr5	Rfc1	-0.3040985	0.039589541	0.061416742	4.562883752	0.023230832	0	365	403	334	468	367	345	342	309	393	324
ENSMUSG00000058587	chr9	Tmod3	-0.3370162	0.039634721	0.061480007	4.486437135	0.029016411	0	300	352	334	592	308	358	371	236	325	327
ENSMUSG00000031028	chr7	Tub	-0.7246122	0.039682194	0.061546814	0.361751584	0.081267564	0	25	14	16	36	19	13	16	14	19	9
ENSMUSG00000080746	chr4	Rpsa-ps12	0.60035794	0.039688967	0.061550488	0.703231441	0.05486088	0	19	12	16	25	17	39	29	23	28	29
ENSMUSG00000022297	chr15	Fzd6	-0.4357054	0.039704557	0.061567834	2.685993575	0.042530932	0	102	109	118	142	73	94	78	89	68	110
ENSMUSG00000087574	chr11	C030037D09Rik	-0.6025791	0.039711193	0.061571292	1.954169857	0.082364756	0	74	63	50	79	72	23	41	62	49	65
ENSMUSG00000031231	chrX	Cox7b	-0.3560027	0.039724987	0.061585848	8.466237814	0.035639732	0	5926	6138	5895	7560	4216	4903	4834	4095	6262	5155
ENSMUSG00000023064	chr14	Sncg	0.68626014	0.039749879	0.061617603	2.750795379	0.120259556	0	38	103	55	90	88	271	91	109	65	144
ENSMUSG00000021597	chr13	Ankrd32	-0.5198246	0.039778149	0.061654586	2.393792833	0.062074931	0	102	84	88	116	64	42	93	52	67	90
ENSMUSG00000070394	chr11	Tmem256	0.43107574	0.039783419	0.061655917	5.640440062	0.051012497	0	704	732	595	609	492	1526	844	737	989	615
ENSMUSG00000041040	chr1	Fam117b	0.41342293	0.039866395	0.061777662	3.243085903	0.040620871	0	105	102	108	164	121	275	181	126	132	170
ENSMUSG00000020283	chr11	Pex13	-0.30477	0.039880623	0.061786178	4.360621047	0.022998693	0	339	382	300	398	265	305	291	271	314	309
ENSMUSG00000024799	chr19	Tm7sf2	0.38198197	0.039880732	0.061786178	3.415547338	0.034831782	0	128	146	130	155	121	294	191	180	154	163
ENSMUSG00000028458	chr4	Tesk1	-0.3165478	0.039947533	0.061882811	5.616601192	0.027003344	0	736	694	662	1123	861	666	733	636	733	785
ENSMUSG00000057982	chr9	Zfp809	-0.5982842	0.040023948	0.061994315	1.618706715	0.07719524	0	49	50	48	69	50	74	42	27	27	25
ENSMUSG00000094936	chr19	Rbm4	0.33821255	0.040059659	0.062042752	3.527639904	0.026456611	0	160	128	153	181	129	244	193	213	206	182
ENSMUSG00000014867	chr2	Surf4	0.30115618	0.040115989	0.06212311	7.398828652	0.025373497	0	2286	2156	1877	2789	2181	3492	3346	2562	2935	2918
ENSMUSG00000072915	chr11	Gm12258	-0.6884169	0.040122281	0.06212597	0.588111915	0.083730514	0	34	33	21	18	20	26	15	16	14	16
ENSMUSG00000026888	chr2	Grb14	-0.5061702	0.040248518	0.062314532	4.159507293	0.068433952	0	189	321	378	502	186	227	149	249	277	287
ENSMUSG00000063800	chr4	Prpf38a	0.32837909	0.040265759	0.062334321	3.843127788	0.025787784	0	184	181	171	215	186	306	284	245	254	204

ENSMUSG00000044320	chr2	1700001O22Rik	-0.9711745	0.040280177	0.062349735	-0.102920569	0.180140931	0	18	16	21	17	8	21	6	11	6	1
ENSMUSG00000097318	chr16	1700007L15Rik	0.83274294	0.040290626	0.062359002	0.014518424	0.113607666	0	12	13	8	10	4	15	9	22	25	20
ENSMUSG00000029836	chr6	Cbx3	-0.3734862	0.040351547	0.062446376	4.025453938	0.035329027	0	295	250	247	347	228	158	275	198	237	277
ENSMUSG00000042726	chr5	Trafd1	0.31943948	0.040375116	0.062475932	5.597830887	0.027606465	0	617	652	539	765	629	1164	783	739	697	1037
ENSMUSG00000089788	chr1	Gm16586	0.47308966	0.040452492	0.062588733	3.150598965	0.055441108	0	123	117	86	116	102	261	148	116	201	111
ENSMUSG00000027204	chr2	Fbn1	-0.3802825	0.04047199	0.06261197	7.478303627	0.040795712	0	2352	2532	2824	4220	3179	3455	2545	2729	1782	2192
ENSMUSG00000022892	chr16	App	-0.3159941	0.040491043	0.062634512	7.253722509	0.028049681	0	2483	2284	2391	3099	2360	2293	2563	1750	1883	2667
ENSMUSG00000051977	chr17	Prdm9	-0.6028548	0.040589815	0.062780351	1.33172089	0.073408956	0	42	44	45	43	40	27	35	14	40	40
ENSMUSG00000029122	chr5	Evc	-0.4647636	0.040596286	0.062781252	3.969744752	0.056975442	0	143	274	366	337	217	217	183	247	195	219
ENSMUSG00000031608	chr8	Galnt7	-0.5261535	0.040599382	0.062781252	2.924777333	0.070307523	0	139	100	106	189	131	126	134	37	87	125
ENSMUSG00000032744	chr4	Heyl	-0.5419403	0.040666182	0.062877593	4.210169943	0.079316739	0	310	266	338	474	256	163	257	404	123	255
ENSMUSG00000006392	chr4	Med8	0.29337583	0.040725906	0.062962972	4.748127295	0.022139439	0	378	358	323	458	284	538	554	422	469	426
ENSMUSG00000097059	chr13	Fam120aos	-0.521077	0.04073222	0.062965767	1.849854853	0.057429225	0	61	54	72	77	43	57	47	27	43	62
ENSMUSG00000062713	chr16	Sim2	-0.6430032	0.040850579	0.063141749	3.54333024	0.111011304	0	143	89	179	525	171	183	108	95	179	174
ENSMUSG00000062515	chr3	Fabp4	0.4020209	0.040904554	0.063218185	7.856819648	0.045880885	0	2301	4223	2789	3148	2302	4097	3728	4075	4285	5302
ENSMUSG00000031824	chr8	6430548M08Rik	0.35020282	0.04092973	0.0632501	4.607191981	0.032466108	0	326	206	269	503	312	504	529	368	398	430
ENSMUSG00000044330	chr3	Gm9790	0.40545334	0.041014245	0.063373697	2.944861782	0.037644786	0	97	96	94	115	83	110	152	130	169	138
ENSMUSG00000020921	chr11	Tmem101	0.31019852	0.041046731	0.063416881	4.200812178	0.023943254	0	268	235	229	282	201	330	306	358	323	325
ENSMUSG00000020790	chr11	Ankfy1	0.31944951	0.041105576	0.063493758	4.751940297	0.026647767	0	325	305	358	446	345	672	525	365	452	440
ENSMUSG00000061080	chr16	Lsamp	-0.8861824	0.041105237	0.063493758	0.770052375	0.173282066	0	32	29	26	26	39	2	23	23	13	29
ENSMUSG00000024962	chr19	Vegfb	-0.3823361	0.041116756	0.063504009	6.364018265	0.041027764	0	1011	1300	1254	2286	1214	1545	957	1271	996	1070
ENSMUSG00000079428	chrX	Tceal7	-0.5080106	0.041133002	0.063522081	6.458075485	0.072878128	0	2372	1185	1348	1453	1293	825	1677	1400	706	1275
ENSMUSG00000030088	chr6	Aldh1l1	-0.4730242	0.041254312	0.063702383	2.90254836	0.055176658	0	94	160	117	130	130	79	91	98	88	146
ENSMUSG00000024413	chr18	Npc1	0.34242987	0.041371619	0.063876463	5.040264948	0.031646698	0	341	406	402	608	412	623	686	380	668	650
ENSMUSG00000022386	chr15	Trmu	0.35137777	0.04142659	0.063953528	3.364934815	0.029224577	0	117	130	135	182	106	197	157	195	188	191
ENSMUSG00000031878	chr8	Nae1	-0.3281281	0.041430684	0.063953528	4.622105166	0.028186884	0	494	369	363	488	327	327	387	270	410	379
ENSMUSG00000037720	chr5	Tmem33	-0.2967198	0.041522025	0.064087445	4.559365947	0.022563684	0	372	377	347	470	363	339	405	266	332	382
ENSMUSG00000037820	chr2	Tgm2	0.30431833	0.04154829	0.064120903	6.651389238	0.025999761	0	1327	1222	1125	1580	1432	2216	1822	1546	1725	1791
ENSMUSG00000044150	chrX	A830080D01Rik	-0.7205621	0.041596176	0.064180631	0.790294892	0.102060264	0	27	22	30	51	22	10	27	14	16	32
ENSMUSG00000044857	chr17	Lemd2	0.31826818	0.041594798	0.064180631	5.205649521	0.027372256	0	480	460	420	652	444	968	585	582	640	581
ENSMUSG00000036381	chr3	P2ry14	-0.5867222	0.041650583	0.064252941	0.993784167	0.062384834	0	31	39	39	31	26	28	18	25	25	26
ENSMUSG00000087644	chrX	Gm14703	-0.6743805	0.041652235	0.064252941	0.398975627	0.071733275	0	21	22	22	33	13	12	13	12	18	20
ENSMUSG00000029775	chr6	Klhdc10	-0.3081823	0.041681735	0.064284256	5.993283593	0.026340129	0	1023	988	941	1309	993	871	907	911	801	1144
ENSMUSG00000051255	chr19	Gm6563	0.39452188	0.041677319	0.064284256	2.942033037	0.035816864	0	114	85	98	128	65	147	160	129	141	123
ENSMUSG00000033208	chr10	S100b	-0.5433561	0.041696359	0.064299636	1.727599611	0.065505667	0	46	56	57	50	69	61	49	28	31	46
ENSMUSG00000086040	chr6	Wipf3	-0.3835693	0.041700909	0.064299636	3.81959929	0.037263438	0	215	177	238	362	205	146	225	184	202	230
ENSMUSG00000035285	chr7	Nat14	0.66279101	0.041756696	0.064378554	1.166718499	0.0948807	0	22	17	20	44	21	81	33	36	32	32
ENSMUSG00000040532	chr5	Abhd11	0.29651119	0.041775981	0.064401182	5.549107446	0.023982496	0	525	629	605	832	546	911	823	831	811	821
ENSMUSG00000029761	chr6	Cald1	-0.3178516	0.041959344	0.064676717	5.390126508	0.027597226	0	640	563	633	1019	644	737	638	605	459	613
ENSMUSG00000045282	chr7	Tmem86b	0.73234989	0.041989782	0.064716497	0.516058716	0.095050015	0	21	14	13	12	12	38	19	34	25	16
ENSMUSG00000048772	chr4	Tmem53	0.77364219	0.042014042	0.064746747	1.55574458	0.144726588	0	43	32	19	47	16	126	31	59	39	38
ENSMUSG00000030254	chr6	Rad18	0.75831907	0.042131107	0.064919995	0.72159258	0.11173624	0	15	17	22	11	17	27	57	23	27	22
ENSMUSG00000023980	chr17	Taf8	-0.3300692	0.042346524	0.065244739	3.83581184	0.026797193	0	212	254	194	323	202	246	165	188	199	229
ENSMUSG00000037085	chr15	Trmt12	0.41442548	0.042369873	0.065273517	2.954609681	0.040503932	0	134	90	82	96	83	128	158	146	120	157
ENSMUSG00000034349	chr3	Smc4	0.39188869	0.042383177	0.065279621	4.014859512	0.040125363	0	247	205	193	205	177	251	439	237	290	268
ENSMUSG00000097101	chr13	1810034E14Rik	0.798547	0.042383122	0.065279621	0.041551257	0.101083593	0	12	6	17	7	6	15	21	15	20	22
ENSMUSG00000045757	chr7	Zfp764	-0.5152295	0.042543504	0.06551934	1.541577653	0.052441921	0	53	35	40	74	46	54	39	31	30	35
ENSMUSG00000024732	chr19	Ccdc86	0.33508066	0.042589166	0.065576628	4.592140475	0.029873053	0	368	290	287	354	280	370	438	511	370	480
ENSMUSG00000037692	chr4	Ahdc1	-0.4122985	0.042590086	0.065576628	5.02558729	0.047155626	0	448	369	448	961	597	433	423	507	332	574
ENSMUSG00000026817	chr2	Ak1	-0.3417162	0.042611031	0.065594423	11.1293968	0.033951745	0	42010	37543	34017	39210	32935	27303	32992	30923	30447	39124
ENSMUSG00000044709	chr7	Gemin7	0.29681959	0.042606459	0.065594423	5.34392726	0.023996882	0	662	477	466	623	483	737	766	637	748	755
ENSMUSG00000039202	chr7	Abhd2	0.4050189	0.042695703	0.065717526	3.539702337	0.041500829	0	124	138	119	201	159	218	293	218	135	208
ENSMUSG00000035011	chr10	Zbtb7a	-0.308843	0.042885507	0.066002405	5.116404093	0.025976895	0	551	519	559	723	507	613	480	442	367	640
ENSMUSG00000039680	chr16	Mrps6	0.34570207	0.04289108	0.066003715	3.835290571	0.03002591	0	184	194	163	231	159	341	304	245	209	200
ENSMUSG00000080316	chr17	Spaca6	0.62352987	0.042978127	0.066130387	1.576095131	0.086948238	0	42	45	24	31	24	100	41	47	53	44
ENSMUSG00000001227	chr17	Sema6b	0.48004326	0.043039635	0.066217739	2.885533813	0.056599115	0	102	105	63	86	92	219	119	104	96	163
ENSMUSG00000031209	chrX	Heph	-0.5720359	0.043073412	0.066262411	1.206080378	0.064089739	0	29	47	29	48	42	40	35	21	20	29
ENSMUSG00000023010	chr15	Tmbim6	0.30843288	0.043145304	0.066351096	7.927364008	0.027562673	0	3333	3077	2663	3927	3223	5638	4586	3774	3805	4330
ENSMUSG00000027966	chr3	Col11a1	-0.5842598	0.043139196	0.066351096	4.645973002	0.096616994	0	708	364	395	450	312	654	344	136	202	347
ENSMUSG00000064360	chrMT	mt-Nd3	-0.7793634	0.043145244	0.066351096	0.408059113	0.110564407	0	18	29	16	40	13	7	21	12	12	20
ENSMUSG00000026578	chr1	Ccdc181	0.36712981	0.04318932	0.066411479	2.911434259	0.030380754	0	116	88	75	126	80	160	129	120	131	142
ENSMUSG00000042804	chr4	Gpr153	0.34067184	0.043265689	0.066521593	4.14227131	0.029904728	0	206	195	250	266	230	376	349	319	220	342
ENSMUSG00000033031	chr16	C330027C09Rik	0.74628851	0.043337481	0.066624643	1.317220668	0.129855459	0	37	26	26	22	19	23	85	31	60	41
ENSMUSG00000022551	chr15	Cyc1	-0.3338178	0.043503427	0.066872404	9.169347373	0.032593106	0	8554	9604	10258	12700	6981	8649	7588	8142	8256	8865
ENSMUSG00000036334	chr3	Igsf10	-0.3248503	0.043512844	0.066879524	4.240732045	0.02759978	0	320	267	295	357	314	331	276	237	191	338

ENSMUSG00000085396	chrX	Firre	-0.6809956	0.04352081	0.066884412	1.173155905	0.104062418	0	34	40	47	42	32	45	10	19	35	26
ENSMUSG00000069379	chr18	Gm4950	0.68981932	0.043531728	0.066893835	0.56496498	0.081333303	0	23	13	16	12	12	39	23	30	24	20
ENSMUSG00000011179	chr12	Odc1	0.39225759	0.043715397	0.067168688	6.441452493	0.044398925	0	1254	1121	998	1146	1039	1139	2113	1585	1802	1321
ENSMUSG00000030166	chr6	Rad52	-0.3705225	0.043757087	0.067225355	2.964393392	0.031620747	0	141	120	104	172	114	138	86	101	106	118
ENSMUSG00000031521	chr8	Aga	-0.3339475	0.043798279	0.067281243	3.887792994	0.028563579	0	272	257	239	242	202	279	234	162	184	211
ENSMUSG00000025782	chr2	Taf3	-0.3538261	0.043807317	0.067287731	3.066775419	0.028748133	0	139	127	121	175	131	127	122	111	90	144
ENSMUSG00000078502	chr4	Gm13212	-0.733407	0.0438405	0.0673313	0.891739319	0.123194316	0	47	33	29	30	22	46	18	8	17	20
ENSMUSG00000024812	chr19	Tjp2	0.39127155	0.043854572	0.067345511	3.141395642	0.037412204	0	117	97	112	154	85	135	209	149	131	181
ENSMUSG00000028409	chr4	Smu1	0.28451259	0.04389575	0.067401341	5.594922155	0.022510629	0	672	643	559	831	552	941	905	767	907	802
ENSMUSG00000033356	chr15	Pus7l	0.5488043	0.043909332	0.067414789	1.445129447	0.059019374	0	35	31	26	33	31	65	64	31	53	40
ENSMUSG00000060149	chr17	BC002059	-0.6065785	0.043933723	0.067444828	1.493764121	0.081250362	0	55	54	47	60	28	42	41	19	49	24
ENSMUSG00000049439	chr1	Cyp20a1	0.40305746	0.04402245	0.067573615	3.14001921	0.039620786	0	103	117	119	125	91	166	228	114	154	149
ENSMUSG00000052921	chr11	Arhgef15	-0.3789226	0.044028493	0.067575469	3.918877163	0.03762542	0	206	233	205	431	217	279	156	203	191	241
ENSMUSG00000015363	chr15	Trabd	0.30680677	0.044043861	0.067589472	5.263547084	0.026044717	0	481	470	458	687	471	886	681	568	759	575
ENSMUSG00000044573	chr12	Acp1	0.62670894	0.044047289	0.067589472	4.437876454	0.111589564	0	274	258	210	291	229	101	584	403	493	520
ENSMUSG00000021114	chr12	Atp6v1d	0.29216516	0.044057473	0.067597678	6.159731891	0.024276917	0	1039	979	840	1176	767	1356	1400	1111	1257	1299
ENSMUSG00000021428	chr13	Riok1	0.36781101	0.044087473	0.067636282	3.089458324	0.031492519	0	125	107	98	114	99	182	161	119	171	140
ENSMUSG00000003992	chr13	Ssbp2	-0.3332867	0.044141423	0.067711615	3.706508542	0.027706995	0	249	196	181	238	209	199	156	159	191	231
ENSMUSG00000057342	chr7	Sphk2	0.35305206	0.044316077	0.067972069	4.309817887	0.033442803	0	237	201	199	370	294	489	295	321	307	406
ENSMUSG00000028443	chr4	Nudt2	-0.2963108	0.044371482	0.068049581	3.793668668	0.021171926	0	243	231	196	271	191	237	209	179	183	203
ENSMUSG00000032840	chr5	2410131K14Rik	-0.342471	0.044389127	0.068069173	3.678138436	0.029031195	0	165	197	234	276	186	173	184	173	192	188
ENSMUSG00000039648	chr2	Ccbl1	-0.3174206	0.044452946	0.068159558	3.995684284	0.02536257	0	232	259	245	359	223	217	221	243	232	232
ENSMUSG00000020547	chr12	Bzw2	-0.3175855	0.044476037	0.068187483	6.9864724	0.029352434	0	2485	2027	1850	2401	1725	1680	1852	1579	1992	2087
ENSMUSG00000034329	chr11	Brip1	0.8917685	0.044518182	0.068244609	0.017840702	0.151588357	0	12	15	7	4	7	10	32	15	23	13
ENSMUSG00000003604	chr2	Aven	0.31731754	0.044565379	0.068309469	4.310216578	0.026453426	0	295	231	198	313	273	331	347	331	340	434
ENSMUSG00000024947	chr19	Men1	0.33147679	0.044669136	0.068460998	3.377881981	0.025694395	0	152	135	121	153	116	218	214	172	156	177
ENSMUSG00000067818	chr2	Myl9	0.38371219	0.044747788	0.068574023	6.636970836	0.042971917	0	1728	1129	911	1263	1363	1918	1914	1996	1286	2076
ENSMUSG00000034656	chr8	Cacna1a	-0.6948602	0.044777247	0.068611644	2.160333555	0.125236338	0	49	92	78	109	74	131	31	35	38	44
ENSMUSG00000022982	chr16	Sod1	0.29385049	0.044868717	0.068744265	7.098650327	0.025198905	0	2001	1846	1581	2138	1609	2961	2458	2170	2421	2341
ENSMUSG00000002768	chr17	Mea1	0.28451758	0.044887639	0.068765718	4.839877912	0.021773678	0	399	372	327	496	333	655	488	478	491	452
ENSMUSG00000078349	chr4	AW011738	-0.6626932	0.044934263	0.068829599	0.570747869	0.072217631	0	29	18	14	42	24	19	15	18	15	19
ENSMUSG00000022951	chr16	Rcan1	0.44429993	0.044943279	0.068835865	6.357467151	0.057778874	0	875	986	1023	1675	710	2091	1846	1474	1497	816
ENSMUSG00000060708	chr5	Bloc1s4	0.38536459	0.044986477	0.068894477	2.877573158	0.034540028	0	94	78	94	129	75	185	136	112	113	127
ENSMUSG00000024538	chr18	Ppic	0.34768757	0.045061783	0.069002244	5.686803268	0.034609888	0	828	722	621	614	553	906	952	965	744	1127
ENSMUSG00000098808	chr3	Mir7009	0.88022051	0.04511439	0.069075231	-0.230881756	0.11518731	0	4	4	11	6	12	10	18	17	13	18
ENSMUSG00000071256	chr17	Zfp213	0.56649115	0.04512686	0.069086756	2.022828823	0.077098	0	36	45	55	60	40	40	88	70	97	84
ENSMUSG00000002274	chr17	Metrn	-0.3268097	0.045215217	0.069214445	4.856039558	0.029532313	0	507	522	475	485	386	347	429	405	387	514
ENSMUSG00000002820	chr9	Atg4d	-0.3199563	0.045228959	0.069227898	5.506433448	0.029047763	0	594	616	701	1046	814	755	638	606	675	620
ENSMUSG00000015647	chr2	Lama5	-0.362453	0.045242184	0.069240557	4.473084106	0.035990112	0	352	305	312	478	410	257	291	361	253	407
ENSMUSG00000031822	chr8	Gse1	-0.3616071	0.045410525	0.069490584	5.146008004	0.03711493	0	560	411	486	915	630	648	494	507	342	547
ENSMUSG00000026770	chr2	Il2ra	-0.7079421	0.045420096	0.06949762	0.33594954	0.086161776	0	26	21	17	19	22	11	15	11	9	25
ENSMUSG00000019969	chr12	Psen1	0.30284791	0.045479061	0.069580224	5.077957109	0.025386552	0	422	448	360	581	444	776	684	480	461	665
ENSMUSG00000026930	chr2	Gpsm1	0.39577995	0.045490281	0.069589773	2.691560293	0.035756621	0	91	82	72	92	70	159	115	99	117	100
ENSMUSG00000032308	chr9	Ulk3	0.4120861	0.045533717	0.069648597	2.560757552	0.039183846	0	63	79	64	110	57	116	89	107	109	116
ENSMUSG00000002064	chr11	Sdf2	0.31295277	0.045661154	0.069828241	5.880124397	0.028143068	0	955	785	691	755	692	1190	998	913	1129	1092
ENSMUSG00000071151	chr10	Gm4799	0.686123	0.045658146	0.069828241	0.820898128	0.094004234	0	21	11	18	28	16	59	32	30	26	19
ENSMUSG00000076275	chr7	Mir675	-0.5390366	0.045675447	0.069842456	8.811051914	0.086355836	0	8466	6984	6809	11188	6680	3341	4106	5335	5115	11917
ENSMUSG00000037999	chr5	Arap2	-0.6093088	0.04569028	0.069857494	1.244199564	0.079253605	0	38	39	35	61	32	38	49	17	19	24
ENSMUSG00000023764	chr11	Sfi1	-0.994271	0.045884002	0.070146009	4.770262841	0.285819082	0	512	519	444	639	578	1118	91	107	142	120
ENSMUSG00000037341	chrX	Slc9a7	-0.6218762	0.045910842	0.070179364	1.564955566	0.088014326	0	51	29	50	75	54	18	37	36	38	52
ENSMUSG00000004508	chr7	Gab2	0.32731738	0.045929609	0.070200373	3.670018508	0.026938433	0	146	168	146	231	148	276	211	203	182	280
ENSMUSG00000005813	chr3	Metap1	-0.3072093	0.045947565	0.070220139	5.959397195	0.027285829	0	1126	966	931	1108	967	808	944	788	907	1080
ENSMUSG00000030528	chr7	Blm	0.57196477	0.046035774	0.070347254	1.315730458	0.065082844	0	34	32	23	25	26	39	68	39	41	43
ENSMUSG00000031728	chr8	Zfp821	0.40655101	0.046053306	0.07036635	2.593155542	0.038149377	0	95	68	61	97	60	143	100	107	100	101
ENSMUSG00000026927	chr2	Sdccag3	0.31235505	0.046068337	0.070381621	4.64229043	0.026536558	0	334	307	316	396	299	623	451	357	463	368
ENSMUSG00000029125	chr5	Stx18	0.29317595	0.046149567	0.070498015	3.779186967	0.020917021	0	178	172	165	229	169	267	246	209	255	247
ENSMUSG00000066233	chr9	Tmem42	-0.3786919	0.046154879	0.070498425	2.993441623	0.034270168	0	130	132	126	167	108	87	124	102	122	119
ENSMUSG00000028576	chr4	Ift74	0.44227614	0.046243012	0.070625323	2.374004181	0.045374501	0	74	58	54	82	53	93	99	73	124	85
ENSMUSG00000026201	chr1	Stk16	0.2912993	0.046268404	0.070656383	4.379205843	0.022208554	0	312	267	268	294	239	421	375	374	333	355
ENSMUSG00000030103	chr6	Bhlhe40	-0.3589975	0.04629371	0.070687303	6.792968308	0.038229412	0	1882	2070	1782	2153	1389	2229	1670	1425	1003	1692
ENSMUSG00000028464	chr4	Tpm2	0.36762221	0.046330554	0.070735833	12.95366615	0.040692338	0	91581	98772	91832	143722	94633	113966	136000	161564	123874	189556
ENSMUSG00000021143	chr12	Pacs2	-0.2930968	0.046385473	0.070811947	6.041415554	0.024890689	0	996	933	979	1477	1047	1028	932	905	861	1105
ENSMUSG00000090698	chr6	Apold1	-0.7263514	0.046407601	0.07083799	2.788725243	0.147378437	0	107	177	181	78	71	163	106	57	34	70
ENSMUSG00000036964	chr11	Trim17	0.34406478	0.046454571	0.070901943	3.377365736	0.028841058	0	149	125	129	166	107	173	214	182	151	217
ENSMUSG00000026766	chr2	Mmadhc	-0.2978851	0.046479284	0.070931914	6.825295302	0.0261959	0	1840	1771	1766	2434	1552	1606	1682	1407	1758	1839

ENSMUSG00000049807	chr11	Arhgap23	0.36334475	0.046520474	0.070979273	4.111598215	0.035940618	0	207	195	178	316	232	450	244	342	246	301
ENSMUSG00000096401	chr8	Gm21811	-0.6774382	0.046520252	0.070979273	0.234648179	0.068981459	0	20	13	22	24	18	15	11	17	11	12
ENSMUSG00000027694	chr3	Gm8325	-0.676757	0.046606463	0.07110271	0.401884889	0.075502657	0	22	18	21	19	29	11	17	17	15	15
ENSMUSG00000059327	chrX	Eda	-0.4558532	0.046640763	0.071147272	2.859996623	0.052636824	0	115	135	101	123	136	62	108	101	95	122
ENSMUSG00000017210	chr11	Med24	-0.2955915	0.046707113	0.071240708	5.60867278	0.025047637	0	754	661	663	1087	858	788	696	670	647	773
ENSMUSG00000026556	chr1	Vangl2	0.56344592	0.046715642	0.071245941	1.574171969	0.06928444	0	34	31	30	41	35	37	60	70	38	70
ENSMUSG00000025931	chr1	Paqr8	0.61342465	0.046728696	0.071258075	0.956670077	0.076537695	0	17	24	20	24	21	43	41	43	32	19
ENSMUSG00000039345	chr16	Mettl22	-0.2976977	0.046753416	0.071287993	6.229703428	0.025935729	0	1207	1074	1123	1508	1248	1216	1134	964	1190	983
ENSMUSG00000019988	chr10	Nedd1	-0.4281297	0.046773674	0.071311101	3.568073757	0.049353213	0	169	184	194	261	198	108	188	116	225	175
ENSMUSG00000071637	chr16	Cebpd	0.77488715	0.046781409	0.071315115	3.569310589	0.171815944	0	144	127	118	142	111	704	191	71	164	136
ENSMUSG00000040124	chr1	Gorab	-0.5074771	0.046819273	0.071365052	1.615721427	0.056334032	0	52	49	51	67	40	53	41	21	48	37
ENSMUSG00000057421	chrX	Las1l	-0.27474	0.046879033	0.071448349	5.15542337	0.020958778	0	559	539	500	768	549	531	566	458	540	529
ENSMUSG00000020652	chr12	Cenpo	0.53111545	0.046887097	0.071452847	1.376332506	0.054383225	0	30	28	32	25	33	62	53	37	45	42
ENSMUSG00000089764	chr17	Gm16580	0.67038962	0.046953958	0.071546939	0.547211699	0.085126892	0	16	14	8	23	16	27	26	13	30	38
ENSMUSG00000027882	chr3	Stxbp3a	-0.266463	0.04698333	0.071583889	4.972079264	0.01944656	0	532	497	423	614	483	527	458	402	427	512
ENSMUSG00000043496	chr6	Tril	0.38688631	0.046989111	0.071584894	3.582997593	0.039578487	0	154	148	113	193	160	239	188	203	151	322
ENSMUSG00000028484	chr4	Psip1	-0.3452918	0.047120064	0.071776569	4.491888202	0.033152963	0	406	364	304	442	353	269	452	241	329	319
ENSMUSG00000094518	chr13	Gm6421	-0.6925692	0.047183958	0.071866063	0.464054757	0.08461644	0	29	28	13	24	22	9	19	14	19	17
ENSMUSG00000025172	chr19	Ankrd2	1.25201776	0.047217853	0.071909853	6.661123427	0.453059706	0	205	337	1071	3068	215	6078	1772	1977	1826	283
ENSMUSG00000035021	chr12	Baz1a	0.61242977	0.047532007	0.072380401	2.324964339	0.098810733	0	52	46	64	84	44	50	159	59	121	90
ENSMUSG00000040025	chr4	Ythdf2	-0.3215586	0.047565128	0.07241113	4.228977682	0.027827146	0	305	259	254	429	309	252	268	208	288	338
ENSMUSG00000040093	chr2	Bmf	0.53499406	0.04757027	0.07241113	2.774131074	0.075595532	0	71	89	92	74	76	109	102	141	79	217
ENSMUSG00000040164	chr2	Kcns1	-0.9464143	0.047560782	0.07241113	0.586478044	0.212120963	0	37	45	16	9	26	7	16	20	8	26
ENSMUSG00000054387	chr1	Mdm4	-0.2900399	0.047572911	0.07241113	4.947274706	0.023615823	0	478	534	480	548	466	602	435	361	433	443
ENSMUSG00000027487	chr2	Cdk5rap1	-0.3973666	0.047597886	0.072441256	3.155216987	0.039695524	0	141	129	122	214	146	111	108	122	162	111
ENSMUSG00000028790	chr4	Khdrbs1	0.31819976	0.047610717	0.072452895	5.297889784	0.029213399	0	532	469	443	689	485	615	926	628	727	646
ENSMUSG00000020180	chr10	Snrpd3	0.2890082	0.047623227	0.072464041	6.121373153	0.024539729	0	962	916	785	1216	813	1497	1345	1083	1220	1115
ENSMUSG00000062081	chr14	Gm6055	-0.5194562	0.047671538	0.072529655	1.690551537	0.059268067	0	62	62	42	75	35	39	48	26	47	49
ENSMUSG00000024072	chr17	Yipf4	-0.3130165	0.047806413	0.072726944	4.350707894	0.026670708	0	325	344	283	474	268	347	349	214	243	338
ENSMUSG00000053192	chr3	Mllt11	-0.3071213	0.047811851	0.0727273	5.825730298	0.027622519	0	1046	883	860	1052	818	693	991	759	800	875
ENSMUSG00000018678	chr11	Sp2	-0.3550832	0.047829932	0.072746885	3.615329259	0.032822157	0	177	193	169	255	222	177	191	162	120	223
ENSMUSG00000029499	chr5	Pxmp2	0.35559446	0.047860787	0.072785893	4.419161476	0.035666839	0	217	265	244	438	247	304	436	349	457	390
ENSMUSG00000042308	chr7	Setd1a	-0.2866215	0.047875413	0.072792294	4.453329123	0.022132198	0	329	322	315	457	366	397	312	287	264	352
ENSMUSG00000071477	chr6	Zfp777	-0.3264248	0.047874296	0.072792294	4.041949273	0.028510892	0	234	220	247	364	296	265	229	178	244	274
ENSMUSG00000059897	chr8	Zfp930	-0.9310599	0.047926175	0.072861549	0.827220371	0.213053315	0	23	42	38	38	21	1	28	12	26	25
ENSMUSG00000067203	chr17	H2-K2	0.91107301	0.047949305	0.072888785	1.681813766	0.221679355	0	23	57	33	29	14	178	47	24	39	52
ENSMUSG00000025235	chr9	Bbs4	-0.4269342	0.047983601	0.072932986	2.548347986	0.043566338	0	120	99	83	113	76	77	79	57	99	87
ENSMUSG00000030309	chr6	Caprin2	0.70801918	0.047991149	0.072936527	3.029116446	0.142166821	0	111	114	61	67	94	42	175	146	177	264
ENSMUSG00000035105	chr12	Egln3	0.48539604	0.048057846	0.073029951	4.347032043	0.068950442	0	161	199	207	581	169	351	423	371	303	478
ENSMUSG00000050821	chr16	Fam131a	-0.4187205	0.048092213	0.07307423	6.780501987	0.052945361	0	2196	1980	2011	1788	1309	1016	1507	1339	1632	2138
ENSMUSG00000026197	chr1	Zfand2b	0.37187699	0.048104138	0.073084405	3.683393875	0.037053132	0	209	132	139	190	157	227	216	191	312	220
ENSMUSG00000006958	chr16	Chrd	0.56737578	0.048126157	0.07310991	2.328538542	0.082247469	0	68	43	65	67	50	140	76	133	51	77
ENSMUSG00000039834	chr2	Zfp335	-0.3301382	0.048158474	0.073151052	3.683428616	0.028488279	0	206	181	231	230	202	208	206	131	193	187
ENSMUSG00000028700	chr4	Pomgnt1	-0.2837912	0.048185804	0.073184611	6.172114559	0.023762075	0	1149	1138	1058	1445	1108	1166	1033	1057	1045	991
ENSMUSG00000052915	chr11	Msl1	-0.3038819	0.04830283	0.073354379	6.312626889	0.027485152	0	1159	1123	1206	1749	1327	1227	1014	1144	1111	1297
ENSMUSG00000028133	chr3	Rwdd3	-0.6581473	0.048320361	0.07337303	1.615883749	0.110003646	0	58	54	51	49	54	81	20	29	21	40
ENSMUSG00000034800	chr2	Zfp661	-0.5623156	0.048445315	0.073554777	1.732790217	0.07439509	0	66	44	49	76	52	35	45	21	63	47
ENSMUSG00000028645	chr4	Slc2a1	0.41277679	0.048471727	0.073586884	3.391054717	0.045579161	0	116	128	143	176	102	303	216	117	153	194
ENSMUSG00000063410	chr14	Stk24	-0.3235926	0.048672513	0.07388368	4.342424101	0.029026037	0	326	321	299	445	291	329	332	187	251	379
ENSMUSG00000015202	chr10	Cnksr3	-0.4653665	0.048713562	0.073937961	2.484951653	0.054512168	0	80	77	105	139	77	120	82	56	55	68
ENSMUSG00000039770	chr17	Ypel5	0.31187171	0.048845988	0.074130907	5.535067176	0.028484324	0	729	672	585	637	441	973	862	711	821	828
ENSMUSG00000068240	chr4	Gm11808	0.27207997	0.048851751	0.074131604	4.835305693	0.020467869	0	398	403	348	472	304	603	514	424	493	515
ENSMUSG00000078234	chr4	Klhdc7a	-1.2583363	0.048862365	0.07413966	0.590171491	0.417044661	0	10	72	24	10	26	4	11	20	2	30
ENSMUSG00000039697	chr10	Ncoa7	-0.4438658	0.048872754	0.074147374	2.249011917	0.045582891	0	89	69	78	83	77	50	71	57	60	82
ENSMUSG00000029344	chr5	Tpst2	0.34075794	0.048944124	0.074245655	4.131118019	0.031902927	0	188	218	218	322	206	476	307	280	273	265
ENSMUSG00000058761	chr7	Rnf169	0.35093732	0.048948159	0.074245655	3.312198941	0.030705586	0	147	118	111	147	119	252	183	130	167	174
ENSMUSG00000047205	chr11	Dusp18	0.62015363	0.049023903	0.074352476	3.147283964	0.111103584	0	64	73	64	281	65	148	163	187	137	224
ENSMUSG00000001774	chr9	Chordc1	-0.2919672	0.049090497	0.074445398	5.285350392	0.024531052	0	669	551	511	910	587	543	640	524	580	561
ENSMUSG00000031432	chrX	Prps1	-0.2900921	0.049106266	0.074461231	4.921328484	0.023799677	0	505	469	420	613	474	497	508	355	485	376
ENSMUSG00000030019	chr6	Fbxl14	0.30602894	0.049377246	0.074864005	3.748288938	0.023766222	0	170	178	162	209	167	284	285	207	216	214
ENSMUSG00000053119	chr6	Chmp3	0.28896966	0.049500824	0.075043228	5.933826179	0.02481037	0	909	844	737	972	640	1251	1069	936	1149	1082
ENSMUSG00000095597	chrX	Gm6472	-0.4297395	0.04959578	0.075179026	4.748237495	0.054807274	0	459	481	488	512	342	698	376	279	295	249
ENSMUSG00000025733	chr17	Rhot2	-0.3253526	0.049638063	0.07523496	6.6502975	0.032149501	0	1384	1594	1558	2476	1406	1291	1364	1532	1442	1597
ENSMUSG00000007739	chr11	Cct4	0.29251801	0.049657825	0.075256752	6.832156195	0.026012632	0	1631	1435	1253	1997	1364	2311	2240	1712	2112	1878
ENSMUSG00000032261	chr9	Sh3bgrl2	0.68372563	0.049667503	0.075263257	1.014364572	0.104525152	0	16	19	21	41	13	49	29	26	24	64

ENSMUSG00000049538	chr13	Adamts16	-0.9047599	0.049711654	0.075321994	0.218220607	0.182312885	0	19	17	19	22	24	18	3	13	2	24
ENSMUSG00000067367	chr5	Lyar	0.38305808	0.049749157	0.075370647	3.957325391	0.041311084	0	155	174	152	317	213	327	365	232	294	209
ENSMUSG00000039660	chr2	D2Wsu81e	0.39819577	0.049894055	0.075581976	3.076305079	0.040252092	0	132	97	119	90	89	190	169	128	148	139
ENSMUSG00000021340	chr13	Gpld1	0.77402141	0.049913558	0.075603325	0.023415521	0.097455308	0	6	11	10	10	11	27	11	10	19	25
ENSMUSG00000042246	chr7	Tmc7	0.81649723	0.05001708	0.07575192	3.145770093	0.195417414	0	80	110	114	72	84	22	225	219	186	237
ENSMUSG00000040236	chr8	Trappc5	-0.2570581	0.050030303	0.075763736	5.057574371	0.018558618	0	551	503	488	682	479	524	491	457	488	508
ENSMUSG00000075012	chr2	Fjx1	0.69241388	0.050086216	0.075840191	1.190077727	0.113730822	0	24	20	33	29	16	71	31	61	26	28
ENSMUSG00000039137	chr4	Whrn	0.82837088	0.050098847	0.075851099	0.830305289	0.158885178	0	17	13	13	16	28	16	36	43	16	60
ENSMUSG00000025857	chr5	Heatr2	-0.3198639	0.05010653	0.075854513	3.760667579	0.027023694	0	226	203	186	246	246	216	234	184	158	186
ENSMUSG00000000567	chr11	Sox9	0.62466823	0.050156207	0.075921493	2.009993473	0.10113362	0	53	32	44	39	57	41	91	99	51	100
ENSMUSG00000021171	chr12	Esyt2	-0.2803681	0.050197276	0.075975431	5.077246432	0.022556392	0	502	500	495	761	513	550	585	379	488	490
ENSMUSG00000053819	chr3	Camk2d	-0.3349564	0.050249012	0.0760455	6.25885262	0.034110588	0	1402	999	1126	1602	1252	859	1305	966	1055	1323
ENSMUSG00000026017	chr1	Carf	-0.5092747	0.050283525	0.076089491	1.693950344	0.056722965	0	58	50	34	84	51	43	40	52	32	42
ENSMUSG00000027890	chr3	Gstm4	0.34768853	0.050411178	0.076274399	3.9108924	0.033160982	0	245	212	131	200	187	265	276	246	304	268
ENSMUSG00000030766	chr7	Arhgap17	0.29440676	0.050450345	0.076325398	4.541037232	0.024068794	0	278	292	313	387	281	518	432	327	340	484
ENSMUSG00000016024	chr2	Lbp	0.48855941	0.050584088	0.076514185	3.995312183	0.069806788	0	197	197	183	243	163	649	216	199	218	266
ENSMUSG00000037892	chr3	Pcdh18	-0.3894126	0.050586081	0.076514185	2.668270076	0.036208868	0	90	97	104	140	98	84	85	73	104	94
ENSMUSG00000005299	chr5	Letm1	-0.3159067	0.050635482	0.076580618	6.214038885	0.030296324	0	1069	1122	1112	1787	1103	972	1038	1176	973	1203
ENSMUSG00000031877	chr8	Ces2g	0.93925416	0.050654892	0.076601684	0.653189924	0.216985458	0	16	16	13	5	21	10	31	15	47	51
ENSMUSG00000039041	chr2	Adrm1	0.27717003	0.050678696	0.076629391	6.15524506	0.023159001	0	1035	883	819	1231	854	1460	1265	1163	1129	1368
ENSMUSG00000028411	chr4	Aptx	-0.2933831	0.050724525	0.07669039	4.261904598	0.023370173	0	356	274	287	376	275	287	290	258	309	251
ENSMUSG00000078427	chr10	Sarnp	0.30171681	0.050844897	0.076864064	4.736725975	0.026047529	0	407	339	323	431	278	520	588	394	490	404
ENSMUSG00000098148	chr8	Gm20204	0.43414776	0.050921108	0.076970951	2.974061716	0.04972266	0	89	83	98	124	96	241	123	130	93	148
ENSMUSG00000029060	chr4	Mib2	-0.2766774	0.050941961	0.076985819	4.260354579	0.020560688	0	297	290	285	382	302	300	265	244	281	318
ENSMUSG00000103009	chr2	RP23-160G19.10	0.74717106	0.050940942	0.076985819	0.219175158	0.095738973	0	16	8	12	12	9	34	29	12	14	18
ENSMUSG00000090952	chr17	Gm17251	0.5487191	0.051040116	0.077125816	2.115816977	0.0773899	0	44	40	42	69	60	96	62	94	41	116
ENSMUSG00000031200	chrX	Mtcp1	-0.5279794	0.051072673	0.077166667	0.940561608	0.049190749	0	32	30	27	41	29	24	21	21	28	26
ENSMUSG00000047434	chr16	Xxylt1	-0.4182501	0.051084915	0.077176821	2.819338688	0.044601598	0	138	87	119	140	108	74	119	78	101	112
ENSMUSG00000048728	chr11	Zfp454	-0.7174455	0.051172492	0.077300773	1.035470568	0.125199575	0	35	29	47	48	21	11	26	12	29	41
ENSMUSG00000020722	chr11	Cacng1	0.34221779	0.051279185	0.077453571	8.426411872	0.036664924	0	5699	4317	3527	4622	4346	8448	5249	5734	5297	6890
ENSMUSG00000032740	chr11	Ccdc88a	-0.4191396	0.051330912	0.077518896	2.73400836	0.044982477	0	99	87	113	161	102	99	110	55	101	94
ENSMUSG00000041679	chr8	Lrrc29	0.89876778	0.051333528	0.077518896	-0.295742385	0.147426062	0	10	9	7	4	5	12	4	21	17	18
ENSMUSG00000020642	chr12	Rnf144a	-0.4497816	0.051346646	0.077519898	3.348186751	0.056488003	0	192	182	169	176	142	116	103	148	98	229
ENSMUSG00000043487	chr12	Acot6	0.49139413	0.051341615	0.077519898	2.196969475	0.061495655	0	48	54	53	88	37	86	76	96	53	114
ENSMUSG00000078681	chr7	Tm2d3	0.30647419	0.051350831	0.077519898	4.136373386	0.025735545	0	247	215	237	274	190	278	318	278	342	355
ENSMUSG00000026179	chr1	Pnkd	0.30029041	0.051356542	0.077520146	5.315420067	0.026738839	0	476	561	490	672	459	813	557	721	680	804
ENSMUSG00000029228	chr5	Lnx1	-0.5679371	0.051417779	0.077604198	1.430369918	0.076766929	0	38	53	37	64	39	64	25	24	26	33
ENSMUSG00000046808	chr5	Atp10d	-0.6187251	0.05155321	0.0778002	1.839072708	0.102009444	0	52	62	69	77	52	96	42	20	30	41
ENSMUSG00000057649	chr13	Brd9	0.30775099	0.051684448	0.077984948	3.79680102	0.024930187	0	197	195	165	203	155	289	250	229	264	211
ENSMUSG00000090523	chr18	Gypc	0.30138188	0.05168679	0.077984948	4.905022335	0.026443169	0	437	377	365	445	363	480	499	474	648	574
ENSMUSG00000035686	chr7	Thrsp	1.06428168	0.051781509	0.078119427	5.160312278	0.343548197	0	83	819	295	114	325	135	644	961	739	1381
ENSMUSG00000065037	chr9	Rn7sk	0.7183595	0.051865245	0.078237309	0.55260319	0.113615612	0	24	7	11	21	13	15	27	25	40	27
ENSMUSG00000027367	chr2	Stard7	-0.3055235	0.052000795	0.078433316	6.976136757	0.029031717	0	1844	2004	2054	2942	1620	1916	1651	1910	1770	1910
ENSMUSG00000074874	chr13	Ctla2b	0.66268018	0.052049469	0.07849826	1.58098346	0.11128817	0	29	38	28	47	24	114	43	35	67	31
ENSMUSG00000022142	chr15	Nup155	-0.3222412	0.052107875	0.07856185	3.685961654	0.02744417	0	206	193	179	297	191	174	233	146	190	183
ENSMUSG00000030291	chr6	Med21	-0.3505019	0.052101991	0.07856185	4.312690584	0.03550065	0	412	340	285	340	268	261	294	204	365	291
ENSMUSG00000048911	chr2	Rnf24	-0.4257292	0.052108497	0.07856185	1.992244623	0.039387321	0	55	59	64	89	64	57	61	48	52	51
ENSMUSG00000027160	chr2	Ccdc34	0.44657254	0.052147674	0.078612436	2.214197932	0.047781915	0	64	64	46	72	40	71	96	91	70	95
ENSMUSG00000031487	chr8	Brf2	0.33920153	0.052184264	0.078659111	3.058404127	0.028478817	0	105	99	107	142	89	157	154	153	121	163
ENSMUSG00000030471	chr7	Zdhhc13	0.40016976	0.052262501	0.078768545	2.57172422	0.039058655	0	97	70	60	84	63	123	130	86	105	98
ENSMUSG00000028996	chr4	Rbp7	-0.9114377	0.052328802	0.078859967	2.934582808	0.249350007	0	105	128	115	212	177	277	24	32	36	81
ENSMUSG00000097052	chr2	Snhg7	0.60728266	0.05237917	0.078927362	1.425933512	0.086280149	0	38	38	32	19	21	78	51	47	36	42
ENSMUSG00000047388	chr8	Atmin	-0.303938	0.052422351	0.078983912	4.60818824	0.026607538	0	369	311	324	546	460	408	343	314	332	382
ENSMUSG00000037339	chr5	Fam53a	-0.2911821	0.052453751	0.079022704	5.743342122	0.025722283	0	862	766	810	1067	879	723	760	733	745	958
ENSMUSG00000064363	chrMT	mt-Nd4	-0.3634581	0.052465003	0.079031136	12.00674907	0.041972864	0	56157	66157	62930	109999	55947	46530	54355	61307	63839	65129
ENSMUSG00000028917	chr4	Plekhm2	0.26846881	0.052563693	0.079171265	5.093328878	0.020965572	0	446	396	420	596	450	690	635	474	574	678
ENSMUSG00000026675	chr1	Hsd17b7	-0.4704272	0.052579906	0.079187152	2.414315037	0.056601186	0	86	91	90	94	87	52	67	71	56	110
ENSMUSG00000097772	chr5	5430416N02Rik	0.70437192	0.052589612	0.079193235	0.223281219	0.078819242	0	17	9	12	9	11	27	19	16	26	17
ENSMUSG00000006678	chrX	Pola1	0.58361782	0.052836194	0.079555984	1.747671262	0.085059721	0	35	34	23	56	46	56	75	37	94	53
ENSMUSG00000035851	chr5	Ythdc1	-0.2590118	0.052846648	0.079563153	4.788913758	0.018988568	0	468	402	385	555	431	446	428	377	386	411
ENSMUSG00000027255	chr2	Arfgap2	-0.2939321	0.052868157	0.079586962	7.32838677	0.027182484	0	2948	2345	2375	3100	2424	2322	2439	1910	2457	2664
ENSMUSG00000056216	chr7	Cebpg	-0.3151625	0.052921092	0.079658071	5.420801303	0.030224462	0	578	612	730	921	694	845	635	450	617	590
ENSMUSG00000028341	chr4	Nr4a3	-0.8934373	0.05295048	0.079693722	2.045199722	0.231215612	0	19	29	75	162	113	92	50	35	34	22
ENSMUSG00000055923	chr5	Aasdh	-0.3887822	0.052969749	0.079714139	2.679227683	0.037290478	0	127	99	97	105	100	113	85	66	91	92
ENSMUSG00000028479	chr4	Gne	-0.3501692	0.053098239	0.079898901	3.272183782	0.032329399	0	145	144	150	217	146	156	140	94	118	183

ENSMUSG00000074925	chr19	Ptar1	-0.7104428	0.053111073	0.079909609	0.491057355	0.099800404	0	28	23	23	32	14	12	24	22	7	14
ENSMUSG00000020135	chr10	Apc2	-0.7223669	0.05311806	0.079911519	0.353435402	0.099264643	0	20	18	19	23	27	9	9	16	11	26
ENSMUSG00000063145	chr2	Bbs5	0.48798172	0.053156279	0.079960409	1.613730752	0.050949701	0	40	41	32	33	34	53	63	63	47	52
ENSMUSG00000046062	chr1	Ppp1r15b	0.30304593	0.053176028	0.079981508	5.044617017	0.027264873	0	372	400	430	577	421	804	666	418	535	575
ENSMUSG00000019303	chr11	Psmc3ip	0.60744737	0.053256844	0.080094442	0.945313043	0.081193231	0	32	14	24	24	12	39	36	24	45	33
ENSMUSG00000029513	chr5	Prkab1	0.32509898	0.053276793	0.080115823	3.870770072	0.029059323	0	206	214	173	210	154	327	237	287	209	258
ENSMUSG00000042590	chr13	Ipo11	-0.3154608	0.053288307	0.080124517	4.250831285	0.028229538	0	315	347	238	379	288	275	297	229	330	242
ENSMUSG00000059201	chr6	Lep	-1.5836824	0.053354308	0.080215126	0.279255993	0.679190339	0	1	69	20	5	24	2	1	11	7	24
ENSMUSG00000032077	chr9	Bud13	0.36728987	0.05336624	0.080224434	2.800434601	0.032655961	0	91	81	84	89	96	145	119	121	117	127
ENSMUSG00000019851	chr10	Perp	-0.5815732	0.053517099	0.080442566	1.065636645	0.070941637	0	35	26	33	41	41	29	34	31	15	20
ENSMUSG00000030286	chr6	Emc3	0.27698198	0.053544971	0.080475806	6.247824084	0.02377434	0	1076	974	879	1270	931	1391	1306	1213	1347	1531
ENSMUSG00000033885	chr14	Pxk	-0.3368041	0.053614101	0.080571041	3.698704658	0.030968631	0	178	222	185	310	186	178	210	136	212	193
ENSMUSG00000040139	chr7	9430038I01Rik	0.57860396	0.053702856	0.080695744	1.722134484	0.082771163	0	29	44	38	33	42	110	53	53	56	41
ENSMUSG00000078480	chr4	Mrpl48-ps	-1.1705534	0.053728041	0.080724909	2.900869357	0.41159	0	158	150	149	177	124	311	13	27	17	28
ENSMUSG00000002205	chr7	Vrk3	0.3138304	0.053835419	0.080877547	4.377974611	0.028270767	0	285	264	287	316	219	539	353	299	367	327
ENSMUSG00000026418	chr1	Tnni1	1.9607865	0.053875928	0.080929705	7.058657141	1.097532099	0	17	81	47	4778	42	6963	1153	6377	1283	1498
ENSMUSG00000081967	chr2	Gm14017	0.66241711	0.053958266	0.081044677	0.536372031	0.088544148	0	20	12	12	17	15	28	13	30	35	25
ENSMUSG00000003528	chr16	Slc25a1	0.57408343	0.05418742	0.081380118	3.943681922	0.100359491	0	97	322	149	110	206	416	267	327	245	239
ENSMUSG00000035919	chr9	Bbs9	-0.4026823	0.054194334	0.081381757	2.716744553	0.041392071	0	108	102	121	137	81	83	99	65	105	102
ENSMUSG00000026305	chr1	Lrrfip1	-0.3346087	0.054201697	0.08138407	7.597163265	0.035778415	0	3659	3024	2788	3669	2940	2093	2966	2514	2816	3527
ENSMUSG00000002083	chr7	Bbc3	0.59351538	0.054230753	0.081410204	1.677808526	0.089702096	0	43	42	42	31	22	79	49	67	30	78
ENSMUSG00000039737	chr5	Prkrip1	0.31005134	0.054230419	0.081410204	3.988026627	0.026690028	0	246	173	205	237	185	327	279	263	309	243
ENSMUSG00000026698	chr1	Pigc	0.29398519	0.05428238	0.081478955	4.433148854	0.02459075	0	318	305	277	292	237	433	398	351	310	447
ENSMUSG00000022556	chr15	Hsf1	-0.3225038	0.054302082	0.081499774	5.111153169	0.031602085	0	488	478	419	822	671	618	489	502	438	457
ENSMUSG00000057706	chr7	Mex3b	-0.6634977	0.054379218	0.081606781	0.972974216	0.101434205	0	32	26	30	44	37	16	23	17	14	47
ENSMUSG00000038518	chr13	Jarid2	-0.2863715	0.05438791	0.081611061	5.34732733	0.024904964	0	686	704	633	789	516	607	668	507	509	706
ENSMUSG00000031819	chr8	Emc8	0.29230736	0.054480514	0.081741241	4.156067729	0.023890718	0	199	222	222	336	216	367	358	255	308	310
ENSMUSG00000039252	chr5	Lgi2	-0.5001522	0.054526305	0.081801163	1.372100253	0.054852571	0	52	46	37	44	36	41	31	20	36	40
ENSMUSG00000023050	chr15	Map3k12	0.45891854	0.054582217	0.081876254	2.11544941	0.050828927	0	48	62	47	60	46	78	67	93	59	99
ENSMUSG00000027559	chr3	Car3	-0.6614674	0.054596532	0.081888939	9.601525382	0.139954872	0	5177	10925	7631	37622	14094	12334	7933	6207	9315	13951
ENSMUSG00000023452	chr5	Pisd	0.27317281	0.054695822	0.08202906	4.870138766	0.021901273	0	417	394	341	501	323	640	489	405	534	548
ENSMUSG00000043531	chr19	Sorcs1	-0.9610877	0.054740563	0.082087351	-0.210414408	0.197325993	0	8	5	20	18	22	7	3	4	16	11
ENSMUSG00000020807	chr11	4933427D14Rik	0.46780561	0.054759418	0.082106816	1.491987814	0.044350519	0	39	35	29	40	25	59	58	39	51	48
ENSMUSG00000029442	chr5	Wdr66	-0.5031099	0.054779651	0.082128341	1.836850749	0.061626307	0	71	76	52	61	41	60	32	38	52	52
ENSMUSG00000028937	chr4	Acot7	0.31852256	0.054805647	0.082158503	4.620199371	0.030131557	0	284	317	310	435	285	606	464	456	313	391
ENSMUSG00000037370	chr10	Enpp1	0.41326172	0.054914677	0.08231312	3.340687821	0.048247816	0	132	126	104	184	101	306	218	150	123	150
ENSMUSG00000069135	chr17	Fgfr1op	-0.2842469	0.054999467	0.082431373	3.971488492	0.021815279	0	266	239	242	330	204	231	238	219	219	238
ENSMUSG00000001305	chr1	Rrp15	0.35061036	0.05501481	0.082445527	3.313359758	0.032682402	0	118	128	118	158	121	249	210	158	139	149
ENSMUSG00000075318	chr2	Scn2a1	-0.6908777	0.055051685	0.082491943	-0.021928098	0.072461496	0	19	13	10	21	17	12	15	7	9	11
ENSMUSG00000009876	chr2	Cox4i2	0.56644017	0.055104576	0.082562344	1.725083629	0.08397332	0	36	50	20	61	27	94	49	64	60	43
ENSMUSG00000020267	chr11	Hint1	0.31518619	0.055158416	0.082634153	7.044303809	0.031803433	0	1847	1732	1545	2122	1531	3374	2439	1794	2447	1988
ENSMUSG00000035725	chrX	Prkx	0.35371015	0.055244942	0.082754909	3.485840937	0.034467083	0	138	122	127	189	151	264	244	127	195	195
ENSMUSG00000036955	chr10	2510003E04Rik	-0.2738864	0.055284813	0.082805761	4.661142929	0.021871643	0	382	425	391	502	356	409	389	306	322	445
ENSMUSG00000041891	chr18	Lman1	-0.2960222	0.055340986	0.082881014	6.045087495	0.027533057	0	1127	962	979	1287	1058	872	1117	841	1053	933
ENSMUSG00000039005	chr4	Tlr4	0.51805157	0.055398986	0.082950099	2.272415971	0.072223498	0	39	66	58	93	36	100	132	55	87	81
ENSMUSG00000043923	chr9	Ccdc84	0.61130826	0.055397567	0.082950099	1.327418786	0.088788205	0	25	20	30	21	41	65	37	49	31	54
ENSMUSG00000028854	chr4	Slc9a1	0.34358671	0.055428906	0.082977119	4.205552505	0.034814575	0	196	229	206	359	227	396	343	303	213	432
ENSMUSG00000085566	chr2	A730017L22Rik	-0.5728733	0.055424915	0.082977119	1.139374469	0.073235333	0	46	34	25	32	47	35	31	26	26	19
ENSMUSG00000086119	chr9	Gm2415	0.52142648	0.055577973	0.083191363	1.219835982	0.058287668	0	22	22	20	38	33	36	52	37	44	42
ENSMUSG00000023044	chr15	Csad	0.43254968	0.055702455	0.083368764	2.797647262	0.050690361	0	75	109	82	79	82	147	100	142	96	155
ENSMUSG00000033295	chr4	Ptprf	-0.3999723	0.055708573	0.083368992	3.25577544	0.045292184	0	172	125	144	187	171	190	160	86	88	151
ENSMUSG00000002455	chr2	Prpf6	0.28119158	0.055752595	0.083425938	5.158636602	0.023995136	0	441	461	383	627	493	666	591	606	565	763
ENSMUSG00000007670	chr17	Khsrp	0.29560044	0.055808361	0.08349703	4.83556625	0.026310744	0	324	348	292	577	386	617	535	462	414	544
ENSMUSG00000025917	chr1	Cops5	-0.2906572	0.055812053	0.08349703	6.775722937	0.027028661	0	1951	1794	1554	2152	1545	1603	1619	1364	1833	1605
ENSMUSG00000089989	chr7	Flt3l	0.44520869	0.055861514	0.083562081	1.793473099	0.042879105	0	49	40	38	46	37	76	72	51	62	54
ENSMUSG00000006920	chr11	Ezh1	-0.2965172	0.0559001	0.083610852	4.979909118	0.026781372	0	504	526	451	581	512	606	379	345	456	537
ENSMUSG00000033196	chr11	Myh2	-0.8170073	0.055950604	0.083677436	10.59194162	0.214237764	0	7922	21709	21269	73500	30206	40078	8195	22052	10724	11649
ENSMUSG00000024319	chr17	Vps52	-0.2838842	0.056004131	0.083748527	5.500041835	0.024893111	0	776	684	601	925	721	665	644	699	568	741
ENSMUSG00000057134	chr10	Ado	-0.2928127	0.056048648	0.083806131	5.188814915	0.026212031	0	546	527	498	881	568	514	601	475	444	640
ENSMUSG00000000001	chr3	Gnai3	0.303506	0.056249191	0.084096993	4.732490371	0.027733169	0	341	350	285	488	317	513	619	333	470	465
ENSMUSG00000085965	chr1	2310016D23Rik	0.62739771	0.056339639	0.08422321	2.132096252	0.11352177	0	42	46	40	93	35	34	83	84	129	83
ENSMUSG00000017144	chr2	Rnd3	0.33936439	0.056427542	0.084345596	3.582033521	0.032479963	0	146	166	157	211	105	249	247	182	229	175
ENSMUSG00000062591	chr17	Tubb4a	0.68438589	0.056461522	0.084387363	1.127823202	0.117242168	0	13	20	20	35	30	23	41	66	34	39
ENSMUSG00000022718	chr16	Dgcr8	-0.2864573	0.056490043	0.084420963	4.045303559	0.023079351	0	274	257	241	300	266	269	243	187	236	276
ENSMUSG00000027291	chr2	Vps39	-0.2552907	0.056506545	0.084436595	4.954769305	0.019363855	0	495	478	484	595	452	542	445	392	434	496

ENSMUSG00000039497	chr10	Dse	0.39205554	0.056571918	0.084525243	3.854001105	0.045475071	0	239	188	159	189	146	294	323	137	278	309
ENSMUSG00000046573	chr13	Lyrm4	0.40380711	0.056625088	0.084595642	2.587419626	0.041550398	0	83	79	71	86	58	127	114	98	126	81
ENSMUSG00000057137	chr6	Tmem140	-0.3421955	0.056631985	0.084596903	4.521510947	0.035680595	0	405	394	342	445	319	365	260	264	264	505
ENSMUSG00000022283	chr15	Pabpc1	0.29939591	0.056932877	0.085037286	6.90037961	0.029023568	0	1559	1471	1308	1977	1671	2239	2536	1630	1875	2537
ENSMUSG00000021241	chr12	Isca2	0.30830623	0.056963824	0.085074418	4.785618927	0.029015005	0	415	420	313	443	246	505	533	508	484	441
ENSMUSG00000050379	chrX	Sept6	0.41879335	0.057026435	0.085158826	2.863918282	0.047815555	0	110	76	94	92	81	154	183	87	135	113
ENSMUSG00000028763	chr4	Hspg2	-0.3511098	0.057264081	0.085495438	8.393732408	0.040573878	0	4637	4623	5383	7125	6297	4854	4647	5608	3420	5537
ENSMUSG00000066829	chr9	Zfp810	0.70229235	0.057261	0.085495438	0.604485729	0.110262433	0	17	17	20	21	4	31	19	21	26	44
ENSMUSG00000022469	chr15	Rapgef3	-0.3905835	0.057496239	0.085832882	3.110998173	0.042255468	0	99	118	139	240	136	148	113	121	107	114
ENSMUSG00000029735	chr6	Tpk1	-0.5906163	0.057534551	0.085880903	0.809000687	0.069814745	0	33	25	22	38	29	21	25	11	18	32
ENSMUSG00000058833	chr8	2810428I15Rik	0.30708332	0.057572354	0.085928152	5.7776566	0.030020148	0	831	688	654	820	649	1402	916	845	1005	804
ENSMUSG00000015944	chr5	Gatsl2	-0.3107432	0.057619781	0.085989755	6.841081042	0.031467302	0	1699	1847	1536	2404	1986	1918	1281	1705	1499	1948
ENSMUSG00000087658	chr6	Hotairm1	0.64594402	0.05774722	0.08617074	0.225214933	0.069240047	0	16	11	11	12	10	22	15	25	20	21
ENSMUSG00000009995	chrX	Taz	-0.2893425	0.057844856	0.086307217	5.448154743	0.026328634	0	799	735	678	786	564	758	647	562	671	566
ENSMUSG00000021750	chr14	Fam107a	-0.9432503	0.057896524	0.086366898	0.929306758	0.254076241	0	21	34	25	32	60	58	13	4	17	12
ENSMUSG00000038119	chr9	Cdon	-0.3179093	0.057898282	0.086366898	5.037732462	0.031600222	0	529	537	473	599	556	555	449	547	306	525
ENSMUSG00000061100	chr16	Retnla	0.74480847	0.057909573	0.086366898	2.919425465	0.170931146	0	75	84	49	57	138	190	68	125	294	75
ENSMUSG00000069565	chr10	Dazap1	0.26071531	0.057906091	0.086366898	4.965470336	0.020506962	0	449	387	374	515	389	542	605	543	532	540
ENSMUSG00000006526	chr14	Tmem110	-0.3206524	0.057983513	0.086467945	3.527295703	0.028104904	0	181	156	183	247	181	211	171	141	174	134
ENSMUSG00000075703	chr5	Ept1	-0.3168652	0.058128603	0.086675062	3.884636806	0.028717739	0	195	210	224	350	242	217	260	204	190	194
ENSMUSG00000045659	chr7	Plekha7	0.58311756	0.058189779	0.086757025	1.452317658	0.085285898	0	24	32	32	43	25	61	48	75	26	44
ENSMUSG00000022206	chr15	Npr3	-0.6547723	0.058279745	0.086881889	2.945646697	0.131233652	0	73	141	103	340	72	136	144	85	59	61
ENSMUSG00000040152	chr2	Thbs1	0.6527374	0.058339327	0.086961436	5.195549292	0.138789754	0	513	266	436	732	230	881	1323	267	886	328
ENSMUSG00000096403	chr6	Gm9825	-1.0158153	0.058419484	0.087071634	3.621816236	0.329270832	0	248	230	224	280	231	524	54	32	44	52
ENSMUSG00000024944	chr19	Arl2	0.27345121	0.058464196	0.087119693	5.332687069	0.023355371	0	544	530	454	705	493	873	599	671	683	773
ENSMUSG00000030157	chr6	Clec2d	0.39670561	0.058460788	0.087119693	5.546287754	0.050947373	0	710	773	547	584	369	1287	817	632	942	686
ENSMUSG00000025016	chr19	Tm9sf3	-0.2744027	0.058533609	0.08721383	6.833773998	0.024608322	0	1962	1732	1637	2347	1660	1683	1928	1392	1660	1771
ENSMUSG00000038375	chr2	Trp53inp2	-0.3728562	0.058541688	0.087216569	9.14745839	0.04630281	0	7817	8386	9477	13753	8673	6136	7344	9089	6599	10902
ENSMUSG00000024317	chr18	Rnf138	-0.3933654	0.058743943	0.087508564	2.579211019	0.039485115	0	103	94	93	123	84	82	110	72	84	65
ENSMUSG00000031060	chrX	Rbm10	0.27051574	0.058868653	0.087684993	4.216569456	0.020929604	0	254	235	224	313	225	391	302	315	330	311
ENSMUSG00000026499	chr1	Acbd3	-0.2802697	0.058913213	0.087742015	4.094877223	0.022361547	0	264	251	246	379	257	261	295	211	225	263
ENSMUSG00000044145	chr2	1810024B03Rik	0.6430021	0.058961206	0.087804135	0.792292019	0.093380091	0	19	17	9	17	30	39	29	38	27	26
ENSMUSG00000024426	chr17	Atat1	0.42833134	0.058982353	0.08782627	2.317034435	0.046650828	0	86	53	54	56	57	90	91	94	86	92
ENSMUSG00000020231	chr10	Dip2a	-0.3349226	0.059072596	0.087947078	3.301836246	0.030566064	0	122	169	150	218	154	164	155	111	144	132
ENSMUSG00000085180	chr4	AI838599	-0.9107093	0.059076071	0.087947078	1.448802142	0.246966835	0	79	44	42	47	41	95	14	20	14	11
ENSMUSG00000002803	chr12	Btbd6	-0.3215618	0.059171817	0.088080234	3.77891542	0.029523817	0	207	190	196	315	227	216	193	233	165	177
ENSMUSG00000042289	chr7	Hsd3b7	0.26464363	0.05931483	0.088283712	4.863600644	0.021195188	0	383	371	347	487	378	600	523	384	516	575
ENSMUSG00000042156	chr14	Dzip1	0.48877467	0.059323046	0.088286539	1.908664865	0.06075697	0	56	49	29	46	44	55	73	83	56	76
ENSMUSG00000014771	chr17	Pdcd2	0.33889515	0.059387447	0.088372973	3.281169015	0.031672112	0	125	137	118	174	83	210	179	148	182	158
ENSMUSG00000025350	chr10	Rdh5	0.29706039	0.059420415	0.088412618	6.296031915	0.02884758	0	1225	1107	945	1121	835	1703	1289	1381	1382	1310
ENSMUSG00000033364	chr1	Usp37	-0.3108742	0.059430591	0.088418346	3.44110802	0.026456533	0	167	173	161	208	176	186	191	128	136	146
ENSMUSG00000033554	chr3	Dph5	0.41343823	0.059443768	0.088428537	2.452725228	0.045053142	0	65	59	59	105	58	98	114	83	121	81
ENSMUSG00000030431	chr7	Tmem238	0.50195603	0.05948489	0.088480292	1.292847849	0.055977616	0	35	31	21	32	24	56	32	40	51	43
ENSMUSG00000029127	chr5	Zbtb49	-0.5545398	0.059547189	0.088563532	1.0087637	0.065448744	0	42	33	31	32	29	26	36	15	20	29
ENSMUSG00000046668	chr18	Cxxc5	0.30332517	0.059568277	0.088585469	4.820026237	0.02878895	0	319	320	321	564	374	446	492	550	485	547
ENSMUSG00000082286	chr11	Pisd-ps1	-0.8505637	0.059640215	0.088683014	3.690610607	0.233541385	0	251	273	201	268	229	518	54	66	64	86
ENSMUSG00000022191	chr15	Drosha	-0.2835445	0.059666607	0.088712819	5.128196691	0.025147001	0	531	474	481	764	616	523	563	537	449	489
ENSMUSG00000042198	chr4	Chchd7	0.28997233	0.059940847	0.089111082	3.997321975	0.024313926	0	212	195	202	296	167	343	311	265	257	251
ENSMUSG00000097624	chr17	Gm5091	-0.8823874	0.059980355	0.089160332	-0.059519715	0.173506646	0	30	9	16	15	11	18	17	3	5	6
ENSMUSG00000014959	chr2	Gorasp2	0.27894449	0.060017457	0.089205995	6.412222837	0.025575743	0	1172	984	947	1552	1117	1547	1678	1330	1485	1577
ENSMUSG00000001761	chr6	Smo	-0.2825773	0.060101486	0.089321391	3.824295492	0.022481274	0	227	210	213	256	238	239	213	170	194	223
ENSMUSG00000030170	chr6	Wnt5b	-0.6379575	0.06014308	0.089364202	1.438239479	0.109564557	0	57	41	29	62	48	66	32	33	14	23
ENSMUSG00000081434	chr2	Gm14165	0.81081105	0.060139587	0.089364202	3.025733041	0.208478121	0	105	73	87	91	74	523	75	87	120	63
ENSMUSG00000036826	chr7	Igflr1	0.6436057	0.06015502	0.089372441	1.140157606	0.105298893	0	30	21	28	27	14	80	35	20	39	36
ENSMUSG00000099843	chr1	Gm7160	0.63565977	0.060210119	0.089444794	0.223050709	0.065385337	0	12	9	10	20	10	24	21	17	24	17
ENSMUSG00000026819	chr2	Slc25a25	-1.0568602	0.060299299	0.089567755	5.963188998	0.364303983	0	232	575	1963	1154	2122	2191	401	202	349	353
ENSMUSG00000000938	chr6	Hoxa10	-0.3106513	0.060332797	0.089607988	4.110983859	0.028696543	0	286	257	249	364	266	201	307	231	213	297
ENSMUSG00000029027	chr4	Dffb	0.62885429	0.060348103	0.089621198	0.996371177	0.092466138	0	34	28	13	22	12	52	30	24	41	39
ENSMUSG00000028582	chr4	Cc2d1b	0.28237817	0.060423517	0.089723659	4.77582559	0.024504154	0	425	381	310	370	337	496	488	424	532	500
ENSMUSG00000020464	chr11	Pnpt1	-0.38054	0.060492006	0.089815816	4.240642361	0.045267806	0	279	327	339	402	240	177	315	224	351	253
ENSMUSG00000039640	chr11	Mrpl12	0.31000038	0.060563683	0.089912687	7.311813215	0.032247196	0	1954	2010	2160	2850	1660	3031	2838	2992	3091	2316
ENSMUSG00000034343	chr1	Ube2f	-0.2661914	0.060653496	0.090036459	6.138274497	0.023162094	0	1189	1047	1085	1336	1059	1068	1092	949	1035	1066
ENSMUSG00000024759	chr19	Atl3	-0.3210937	0.060865495	0.090341564	4.304656704	0.031791129	0	309	357	316	362	276	278	386	193	287	288
ENSMUSG00000078652	chr11	Psme3	0.26258287	0.061010391	0.090547014	6.006795921	0.022498871	0	859	827	776	1143	769	1273	1235	1044	1039	1136
ENSMUSG00000005674	chr1	Tomm40l	-0.3005531	0.061041687	0.090583842	5.764219006	0.029540642	0	932	946	909	991	671	739	832	741	905	730

ENSMUSG00000031533	chr8	Mrps31	-0.266722	0.061109755	0.090675224	4.795982694	0.021797711	0	476	456	406	551	369	408	428	361	452	397
ENSMUSG00000020544	chr11	Cox11	-0.2919561	0.061127657	0.090692159	4.346062365	0.02565369	0	361	325	303	414	263	248	324	261	297	351
ENSMUSG00000036339	chr14	Tmem260	0.40340686	0.061275425	0.090901746	2.374800537	0.041346816	0	59	53	71	75	65	110	91	76	77	119
ENSMUSG00000042745	chr2	Id1	0.47273046	0.061373494	0.091037567	3.933085686	0.071133258	0	96	207	218	233	185	521	287	208	235	212
ENSMUSG00000022109	chr14	Med4	0.283364	0.061520503	0.091245946	4.33376401	0.024027926	0	296	281	224	320	229	485	375	295	310	346
ENSMUSG00000075600	chr15	Zc3h3	0.50238324	0.061529812	0.091250069	2.377039212	0.072039384	0	74	75	39	63	60	110	77	131	58	107
ENSMUSG00000029213	chr5	Commd8	-0.3008277	0.061544645	0.091262382	4.304909038	0.027667466	0	371	354	317	324	241	313	306	227	299	296
ENSMUSG00000025666	chrX	Tmem47	-0.3468201	0.061690517	0.091459283	3.394306738	0.034373018	0	169	164	149	241	152	116	146	139	142	202
ENSMUSG00000039768	chr4	Dnajc11	0.28339971	0.061687358	0.091459283	5.703469701	0.026311874	0	712	607	603	975	632	1003	957	1026	767	897
ENSMUSG00000021025	chr12	Nfkbia	0.45797941	0.061703657	0.091469062	4.778245848	0.068871941	0	287	293	384	413	331	1063	529	335	351	371
ENSMUSG00000089810	chr9	Gm16536	0.35578961	0.061853294	0.091681158	3.12029707	0.035042216	0	119	128	95	137	83	186	134	162	122	183
ENSMUSG00000026803	chr2	Ttf1	-0.3636176	0.061865007	0.091688795	2.875323193	0.03530288	0	143	95	96	164	113	105	110	78	104	120
ENSMUSG00000028648	chr4	Ndufs5	0.27613107	0.061894327	0.091722523	6.576894351	0.025494616	0	1347	1299	1143	1560	1093	1942	1501	1681	1724	1668
ENSMUSG00000036362	chr3	P2ry13	0.59956659	0.061997022	0.091864968	0.361416552	0.061279181	0	14	13	13	15	13	25	29	19	15	26
ENSMUSG00000022528	chr16	Hes1	0.43929378	0.062072948	0.091967722	3.361457361	0.058939652	0	102	170	139	140	87	264	210	215	116	153
ENSMUSG00000037965	chr16	Zc3h7a	0.30212415	0.062114665	0.092019775	4.220902796	0.027591836	0	280	232	219	280	224	415	365	235	369	295
ENSMUSG00000027189	chr2	Trim44	-0.2659588	0.062181925	0.092105141	4.715137935	0.021767471	0	398	411	358	578	398	396	441	323	346	439
ENSMUSG00000032386	chr9	Trip4	-0.2645041	0.062185469	0.092105141	4.297411189	0.020565846	0	295	303	288	407	301	294	291	271	300	291
ENSMUSG00000054641	chr6	Mmrn1	-0.6892198	0.062214275	0.092138043	1.680092802	0.136838761	0	91	18	46	89	46	59	35	17	45	39
ENSMUSG00000026280	chr1	Atg4b	0.25156647	0.062221649	0.0921392	4.792319546	0.019363222	0	366	335	371	474	335	547	494	457	474	477
ENSMUSG00000020212	chr10	Mdm1	0.69527546	0.062270145	0.092201245	0.882384217	0.115961497	0	25	24	19	15	13	41	56	16	39	22
ENSMUSG00000027952	chr3	Pmvk	0.32311826	0.062283642	0.09221146	3.65271108	0.030089334	0	146	181	163	179	150	233	278	204	229	184
ENSMUSG00000100493	chr4	Gm29294	-1.1523961	0.062433664	0.092423778	0.502918378	0.382427425	0	28	30	20	35	21	53	2	5	5	4
ENSMUSG00000087687	chr8	Pet100	0.34458565	0.062532191	0.092559829	4.158458537	0.036924533	0	270	263	236	230	158	410	312	289	357	253
ENSMUSG00000064208	chr10	Gm10145	0.61965043	0.062564239	0.092597459	0.229297182	0.058954717	0	11	11	12	15	12	20	23	16	23	21
ENSMUSG00000054199	chr3	Gon4l	-0.286817	0.062612161	0.092658573	3.93850393	0.024082112	0	243	239	240	323	207	298	242	192	189	206
ENSMUSG00000054256	chr5	Msi1	0.7891444	0.06265295	0.092709119	0.066970854	0.128837473	0	12	7	10	14	7	35	23	17	5	16
ENSMUSG00000020142	chr11	Slc1a4	0.50856225	0.062661103	0.092711368	1.790493284	0.068866137	0	35	42	29	63	38	107	68	55	42	51
ENSMUSG00000032363	chr9	Adamts7	0.62997916	0.062770986	0.092864116	2.240155956	0.118467556	0	53	66	75	43	27	101	76	125	39	114
ENSMUSG00000046167	chr9	Gldn	-0.6699025	0.062917558	0.093071104	0.745397347	0.10563907	0	13	20	23	48	40	24	17	22	14	21
ENSMUSG00000021983	chr14	Atp8a2	-0.5520319	0.062953218	0.093113999	2.145631512	0.090155368	0	93	92	69	66	58	115	54	38	45	39
ENSMUSG00000031595	chr8	Pdgfrl	0.52660067	0.062974166	0.093125271	4.236959764	0.091381826	0	256	228	239	219	190	656	225	450	143	353
ENSMUSG00000098374	chr17	Gm28043	-0.2791519	0.062972898	0.093125271	5.773386809	0.02574706	0	899	847	791	1078	848	723	802	728	754	1016
ENSMUSG00000039016	chr9	Timm8b	-0.3075993	0.063031431	0.093200093	5.877156804	0.031598315	0	1051	985	952	1162	698	837	922	643	1036	839
ENSMUSG00000030091	chr6	Nup210	-0.3008843	0.063075833	0.093255881	5.125248514	0.029348542	0	522	526	473	717	626	504	579	544	507	396
ENSMUSG00000021481	chr13	Zfp346	0.27202656	0.063185622	0.093391576	4.388472373	0.022417693	0	297	287	220	334	269	421	328	358	355	398
ENSMUSG00000029920	chr6	Smarcad1	-0.3321935	0.06318766	0.093391576	3.112554296	0.030169854	0	161	130	121	177	123	154	131	85	125	126
ENSMUSG00000071281	chr13	Zfp65	-0.4153972	0.063179929	0.093391576	2.083174845	0.043266024	0	83	71	68	84	46	55	63	52	54	64
ENSMUSG00000023915	chr17	Tnfrsf21	0.32048322	0.063293259	0.093537759	5.050109673	0.033638655	0	378	447	397	598	382	451	606	592	519	813
ENSMUSG00000022199	chr14	Slc22a17	0.47447243	0.063309555	0.093542059	2.101070043	0.060033362	0	57	60	36	48	56	94	54	86	65	96
ENSMUSG00000062329	chr5	Cytl1	-0.6919733	0.063303227	0.093542059	1.759560717	0.142260376	0	26	76	49	68	79	87	21	34	32	34
ENSMUSG00000051355	chr11	Commd1	0.28094536	0.0633595	0.093605959	5.821719931	0.02620358	0	786	829	688	895	603	1161	1050	796	1118	942
ENSMUSG00000014402	chr7	Tsg101	0.26124635	0.063382138	0.093629506	5.485365552	0.022210719	0	687	567	518	730	535	910	764	731	740	840
ENSMUSG00000022553	chr15	Maf1	-0.2863183	0.06346741	0.093745564	6.313709184	0.027664289	0	1329	1272	1075	1677	1188	1539	999	934	1158	1255
ENSMUSG00000084384	chr11	Gm12251	0.34094386	0.063475577	0.093747719	3.495778663	0.034547779	0	141	166	135	181	112	268	152	216	192	190
ENSMUSG00000024076	chr17	Vit	-0.7107558	0.063509499	0.093787907	1.387105586	0.148689328	0	67	25	50	51	38	65	31	11	34	17
ENSMUSG00000028920	chr4	Fbxo42	-0.2951538	0.063684314	0.094036131	3.938492371	0.025970191	0	217	209	226	354	253	282	221	179	194	248
ENSMUSG00000022248	chr15	Rad1	0.40022096	0.063835759	0.094249796	2.398459538	0.041829562	0	71	60	59	86	56	110	120	74	100	75
ENSMUSG00000062867	chr9	Impdh2	0.29981276	0.063852536	0.094264608	5.505956912	0.029876275	0	587	497	465	879	634	1016	949	711	716	713
ENSMUSG00000039501	chr2	Znfx1	-0.3135973	0.063875934	0.09428919	4.627269128	0.031540881	0	354	329	389	568	405	367	336	301	289	507
ENSMUSG00000027188	chr2	Pamr1	0.46581059	0.063906895	0.09432493	3.798424316	0.070534574	0	293	106	148	226	103	233	236	264	194	378
ENSMUSG00000038736	chr15	Nudcd1	-0.4565696	0.063948822	0.094366882	2.624885117	0.060037249	0	101	94	80	128	119	52	123	72	87	80
ENSMUSG00000103578	chr10	AC153941.1	0.65006064	0.063944813	0.094366882	1.558634422	0.119828018	0	39	54	9	29	31	54	65	39	49	75
ENSMUSG00000036862	chr7	Dchs1	-0.4279966	0.06396029	0.09437379	3.769925056	0.058668607	0	189	199	206	374	208	285	160	186	89	234
ENSMUSG00000098188	chr10	Sowahc	0.65006017	0.063967009	0.09437379	1.558634422	0.119851774	0	39	54	9	29	31	54	65	39	49	75
ENSMUSG00000038827	chr4	Fam206a	0.45113507	0.06404866	0.094484281	2.114895859	0.053528574	0	32	55	46	78	55	96	98	66	69	69
ENSMUSG00000040272	chr2	Accs	0.42761541	0.06406705	0.094501435	1.946520487	0.044457775	0	55	53	38	50	40	78	71	64	53	84
ENSMUSG00000091989	chr7	Gm17257	0.59963416	0.06414604	0.094607963	0.731001811	0.072871811	0	15	15	22	21	17	45	27	23	35	21
ENSMUSG00000015126	chr17	Tsr3	0.27617571	0.064244368	0.094732991	4.112343391	0.022678701	0	268	213	200	272	206	340	354	252	298	296
ENSMUSG00000038422	chr4	Hdhd3	0.44254379	0.064241056	0.094732991	2.881852207	0.058956175	0	82	94	110	115	57	179	125	171	89	117
ENSMUSG00000060260	chr7	Pwwp2b	0.4147887	0.064273105	0.094765367	2.312330147	0.046178446	0	52	53	55	98	55	126	93	65	89	82
ENSMUSG00000030551	chr7	Nr2f2	-0.3265281	0.064309952	0.094809693	3.937602098	0.032936562	0	227	231	238	281	276	188	238	186	188	303
ENSMUSG00000027508	chr3	Pag1	-0.4111179	0.064339473	0.09484321	2.645559231	0.048387894	0	94	114	75	129	111	83	106	54	79	111
ENSMUSG00000033773	chr5	Rpap2	0.49302281	0.064396048	0.094916597	3.247240011	0.077268435	0	141	112	92	151	89	75	181	164	226	236
ENSMUSG00000024240	chr18	Epc1	-0.2810039	0.064420478	0.094942593	4.264643285	0.024102702	0	296	268	289	433	288	311	254	225	277	347

ENSMUSG00000068699	chr6	Flnc	-0.4436625	0.064475982	0.095014374	9.212163167	0.068538154	0	7500	6229	8007	20031	10839	12647	7479	7616	7151	6489
ENSMUSG00000029173	chr5	Sepsecs	-0.3225546	0.064496407	0.095034452	3.262114387	0.028725907	0	173	141	122	210	145	131	156	113	149	138
ENSMUSG00000098253	chr18	Mir7219	-0.4488562	0.064662372	0.095268955	2.04173255	0.051448188	0	60	70	66	94	56	43	55	65	62	48
ENSMUSG00000036752	chr2	Tubb4b	-0.3646452	0.064793345	0.095451859	7.818627175	0.046284215	0	4642	2769	3031	4767	3830	3082	3995	2807	3875	2267
ENSMUSG00000030048	chr6	Gkn3	0.73926018	0.064883395	0.095574444	0.229023902	0.118052685	0	9	8	13	15	13	7	28	25	23	22
ENSMUSG00000038530	chr1	Rgs4	-0.422824	0.064894673	0.095580984	3.379362214	0.055477455	0	115	178	134	347	133	131	158	115	155	158
ENSMUSG00000022022	chr14	Mtrf1	-0.3188476	0.064906045	0.095587659	3.1366228	0.028033761	0	160	127	131	173	128	119	123	111	125	152
ENSMUSG00000053641	chr9	Dennd4a	0.42187954	0.065029194	0.095758931	2.9460249	0.053181557	0	99	104	77	124	81	237	150	82	133	118
ENSMUSG00000054280	chr5	Prr14l	-0.3317199	0.065059737	0.095793814	3.1576803	0.030992453	0	142	141	156	170	121	175	121	110	121	113
ENSMUSG00000029145	chr5	Eif2b4	0.26495152	0.065128697	0.095885248	5.870194072	0.023596539	0	783	721	722	1023	720	1101	973	1059	1065	985
ENSMUSG00000052752	chr17	Traf7	0.25798344	0.065228154	0.096021559	4.949439201	0.021256179	0	382	400	363	542	409	673	564	509	506	492
ENSMUSG00000000282	chr11	Mnt	0.39736046	0.06536737	0.096216363	3.616201445	0.049224158	0	139	164	174	153	141	339	230	200	121	252
ENSMUSG00000032295	chr9	Man2c1	0.26038648	0.065377646	0.096221354	4.433520573	0.020823771	0	294	262	244	388	278	457	368	366	323	404
ENSMUSG00000010660	chr9	Plcd1	0.28859057	0.065430169	0.096278379	3.990731007	0.025104111	0	243	206	177	238	193	275	259	292	289	294
ENSMUSG00000084790	chr16	Gm15879	-0.6464926	0.065426872	0.096278379	0.268414438	0.08499178	0	16	16	25	21	20	9	20	10	11	19
ENSMUSG00000062619	chr17	2310039H08Rik	0.32227214	0.06563167	0.096564715	3.760282739	0.03152203	0	219	183	166	180	137	215	257	228	272	239
ENSMUSG00000067931	chr17	Zfp948	-0.5533106	0.065807168	0.096812735	1.366956022	0.079326933	0	38	35	56	49	39	23	39	34	43	22
ENSMUSG00000022324	chr15	Matn2	-0.2783912	0.065839178	0.096849632	4.212516927	0.023860155	0	344	278	294	330	255	299	298	259	213	294
ENSMUSG00000024571	chr18	Gm16286	0.26327784	0.065928711	0.096971129	6.079842624	0.023550204	0	965	803	816	1147	858	1404	1228	1014	1224	1161
ENSMUSG00000032479	chr9	Map4	-0.2793951	0.066036342	0.097119217	8.746981834	0.027508051	0	6952	6132	6118	9048	6990	6855	6007	6270	5675	6877
ENSMUSG00000038838	chr17	Vars2	-0.3223456	0.066140753	0.097262539	3.860305251	0.031995716	0	202	219	243	301	228	174	207	223	173	264
ENSMUSG00000078350	chr4	Smim1	0.4738655	0.0661567	0.097275754	2.431835193	0.063990047	0	66	68	57	54	78	104	66	118	82	128
ENSMUSG00000032355	chr9	Mlip	-0.2923778	0.066455659	0.09770506	6.483165352	0.029611576	0	1606	1264	1234	1807	1441	1187	1323	1074	1445	1519
ENSMUSG00000030711	chr7	Sult1a1	-0.4245735	0.06652059	0.09777995	3.837920519	0.059413708	0	232	289	219	270	198	369	121	141	164	213
ENSMUSG00000092187	chr7	Gm20457	0.60933064	0.066518132	0.09777995	0.590612704	0.074337017	0	18	15	9	19	20	19	35	27	25	29
ENSMUSG00000032232	chr9	Cgnl1	0.29269253	0.066620119	0.097915951	3.80953203	0.02575564	0	210	161	156	236	172	253	249	278	209	256
ENSMUSG00000083458	chr19	Gm5510	-0.7799006	0.066706788	0.098033025	0.208549792	0.156508164	0	22	19	20	20	16	32	8	3	7	14
ENSMUSG00000001508	chr11	Sgca	-0.2794025	0.066763453	0.098105707	7.543123117	0.027452163	0	3015	2936	2378	3787	3152	2707	2931	2487	2546	3083
ENSMUSG00000045761	chr17	Fam179a	0.52217671	0.066770284	0.098105707	2.840388139	0.086372991	0	56	93	96	129	60	198	114	152	148	63
ENSMUSG00000038365	chr8	Fbxo25	-0.316543	0.066842227	0.09820109	3.415329533	0.029494275	0	211	184	160	179	135	162	146	135	149	176
ENSMUSG00000027433	chr2	Xrn2	0.28190174	0.066882311	0.098249651	4.267004854	0.024737666	0	259	249	240	325	218	357	433	253	309	371
ENSMUSG00000037032	chr7	Apbb1	0.40934586	0.066928418	0.098307048	3.791249953	0.054840448	0	202	150	153	232	148	270	168	390	216	216
ENSMUSG00000083649	chr7	Rasl2-9	-0.6074609	0.066966024	0.09835195	0.541720858	0.075557945	0	25	21	28	27	19	22	10	18	23	13
ENSMUSG00000003438	chr7	Timm50	0.25932374	0.067090528	0.098524453	5.495813278	0.0225429	0	594	579	514	793	587	946	773	731	800	759
ENSMUSG00000024174	chr17	Pot1b	0.48187521	0.067404663	0.09897537	1.055474051	0.048912317	0	25	22	27	29	18	36	38	33	40	38
ENSMUSG00000024498	chr18	Tcerg1	-0.2683287	0.067438309	0.098993573	4.769622666	0.023239419	0	414	408	409	587	405	386	491	348	408	377
ENSMUSG00000027597	chr2	Ahcy	-0.2945415	0.067433075	0.098993573	4.608554024	0.028173516	0	395	374	369	483	373	307	387	297	444	336
ENSMUSG00000053390	chr17	Zfp952	-0.3715784	0.067427975	0.098993573	2.455316966	0.035606208	0	85	93	71	122	83	71	75	71	79	85
ENSMUSG00000039759	chr4	Thap3	0.26884587	0.06745092	0.099001686	5.172643383	0.023973886	0	525	514	466	545	376	741	632	592	664	578
ENSMUSG00000037605	chr5	Lphn3	0.7904913	0.067520426	0.099093298	0.197282817	0.149748104	0	11	6	14	12	12	5	22	23	21	33
ENSMUSG00000032563	chr9	Mrpl3	-0.2775446	0.067618118	0.099226252	5.361261497	0.025935828	0	692	709	660	768	515	571	630	560	656	597
ENSMUSG00000026248	chr1	Mrpl44	0.26985419	0.067717428	0.099359337	5.254034453	0.024429443	0	523	517	465	697	391	688	628	638	621	821
ENSMUSG00000038806	chr1	Sde2	-0.288417	0.067723028	0.099359337	3.629536055	0.024301186	0	217	190	177	269	160	227	177	144	167	192
ENSMUSG00000079469	chr9	Pigb	-0.4313343	0.067998426	0.099752913	2.099274194	0.049481432	0	78	68	57	80	73	48	74	51	43	74
ENSMUSG00000025340	chr5	Rabgef1	-0.2837031	0.06821917	0.100066238	6.006805161	0.027927922	0	1087	956	970	1251	988	845	936	826	894	1225
ENSMUSG00000024958	chr19	Gpr137	0.37084134	0.068310295	0.100189389	3.573559343	0.043939361	0	139	121	162	237	117	318	159	229	195	187
ENSMUSG00000013465	chr2	Nelfb	0.24803032	0.068449228	0.100372092	4.968260034	0.020009801	0	418	426	353	511	417	585	539	486	549	607
ENSMUSG00000026083	chr1	Eif5b	0.29500813	0.068447082	0.100372092	6.869208531	0.030843295	0	1600	1394	1238	2210	1463	1884	1940	2331	1968	2312
ENSMUSG00000023007	chr15	Prpf40b	-0.2750773	0.068521466	0.10046748	4.084265415	0.023183659	0	279	244	221	357	280	258	259	225	262	239
ENSMUSG00000040767	chr11	Snrnp25	0.37709247	0.068597557	0.10056649	3.178363655	0.043200246	0	136	122	88	119	111	229	154	151	177	114
ENSMUSG00000063412	chr8	Gm10131	0.5131938	0.068603386	0.10056649	1.399401727	0.067189131	0	42	22	18	51	24	53	56	48	36	48
ENSMUSG00000022136	chr14	Dnajc3	-0.2809318	0.068694293	0.100689191	5.465303623	0.027022071	0	707	686	654	915	653	740	817	469	636	606
ENSMUSG00000032497	chr9	Lrrfip2	0.26167881	0.068747145	0.100756093	5.966266169	0.023692126	0	882	763	779	1056	762	1107	1050	1022	1139	1228
ENSMUSG00000053730	chr4	Tmem39b	0.43844974	0.068803642	0.100828321	1.673751674	0.046561226	0	33	32	36	57	37	65	67	58	43	55
ENSMUSG00000038502	chr7	Ptov1	0.30867512	0.068847264	0.10088167	6.78912373	0.033828386	0	1436	1244	1210	1971	1539	2761	1692	1984	1520	2091
ENSMUSG00000068479	chr2	Mfap1a	-0.2915172	0.068882962	0.100923396	3.489871036	0.024587038	0	176	177	143	241	180	184	176	132	148	180
ENSMUSG00000037847	chr19	Nmrk1	0.59047814	0.068985015	0.101062324	1.575862871	0.10041984	0	49	42	24	32	22	32	71	38	73	64
ENSMUSG00000025821	chr6	Zfp282	-0.2725232	0.069167025	0.101318346	3.686254663	0.021663475	0	196	185	188	272	203	202	195	164	179	205
ENSMUSG00000078923	chr2	Ube2v1	-0.2729023	0.069254823	0.101436325	5.145317168	0.02508588	0	589	467	552	692	575	456	541	465	530	610
ENSMUSG00000031447	chr8	Lamp1	0.27843217	0.069286838	0.101472582	9.130243605	0.028010151	0	7805	7439	6593	9051	6890	12032	10600	7532	9566	10779
ENSMUSG00000027313	chr2	Chac1	-0.6457501	0.069307565	0.101492302	4.664852726	0.146784755	0	473	984	264	299	237	564	217	340	179	331
ENSMUSG00000024379	chr18	Tslp	0.80973702	0.069332391	0.10151802	0.647545271	0.179295052	0	18	31	12	13	3	33	27	40	13	36
ENSMUSG00000029028	chr4	Lrrc47	0.2816143	0.069395777	0.101600187	5.026185536	0.026758783	0	379	370	391	613	446	699	525	631	467	588
ENSMUSG00000028348	chr4	Murc	-0.2864794	0.069638144	0.101944349	7.510443414	0.029471828	0	3013	2404	2422	3963	3208	2873	2467	2536	2782	2726
ENSMUSG00000020346	chr11	Mgat1	0.27558123	0.069686851	0.102004967	5.733367101	0.026326126	0	778	654	681	859	612	1297	827	786	908	963

ENSMUSG00000038122	chr10	Tbc1d32	-0.5598901	0.069820305	0.10218961	1.452993113	0.085897477	0	48	47	50	61	28	22	49	19	36	47
ENSMUSG00000020074	chr10	Ccar1	-0.2711227	0.069924069	0.102311896	4.764403205	0.024301207	0	446	413	393	533	422	362	454	310	433	443
ENSMUSG00000021991	chr14	Cacna2d3	-0.6769241	0.069917753	0.102311896	0.484795123	0.106096731	0	33	17	30	17	19	9	15	14	19	23
ENSMUSG00000023923	chr17	Tbc1d5	0.30580867	0.069925818	0.102311896	3.64133904	0.028567929	0	147	158	120	232	173	274	241	171	201	236
ENSMUSG00000036270	chr8	Edc4	-0.2518681	0.069943574	0.102327164	4.795893119	0.020776087	0	441	399	408	536	455	477	431	385	338	438
ENSMUSG00000026575	chr1	Nme7	0.55671041	0.070002904	0.102403243	1.644121764	0.085777202	0	46	42	45	27	18	71	61	67	43	49
ENSMUSG00000027523	chr2	Gnas	-0.3028429	0.070022262	0.102420841	10.05020408	0.033377827	0	17393	15996	15315	22115	16743	14628	14638	15186	12555	20512
ENSMUSG00000004500	chr7	Zfp324	-0.435374	0.070062478	0.102458218	1.705217624	0.044357718	0	47	50	50	76	48	36	44	44	44	49
ENSMUSG00000036863	chr3	Syde2	-0.5799793	0.070061003	0.102458218	0.466059956	0.070711241	0	24	23	23	22	20	25	15	9	20	14
ENSMUSG00000026374	chr1	Tsn	0.25492933	0.070123889	0.102537296	5.623720253	0.022349019	0	716	677	604	787	561	969	959	783	842	822
ENSMUSG00000032175	chr9	Tyk2	0.30290328	0.070194388	0.102629644	3.767341593	0.028028395	0	178	182	173	189	172	320	253	175	251	226
ENSMUSG00000031723	chr8	Txnl4b	0.28932358	0.07021633	0.102650986	3.694080443	0.025458792	0	191	164	160	210	137	256	230	212	253	198
ENSMUSG00000024091	chr17	Vapa	-0.2737865	0.070389727	0.102891979	6.807060684	0.026813649	0	1922	1610	1619	2190	1789	1521	1869	1462	1583	1828
ENSMUSG00000042305	chr1	Tmem183a	0.26711967	0.0703959	0.102891979	4.392629094	0.022717007	0	300	254	275	329	253	463	426	318	316	350
ENSMUSG00000025432	chr10	Avil	-0.6141655	0.070498364	0.103030967	0.797681062	0.092814581	0	42	29	21	25	28	36	23	10	18	19
ENSMUSG00000020692	chr11	Nle1	0.37261142	0.07062438	0.103200747	2.953869593	0.04081526	0	108	91	75	104	114	162	185	111	128	119
ENSMUSG00000097177	chr9	9330159M07Rik	0.63129895	0.070629304	0.103200747	1.169205885	0.11320397	0	25	15	31	37	17	18	38	45	54	52
ENSMUSG00000075224	chr2	Lrrc55	-0.7364799	0.070655841	0.103228731	0.555217747	0.141584902	0	33	35	27	20	10	14	21	26	8	13
ENSMUSG00000037426	chr5	Depdc5	-0.3346197	0.070669629	0.103238082	3.324508424	0.034094846	0	149	123	157	196	195	176	131	146	122	141
ENSMUSG00000021693	chr13	Kif2a	-0.2741701	0.070854833	0.10349782	3.812893888	0.022900978	0	223	212	211	262	226	225	247	173	187	201
ENSMUSG00000050064	chr3	Zfp697	0.750537	0.070898921	0.103551397	-0.17231021	0.119104106	0	12	7	3	17	4	10	22	14	17	14
ENSMUSG00000032673	chr11	Prorsd1	-0.3070349	0.070921261	0.103573202	3.879875789	0.029843202	0	311	235	221	267	171	220	220	191	232	201
ENSMUSG00000037890	chr5	Wdr19	0.45473518	0.070928727	0.103573283	1.465703854	0.048425886	0	43	29	31	35	27	65	43	48	45	48
ENSMUSG00000030256	chr6	Bhlhe41	-0.3542802	0.071032669	0.103714228	5.644014303	0.044706054	0	945	811	959	791	623	602	789	690	511	986
ENSMUSG00000028698	chr4	Pik3r3	-0.3312353	0.071047785	0.103718936	3.389822615	0.033107546	0	185	159	161	233	130	166	118	164	122	179
ENSMUSG00000068115	chr2	Ninl	0.63942633	0.071050736	0.103718936	0.765582457	0.110206244	0	22	20	11	23	16	18	21	46	40	28
ENSMUSG00000029687	chr6	Ezh2	0.35884589	0.071062151	0.103724765	2.951316124	0.038499499	0	89	99	98	133	80	145	177	108	156	112
ENSMUSG00000037251	chr8	Pomk	0.34832313	0.071190785	0.103879976	3.78314955	0.039480253	0	206	157	172	186	168	171	256	233	305	270
ENSMUSG00000066058	chr4	Cldn19	-0.5324645	0.071188227	0.103879976	1.994809289	0.085710651	0	48	30	66	122	81	59	54	44	43	59
ENSMUSG00000074521	chr2	Gm14327	-0.6030237	0.071179009	0.103879976	0.250860385	0.062141238	0	18	18	14	29	18	12	13	12	15	17
ENSMUSG00000016262	chr1	Sertad4	0.37917705	0.071273196	0.103989371	3.140510466	0.044885126	0	119	117	97	132	98	137	173	209	108	169
ENSMUSG00000031021	chr7	Tmem9b	0.25166182	0.071307498	0.104028559	5.355000438	0.021696829	0	591	528	489	687	490	723	793	651	734	716
ENSMUSG00000024810	chr19	Il33	0.51089144	0.071322043	0.104038917	3.12682997	0.086687182	0	110	122	113	100	78	331	177	125	122	87
ENSMUSG00000026885	chr2	Ttll11	0.44556991	0.07147241	0.104243586	1.464519688	0.046675612	0	30	26	29	43	38	47	49	50	45	56
ENSMUSG00000038612	chr3	Mcl1	0.33097522	0.071477267	0.104243586	7.697540334	0.039989914	0	2474	2690	2570	3694	2355	6125	3836	2611	3078	3554
ENSMUSG00000001786	chr10	Fbxo7	0.3157075	0.071619357	0.104439913	3.411938609	0.030077004	0	160	118	128	179	117	233	185	154	218	164
ENSMUSG00000044167	chr3	Foxo1	-0.3211592	0.071815147	0.104714501	4.178606659	0.034427264	0	229	275	261	401	328	340	225	234	192	326
ENSMUSG00000027377	chr2	Mall	0.45400023	0.072103313	0.105112747	2.106402834	0.059772716	0	54	50	32	79	51	73	79	85	51	106
ENSMUSG00000047766	chr9	Lrrc49	0.47224503	0.072100235	0.105112747	2.12350423	0.065860348	0	61	49	45	71	40	60	87	48	110	95
ENSMUSG00000029462	chr5	Vps29	0.28472039	0.072185403	0.105221443	4.509437351	0.027040578	0	343	299	289	362	232	412	480	330	450	358
ENSMUSG00000020022	chr10	Ndufa12	0.26037568	0.072238827	0.105288335	7.339643178	0.024722326	0	2229	2120	1819	2790	2066	3134	2823	2811	2707	2922
ENSMUSG00000080059	chr4	Rps19-ps3	0.622888	0.072251094	0.105295234	0.327823819	0.075055699	0	18	9	14	16	9	27	17	28	19	20
ENSMUSG00000038539	chr7	Atf5	-0.3762544	0.072303955	0.105361284	5.880447976	0.051175469	0	671	736	785	1734	1128	1235	755	762	723	737
ENSMUSG00000078517	chr4	Emc1	0.25934074	0.072330888	0.105389542	5.596548934	0.023498351	0	642	573	599	774	680	1016	889	828	747	823
ENSMUSG00000010097	chr19	Nxf1	0.26154304	0.072399878	0.105479068	6.338512309	0.024530037	0	1184	973	1061	1283	974	1711	1380	1290	1427	1401
ENSMUSG00000009647	chr10	Mcu	0.26794347	0.072474696	0.105577064	5.668301782	0.025343384	0	662	606	587	926	672	1069	822	916	755	972
ENSMUSG00000094114	chr13	Gm21967	0.50613486	0.072548856	0.105674081	1.817094941	0.073960382	0	43	33	32	61	42	39	90	76	53	64
ENSMUSG00000032376	chr9	Usp3	0.31484699	0.072565707	0.105687611	3.570825284	0.031009577	0	164	151	162	173	128	206	207	175	268	204
ENSMUSG00000027635	chr2	Dsn1	0.57048084	0.072678587	0.105840984	1.256026313	0.085157402	0	27	31	35	21	19	58	55	24	49	36
ENSMUSG00000048078	chr7	Tenm4	0.64084171	0.07269097	0.105847989	2.004460165	0.130713971	0	24	62	37	45	55	30	76	106	74	93
ENSMUSG00000021782	chr14	Dlg5	-0.3678567	0.072810954	0.106011656	2.768242993	0.039904577	0	117	88	100	152	109	121	97	74	68	122
ENSMUSG00000021377	chr13	Dek	-0.3246958	0.072821734	0.106016307	4.850159387	0.0367779	0	457	429	410	629	468	343	608	297	450	384
ENSMUSG00000018906	chr11	P4ha2	0.28610383	0.07288836	0.106080154	4.645248543	0.027789775	0	271	308	298	462	342	505	440	499	354	433
ENSMUSG00000024085	chr17	Man2a1	0.28190483	0.07288781	0.106080154	4.934094435	0.027217015	0	318	386	376	502	460	612	585	449	454	644
ENSMUSG00000046806	chr6	3110062M04Rik	0.37756092	0.072873522	0.106080154	2.498149094	0.039560672	0	83	62	70	75	66	93	90	98	110	116
ENSMUSG00000018809	chr11	Smyd4	-0.3718346	0.072996145	0.106225961	2.389221618	0.037740282	0	75	76	94	115	72	71	74	70	67	82
ENSMUSG00000093574	chr5	Gm20671	-0.2970954	0.073008552	0.106232954	3.989874624	0.028669171	0	283	249	230	337	206	289	231	149	245	251
ENSMUSG00000039959	chr5	Hip1	0.27377202	0.07305721	0.106292688	5.606737901	0.026491759	0	784	642	551	710	586	934	900	790	696	1040
ENSMUSG00000037003	chr15	Tenc1	-0.3208734	0.073157916	0.106428129	5.32801103	0.036705455	0	525	616	605	903	681	904	479	540	518	491
ENSMUSG00000034949	chr10	Zfr2	0.51069662	0.073166964	0.106430214	1.156039929	0.061427494	0	26	30	19	31	23	43	27	48	43	39
ENSMUSG00000098812	chr2	Mir7578	-0.6431859	0.073658844	0.107134562	0.443652648	0.09790735	0	20	20	17	29	27	6	13	19	17	23
ENSMUSG00000030768	chr1	Disp1	-0.3714092	0.073756595	0.107256487	2.715413216	0.040491403	0	93	101	90	157	106	77	99	101	76	104
ENSMUSG00000097062	chr11	Gm17586	0.38831708	0.073758021	0.107256487	2.185694158	0.040433251	0	61	50	58	67	49	77	101	76	82	72
ENSMUSG00000031730	chr8	Dhodh	-0.287778	0.073771434	0.107264832	3.612838632	0.025595791	0	202	200	200	232	158	165	188	151	184	202
ENSMUSG00000096983	chr11	2010015M23Rik	0.77012423	0.073817883	0.107321204	-0.130197491	0.123066423	0	4	7	12	6	13	26	9	15	17	14

ENSMUSG00000048170	chr7	Mcmbp	-0.2785074	0.074087549	0.107690856	4.351233511	0.025607648	0	337	291	261	472	315	307	347	257	325	260
ENSMUSG00000079499	chr2	6530402F18Rik	-0.4907675	0.074081439	0.107690856	2.48046247	0.075597893	0	106	57	84	172	70	52	68	64	102	81
ENSMUSG00000020467	chr11	Efemp1	-0.3755923	0.074127815	0.10773818	2.96921024	0.044238372	0	107	123	139	129	143	99	96	91	113	149
ENSMUSG00000003464	chr1	Pex19	-0.260628	0.074144988	0.107751935	6.982243777	0.024972727	0	2096	2035	1837	2612	1731	1933	1787	1792	1706	2167
ENSMUSG00000016520	chr5	Lnx2	-0.3916883	0.07423506	0.107871615	2.636443528	0.046056966	0	93	115	85	133	92	119	87	87	51	90
ENSMUSG00000018651	chr11	Tada2a	0.29196788	0.074273524	0.107916288	3.601167335	0.026193014	0	198	149	153	174	129	221	228	206	215	207
ENSMUSG00000040964	chr4	Arhgef10l	-0.2731786	0.074318415	0.107970287	6.015949382	0.026964321	0	985	870	867	1511	1088	1018	956	931	934	930
ENSMUSG00000047166	chr15	Tigd5	0.49959298	0.074543517	0.108286061	1.026322208	0.056043305	0	21	28	22	25	21	44	28	35	42	33
ENSMUSG00000031546	chr8	Gins4	0.29921834	0.074687001	0.108483219	3.731196104	0.028344924	0	195	173	155	191	162	259	281	178	262	207
ENSMUSG00000042978	chr7	Sbk1	-0.2671102	0.074741039	0.108550427	5.810439684	0.025666574	0	910	910	841	1079	817	781	748	889	766	947
ENSMUSG00000024312	chr17	Wdr46	0.31809787	0.07475971	0.108566262	3.321817523	0.031339881	0	129	121	96	185	130	231	199	169	142	158
ENSMUSG00000033949	chr18	Trim36	0.77844281	0.07490752	0.108769611	0.102600136	0.151338359	0	4	7	15	19	7	24	33	7	19	15
ENSMUSG00000043068	chr8	Fam89a	-0.7250595	0.07497884	0.10886186	-0.103279951	0.103979961	0	15	20	9	22	10	16	14	9	4	7
ENSMUSG00000051375	chr18	Pcdh1	-0.3402346	0.075151871	0.10910175	4.240686566	0.040127508	0	308	330	319	361	244	327	189	295	188	359
ENSMUSG00000026730	chr2	Pter	-0.3273185	0.075216912	0.109184832	3.596303688	0.034582792	0	192	190	147	247	219	138	179	144	187	217
ENSMUSG00000047139	chr10	Cd24a	0.4392031	0.075432102	0.10948583	6.616541372	0.072026948	0	1074	1350	1461	1251	993	1143	1837	1383	3032	1685
ENSMUSG00000048856	chr12	Slc25a47	0.72877494	0.075441395	0.109487948	0.777267506	0.14933715	0	18	7	27	19	17	11	37	32	43	36
ENSMUSG00000020448	chr11	Rnf185	0.24749137	0.075458512	0.109501419	4.831575408	0.02081847	0	357	331	389	493	365	521	515	430	512	536
ENSMUSG00000096433	chr17	Gm4944	0.55706173	0.075549282	0.109621758	1.500852054	0.089328136	0	37	40	18	28	38	31	65	45	55	65
ENSMUSG00000024350	chr18	Dnajc18	-0.2431292	0.075570037	0.10964049	5.039264945	0.020369099	0	597	505	454	601	488	518	459	462	477	533
ENSMUSG00000030983	chr7	Bccip	-0.271091	0.075818114	0.109988994	5.482464751	0.026347916	0	720	642	615	1003	686	660	767	542	721	608
ENSMUSG00000046916	chr10	Myct1	-0.3563384	0.075859779	0.110038014	3.285931671	0.040890531	0	177	175	161	203	95	132	124	132	119	183
ENSMUSG00000025981	chr1	Coq10b	-0.3299556	0.075927445	0.110124738	4.498813996	0.038477427	0	308	375	450	471	264	455	373	224	298	296
ENSMUSG00000049396	chr11	Gemin4	0.35723957	0.076039654	0.110276041	2.560299331	0.036823343	0	80	74	50	103	73	117	113	97	107	95
ENSMUSG00000056952	chr6	Tatdn2	-0.2879492	0.076373308	0.110748429	4.491340148	0.028530273	0	342	317	339	531	324	364	366	223	384	314
ENSMUSG00000025555	chr14	Farp1	0.34522717	0.07651531	0.110942834	3.045687231	0.037091136	0	86	90	103	157	102	172	133	157	111	171
ENSMUSG00000043858	chr7	Nup62	0.26343448	0.076601235	0.111055898	4.91464859	0.024283523	0	400	348	324	546	429	649	552	534	435	513
ENSMUSG00000020268	chr11	Lyrm7	-0.3814072	0.076783365	0.111304049	3.675349681	0.050039614	0	221	224	218	256	150	103	220	161	212	193
ENSMUSG00000061024	chr1	Rrs1	0.28932824	0.076788326	0.111304049	4.098187196	0.028035844	0	215	228	200	300	203	295	418	264	263	289
ENSMUSG00000075254	chr16	Heg1	-0.3541681	0.076812112	0.111326981	5.338743526	0.04620109	0	633	626	622	771	708	572	654	695	295	675
ENSMUSG00000020591	chr12	Ntsr2	-0.5482227	0.076821147	0.111328531	1.249573134	0.085505367	0	38	43	26	43	49	55	27	25	17	28
ENSMUSG00000068917	chr3	Clk2	0.27636215	0.077078928	0.111690524	3.855997298	0.024343664	0	201	184	193	219	168	329	233	234	255	236
ENSMUSG00000028358	chr4	Zfp618	-0.6619475	0.077157505	0.111792794	0.149676905	0.094480777	0	12	20	25	21	12	18	13	10	6	16
ENSMUSG00000024451	chr18	Arap3	-0.3278116	0.077243458	0.111905729	4.283239083	0.037674843	0	290	299	306	493	242	449	248	251	212	258
ENSMUSG00000014195	chr11	Dnajc7	0.25630514	0.077377927	0.112088921	6.922478139	0.024691246	0	1644	1594	1522	2188	1341	2388	2193	2105	2052	2026
ENSMUSG00000045216	chr1	Hs6st1	-0.2529396	0.07741709	0.112134029	5.318884316	0.022875639	0	641	537	610	821	625	610	602	560	515	681
ENSMUSG00000006057	chr11	Atp5g1	0.28442343	0.077480299	0.112213955	8.821973983	0.030926961	0	5540	6096	6077	7934	4893	9497	6996	8436	7832	7748
ENSMUSG00000097743	chr14	Gm16973	0.55882563	0.077567697	0.112328891	0.762633035	0.074859248	0	18	22	14	27	14	39	27	27	40	19
ENSMUSG00000089698	chr16	Gm2541	-0.6337367	0.07761077	0.112379623	0.648267744	0.103378524	0	21	24	19	37	31	7	28	17	15	25
ENSMUSG00000032526	chr9	Deb1	0.27891722	0.077820115	0.11267108	5.142593815	0.028115825	0	567	460	403	571	379	572	647	647	705	555
ENSMUSG00000037196	chr17	Pacrg	0.64843153	0.077843115	0.112692705	0.348923052	0.090582439	0	7	11	20	11	16	28	17	23	22	24
ENSMUSG00000040734	chr7	Ppp1r13l	0.56230241	0.077885003	0.112741667	1.814850409	0.098910811	0	31	31	29	75	42	123	40	60	46	65
ENSMUSG00000068328	chr6	Aup1	0.25193704	0.077952248	0.112827321	5.725267745	0.023146156	0	807	663	620	828	672	1108	1029	779	848	945
ENSMUSG00000005873	chr18	Reep5	0.2643216	0.078149899	0.113101687	7.606723878	0.026623495	0	2910	2535	2269	3111	2381	3333	3466	3176	3602	3739
ENSMUSG00000041734	chr3	Kirrel	0.28010566	0.078227851	0.11320278	3.844753119	0.025525008	0	184	161	161	255	202	293	299	233	218	236
ENSMUSG00000031834	chr8	Pik3r2	0.27578169	0.078344834	0.113360327	4.979130045	0.027166629	0	461	365	386	485	417	602	474	572	449	715
ENSMUSG00000031438	chrX	Rnf128	-0.3206513	0.078409272	0.113441821	4.586407461	0.036850484	0	335	367	342	619	347	340	389	230	299	492
ENSMUSG00000041712	chr12	Ubr7	-0.2692996	0.078516789	0.113585617	4.428688483	0.024845524	0	335	328	328	441	317	271	339	259	333	382
ENSMUSG00000099966	chr14	2810402E24Rik	0.4308628	0.078543367	0.113612306	2.003816883	0.052219946	0	48	66	35	46	49	68	78	70	67	80
ENSMUSG00000047583	chr3	Tyw3	-0.4496076	0.078676232	0.113792716	1.508079362	0.052863537	0	42	52	48	49	42	40	46	29	44	29
ENSMUSG00000019878	chr10	Hsf2	-0.2565341	0.078960293	0.114191748	4.593037652	0.022636288	0	389	337	341	538	360	346	364	328	319	431
ENSMUSG00000030058	chr6	Copg1	0.26152824	0.078995689	0.114231118	5.866584882	0.025397705	0	709	701	693	1028	827	1121	1067	965	1090	932
ENSMUSG00000009281	chr6	Rarres2	0.40705094	0.079029831	0.114268665	4.673615432	0.061075045	0	303	361	301	309	332	916	323	343	446	379
ENSMUSG00000044906	chr18	4930503L19Rik	0.70627743	0.079042655	0.114275384	0.835486295	0.140474125	0	28	13	17	18	17	25	52	13	53	24
ENSMUSG00000041870	chr5	Ankrd13a	0.245753	0.07906173	0.114291139	4.995062141	0.021355308	0	382	422	409	591	376	668	601	479	545	531
ENSMUSG00000043572	chr4	Pars2	0.44530279	0.07912892	0.114376439	1.995860241	0.058418503	0	47	55	42	51	47	56	56	71	92	85
ENSMUSG00000091243	chr16	Vgll3	-0.3812859	0.079245839	0.114533592	2.659095364	0.044468841	0	141	100	68	118	97	92	80	95	83	88
ENSMUSG00000026283	chr1	Ing5	0.36417499	0.07927428	0.114562852	2.658333142	0.039499506	0	81	71	74	107	72	159	129	77	106	103
ENSMUSG00000082575	chr4	Gm13050	0.46546984	0.07940358	0.114737845	1.772501003	0.064695051	0	57	30	23	62	37	68	53	66	51	73
ENSMUSG00000103922	chr1	RP23-34E15.4	-0.4439925	0.079435349	0.114771884	1.617668335	0.052362899	0	51	63	44	56	39	50	31	45	34	44
ENSMUSG00000031216	chrX	Stard8	-0.2796604	0.079471249	0.114811885	5.192909652	0.028599611	0	523	484	521	890	597	671	496	401	514	629
ENSMUSG00000016308	chrX	Ube2a	0.25357626	0.079502449	0.114845088	4.924243338	0.022884233	0	427	438	337	535	333	543	589	440	574	540
ENSMUSG00000038214	chr10	Bend3	-0.3115742	0.079591242	0.114961472	3.053148064	0.030004356	0	132	123	127	170	125	164	117	103	92	125
ENSMUSG00000021703	chr13	Serinc5	-0.3515983	0.079610928	0.114978024	3.616034466	0.041954372	0	205	183	180	302	159	129	176	183	134	246
ENSMUSG00000069833	chr19	Ahnak	0.27124718	0.079640221	0.115008445	8.19079913	0.028441826	0	3946	3551	3493	5004	3798	6879	5528	4074	4651	5190

ENSMUSG00000030865	chr7	Chp2	-0.4198697	0.079649512	0.115009978	1.719670673	0.045668161	0	58	49	47	65	52	34	49	41	42	55
ENSMUSG00000062762	chr9	Ei24	-0.2501381	0.079719392	0.11509899	6.44549572	0.023628059	0	1363	1350	1318	1797	1244	1464	1317	1220	1255	1239
ENSMUSG00000094910	chr12	D430019H16Rik	0.63852966	0.079776407	0.115169411	0.936257234	0.114473886	0	27	14	17	21	24	58	27	39	13	42
ENSMUSG00000054716	chr7	Zfp771	0.31141434	0.0798203	0.115220876	3.418981513	0.030963693	0	130	136	128	164	143	264	166	174	146	213
ENSMUSG00000038721	chr11	Hoxb7	0.65291638	0.07983117	0.115224665	0.471906895	0.101605706	0	15	16	15	20	7	45	15	26	22	18
ENSMUSG00000023883	chr17	Phf10	-0.258695	0.079845394	0.115233295	5.652331498	0.024758097	0	873	704	740	1059	722	836	733	611	829	726
ENSMUSG00000039801	chr15	2410089E03Rik	-0.3352117	0.079873555	0.115262034	2.645552342	0.033809905	0	110	96	98	104	99	98	92	71	79	105
ENSMUSG00000021368	chr13	Tbc1d7	0.30816077	0.08012475	0.115612585	4.070816563	0.033216719	0	187	223	170	308	230	239	323	326	288	319
ENSMUSG00000004268	chr6	Emg1	0.26214668	0.080204848	0.115713458	5.718420001	0.025607192	0	692	640	647	914	679	1094	978	812	1020	776
ENSMUSG00000038208	chr11	Pgap3	0.40182635	0.080211218	0.115713458	2.105129845	0.046506928	0	48	52	53	72	44	101	64	62	62	102
ENSMUSG00000038855	chr1	Itpkb	-0.333952	0.080334485	0.115879324	5.450768851	0.042082597	0	517	719	647	1152	646	990	570	505	489	642
ENSMUSG00000093606	chr16	B130034C11Rik	0.78545512	0.080369769	0.115918256	-0.080496515	0.131985611	0	9	2	14	9	10	11	13	14	19	27
ENSMUSG00000004127	chr3	Trmt10a	0.54884223	0.080416172	0.115973214	1.241965967	0.08346983	0	23	24	20	29	38	50	64	40	37	26
ENSMUSG00000028833	chr4	Ncdn	0.28596024	0.080468145	0.116036194	4.436431199	0.028847113	0	304	255	205	358	327	509	353	379	337	360
ENSMUSG00000021285	chr12	Ppp1r13b	-0.2953234	0.080503169	0.116062982	3.511570564	0.028076108	0	159	173	167	262	173	198	137	170	161	161
ENSMUSG00000068697	chr14	Myoz1	-0.2965841	0.080503331	0.116062982	10.94520271	0.034433045	0	35003	31351	29170	35205	30576	26112	26628	24466	28812	38459
ENSMUSG00000000776	chr14	Polr3d	-0.2795255	0.080614053	0.116210624	4.085864899	0.026501067	0	248	235	237	389	280	274	273	213	270	214
ENSMUSG00000033542	chr6	Arhgef5	-0.3408104	0.080777466	0.116434186	2.917470363	0.03624552	0	121	128	134	142	93	112	89	100	124	109
ENSMUSG00000024037	chr17	Wdr4	0.31842661	0.080913649	0.116618455	2.98401354	0.030868295	0	119	105	89	116	87	169	159	112	141	127
ENSMUSG00000025545	chr14	Clybl	0.28114461	0.08099318	0.116721043	5.635963598	0.029734955	0	668	696	676	796	503	802	805	935	926	944
ENSMUSG00000028399	chr4	Ptprd	-0.4405479	0.081016148	0.116742106	2.943631794	0.066906743	0	118	143	111	135	138	56	103	109	91	162
ENSMUSG00000041920	chr11	Slc16a6	-0.4205727	0.081139692	0.116908075	3.566680373	0.062711095	0	190	189	201	256	168	75	216	133	180	209
ENSMUSG00000047238	chrX	Mageh1	0.36604046	0.081367106	0.117223655	2.628245726	0.041366805	0	80	87	79	92	56	107	110	129	91	117
ENSMUSG00000016257	chr2	Slmo2	0.27293351	0.081528113	0.117443507	5.84308382	0.028313282	0	790	674	684	1138	634	911	1121	1075	885	1105
ENSMUSG00000017774	chr11	Myo1c	0.25459615	0.081621319	0.11755354	6.373445999	0.024797329	0	1067	978	990	1502	1120	1629	1550	1268	1468	1452
ENSMUSG00000046671	chr4	Mtfr1l	-0.252133	0.081619247	0.11755354	6.902988092	0.024549528	0	2150	1894	1785	2184	1661	1863	1745	1664	1771	1860
ENSMUSG00000020099	chr10	Unc5b	-0.3718471	0.081644144	0.117562184	3.529387294	0.048404816	0	204	189	193	229	147	189	133	188	88	218
ENSMUSG00000033767	chr3	D930015E06Rik	0.36084352	0.081643485	0.117562184	3.781559818	0.046644744	0	137	152	172	317	132	374	203	248	196	239
ENSMUSG00000026811	chr2	St6galnac6	0.27305175	0.081655804	0.117566861	5.744369566	0.028153586	0	809	629	642	829	697	865	966	771	978	1200
ENSMUSG00000024535	chr18	Snx24	-0.2928433	0.081691365	0.117605945	3.779238502	0.028803728	0	236	220	184	286	197	184	228	140	226	222
ENSMUSG00000028454	chr4	Pigo	-0.3221383	0.081708534	0.117618547	3.310520407	0.033626637	0	134	141	163	217	159	137	123	166	130	151
ENSMUSG00000035637	chr4	Grhpr	0.31502988	0.081727267	0.117633397	4.994317398	0.03707952	0	450	420	285	517	443	457	537	616	486	763
ENSMUSG00000021136	chr12	Smoc1	0.7714693	0.08185405	0.117791619	1.177345015	0.190672143	0	11	50	11	10	31	58	42	44	27	50
ENSMUSG00000084691	chr12	Gm24895	0.82455367	0.081845745	0.117791619	1.506826543	0.233066967	0	45	24	24	29	23	24	32	18	64	146
ENSMUSG00000010057	chr9	Nprl2	0.29753098	0.081889824	0.117830967	3.30546408	0.027955347	0	127	130	104	181	116	219	176	170	167	148
ENSMUSG00000032181	chr9	Scg3	-0.523584	0.081964132	0.117925747	0.848988427	0.065084803	0	32	20	31	31	33	33	21	22	19	18
ENSMUSG00000022710	chr16	Usp7	-0.2574037	0.081983132	0.117934744	6.166720492	0.025314961	0	1151	1008	1047	1481	1151	1307	1154	851	1048	1004
ENSMUSG00000078484	chr4	Klhl17	-0.3099705	0.081987262	0.117934744	3.343626023	0.031596179	0	198	184	143	158	139	166	130	147	137	151
ENSMUSG00000041303	chr1	Gtf3c3	-0.2904644	0.082053784	0.118018287	3.466427434	0.026891632	0	184	184	179	220	132	170	175	138	136	187
ENSMUSG00000040219	chr9	Ttc12	0.56599487	0.08233906	0.118416414	1.678538223	0.101354579	0	46	43	28	49	20	117	45	47	56	38
ENSMUSG00000022685	chr16	Parn	0.31562311	0.082376174	0.118447319	3.501474859	0.03340432	0	158	134	139	174	138	303	182	192	146	200
ENSMUSG00000049577	chr8	Zfpm1	-0.4975318	0.0823775	0.118447319	2.178605866	0.081234093	0	47	54	74	138	79	55	52	55	43	94
ENSMUSG00000024393	chr17	Prrc2a	-0.2970632	0.082407987	0.118475711	7.513521773	0.034641008	0	2456	2351	2549	4199	3534	3244	2753	2487	2277	2675
ENSMUSG00000025159	chr19	Mms19	0.29500143	0.0824142	0.118475711	4.319506076	0.030762411	0	269	302	241	257	246	518	330	312	323	315
ENSMUSG00000020357	chr11	Flt4	-0.4105715	0.082565577	0.118681118	2.947981887	0.057684948	0	132	107	97	230	98	181	92	86	82	99
ENSMUSG00000004043	chr11	Stat5a	0.33652562	0.082726161	0.118899715	4.227315486	0.041589187	0	181	256	183	408	221	290	336	323	281	464
ENSMUSG00000027787	chr3	Nmd3	-0.2836837	0.082744621	0.118914018	4.32044433	0.028537389	0	340	316	306	433	243	336	338	216	331	246
ENSMUSG00000029162	chr5	Khk	0.2822584	0.08291477	0.11914629	4.10515153	0.027742141	0	262	240	192	265	191	332	260	257	364	316
ENSMUSG00000037752	chr4	Xkr8	0.42971077	0.083077667	0.119368096	1.80932364	0.054859739	0	51	32	40	59	34	55	70	73	46	71
ENSMUSG00000001248	chr7	Gramd1a	-0.3110821	0.083176263	0.119497476	5.210980005	0.036870676	0	616	650	561	679	532	910	455	432	451	482
ENSMUSG00000026245	chr1	Farsb	0.2580979	0.08325102	0.119586312	5.695094811	0.025307296	0	615	630	597	968	721	1038	1011	856	853	844
ENSMUSG00000028798	chr4	Eif3i	0.25695156	0.08325521	0.119586312	6.639995613	0.025662943	0	1468	1357	1205	1509	1210	2042	1805	1593	1827	1594
ENSMUSG00000033499	chr13	Larp4b	-0.251943	0.083339293	0.119688297	6.671090923	0.02466927	0	1651	1471	1520	2179	1475	1585	1472	1534	1450	1528
ENSMUSG00000042751	chr1	Nmnat2	0.69489061	0.083343339	0.119688297	-0.11765691	0.09337378	0	8	12	4	12	9	18	10	16	12	24
ENSMUSG00000059439	chr11	Bcas3	-0.2612718	0.083395401	0.119750757	4.799651974	0.024844373	0	451	431	384	553	438	483	361	433	314	473
ENSMUSG00000020321	chr11	Mdh1	-0.3227404	0.083480931	0.119861259	9.33178581	0.04147637	0	8632	11322	10878	16278	7042	10845	8388	9862	9278	8243
ENSMUSG00000004896	chr3	Rrnad1	0.35066117	0.083493042	0.119866333	2.784650374	0.038488224	0	102	87	88	93	71	137	116	143	113	107
ENSMUSG00000024158	chr17	Hagh	-0.2656563	0.083559835	0.119949903	5.629874324	0.026870397	0	851	855	783	893	628	842	618	678	737	791
ENSMUSG00000042500	chr4	Ago4	-0.3036171	0.083571462	0.119954273	3.320127244	0.029471032	0	129	169	154	215	148	130	153	143	135	158
ENSMUSG00000034881	chr10	Tbxa2r	0.63922676	0.08361647	0.12000655	0.690194803	0.117555401	0	18	14	13	32	11	51	23	29	11	35
ENSMUSG00000005501	chr1	Usp40	-0.3222997	0.083637887	0.120024962	3.839751173	0.03642953	0	261	189	253	295	182	150	213	212	202	246
ENSMUSG00000035295	chr2	Wdr38	1.09096977	0.083683194	0.12007765	0.415052618	0.407261722	0	8	8	1	28	15	19	6	70	9	25
ENSMUSG00000044952	chr7	Kctd21	-0.3793151	0.083857604	0.12031556	2.363708454	0.04327708	0	76	72	87	103	85	55	79	65	78	78
ENSMUSG00000030246	chr6	Ldhb	-0.7306666	0.083939994	0.120421408	6.732836094	0.209517032	0	599	2199	1888	4424	1199	2484	575	1627	1394	450
ENSMUSG00000011960	chr15	Ccnt1	-0.2763507	0.083995233	0.120488287	4.239569755	0.027103342	0	250	265	296	433	299	325	284	209	243	336

ENSMUSG00000062101	chr17	Zfp119b	-0.5100809	0.084074536	0.120589668	1.396908663	0.074007537	0	54	34	39	64	32	22	47	28	42	29
ENSMUSG00000056050	chr1	Mia3	-0.2622697	0.0841157	0.120636328	6.033654838	0.026552236	0	958	954	975	1394	1053	879	1066	926	891	1083
ENSMUSG00000090691	chr14	Gm3667	0.85440676	0.084177211	0.120712158	-0.261039553	0.180525639	0	6	10	11	7	3	6	7	15	27	18
ENSMUSG00000022244	chr15	Amacr	-0.253474	0.084243773	0.120795217	4.438561903	0.022615991	0	350	361	344	430	267	351	291	327	294	342
ENSMUSG00000029415	chr5	Sdad1	-0.2857129	0.084259334	0.120805134	4.043885252	0.028715215	0	248	220	268	311	288	219	294	210	219	263
ENSMUSG00000058239	chr7	Usf2	0.25280495	0.084322019	0.120882607	5.675979827	0.024413066	0	677	568	604	982	671	958	952	774	875	978
ENSMUSG00000026663	chr1	Atf6	-0.2374737	0.084371184	0.120940683	5.273969596	0.020960599	0	651	543	566	751	602	599	617	486	553	642
ENSMUSG00000075514	chr2	Gm13375	-0.5150349	0.084381719	0.120943381	1.741845322	0.085280468	0	63	42	43	82	56	83	45	31	23	39
ENSMUSG00000038175	chr13	Mylip	0.41498341	0.084491696	0.121088592	3.526345788	0.06218727	0	118	154	153	176	125	197	166	166	149	393
ENSMUSG00000044627	chr2	Swi5	0.27280703	0.084507741	0.121099168	6.239649556	0.029054136	0	1104	1040	898	1244	824	1608	1426	1211	1440	1058
ENSMUSG00000062127	chr3	Cttnbp2nl	0.31727367	0.084581581	0.121192555	3.649490884	0.035062279	0	134	177	162	221	134	346	212	184	185	211
ENSMUSG00000029131	chr5	Dnajb6	-0.2516337	0.08462721	0.121233076	5.584087485	0.024063192	0	835	718	681	939	711	642	773	673	662	810
ENSMUSG00000073079	chr12	Srp54a	-0.6233436	0.084619482	0.121233076	1.018726576	0.114581515	0	50	32	33	28	28	13	26	13	38	32
ENSMUSG00000032309	chr9	Fbxo22	-0.257487	0.08489247	0.121600611	4.545910397	0.023745034	0	389	348	339	473	343	297	387	300	363	377
ENSMUSG00000037640	chr7	Zfp60	-0.303976	0.085025385	0.121778518	3.040718313	0.028611203	0	123	127	112	195	118	128	121	115	118	110
ENSMUSG00000044026	chr19	Slc35g1	-0.5115929	0.085036767	0.12178234	1.217621217	0.07184686	0	27	37	40	64	28	32	44	20	27	26
ENSMUSG00000015843	chr1	Rxrg	-0.342385	0.085229737	0.122046189	5.387612806	0.045583166	0	729	577	572	822	775	360	630	598	627	762
ENSMUSG00000004347	chr6	Pde1c	-0.6512736	0.085289342	0.122119029	0.305645965	0.096805167	0	20	18	19	20	24	13	13	25	10	9
ENSMUSG00000023832	chr17	Acat2	0.3754765	0.085300496	0.122122488	2.782490343	0.045636031	0	93	112	79	77	72	134	131	134	119	102
ENSMUSG00000089755	chr17	0610012D04Rik	-0.5440826	0.085423646	0.122286272	0.614596509	0.067920254	0	28	24	30	24	18	24	14	18	14	24
ENSMUSG00000075273	chr2	Ttc30b	-0.4355772	0.085437046	0.122292929	1.894339092	0.056825609	0	58	70	60	76	45	44	36	49	49	71
ENSMUSG00000025893	chr9	Kbtbd3	-0.367571	0.085457671	0.122309924	3.026063614	0.045733562	0	167	140	135	139	91	96	136	87	134	118
ENSMUSG00000027739	chr3	Rab33b	-0.287567	0.085680063	0.122615662	3.28893392	0.026339036	0	149	165	138	186	152	140	136	128	134	172
ENSMUSG00000040264	chr3	Gbp5	-0.518677	0.085707443	0.122642287	1.210485469	0.07632358	0	41	34	44	42	31	23	32	18	25	50
ENSMUSG00000058267	chr1	Mrps14	-0.2706254	0.08575569	0.122698763	5.684619132	0.028424599	0	867	833	717	1044	737	1096	759	648	683	644
ENSMUSG00000002102	chr2	Psmc3	0.25390759	0.08578543	0.12270363	7.784122819	0.02586327	0	3157	2936	2435	3738	2771	4046	3835	3676	3919	4063
ENSMUSG00000002550	chr2	Uck1	0.26510022	0.085785106	0.12270363	3.896817719	0.023847382	0	180	216	179	236	187	254	270	266	236	287
ENSMUSG00000028713	chr4	Cyp4b1	-0.3841564	0.085774474	0.122270363	1.917742364	0.041709282	0	64	71	54	67	52	55	55	41	47	62
ENSMUSG00000059981	chr7	Taok2	-0.2360604	0.085820217	0.122740827	5.170023797	0.020785962	0	558	514	572	704	544	622	501	485	501	589
ENSMUSG00000032507	chr9	Fbxl2	0.62084744	0.086230593	0.12331513	1.231593752	0.120772312	0	47	29	12	19	22	72	38	46	29	36
ENSMUSG00000021120	chr12	Pigh	0.43432234	0.086273396	0.123363719	1.717244453	0.05310189	0	41	54	31	40	33	66	67	58	43	63
ENSMUSG00000044072	chr11	Eml6	-0.5290121	0.086328352	0.123429673	0.708275925	0.066804205	0	29	33	24	28	19	15	23	17	18	28
ENSMUSG00000029059	chr4	Fam213b	0.2730737	0.086399075	0.123518153	7.021012767	0.029827822	0	2041	1784	1503	1795	1588	2273	2166	2301	2083	2753
ENSMUSG00000038369	chr2	Ncoa6	-0.2788393	0.086425045	0.123542644	4.351209259	0.028418633	0	247	290	322	448	355	365	325	266	238	312
ENSMUSG00000026202	chr1	Tuba4a	-0.3838374	0.086537314	0.123690478	9.246492963	0.059765374	0	11974	8409	8373	12132	10428	8479	9758	7250	12313	4878
ENSMUSG00000038212	chr13	Hiatl1	-0.3269963	0.086607304	0.123777859	3.691216836	0.038245527	0	197	217	197	271	183	162	239	112	182	237
ENSMUSG00000003813	chr8	Rad23a	-0.2505847	0.086628655	0.123795714	6.906480816	0.025056395	0	1994	1771	1590	2515	1888	2190	1646	1608	1723	1800
ENSMUSG00000035578	chr16	Iqcg	-0.4475814	0.086789577	0.124012997	2.215594699	0.0663528	0	74	92	95	68	55	93	46	63	58	54
ENSMUSG00000028779	chr4	Pef1	0.23125703	0.086814321	0.124035672	5.068719009	0.019816673	0	500	445	383	535	430	619	595	569	531	634
ENSMUSG00000066838	chr7	Zfp772	-0.4578821	0.086998352	0.124285121	1.373149258	0.060640039	0	40	52	32	39	48	43	34	22	36	36
ENSMUSG00000087178	chr7	A230056P14Rik	-0.6128263	0.087006699	0.124285121	0.189684958	0.087038912	0	21	20	19	21	11	16	22	11	8	9
ENSMUSG00000024353	chr18	Mzb1	0.61083678	0.087018882	0.12428982	0.17338299	0.08231766	0	9	7	9	18	16	15	18	19	21	25
ENSMUSG00000070822	chr7	Zscan18	0.55423942	0.087163866	0.124484181	1.056414495	0.088322979	0	25	24	20	24	24	40	28	52	46	21
ENSMUSG00000013593	chr1	Ndufs2	-0.2805431	0.087269004	0.124621601	9.876921969	0.032153374	0	14286	15966	15827	19743	11347	15870	12628	12771	14838	13179
ENSMUSG00000044770	chr10	Scml4	0.50060343	0.087388063	0.124778869	1.554631095	0.075995211	0	35	24	30	47	38	47	52	79	34	54
ENSMUSG00000087014	chr10	Gm16364	-0.4949721	0.087470906	0.124884399	0.966005683	0.062672284	0	33	36	32	32	26	22	30	17	32	23
ENSMUSG00000051234	chr9	Rnf7	0.24483127	0.087644545	0.125119526	6.466696712	0.023854313	0	1321	1088	1098	1457	1073	1651	1629	1452	1509	1579
ENSMUSG00000039456	chr16	Morc3	-0.2567057	0.087666962	0.125138746	4.132497701	0.023217894	0	298	269	273	319	251	261	301	215	272	247
ENSMUSG00000030733	chr7	Sh2b1	-0.2732388	0.087688824	0.125157169	6.332566632	0.029803282	0	1441	1184	1132	1439	1342	1019	1215	1092	1236	1365
ENSMUSG00000021686	chr13	Ap3b1	0.24705656	0.087839926	0.125360033	4.493358743	0.022094772	0	288	279	249	416	305	443	417	321	369	444
ENSMUSG00000033805	chr5	Ephx4	0.6681761	0.087902908	0.125437108	0.266060327	0.108891026	0	19	19	6	8	9	15	25	20	22	25
ENSMUSG00000097180	chr5	2700038G22Rik	-0.7982446	0.087953553	0.125496565	0.95923158	0.222812451	0	48	28	38	25	31	66	14	14	9	10
ENSMUSG00000034403	chrX	Pja1	0.25322927	0.088071376	0.125651853	4.493256807	0.023489702	0	323	269	230	407	305	431	403	404	345	405
ENSMUSG00000024410	chr18	3110002H16Rik	0.29292507	0.088111461	0.125683382	3.783337601	0.030295335	0	169	197	180	226	143	263	248	193	304	217
ENSMUSG00000031482	chr8	Slc25a15	-0.2935036	0.088109395	0.125683382	4.136343865	0.031338431	0	298	285	286	351	217	192	268	243	278	292
ENSMUSG00000023330	chr2	Dtwd1	-0.3851917	0.088302041	0.125942374	2.376022317	0.04871808	0	91	86	92	103	57	107	67	50	66	73
ENSMUSG00000014077	chr2	Chp1	0.32117498	0.088333788	0.125974799	5.920739538	0.041385704	0	786	819	647	1033	741	689	1200	1066	1058	1430
ENSMUSG00000035845	chr15	Alg12	0.34702879	0.088606254	0.126350475	2.290737685	0.035315363	0	63	64	55	77	54	81	99	78	84	93
ENSMUSG00000066278	chr5	Vps37b	0.27553322	0.088640736	0.12638675	3.344315439	0.024292372	0	131	150	114	155	125	203	185	161	171	178
ENSMUSG00000005102	chr2	Eif2ak4	-0.3642643	0.088785159	0.126579759	2.625670881	0.043075358	0	89	95	92	145	91	78	104	66	106	77
ENSMUSG00000028420	chr4	Tmem38b	-0.2461974	0.088866617	0.126682971	5.79561341	0.023861608	0	892	777	860	1201	782	911	811	646	858	929
ENSMUSG00000040562	chr3	Gstm2	0.31377909	0.088948848	0.126787262	5.940903301	0.039577748	0	828	707	487	1037	1029	1395	1227	975	931	1054
ENSMUSG00000019952	chr10	Poc1b	0.33086511	0.089158032	0.127072472	2.493923795	0.032900413	0	70	76	59	100	61	109	103	97	89	103
ENSMUSG00000082044	chr2	Gm14284	0.49636503	0.089381751	0.127378337	0.969784576	0.060287148	0	20	27	20	28	18	41	46	29	34	25
ENSMUSG00000025956	chr1	Mettl21a	0.29993401	0.089450246	0.127462952	3.720460028	0.031685087	0	201	197	176	161	129	255	231	195	229	269

ENSMUSG00000028861	chr4	Mrps15	0.26209624	0.08952118	0.127551026	5.552339534	0.027120532	0	719	602	559	803	508	1074	772	832	794	701
ENSMUSG00000033006	chr15	Sox10	-0.5183909	0.089735457	0.127843297	1.397309452	0.083964813	0	28	25	57	72	41	38	31	34	25	41
ENSMUSG00000031242	chrX	2610002M06Rik	-0.3333651	0.089778242	0.127891215	2.690928822	0.034916795	0	123	92	79	131	104	99	98	71	96	95
ENSMUSG00000030737	chr7	Slco2b1	0.29757972	0.089868841	0.128007228	3.897263036	0.031924932	0	158	194	197	239	197	322	216	221	227	353
ENSMUSG00000016619	chr15	Nup50	0.24248503	0.089887076	0.128020154	4.630191967	0.021739213	0	316	307	308	448	312	494	511	352	418	414
ENSMUSG00000033849	chr1	B3galt2	-0.4962423	0.089957781	0.1281078	2.704387009	0.090962449	0	101	133	115	127	81	39	71	77	96	147
ENSMUSG00000027500	chr3	Stmn2	-0.4562023	0.090207467	0.128450286	1.350347291	0.056384064	0	48	41	35	50	36	45	27	21	42	33
ENSMUSG00000024566	chr18	Atp9b	0.26528542	0.090248423	0.128482424	4.405687037	0.025963873	0	270	279	224	337	314	504	380	316	337	354
ENSMUSG00000051034	chr5	Zfp11	-0.4622093	0.090245103	0.128482424	1.535352954	0.063367539	0	50	48	53	51	37	24	42	37	34	53
ENSMUSG00000090247	chr10	Bloc1s1	0.26770832	0.090334429	0.128591768	6.309897595	0.029038792	0	1258	1132	958	1134	859	1710	1278	1369	1389	1324
ENSMUSG00000058392	chr17	Rrp1b	0.31773431	0.090430589	0.128715543	3.045136353	0.033197393	0	100	87	104	139	110	159	181	122	150	125
ENSMUSG00000049800	chr11	Sertad2	-0.2716475	0.090452756	0.128733984	3.95186423	0.026469699	0	237	226	249	323	221	260	290	181	213	197
ENSMUSG00000031214	chrX	Ophn1	0.35385578	0.090597873	0.128927388	2.889607166	0.041686438	0	121	88	73	91	100	162	125	108	153	120
ENSMUSG00000069520	chr10	Tmem19	0.27386747	0.090742159	0.12911957	4.36018812	0.027850515	0	262	268	267	329	250	544	342	283	349	324
ENSMUSG00000034880	chr8	Mrpl34	0.26421832	0.090839563	0.129231853	4.625455177	0.026596889	0	317	283	328	459	288	471	460	495	377	377
ENSMUSG00000038286	chr13	Bphl	-0.3045238	0.090838201	0.129231853	4.036338848	0.03441978	0	275	267	282	311	205	191	201	240	264	285
ENSMUSG00000027560	chr2	Dok5	0.44241835	0.09091548	0.129326693	2.436419913	0.069273204	0	55	58	78	95	50	59	99	126	106	99
ENSMUSG00000060376	chr7	Bckdha	-0.2792503	0.091090313	0.129562204	6.891163082	0.03211632	0	1811	2175	1836	2562	1373	2107	1413	1572	1828	1843
ENSMUSG00000022456	chr15	Sept3	-0.6144973	0.091197267	0.12970113	0.107775196	0.087606823	0	12	13	18	21	22	21	8	12	9	12
ENSMUSG00000020076	chr10	Ddx50	-0.2487936	0.091609537	0.130274205	5.267047945	0.024241544	0	643	556	555	812	559	569	600	450	666	578
ENSMUSG00000022353	chr15	Mtss1	0.26310654	0.091632622	0.130280522	4.62821017	0.026264574	0	289	375	329	418	259	530	486	342	369	482
ENSMUSG00000028950	chr4	Tas1r1	0.46156166	0.091625111	0.130280522	2.210128952	0.07285912	0	73	44	63	50	49	62	66	111	94	86
ENSMUSG00000069631	chr11	Strada	-0.253128	0.091662561	0.130309832	4.908435398	0.024682611	0	533	428	427	579	460	383	493	377	446	527
ENSMUSG00000035356	chr16	Nfkbiz	0.53343006	0.091793506	0.130469738	1.284067356	0.085974521	0	37	32	26	30	15	77	41	31	29	48
ENSMUSG00000074221	chr7	Zfp568	-0.2604186	0.09179544	0.130469738	4.888958204	0.026161367	0	494	417	390	595	506	404	389	474	422	491
ENSMUSG00000097493	chr15	9930014A18Rik	0.61725774	0.091803048	0.130469738	0.065522943	0.086299538	0	11	14	4	14	11	16	17	18	24	15
ENSMUSG00000087119	chr3	Atg4a-ps	-0.7174136	0.091845179	0.130516342	0.352623455	0.14814131	0	22	21	23	28	14	2	11	14	24	19
ENSMUSG00000036278	chr19	Macrod1	-0.2485758	0.091855083	0.130517145	7.593625764	0.025704023	0	3091	3093	2891	3734	2814	3429	2654	2582	2957	2809
ENSMUSG00000027800	chr3	Tm4sf1	0.28170384	0.091875735	0.130533219	4.715706892	0.030830775	0	321	325	324	497	308	721	435	392	428	390
ENSMUSG00000027424	chr2	Mgme1	-0.3725208	0.092002677	0.130700286	3.003382945	0.049698992	0	133	118	123	163	128	75	117	80	139	149
ENSMUSG00000024309	chr17	Pfdn6	0.24885756	0.092239201	0.131022977	5.004519037	0.023986459	0	476	428	353	505	416	761	531	511	545	500
ENSMUSG00000052727	chr13	Map1b	-0.3854696	0.092326947	0.131134289	4.769133531	0.059988454	0	441	375	379	569	529	442	327	562	191	391
ENSMUSG00000005804	chr2	Bloc1s6	-0.2427876	0.092349742	0.131153338	5.00669851	0.022792456	0	619	474	412	630	464	487	493	395	476	549
ENSMUSG00000044006	chr8	Cilp2	0.48067985	0.092429151	0.131252775	5.321571093	0.095310902	0	768	369	420	635	320	1611	823	402	546	524
ENSMUSG00000044037	chr9	Als2cl	-0.3739157	0.092730887	0.131667874	2.463936313	0.046965716	0	97	89	109	83	71	96	63	67	78	81
ENSMUSG00000038984	chr15	Tspyl5	-0.5255686	0.092763215	0.131700395	0.732809509	0.068184302	0	34	26	20	32	24	20	16	23	14	30
ENSMUSG00000028910	chr4	Mecr	0.27241674	0.092817051	0.131763443	4.227505244	0.027842551	0	251	279	221	303	204	382	336	341	345	253
ENSMUSG00000032883	chr1	Acsl3	-0.2970555	0.092926864	0.131892541	4.461911278	0.034505137	0	443	386	360	302	287	369	324	303	244	373
ENSMUSG00000045275	chr16	Lca5l	0.54426701	0.092922895	0.131892541	0.901632573	0.084664157	0	27	24	10	16	27	32	35	36	27	38
ENSMUSG00000019494	chr5	Cops6	0.24528875	0.093102406	0.132114857	6.375189069	0.024751271	0	1216	1083	978	1371	1018	1594	1375	1348	1568	1447
ENSMUSG00000062184	chrX	Hs6st2	-0.4931467	0.09309943	0.132114857	3.13893936	0.094182678	0	202	162	103	117	163	66	168	63	134	159
ENSMUSG00000030042	chr6	Pole4	-0.2635077	0.093118693	0.132124554	4.715868348	0.026945488	0	528	387	374	481	359	412	489	295	378	375
ENSMUSG00000018909	chr7	Arrb1	0.28827892	0.093150834	0.13215674	4.527011733	0.032362003	0	264	240	242	471	341	548	392	318	375	444
ENSMUSG00000027245	chr2	Hypk	0.30106756	0.093230351	0.132256129	6.08831447	0.037476206	0	940	812	768	1212	837	2003	1078	1096	1006	1010
ENSMUSG00000032289	chr9	Thsd4	-0.5140707	0.093374745	0.132447523	1.444870947	0.083191284	0	46	23	43	76	44	48	42	35	19	32
ENSMUSG00000032185	chr9	Carm1	-0.2795379	0.093428304	0.132510045	6.316855253	0.032399834	0	1281	1327	1250	1443	1176	1008	1290	1100	938	1536
ENSMUSG00000039656	chr17	Rxrb	-0.2337793	0.093439834	0.132512949	5.212138113	0.021449879	0	624	519	545	732	562	672	496	502	555	554
ENSMUSG00000083854	chr7	Dnajc19-ps	-0.4365163	0.093523629	0.132618328	1.132161459	0.048727586	0	45	32	33	36	31	34	28	24	28	30
ENSMUSG00000036186	chr2	Fam69b	0.54925388	0.093551822	0.132631392	1.486673055	0.101609622	0	20	40	32	48	23	36	62	66	61	30
ENSMUSG00000078813	chr7	Leng1	0.3055001	0.093551199	0.132631392	3.1927225	0.032075546	0	92	108	122	165	116	161	171	173	145	161
ENSMUSG00000061898	chr5	Rbak	-0.3421611	0.093572113	0.132646703	2.18400673	0.034923312	0	81	72	64	82	69	73	58	59	59	70
ENSMUSG00000007415	chr5	Gatad1	-0.2393092	0.093717599	0.132839468	5.746849085	0.023124607	0	874	792	831	1131	720	783	871	708	806	842
ENSMUSG00000025332	chrX	Kdm5c	-0.3747885	0.093842392	0.133002867	5.052956578	0.057678653	0	408	405	387	932	701	768	430	416	369	398
ENSMUSG00000024841	chr19	Eif1ad	0.24820381	0.093973289	0.133174882	4.536890299	0.023434805	0	285	290	293	442	276	476	482	375	345	376
ENSMUSG00000058581	chr14	Gm5801	-1.0453863	0.094074399	0.133304653	1.797911842	0.426982394	0	70	60	64	73	68	149	9	8	18	7
ENSMUSG00000059423	chr4	Zfp933	-0.5128945	0.094086148	0.133307786	2.784765928	0.100030605	0	116	93	154	134	94	31	101	112	102	101
ENSMUSG00000053297	chr6	AI854703	0.61058749	0.094175171	0.133420394	0.527404885	0.096501412	0	13	16	12	19	17	23	20	16	22	49
ENSMUSG00000001942	chr9	Siae	0.38367409	0.094284577	0.133561854	2.863217837	0.052773694	0	91	99	76	105	90	89	133	106	134	197
ENSMUSG00000018171	chr11	Vmp1	-0.2534066	0.094397877	0.1337088	5.689091149	0.026221743	0	911	799	835	938	681	813	876	571	776	814
ENSMUSG00000042487	chr9	Leo1	-0.3423364	0.094449482	0.133768338	4.257717271	0.046202724	0	288	229	206	547	351	255	289	283	204	337
ENSMUSG00000025964	chr1	Adam23	0.4029237	0.094475786	0.133792035	2.019941799	0.05154492	0	57	43	56	55	40	73	60	55	86	91
ENSMUSG00000037580	chr14	Gch1	0.44519302	0.094803409	0.134242395	2.247532554	0.069171606	0	41	63	45	92	54	120	111	49	93	66
ENSMUSG00000018196	chr1	Glrx2	-0.2271232	0.094848448	0.134292565	5.062390762	0.020113249	0	619	513	461	647	446	559	513	435	493	510
ENSMUSG00000028042	chr3	Zbtb7b	-0.2490667	0.094916669	0.134375543	5.009290924	0.024484324	0	516	455	475	672	490	424	517	381	521	549
ENSMUSG00000053907	chr6	Mat2a	-0.3072529	0.09505112	0.134552259	7.463286212	0.040149057	0	3408	2537	2844	2859	2762	2141	2541	1926	3108	3124

ENSMUSG00000037894	chr3	H2afz	0.28378403	0.095112841	0.134625994	5.749536318	0.033290018	0	782	633	677	833	678	978	1366	723	945	815
ENSMUSG00000029321	chr5	Slc10a6	1.1210433	0.09532299	0.134909783	0.579336014	0.447321616	0	11	4	22	10	14	114	9	8	20	8
ENSMUSG00000029578	chr5	Wipi2	-0.2389795	0.095626223	0.135325242	5.35759128	0.023043607	0	700	644	627	750	572	734	561	497	625	658
ENSMUSG00000021701	chr13	Plk2	0.33035896	0.095694717	0.13540846	4.167497335	0.042927529	0	306	253	249	224	139	349	407	266	256	354
ENSMUSG00000030264	chr6	Thumpd3	-0.2574414	0.095719316	0.135429557	3.888301913	0.023944353	0	234	232	192	290	245	222	237	183	237	213
ENSMUSG00000042050	chr12	Wdr60	-0.3490135	0.095776992	0.135497443	2.938516505	0.043676445	0	171	98	121	133	106	105	98	89	104	147
ENSMUSG00000035842	chr17	Ddx11	0.52723542	0.095788584	0.135500127	0.988232276	0.079145705	0	19	17	20	35	23	44	52	32	31	20
ENSMUSG00000050931	chr3	Sgms2	0.42362823	0.095819046	0.135529499	2.095555483	0.060065281	0	61	41	52	59	50	57	87	61	66	117
ENSMUSG00000014075	chr16	Tctex1d2	0.38120958	0.095923848	0.135664005	2.841746827	0.052788005	0	113	80	76	109	79	201	141	98	132	84
ENSMUSG00000103766	chr3	RHBG	0.49899983	0.095970493	0.135716241	0.797071348	0.061798182	0	16	21	18	24	20	34	27	31	38	23
ENSMUSG00000097919	chr8	Gm27021	0.43063647	0.096104673	0.135892241	1.700950487	0.056902185	0	28	36	29	52	53	54	65	55	55	63
ENSMUSG00000067276	chrX	Capn6	0.42441018	0.096167287	0.135967021	4.609126569	0.074564562	0	405	287	289	267	279	343	339	586	262	727
ENSMUSG00000039089	chr10	L3mbtl3	-0.288907	0.096251851	0.136072817	3.183218953	0.028858413	0	147	120	137	180	151	153	123	125	106	154
ENSMUSG00000022773	chr16	Ypel1	0.64840318	0.096295434	0.136120662	0.5022712	0.118978214	0	21	15	15	8	14	30	19	26	12	42
ENSMUSG00000026779	chr2	Mastl	0.63728082	0.096553221	0.13647126	0.377427499	0.113095321	0	18	14	6	15	15	25	37	20	24	10
ENSMUSG00000032419	chr9	Tbx18	0.53264139	0.096595343	0.136516991	0.954394615	0.079941852	0	18	18	28	29	17	41	21	25	40	48
ENSMUSG00000066621	chr5	Tecpr1	-0.2873058	0.096669921	0.136608576	4.956270098	0.033665836	0	515	494	406	595	522	461	390	375	371	690
ENSMUSG00000022883	chr16	Robo1	-0.3652764	0.096715387	0.136642628	2.074690818	0.040408503	0	79	61	65	77	61	54	69	55	48	66
ENSMUSG00000029287	chr5	Tgfbr3	0.28371532	0.096723349	0.136642628	5.018009532	0.032718658	0	428	435	413	547	354	922	526	499	416	570
ENSMUSG00000074063	chr8	Osgin1	-0.3194113	0.09671648	0.136642628	3.407021143	0.038166099	0	143	187	198	191	143	151	206	133	143	129
ENSMUSG00000021468	chr13	Sptlc1	0.25474009	0.096926205	0.136915367	4.124400092	0.024084214	0	242	226	198	272	237	350	379	254	260	303
ENSMUSG00000036944	chr15	Tmem71	0.48736727	0.096964585	0.136955739	0.976429857	0.063656115	0	25	26	15	27	21	45	26	24	38	43
ENSMUSG00000067787	chr2	Blcap	-0.2564022	0.096984137	0.136969513	4.605555849	0.025893872	0	379	421	383	461	320	501	320	308	350	335
ENSMUSG00000037275	chr11	Gemin5	0.31946569	0.0971879	0.137243417	3.888714222	0.039924818	0	197	163	160	283	182	191	317	195	289	337
ENSMUSG00000024359	chr18	Hspa9	-0.2690668	0.097397534	0.137502828	8.845766888	0.031394528	0	6475	7287	6949	10971	6226	6948	6835	6619	7298	6229
ENSMUSG00000030409	chr7	Dmpk	-0.3047481	0.097401116	0.137502828	8.700469205	0.040269539	0	6669	5909	6056	8248	7339	4410	5645	6250	6443	7356
ENSMUSG00000062931	chr10	Zfp938	-0.3110556	0.097395386	0.137502828	3.077407744	0.034395091	0	138	152	133	144	116	153	93	104	118	141
ENSMUSG00000095690	chr19	Rab11b-ps2	-0.3705896	0.097436737	0.137539222	2.143458654	0.042967767	0	75	53	62	105	70	68	65	59	45	70
ENSMUSG00000080242	chr6	Gm15487	-0.919285	0.097450786	0.137545161	3.902465709	0.353442955	0	282	245	214	426	297	673	84	34	45	64
ENSMUSG00000044751	chr11	Gm12231	-0.2736239	0.097485011	0.137579574	3.924294735	0.027910911	0	209	249	226	375	187	242	200	200	208	266
ENSMUSG00000029095	chr5	Ablim2	-0.252099	0.097532153	0.137632206	5.873833946	0.026574168	0	1014	826	821	1039	1019	961	777	845	914	856
ENSMUSG00000040105	chr19	Ppapdc2	0.43977214	0.097545766	0.137637519	2.070938293	0.068497148	0	43	76	34	68	38	81	59	77	61	105
ENSMUSG00000042133	chr2	Ppig	-0.2450466	0.097574011	0.137663474	4.74479164	0.02359563	0	405	391	376	609	397	402	432	304	434	426
ENSMUSG00000003518	chr11	Dusp3	-0.276156	0.097645069	0.137749822	7.459781242	0.032889906	0	3529	2527	2533	3081	2652	2210	2768	2416	2440	3127
ENSMUSG00000010048	chr9	Ifrd2	-0.2627263	0.097751994	0.137872829	5.078257988	0.028046662	0	474	413	526	807	544	494	601	438	497	468
ENSMUSG00000070699	chr7	Sars2	0.24774015	0.097749034	0.137872829	4.127085232	0.023046232	0	237	211	199	319	224	320	285	316	269	346
ENSMUSG00000073435	chr17	Nme3	0.37291479	0.097775715	0.137892371	2.766311727	0.050519851	0	114	86	70	101	64	197	102	101	114	107
ENSMUSG00000020783	chr11	1200014J11Rik	0.26941178	0.097810989	0.137914284	3.520336607	0.025906277	0	170	130	150	186	132	194	238	188	194	197
ENSMUSG00000048965	chr7	Mrgpre	0.54776595	0.097808091	0.137914284	1.177073181	0.095431321	0	45	19	24	22	18	62	38	33	25	51
ENSMUSG00000097882	chr8	0610038B21Rik	-0.5825314	0.097866606	0.137978785	0.402369623	0.082852456	0	28	19	21	21	18	8	20	12	20	18
ENSMUSG00000020473	chr11	Aebp1	0.37762371	0.098392317	0.138705973	6.102121041	0.061326999	0	806	674	578	1365	1085	1964	1079	1083	732	1574
ENSMUSG00000030614	chr7	Tmem126b	-0.3271249	0.098569948	0.138942369	4.312850108	0.043182664	0	378	322	305	382	254	183	319	249	375	290
ENSMUSG00000041396	chr1	Mettl18	-0.4049772	0.098676079	0.139077942	1.791896898	0.051638119	0	74	63	45	51	49	54	51	45	43	42
ENSMUSG00000053684	chr10	BC048403	0.52738784	0.098721153	0.139127441	0.85112215	0.082309577	0	16	24	15	31	17	21	41	21	37	41
ENSMUSG00000040414	chr19	Slc25a28	0.24116366	0.098805715	0.139232574	4.238644951	0.021815887	0	281	237	232	299	232	412	297	284	307	367
ENSMUSG00000033096	chr2	Apmap	0.23745907	0.0988457	0.139274876	4.968691748	0.0225876	0	456	465	358	489	365	600	647	504	500	508
ENSMUSG00000030272	chr6	Camk1	0.24265408	0.098919288	0.139364513	5.227526372	0.024083995	0	560	502	431	608	453	762	656	545	755	589
ENSMUSG00000031668	chr6	Eif2ak3	-0.2929753	0.098968578	0.13940585	3.158473288	0.030123305	0	130	135	150	178	130	147	144	93	114	153
ENSMUSG00000032643	chr4	Fhl3	0.30333631	0.098961717	0.13940585	6.484869289	0.03975502	0	967	1037	1079	1946	1048	1587	1335	1998	1481	1595
ENSMUSG00000029247	chr5	Paics	-0.2580166	0.099005829	0.139444267	6.627321456	0.028611371	0	1685	1573	1456	1944	1374	1333	1595	1182	1402	1843
ENSMUSG00000045790	chr5	Ccdc149	0.46696125	0.099037985	0.139475502	1.334252585	0.066115928	0	33	33	20	42	23	39	49	39	62	36
ENSMUSG00000038290	chr11	Smg6	-0.2371549	0.099056263	0.139487188	4.569381801	0.021853333	0	356	354	347	464	383	362	321	357	343	383
ENSMUSG00000064725	chr11	Snord96a	0.5992692	0.099128419	0.139574732	0.204545431	0.087289514	0	13	10	11	19	8	21	25	8	24	23
ENSMUSG00000045664	chr19	Cdc42ep2	0.32112664	0.099139372	0.139576092	4.753816234	0.042917699	0	288	255	334	551	373	616	398	603	388	424
ENSMUSG00000017417	chr11	Plxdc1	-0.3112076	0.099171161	0.139584031	2.935257193	0.033558995	0	113	120	110	172	111	115	122	109	77	127
ENSMUSG00000026674	chr1	Ddr2	-0.2384902	0.099174973	0.139584031	5.351897242	0.023409178	0	670	637	605	711	644	646	632	612	603	549
ENSMUSG00000033983	chr11	Coil	-0.3987404	0.099155864	0.139584031	2.007895213	0.05094536	0	69	61	59	70	70	43	63	41	67	60
ENSMUSG00000006315	chr7	Tmem147	-0.2384843	0.099280949	0.139719116	6.759218221	0.024459042	0	1784	1704	1561	2038	1634	1890	1574	1607	1473	1568
ENSMUSG00000006464	chr19	Bbs1	-0.4292948	0.099333993	0.139765948	1.623138587	0.056760688	0	50	44	40	60	59	38	32	33	44	59
ENSMUSG00000015937	chr13	H2afy	0.24073723	0.099334227	0.139765948	6.134819159	0.024580046	0	975	877	830	1166	949	1470	1315	1115	1219	1097
ENSMUSG00000022476	chr15	Polr3h	0.28215554	0.099376463	0.139811299	3.53129615	0.028888549	0	153	146	120	185	165	250	217	206	187	165
ENSMUSG00000021555	chr13	Naa35	0.23558571	0.099645503	0.140147484	4.420053415	0.021369115	0	305	260	261	357	276	401	386	354	398	336
ENSMUSG00000022217	chr14	Emc9	0.24527895	0.0996319	0.140147484	4.329564729	0.023294726	0	252	265	254	352	244	345	315	369	369	362
ENSMUSG00000091537	chr9	Tma7	0.25541797	0.099645283	0.140147484	5.589297991	0.027381628	0	748	648	595	713	551	879	994	790	887	707
ENSMUSG00000034729	chr17	Mrps10	0.23012245	0.099678238	0.140174746	4.788884549	0.02096218	0	415	366	331	444	333	456	505	445	491	523

ENSMUSG00000103515	chr8	AL591003.1	0.58130751	0.099684946	0.140174746	0.602702855	0.095497389	0	13	23	18	22	7	21	37	22	20	36
ENSMUSG00000033285	chr3	Wdr3	-0.28228	0.099715555	0.140192589	3.826612949	0.030422754	0	238	209	214	271	218	238	249	154	237	161
ENSMUSG00000096199	chr12	Ptrhd1	0.29210123	0.099717697	0.140192589	3.153569357	0.029990893	0	122	92	100	153	123	196	163	125	159	149
ENSMUSG00000074682	chr2	Zcchc3	0.40342717	0.09982897	0.140334912	1.754801584	0.047430476	0	41	50	41	43	32	68	59	45	58	73
ENSMUSG00000043614	chr5	Vps37d	0.64936431	0.100202584	0.140845953	0.470066027	0.122271	0	30	12	10	9	11	32	19	32	17	25
ENSMUSG00000002031	chr9	Ift46	0.27238056	0.100426099	0.141145933	4.05876758	0.028598247	0	248	245	208	239	173	382	264	293	242	302
ENSMUSG00000022114	chr14	Spry2	-0.2670959	0.100460301	0.141179806	3.951467119	0.027189403	0	247	247	228	328	207	239	293	214	169	226
ENSMUSG00000098905	chr13	Zfp953	-0.6500403	0.10063942	0.141417307	0.522143336	0.127006578	0	23	36	15	39	9	23	11	9	17	24
ENSMUSG00000022894	chr16	Adamts5	-0.2371657	0.10068426	0.141465881	4.28522881	0.021595913	0	287	293	286	397	303	354	278	232	296	299
ENSMUSG00000052296	chr7	Ppp6r1	-0.2358519	0.100694232	0.141465881	6.240926353	0.023845334	0	1145	1110	1107	1547	1192	1234	1100	1018	1033	1291
ENSMUSG00000039781	chr11	Cep131	0.33404887	0.100718682	0.141486009	2.850933554	0.039535418	0	86	83	83	120	96	114	128	150	100	150
ENSMUSG00000020525	chr11	Ppm1d	-0.3308332	0.100920504	0.141755273	2.744983942	0.038163956	0	97	94	116	164	82	102	100	73	93	110
ENSMUSG00000024949	chr19	Sf1	0.27048889	0.101032932	0.141898874	6.188108087	0.031635897	0	923	826	734	1313	1146	1556	1392	1233	1039	1306
ENSMUSG00000063172	chr4	Hspb11	0.38211922	0.101043045	0.141898874	1.861394596	0.043235458	0	53	47	41	48	37	76	66	54	71	57
ENSMUSG00000057967	chr11	Fgf18	-0.5150626	0.101281446	0.14221938	1.033636274	0.083756934	0	31	28	49	26	32	22	34	19	23	32
ENSMUSG00000024580	chr18	Grpel2	-0.2450308	0.101296072	0.142225628	4.431620853	0.023542444	0	313	355	346	425	296	293	368	314	309	314
ENSMUSG00000032044	chr9	Rpusd4	0.26915296	0.101336256	0.142267756	3.438685534	0.025864182	0	142	142	148	169	122	212	182	163	213	186
ENSMUSG00000004789	chr12	Dlst	-0.266231	0.101414717	0.142363609	8.533841078	0.031438982	0	5313	5781	5659	8653	5061	5685	5072	6050	4823	5740
ENSMUSG00000029516	chr5	Cit	0.46744244	0.101447574	0.14239543	1.358850434	0.067594014	0	25	32	20	37	38	38	56	55	40	40
ENSMUSG00000020362	chr11	Cnot6	-0.259021	0.101580629	0.142567872	4.428758779	0.026807379	0	344	325	321	477	287	380	414	247	291	270
ENSMUSG00000002055	chr11	Spag5	0.3598193	0.101605875	0.142582904	2.979156904	0.048042636	0	126	85	93	88	108	122	196	130	131	131
ENSMUSG00000020522	chr11	Mfap3	-0.2575445	0.101611743	0.142582904	3.912896113	0.025325541	0	248	254	202	260	243	242	233	164	226	251
ENSMUSG00000001870	chr17	Ltbp1	0.26817263	0.101707212	0.142696816	4.70990765	0.029640615	0	376	306	335	474	284	511	493	546	333	436
ENSMUSG00000034781	chr10	Gna11	-0.2280051	0.101713343	0.142696816	5.462485695	0.021728129	0	711	689	670	840	625	745	627	621	632	685
ENSMUSG00000040234	chr6	Tm7sf3	0.23910136	0.1017378	0.142716801	4.386824353	0.02226541	0	253	303	267	349	250	371	424	331	348	364
ENSMUSG00000026767	chr2	Fam188a	-0.342856	0.101902822	0.142933947	2.842051657	0.042843697	0	118	118	87	158	111	90	138	78	112	89
ENSMUSG00000003752	chr7	Itpkc	0.32374932	0.101943433	0.14297656	2.691569245	0.035851763	0	92	70	70	108	81	154	108	85	113	119
ENSMUSG00000029326	chr5	Enoph1	0.32724387	0.102042182	0.143068938	2.900297311	0.038465574	0	89	80	95	126	96	149	161	91	150	118
ENSMUSG00000032377	chr9	Plscr4	0.38514196	0.102050247	0.143068938	1.938473011	0.046316956	0	48	53	39	60	40	56	83	56	69	78
ENSMUSG00000051817	chr2	Sox12	0.36321859	0.102048844	0.143068938	2.436568362	0.044525888	0	75	64	83	70	50	108	97	104	79	97
ENSMUSG00000087231	chr6	E230016M11Rik	0.62189253	0.102040651	0.143068938	0.29982896	0.098128936	0	15	16	16	11	6	13	26	26	21	22
ENSMUSG00000036371	chr6	Serbp1	-0.260685	0.102526953	0.143722838	7.997615725	0.030254909	0	4076	3572	3491	5585	4169	3395	4129	3241	3941	4241
ENSMUSG00000024383	chr18	Map3k2	-0.3349548	0.102615778	0.143832927	3.465622819	0.044248579	0	145	165	161	274	174	247	172	117	103	163
ENSMUSG00000000538	chr11	Tom1l2	-0.2565013	0.102715682	0.14395852	6.595379601	0.028841165	0	1431	1412	1402	2226	1440	1282	1445	1320	1595	1510
ENSMUSG00000048164	chr16	Gm7204	0.84565289	0.102766222	0.144014912	-0.147812742	0.205904627	0	5	20	1	10	5	17	24	9	21	10
ENSMUSG00000040720	chr4	1110037F02Rik	-0.2650575	0.102978518	0.144297952	4.230048184	0.027774938	0	283	261	272	432	283	227	333	243	281	295
ENSMUSG00000022552	chr15	Sharpin	0.23400854	0.103049367	0.144382752	4.684639343	0.02191601	0	398	307	322	388	333	504	459	425	379	497
ENSMUSG00000027405	chr2	Nop56	0.26214988	0.103122625	0.144470911	4.83977826	0.028552376	0	389	326	323	500	402	602	639	379	512	420
ENSMUSG00000027353	chr2	Mcm8	-0.513342	0.103149171	0.144493617	0.808212121	0.075101026	0	23	31	25	30	33	21	34	13	23	19
ENSMUSG00000104204	chr6	RP23-291E6.6	-0.4959812	0.103166082	0.144502823	0.948004078	0.065901903	0	38	23	33	43	22	22	18	24	26	32
ENSMUSG00000050052	chr8	Tdrp	-0.4387248	0.103346032	0.14474037	2.663684481	0.07477089	0	99	107	109	119	97	37	96	86	84	124
ENSMUSG00000029054	chr4	Gabrd	0.68025483	0.103489343	0.144915796	2.072177984	0.186807585	0	109	36	38	24	24	66	70	141	70	54
ENSMUSG00000031373	chrX	Car5b	0.60808503	0.103492027	0.144915796	1.8362599	0.139172684	0	18	73	37	26	43	64	102	51	41	84
ENSMUSG00000060090	chrX	Rp2h	-0.4364793	0.103553967	0.144988003	2.454463338	0.073301916	0	76	92	107	99	82	62	86	34	101	90
ENSMUSG00000022419	chr15	Deptor	-0.3008018	0.103683861	0.145155328	6.504052234	0.040100315	0	1500	1349	1473	1772	1357	882	1336	1204	1417	1749
ENSMUSG00000070315	chr9	4930581F22Rik	0.70630247	0.10370446	0.145169625	-0.286535753	0.11191408	0	6	9	7	11	6	23	4	14	15	14
ENSMUSG00000003345	chr10	Csnk1g2	-0.2316884	0.10372922	0.145189743	6.587107506	0.02357925	0	1576	1398	1439	1960	1385	1582	1380	1335	1463	1450
ENSMUSG00000045005	chr1	Fzd5	0.42521443	0.103745175	0.145197534	1.87914616	0.061907055	0	35	40	49	65	38	74	73	80	38	67
ENSMUSG00000020928	chr11	Higd1b	0.4353218	0.103757552	0.145200315	1.378918532	0.057620261	0	34	26	27	46	25	65	46	41	28	54
ENSMUSG00000040731	chr5	Eif4h	0.23883732	0.103805753	0.145253224	7.218589655	0.025377997	0	1962	1821	1713	2693	2041	3023	2671	2469	2397	2619
ENSMUSG00000051504	chr7	Siglech	0.79365125	0.103849348	0.145299679	0.246703674	0.193808914	0	10	20	8	8	10	55	21	14	9	13
ENSMUSG00000025209	chr19	Peo1	-0.2378968	0.104371538	0.146015677	4.635876442	0.022850723	0	353	387	334	574	368	418	331	355	346	406
ENSMUSG00000084289	chrX	Gm6977	0.38380523	0.104424416	0.146075032	2.188758711	0.050474324	0	77	50	40	61	58	83	67	81	75	103
ENSMUSG00000043300	chr3	B3galnt1	0.37250755	0.104548283	0.146233667	2.229608803	0.047296503	0	60	61	40	79	58	107	99	53	79	86
ENSMUSG00000030138	chr6	Bms1	-0.2392438	0.104650051	0.146361364	5.025855202	0.023877215	0	480	478	456	705	515	435	526	407	520	539
ENSMUSG00000031901	chr8	Dus2	0.28239863	0.104673015	0.146378833	3.482875167	0.030080544	0	142	138	143	181	139	208	195	227	196	158
ENSMUSG00000038605	chr2	Samd10	0.40994994	0.104902935	0.14667101	1.681030811	0.051644877	0	32	32	35	52	46	75	57	38	54	65
ENSMUSG00000063200	chr13	Nol7	-0.2609503	0.104898443	0.14667101	5.6331941	0.029575826	0	896	749	670	1044	693	655	874	589	833	719
ENSMUSG00000032952	chr3	Ap4b1	-0.2483494	0.105022087	0.146822916	3.909828377	0.02347415	0	253	256	223	270	202	226	212	230	217	224
ENSMUSG00000044317	chr7	Gpr4	-0.4939689	0.105046175	0.146841902	2.303330153	0.095764031	0	53	75	82	143	74	118	35	74	48	54
ENSMUSG00000029469	chr5	Ift81	0.4639859	0.105099561	0.146901837	2.131274331	0.084020299	0	48	48	36	115	30	102	61	94	73	71
ENSMUSG00000073758	chr4	Sh3d21	0.55129143	0.105182961	0.147003706	0.47704533	0.085753815	0	20	17	13	16	10	36	14	26	17	30
ENSMUSG00000019849	chr10	Prep	0.25341729	0.105252873	0.147072001	4.90802597	0.027138957	0	377	334	358	579	403	494	654	532	443	527
ENSMUSG00000025451	chr13	Paip1	-0.2402074	0.105249055	0.147072001	5.464996971	0.02473601	0	782	607	630	981	593	695	705	548	696	657
ENSMUSG00000040811	chr7	Eml2	0.24152083	0.105271151	0.147082836	3.984955382	0.022249529	0	196	211	185	268	214	331	268	267	262	263

ENSMUSG00000072761	chr17	Gm6712	-0.6654613	0.1053886	0.147232215	0.341918048	0.136807847	0	18	33	22	18	13	7	24	9	21	11
ENSMUSG00000051043	chr11	Gprc5c	-0.2920178	0.105439581	0.147288714	6.415266552	0.038113406	0	1530	1488	1342	1337	1226	990	1301	1450	1077	1386
ENSMUSG00000063698	chr19	Sfxn4	-0.4129345	0.105475466	0.147324117	1.412245865	0.051717461	0	34	48	38	52	44	46	34	39	30	29
ENSMUSG00000039684	chr10	Gm5422	-0.4298378	0.105545077	0.147406616	1.332697976	0.056967933	0	35	38	37	50	45	47	23	25	32	41
ENSMUSG00000030638	chr7	Sh3gl3	0.62463543	0.105611856	0.147485142	-0.090024479	0.082555694	0	12	11	11	8	5	13	16	17	13	21
ENSMUSG00000063931	chr7	Pepd	0.24349747	0.105633626	0.147500804	5.318068253	0.025310462	0	609	541	482	582	490	858	788	547	703	643
ENSMUSG00000063801	chr7	Ap3s2	-0.2407728	0.105697605	0.147575397	5.489923477	0.024990217	0	801	699	682	816	615	620	717	617	711	678
ENSMUSG00000024667	chr19	Tmem216	0.46408562	0.105862146	0.147790365	1.287110451	0.068648506	0	31	20	31	32	30	46	45	56	42	28
ENSMUSG00000063696	chr8	Gm8730	-1.172276	0.106001083	0.147969551	6.876399246	0.596723613	0	2754	2235	2193	2855	2097	5675	209	202	180	164
ENSMUSG00000038351	chr11	Sgsm2	0.37076372	0.106083775	0.148070193	2.922381765	0.052393449	0	102	103	96	99	81	202	116	129	78	169
ENSMUSG00000031090	chr7	Nadsyn1	0.39096379	0.106252414	0.148277447	1.597583597	0.04592797	0	34	45	31	41	35	63	52	52	56	45
ENSMUSG00000051065	chr16	Mb21d2	-0.27196	0.106264089	0.148277447	3.274088262	0.026439054	0	168	148	120	216	135	173	144	129	131	132
ENSMUSG00000070304	chr9	Scn2b	-0.7239898	0.106253539	0.148277447	0.106782052	0.149523807	0	14	19	5	23	28	20	8	15	6	10
ENSMUSG00000043687	chr8	1190005I06Rik	0.63463206	0.106456643	0.148518509	-0.077503525	0.098409183	0	9	14	5	14	6	17	10	20	12	22
ENSMUSG00000073402	chr17	Gm8909	-1.6939513	0.106458101	0.148518509	0.857565208	1.143425603	0	61	20	44	17	46	70	0	0	0	2
ENSMUSG00000032469	chr9	Dbr1	0.31551513	0.106541942	0.148620639	2.463242286	0.033463981	0	82	70	61	84	61	95	105	89	96	102
ENSMUSG00000031628	chr8	Casp3	-0.5662544	0.106561907	0.148633653	1.724898475	0.122097958	0	66	71	50	54	41	17	71	26	35	61
ENSMUSG00000024077	chr17	Strn	-0.2665242	0.106780683	0.148923942	3.5641012	0.027301507	0	182	181	174	226	189	235	175	121	166	179
ENSMUSG00000025466	chr7	Fuom	0.28265562	0.106828057	0.148968913	4.161096267	0.032813842	0	200	269	250	284	189	413	294	322	317	246
ENSMUSG00000037266	chr4	Rsrp1	-0.3484593	0.106834245	0.148968913	7.286533412	0.055394234	0	2829	2766	2244	2364	2655	3993	1735	1583	2242	1835
ENSMUSG00000035007	chr11	Rundc1	0.24728195	0.106869829	0.149003664	3.741510957	0.022780393	0	190	182	157	199	172	287	214	218	218	240
ENSMUSG00000035566	chr14	Pcdh17	-0.6038917	0.10699408	0.149147144	1.026101874	0.12312082	0	25	36	50	41	20	14	15	30	24	40
ENSMUSG00000078772	chr4	Gm12353	-0.3486796	0.106990967	0.149147144	2.744001766	0.045166512	0	112	127	118	121	70	101	76	85	105	105
ENSMUSG00000038542	chr8	Pcid2	0.26304168	0.107222001	0.149435051	3.752141162	0.026683968	0	188	151	152	229	187	329	223	209	208	228
ENSMUSG00000049858	chr10	Suox	-0.2555764	0.107211735	0.149435051	5.131087119	0.02812815	0	608	551	522	655	495	440	454	541	490	661
ENSMUSG00000023990	chr17	Tfeb	-0.236833	0.107389672	0.149653809	6.136398372	0.024945416	0	1271	1019	979	1393	1021	1145	932	949	1047	1196
ENSMUSG00000059409	chr17	Ppp2r5d	-0.2191374	0.107497926	0.149789733	5.168497737	0.020308938	0	568	523	504	738	552	552	587	480	502	587
ENSMUSG00000030494	chr7	Rhpn2	-0.5362136	0.107593243	0.149907603	0.911149208	0.093934138	0	24	30	27	48	28	25	13	30	13	36
ENSMUSG00000027641	chr2	Rbl1	0.40964425	0.10778872	0.150164988	2.185072837	0.061318214	0	69	61	48	55	48	83	114	44	88	85
ENSMUSG00000079662	chr17	Ntn3	0.56704997	0.107828631	0.150205617	0.834051428	0.103841684	0	18	27	14	23	17	31	23	39	16	52
ENSMUSG00000062981	chr10	Mrpl42	-0.245384	0.107903065	0.150294323	7.557727204	0.027534868	0	3244	2956	2974	3674	2405	2926	2771	2788	2916	2619
ENSMUSG00000037624	chr1	Kcnk2	-0.5186294	0.108034421	0.150462289	1.32928955	0.092219627	0	38	45	42	50	35	43	27	44	11	36
ENSMUSG00000001661	chr15	Hoxc6	-0.3220511	0.108305636	0.150809961	3.182702501	0.040368556	0	167	134	133	155	149	157	129	153	81	131
ENSMUSG00000032712	chr6	2810474O19Rik	0.28348147	0.108299728	0.150809961	3.981798459	0.032728819	0	226	247	200	201	170	274	310	311	256	246
ENSMUSG00000053226	chr8	Dand5	0.30774672	0.108437577	0.150978638	2.907252204	0.034520981	0	110	87	86	115	93	111	126	135	137	153
ENSMUSG00000028018	chr3	Gstcd	0.43841699	0.108612638	0.151207314	1.402403091	0.057010954	0	31	27	41	29	29	56	59	41	38	43
ENSMUSG00000028797	chr4	Tmem234	0.23190796	0.108654144	0.151250032	5.395742602	0.023348876	0	645	529	560	635	500	798	712	626	730	844
ENSMUSG00000070443	chr3	Gm10291	0.59189171	0.109166812	0.151948548	0.301855529	0.086368493	0	15	17	8	12	13	14	29	20	17	28
ENSMUSG00000001143	chr1	Lman2l	-0.2300553	0.10932971	0.15216013	4.905306568	0.022418187	0	538	421	422	559	461	470	455	481	385	447
ENSMUSG00000027845	chr3	Dclre1b	-0.3750691	0.109399035	0.152241453	1.971017173	0.0478538	0	66	53	53	68	78	55	58	42	50	66
ENSMUSG00000036620	chr11	Mgat4b	0.26330283	0.109502918	0.152370847	5.313580359	0.030629738	0	448	481	487	722	558	1036	623	612	600	694
ENSMUSG00000037010	chrX	Apln	-0.4945262	0.10951717	0.152375507	3.386210148	0.106301735	0	202	263	204	138	81	136	134	200	68	159
ENSMUSG00000006651	chr7	Aplp1	0.53116489	0.109774992	0.152719021	0.706683058	0.078088557	0	24	13	22	19	13	40	28	27	16	35
ENSMUSG00000067995	chr14	Gtf2f2	0.29587532	0.109787635	0.152721409	3.530517389	0.035011741	0	158	156	119	211	128	251	236	160	234	150
ENSMUSG00000020085	chr10	Aifm2	0.28834546	0.110198898	0.153278245	4.046728884	0.035132679	0	160	259	170	341	186	303	278	310	273	304
ENSMUSG00000020102	chr10	Slc16a7	0.73342489	0.110213235	0.153282931	0.31617644	0.176532703	0	8	21	13	10	9	18	39	6	16	36
ENSMUSG00000024829	chr19	Mrpl21	0.22208353	0.11022553	0.153284776	5.122051849	0.021294906	0	484	477	421	628	393	687	625	616	570	550
ENSMUSG00000013539	chr16	Tango2	-0.2766762	0.110274214	0.153337222	4.525063333	0.032959678	0	309	388	363	516	307	466	320	257	384	274
ENSMUSG00000031448	chr8	Adprhl1	0.39415157	0.110301309	0.15335964	5.03750524	0.070670755	0	329	360	405	743	321	1134	366	625	434	515
ENSMUSG00000073888	chr4	Ccl27a	0.35051457	0.110326653	0.153379618	2.475195034	0.044279659	0	87	65	68	77	58	125	79	112	81	100
ENSMUSG00000040620	chr11	Dhx33	-0.2658579	0.110366269	0.153419433	3.43166261	0.026975093	0	175	172	152	213	158	176	192	126	163	136
ENSMUSG00000021786	chr14	Oxsm	-0.334502	0.110479389	0.153561406	3.676888876	0.046727062	0	220	194	192	277	177	103	205	160	205	235
ENSMUSG00000042579	chr3	4632404H12Rik	-0.4561953	0.110665939	0.153805406	0.968205903	0.059039543	0	29	27	22	43	38	22	31	23	25	25
ENSMUSG00000097820	chr9	E530011L22Rik	0.50884295	0.110833615	0.154023128	0.796452773	0.077105781	0	24	18	23	24	10	31	25	32	40	25
ENSMUSG00000019794	chr10	Katna1	0.23301965	0.111005196	0.154246234	4.00099527	0.021337487	0	209	215	183	274	210	311	291	256	277	267
ENSMUSG00000006675	chr9	P4htm	-0.4017202	0.111047995	0.154290365	1.982043119	0.059959704	0	50	64	55	64	88	73	58	42	42	57
ENSMUSG00000033308	chr3	Dpyd	-0.6551342	0.111094227	0.154339257	0.335021396	0.134994387	0	18	33	12	22	19	4	15	21	16	15
ENSMUSG00000024170	chr17	Telo2	0.29540771	0.111403553	0.154753609	3.232924107	0.033571071	0	126	104	128	136	123	174	137	183	179	156
ENSMUSG00000029505	chr5	Ep400	-0.2420206	0.11152699	0.154909681	4.730900354	0.025080374	0	370	392	354	609	429	406	446	364	317	450
ENSMUSG00000037740	chr2	Mrps26	0.22850962	0.111639636	0.155050736	4.901815013	0.022466661	0	379	410	386	536	342	651	495	480	538	463
ENSMUSG00000024480	chr18	Ap3s1	0.31499147	0.111690228	0.155105587	3.634466435	0.041242856	0	171	170	134	210	136	169	306	158	203	279
ENSMUSG00000049300	chr3	Prmt6	0.32940715	0.11179725	0.155238785	2.459801736	0.039263846	0	81	69	55	101	53	102	107	77	107	96
ENSMUSG00000070407	chr11	Hs3st3b1	-0.5930927	0.111910685	0.15538086	-0.129269848	0.085466466	0	9	15	13	18	16	17	12	5	8	10
ENSMUSG00000023079	chr5	Gtf2ird1	-0.3267293	0.112010276	0.155503687	2.845626882	0.040735937	0	116	109	88	153	123	141	78	100	105	89
ENSMUSG00000098702	chr18	1500015A07Rik	0.45631103	0.112052315	0.155546598	1.169710275	0.06478059	0	22	33	24	32	22	28	53	42	36	40

ENSMUSG00000037904	chr12	Ankrd9	-0.2497703	0.112125067	0.155632131	6.402240389	0.028852409	0	1439	1171	1342	1459	1381	1406	1221	1006	1141	1563
ENSMUSG00000020941	chr11	Map3k14	0.30727146	0.112235703	0.155754759	3.075497011	0.036372696	0	104	82	104	174	97	187	166	136	141	122
ENSMUSG00000037808	chr9	Fam76b	-0.3031114	0.11223341	0.155754759	2.975975658	0.034539347	0	129	124	140	156	90	123	125	82	112	127
ENSMUSG00000030846	chr7	Tial1	-0.2349973	0.112305522	0.155836177	5.248111784	0.02446468	0	703	548	577	718	511	597	662	440	589	561
ENSMUSG00000030662	chr14	Ipo5	-0.2574874	0.112401825	0.155954324	7.048435668	0.030966311	0	1999	1786	1807	3281	2023	2115	2273	1588	2089	1787
ENSMUSG00000044285	chr14	Gm1821	0.59923168	0.112502015	0.156077841	3.192371111	0.160364482	0	127	93	94	120	99	132	76	54	278	349
ENSMUSG00000005716	chr15	Pvalb	-0.3494463	0.112573446	0.156158478	14.26306027	0.057943332	0	477538	333602	282534	245186	279199	218318	322227	232475	282040	354326
ENSMUSG00000034263	chr9	Vwa9	-0.238693	0.112582486	0.156158478	4.593556415	0.024274208	0	434	361	331	471	347	335	386	292	339	451
ENSMUSG00000022336	chr15	Eif3e	-0.2425367	0.112636507	0.156217904	6.567046502	0.0272842	0	1675	1525	1353	1874	1251	1606	1533	1070	1541	1358
ENSMUSG00000007207	chr5	Stx1a	0.54651822	0.112780157	0.156389058	0.422236594	0.085601389	0	20	17	9	15	12	38	15	18	25	22
ENSMUSG00000027185	chr2	Nat10	-0.2533179	0.112782292	0.156389058	4.353029522	0.027152826	0	327	302	281	383	350	285	343	259	354	267
ENSMUSG00000009575	chr15	Cbx5	-0.2361355	0.112891227	0.156524583	5.862917912	0.025395773	0	972	880	841	1069	909	853	984	926	743	835
ENSMUSG00000024151	chr17	Msh2	0.24216836	0.113005845	0.156667959	3.705769799	0.022749635	0	159	185	155	235	153	245	234	204	204	259
ENSMUSG00000042453	chr5	Reln	-0.3958017	0.113192341	0.156910946	2.152721188	0.058534701	0	62	46	71	125	69	77	77	49	50	54
ENSMUSG00000022827	chr16	Rabl3	0.29277037	0.113217158	0.156929783	2.783426386	0.031129453	0	92	87	87	119	70	154	123	110	107	116
ENSMUSG00000034111	chr12	Tmed8	-0.3184176	0.113464269	0.157256707	2.372882203	0.034081904	0	89	78	69	110	75	72	81	69	74	71
ENSMUSG00000048100	chr3	Taf13	0.23862734	0.113762671	0.157654644	4.429061042	0.024258363	0	323	278	253	384	237	333	385	335	396	439
ENSMUSG00000031532	chr8	Saraf	-0.2992226	0.113852155	0.15776301	7.184078828	0.042351537	0	2531	2202	2055	2901	2280	1332	2426	1974	2189	2638
ENSMUSG00000029563	chr6	Foxp2	-0.5494991	0.113877049	0.157781861	0.499975862	0.08565114	0	24	23	30	23	14	16	13	25	14	17
ENSMUSG00000037822	chr5	Smim14	0.25520781	0.113942543	0.157856958	5.337989371	0.029429448	0	525	568	497	680	476	1067	666	575	557	764
ENSMUSG00000009293	chr10	Ube2g2	0.24594576	0.114081857	0.158034298	6.410727987	0.028272896	0	1187	1099	957	1633	984	1633	1289	1377	1692	1520
ENSMUSG00000058325	chr7	Dock1	-0.251773	0.114275729	0.158287174	3.849077961	0.025956279	0	228	238	215	271	205	265	232	181	154	242
ENSMUSG00000025217	chr19	Btrc	-0.2374055	0.114551066	0.158651714	4.73082184	0.024477948	0	371	426	388	533	415	363	366	386	385	475
ENSMUSG00000030521	chr7	Mphosph10	-0.264716	0.114561613	0.158651714	4.05340058	0.029671304	0	315	235	229	319	246	317	284	181	247	202
ENSMUSG00000040170	chr1	Fmo2	-0.470968	0.114601148	0.15869074	2.484027027	0.09154486	0	58	114	92	147	69	38	88	54	95	97
ENSMUSG00000034659	chr19	Tmem109	-0.2569382	0.114660234	0.158756829	8.515239347	0.031579823	0	5905	5208	5046	6913	6532	4822	6023	5126	5269	5888
ENSMUSG00000029600	chr5	Rita1	-0.3803452	0.11471798	0.158821049	2.270468589	0.053050242	0	85	87	74	106	48	62	63	71	80	55
ENSMUSG00000020042	chr10	Btbd11	0.48193262	0.114750744	0.158850673	0.632020388	0.061968483	0	13	16	14	22	23	25	33	24	25	28
ENSMUSG00000031950	chr8	Gabarapl2	-0.2253188	0.114784716	0.158881965	5.737520058	0.023185577	0	944	843	743	1079	692	946	828	657	789	805
ENSMUSG00000029394	chr5	Cdk2ap1	-0.2261938	0.114872336	0.158956016	5.494394991	0.023167814	0	812	681	577	883	673	827	669	601	610	692
ENSMUSG00000032615	chr11	Nt5m	0.25707247	0.114862875	0.158956016	4.034461959	0.027572185	0	211	178	239	282	196	331	245	283	250	339
ENSMUSG00000034928	chr13	Rnf44	-0.2651409	0.114866721	0.158956016	4.905845763	0.031525164	0	399	465	424	690	471	437	453	445	307	577
ENSMUSG00000037224	chr5	Zfyve28	-0.5817281	0.114942338	0.159037137	0.238998577	0.103319548	0	21	18	23	18	14	16	16	9	5	24
ENSMUSG00000049929	chrX	Lpar4	-0.4908488	0.115102052	0.159242356	1.503122507	0.0873966	0	40	48	54	51	42	22	28	44	29	60
ENSMUSG00000034341	chr11	Wbp2	0.24495867	0.115196261	0.159356918	6.347876742	0.028111146	0	1145	1034	869	1393	1126	1714	1399	1289	1129	1717
ENSMUSG00000037031	chr10	Tspan15	-0.2931876	0.115333353	0.159530775	3.738129347	0.036078229	0	239	222	183	264	181	175	147	160	241	244
ENSMUSG00000003865	chr7	Gys1	-0.289355	0.115526975	0.159780764	8.533092395	0.040249762	0	5157	5171	5636	9379	5459	4572	5083	6172	4587	6623
ENSMUSG00000017446	chr11	C1qtnf1	-0.3498264	0.115548381	0.159780764	3.811068284	0.054022758	0	192	184	197	290	297	143	192	181	167	315
ENSMUSG00000018707	chr12	Dync1h1	-0.2493513	0.11554134	0.159780764	7.435751397	0.029676902	0	2509	2363	2361	3734	3097	3016	2450	2435	2213	2837
ENSMUSG00000031828	chr8	Klhl36	0.49272453	0.115646409	0.159900496	1.050865847	0.073850675	0	35	20	27	20	17	38	42	33	25	48
ENSMUSG00000024793	chr4	Tnfrsf25	0.64263978	0.115779142	0.160068185	0.498226658	0.131666499	0	17	16	19	10	11	52	16	21	26	14
ENSMUSG00000022787	chr16	Wdr53	0.31032309	0.115884076	0.160197413	2.625156983	0.034347805	0	80	85	71	96	70	123	102	101	123	96
ENSMUSG00000052446	chr8	Zfp961	0.39807909	0.115921401	0.160233162	1.564636203	0.05310922	0	37	30	37	56	24	57	67	38	45	57
ENSMUSG00000005198	chr11	Polr2a	0.31629938	0.115938142	0.160240454	6.195759424	0.047459696	0	791	777	777	1356	1183	1440	1256	1419	810	1723
ENSMUSG00000055184	chr1	Fam72a	0.61402487	0.115994352	0.160302291	-0.021253293	0.080557216	0	6	12	7	12	13	26	16	13	15	15
ENSMUSG00000029722	chr5	Agfg2	0.33119618	0.116063722	0.1603823	2.668305407	0.04097771	0	82	78	85	81	81	121	134	94	127	90
ENSMUSG00000021417	chr13	Eci2	-0.2350499	0.116084602	0.160393096	5.980494258	0.025686032	0	897	1022	939	1405	856	998	879	826	1012	1011
ENSMUSG00000069919	chr11	Hba-a1	0.55858282	0.116094487	0.160393096	6.979078379	0.149102202	0	1602	1394	1919	1686	964	5579	864	1167	1584	3527
ENSMUSG00000024036	chr17	Slc37a1	0.53383089	0.116122869	0.160416449	0.842308259	0.096659944	0	17	16	17	37	16	45	23	18	47	28
ENSMUSG00000038240	chr10	Pdss2	-0.2302879	0.116151644	0.160440342	4.526131263	0.022620806	0	348	368	330	517	299	351	345	342	298	386
ENSMUSG00000082675	chrX	Gm6382	0.58582813	0.116213704	0.160510201	0.224122441	0.087721988	0	10	14	9	11	17	21	32	17	15	17
ENSMUSG00000061559	chr9	Wdr61	0.2429505	0.1162836	0.160590869	3.983663118	0.024175081	0	244	214	201	243	169	319	320	229	263	263
ENSMUSG00000029176	chr5	Anapc4	0.2265097	0.116323022	0.160629439	5.373477561	0.023300492	0	595	532	531	685	499	702	741	651	811	722
ENSMUSG00000027878	chr3	Notch2	0.2317168	0.116462823	0.1608066	4.549820435	0.022949052	0	326	315	274	338	334	463	394	350	376	479
ENSMUSG00000058571	chr14	Gpc6	-0.3421156	0.116572963	0.160942776	3.064150901	0.048734766	0	104	132	135	193	127	141	96	120	74	166
ENSMUSG00000022131	chr14	Gpr180	-0.2195955	0.116626722	0.160986197	4.843865605	0.021085671	0	480	447	373	593	414	469	476	334	441	445
ENSMUSG00000025220	chr19	Mgea5	-0.2320965	0.11662745	0.160986197	5.562995684	0.024800054	0	754	759	603	937	752	736	748	591	613	868
ENSMUSG00000032060	chr9	Cryab	0.3718282	0.116867571	0.161301716	9.111501028	0.067004195	0	7218	5859	7996	10494	4828	16725	9698	10373	9062	5424
ENSMUSG00000015149	chr7	Sirt2	-0.2410278	0.116886303	0.161311639	6.352036861	0.027463213	0	1251	1168	1227	1743	1230	1194	1199	1107	1061	1553
ENSMUSG00000062202	chr17	Btbd9	-0.2451503	0.116971355	0.161413079	4.012768443	0.024935241	0	253	254	204	370	229	294	210	205	228	266
ENSMUSG00000020475	chr11	Pgam2	0.2834793	0.117002076	0.161439532	11.41490769	0.039120908	0	38968	33034	31210	44725	35958	34716	51407	50618	47919	58062
ENSMUSG00000028343	chr4	Erp44	0.24087898	0.11705429	0.161479692	5.385876847	0.026587773	0	619	541	502	645	536	821	938	580	710	653
ENSMUSG00000049281	chr9	Scn3b	0.44439254	0.117048101	0.161479692	2.013726605	0.077584141	0	41	30	41	81	57	103	68	53	94	51
ENSMUSG00000028396	chr4	2310002L09Rik	-0.3713422	0.117156141	0.161604247	4.890011442	0.064433599	0	416	464	548	688	383	194	491	485	485	409
ENSMUSG00000000751	chr11	Rpa1	-0.2314127	0.117248037	0.161715046	6.269965878	0.025277422	0	1430	1138	1076	1411	1144	1200	1196	958	1182	1260

ENSMUSG00000032498	chr9	Mlh1	0.29101613	0.117445996	0.161972097	2.98277032	0.031897981	0	85	116	106	115	96	152	148	137	118	144
ENSMUSG00000040841	chr7	Six5	0.33580419	0.11747017	0.161989451	2.490452375	0.041093245	0	87	77	62	68	65	131	86	93	90	102
ENSMUSG00000061894	chr4	Zscan20	-0.3717326	0.117856105	0.162501717	1.606731202	0.04469246	0	38	46	49	58	54	42	42	39	40	45
ENSMUSG00000089979	chr16	Gm15954	0.25534344	0.117864905	0.162501717	3.3621055	0.025378602	0	127	126	125	188	128	211	177	150	195	171
ENSMUSG00000038416	chr8	Cdc16	-0.2186047	0.117944442	0.162595336	5.096957099	0.021427814	0	562	519	536	673	450	530	592	430	527	497
ENSMUSG00000032590	chr9	Apeh	0.2313392	0.118119378	0.162820439	5.257878384	0.024489043	0	606	460	437	608	505	671	636	711	617	716
ENSMUSG00000030929	chr7	Eri2	0.51682003	0.118233184	0.16296124	0.817069726	0.083554236	0	28	13	22	17	19	26	28	25	44	33
ENSMUSG00000046032	chrX	Snx12	0.21998418	0.118309329	0.163050111	4.920853562	0.021452562	0	458	386	371	491	373	567	616	409	513	556
ENSMUSG00000019808	chr10	Adat2	0.47885204	0.118364017	0.163109397	1.265102953	0.078683778	0	22	32	29	28	29	27	60	33	52	43
ENSMUSG00000045973	chr4	Slc25a51	-0.2292512	0.118392955	0.163133189	6.093133102	0.024803923	0	1082	1047	965	1403	1007	1005	1046	1012	872	1185
ENSMUSG00000029851	chr6	Fam115c	0.40612474	0.118422764	0.163158177	2.067807091	0.063845366	0	56	58	39	58	49	62	50	96	75	91
ENSMUSG00000020190	chr10	Mknk2	-0.25669	0.118643338	0.163445963	7.744786232	0.032095616	0	3529	3150	3204	4421	3156	4585	2678	2959	2563	3304
ENSMUSG00000045795	chr7	Whamm	0.28952239	0.118758902	0.163589041	2.881513958	0.031141996	0	90	82	94	127	94	146	122	105	122	158
ENSMUSG00000003527	chr16	Dgcr14	0.29434098	0.1188098	0.163643023	3.387754077	0.035558851	0	160	136	103	161	133	266	148	149	162	214
ENSMUSG00000104139	chr14	AC102815.1	-0.38295	0.119020926	0.163917664	3.842136985	0.067057746	0	247	207	227	348	186	132	250	102	205	324
ENSMUSG00000026879	chr2	Gsn	-0.2524935	0.119083617	0.163987845	9.666885929	0.031348554	0	11124	13137	11586	15576	14206	12601	13303	10594	12664	11375
ENSMUSG00000035772	chr2	Mrps2	0.22464236	0.119100153	0.163994457	4.607506839	0.022213725	0	347	300	303	431	294	428	416	465	390	426
ENSMUSG00000015671	chr13	Psma2	0.24306092	0.119713298	0.164816971	6.504573412	0.028480177	0	1437	1211	1093	1447	1013	1686	1736	1319	1820	1460
ENSMUSG00000035545	chr7	Leng8	-0.2741478	0.119721085	0.164816971	5.523135863	0.035798988	0	899	750	722	653	671	964	553	602	588	711
ENSMUSG00000098955	chr11	Mir6935	-0.5577751	0.119797191	0.1649055	1.459423888	0.122657196	0	66	43	36	55	35	27	16	23	64	42
ENSMUSG00000098496	chr7	1810026B05Rik	0.28560437	0.120137113	0.165357129	2.839743175	0.03054936	0	92	100	90	116	75	140	135	111	104	143
ENSMUSG00000022415	chr15	Syngr1	-0.2729018	0.120222479	0.165428678	4.890211385	0.034816407	0	489	524	471	516	397	564	495	243	452	456
ENSMUSG00000022748	chr16	Cmss1	-0.2394242	0.120224605	0.165428678	4.258052146	0.024806116	0	322	313	300	365	236	308	321	253	301	240
ENSMUSG00000024785	chr19	Rcl1	-0.343644	0.12021961	0.165428678	3.360557359	0.051347719	0	160	210	166	188	120	121	172	149	90	199
ENSMUSG00000029798	chr6	Herc6	0.40603992	0.120369415	0.16561163	1.402737365	0.050549384	0	35	38	31	31	25	52	57	37	38	51
ENSMUSG00000078768	chr7	Zfp566	-0.4335207	0.120413808	0.165656401	1.045111798	0.059356053	0	37	26	42	37	24	30	27	21	31	26
ENSMUSG00000028085	chr3	Gatb	-0.2427178	0.120494449	0.165751026	4.218171685	0.025419587	0	289	335	262	370	242	258	258	254	307	301
ENSMUSG00000024277	chr18	Mapre2	-0.2331985	0.120521968	0.165756251	5.323836318	0.025388182	0	678	569	594	817	572	726	702	421	574	599
ENSMUSG00000099519	chr1	Gm29253	-0.2354231	0.120512703	0.165756251	7.060892216	0.027027653	0	2103	1910	1735	2736	2299	2034	1993	1899	1833	2244
ENSMUSG00000038417	chr10	Fig4	-0.2728449	0.120573847	0.165811285	3.307721826	0.029670567	0	181	147	149	185	136	139	158	110	168	148
ENSMUSG00000025410	chr10	Dctn2	0.23025566	0.120708294	0.165966893	6.950714737	0.025813084	0	1827	1709	1555	1930	1446	2479	1980	1836	2299	2321
ENSMUSG00000059878	chr6	Zfp422	0.23496766	0.120710752	0.165966893	3.89695535	0.022699589	0	227	187	182	229	185	267	298	235	224	282
ENSMUSG00000032501	chr15	Trib1	0.32008157	0.120779245	0.166044731	5.006212727	0.048831438	0	323	409	468	704	259	850	632	460	552	435
ENSMUSG00000062077	chr5	Trim54	-0.2357637	0.120798066	0.16605427	7.680586303	0.027324771	0	3283	2868	2679	4492	3332	3122	3089	2757	3035	3372
ENSMUSG00000074890	chr2	Lcmt2	0.35225405	0.120895203	0.166171455	2.635946059	0.049893316	0	98	96	60	84	60	99	91	110	113	142
ENSMUSG00000090136	chr9	Gm10177	0.38134645	0.120926982	0.166198791	2.359017454	0.057503039	0	72	59	72	73	47	99	94	65	130	73
ENSMUSG00000050103	chr12	Agmo	-0.433095	0.121013601	0.166301484	1.549180711	0.06676436	0	40	48	51	58	43	26	32	39	37	60
ENSMUSG00000020828	chr11	Pld2	0.25289252	0.121260259	0.166624067	3.916193048	0.027184163	0	226	197	159	227	207	265	247	212	286	320
ENSMUSG00000006127	chr11	Inpp5k	-0.2287661	0.121437983	0.166851872	5.141619362	0.024320398	0	569	573	489	679	522	738	481	409	497	545
ENSMUSG00000027615	chr3	Hps3	0.3010867	0.121476785	0.166888778	2.843135319	0.034456428	0	86	105	97	102	78	143	147	100	127	120
ENSMUSG00000030822	chr7	Prr14	0.25485877	0.121588021	0.167022604	4.17500211	0.028645054	0	241	229	222	346	194	464	317	257	252	322
ENSMUSG00000080824	chr6	Gm9001	-0.6292254	0.121598096	0.167022604	-0.104030742	0.101968635	0	16	8	8	23	19	18	8	8	9	9
ENSMUSG00000045287	chr11	Rtn4rl1	0.43726444	0.121783125	0.167260314	1.448251533	0.064745191	0	28	40	30	38	28	67	30	50	39	59
ENSMUSG00000101316	chr11	Gm12663	-0.594539	0.12189002	0.167390677	0.722007796	0.12240668	0	23	15	37	40	23	16	30	11	30	12
ENSMUSG00000050786	chr6	Ccdc126	-0.4560206	0.122002182	0.167528246	1.27021291	0.072242357	0	34	44	43	45	31	49	38	23	31	18
ENSMUSG00000025049	chr19	Taf5	-0.3745556	0.122138285	0.167698661	1.878605066	0.05137064	0	56	59	39	85	63	59	63	36	51	45
ENSMUSG00000043311	chr17	D17H6S53E	0.2702768	0.122208326	0.167778347	3.613068182	0.03088959	0	164	187	168	195	105	244	199	217	194	227
ENSMUSG00000055065	chr15	Ddx17	-0.2375567	0.122294919	0.167880737	6.622115712	0.027659539	0	1740	1524	1458	1717	1463	1977	1440	1280	1381	1340
ENSMUSG00000021217	chr7	Tshz3	0.34500141	0.122492668	0.168135683	2.078800956	0.044170864	0	54	46	39	81	52	75	84	73	78	63
ENSMUSG00000025427	chr18	Rnf165	-0.5734374	0.122639951	0.168321315	0.317557683	0.094523636	0	17	18	10	41	17	15	12	16	18	12
ENSMUSG00000045078	chr5	Rnf216	-0.2287392	0.122902383	0.168664936	4.706638477	0.023660189	0	396	381	399	542	380	379	367	387	335	485
ENSMUSG00000030647	chr7	Ndufc2	0.22560728	0.122938921	0.168698514	6.898431033	0.025059097	0	1670	1652	1606	2011	1270	2428	2127	1901	2039	2013
ENSMUSG00000085829	chr14	Gm4285	0.63053152	0.123013988	0.16878495	0.058312847	0.106343024	0	13	4	18	12	6	17	19	22	15	17
ENSMUSG00000057265	chr12	Ccdc176	-0.5100419	0.123206341	0.169032278	0.078104205	0.058026339	0	16	15	16	21	14	15	14	9	11	14
ENSMUSG00000030774	chr7	Pak1	-0.3435692	0.123389185	0.169266515	6.810585654	0.058810773	0	2765	1938	1542	1425	1557	1451	1337	1242	1751	2295
ENSMUSG00000026112	chr1	Coa5	-0.2746778	0.123401637	0.169266982	7.467191081	0.037640029	0	2871	2789	2891	3446	2430	1841	2819	2784	2436	3078
ENSMUSG00000034575	chr13	Papd7	-0.2525211	0.123790509	0.169783724	3.316687262	0.025422185	0	156	153	157	206	129	160	172	127	138	138
ENSMUSG00000022515	chr16	Anks3	0.26313243	0.124008598	0.170066154	3.643440375	0.02904361	0	177	158	157	169	170	270	234	220	203	175
ENSMUSG00000000531	chr15	Grasp	0.33206342	0.1240984	0.17017261	2.830165262	0.046004215	0	68	95	99	111	86	131	109	153	96	144
ENSMUSG00000046441	chr8	Cmtr2	-0.3736267	0.124156739	0.170235906	2.227572425	0.054314032	0	59	69	72	117	71	57	80	43	59	87
ENSMUSG00000028995	chr5	Fam126a	-0.2605818	0.12426614	0.170369195	3.71713974	0.029352492	0	187	203	217	291	168	263	208	139	174	194
ENSMUSG00000039047	chr3	Pigk	-0.221564	0.12434914	0.170451909	5.262306003	0.023124466	0	619	504	563	782	611	562	628	489	550	659
ENSMUSG00000070730	chr2	Rmdn3	-0.2923564	0.124350863	0.170451909	3.28806067	0.036350723	0	134	146	160	200	152	207	149	134	114	109
ENSMUSG00000020375	chr11	Rufy1	-0.2213587	0.124432228	0.170516143	4.693238979	0.022235293	0	422	397	378	545	338	459	409	293	405	385
ENSMUSG00000028978	chr5	Nos3	-0.3249268	0.124434326	0.170516143	3.33189855	0.046068247	0	114	152	142	292	143	175	122	159	111	155

ENSMUSG00000044250	chr15	Pced1b	0.53170719	0.124421598	0.170516143	1.057197282	0.102509217	0	34	26	17	16	24	47	21	39	27	55
ENSMUSG00000034429	chr15	Zfp707	0.36310119	0.124533955	0.170630935	1.892650689	0.047103878	0	44	54	36	48	50	75	73	67	58	56
ENSMUSG00000039633	chr8	Lonrf1	-0.3268901	0.124542513	0.170630935	3.425989282	0.04779338	0	220	198	160	151	143	138	150	106	197	178
ENSMUSG00000042369	chr2	Rbm45	0.29974978	0.124762188	0.170915148	3.812873487	0.040536057	0	237	197	142	216	142	386	245	235	174	228
ENSMUSG00000078154	chr11	Gm12184	-0.3763267	0.124875646	0.17105381	1.358067738	0.041932913	0	44	43	35	49	35	42	38	29	33	32
ENSMUSG00000069255	chr13	Dusp22	0.22392503	0.124968446	0.171164151	4.877596349	0.023290182	0	353	377	404	552	339	567	514	525	505	458
ENSMUSG00000026104	chr1	Stat1	0.2355173	0.125040098	0.17122873	4.605253755	0.0252582	0	339	340	328	372	274	424	500	321	396	506
ENSMUSG00000033327	chr17	Tnxb	-0.2809885	0.125038798	0.17122873	6.832694223	0.039564834	0	1672	1577	1828	2125	2052	1668	1512	1839	1169	2204
ENSMUSG00000085704	chr2	4921531C22Rik	0.55444675	0.125083974	0.171272031	0.894863025	0.108910207	0	15	38	19	12	18	33	31	40	34	29
ENSMUSG00000041278	chr11	Ttc1	-0.2169397	0.125132368	0.17132151	5.324512885	0.022306184	0	695	598	594	729	580	696	562	525	637	601
ENSMUSG00000041164	chr11	Zmiz2	-0.2512101	0.125155927	0.171336981	5.763349758	0.030916493	0	805	683	750	1131	1028	930	781	701	658	995
ENSMUSG00000028082	chr3	Sh3d19	-0.2620541	0.125183851	0.171358424	4.03920987	0.031016803	0	299	273	241	251	250	297	208	245	187	279
ENSMUSG00000030751	chr7	Psma1	0.23813429	0.1254475	0.171702503	6.207858508	0.028018218	0	1046	989	986	1227	808	1204	1459	1123	1453	1262
ENSMUSG00000036438	chr17	Calm2	0.24300274	0.12577581	0.17213501	7.836877228	0.029881354	0	3341	2840	2807	3932	2747	3639	4724	3242	3936	4705
ENSMUSG00000022546	chr15	Gpt	0.25955468	0.125842732	0.172206261	4.654023003	0.031859907	0	270	372	252	491	331	432	370	444	471	502
ENSMUSG00000053536	chr19	Cstf2t	-0.217696	0.125852515	0.172206261	4.747167974	0.021553401	0	421	395	353	626	375	446	445	371	371	389
ENSMUSG00000103906	chr15	TIGD5	0.42142341	0.126208897	0.172676999	1.260088914	0.057815488	0	27	32	25	28	31	50	30	46	46	39
ENSMUSG00000051451	chr7	Crebzf	-0.2458545	0.126371332	0.172882316	3.566992282	0.02504749	0	216	165	171	234	166	174	213	150	157	184
ENSMUSG00000060579	chr14	Fhit	0.65693542	0.126407176	0.172914426	0.486118064	0.153546718	0	25	15	9	12	12	11	18	18	36	43
ENSMUSG00000034040	chr5	Wbscr17	0.32936162	0.12650588	0.173032509	4.162727498	0.051638222	0	169	182	260	347	225	429	222	377	222	371
ENSMUSG00000025417	chr10	Pip4k2c	0.25712529	0.126621503	0.173173708	4.230913054	0.029939307	0	263	257	217	291	237	500	320	235	280	346
ENSMUSG00000025758	chr3	Plk4	0.58518773	0.127049655	0.173742268	1.423275361	0.142215875	0	35	44	17	29	26	43	103	26	49	30
ENSMUSG00000025505	chr7	Tmem80	-0.2438527	0.127097618	0.173790853	3.662030329	0.024941287	0	223	196	191	205	191	180	196	176	188	195
ENSMUSG00000039067	chr8	Psmd7	-0.2260517	0.127424508	0.174220791	7.152462881	0.025875853	0	2525	2265	1949	2798	1930	2542	2162	1731	2184	2124
ENSMUSG00000026970	chr2	Rbms1	0.2281027	0.127812889	0.174734709	5.169101294	0.025014447	0	457	473	459	683	410	748	750	500	624	551
ENSMUSG00000019732	chr8	Calr3	0.52736219	0.12800135	0.174975241	0.866385492	0.101717845	0	20	20	14	30	20	45	18	16	47	38
ENSMUSG00000059195	chr4	Gm12715	0.39929766	0.128137555	0.175127173	2.454318107	0.068027226	0	66	59	76	82	60	118	143	43	86	114
ENSMUSG00000073096	chr6	Lrrc61	-0.2291864	0.128127474	0.175127173	4.331813253	0.0238108	0	325	321	270	397	301	347	261	288	245	369
ENSMUSG00000049086	chr2	Bmyc	0.31818685	0.128196702	0.175187747	2.953706099	0.042836389	0	119	85	72	111	117	180	118	147	109	138
ENSMUSG00000063146	chr5	Clip2	0.29973848	0.128206946	0.175187747	3.095619906	0.038376828	0	115	98	125	121	100	169	136	184	116	151
ENSMUSG00000025236	chr9	Adpgk	0.30642383	0.128359167	0.175378601	3.043814637	0.039446343	0	127	96	80	133	107	211	169	107	125	129
ENSMUSG00000024104	chr6	Fam21	-0.2294846	0.128428717	0.175456476	5.171654247	0.025498545	0	626	592	507	659	504	639	579	366	566	569
ENSMUSG00000045160	chr6	Bola3	-0.2453672	0.128645158	0.175734995	6.330906499	0.030361596	0	1370	1391	1317	1573	866	1353	1136	1159	1198	1156
ENSMUSG00000037958	chr11	Ccdc55	-0.2378532	0.128679797	0.175765133	3.738451269	0.024294033	0	241	171	187	263	208	236	193	173	170	224
ENSMUSG00000041840	chr18	Haus1	0.27879134	0.128760619	0.175858341	3.356005199	0.033139156	0	142	137	151	148	100	205	203	174	180	142
ENSMUSG00000056204	chr8	Pgpep1	0.23123884	0.128814125	0.175914228	4.653631357	0.025094264	0	297	310	338	448	328	429	395	473	408	494
ENSMUSG00000024871	chr19	Doc2g	0.60400704	0.128830315	0.175919149	0.123172949	0.124308001	0	9	7	7	25	10	35	17	15	18	10
ENSMUSG00000044716	chr5	Dok7	-0.233405	0.12886273	0.175946221	4.475285607	0.025262533	0	342	292	333	495	334	419	391	285	259	319
ENSMUSG00000090262	chr5	Mpv17	-0.2524386	0.128926884	0.17601662	5.159743894	0.031217271	0	624	581	580	615	473	464	536	393	594	668
ENSMUSG00000018932	chr11	Map2k3	-0.2227805	0.129061554	0.176183266	7.595707002	0.025468182	0	3033	3006	2969	3706	2796	2975	2893	2602	2738	3375
ENSMUSG00000056091	chr6	St3gal5	-0.2989351	0.129124045	0.176251357	5.699735971	0.044996759	0	607	801	950	1378	597	903	691	888	582	728
ENSMUSG00000074415	chr9	2610203C20Rik	-0.336491	0.129147108	0.176265623	2.94926957	0.049126969	0	174	122	115	102	112	127	94	88	133	107
ENSMUSG00000006586	chr4	Runx1t1	0.5652752	0.129356693	0.176534434	1.248170702	0.122598368	0	28	34	39	13	17	52	32	44	28	64
ENSMUSG00000027286	chr2	Lrrc57	-0.2393178	0.129405476	0.176583766	3.823377436	0.024960235	0	235	236	222	250	186	198	243	190	212	206
ENSMUSG00000025141	chr11	Myadml2	-0.2226585	0.129612791	0.176849397	6.229133494	0.024921884	0	1244	1023	1107	1557	1110	1089	1244	1015	1137	1151
ENSMUSG00000038766	chr3	Gabpb2	-0.2381886	0.129626871	0.176851343	4.10282298	0.02582835	0	261	270	270	315	256	300	311	184	251	240
ENSMUSG00000035722	chr10	Abca7	0.24280859	0.129749816	0.177001799	3.802744236	0.025568708	0	167	167	160	232	217	293	244	216	214	262
ENSMUSG00000034437	chr3	Gm9761	0.50864104	0.129836393	0.177085334	0.754172159	0.091704627	0	23	16	16	30	12	32	38	19	42	18
ENSMUSG00000097162	chr7	2310010J17Rik	0.4428233	0.129829106	0.177085334	1.10736994	0.06158742	0	20	29	27	28	23	49	41	21	39	42
ENSMUSG00000040280	chr10	Ndufa4l2	0.28807642	0.129920841	0.177183223	3.642869304	0.037469573	0	187	126	165	223	135	319	167	222	175	234
ENSMUSG00000029047	chr4	Pex10	-0.2576629	0.129970311	0.177233396	3.216859629	0.027055869	0	150	132	129	185	150	137	131	144	132	136
ENSMUSG00000092368	chr17	A930015D03Rik	-0.9702641	0.130019062	0.177282576	0.241820121	0.407212525	0	18	23	19	24	20	46	7	0	3	6
ENSMUSG00000038215	chr8	Cep44	0.32616869	0.130094303	0.177367864	2.610790045	0.042930613	0	84	79	83	73	72	105	145	86	101	107
ENSMUSG00000023988	chr17	Bysl	0.23494553	0.130258831	0.177574856	4.830481519	0.026627456	0	391	302	326	549	390	493	572	527	447	453
ENSMUSG00000003545	chr7	Fosb	0.80089935	0.13030479	0.177620184	1.296673805	0.292170075	0	15	24	62	9	10	98	50	50	17	31
ENSMUSG00000059213	chr15	Ddn	-0.5842312	0.130353931	0.17766984	-0.024641051	0.092948829	0	12	14	15	19	17	8	9	14	6	19
ENSMUSG00000049536	chrX	Tceal1	-0.3590197	0.130453899	0.177788756	2.194083171	0.051743684	0	73	90	61	81	67	63	57	67	44	88
ENSMUSG00000019802	chr10	Sec63	0.21327061	0.130540185	0.177889004	5.419823184	0.022310261	0	575	528	539	817	513	771	841	652	700	784
ENSMUSG00000069793	chr11	Slfn9	0.55937799	0.130597501	0.177949759	0.282401568	0.098788927	0	16	8	13	14	14	18	35	10	23	20
ENSMUSG00000041658	chrX	Rragb	-0.6671263	0.130764995	0.178160613	0.296560139	0.160120394	0	5	20	23	44	12	11	16	10	20	12
ENSMUSG00000042548	chr2	Asxl1	-0.2552644	0.130981226	0.178437823	4.119836749	0.030085329	0	246	234	213	412	310	261	296	245	209	276
ENSMUSG00000074182	chr3	Znhit6	0.28908636	0.131088103	0.178566016	3.440406535	0.038086288	0	153	105	106	231	138	215	213	157	218	161
ENSMUSG00000029655	chr5	N4bp2l2	-0.2295456	0.13132065	0.178865355	4.063285515	0.02353025	0	295	238	253	328	225	258	257	209	276	247
ENSMUSG00000027263	chr2	Tubgcp4	0.26020685	0.131335324	0.17886791	3.522972692	0.029453703	0	162	153	147	190	121	208	230	159	236	178
ENSMUSG00000049119	chr4	Fam110b	0.33703109	0.131451307	0.179008426	2.528287088	0.046947408	0	79	74	47	90	82	89	100	116	90	116

ENSMUSG00000062014	chr14	Gmfb	0.2171647	0.131560159	0.179139203	5.002650517	0.022646553	0	458	448	410	504	378	580	698	492	500	538
ENSMUSG00000036718	chr5	Micall2	0.3654145	0.131625167	0.179210261	1.864538775	0.048136119	0	52	53	44	53	27	77	65	57	56	69
ENSMUSG00000015790	chr2	Surf1	0.21510318	0.131696537	0.179289966	4.580711486	0.021584868	0	347	339	300	403	258	465	420	389	427	386
ENSMUSG00000091478	chr11	Gm10039	0.22122339	0.131793121	0.179403979	5.408133781	0.024288002	0	534	538	549	829	492	861	651	721	718	772
ENSMUSG00000031583	chr8	Wrn	-0.3880218	0.131989963	0.179654434	1.928103108	0.060387743	0	57	61	70	74	49	40	42	44	56	78
ENSMUSG00000028868	chr4	Wasf2	0.22702519	0.132140438	0.179841734	5.486513106	0.025645497	0	558	567	609	785	558	950	828	675	602	912
ENSMUSG00000032434	chr9	Cmtm6	0.23952358	0.132264238	0.179992696	4.491815251	0.0271263	0	251	293	309	397	282	547	366	309	385	387
ENSMUSG00000074748	chr10	Atxn7l3b	0.20657839	0.132380105	0.180132835	5.172376221	0.020613743	0	503	480	451	597	457	725	702	529	534	671
ENSMUSG00000097787	chr19	2700046G09Rik	0.47231793	0.132398805	0.180140742	1.039944916	0.080990479	0	38	27	19	23	13	43	27	29	42	42
ENSMUSG00000085498	chr2	Gm14023	0.55048294	0.132466673	0.180215538	0.126164182	0.077281109	0	15	10	14	13	6	15	18	20	16	24
ENSMUSG00000034353	chr1	Ramp1	-0.3064446	0.132552081	0.180314179	5.359965929	0.047944238	0	570	860	767	753	410	646	439	516	703	682
ENSMUSG00000046949	chr13	Nqo2	-0.2269719	0.132597776	0.180358785	4.900596112	0.024933675	0	482	531	436	558	384	388	467	413	452	511
ENSMUSG00000019235	chr12	Rps6kl1	-0.6845002	0.133062555	0.180973362	-0.225645511	0.14851383	0	11	11	8	21	17	17	9	4	14	2
ENSMUSG00000034334	chr13	Fam151b	0.42912165	0.133204271	0.181148477	0.975601171	0.056531204	0	31	24	18	28	16	43	33	25	33	39
ENSMUSG00000026942	chr2	Traf2	0.23757508	0.133242733	0.181183152	4.405390789	0.026776701	0	275	229	285	387	272	399	366	287	441	369
ENSMUSG00000089774	chr16	Slc5a3	-0.3139915	0.133278062	0.181213561	2.982653543	0.043884725	0	100	108	117	204	123	165	123	93	82	110
ENSMUSG00000097989	chr15	Gm4335	0.52390978	0.133338938	0.181278696	0.799206009	0.097415942	0	18	27	13	16	23	21	47	27	23	37
ENSMUSG00000055723	chr7	Rras2	0.25591652	0.133414474	0.181363747	4.439758554	0.031860791	0	269	241	240	456	282	444	476	373	332	295
ENSMUSG00000021704	chr13	Mtx3	-0.3026098	0.133435001	0.18137401	2.943505244	0.038474411	0	128	148	88	159	104	106	105	121	117	101
ENSMUSG00000024570	chr18	Rbfa	0.21539014	0.133504814	0.181451257	5.19386663	0.022833115	0	509	500	424	671	431	844	623	559	536	662
ENSMUSG00000025873	chr13	Faf2	0.21128165	0.133538984	0.18148005	4.213391689	0.019978332	0	234	252	238	320	231	364	336	275	296	349
ENSMUSG00000030335	chr6	Mrpl51	0.22402766	0.133730553	0.181722723	6.957963327	0.02623675	0	1657	1620	1533	2455	1377	2301	2170	2216	2058	2158
ENSMUSG00000032959	chr5	Pebp1	0.2188873	0.133781887	0.181774806	7.623032936	0.025198646	0	2885	2659	2363	3359	2354	3743	3376	3379	3093	3718
ENSMUSG00000021028	chr12	Mbip	-0.3711564	0.134058945	0.182080448	2.069141047	0.05560639	0	66	76	52	87	63	51	58	41	83	56
ENSMUSG00000030801	chr7	Kat8	-0.2338403	0.134055772	0.182080448	3.852734988	0.024189779	0	232	217	169	313	232	230	208	206	205	226
ENSMUSG00000035297	chr5	Cops4	-0.2187548	0.134035398	0.182080448	6.150984253	0.02454545	0	1121	1011	1016	1540	1041	1094	1051	918	1145	1144
ENSMUSG00000055652	chr7	Klhl25	0.32592843	0.134036012	0.182080448	2.570008855	0.043701669	0	68	66	61	96	93	150	95	95	91	100
ENSMUSG00000041781	chr12	Cpsf2	-0.2348005	0.134100033	0.182118557	4.868772307	0.027009207	0	444	457	463	594	393	426	508	354	516	374
ENSMUSG00000024604	chr18	Rbm22	0.22642702	0.134180985	0.18221079	4.344219102	0.023965794	0	272	295	220	351	254	476	337	317	335	321
ENSMUSG00000037933	chr13	Bicd2	-0.2312681	0.134267495	0.182310552	5.309534391	0.026714475	0	545	543	540	968	628	586	603	566	598	610
ENSMUSG00000038828	chr5	Tmem214	0.21996322	0.134435881	0.182521456	5.102301301	0.023826535	0	436	405	449	564	497	560	669	521	623	629
ENSMUSG00000024018	chr17	Ccdc167	-0.3249468	0.134484008	0.182569063	2.453062487	0.042598452	0	90	75	88	99	90	77	76	74	96	63
ENSMUSG00000050147	chr8	F2rl3	-0.4197239	0.134543283	0.182631791	1.379517021	0.065140917	0	49	44	50	34	32	37	32	29	44	31
ENSMUSG00000016933	chr2	Plcg1	-0.2271284	0.134626514	0.182718203	5.063733592	0.025558648	0	469	516	528	674	494	545	408	509	431	615
ENSMUSG00000031792	chr8	Usb1	0.27592213	0.134633089	0.182718203	3.196332792	0.032948733	0	123	118	105	161	106	235	156	117	160	148
ENSMUSG00000019689	chr6	1110001J03Rik	-0.2225963	0.134663095	0.18274118	5.215505771	0.024648306	0	535	597	548	830	489	718	518	490	570	505
ENSMUSG00000005374	chr5	Tbl2	0.22466721	0.134868159	0.183001688	3.889245979	0.022320387	0	201	190	166	252	203	302	277	242	213	263
ENSMUSG00000007097	chr1	Atp1a2	-0.2569382	0.135023763	0.183195041	10.5936007	0.03534225	0	20042	25281	22382	35285	23362	22629	20684	24983	19376	26926
ENSMUSG00000034518	chr8	Hmgxb4	-0.2662476	0.135361403	0.183630408	3.076636547	0.029684654	0	136	130	134	170	109	146	136	87	114	138
ENSMUSG00000097785	chr19	B230217O12Rik	-0.5778835	0.135370928	0.183630408	0.04229792	0.092749795	0	19	18	16	17	11	5	11	12	12	19
ENSMUSG00000096768	chrY	Erdr1	1.24942531	0.135406465	0.183660788	1.417466281	0.757437582	0	19	10	12	32	38	56	150	0	1	93
ENSMUSG00000029711	chr5	Epo	-0.5491093	0.13545522	0.183709089	0.461636863	0.102663525	0	14	24	16	33	25	16	7	15	18	27
ENSMUSG00000042197	chr1	Zfp451	-0.2431034	0.135637558	0.183938532	3.476577806	0.025540936	0	193	169	153	212	164	214	180	127	145	164
ENSMUSG00000022722	chr16	Arl6	0.45903303	0.135657428	0.183947629	1.435807207	0.082991545	0	36	29	37	31	27	44	80	25	45	51
ENSMUSG00000030613	chr7	Ccdc90b	-0.2271979	0.13569389	0.183979221	4.142453772	0.023696876	0	300	279	214	374	254	274	263	224	292	266
ENSMUSG00000022008	chr14	Gpalpp1	-0.232573	0.135775698	0.184072282	3.86010193	0.024567572	0	241	232	229	269	188	263	252	174	200	198
ENSMUSG00000027082	chr2	Tfpi	0.32601754	0.13603894	0.184411274	2.427411473	0.043864169	0	68	77	69	86	48	89	108	69	96	116
ENSMUSG00000031660	chr8	Brd7	-0.2171205	0.136095779	0.184452541	6.060202596	0.024369908	0	1183	978	920	1349	935	985	1108	888	1024	1020
ENSMUSG00000032459	chr9	Mrps22	-0.2371833	0.13609136	0.184452541	4.224166709	0.026519501	0	302	278	309	350	256	231	312	262	300	279
ENSMUSG00000045639	chr7	Zfp629	-0.2348837	0.136408463	0.1848584	3.916846546	0.025194507	0	199	243	215	321	234	275	224	228	191	208
ENSMUSG00000004631	chr6	Sgce	0.23807479	0.136480256	0.18493776	3.724178556	0.025320242	0	192	181	173	196	150	228	237	246	223	217
ENSMUSG00000042659	chr7	Arrdc4	0.2795742	0.136599668	0.185081625	3.295302	0.034658069	0	103	122	132	157	136	220	161	163	124	205
ENSMUSG00000055707	chr8	Klhl26	-0.2252576	0.136745573	0.185261355	3.643899466	0.022265163	0	198	198	164	239	196	205	180	172	187	188
ENSMUSG00000090641	chr13	Zfp712	-0.5263956	0.136804495	0.185323216	0.13181139	0.068361136	0	18	16	14	22	16	9	18	9	13	16
ENSMUSG00000027829	chr3	Ccnl1	0.27088645	0.136851616	0.185369082	3.76528283	0.034191981	0	196	157	205	208	142	346	240	168	238	223
ENSMUSG00000020495	chr11	Smg8	-0.2686475	0.13689898	0.185374207	3.165777529	0.031309752	0	147	136	123	209	115	133	150	102	113	161
ENSMUSG00000026109	chr1	Tmeff2	0.42934381	0.136876003	0.185374207	2.050123061	0.082422166	0	41	51	46	52	62	41	70	79	68	115
ENSMUSG00000027933	chr3	Ints3	-0.2158611	0.136898504	0.185374207	4.665346036	0.022431857	0	429	332	364	510	394	395	405	381	374	348
ENSMUSG00000074884	chr2	Serf2	0.22837029	0.136908455	0.185374207	8.131050639	0.027998752	0	4351	3787	3590	4490	3041	5908	4679	4658	4780	4697
ENSMUSG00000063884	chr6	Ptcd3	-0.3194661	0.136946043	0.185407139	5.664118425	0.053655229	0	868	775	804	1033	716	376	744	726	903	874
ENSMUSG00000033545	chr8	Znrf1	-0.218556	0.137081524	0.185572587	6.194332773	0.024929791	0	1117	1107	1157	1523	982	1173	994	1078	1104	1159
ENSMUSG00000021716	chr13	Srek1ip1	-0.2342595	0.137103686	0.185584611	3.943561257	0.025053114	0	229	218	230	313	242	233	202	255	216	234
ENSMUSG00000087413	chr4	Gm11266	-0.463878	0.137264309	0.185784039	2.273815047	0.099876022	0	129	100	80	60	35	54	61	69	74	63
ENSMUSG00000100725	chr1	Gm28062	0.23343728	0.137278918	0.185785819	6.800608792	0.028977977	0	1367	1378	1287	2278	1419	2115	2318	1551	1937	1939
ENSMUSG00000073485	chr1	H3f3aos	-0.5220474	0.137300441	0.185792072	0.169793705	0.072247432	0	22	18	16	18	14	10	17	9	17	14

ENSMUSG00000095123	chr10	Gm21781	0.48727649	0.137310126	0.185792072	0.787830631	0.077304969	0	28	19	19	16	16	47	22	30	24	30
ENSMUSG00000060380	chr9	C030014I23Rik	-0.5213769	0.137444264	0.185919718	0.860882892	0.103389351	0	33	33	15	55	17	36	25	21	17	15
ENSMUSG00000086914	chr9	Gm16124	-0.3198655	0.13742214	0.185919718	2.642551903	0.044777002	0	94	110	100	131	74	85	80	63	107	110
ENSMUSG00000097978	chr5	Gm5864	0.7687728	0.137444371	0.185919718	0.832558977	0.274195394	0	5	14	9	58	11	64	17	47	19	22
ENSMUSG00000063015	chr5	Ccni	-0.2386083	0.137514291	0.185996296	5.98032654	0.029843935	0	927	1056	871	1384	885	1085	919	849	690	1209
ENSMUSG00000027351	chr2	Spred1	0.23268261	0.137569341	0.18603866	4.323917753	0.025992741	0	266	237	263	386	225	449	412	290	272	348
ENSMUSG00000058297	chr10	Spock2	-0.3064615	0.137572235	0.18603866	2.882264046	0.041739875	0	104	110	114	124	140	149	117	82	83	104
ENSMUSG00000063415	chr6	Cyp26b1	-0.8481238	0.137594155	0.1860503	2.322193898	0.363647309	0	188	25	82	40	123	25	44	139	12	56
ENSMUSG00000026799	chr2	Med27	0.25265611	0.137629334	0.186079866	3.482119607	0.028786921	0	137	126	144	204	144	211	168	213	168	219
ENSMUSG00000022995	chr1	Enah	0.2918425	0.137709412	0.186152118	5.771430416	0.045097444	0	654	530	645	1241	663	1173	842	1206	658	1014
ENSMUSG00000068457	chrY	Uty	-1.4975827	0.137705959	0.186152118	2.678257357	1.097008756	0	263	187	216	0	1	2	71	31	61	103
ENSMUSG00000033460	chrX	Armcx1	0.32364708	0.137750293	0.186171434	2.396568298	0.043834657	0	75	68	66	79	52	73	89	94	100	107
ENSMUSG00000079139	chr1	Gm4204	0.38047287	0.137750343	0.186171434	3.268098682	0.070972808	0	130	119	102	140	123	280	230	153	147	76
ENSMUSG00000078429	chr10	Ctdsp2	-0.2380057	0.137955136	0.186430186	7.229496226	0.030381595	0	2267	2325	2309	3129	2113	2647	1939	2221	1727	2747
ENSMUSG00000015120	chr17	Ube2i	0.2116099	0.138040639	0.186521088	4.482957206	0.021189617	0	311	309	275	364	277	473	449	328	341	368
ENSMUSG00000031174	chrX	Rpgr	-0.4168577	0.138049094	0.186521088	1.163045945	0.058814965	0	37	32	24	56	34	24	34	23	29	38
ENSMUSG00000020894	chr11	Vamp2	0.25528338	0.138254947	0.18676311	5.858297866	0.034308491	0	732	707	712	1064	743	1615	864	974	850	888
ENSMUSG00000081111	chr8	Gm5913	0.59299883	0.138252795	0.18676311	0.709461739	0.133270847	0	20	15	18	19	17	7	38	33	28	40
ENSMUSG00000066150	chr4	Slc31a1	-0.2039985	0.13847644	0.187044237	4.822678793	0.020398951	0	434	437	431	525	417	514	468	387	389	387
ENSMUSG00000047363	chr2	Cstad	0.63764683	0.138516831	0.187080714	0.578127592	0.160198014	0	33	21	6	10	9	16	30	29	32	27
ENSMUSG00000022510	chr16	Trp63	0.39749169	0.13855598	0.187115507	2.74589144	0.073537708	0	126	62	84	78	70	179	111	85	74	172
ENSMUSG00000071178	chr12	Serpina1b	-1.7173348	0.138569518	0.187115708	1.106329009	1.38879268	0	21	68	26	64	54	85	0	0	0	0
ENSMUSG00000027547	chr2	Sall4	0.6649276	0.138627704	0.187176195	0.486150574	0.187756689	0	10	17	21	18	7	5	28	25	24	44
ENSMUSG00000068394	chr2	Cep152	-0.3881365	0.138748043	0.187320581	1.299333043	0.052493381	0	45	33	39	47	34	43	36	19	30	39
ENSMUSG00000018379	chr11	Srsf1	0.24468487	0.13886469	0.187459955	5.950648909	0.031653479	0	837	731	728	1154	795	1120	1475	904	1081	892
ENSMUSG00000039509	chr8	Nup133	-0.207982	0.138890807	0.187477103	4.380737963	0.020375675	0	321	332	287	418	302	372	325	298	279	299
ENSMUSG00000001138	chr1	Cnnm3	-0.2609957	0.138958401	0.187532118	3.912721571	0.032773137	0	225	254	229	285	219	244	186	219	158	307
ENSMUSG00000021595	chr13	Nsun2	0.23578083	0.138958261	0.187532118	5.624253652	0.029042025	0	684	627	580	861	630	880	1083	701	966	712
ENSMUSG00000035890	chr10	Rnf126	0.22096827	0.138984527	0.187549266	4.545065047	0.023699125	0	303	249	297	406	345	460	452	360	364	411
ENSMUSG00000029535	chr5	Triap1	0.22906141	0.13917495	0.187788096	4.237536822	0.02500996	0	287	264	229	299	208	382	373	258	351	292
ENSMUSG00000062169	chr1	Cnih4	0.22566326	0.139239857	0.187857538	4.875936257	0.025498553	0	410	393	370	458	373	490	641	415	558	467
ENSMUSG00000027778	chr3	Ift80	-0.3402019	0.139370052	0.188015044	2.17897006	0.04801034	0	78	91	56	73	67	55	67	53	69	73
ENSMUSG00000018604	chr5	Tbx3	-0.3622634	0.139618868	0.188332525	2.533184005	0.059193981	0	64	106	64	147	100	96	69	86	57	98
ENSMUSG00000047909	chr2	Ankrd16	-0.2289065	0.139645993	0.188350936	3.893420701	0.024211866	0	281	227	213	253	208	237	203	203	211	255
ENSMUSG00000034007	chr9	Scaper	-0.2887572	0.139719762	0.188414067	2.989650196	0.037276244	0	124	135	86	156	141	126	126	83	123	119
ENSMUSG00000035158	chr6	Mitf	-0.2925862	0.139712598	0.188414067	3.554442041	0.041089935	0	187	176	200	278	125	193	213	101	158	197
ENSMUSG00000026676	chr2	Ccdc3	-0.2867473	0.139851749	0.188573859	3.466462003	0.038494433	0	240	150	149	246	123	225	162	127	150	147
ENSMUSG00000026895	chr2	Ndufa8	0.23301818	0.140107795	0.188900883	7.607548204	0.029547191	0	2450	2616	2538	3708	2160	3918	3139	3713	2919	3491
ENSMUSG00000030064	chr6	Frmd4b	0.23755694	0.140176677	0.18897456	4.042903875	0.026611578	0	252	232	196	227	205	272	335	245	269	325
ENSMUSG00000040112	chr6	Mrps35	0.24025016	0.140189484	0.18897456	4.586664677	0.029059001	0	277	343	318	471	241	519	370	443	395	386
ENSMUSG00000014245	chr11	Pigl	0.37993157	0.140254203	0.189043566	1.511025877	0.054030146	0	37	46	31	34	27	44	53	54	46	53
ENSMUSG00000032000	chr9	Birc3	0.28503668	0.140278772	0.189058449	2.848899965	0.03450461	0	89	83	83	129	94	172	133	92	121	122
ENSMUSG00000086629	chrX	2810403D21Rik	0.53938732	0.140337943	0.189119958	0.057725328	0.086362313	0	10	13	5	19	9	19	14	21	12	22
ENSMUSG00000080741	chr13	Gm11398	-0.4351525	0.140481868	0.18929566	1.620434964	0.079716677	0	67	43	36	59	49	22	48	41	33	60
ENSMUSG00000005262	chr16	Ufd1l	-0.2138138	0.140561875	0.189366952	5.602817041	0.023877175	0	845	792	724	870	643	821	804	570	719	768
ENSMUSG00000020319	chr11	Wdpcp	0.39803348	0.140557995	0.189366952	1.244962215	0.055541833	0	26	26	27	47	20	34	45	40	45	43
ENSMUSG00000034501	chr12	Pcnxl4	0.27863388	0.140622389	0.189411961	2.789649201	0.032746666	0	89	103	83	99	81	119	123	102	128	135
ENSMUSG00000099112	chr15	Gm27406	-0.2692121	0.140618672	0.189411961	3.861607235	0.034998787	0	223	219	183	313	243	160	243	184	196	283
ENSMUSG00000028218	chr4	Fam92a	0.3044914	0.140961171	0.189849987	2.816085301	0.040900432	0	91	89	100	111	70	106	159	95	125	139
ENSMUSG00000059278	chr11	Naa38	0.22017587	0.141052048	0.189954078	4.645033483	0.024020501	0	361	352	303	404	295	536	393	369	491	402
ENSMUSG00000036825	chr3	Ssx2ip	-0.2770513	0.141215055	0.190155276	4.825100255	0.039765063	0	473	408	424	592	418	267	368	457	428	541
ENSMUSG00000011305	chr17	Plin5	-0.4360441	0.141254919	0.19019063	4.204895797	0.100318902	0	136	261	229	675	328	318	244	254	314	135
ENSMUSG00000036402	chr6	Gng12	-0.2095938	0.141272995	0.190196645	4.888467977	0.022072264	0	429	430	477	599	427	469	465	345	443	520
ENSMUSG00000096458	chr12	Moap1	-0.2812846	0.141343942	0.190273833	2.819582089	0.033763569	0	110	127	105	141	86	97	100	94	111	108
ENSMUSG00000074030	chr8	Exoc8	0.24860272	0.141365268	0.190284213	3.631962437	0.028109905	0	155	169	146	216	153	313	218	186	175	206
ENSMUSG00000085741	chr2	5430405H02Rik	-0.5196786	0.1415798	0.190554631	1.667906385	0.128868016	0	72	47	40	66	45	98	19	29	30	34
ENSMUSG00000022967	chr16	Ifnar1	0.25240885	0.1416125	0.190580289	4.595610981	0.03224669	0	365	325	320	356	265	561	456	275	480	380
ENSMUSG00000018733	chr11	Pex12	-0.2863198	0.141994948	0.191076583	3.255566451	0.037969055	0	188	169	118	180	120	127	125	137	119	185
ENSMUSG00000059842	chr2	Zfp341	-0.3985777	0.142068953	0.191157763	1.582545935	0.064702985	0	38	54	34	72	48	56	38	47	25	37
ENSMUSG00000018395	chr11	Kif3a	0.27731752	0.142091085	0.191169138	3.049176646	0.033812647	0	112	122	100	119	94	197	122	141	139	132
ENSMUSG00000009633	chr1	G0s2	-0.2819214	0.142323051	0.191462793	4.208473671	0.040087633	0	191	296	320	465	247	256	256	307	263	262
ENSMUSG00000025408	chr10	Ddit3	0.29064207	0.142373013	0.191474563	3.440993593	0.040587536	0	136	132	152	212	96	279	158	160	205	168
ENSMUSG00000037005	chrX	Xpnpep2	-0.5304521	0.142386548	0.191474563	0.989564587	0.115035999	0	17	29	30	33	53	18	30	21	18	38
ENSMUSG00000049038	chr10	Mterf2	-0.3134473	0.142358547	0.191474563	3.802602458	0.049156615	0	213	276	241	251	157	148	162	233	243	207
ENSMUSG00000079018	chr15	Ly6c1	0.25759991	0.142386601	0.191474563	5.722407562	0.035547393	0	672	742	687	916	573	1506	785	731	783	946

ENSMUSG00000025578	chr11	Cbx8	0.35402411	0.142405237	0.1914812	2.043795237	0.050084055	0	44	61	46	63	47	96	57	69	55	91
ENSMUSG00000054051	chr14	Ercc6	-0.270968	0.142430232	0.191496385	2.865747339	0.031543209	0	122	103	104	146	111	128	119	74	104	109
ENSMUSG00000097239	chr11	Gm27029	0.23018338	0.142445557	0.191498567	6.582997059	0.028805829	0	1525	1224	1096	1525	1204	1520	1870	1700	1704	1598
ENSMUSG00000032413	chr9	Rasa2	-0.3294158	0.142948055	0.192155623	2.16522415	0.04551671	0	83	77	61	89	54	91	67	54	55	51
ENSMUSG00000050244	chr13	Heatr1	0.28991735	0.143264428	0.192562382	3.576195304	0.041032095	0	144	130	133	206	180	255	269	163	231	145
ENSMUSG00000028345	chr4	Tex10	-0.2349941	0.143487259	0.192843343	3.582479355	0.025128782	0	200	180	157	248	176	181	222	148	171	169
ENSMUSG00000056749	chr13	Nfil3	0.31791888	0.14354195	0.192879752	3.96728939	0.051560409	0	143	154	218	257	252	451	215	218	258	281
ENSMUSG00000066554	chr5	Gm10167	0.43200538	0.143535452	0.192879752	0.622208372	0.05447509	0	18	17	12	26	17	27	29	25	27	24
ENSMUSG00000030888	chr7	Rrp8	0.22322384	0.143558075	0.192882875	3.988330995	0.023468595	0	233	181	191	263	216	306	321	256	233	272
ENSMUSG00000009863	chr4	Sdhb	-0.2399649	0.143612474	0.192937416	8.812946918	0.032088377	0	6438	7321	7124	10399	5402	7861	5883	6513	6651	6762
ENSMUSG00000040842	chr4	Szrd1	-0.2367862	0.143849779	0.19323765	7.138825741	0.030931682	0	2407	2055	2092	2780	2044	1715	2236	1829	2347	2381
ENSMUSG00000006641	chr5	Slc5a6	0.2951637	0.143912627	0.193303496	2.886673167	0.038838164	0	82	111	87	105	98	122	131	151	124	121
ENSMUSG00000036989	chr7	Trim3	0.24734785	0.144212914	0.193688227	4.3093059	0.030543735	0	254	282	238	304	260	524	290	263	320	369
ENSMUSG00000092650	chr13	Gm25241	0.51408077	0.144306141	0.193794814	0.089744965	0.072642701	0	12	8	10	20	8	24	20	18	13	15
ENSMUSG00000004929	chr10	Thop1	0.24484337	0.144345531	0.193829087	4.752356998	0.031256806	0	368	317	304	472	376	434	494	593	408	425
ENSMUSG00000018263	chr5	Tbx5	-0.4961573	0.144406763	0.193874056	0.473534282	0.082720431	0	30	10	23	22	25	19	20	13	17	17
ENSMUSG00000031725	chr8	Ces1f	1.05949533	0.144401791	0.193874056	0.075819008	0.506088805	0	1	22	2	4	14	2	12	25	17	45
ENSMUSG00000094935	chr12	Gm9726	-0.8211334	0.14444628	0.193908483	0.001884316	0.279727779	0	24	20	11	14	14	36	5	5	2	6
ENSMUSG00000099876	chrY	Gm29650	1.22220519	0.144762128	0.194313821	-0.016527941	0.669604697	0	13	10	14	0	0	0	24	22	37	13
ENSMUSG00000020255	chr10	D10Wsu102e	0.26362813	0.144854937	0.194419725	3.170938935	0.031993049	0	115	119	101	174	99	193	189	112	149	154
ENSMUSG00000021694	chr13	Ercc8	-0.328154	0.144948309	0.194526366	2.468211533	0.047069008	0	104	89	84	114	61	108	86	53	82	66
ENSMUSG00000056973	chr8	Ces1d	-0.8005129	0.145064968	0.194664233	3.092771222	0.341522701	0	73	333	119	123	133	16	59	179	31	206
ENSMUSG00000037703	chr2	Lzts3	-0.3300165	0.145190553	0.194814052	2.077472943	0.044661824	0	58	56	60	94	74	69	48	61	62	56
ENSMUSG00000001211	chr10	Agpat3	-0.2539494	0.145396189	0.195071243	6.857360355	0.035797203	0	1489	1724	1546	2840	1907	2083	1544	1969	1391	1632
ENSMUSG00000027305	chr2	Ndufaf1	0.23901481	0.145417207	0.195080714	5.557016268	0.03089298	0	645	669	603	809	497	684	795	941	771	925
ENSMUSG00000039234	chr3	Sec24d	0.2348614	0.145581874	0.195237908	4.057090897	0.02716616	0	227	207	194	301	209	251	365	247	282	312
ENSMUSG00000048707	chr2	Tprn	0.36358598	0.145559383	0.195237908	1.99294283	0.055588055	0	66	36	39	62	49	97	52	56	71	80
ENSMUSG00000048852	chr11	Gm12185	-0.5132462	0.14556493	0.195237908	0.940735061	0.104749604	0	43	39	23	33	20	11	23	23	26	37
ENSMUSG00000061887	chr4	Ssbp3	0.22867563	0.14559026	0.195237908	4.584853445	0.026648541	0	343	337	280	401	282	534	363	413	312	493
ENSMUSG00000102752	chr1	Gm7694	0.56706848	0.145744051	0.195425392	-0.189919012	0.086965728	0	10	8	5	13	9	19	8	15	11	20
ENSMUSG00000049287	chr11	Iba57	0.2285961	0.146138551	0.195935571	4.270080609	0.02626851	0	226	247	233	365	253	325	296	370	330	358
ENSMUSG00000001657	chr15	Hoxc8	-0.3927108	0.146179016	0.195971024	1.819861047	0.066438725	0	67	60	40	62	59	63	47	61	27	43
ENSMUSG00000073530	chr1	Pappa2	-0.6021526	0.146210476	0.195994399	0.346567959	0.137248668	0	28	23	9	14	28	29	12	8	11	16
ENSMUSG00000006276	chr8	Eps15l1	-0.2167499	0.146403641	0.196234515	4.201971968	0.022851449	0	293	258	262	407	258	283	283	243	237	339
ENSMUSG00000087090	chr7	Nctc1	-0.3141513	0.146432885	0.196254891	6.257392572	0.055010499	0	1775	1357	952	1131	1052	852	1042	840	1468	1327
ENSMUSG00000023800	chr17	Tiam2	-0.4433171	0.146558196	0.196404003	1.929694854	0.092850759	0	70	36	71	87	55	90	62	45	28	34
ENSMUSG00000064343	chrMT	mt-Tq	0.82299312	0.146599045	0.196439909	0.050243894	0.303303163	0	5	0	9	27	10	7	11	28	22	24
ENSMUSG00000036103	chr18	Colec12	0.32575071	0.146623378	0.196453679	4.58454479	0.056867927	0	364	306	341	308	246	753	415	213	394	441
ENSMUSG00000003746	chr10	Man1a	-0.2535893	0.146745323	0.196579377	4.044239337	0.032701284	0	200	292	270	288	266	280	254	169	255	269
ENSMUSG00000082691	chr6	Dynlt1-ps1	-0.3807441	0.146736309	0.196579377	2.355233958	0.069282066	0	104	76	70	80	88	113	95	43	58	51
ENSMUSG00000073236	chr2	2500004C02Rik	-0.6079831	0.146768452	0.196591516	0.538707064	0.160303427	0	36	19	25	21	18	32	6	7	13	30
ENSMUSG00000033065	chr15	Pfkm	-0.2543579	0.147045976	0.196944376	11.31707405	0.036814124	0	38902	36415	34477	59283	40010	30964	35710	37620	36589	48170
ENSMUSG00000021715	chr13	Cwc27	0.27425041	0.147091771	0.196986834	3.513450892	0.037419754	0	162	136	119	232	125	209	234	142	249	176
ENSMUSG00000024006	chr17	Stk38	0.20466886	0.147142805	0.197036298	5.391372247	0.022213426	0	593	559	532	704	514	928	725	632	708	682
ENSMUSG00000036882	chr7	Arhgap33	0.5128641	0.147195676	0.197088213	0.346594328	0.070705521	0	14	17	16	10	12	27	22	21	15	25
ENSMUSG00000079555	chr5	Haus3	0.34452294	0.147224738	0.197108242	2.170462403	0.053038226	0	69	47	59	80	35	85	96	69	87	62
ENSMUSG00000057963	chr12	Itpk1	0.25898295	0.147417812	0.19734783	3.333162066	0.030923823	0	130	138	104	157	145	239	168	136	179	169
ENSMUSG00000003923	chr10	Tfam	-0.2034552	0.147813635	0.197847344	5.309186413	0.021895788	0	654	543	582	833	561	597	623	533	601	645
ENSMUSG00000029090	chr5	Gpr125	-0.2290144	0.147819259	0.197847344	3.918262915	0.025422654	0	255	250	224	275	201	206	278	207	197	239
ENSMUSG00000060679	chr1	Mrps9	0.25042232	0.147983611	0.198048353	5.099410123	0.033993611	0	385	481	487	685	314	734	539	636	610	505
ENSMUSG00000004105	chr2	Angptl2	-0.2573681	0.148107834	0.198195624	7.457514603	0.037524285	0	3263	2850	2518	2937	2607	2314	2700	2808	1885	3333
ENSMUSG00000033813	chr1	Tcea1	-0.449022	0.148222841	0.198330534	3.951908598	0.109674659	0	256	237	265	339	229	53	314	185	265	227
ENSMUSG00000020484	chr11	Xbp1	0.24807267	0.148266706	0.198370236	6.134335583	0.034291046	0	1023	864	705	1281	945	1417	1344	810	1466	1209
ENSMUSG00000034101	chr2	Ctnnd1	-0.2169625	0.148300494	0.198377461	6.052391861	0.025941695	0	985	967	952	1460	984	1218	931	1010	817	1041
ENSMUSG00000102824	chr1	RP23-411B11.2	0.29759741	0.148290772	0.198377461	2.945776819	0.041203895	0	132	73	83	108	109	129	140	130	150	130
ENSMUSG00000025190	chr19	Got1	-0.2952352	0.148359356	0.198437206	8.044945615	0.049606486	0	2934	4084	3934	7644	3598	3154	3958	4474	3747	3825
ENSMUSG00000037134	chr8	Prmt10	0.26192658	0.148613579	0.198748625	3.180904875	0.030963992	0	126	142	105	135	97	183	173	126	169	147
ENSMUSG00000057123	chr3	Gja5	0.37712244	0.148620627	0.198748625	2.502061633	0.069801803	0	64	68	42	116	75	135	62	127	91	94
ENSMUSG00000049504	chr3	Proser1	-0.2993665	0.148677077	0.198805093	3.220379278	0.044420484	0	122	141	125	181	185	157	154	89	104	177
ENSMUSG00000035367	chr13	Rmi1	0.30692906	0.148751887	0.198886098	2.387440248	0.039931721	0	67	68	73	77	54	116	109	78	81	79
ENSMUSG00000025738	chr17	Fbxl16	-0.3540258	0.148803025	0.198935439	1.986108723	0.053235253	0	72	48	58	75	68	39	58	52	55	70
ENSMUSG00000000811	chr6	Txnrd3	0.26996165	0.148974381	0.19913451	2.932663402	0.031804246	0	98	102	91	117	98	119	156	135	117	141
ENSMUSG00000005687	chr3	Bcas2	0.19537238	0.148980426	0.19913451	5.145942067	0.0201084	0	501	465	425	641	434	647	665	574	595	593
ENSMUSG00000014633	chr8	Cmc2	0.23750696	0.149209396	0.199421489	4.402607123	0.029382643	0	308	277	276	377	210	427	373	394	377	280
ENSMUSG00000040383	chr2	Aqr	-0.2334826	0.149307415	0.199533412	4.029763645	0.027071158	0	260	258	207	348	242	222	302	199	221	275

ENSMUSG00000024403	chr17	Atp6v1g2	0.36995612	0.149604312	0.199911068	1.296318935	0.047004023	0	33	32	31	34	21	46	38	43	39	48
ENSMUSG00000084799	chr1	Ino80dos	-0.4441963	0.14966358	0.199971146	0.648453752	0.065994197	0	30	25	18	26	25	17	19	18	16	30
ENSMUSG00000042854	chr2	Trp53rk	0.37251439	0.149715087	0.200020844	1.74972085	0.058387016	0	53	33	37	48	39	64	48	59	78	47
ENSMUSG00000001741	chr7	Il16	0.30136711	0.149813769	0.200133554	2.672945653	0.039836081	0	90	89	89	91	57	136	118	81	107	125
ENSMUSG00000058318	chr2	Phf21a	-0.2353597	0.149946458	0.200291666	3.999510783	0.027609282	0	248	248	192	343	257	265	208	227	197	297
ENSMUSG00000042626	chr3	Shc1	0.21006392	0.150037504	0.200394128	5.31307796	0.02370776	0	552	533	516	630	502	701	731	577	611	863
ENSMUSG00000022031	chr14	Elp3	-0.2123205	0.150398647	0.200857285	5.899397744	0.024967519	0	1047	881	871	1071	885	878	962	782	988	887
ENSMUSG00000019761	chr11	Krt10	-0.3857982	0.150444655	0.200880337	1.440959248	0.055958547	0	57	31	39	49	43	31	37	31	43	41
ENSMUSG00000091811	chr7	Inafm1	0.25038114	0.150440905	0.200880337	4.077671809	0.032007038	0	213	193	204	296	238	438	232	246	266	319
ENSMUSG00000004096	chr9	Cwc15	0.2067256	0.150473663	0.200899877	5.951055106	0.023726904	0	875	786	697	1185	772	1114	1174	992	982	1144
ENSMUSG00000031613	chr8	Hpgd	-0.4321538	0.150543316	0.200973673	1.702520775	0.085721637	0	56	64	57	55	35	82	37	41	26	35
ENSMUSG00000051671	chr8	Coa6	-0.2454136	0.151029025	0.201602833	3.39852911	0.028022277	0	194	168	161	196	125	160	180	135	157	147
ENSMUSG00000001627	chr12	Ifrd1	0.35566357	0.151518233	0.202217229	5.042583846	0.071488779	0	294	314	411	867	335	847	728	404	687	367
ENSMUSG00000026439	chr1	Rbbp5	-0.2103357	0.151506915	0.202217229	4.595863982	0.022949536	0	373	384	314	455	396	377	433	338	331	343
ENSMUSG00000049871	chr16	Nlrc3	0.86717247	0.1518583	0.202651733	2.293012844	0.413165579	0	14	20	13	227	13	209	93	66	70	72
ENSMUSG00000031516	chr8	Dctn6	0.19882137	0.151880663	0.202662226	4.934811502	0.02093935	0	449	378	356	569	379	571	597	468	531	493
ENSMUSG00000031343	chrX	Gabra3	0.54997218	0.151914232	0.202673036	0.424363032	0.116737384	0	7	13	12	20	21	25	14	22	16	41
ENSMUSG00000040543	chr11	Pitpnm3	-0.4765756	0.151917768	0.202673036	2.174722854	0.113735275	0	47	94	90	78	68	26	43	67	83	76
ENSMUSG00000073838	chr7	Tufm	0.24047833	0.151992616	0.202753537	7.023900882	0.033259004	0	1510	1587	1656	2639	1596	2342	2248	2691	1829	2338
ENSMUSG00000022679	chr16	Mpv17l	0.55803133	0.152195257	0.203004477	0.785920179	0.127468177	0	34	11	22	9	18	27	26	31	25	46
ENSMUSG00000051391	chr5	Ywhag	-0.2149302	0.152306149	0.203133003	8.197180441	0.026781761	0	4915	4227	4023	5891	4515	4369	4778	3919	4135	4989
ENSMUSG00000038022	chr6	Fam188b	0.398488	0.152332734	0.203149074	1.391114528	0.058831905	0	33	32	35	32	27	60	39	43	30	61
ENSMUSG00000020918	chr11	Kat2a	0.20355435	0.152389049	0.203204785	4.392448486	0.020882793	0	273	257	260	355	301	413	381	336	341	356
ENSMUSG00000022051	chr14	Bnip3l	-0.2467607	0.152532012	0.203376016	5.442308765	0.034043928	0	775	715	668	807	543	553	662	485	659	884
ENSMUSG00000021831	chr14	Ero1l	0.30645542	0.152558874	0.203392428	2.774878561	0.043811124	0	92	90	84	117	67	160	152	77	119	104
ENSMUSG00000039934	chr5	Gsap	0.4675496	0.152705931	0.203569066	2.296643196	0.110601689	0	38	63	84	63	47	178	96	74	66	47
ENSMUSG00000093752	chr2	Gm20716	-0.2075882	0.152765605	0.203629194	6.260811802	0.02438167	0	1178	1223	1099	1506	1119	1178	1314	950	1104	1271
ENSMUSG00000052033	chr2	Pfdn4	0.27646302	0.152899015	0.203787587	3.244482622	0.037943654	0	126	149	108	163	88	150	203	147	187	146
ENSMUSG00000030826	chr7	Bcat2	-0.239905	0.153172622	0.20413279	6.225632919	0.03291923	0	1248	1304	919	1422	1143	1640	964	864	1018	1172
ENSMUSG00000003135	chr1	Cnot11	-0.2087268	0.153252548	0.204180897	4.802869943	0.023014428	0	457	373	423	553	419	395	438	450	392	420
ENSMUSG00000030871	chr7	Ears2	0.25366323	0.153238837	0.204180897	3.322795777	0.030818787	0	129	112	134	181	119	189	142	186	190	166
ENSMUSG00000043488	chr19	Frmd8os	-0.4548641	0.153237229	0.204180897	0.862964277	0.075859071	0	39	29	17	35	27	29	24	14	17	34
ENSMUSG00000039048	chr9	Foxred1	0.23418214	0.153284989	0.204204652	4.892973487	0.029909183	0	381	440	403	481	320	431	469	532	514	650
ENSMUSG00000034157	chr12	Cipc	-0.20506	0.153372909	0.204302304	5.263308861	0.022955105	0	642	548	560	784	537	592	668	461	518	678
ENSMUSG00000044807	chr11	Zfp354c	-0.2911593	0.153717287	0.204741523	2.613806748	0.039266577	0	127	81	81	104	98	101	82	80	76	103
ENSMUSG00000027777	chr3	Schip1	-0.2432184	0.153886231	0.204947014	6.271655351	0.033899104	0	1223	1245	1361	1543	874	986	1076	1152	1207	1312
ENSMUSG00000097099	chr9	Gm9917	-0.5808648	0.154233662	0.205390153	0.992857233	0.157426775	0	25	46	27	45	25	38	10	33	7	35
ENSMUSG00000063760	chr10	Rnf217	-0.2572146	0.154312881	0.20547607	4.497480973	0.035826814	0	294	303	309	520	410	285	334	335	275	439
ENSMUSG00000031776	chr8	Arl2bp	0.2206649	0.154330484	0.205479931	6.147995486	0.027791141	0	1135	964	833	1095	844	1168	1229	1301	1112	1388
ENSMUSG00000047632	chr19	Fgfbp3	0.51616606	0.154459451	0.205632052	0.143619439	0.080678359	0	10	10	12	18	10	16	21	10	19	28
ENSMUSG00000071660	chr19	Ttc9c	-0.2479482	0.154506498	0.205675095	3.56780587	0.030123397	0	187	178	193	226	165	146	230	160	163	175
ENSMUSG00000002963	chr7	Pnkp	-0.225827	0.15454853	0.205711454	4.428374915	0.026881671	0	378	323	261	403	356	325	294	265	383	342
ENSMUSG00000033540	chr5	Idua	0.31479661	0.154600394	0.205760889	2.985917516	0.049553339	0	77	107	97	147	93	95	172	124	132	180
ENSMUSG00000031839	chr8	Hsbp1	0.20555877	0.154766946	0.205962944	6.580718383	0.024279143	0	1440	1370	1156	1517	1133	1931	1628	1491	1592	1740
ENSMUSG00000028436	chr4	Dcaf12	-0.1995075	0.155086993	0.20636921	5.612398367	0.022226233	0	763	742	717	966	708	861	748	703	603	808
ENSMUSG00000063049	chr8	Ing2	0.24916764	0.155174178	0.206465566	3.680640169	0.031381393	0	200	139	133	204	189	216	199	205	252	250
ENSMUSG00000038225	chr8	Primpol	0.35224522	0.155249387	0.206545972	1.763211718	0.051895736	0	57	41	42	38	34	72	61	57	59	50
ENSMUSG00000020368	chr11	Canx	0.23302749	0.155296989	0.206589636	6.842453337	0.03162119	0	1549	1384	1270	2193	1534	2313	2546	1491	2061	1754
ENSMUSG00000019715	chr2	Gle1	-0.2014914	0.155552627	0.206904454	5.103862597	0.022097738	0	541	508	462	682	545	531	494	438	580	558
ENSMUSG00000025409	chr10	Mbd6	0.23682041	0.155563252	0.206904454	4.223408065	0.029453713	0	202	268	249	333	221	422	299	301	242	387
ENSMUSG00000034487	chr9	Kdelc2	0.23358363	0.155830549	0.207240246	3.595324204	0.02652656	0	176	152	154	204	136	237	242	190	152	240
ENSMUSG00000002617	chr17	Zfp40	-0.4708229	0.155883771	0.207291302	1.029962975	0.095178004	0	38	30	32	36	30	11	35	17	30	38
ENSMUSG00000035142	chr12	Nubpl	-0.3461747	0.156068781	0.20751758	2.517492756	0.058087264	0	87	86	103	129	66	85	67	56	119	75
ENSMUSG00000040752	chr14	Myh6	-1.7401511	0.156177623	0.207642548	5.202647992	1.581208087	0	12	66	38	4968	54	1394	31	30	43	9
ENSMUSG00000037787	chr12	Apopt1	0.19917378	0.156668916	0.208275922	4.952147319	0.021550412	0	418	447	379	533	368	498	572	514	546	551
ENSMUSG00000042549	chr11	Map2k3os	-0.382461	0.156830736	0.208471216	2.009499219	0.068577991	0	43	58	71	99	61	79	57	43	64	35
ENSMUSG00000024870	chr19	Rab1b	0.20730284	0.156901813	0.208545862	7.149500961	0.025220378	0	1998	1935	1715	2415	1774	2749	2187	2259	2485	2742
ENSMUSG00000055862	chr10	Izumo4	0.54260541	0.157162915	0.208873041	1.179541544	0.139774658	0	41	34	16	14	22	69	19	34	36	51
ENSMUSG00000021670	chr13	Hmgcr	0.28144747	0.157212069	0.208918501	3.460526711	0.040568347	0	127	122	167	190	127	254	257	139	180	153
ENSMUSG00000028373	chr4	Astn2	-0.4862	0.157336547	0.209064041	0.685330121	0.092703363	0	19	21	22	32	35	31	29	16	14	12
ENSMUSG00000049107	chr6	Ntf3	-0.4167349	0.157459933	0.209208101	1.009933096	0.063631664	0	24	43	26	43	26	34	32	23	19	25
ENSMUSG00000044338	chr2	Aplnr	0.31851693	0.157559093	0.20931995	5.277076576	0.058949628	0	576	558	569	615	255	609	512	870	590	891
ENSMUSG00000040794	chr2	C1qtnf4	0.3264287	0.157678359	0.209458487	2.407089428	0.050349907	0	87	56	53	72	73	93	82	70	113	112
ENSMUSG00000028743	chr4	Akr7a5	0.20765282	0.158017699	0.209889314	5.067769423	0.023864519	0	479	408	371	572	486	719	491	575	542	602
ENSMUSG00000026425	chr1	Srgap2	0.19568408	0.158365717	0.210331584	4.684651863	0.020293118	0	341	329	330	421	354	518	417	421	417	461

ENSMUSG00000032875	chr7	Arhgef17	-0.2886724	0.158428297	0.210394705	5.603191056	0.048600191	0	905	722	632	931	788	410	778	651	703	999
ENSMUSG00000054942	chr3	Fam73a	-0.2844961	0.158470951	0.210411363	2.907630013	0.038388984	0	127	86	119	176	103	93	129	102	105	113
ENSMUSG00000092072	chr3	Gm4540	0.42791704	0.15846114	0.210411363	0.671031829	0.061826914	0	19	20	15	23	16	21	34	22	24	36
ENSMUSG00000024493	chr18	Lars	-0.2048221	0.158543303	0.210467439	5.532532631	0.023742247	0	770	654	655	950	674	735	717	630	777	636
ENSMUSG00000026039	chr1	Sgol2	0.50378083	0.15854124	0.210467439	0.738376568	0.108090603	0	29	10	22	28	7	28	38	22	34	25
ENSMUSG00000031832	chr8	Taf1c	0.3002167	0.158558567	0.210467712	2.831883214	0.044323778	0	87	86	68	137	94	184	118	117	86	131
ENSMUSG00000090088	chr10	Gm15934	0.55674109	0.158588754	0.210487789	0.063420458	0.112574049	0	14	10	6	18	8	13	16	29	10	20
ENSMUSG00000034254	chr17	Agpat1	-0.2122598	0.158648142	0.210546618	5.995355966	0.026125429	0	1005	883	917	1187	1088	1087	1061	940	789	950
ENSMUSG00000050846	chr15	Zfp623	-0.3041954	0.158692067	0.210584916	2.481398127	0.042416509	0	76	73	74	146	88	81	90	69	84	75
ENSMUSG00000005483	chr8	Dnajb1	0.32535835	0.158715097	0.210595481	3.584527943	0.056841388	0	103	157	139	187	194	351	240	134	196	174
ENSMUSG00000063052	chr3	Lrrc40	-0.2767794	0.158746776	0.210617519	2.883874134	0.037302701	0	132	119	98	136	108	143	120	83	111	82
ENSMUSG00000022404	chr15	Slc25a17	0.24144261	0.158786638	0.210650409	3.384823067	0.028359761	0	140	132	140	167	125	155	206	161	177	212
ENSMUSG00000026988	chr2	Wdsub1	-0.2812378	0.15881836	0.210672494	3.726798345	0.042768997	0	301	211	204	160	181	224	179	157	191	220
ENSMUSG00000028439	chr4	Fam219a	-0.2341875	0.159052013	0.210952547	5.037291432	0.031040248	0	575	532	470	574	476	439	418	442	448	708
ENSMUSG00000063870	chr6	Chd4	0.24561126	0.159059669	0.210952547	7.052913946	0.035913618	0	1564	1444	1444	2620	2058	2544	2448	2224	1751	2831
ENSMUSG00000000876	chr2	Pxmp4	-0.2025013	0.159225975	0.211153072	4.265281201	0.021241283	0	306	265	302	365	285	303	271	270	276	331
ENSMUSG00000021281	chr12	Tnfaip2	-0.3115914	0.1592544	0.21117073	7.023127992	0.058012769	0	2750	2139	1842	1818	2042	1125	1751	1985	2171	2312
ENSMUSG00000029009	chr4	Mthfr	0.24054882	0.159358274	0.21128842	3.265380569	0.027207484	0	123	122	120	157	126	198	138	143	174	188
ENSMUSG00000049760	chr17	2410015M20Rik	0.20467257	0.159423144	0.211354379	5.611416655	0.023958485	0	672	708	658	835	513	1004	817	802	819	827
ENSMUSG00000026566	chr1	Mpzl1	-0.2383005	0.159551741	0.211504803	3.933901608	0.030039081	0	215	245	244	312	210	327	189	207	177	246
ENSMUSG00000030546	chr7	Plin1	-1.0398067	0.159576748	0.21151789	2.45539304	0.605277656	0	21	273	66	19	134	5	24	103	22	128
ENSMUSG00000087651	chr10	1500009L16Rik	0.58386776	0.15982556	0.211827599	0.052359836	0.117990799	0	8	14	12	15	5	35	16	9	17	13
ENSMUSG00000024232	chr18	Bambi	0.34232726	0.15986943	0.21186565	2.107907474	0.05381668	0	72	60	56	46	38	88	73	63	85	73
ENSMUSG00000032235	chr9	Ice2	-0.2980501	0.159997215	0.212014893	2.280712051	0.039114066	0	90	78	64	90	68	90	76	53	68	62
ENSMUSG00000032078	chr9	Zpr1	0.23841379	0.160158145	0.212208023	4.613601487	0.031750924	0	358	288	277	445	310	552	467	368	474	296
ENSMUSG00000041921	chr2	Metap1d	-0.2274942	0.160312034	0.212371657	4.625409116	0.028620917	0	388	399	368	481	341	415	330	282	476	344
ENSMUSG00000049728	chr7	Zfp668	0.32672787	0.160308054	0.212371657	2.274939189	0.04860345	0	76	56	37	78	66	113	86	74	67	91
ENSMUSG00000041261	chr4	Car8	-0.5477016	0.160468928	0.212559354	1.548376788	0.153616159	0	30	53	38	90	43	9	55	31	50	38
ENSMUSG00000058407	chr1	Txndc9	0.2044117	0.160629913	0.212752433	5.152058105	0.023571707	0	568	458	435	594	407	591	694	578	638	587
ENSMUSG00000021338	chr13	Lrrc16a	0.50107097	0.160687109	0.21280802	0.467879768	0.09374218	0	18	15	19	10	14	13	29	25	26	26
ENSMUSG00000086606	chr4	Gm13205	0.58001083	0.160752612	0.212874598	-0.253273487	0.095361603	0	12	8	9	7	6	11	19	15	16	8
ENSMUSG00000030616	chr7	Sytl2	0.35216724	0.160768181	0.212875045	3.724809451	0.070024956	0	249	189	115	120	171	164	324	262	204	235
ENSMUSG00000085095	chr7	Gm15635	-0.5462666	0.160939106	0.213081181	2.166030708	0.165230005	0	86	72	56	101	74	128	15	26	76	51
ENSMUSG00000034687	chr5	Fras1	-0.3138139	0.161178437	0.213377839	3.185862475	0.051716949	0	183	145	137	128	140	107	134	176	100	130
ENSMUSG00000029094	chr5	Afap1	-0.2521748	0.161233905	0.213431053	3.414043124	0.032204595	0	169	147	168	187	178	170	177	162	107	171
ENSMUSG00000019978	chr10	Epb4.1l2	0.21180306	0.161395278	0.213624434	5.487717991	0.025753859	0	655	600	554	669	598	970	895	619	756	704
ENSMUSG00000041939	chr5	Mvk	0.23567633	0.16142433	0.213642654	3.499223568	0.027347076	0	175	160	134	151	140	209	219	192	183	183
ENSMUSG00000000440	chr6	Pparg	0.44279394	0.161903368	0.214256366	2.400308007	0.102811108	0	32	91	37	68	93	87	113	72	77	138
ENSMUSG00000027166	chr2	Dnajc24	0.33802146	0.162141344	0.214550977	1.785308235	0.047682573	0	49	42	39	54	35	55	75	47	69	56
ENSMUSG00000035311	chr10	Gnptab	0.2904298	0.162159622	0.21455485	4.225489989	0.047688587	0	257	204	232	319	238	338	529	180	277	364
ENSMUSG00000020787	chr11	P2rx1	0.63766611	0.162395328	0.214826039	0.411387177	0.187697551	0	17	12	4	19	18	55	15	13	27	11
ENSMUSG00000025732	chr17	Fam195a	0.24022559	0.162390907	0.214826039	4.933632674	0.033361531	0	310	415	424	653	308	514	493	565	551	553
ENSMUSG00000078185	chr1	Chml	-0.3677795	0.16261311	0.215093775	1.64545421	0.057924847	0	47	48	41	78	42	54	56	38	24	44
ENSMUSG00000015474	chr17	Ppt2	0.20173852	0.162678909	0.215160446	5.316894915	0.023179414	0	551	533	463	617	580	809	729	620	586	742
ENSMUSG00000091509	chr14	Gm17066	0.30847648	0.163032299	0.215607438	2.281011554	0.042778833	0	68	57	46	84	62	82	98	90	64	93
ENSMUSG00000049641	chr10	Vgll2	-0.3112692	0.1630879	0.215660563	5.126198794	0.057403539	0	427	520	520	947	511	776	438	636	352	340
ENSMUSG00000022106	chr14	Rcbtb2	0.2264883	0.163151293	0.215703573	4.76709554	0.028933378	0	375	383	314	395	383	417	462	387	547	567
ENSMUSG00000042622	chr15	Maff	0.50755016	0.163142814	0.215703573	1.79544299	0.137509137	0	45	33	40	63	27	157	48	45	44	34
ENSMUSG00000069920	chr8	B3gnt9	0.30628953	0.163524348	0.216176342	2.483105846	0.044830496	0	91	73	76	67	54	95	115	81	101	101
ENSMUSG00000030533	chr7	Unc45a	0.22217993	0.163555556	0.216197149	3.641591011	0.024969541	0	183	147	141	206	174	249	240	195	172	235
ENSMUSG00000060470	chr8	Gpr97	0.73700795	0.163571397	0.216197639	0.111225926	0.252576878	0	12	13	7	21	1	47	19	9	6	18
ENSMUSG00000031711	chr8	Zfp330	-0.2182842	0.163959266	0.216689806	4.195740612	0.025623915	0	294	293	244	389	250	297	294	195	316	276
ENSMUSG00000039065	chr15	Fam173b	0.23243968	0.164119861	0.21688154	3.52666352	0.027038101	0	178	157	123	165	155	242	189	188	202	185
ENSMUSG00000046909	chr11	Tefm	-0.266378	0.164199224	0.216965903	3.726378639	0.038165834	0	212	186	242	278	154	154	205	182	241	182
ENSMUSG00000074922	chr19	Fam122a	0.2671671	0.164236607	0.216994784	2.876215682	0.034716478	0	79	101	90	123	95	121	128	133	108	152
ENSMUSG00000021179	chr12	Nrde2	0.21776741	0.164287924	0.217032301	3.634499366	0.023720593	0	177	154	134	210	174	225	211	196	203	245
ENSMUSG00000034473	chr16	Sec22a	0.25602835	0.16429606	0.217032301	3.334821397	0.032828284	0	173	138	122	136	105	189	170	153	202	170
ENSMUSG00000016327	chrX	Atp1b4	0.34592324	0.164348608	0.217079395	5.287946757	0.072007337	0	561	440	461	596	496	550	485	651	476	1408
ENSMUSG00000030816	chr7	Rnf40	0.20297471	0.164362776	0.217079395	5.382241376	0.023907643	0	568	495	524	779	535	941	722	669	665	652
ENSMUSG00000028031	chr3	Dkk2	-0.3425853	0.164490609	0.217210326	3.305797273	0.065406796	0	188	196	108	121	187	172	98	102	139	198
ENSMUSG00000052331	chr1	Ankrd44	-0.2825408	0.164492994	0.217210326	3.233125007	0.041876482	0	144	128	99	202	190	175	135	99	124	157
ENSMUSG00000070047	chr8	Fat1	0.28476235	0.164775825	0.217563243	4.359687213	0.046615157	0	283	243	223	341	284	563	417	319	183	377
ENSMUSG00000047804	chr11	Akap10	-0.2549256	0.165329499	0.218273671	3.456671855	0.034621762	0	138	150	188	241	167	194	194	118	128	182
ENSMUSG00000002280	chr17	Narfl	-0.2012687	0.165386302	0.218314919	4.97473314	0.022910558	0	428	465	496	697	429	480	454	459	491	489
ENSMUSG00000005982	chr16	Naa60	-0.2029768	0.165391984	0.218314919	5.072117984	0.023627823	0	548	546	511	592	467	445	588	458	485	564

ENSMUSG00000027519	chr2	Rab22a	-0.1943635	0.16552874	0.218454171	5.98893577	0.022453761	0	966	929	916	1316	938	1025	969	870	918	1051
ENSMUSG00000033126	chr10	Ybey	-0.2495586	0.16551748	0.218454171	3.040660782	0.030267659	0	113	137	137	164	106	123	129	100	116	138
ENSMUSG00000022568	chr15	Scrib	0.29991244	0.165679429	0.218632395	4.888686912	0.053760097	0	341	311	336	590	415	607	444	794	387	398
ENSMUSG00000007035	chr17	Msh5	0.99381393	0.165852162	0.218839673	0.311258182	0.499620256	0	13	15	13	2	9	91	12	14	4	5
ENSMUSG00000044468	chr3	Fam46c	0.34558805	0.166078214	0.219117258	2.26308324	0.057888929	0	65	71	58	59	51	83	81	50	105	109
ENSMUSG00000034220	chr1	Gpc1	-0.2183192	0.166157166	0.219200731	8.331452944	0.029567141	0	5281	4370	4574	6416	5218	4542	4653	4746	4594	5707
ENSMUSG00000094530	chr8	Gm21399	0.47736328	0.166378944	0.219472593	0.630519277	0.07881016	0	18	19	12	14	24	39	25	17	25	30
ENSMUSG00000042613	chr3	Pbxip1	-0.2332626	0.166489483	0.219597679	8.695758346	0.033871385	0	7735	6178	5582	7625	6264	5221	5841	5959	6851	7045
ENSMUSG00000031072	chr7	Oraov1	-0.2231694	0.166546414	0.219652041	3.877317661	0.026658124	0	281	244	199	234	206	255	202	183	226	235
ENSMUSG00000090258	chr12	Churc1	0.19954702	0.166583408	0.219680101	5.19971294	0.02309603	0	487	524	485	626	423	706	650	664	609	560
ENSMUSG00000063018	chrX	2010204K13Rik	0.56673438	0.166672972	0.219777474	0.027039714	0.099997306	0	7	15	15	12	4	21	21	11	19	15
ENSMUSG00000022403	chr15	St13	-0.2178522	0.167322224	0.220612774	6.144082528	0.028780891	0	1134	1020	889	1591	1084	930	1218	937	1080	1153
ENSMUSG00000048007	chrX	Timm8a1	0.35026735	0.167340762	0.220616404	2.041029901	0.060837939	0	57	32	52	87	38	74	93	74	64	59
ENSMUSG00000010476	chr7	Ebf3	-0.2352687	0.167396397	0.220668935	3.354764704	0.027924432	0	134	166	163	217	138	181	145	120	160	155
ENSMUSG00000039328	chr8	Rnf122	-0.2307605	0.167799465	0.221179414	3.947677233	0.028827661	0	194	209	215	359	265	259	210	235	207	239
ENSMUSG00000004771	chr9	Rab11a	0.19967754	0.168028386	0.221443177	5.721850129	0.023903927	0	701	649	616	1060	670	1096	917	763	902	938
ENSMUSG00000038335	chr11	Tsr1	-0.218966	0.16803126	0.221443177	4.767240063	0.027700261	0	423	407	343	566	445	505	490	333	407	320
ENSMUSG00000033268	chr2	Duox1	-0.885666	0.168084598	0.221492584	0.793991271	0.424881884	0	25	35	25	47	25	76	4	4	4	10
ENSMUSG00000004939	chr10	Nmrk2	-0.4796539	0.168165614	0.22157845	7.046226566	0.143192863	0	1575	1214	1312	4106	3503	1358	1787	1368	3376	962
ENSMUSG00000032735	chr18	Ablim3	-0.3073917	0.168695156	0.222255231	4.847269123	0.057054259	0	430	536	466	566	365	468	284	612	249	465
ENSMUSG00000003033	chr8	Ap1m1	0.18896618	0.169070911	0.222708299	4.737348971	0.020051743	0	357	353	315	475	356	554	425	419	437	481
ENSMUSG00000050390	chr4	C77080	0.51422701	0.169058542	0.222708299	2.774358856	0.155250954	0	99	77	74	106	58	317	79	93	36	142
ENSMUSG00000031636	chr8	Pdlim3	-0.2686931	0.169131939	0.222767693	9.05021036	0.045572989	0	9542	7073	6929	10143	9466	12390	6445	5517	8295	7096
ENSMUSG00000042105	chr7	Inpp5f	0.32649811	0.169322994	0.22299832	2.094512421	0.048963626	0	40	65	51	70	48	72	100	61	66	78
ENSMUSG00000058240	chr16	Cryzl1	-0.2291796	0.169441869	0.223133851	3.654505436	0.027832864	0	229	228	158	222	166	206	218	149	168	201
ENSMUSG00000027498	chr2	Cstf1	0.19760558	0.169497264	0.22318577	4.357633309	0.021511502	0	297	222	259	384	263	400	359	319	315	390
ENSMUSG00000025076	chr19	Casp7	-0.288324	0.16980985	0.223576304	2.590501083	0.040300071	0	100	93	107	120	65	85	84	71	92	102
ENSMUSG00000063787	chr14	Chchd1	-0.2277824	0.169845318	0.223601938	5.787047392	0.031711266	0	951	905	827	1103	664	870	1042	627	921	690
ENSMUSG00000030630	chr7	Fah	0.49895977	0.170243992	0.224094879	2.033777895	0.135775567	0	33	76	42	41	48	159	54	79	35	59
ENSMUSG00000048277	chr11	Syngr2	-0.2195153	0.170251819	0.224094879	7.659569106	0.030373919	0	3360	3019	2798	3902	3139	4364	3014	2620	2655	2729
ENSMUSG00000104496	chr1	RP23-13N24.1	0.51485108	0.170455365	0.224341669	0.013977667	0.079301898	0	9	10	10	15	10	19	18	7	20	21
ENSMUSG00000029521	chr5	Chek2	-0.3917107	0.1705517	0.224447322	1.868698881	0.078867142	0	62	56	76	58	44	34	75	38	38	65
ENSMUSG00000002814	chr11	Top3a	-0.2653763	0.170620796	0.224517112	2.709782643	0.034332329	0	107	80	89	143	107	103	95	98	82	98
ENSMUSG00000029681	chr5	Bcl7b	0.19557556	0.170866909	0.2248198	4.514258161	0.021444643	0	298	271	309	422	287	465	371	369	351	431
ENSMUSG00000038068	chr13	Rnf144b	-0.2057015	0.17099022	0.224960869	4.169308308	0.023390967	0	284	277	272	357	241	352	284	201	261	268
ENSMUSG00000026455	chr1	Klhl12	-0.2188568	0.171261359	0.225296382	4.527236562	0.027407273	0	408	371	329	447	290	284	354	370	346	364
ENSMUSG00000003131	chr9	Pafah1b2	0.19262675	0.171359302	0.22540401	4.881197725	0.021397611	0	353	401	379	538	378	570	556	451	420	570
ENSMUSG00000028197	chr3	Col24a1	-0.4920322	0.171384342	0.225408972	2.818671378	0.143229434	0	139	132	142	87	93	28	68	83	122	164
ENSMUSG00000031490	chr8	Eif4ebp1	0.27703085	0.171395331	0.225408972	5.623952124	0.047523238	0	742	689	590	691	586	1589	712	669	811	690
ENSMUSG00000030279	chr6	C2cd5	0.23542329	0.171650678	0.225723549	3.714559667	0.030322562	0	153	150	187	231	170	205	211	227	263	234
ENSMUSG00000056220	chr1	Pla2g4a	0.45622998	0.171769367	0.225858375	1.760245437	0.107624813	0	41	40	55	33	32	60	96	35	81	36
ENSMUSG00000040464	chr5	Gtpbp10	-0.2297558	0.172021375	0.226168461	3.557570872	0.027912492	0	192	184	199	240	127	206	186	146	171	170
ENSMUSG00000019797	chr10	1700021F05Rik	0.2104595	0.172407988	0.226634128	5.752314594	0.027332815	0	659	723	662	1054	653	910	868	1046	907	950
ENSMUSG00000027978	chr3	Prss12	0.47829469	0.172403132	0.226634128	1.42724667	0.113815205	0	36	31	28	35	29	20	43	57	37	84
ENSMUSG00000032127	chr9	Vps11	0.18957973	0.172433201	0.226645953	4.773988532	0.020567105	0	375	335	363	482	347	568	438	400	442	533
ENSMUSG00000033318	chr10	Gstt2	0.36376691	0.172553927	0.226783307	2.332635445	0.068713094	0	68	78	56	61	54	160	64	61	82	91
ENSMUSG00000034826	chr5	Nup54	-0.2640825	0.1725868	0.226805183	3.009881049	0.035457462	0	139	122	104	167	117	123	136	107	134	87
ENSMUSG00000044134	chr5	Fam109a	0.25680508	0.172871722	0.227139697	3.172107976	0.034086548	0	128	143	108	140	85	202	142	153	131	165
ENSMUSG00000087138	chr7	Gm15545	0.42238665	0.172873852	0.227139697	0.828867194	0.073756043	0	23	20	14	26	22	34	18	32	26	44
ENSMUSG00000037503	chr1	Fam168b	-0.1954785	0.173231116	0.227587712	5.911497124	0.023573349	0	861	948	867	1261	866	1057	939	719	887	995
ENSMUSG00000044199	chr10	S1pr4	0.48081676	0.173648267	0.228114313	0.197849841	0.07243021	0	11	11	8	22	12	24	24	19	14	16
ENSMUSG00000038717	chr9	Atp5l	0.22385566	0.173740822	0.228214448	8.255049042	0.032218256	0	4050	4448	4258	5236	3066	6545	5046	5090	5545	4648
ENSMUSG00000024869	chr19	Nudt8	0.2614311	0.173827127	0.228287798	3.84474375	0.03978656	0	162	166	179	318	158	343	220	265	253	187
ENSMUSG00000039298	chr4	Cdk5rap2	-0.2546074	0.173842472	0.228287798	3.092418196	0.033543028	0	126	110	111	218	128	134	136	127	108	121
ENSMUSG00000042082	chr13	Arsb	0.27899764	0.173877538	0.228287798	3.850550123	0.044801879	0	145	225	182	214	190	384	253	167	186	312
ENSMUSG00000047604	chr19	Frat2	-0.2421508	0.173871372	0.228287798	4.192315938	0.034015864	0	249	256	286	353	318	213	240	272	290	334
ENSMUSG00000074405	chr7	Zfp865	-0.2412631	0.173878335	0.228287798	3.463324797	0.031531655	0	142	163	155	245	181	180	143	134	150	213
ENSMUSG00000037669	chr12	1110057K04Rik	0.21871376	0.174108567	0.228568601	3.514055337	0.024403353	0	169	151	145	180	133	214	233	164	173	212
ENSMUSG00000024084	chr17	Qpct	0.53805805	0.174255117	0.228739505	2.298280473	0.168419042	0	48	72	53	59	56	22	146	46	101	147
ENSMUSG00000058704	chr17	Memo1	-0.2264456	0.174298426	0.228774869	5.430414442	0.03162377	0	793	573	657	851	594	527	742	504	715	742
ENSMUSG00000070738	chr1	Dgkd	-0.2152828	0.174411052	0.228901198	5.782692172	0.028856619	0	654	866	894	1236	776	1037	759	728	775	872
ENSMUSG00000054364	chr12	Rhob	0.27933719	0.174463592	0.228948654	6.019736659	0.049367042	0	667	824	982	933	904	1964	1133	891	787	1131
ENSMUSG00000009905	chr1	Kdsr	-0.28757	0.174490406	0.228962344	2.513544063	0.04170261	0	74	104	98	104	76	93	80	60	82	98
ENSMUSG00000087478	chr17	4930506C21Rik	-0.9990192	0.174766487	0.229303082	-0.62548041	0.447306156	0	5	7	1	22	19	0	2	17	4	4
ENSMUSG00000035104	chr6	Eva1a	-0.4752261	0.174981333	0.229563419	0.689010541	0.10447991	0	30	32	24	27	16	39	11	20	12	21

ENSMUSG00000024974	chr19	Smc3	-0.2073658	0.175023037	0.22959658	4.838578434	0.025585749	0	409	396	397	612	473	435	522	328	451	428
ENSMUSG00000039018	chr7	Mtg1	0.20290243	0.175098393	0.229673875	4.590606879	0.02392721	0	377	351	279	361	289	426	463	401	421	378
ENSMUSG00000039458	chr15	Mtmr12	-0.2967171	0.175273543	0.229882042	2.626255513	0.046133897	0	91	89	107	125	86	135	96	62	64	93
ENSMUSG00000037533	chr11	Rapgef6	-0.3056541	0.17530254	0.229898498	3.327692741	0.053660387	0	174	139	173	193	138	106	177	91	128	226
ENSMUSG00000001763	chr6	Tspan33	0.36166596	0.175332547	0.229916277	1.629336215	0.061449597	0	41	26	32	51	44	61	50	71	40	49
ENSMUSG00000015749	chr3	Anp32e	-0.2045091	0.175389882	0.229969884	6.427344507	0.026494581	0	1376	1230	1198	1811	1285	1449	1594	1157	1089	1257
ENSMUSG00000027014	chr2	Cwc22	-0.235508	0.175498763	0.230084186	3.407649208	0.029022229	0	174	173	141	226	138	135	170	139	174	166
ENSMUSG00000038990	chr2	Cables2	-0.2077045	0.175509982	0.230084186	3.764852958	0.023361461	0	197	205	194	258	221	253	217	174	172	211
ENSMUSG00000028088	chr3	Fmo5	-0.2696669	0.175564785	0.230134444	2.754945505	0.037630974	0	86	118	114	134	88	100	93	95	84	119
ENSMUSG00000068874	chr3	Selenbp1	0.24780744	0.175726613	0.230324969	3.902711001	0.035424526	0	141	253	154	273	194	314	233	230	274	266
ENSMUSG00000044502	chr11	Bod1	-0.1984004	0.176280813	0.231029693	6.977778787	0.02523433	0	2185	1997	1758	2377	1727	1952	1870	1891	1942	1890
ENSMUSG00000023277	chr9	Twf2	0.32236511	0.176323413	0.231063856	6.346348755	0.067134668	0	698	945	849	2142	932	2285	1228	1477	1417	999
ENSMUSG00000054455	chr2	Vapb	-0.2245133	0.176459827	0.23122094	7.501490872	0.032662013	0	3134	2796	2524	3294	2769	2319	2570	2460	2652	3609
ENSMUSG00000030653	chr7	Pde2a	0.235424	0.17654247	0.231307543	5.579302081	0.035001551	0	679	569	593	865	580	631	763	996	811	962
ENSMUSG00000026239	chr1	Pde6d	0.20202239	0.176562704	0.231312369	4.458420854	0.023704689	0	334	298	251	378	261	352	402	342	343	471
ENSMUSG00000022018	chr14	Rgcc	0.38790517	0.176796115	0.231596448	4.261999378	0.094425254	0	192	212	263	390	191	794	366	232	214	210
ENSMUSG00000008604	chr3	Ubqln4	-0.1981239	0.176849576	0.231644768	6.447015804	0.024981232	0	1303	1281	1197	1839	1355	1424	1418	1238	1310	1232
ENSMUSG00000081683	chr5	Fzd10	0.48835146	0.177585017	0.23258628	1.495577697	0.131899144	0	22	27	24	78	23	24	47	64	51	66
ENSMUSG00000047879	chr18	Usp14	-0.2099628	0.177670539	0.232676486	5.348706345	0.027346096	0	704	626	562	818	554	558	800	487	595	640
ENSMUSG00000020459	chr11	Mtif2	-0.2138871	0.177760771	0.232751034	4.473871579	0.026752238	0	349	350	333	468	280	277	349	342	363	327
ENSMUSG00000020946	chr11	Gosr2	-0.1951278	0.177759454	0.232751034	6.14650716	0.024164835	0	1145	1136	1039	1293	1004	1079	1145	918	1123	1118
ENSMUSG00000022701	chr16	2610015P09Rik	0.36639713	0.177975215	0.233009987	1.165334171	0.055835955	0	26	21	24	43	25	57	35	31	31	42
ENSMUSG00000087404	chr11	Gm11752	0.61626174	0.178043604	0.233077689	0.129552343	0.170526686	0	6	6	7	19	19	11	16	9	27	32
ENSMUSG00000019984	chr10	Med23	-0.2563191	0.178138537	0.233180125	3.278204317	0.035985407	0	129	149	133	194	172	122	176	115	126	175
ENSMUSG00000017405	chr11	Nek8	0.37605713	0.178177819	0.233209703	1.063043064	0.053043618	0	22	28	26	31	20	34	33	33	44	36
ENSMUSG00000020936	chr11	Nmt1	0.20006688	0.178414962	0.233498222	6.12161606	0.025465388	0	981	973	908	1157	807	1607	1156	1045	1143	1153
ENSMUSG00000074282	chr7	Zfp94	0.43990445	0.178508753	0.233599095	0.809135752	0.07983064	0	27	15	15	26	20	20	40	31	22	39
ENSMUSG00000030770	chr7	Parva	0.19190234	0.178584953	0.233676932	5.079106494	0.022303124	0	497	398	447	551	448	690	603	605	487	550
ENSMUSG00000004897	chr3	Hdgf	0.19919088	0.178611009	0.233689146	7.970779602	0.02601929	0	3604	3126	2904	4480	3372	4478	4587	4131	4164	4506
ENSMUSG00000061816	chr1	Myl1	-0.3785427	0.178818797	0.23393911	13.17023928	0.094500558	0	188829	148207	133193	157897	144301	45561	140998	108226	159039	192962
ENSMUSG00000057691	chr6	Zfp746	-0.227657	0.178901617	0.234025552	3.450927067	0.027666411	0	155	170	145	217	183	146	167	156	159	183
ENSMUSG00000028114	chr3	Mettl14	-0.2186759	0.179028811	0.23417002	3.798770245	0.02659329	0	227	241	190	274	178	184	235	183	191	248
ENSMUSG00000020288	chr11	Ahsa2	-0.2052176	0.179065453	0.234196029	5.139277367	0.025880773	0	649	529	458	658	514	491	523	494	626	515
ENSMUSG00000022802	chr16	Lmln	-0.3140453	0.179377937	0.234560821	1.888457272	0.044592798	0	59	52	50	82	55	45	55	53	59	47
ENSMUSG00000035242	chr10	Oaz1	0.20342053	0.179371969	0.234560821	8.447940418	0.02730277	0	5388	4532	4259	5529	4458	7597	5746	5525	5458	6326
ENSMUSG00000103627	chr6	IFFO1	0.277738	0.179574473	0.23479585	3.949368167	0.046619299	0	264	179	188	205	190	187	238	312	260	360
ENSMUSG00000029030	chr4	Tprgl	-0.1959946	0.179639117	0.2348584	6.471408987	0.024800576	0	1481	1384	1261	1693	1243	1525	1225	1151	1396	1461
ENSMUSG00000063576	chr17	Klhdc3	-0.2070854	0.179920323	0.235204044	7.340902254	0.028149118	0	2325	2458	2467	3448	2307	2959	2096	2416	2122	2719
ENSMUSG00000004032	chr3	Gstm5	-0.2121883	0.179939926	0.23520767	5.70795854	0.028652507	0	912	812	731	903	797	735	873	724	905	688
ENSMUSG00000029147	chr5	Ppm1g	0.20263551	0.180053559	0.235318398	5.348899437	0.025776987	0	530	456	471	834	559	809	810	618	659	665
ENSMUSG00000030265	chr6	Kras	-0.2492878	0.180058311	0.235318398	4.431532036	0.03795251	0	296	252	306	558	353	318	403	237	365	279
ENSMUSG00000025104	chr7	Hdgfrp3	-0.3022283	0.180173765	0.235447268	2.068646118	0.04121084	0	64	49	66	101	59	63	63	55	56	61
ENSMUSG00000038604	chr8	Fam65a	-0.2037887	0.180330025	0.235629434	4.650626151	0.024907809	0	324	401	343	563	379	457	338	370	331	406
ENSMUSG00000001493	chr11	Meox1	0.27364606	0.180434566	0.235743993	2.974947717	0.040874192	0	105	133	88	116	79	151	148	158	114	118
ENSMUSG00000018697	chr11	Aatf	0.26817749	0.180492818	0.235798058	3.5906434	0.042116658	0	144	129	130	237	174	305	252	172	196	147
ENSMUSG00000021606	chr13	Ndufs6	0.21362552	0.180593023	0.235904104	7.259560404	0.030046018	0	2174	2299	2045	2451	1596	3110	2417	2471	2940	2476
ENSMUSG00000027804	chr3	Ppid	-0.2142444	0.18060775	0.235904104	5.518230254	0.029128724	0	839	705	585	892	653	750	858	614	694	540
ENSMUSG00000028140	chr3	Mrpl9	0.21492303	0.180625104	0.235904724	6.177218657	0.029960035	0	977	1014	1031	1269	713	1169	1213	1313	1250	1358
ENSMUSG00000043885	chr9	Slc36a4	0.26398899	0.180767442	0.236055133	3.123440372	0.037683285	0	131	120	103	126	100	178	171	98	127	199
ENSMUSG00000055313	chr13	Pgbd1	-0.5837265	0.180774048	0.236055133	-0.102064108	0.126931508	0	19	5	16	21	12	11	20	5	9	8
ENSMUSG00000030035	chr6	Wbp1	-0.2276687	0.180825413	0.236100147	4.424690318	0.031445596	0	360	384	354	364	247	390	266	355	279	315
ENSMUSG00000054434	chr5	Tmem120b	0.26528549	0.180900848	0.236176577	3.439080832	0.041080782	0	141	143	116	198	133	181	154	246	142	226
ENSMUSG00000035266	chr5	Helq	0.30371342	0.180981164	0.236259364	2.00888334	0.044001152	0	44	57	50	65	44	72	90	65	55	70
ENSMUSG00000053604	chr6	Rpia	0.19518797	0.181266714	0.236610031	4.34130817	0.022198304	0	238	255	270	390	256	406	373	305	346	330
ENSMUSG00000027378	chr2	Nphp1	-0.2092505	0.181301464	0.23663329	4.51260356	0.026098038	0	391	348	322	446	313	301	307	339	391	370
ENSMUSG00000059939	chr4	9430015G10Rik	0.36044237	0.181736687	0.237179189	1.689653589	0.060943118	0	32	40	42	37	48	80	51	37	54	65
ENSMUSG00000074121	chr7	Ntf5	-0.3540729	0.181985769	0.237482083	2.621597134	0.072331077	0	113	86	110	119	77	43	79	101	85	119
ENSMUSG00000005125	chr15	Ndrg1	0.28180642	0.182435092	0.2380462	4.902033299	0.050949464	0	275	345	383	577	434	934	429	448	383	518
ENSMUSG00000006024	chr7	Napa	0.22091631	0.182512935	0.238125539	7.029850924	0.032337771	0	2010	1726	1385	1875	1938	2354	2111	2107	2012	2910
ENSMUSG00000042842	chr13	Serpinb6b	-0.4485263	0.182674554	0.238314157	1.521510941	0.107074732	0	50	48	53	61	26	21	27	30	43	68
ENSMUSG00000044465	chr7	Fam160a2	-0.2013324	0.182844064	0.238513033	4.022509604	0.023109319	0	268	256	217	338	216	294	241	217	203	277
ENSMUSG00000030881	chr7	Arfip2	0.22863151	0.183095214	0.238818358	3.383738307	0.028661272	0	163	149	114	174	111	191	182	140	187	211
ENSMUSG00000050382	chr7	Kif7	0.40470185	0.183117394	0.238825	0.9206992	0.066684896	0	24	22	16	33	19	51	33	23	22	37
ENSMUSG00000036040	chr2	Adamtsl2	-0.4100989	0.183247519	0.238972411	3.076362181	0.104591506	0	113	126	132	173	161	268	107	94	69	60
ENSMUSG00000031221	chrX	Igbp1	-0.1824051	0.183281082	0.238993879	5.095403756	0.020540007	0	591	563	484	614	446	587	532	458	519	514

ENSMUSG00000025870	chr13	Arl10	-0.3612756	0.183383941	0.239105696	1.002272855	0.051345112	0	31	34	30	33	29	29	29	18	26	33
ENSMUSG00000060989	chr4	Gm11847	0.90377872	0.183423485	0.239134946	-0.273342168	0.403315318	0	11	3	1	7	14	1	5	18	20	29
ENSMUSG00000078816	chr7	Prkcg	-0.4519194	0.183586787	0.239325524	0.957030541	0.101920637	0	46	36	35	22	16	25	27	24	16	34
ENSMUSG00000016528	chr1	Mapkapk2	-0.2238836	0.183625368	0.239353493	7.953667932	0.033666118	0	3188	3490	3354	6268	3906	4626	3664	3549	3425	3452
ENSMUSG00000030329	chr6	Pianp	0.74055964	0.183819681	0.239584432	3.297185883	0.353588056	0	91	102	97	149	103	688	66	54	24	223
ENSMUSG00000072407	chr10	Gm6419	-0.4162159	0.183876834	0.239636575	0.477373088	0.063943969	0	24	18	16	30	21	26	12	18	15	18
ENSMUSG00000004356	chr10	Utp20	-0.2685877	0.184057562	0.239849743	3.945997223	0.044584825	0	272	210	221	304	241	305	325	144	214	157
ENSMUSG00000021508	chr13	Cxcl14	0.43555918	0.184400812	0.240274636	6.056206763	0.12675409	0	872	906	884	629	823	3062	1270	787	774	555
ENSMUSG00000043969	chr19	Emx2	-0.4303566	0.184564106	0.24046499	0.619031789	0.075994804	0	16	33	17	30	25	24	20	13	16	26
ENSMUSG00000068040	chr2	Tm9sf4	0.19242656	0.184596795	0.240485161	5.046060095	0.023215805	0	456	384	382	612	469	527	619	545	539	630
ENSMUSG00000003849	chr8	Nqo1	-0.3430547	0.184880164	0.240821321	2.997300211	0.069680638	0	156	122	104	162	115	77	108	84	193	97
ENSMUSG00000024325	chr17	Ring1	0.19473666	0.184889294	0.240821321	4.169205169	0.022081051	0	282	227	219	313	207	364	278	293	289	336
ENSMUSG00000096232	chr16	0610012G03Rik	0.19564937	0.185206936	0.241212575	5.110968375	0.024162821	0	468	466	444	663	374	810	577	524	497	618
ENSMUSG00000016552	chr15	Foxred2	0.36684581	0.185268065	0.241269705	1.653481459	0.066053214	0	28	51	33	38	44	51	70	37	59	61
ENSMUSG00000024142	chr17	Mlst8	-0.1973806	0.185347978	0.241335199	4.150955631	0.022648699	0	263	251	292	363	240	264	284	233	270	291
ENSMUSG00000047417	chr10	Rexo1	-0.2139364	0.185352893	0.241335199	3.917983251	0.02701579	0	221	216	235	294	234	315	214	189	175	252
ENSMUSG00000074212	chr3	Dnajb14	-0.202602	0.185706279	0.241772796	4.731893344	0.02555232	0	364	362	378	546	463	469	422	381	309	436
ENSMUSG00000041506	chr9	Rrp9	0.23161591	0.185755142	0.241813884	3.967709118	0.032483752	0	202	177	188	313	196	327	317	254	280	191
ENSMUSG00000048755	chr15	Mcat	-0.1917073	0.185807823	0.241859936	4.500036914	0.022151876	0	350	342	339	428	329	402	302	293	375	346
ENSMUSG00000019977	chr10	Hbs1l	-0.1919715	0.186576001	0.242828918	6.088981474	0.024275006	0	1174	948	953	1373	979	1107	946	942	1085	1096
ENSMUSG00000059669	chr12	Taf1b	-0.2783675	0.186586989	0.242828918	2.731219783	0.042683331	0	132	106	105	106	81	91	123	92	78	97
ENSMUSG00000022858	chr16	Tra2b	0.22544237	0.186885858	0.243195228	5.051916048	0.032911793	0	384	377	429	651	448	653	714	496	629	417
ENSMUSG00000025982	chr1	Sf3b1	-0.1997485	0.186932378	0.243211078	6.761994734	0.026820414	0	1798	1641	1492	2223	1532	1871	1832	1246	1763	1559
ENSMUSG00000075419	chr2	Dolk	-0.197295	0.186932842	0.243211078	4.569266864	0.023847755	0	451	363	285	420	361	364	383	334	340	375
ENSMUSG00000032968	chr1	Inha	0.35638573	0.187377053	0.24376633	3.699996081	0.082224607	0	260	168	111	202	109	134	188	264	209	373
ENSMUSG00000071656	chr19	Lrrn4cl	-0.2236953	0.187514323	0.243922206	3.450816989	0.028518255	0	157	169	190	199	150	180	166	145	129	198
ENSMUSG00000079491	chr17	H2-T10	-0.5627798	0.187548712	0.243944235	2.021107617	0.1986434	0	89	34	73	48	98	129	21	50	25	42
ENSMUSG00000045252	chr7	Zfp574	0.2809988	0.187970504	0.244470107	3.231421594	0.04690086	0	87	117	93	196	138	184	184	166	108	191
ENSMUSG00000064210	chr15	Ano6	-0.1949912	0.188014084	0.244504032	6.349912188	0.025508219	0	1297	1142	1295	1500	1228	1569	1253	1032	1107	1283
ENSMUSG00000028988	chr4	Ctnnbip1	-0.2008309	0.188280092	0.244827183	5.6715477	0.026578776	0	868	730	695	930	823	752	718	657	799	937
ENSMUSG00000056412	chr4	Gm12396	0.33552658	0.188496219	0.245085418	2.198144637	0.060690527	0	61	47	70	68	47	118	76	53	99	63
ENSMUSG00000063810	chr6	Alms1	0.43327517	0.188545302	0.245126432	0.721715397	0.077201468	0	19	13	23	23	18	28	27	15	35	38
ENSMUSG00000032437	chr9	Stt3b	-0.1957883	0.188665337	0.245259674	6.429070264	0.025802988	0	1371	1246	1190	1678	1370	1477	1506	1078	1297	1212
ENSMUSG00000003068	chr10	Stk11	-0.1954745	0.18903561	0.245718163	6.471676958	0.025751308	0	1361	1262	1162	1955	1374	1586	1325	1279	1159	1419
ENSMUSG00000026922	chr2	Agpat2	0.39957502	0.189086874	0.245739088	3.515416468	0.103446581	0	58	262	125	123	143	199	178	265	175	225
ENSMUSG00000059534	chr11	Uqcr10	0.20855269	0.189083752	0.245739088	8.093586744	0.029972265	0	3685	3880	3784	4788	2818	4859	4540	4532	5196	4691
ENSMUSG00000034931	chr11	Dhx8	-0.190535	0.189373145	0.246088245	4.080717674	0.021339278	0	274	257	241	321	243	300	287	206	233	262
ENSMUSG00000032243	chr9	Itga11	-0.3056732	0.189426151	0.24613424	3.249372951	0.057810744	0	179	131	140	164	156	157	136	122	66	212
ENSMUSG00000086688	chr11	Gm11560	-0.4553685	0.18950381	0.246212257	0.263950465	0.069478867	0	15	13	17	24	24	15	17	15	15	12
ENSMUSG00000004952	chr5	Rasa4	0.18683988	0.18955737	0.246254155	5.065105849	0.022244612	0	514	433	390	561	432	632	496	517	562	697
ENSMUSG00000046794	chr8	Ppp1r3b	-0.3463865	0.189571297	0.246254155	1.852347062	0.062493256	0	47	83	57	68	36	55	62	39	44	52
ENSMUSG00000022064	chr14	Pibf1	0.37513445	0.189650934	0.246334708	2.069359517	0.079385267	0	64	68	44	52	35	42	83	80	91	74
ENSMUSG00000021116	chr12	Eif2s1	-0.2145817	0.189903257	0.246639524	5.316372429	0.030316289	0	685	594	591	813	515	577	738	432	698	559
ENSMUSG00000037935	chr11	Smarce1	0.19836712	0.189995557	0.246736472	5.480741838	0.025902871	0	731	630	508	689	532	732	814	701	776	856
ENSMUSG00000078670	chr7	Fam174b	0.40934411	0.190099086	0.246847982	1.008514457	0.080937429	0	27	33	10	30	21	46	25	31	32	42
ENSMUSG00000023484	chr15	Prph	0.61548899	0.190229871	0.246971917	0.96529903	0.214680765	0	31	17	24	26	9	97	31	26	13	18
ENSMUSG00000034848	chr2	Ttc21b	0.31615243	0.190224331	0.246971917	1.791480998	0.048706297	0	49	46	36	60	32	49	67	62	62	60
ENSMUSG00000035275	chr4	Raver2	-0.3861723	0.190254768	0.246981296	1.916617605	0.081303837	0	40	68	82	81	38	40	56	55	63	42
ENSMUSG00000021917	chr14	Spcs1	0.20662455	0.190483064	0.247254695	6.300098782	0.028946517	0	1336	1138	957	1134	863	1471	1401	1226	1435	1347
ENSMUSG00000045969	chr8	Ing1	-0.2081689	0.190585163	0.24736425	3.737283838	0.025310177	0	232	206	198	240	179	223	245	150	193	195
ENSMUSG00000083327	chrX	Vcp-rs	-0.185011	0.190704052	0.247495573	4.990140897	0.021730961	0	509	493	407	648	467	484	492	462	414	569
ENSMUSG00000030346	chr6	Rad51ap1	0.39471561	0.19084881	0.247660443	1.485079766	0.082644569	0	30	46	41	37	17	66	56	50	44	32
ENSMUSG00000101628	chr1	Gm28177	-0.2604155	0.191214358	0.248111769	3.741101494	0.042363918	0	222	211	230	248	164	155	244	129	189	271
ENSMUSG00000021938	chr14	Pspc1	0.24306711	0.191537345	0.248507792	3.296328662	0.035001192	0	119	147	95	199	111	179	202	130	185	164
ENSMUSG00000000489	chr15	Pdgfb	0.20971569	0.191870113	0.24891643	5.370929925	0.029310546	0	595	485	500	771	523	826	610	755	542	888
ENSMUSG00000097081	chr12	Gm10425	0.63502302	0.191985254	0.249042687	0.531907838	0.209367849	0	34	15	10	3	13	15	25	31	20	39
ENSMUSG00000058135	chr3	Gstm1	0.23983064	0.19202597	0.249072386	6.973524059	0.039901059	0	1492	1465	1169	2309	2183	2284	2420	1928	1801	2714
ENSMUSG00000041609	chr5	Ccdc64	0.34089582	0.192227631	0.249310818	1.515607926	0.05162669	0	32	35	30	37	44	68	46	48	42	46
ENSMUSG00000026398	chr1	Nr5a2	-0.5548116	0.192312409	0.249397627	-0.115951423	0.12271068	0	24	16	9	13	9	9	12	10	4	18
ENSMUSG00000039531	chr10	Zufsp	0.29499561	0.1926249	0.2497797	2.23519629	0.04463122	0	72	57	63	68	46	91	87	57	96	82
ENSMUSG00000032458	chr9	Copb2	0.19468747	0.192686172	0.249812796	6.578611831	0.026054406	0	1373	1272	1184	1626	1194	1679	1836	1407	1839	1547
ENSMUSG00000059540	chr2	Tcea2	0.35527816	0.19267376	0.249812796	1.856620229	0.068853163	0	54	53	32	54	36	94	53	51	80	43
ENSMUSG00000083774	chr7	Gm7180	-0.4541516	0.192720493	0.249834117	0.683074501	0.10038317	0	14	35	20	28	30	21	18	12	18	34
ENSMUSG00000027257	chr2	Pacsin3	0.2098657	0.192836854	0.249961777	8.064929601	0.030859043	0	3791	3093	3412	4673	3584	6100	3817	4501	4597	4483
ENSMUSG00000035547	chr7	Capn5	0.2912819	0.192876421	0.249989879	2.384508383	0.04454182	0	86	57	60	71	66	122	86	82	67	104

ENSMUSG00000029192	chr5	Tbc1d14	-0.190487	0.193045134	0.250185348	4.367217237	0.022498384	0	328	337	298	392	277	387	329	227	308	325
ENSMUSG00000075010	chr19	AW112010	-0.2692533	0.193071763	0.250196658	2.910596066	0.042484743	0	122	143	119	127	89	137	89	102	84	139
ENSMUSG00000002949	chr8	Timm44	-0.201626	0.193227028	0.250374647	6.314035522	0.027859592	0	1137	1312	1254	1647	1010	1184	1155	1178	1296	1194
ENSMUSG00000030505	chr7	Prmt3	0.22211574	0.193337957	0.250495159	4.078708425	0.030971477	0	259	161	182	314	247	334	318	290	277	255
ENSMUSG00000081272	chr2	Gm13509	0.25364311	0.193598677	0.250809707	2.973472444	0.036891212	0	93	94	94	139	107	132	174	94	145	143
ENSMUSG00000057606	chr14	Colq	0.21662487	0.193696506	0.250913187	3.934711712	0.028716814	0	165	196	189	290	211	270	243	223	254	344
ENSMUSG00000026694	chr1	Mettl13	-0.2183061	0.193798226	0.251021688	3.644497077	0.028408817	0	224	202	156	222	188	258	199	148	163	175
ENSMUSG00000021713	chr13	Ppwd1	-0.2929615	0.193879687	0.251082464	2.097866486	0.042602772	0	61	69	71	77	62	64	66	48	73	54
ENSMUSG00000038055	chr16	Dexi	-0.1893424	0.193881078	0.251082464	4.9435128	0.023289686	0	507	436	425	591	478	590	452	455	353	501
ENSMUSG00000036957	chr7	Lrfn3	0.40556406	0.193951194	0.251149994	1.450980969	0.088974167	0	26	34	26	57	27	35	45	74	34	51
ENSMUSG00000085653	chr1	Gm15179	-0.2445442	0.193969171	0.251150003	3.215115616	0.03506429	0	149	167	136	144	138	155	136	134	151	107
ENSMUSG00000028542	chr4	Slc6a9	-0.2508765	0.19400345	0.251171118	3.050963245	0.035846675	0	128	128	103	149	151	134	94	115	120	146
ENSMUSG00000037049	chr7	Smpd1	-0.198162	0.194625456	0.251953073	6.13876681	0.026944924	0	1178	1028	1020	1408	989	1000	1087	1148	897	1199
ENSMUSG00000020477	chr11	Mrps24	0.18545703	0.194862993	0.252237213	5.507613205	0.023096733	0	689	539	584	864	518	898	766	709	771	805
ENSMUSG00000042116	chr4	Vwa1	-0.1978541	0.195368685	0.252868377	4.264056743	0.024458996	0	307	326	275	339	269	299	269	276	245	365
ENSMUSG00000031398	chrX	Plxna3	0.3523248	0.195529241	0.253029322	1.678782506	0.064140959	0	54	37	29	39	41	90	55	49	43	47
ENSMUSG00000058301	chr8	Upf1	0.20547571	0.195524739	0.253029322	5.373805483	0.028580456	0	539	497	429	781	635	686	790	702	621	813
ENSMUSG00000031605	chr8	Klhl2	0.28489678	0.19600122	0.253616614	2.6822514	0.046300137	0	70	91	52	129	86	143	128	86	104	107
ENSMUSG00000058655	chr15	Eif4b	-0.1974053	0.19623037	0.253889618	7.668141588	0.027635655	0	3672	3269	2661	3675	2906	3890	2925	2630	2918	3186
ENSMUSG00000006471	chr2	Ndor1	-0.2614302	0.196263738	0.253909284	3.078026442	0.041295733	0	143	145	107	137	140	182	133	84	118	108
ENSMUSG00000055491	chr19	Pprc1	0.28719902	0.19635871	0.254008638	4.233918968	0.055147983	0	213	185	221	354	289	563	358	226	335	219
ENSMUSG00000061533	chr12	Cep128	0.43528511	0.196500957	0.254169124	0.970468608	0.095531825	0	27	33	17	26	13	45	32	22	49	24
ENSMUSG00000103974	chr13	AL589742.1	0.32409064	0.196781288	0.254508169	4.521820521	0.071881766	0	301	313	328	329	233	850	240	376	323	322
ENSMUSG00000014767	chr17	Tbp	-0.2525167	0.196839291	0.25455963	2.727856941	0.035649666	0	115	115	72	133	95	110	103	78	99	96
ENSMUSG00000035392	chr2	Dennd1a	-0.1995074	0.197119952	0.254875423	4.508851006	0.025642283	0	348	304	306	423	418	333	361	308	349	368
ENSMUSG00000078249	chr11	Hmga1-rs1	-0.8625622	0.197102648	0.254875423	3.378596104	0.508689297	0	186	188	186	236	190	538	36	13	17	43
ENSMUSG00000069045	chrY	Ddx3y	-1.5676602	0.197149121	0.254889557	4.737167011	1.566300404	0	1048	881	906	1	0	1	276	179	244	380
ENSMUSG00000022220	chr14	Adcy4	0.25888142	0.197284919	0.255041535	2.917207495	0.039320326	0	93	76	84	154	103	175	107	123	114	145
ENSMUSG00000034432	chr1	Cops8	-0.1847177	0.197518862	0.255320349	6.393567635	0.023806402	0	1386	1303	1166	1584	1222	1283	1352	1156	1244	1380
ENSMUSG00000030161	chr6	Gabarapl1	0.2008945	0.19780767	0.255670027	5.101933367	0.027026564	0	496	520	412	553	393	753	541	518	455	746
ENSMUSG00000101335	chr9	Gm28229	0.40070675	0.197949037	0.255829086	0.780194661	0.068185169	0	25	18	13	24	22	34	37	30	17	30
ENSMUSG00000020648	chr12	Dus4l	0.30398776	0.198230159	0.25616872	1.726083652	0.044241521	0	38	44	39	52	39	57	75	47	56	52
ENSMUSG00000069117	chr13	Gm10260	-1.4876661	0.198289465	0.256221669	4.591160686	1.433095276	0	565	511	464	574	510	1132	3	2	2	2
ENSMUSG00000048756	chr10	Foxo3	-0.2119269	0.198320778	0.256238439	5.133967823	0.030623773	0	515	504	423	748	624	739	465	446	422	603
ENSMUSG00000025133	chr7	Ints4	0.21165196	0.198593338	0.256566878	4.408600955	0.029228877	0	309	257	252	339	299	284	417	367	378	391
ENSMUSG00000079941	chr13	Gm11273	0.32277958	0.198877113	0.256909745	4.521094056	0.071971997	0	301	313	328	329	233	849	239	376	323	322
ENSMUSG00000026209	chr1	Dnpep	0.18544375	0.198916626	0.256937039	5.493138515	0.023455165	0	625	646	590	753	521	816	726	730	831	791
ENSMUSG00000026043	chr1	Col3a1	0.24675525	0.198984308	0.256953219	11.07763446	0.04414355	0	28238	27037	30315	32705	28160	30080	36688	37928	30233	56207
ENSMUSG00000026273	chr1	Mterf4	0.23723786	0.19897173	0.256953219	3.303588549	0.033345718	0	162	125	142	143	93	171	162	165	184	176
ENSMUSG00000087336	chr5	Gm15860	0.53354851	0.198963584	0.256953219	-0.213034329	0.097019154	0	9	9	10	7	9	18	6	11	17	19
ENSMUSG00000098650	chr11	Gm28048	0.19806254	0.199238723	0.257257982	5.579010269	0.02702605	0	671	682	626	801	535	971	962	594	879	776
ENSMUSG00000021065	chr12	Fut8	-0.2475725	0.199329191	0.257351018	3.811307931	0.039475788	0	199	214	218	299	201	155	270	146	197	273
ENSMUSG00000089781	chr6	Gm15756	-0.3856614	0.199482433	0.257525076	2.112048929	0.090365304	0	68	61	64	96	68	25	63	48	59	101
ENSMUSG00000007036	chr17	Abhd16a	-0.1901047	0.199644861	0.257675317	5.709940321	0.024975914	0	837	820	682	1054	773	756	797	659	846	924
ENSMUSG00000048897	chr7	Zfp710	0.20119471	0.199654122	0.257675317	4.763337175	0.027028421	0	292	388	343	548	322	550	424	386	510	497
ENSMUSG00000063873	chr2	Slc24a3	-0.3328491	0.199628098	0.257675317	2.189716984	0.065361851	0	77	97	63	69	60	90	74	54	34	73
ENSMUSG00000051403	chr7	Ppp1r37	-0.1954677	0.19974053	0.257763033	5.651463749	0.026390333	0	786	689	665	1069	806	715	725	707	799	860
ENSMUSG00000031016	chr7	Wee1	-0.375742	0.199882557	0.257922502	1.776264681	0.080797009	0	66	52	64	48	45	64	38	27	68	39
ENSMUSG00000004567	chr8	Mcoln1	0.19762833	0.200030271	0.258089279	4.541722397	0.02543275	0	370	335	258	373	275	498	394	303	435	401
ENSMUSG00000030584	chr7	Dpf1	0.45575914	0.200143326	0.258211311	0.842148764	0.099079065	0	21	24	24	11	22	29	19	36	37	35
ENSMUSG00000018559	chr11	Ctdnep1	0.20584966	0.200293107	0.258375235	7.259957757	0.030530905	0	1829	1798	1752	3225	2140	3110	2609	2629	2280	2795
ENSMUSG00000045519	chr9	Zfp560	0.26217496	0.200307361	0.258375235	2.82428455	0.039823126	0	117	84	98	96	74	144	99	107	132	138
ENSMUSG00000032180	chr9	Tmed1	0.17999263	0.200645502	0.258787517	5.049175809	0.021647214	0	462	510	415	552	369	598	576	519	603	561
ENSMUSG00000022257	chr15	Laptm4b	-0.2258538	0.200933622	0.259135213	4.79290167	0.03478769	0	448	421	316	527	505	325	471	377	365	536
ENSMUSG00000031342	chrX	Gpm6b	-0.265359	0.200963465	0.259149786	2.780776643	0.04174915	0	106	97	107	145	97	130	103	63	80	131
ENSMUSG00000028270	chr3	Gbp2	0.27358854	0.201225926	0.2594643	3.273794408	0.047052422	0	123	146	108	153	114	167	130	175	121	261
ENSMUSG00000031758	chr8	Cdyl2	0.28172446	0.201321708	0.259563855	2.574411755	0.0467155	0	63	70	72	123	69	115	88	128	85	104
ENSMUSG00000102781	chr2	Pla2r1	-0.3755042	0.201409922	0.259653636	1.283903224	0.068172621	0	42	33	39	47	34	18	35	38	29	43
ENSMUSG00000034908	chr9	Sidt2	-0.1988192	0.201523194	0.259775702	6.026779337	0.028017048	0	936	922	914	1332	1091	1264	869	882	832	1134
ENSMUSG00000001674	chr1	Ddx18	0.22192244	0.201890857	0.26022564	3.897244954	0.031548691	0	191	194	167	271	199	277	315	184	305	220
ENSMUSG00000024583	chr18	Txnl1	-0.1875636	0.201914603	0.260232247	5.848713122	0.024682059	0	988	901	825	1120	746	1009	995	769	879	746
ENSMUSG00000085148	chr11	Mir22hg	0.21175369	0.202120653	0.260473789	4.929896043	0.030680454	0	508	444	384	456	303	538	462	484	476	704
ENSMUSG00000026187	chr1	Xrcc5	-0.2761709	0.202427012	0.260844543	4.789428226	0.053474802	0	512	374	350	494	510	223	517	341	445	493
ENSMUSG00000036712	chr8	Cyld	-0.1911224	0.202488938	0.260900285	4.609412721	0.023988036	0	399	347	352	532	318	344	431	307	343	430
ENSMUSG00000038236	chr6	Hoxa7	0.22561773	0.202758535	0.26122093	3.507477814	0.03100211	0	168	146	156	170	130	218	180	232	155	202

ENSMUSG00000079179	chr12	Rab10os	-0.2593896	0.202775177	0.26122093	2.820294078	0.04052935	0	106	109	102	120	123	146	107	79	75	115
ENSMUSG00000036306	chr8	Lzts1	0.45648186	0.202812838	0.261245366	2.37800398	0.138181263	0	19	69	75	119	43	92	75	142	57	108
ENSMUSG00000007570	chr17	Fance	0.2162618	0.203104782	0.261597312	3.048208634	0.026114723	0	106	110	102	143	102	157	147	136	120	156
ENSMUSG00000012429	chr13	Mplkip	0.30113785	0.203306815	0.261833399	2.008279108	0.046196639	0	67	53	42	52	45	73	77	72	54	75
ENSMUSG00000070282	chr9	3000002C10Rik	0.50671058	0.203479764	0.26203199	0.069834993	0.104863	0	14	11	13	16	3	16	17	21	10	24
ENSMUSG00000075327	chr10	Zbtb2	-0.2456054	0.203584271	0.262142415	2.665089755	0.034191172	0	98	96	107	125	78	103	109	72	84	99
ENSMUSG00000027420	chr2	Bfsp1	0.43751268	0.203617281	0.262160766	-0.023801625	0.065062342	0	11	11	10	13	9	12	17	15	17	19
ENSMUSG00000030428	chr7	Ttyh1	-0.4268223	0.203673865	0.262209464	0.616661958	0.086850367	0	22	20	17	32	30	26	31	11	18	13
ENSMUSG00000086350	chr1	B230369F24Rik	-0.3766124	0.203702583	0.262222281	0.707756601	0.058518942	0	27	19	24	29	28	17	22	21	20	27
ENSMUSG00000090210	chr3	Itga10	0.37722979	0.20393626	0.262498911	1.573229561	0.080680283	0	55	32	28	37	32	85	46	55	29	50
ENSMUSG00000030583	chr7	Sipa1l3	-0.2430752	0.204077746	0.262656836	2.897226034	0.033491429	0	107	99	104	169	118	112	127	95	88	128
ENSMUSG00000019889	chr10	Ptprk	-0.2657357	0.204152526	0.26268051	3.226309255	0.044720505	0	131	137	144	218	129	190	113	158	85	142
ENSMUSG00000024505	chr18	Dtwd2	-0.3065169	0.204115312	0.26268051	1.921535516	0.048995956	0	66	47	64	66	58	53	63	37	62	53
ENSMUSG00000034189	chr8	Hsdl1	-0.1780759	0.204141258	0.26268051	4.32087565	0.02022686	0	329	301	289	375	279	341	309	240	301	337
ENSMUSG00000029068	chr4	Ccnl2	0.20121905	0.204199958	0.262699371	5.099080902	0.027877736	0	534	440	474	470	430	737	482	498	658	615
ENSMUSG00000050966	chr4	Lin28a	0.51161911	0.204204778	0.262699371	0.997074547	0.149640212	0	36	26	19	15	17	16	35	24	35	69
ENSMUSG00000053004	chr6	Hrh1	-0.4819949	0.204285572	0.262779121	0.025107399	0.083963322	0	8	18	17	22	13	17	14	12	10	8
ENSMUSG00000028125	chr3	Abca4	0.5260819	0.204686203	0.263246008	0.073423961	0.118660683	0	16	16	7	10	7	12	24	8	22	23
ENSMUSG00000030512	chr7	Snrpa1	0.26435319	0.204674728	0.263246008	4.219211584	0.048224108	0	251	171	213	373	260	477	398	239	338	211
ENSMUSG00000022159	chr14	Rab2b	0.31714488	0.204734299	0.263283637	2.192462216	0.056964185	0	56	55	66	60	55	111	66	63	55	112
ENSMUSG00000049823	chr17	Zbtb12	-0.2735294	0.204836291	0.263390561	2.820267331	0.045220715	0	92	103	102	160	113	72	122	95	98	124
ENSMUSG00000089739	chr2	Gm20431	-0.1950896	0.205162087	0.263785218	5.453539696	0.02683394	0	710	584	652	819	706	591	727	571	669	765
ENSMUSG00000022757	chr16	Tfg	-0.1997833	0.205242793	0.263864711	5.659394614	0.028373804	0	842	710	688	1017	776	628	886	694	732	882
ENSMUSG00000097233	chr19	Gm17552	-0.6493093	0.205432095	0.26408379	-0.296776517	0.192038188	0	19	10	15	6	12	3	5	5	11	20
ENSMUSG00000084514	chr18	Mir1893	-0.4058162	0.205778326	0.264504542	0.788345899	0.076592059	0	31	26	34	29	16	25	17	15	27	29
ENSMUSG00000028577	chr4	Plaa	-0.1885952	0.205814352	0.264526521	5.565112484	0.025147574	0	774	710	681	996	616	730	796	533	756	800
ENSMUSG00000096944	chr4	Gm26722	0.21673845	0.205881546	0.26458855	4.061537341	0.031113893	0	291	197	217	270	171	298	241	310	278	322
ENSMUSG00000100164	chr6	2610306M01Rik	0.30976208	0.206007354	0.26472589	2.582301504	0.05989907	0	83	100	60	101	49	142	71	95	126	96
ENSMUSG00000035521	chr17	Gnptg	0.21015963	0.206062091	0.264771884	3.615369243	0.027215085	0	203	169	144	190	133	227	220	161	227	230
ENSMUSG00000025854	chr5	Fam20c	0.26310971	0.206093985	0.264788521	5.02885719	0.049465814	0	508	356	342	487	503	530	859	377	410	749
ENSMUSG00000101599	chr1	Gm20342	0.44592348	0.206217642	0.264923041	0.290700572	0.07687605	0	14	14	15	11	14	31	19	11	20	23
ENSMUSG00000079415	chr19	Cntf	-0.4305621	0.206239189	0.264926371	1.07900752	0.100045605	0	19	43	37	42	29	46	21	27	30	15
ENSMUSG00000029486	chr5	Mrpl1	-0.1830017	0.206273673	0.264946315	5.027326093	0.02295789	0	496	516	523	632	411	487	517	426	554	496
ENSMUSG00000003299	chr9	Mrpl4	0.18611701	0.206420827	0.26511096	5.574090011	0.024663535	0	586	606	563	966	628	887	847	839	741	811
ENSMUSG00000001065	chr8	Zfp276	-0.2422293	0.206476511	0.265158111	3.012120445	0.035468853	0	113	103	132	163	131	135	120	92	141	107
ENSMUSG00000028266	chr3	Lmo4	-0.2054027	0.206930554	0.265716779	4.292416211	0.028321331	0	278	287	358	395	239	392	310	243	274	268
ENSMUSG00000001472	chr8	Tcf25	0.20481548	0.206965776	0.265737592	7.251654744	0.031101608	0	2280	1795	1792	2485	2188	2329	2697	2341	2644	3281
ENSMUSG00000046756	chr11	Mrps7	0.18959011	0.207061665	0.265836288	6.12227868	0.026100619	0	1055	906	949	1169	773	1161	1214	1208	1242	1197
ENSMUSG00000036352	chr2	Ubac1	-0.1932525	0.207248024	0.266051106	8.002292491	0.02786065	0	4361	3803	3699	4812	3709	3687	3737	4030	3823	4155
ENSMUSG00000061740	chr15	Cyp2d22	0.22886363	0.207481377	0.266326205	3.19915812	0.032707891	0	117	123	114	175	98	180	131	178	133	175
ENSMUSG00000048731	chr17	Ggnbp1	-0.2015388	0.207521548	0.266353306	4.048877179	0.026577496	0	298	262	260	282	204	312	255	216	249	220
ENSMUSG00000031775	chr8	Pllp	-0.4015197	0.207815214	0.266705733	1.141777955	0.091056503	0	25	30	53	42	26	37	27	26	16	42
ENSMUSG00000010392	chr11	Gosr1	-0.1844064	0.20803912	0.266968575	4.497195519	0.022758054	0	331	341	375	435	299	402	394	297	305	326
ENSMUSG00000030257	chr6	Srgap3	0.34234911	0.208077261	0.266993004	2.463196713	0.074749564	0	77	41	71	106	63	168	69	99	64	97
ENSMUSG00000093798	chr10	Gm8355	0.24505372	0.208311717	0.267269306	3.622062231	0.03980634	0	182	136	121	242	161	334	227	190	163	177
ENSMUSG00000028437	chr4	Ubap1	-0.1878156	0.208393312	0.267349452	5.669495197	0.025374688	0	916	811	697	931	679	810	748	635	760	934
ENSMUSG00000021453	chr13	Gadd45g	0.41254173	0.208761654	0.267774621	4.86981241	0.125029808	0	277	226	528	231	527	1105	376	324	555	415
ENSMUSG00000032478	chr9	Nme6	0.20942869	0.208763042	0.267774621	4.219121264	0.029554991	0	255	265	210	317	235	381	293	279	403	261
ENSMUSG00000084403	chr4	Rps15a-ps8	-1.2997829	0.208797144	0.267793786	0.032517075	1.069689867	0	24	19	15	21	16	46	0	0	0	0
ENSMUSG00000025135	chr11	Anapc11	0.18405778	0.208833223	0.267795656	4.819286643	0.023062388	0	360	381	379	467	371	651	514	402	450	441
ENSMUSG00000037827	chr6	Gm5884	-0.2645447	0.208836925	0.267795656	2.35925326	0.038343895	0	79	76	59	119	79	77	79	60	79	77
ENSMUSG00000045095	chr6	Magi1	-0.2725524	0.209056582	0.268052733	2.426716939	0.042668659	0	75	81	100	99	72	101	79	73	56	82
ENSMUSG00000024955	chr19	Esrra	-0.2126574	0.209337836	0.268388735	6.328415263	0.033423895	0	1041	1242	1349	1856	993	1108	1214	1290	1230	1186
ENSMUSG00000036781	chr9	Rps27l	0.19008134	0.209436637	0.268490775	5.87228779	0.026275962	0	909	779	788	929	662	1154	1134	862	1071	872
ENSMUSG00000026697	chr1	Myoc	-0.2220816	0.209479316	0.268520859	4.397779946	0.034348177	0	409	351	279	323	308	340	380	220	363	281
ENSMUSG00000013858	chr10	Tmem259	0.1902624	0.20949983	0.268522527	6.363121521	0.026743003	0	1044	1020	1028	1591	1084	1638	1367	1497	1224	1426
ENSMUSG00000032578	chr9	Cish	0.66163456	0.210296886	0.26951942	4.753070035	0.324000749	0	414	719	113	253	49	277	785	427	962	178
ENSMUSG00000027811	chr3	4930579G24Rik	0.40033351	0.210328798	0.269535602	1.269369999	0.083261612	0	29	28	21	23	43	38	62	33	42	37
ENSMUSG00000004880	chr1	Lbr	-0.2071665	0.210488323	0.269715302	4.427511735	0.029803531	0	347	348	343	363	298	398	402	230	334	268
ENSMUSG00000038497	chr8	Tmco3	-0.2047236	0.210989871	0.27033319	3.753469725	0.026876896	0	203	206	185	256	216	176	218	187	179	253
ENSMUSG00000025169	chr11	Ogfod3	0.22352841	0.211060229	0.270369507	3.600122623	0.032222337	0	166	155	120	197	187	302	192	170	189	212
ENSMUSG00000046020	chr2	Pofut1	0.1739345	0.211076251	0.270369507	4.757313779	0.02063917	0	388	340	340	485	341	507	447	377	473	533
ENSMUSG00000048481	chr7	Mypop	0.25869997	0.211052173	0.270369507	2.355765388	0.037714687	0	70	56	59	98	59	86	89	84	77	108
ENSMUSG00000079669	chr9	Gm17396	0.38913833	0.211409638	0.270771728	1.740472501	0.092272621	0	56	41	43	39	27	49	50	68	34	96
ENSMUSG00000083022	chr11	Rps15a-ps6	-0.4681422	0.211552074	0.270929331	2.63800941	0.155237674	0	88	90	82	156	117	221	46	58	71	34

ENSMUSG00000043313	chr18	Pcdhb19	-0.4615903	0.21175155	0.271159947	0.353861385	0.101523536	0	25	20	16	17	21	21	18	17	4	20
ENSMUSG00000053289	chr9	Ddx10	-0.233793	0.211901163	0.271326675	3.504806074	0.034981988	0	166	160	141	275	175	150	208	129	190	165
ENSMUSG00000024081	chr17	Cebpz	-0.1777216	0.212084362	0.271536372	4.441227694	0.021072288	0	336	327	289	470	302	390	342	259	337	335
ENSMUSG00000028145	chr3	Them4	-0.2784566	0.212246889	0.271719568	3.057134604	0.050034212	0	126	143	144	156	100	75	135	110	143	137
ENSMUSG00000026646	chr2	Suv39h2	-0.3718463	0.212374696	0.271858285	1.000157306	0.064234253	0	38	30	19	41	31	32	32	18	31	21
ENSMUSG00000036622	chr4	Atp13a2	0.19610108	0.212488534	0.271979097	5.179114686	0.027564026	0	487	447	470	576	519	652	622	468	579	845
ENSMUSG00000040016	chr3	Ptger3	-0.7190992	0.21252692	0.272003318	-0.220265552	0.265109671	0	4	28	5	7	23	6	6	15	10	8
ENSMUSG00000071072	chr10	Ptges3	0.19574824	0.212553824	0.272012842	5.790431841	0.028331706	0	831	718	611	1029	682	1097	1236	787	902	812
ENSMUSG00000048307	chr15	Ankrd46	-0.1805749	0.212784872	0.27228359	4.713467308	0.022493657	0	447	448	341	478	355	393	442	352	409	401
ENSMUSG00000021069	chr12	Pygl	0.45137894	0.212854617	0.272330945	3.437705639	0.146594229	0	46	246	156	61	136	255	190	138	207	229
ENSMUSG00000023170	chr11	Gps2	0.1924881	0.21286085	0.272330945	4.401322176	0.025495276	0	291	227	240	431	290	443	352	342	309	391
ENSMUSG00000024914	chr19	Drap1	0.19632424	0.213025828	0.272517069	8.206583661	0.029549468	0	4839	3854	3420	4596	3789	4932	5160	4541	5481	5583
ENSMUSG00000033453	chr9	Adamts15	0.45297376	0.21329798	0.27284025	2.766165058	0.144675298	0	54	63	72	114	116	255	52	122	54	160
ENSMUSG00000026229	chr1	Psmd1	-0.1839396	0.213378051	0.272917693	7.437616083	0.025788564	0	2932	2529	2399	3333	2566	2607	2933	2302	2693	2702
ENSMUSG00000025887	chr9	Casp12	-0.3243105	0.213468979	0.273009008	2.665793579	0.070097022	0	115	120	138	86	50	92	100	79	85	96
ENSMUSG00000020937	chr11	Plcd3	-0.3124272	0.213537602	0.273027415	2.331578504	0.061669044	0	79	66	55	110	98	106	81	63	41	71
ENSMUSG00000026727	chr2	Rsu1	0.18251985	0.213541977	0.273027415	4.895675632	0.023450706	0	434	416	354	483	382	457	591	471	456	596
ENSMUSG00000052798	chr10	Nup107	0.25515404	0.213515613	0.273027415	3.205693488	0.0426188	0	114	112	131	148	112	160	232	133	166	117
ENSMUSG00000031503	chr8	Col4a2	-0.2237305	0.213702492	0.27320765	8.397915922	0.038558909	0	4561	4732	5133	7732	5145	5966	4376	5546	3509	6066
ENSMUSG00000010205	chr9	Raver1	0.17897054	0.213823521	0.273337376	4.981094575	0.022613722	0	412	359	405	578	453	656	595	498	463	527
ENSMUSG00000036686	chr8	Cc2d1a	-0.1885041	0.213893791	0.273402197	4.212325832	0.023804534	0	293	251	231	386	309	315	270	243	252	331
ENSMUSG00000069808	chr11	Fam57a	0.2956841	0.214010062	0.2735258	1.75353681	0.043764554	0	45	46	41	41	42	68	64	54	55	51
ENSMUSG00000050222	chr14	Il17d	0.34838852	0.214183613	0.273722584	1.445206043	0.063122737	0	36	46	19	33	35	47	55	47	40	48
ENSMUSG00000022146	chr15	Osmr	0.31583064	0.214382549	0.273951769	2.838920561	0.06802045	0	64	84	61	177	93	184	139	94	132	92
ENSMUSG00000037169	chr12	Mycn	-0.5204237	0.214463647	0.274030346	0.290985511	0.130722552	0	21	18	19	35	6	6	17	14	14	22
ENSMUSG00000093470	chr11	Gm20645	0.32379266	0.215295166	0.27506767	2.182218756	0.06571501	0	48	41	44	105	60	106	92	46	71	90
ENSMUSG00000037148	chr8	Arhgap10	-0.1990582	0.215400499	0.275166845	5.346815798	0.029080033	0	565	558	493	975	683	593	599	591	592	704
ENSMUSG00000040795	chr4	Iqcc	-0.2165715	0.215412167	0.275166845	3.426167238	0.030098407	0	168	188	163	202	131	220	138	149	142	158
ENSMUSG00000063286	chr7	Gm8995	0.32668799	0.215548412	0.275315719	2.770626654	0.072766305	0	58	91	105	118	71	79	149	77	146	156
ENSMUSG00000028550	chr4	Atg4c	-0.2907634	0.215592592	0.275346986	2.939694323	0.056348901	0	141	116	92	170	107	68	124	81	134	145
ENSMUSG00000041057	chr17	Wdr43	-0.1984457	0.215843494	0.27564224	4.700265634	0.028036684	0	427	379	346	561	366	413	479	281	448	351
ENSMUSG00000022184	chr15	Fbxo4	0.28479279	0.21595336	0.275757347	2.370719052	0.048562364	0	73	82	64	73	46	92	101	60	96	105
ENSMUSG00000034024	chr10	Cct2	0.18502836	0.21603231	0.275807762	6.855709881	0.02623408	0	1744	1447	1294	2123	1521	2092	2388	1728	1931	1926
ENSMUSG00000042340	chr7	Ctf1	0.25915338	0.216031191	0.275807762	3.298285849	0.044828654	0	158	160	120	123	93	151	149	168	165	228
ENSMUSG00000024525	chr18	Impa2	0.26298143	0.216231484	0.276036831	2.8806443	0.044932378	0	88	108	96	131	70	157	94	147	131	113
ENSMUSG00000041720	chr16	Pi4ka	-0.1881109	0.216497832	0.276351603	4.483159276	0.024837492	0	332	331	312	451	345	444	375	238	332	324
ENSMUSG00000097333	chr13	Zfp87	0.27726316	0.216654899	0.276526837	2.049513051	0.042611833	0	50	59	47	64	50	99	70	55	73	64
ENSMUSG00000029012	chr5	Orc5	0.21802821	0.216805909	0.27669431	3.636624619	0.031328689	0	201	178	150	188	131	241	236	143	230	237
ENSMUSG00000047777	chr4	Phf13	0.22377995	0.217266856	0.277257267	3.164453056	0.031799131	0	116	107	102	159	126	220	137	135	139	152
ENSMUSG00000052533	chr2	Nup188	0.20040714	0.217384859	0.277382525	3.57144032	0.025220186	0	142	147	150	218	162	263	214	173	172	212
ENSMUSG00000037458	chr15	Azin1	-0.2124157	0.217831555	0.277927132	6.192293748	0.034607057	0	1208	834	1101	1555	1175	998	1403	870	1172	1077
ENSMUSG00000032593	chr9	Amigo3	-0.3647085	0.21794769	0.278049924	1.683482054	0.07891601	0	39	42	72	80	29	42	55	47	35	41
ENSMUSG00000098816	chr7	Gm27786	-0.8370116	0.218049785	0.278154782	1.375606793	0.499914198	0	26	26	8	92	91	10	3	59	11	58
ENSMUSG00000020674	chr12	Pxdn	-0.2101391	0.218132344	0.278221777	6.007746135	0.033835523	0	1005	1028	1040	1193	859	1034	901	938	677	1334
ENSMUSG00000093483	chr11	AA465934	-0.494994	0.218142118	0.278221777	0.762550782	0.145925906	0	35	24	20	35	24	49	23	8	20	9
ENSMUSG00000102422	chr3	SCHIP1	-0.2099695	0.218235496	0.278315476	6.22966067	0.033850144	0	1177	1197	1310	1492	829	978	1061	1134	1179	1287
ENSMUSG00000005442	chr7	Cic	0.21941752	0.218256161	0.278316433	5.504616192	0.036397782	0	540	524	571	859	642	1125	777	564	583	990
ENSMUSG00000062040	chr7	Zfp27	-0.2790231	0.218489053	0.278585132	2.392262543	0.047577548	0	99	90	63	106	64	69	80	54	93	82
ENSMUSG00000091154	chr8	Proscos	0.43330544	0.218506741	0.278585132	0.041724531	0.077511009	0	10	8	10	22	8	16	17	19	18	14
ENSMUSG00000067713	chr15	Prkag1	0.17840232	0.218609666	0.278690932	5.733883758	0.023981188	0	769	711	701	985	574	928	956	827	964	921
ENSMUSG00000053740	chr18	Gm6457	-0.4567284	0.218905363	0.279042444	0.166589146	0.09452059	0	16	25	8	18	19	13	19	11	9	17
ENSMUSG00000046679	chr6	C87436	-0.2162239	0.219218658	0.279416322	3.092286321	0.029623128	0	133	107	126	167	141	158	124	105	110	142
ENSMUSG00000029319	chr5	Coq2	-0.1811254	0.219380175	0.279545707	5.42288235	0.024418324	0	675	644	666	813	590	595	714	569	707	680
ENSMUSG00000043467	chr1	Zbtb37	-0.2967109	0.219366411	0.279545707	2.56097793	0.055410011	0	135	86	72	100	82	58	101	81	85	96
ENSMUSG00000086096	chr4	Gm12688	0.47909753	0.219360275	0.279545707	0.456604175	0.108823609	0	19	11	14	12	20	38	19	15	13	35
ENSMUSG00000024743	chr19	Syt7	-0.3663798	0.219414889	0.279564454	0.983312101	0.069677322	0	28	20	27	52	31	38	19	23	22	31
ENSMUSG00000042203	chr17	Tbc1d22b	-0.1954486	0.219566222	0.27973177	3.788786404	0.02530239	0	207	183	192	281	230	242	221	211	164	207
ENSMUSG00000035649	chr4	Zcchc7	0.21744305	0.219861761	0.280082762	3.351422783	0.03063984	0	156	150	114	151	122	188	159	171	205	158
ENSMUSG00000022847	chr16	Thpo	0.37256033	0.220192797	0.280478904	1.290939178	0.081606287	0	29	24	32	51	17	71	32	42	33	37
ENSMUSG00000086877	chrX	A230072C01Rik	-0.448057	0.220372893	0.280682725	0.22972709	0.083328643	0	23	21	20	17	9	20	17	11	10	15
ENSMUSG00000051243	chr9	Islr2	0.43159905	0.22052916	0.280856164	1.688018448	0.124280135	0	27	31	57	51	30	65	39	103	37	42
ENSMUSG00000020282	chr11	Rhbdf1	0.18919494	0.220641319	0.280973401	4.55614694	0.025583978	0	299	313	285	425	314	558	391	400	335	362
ENSMUSG00000017167	chr11	Cntnap1	-0.3880533	0.220784143	0.281129663	1.131776055	0.083280594	0	34	43	25	41	32	21	45	17	24	40
ENSMUSG00000022466	chr15	Rpap3	-0.1960024	0.221232598	0.281675029	3.885910239	0.025797327	0	262	212	208	288	201	201	224	188	254	246
ENSMUSG00000021840	chr14	Mapk1ip1l	0.19589387	0.221348963	0.281771847	4.630241059	0.027838082	0	341	277	312	428	356	429	573	366	351	436

ENSMUSG00000026158	chr1	Ogfrl1	-0.2430863	0.221348086	0.281771847	3.000887783	0.039082647	0	121	127	109	158	123	124	128	73	149	117
ENSMUSG00000085586	chr11	Gm11613	-0.2804291	0.22156277	0.282018331	2.847367118	0.053032902	0	135	112	112	129	90	86	83	75	128	149
ENSMUSG00000030869	chr7	Ndufab1	0.19133793	0.221639099	0.282089796	7.748739154	0.029072059	0	2739	2910	2833	4296	2349	4318	3629	3831	3317	3619
ENSMUSG00000017764	chr2	Zswim1	0.22458924	0.221690927	0.282130066	2.986239227	0.031206599	0	110	107	90	136	95	177	141	137	103	131
ENSMUSG00000055302	chr5	Mrfap1	0.17617624	0.221910307	0.282383542	7.617975346	0.024587637	0	2987	2600	2486	3318	2378	3792	3448	3142	3249	3393
ENSMUSG00000027746	chr3	Ufm1	0.1874867	0.221977281	0.282443052	4.779553448	0.025635569	0	433	367	340	451	318	599	490	354	524	422
ENSMUSG00000074652	chr2	Myh7b	-0.6006924	0.222143157	0.282628381	1.663201582	0.26166548	0	21	61	30	132	42	97	27	45	10	22
ENSMUSG00000027474	chr2	Ccm2l	-0.3018442	0.222319486	0.282818404	2.071689928	0.05689079	0	78	60	59	77	62	89	34	56	59	62
ENSMUSG00000033111	chr14	3830406C13Rik	-0.2221812	0.222332986	0.282818404	3.577325118	0.034109309	0	209	206	173	206	152	229	191	146	198	129
ENSMUSG00000039740	chr4	Alg2	-0.1963568	0.222473793	0.282971762	4.296796581	0.027650356	0	340	281	244	333	349	297	349	262	248	334
ENSMUSG00000052713	chr18	Zfp608	-0.2631673	0.222540703	0.28303111	2.665775283	0.045380603	0	113	84	91	144	80	127	106	66	63	106
ENSMUSG00000019868	chr10	Vta1	0.18093649	0.223009375	0.283601367	4.258336439	0.02278374	0	314	257	240	300	217	333	315	316	319	364
ENSMUSG00000002847	chr16	Pla1a	-0.3376204	0.223459072	0.284147392	2.360554868	0.076969798	0	60	105	93	85	70	108	59	92	55	48
ENSMUSG00000029034	chr4	Cpsf3l	0.17609953	0.223610895	0.28431458	4.321506676	0.021485953	0	283	244	269	337	258	415	377	293	334	308
ENSMUSG00000026748	chr2	Plxdc2	-0.1933686	0.22382514	0.284561099	5.037399517	0.028378146	0	603	535	469	535	447	715	496	427	382	499
ENSMUSG00000028549	chr4	Itgb3bp	0.32305892	0.224409401	0.28527795	2.186425837	0.068058841	0	70	47	34	73	70	62	92	71	105	68
ENSMUSG00000023156	chr14	Rpp14	-0.1796478	0.224715679	0.285641322	4.651197835	0.023305287	0	403	354	373	529	334	356	432	328	414	381
ENSMUSG00000053835	chr17	H2-T24	-0.3880386	0.224809968	0.285735187	2.447154075	0.108297475	0	73	103	69	127	82	159	79	39	33	79
ENSMUSG00000073374	chr17	C030034I22Rik	-0.3996881	0.224969094	0.285911436	0.282662176	0.065715962	0	23	18	20	22	10	16	17	13	14	17
ENSMUSG00000024587	chr18	Nars	-0.1839695	0.225089822	0.286038857	6.684838339	0.026871694	0	1642	1477	1443	2106	1517	1572	1781	1279	1728	1493
ENSMUSG00000022351	chr15	Sqle	0.33468661	0.225145496	0.286083594	2.822507797	0.080354815	0	111	83	84	88	88	122	187	84	172	66
ENSMUSG00000099481	chr7	Xndc1	0.25038326	0.225252065	0.286192987	2.476232287	0.037580191	0	69	74	64	99	66	131	105	84	73	93
ENSMUSG00000039307	chr11	Hexdc	0.21802409	0.225586855	0.286592299	3.165572412	0.030917515	0	143	114	92	137	123	169	142	130	170	166
ENSMUSG00000020474	chr11	Polm	0.26502676	0.225700299	0.286655299	2.349198647	0.042991861	0	76	71	61	71	56	100	72	100	72	98
ENSMUSG00000024456	chr18	Diap1	0.20606216	0.225726314	0.286655299	6.160487287	0.033785994	0	813	749	923	1662	895	1436	1275	1092	1267	1187
ENSMUSG00000031994	chr9	Adamts8	0.5823503	0.225684112	0.286655299	1.92641849	0.251646025	0	21	33	33	122	23	167	87	55	19	40
ENSMUSG00000040612	chr1	Ildr2	-0.3881646	0.225658858	0.286655299	1.040270157	0.082020074	0	22	26	34	46	36	36	33	22	32	14
ENSMUSG00000068396	chr6	Rpl34-ps1	0.37482255	0.225738997	0.286655299	2.282318156	0.098110599	0	62	76	50	76	44	178	96	51	71	50
ENSMUSG00000031641	chr8	Cbr4	-0.1958575	0.22603541	0.287005623	4.265351213	0.027618744	0	309	331	311	341	225	261	282	274	314	317
ENSMUSG00000042035	chr3	Igsf3	0.21627351	0.226074108	0.287028682	3.826979453	0.033216724	0	212	169	154	238	199	272	219	268	170	307
ENSMUSG00000030615	chr7	Tmem126a	-0.1857702	0.226108674	0.287046492	5.695239291	0.026843788	0	944	761	710	1000	701	717	968	678	775	808
ENSMUSG00000020843	chr11	Timm22	0.17575763	0.226225072	0.287168175	5.345721571	0.023623167	0	636	553	509	667	476	698	749	693	716	642
ENSMUSG00000020709	chr11	Adap2	-0.390976	0.226289069	0.287197242	1.467760859	0.097737634	0	37	36	58	49	42	28	47	16	54	42
ENSMUSG00000034205	chr14	Loxl2	0.22834438	0.226284666	0.287197242	5.707302779	0.041233129	0	802	614	654	846	664	1177	997	1001	487	959
ENSMUSG00000021974	chr14	Fgf9	0.46539259	0.226515275	0.28745823	0.470465501	0.123560233	0	6	15	14	37	9	35	22	21	24	17
ENSMUSG00000046861	chr4	Hectd3	-0.1694768	0.226786737	0.287776597	4.907561573	0.021370468	0	512	479	440	503	414	514	424	421	423	520
ENSMUSG00000006732	chr10	Mettl1	0.23859322	0.227329142	0.288438683	4.131691108	0.042511069	0	268	251	226	239	198	290	400	235	387	221
ENSMUSG00000092310	chr9	Gm20509	-0.2696229	0.227426842	0.288536451	2.863501469	0.051017339	0	130	103	119	127	102	105	126	59	140	101
ENSMUSG00000025591	chr8	Tma16	-0.2970634	0.227551509	0.288668411	2.525330629	0.059571892	0	76	94	84	128	84	64	103	55	116	73
ENSMUSG00000026034	chr1	Clk1	0.22238377	0.227573197	0.288669723	4.69319497	0.037491609	0	364	369	340	341	338	715	439	294	430	419
ENSMUSG00000038637	chr7	Lrrc56	0.36623558	0.227895092	0.289051802	1.087355747	0.071832801	0	22	31	30	33	14	47	32	26	30	50
ENSMUSG00000034586	chr11	Hid1	0.29957544	0.227975687	0.289127787	1.803717079	0.048973261	0	37	49	53	48	36	73	56	56	49	70
ENSMUSG00000038895	chr9	Zfp653	0.32215127	0.228050965	0.289197013	1.931449192	0.063244639	0	54	41	64	58	27	89	66	45	67	70
ENSMUSG00000069727	chr7	Gm5595	-0.4450971	0.228101269	0.289234562	0.90487009	0.118068028	0	43	27	27	23	29	8	28	24	26	34
ENSMUSG00000024197	chr17	Plin3	0.19931304	0.228139829	0.289257212	5.145022578	0.030718889	0	435	523	556	618	320	777	658	512	533	619
ENSMUSG00000032786	chr9	Alas1	-0.2129965	0.228378755	0.289533879	7.13497825	0.036930353	0	1661	2112	2444	3432	1726	2426	1994	2148	1732	2340
ENSMUSG00000030905	chr7	Crym	0.28725696	0.228604914	0.28979431	3.013993981	0.059111563	0	80	96	138	124	92	130	117	105	137	227
ENSMUSG00000090958	chr7	Lrrc32	0.27296471	0.229168085	0.290481875	3.500909451	0.054206286	0	129	128	147	158	185	231	174	214	110	276
ENSMUSG00000008035	chrX	Mid1ip1	0.36630546	0.229205973	0.290503553	4.844081353	0.107801808	0	223	471	579	419	153	944	410	498	421	390
ENSMUSG00000020329	chr10	Polrmt	-0.1789373	0.229266221	0.290527219	4.388201944	0.023017294	0	311	299	300	434	311	315	320	347	278	329
ENSMUSG00000022208	chr14	Jph4	-0.5115386	0.22926344	0.290527219	-0.111269886	0.118359332	0	14	12	11	21	13	20	3	15	7	9
ENSMUSG00000047044	chr19	D030056L22Rik	0.27802647	0.229472086	0.290761729	2.507460694	0.050739417	0	75	83	71	91	55	108	146	77	93	75
ENSMUSG00000022781	chr16	Pak2	0.17121827	0.229714249	0.291042186	5.262162503	0.022509504	0	496	520	491	699	487	797	755	520	625	631
ENSMUSG00000049411	chr18	Tmem241	0.34008662	0.229797008	0.291120648	1.533938101	0.070270761	0	24	44	46	42	25	41	49	45	61	55
ENSMUSG00000081769	chr11	Gm12216	0.4224327	0.22998837	0.291336668	0.228799771	0.07843167	0	15	13	9	20	10	15	14	18	24	26
ENSMUSG00000003378	chr7	Grik5	0.29424307	0.230685711	0.292193538	2.272999934	0.055652564	0	69	54	60	66	64	114	60	92	57	102
ENSMUSG00000051224	chrX	Tceanc	-0.3681176	0.230814879	0.292330653	1.413467241	0.085496935	0	37	54	49	33	37	27	31	47	28	47
ENSMUSG00000055943	chr2	Emc7	0.17405318	0.230945598	0.292443398	5.648925219	0.023937411	0	737	679	624	881	599	850	1003	722	831	933
ENSMUSG00000070610	chr4	Gm13127	0.30946296	0.230945749	0.292443398	1.388708197	0.048689796	0	38	23	27	47	32	54	46	40	35	51
ENSMUSG00000025064	chr19	Col17a1	0.46503645	0.231281925	0.292842561	0.079175157	0.095623484	0	14	10	4	21	10	18	15	13	15	27
ENSMUSG00000098004	chr2	Gm27027	0.19945403	0.231598124	0.293216359	3.495907808	0.027095026	0	164	138	163	189	121	200	212	202	178	179
ENSMUSG00000007589	chr14	Tinf2	0.21764839	0.231680254	0.29329377	3.60482709	0.033150592	0	192	174	158	151	146	235	199	172	255	195
ENSMUSG00000009090	chr11	Ap1b1	0.19491914	0.231722878	0.293321161	5.925741324	0.030706719	0	801	714	652	1216	879	1472	960	891	999	1005
ENSMUSG00000042320	chr12	Prox2	-0.4107607	0.23185766	0.293465192	0.532147262	0.079930152	0	27	16	29	22	18	12	19	20	22	19
ENSMUSG00000028894	chr4	Inpp5b	-0.1916773	0.231910316	0.293505259	3.579673561	0.025314071	0	170	169	173	214	210	211	178	162	160	194

ENSMUSG00000048450	chr5	Msx1	0.29087213	0.231984513	0.293572578	2.077416242	0.053038794	0	66	46	52	62	48	85	66	77	45	96
ENSMUSG00000001157	chr6	Gmcl1	-0.2461044	0.232145682	0.293749937	2.554467182	0.039377823	0	99	80	92	100	92	117	99	73	67	77
ENSMUSG00000036281	chr2	Snapc4	0.24079483	0.232173812	0.293758935	2.620928228	0.035450054	0	84	78	74	87	86	133	92	105	103	100
ENSMUSG00000029345	chr5	Tfip11	-0.1748164	0.232339736	0.29394226	4.158183258	0.021853797	0	310	265	241	350	242	311	305	222	234	296
ENSMUSG00000055760	chr17	Gemin6	0.27300463	0.232434562	0.294035611	2.538464707	0.050580556	0	71	87	69	99	59	106	108	79	137	76
ENSMUSG00000014601	chr3	Strip1	-0.1673783	0.23264851	0.294252994	5.064897973	0.021449729	0	519	447	517	667	486	532	550	454	551	475
ENSMUSG00000014980	chr1	Tsen15	0.19059612	0.232636479	0.294252994	3.478908232	0.024120737	0	159	138	135	208	133	218	209	166	194	174
ENSMUSG00000097204	chr3	Gm17690	0.33800623	0.233246467	0.294982592	1.442632441	0.071472459	0	44	44	21	44	19	44	44	40	46	62
ENSMUSG00000033557	chr1	Fam20b	-0.1645496	0.233428568	0.29518618	5.803520931	0.021590095	0	835	813	823	1129	805	931	873	829	825	830
ENSMUSG00000022442	chr15	Ttll1	0.24735231	0.233464648	0.295205096	2.698352627	0.04074816	0	91	71	83	111	79	104	95	113	98	153
ENSMUSG00000033703	chr8	Fuk	-0.253305	0.233704277	0.295481362	2.474762169	0.040727611	0	91	71	81	108	90	71	70	86	79	97
ENSMUSG00000024096	chr17	Ralbp1	-0.1622312	0.23398288	0.295806851	4.990142643	0.020073313	0	453	460	456	670	467	530	494	416	471	535
ENSMUSG00000025231	chr19	Sufu	0.19734007	0.234054291	0.295870366	3.536537717	0.026832983	0	145	166	132	203	153	187	215	189	169	241
ENSMUSG00000032531	chr9	Amotl2	-0.2948985	0.2341974	0.29599922	4.410884944	0.070529613	0	256	362	351	379	372	572	261	240	146	370
ENSMUSG00000062012	chr17	Zfp13	0.32910254	0.234198581	0.29599922	1.135220818	0.057837404	0	23	31	17	42	25	37	38	37	30	46
ENSMUSG00000070392	chr3	Gm20634	-0.3811981	0.234687731	0.296590626	2.15891549	0.105806149	0	69	60	50	106	85	27	85	59	39	97
ENSMUSG00000041809	chr1	Efhc1	0.48308903	0.234838992	0.29675495	-0.172882383	0.099386849	0	11	15	4	10	7	15	11	18	10	18
ENSMUSG00000024069	chr17	Slc30a6	0.24653135	0.235385554	0.297418723	2.796308019	0.041722255	0	122	82	88	90	80	111	151	111	102	129
ENSMUSG00000051980	chr16	Casr	-0.537781	0.235631211	0.297702206	0.893670579	0.190110382	0	27	14	21	67	30	6	19	19	39	30
ENSMUSG00000048814	chr1	Lonrf2	-0.431409	0.235658256	0.297709462	0.221016318	0.081863085	0	19	18	9	25	19	11	13	18	11	19
ENSMUSG00000094685	chr7	Gm5900	-0.8765902	0.235834856	0.297905635	2.826393499	0.617866824	0	160	127	144	138	99	383	9	9	13	23
ENSMUSG00000094483	chr11	Purb	-0.1959038	0.235865439	0.297917341	5.978914125	0.031592411	0	1047	912	884	1264	922	905	1265	960	698	964
ENSMUSG00000001334	chr4	Fndc5	-0.3144352	0.235894947	0.297927686	6.349122506	0.082999422	0	618	1451	1355	2542	943	1327	832	1546	1137	1026
ENSMUSG00000020832	chr11	Eral1	-0.1743177	0.235977032	0.298004427	4.566143537	0.022965104	0	366	402	371	431	290	370	368	333	376	358
ENSMUSG00000080836	chr5	Gm6444	0.34277589	0.236101311	0.298134435	1.548870885	0.071271616	0	36	48	32	34	32	61	33	41	70	50
ENSMUSG00000021130	chr12	Galnt16	0.19469809	0.23665483	0.298806388	3.682288064	0.026640741	0	156	181	166	203	174	259	208	238	176	227
ENSMUSG00000057842	chr13	Zfp595	-0.3379863	0.236742309	0.298889838	0.923437724	0.053992826	0	24	29	35	33	26	26	29	21	26	26
ENSMUSG00000001924	chrX	Uba1	0.19571615	0.236827481	0.298916362	7.404953194	0.032399316	0	2100	1992	1866	3401	2526	3505	3046	2922	2272	3073
ENSMUSG00000020163	chr10	Uqcr11	0.19321322	0.236792984	0.298916362	8.190292926	0.031725825	0	3906	4165	4140	5088	3064	6089	4242	4878	5350	4864
ENSMUSG00000094870	chr13	Zfp131	-0.2520453	0.23682487	0.298916362	3.389356176	0.046979397	0	173	160	180	186	137	95	188	132	182	169
ENSMUSG00000025086	chr19	Trub1	-0.2299831	0.236957419	0.299053358	2.894045145	0.036036904	0	118	128	109	141	93	108	124	119	79	119
ENSMUSG00000005124	chr15	Wisp1	0.31869527	0.237184678	0.299287574	3.188689025	0.078705561	0	157	84	135	155	70	219	237	154	79	134
ENSMUSG00000032834	chr10	Pwp2	0.19659508	0.237185831	0.299287574	4.088367097	0.028993608	0	201	194	208	324	252	371	329	260	277	241
ENSMUSG00000027011	chr2	Ube2e3	0.16851171	0.237359444	0.299452572	4.517751535	0.021423015	0	339	276	275	422	297	415	414	364	332	448
ENSMUSG00000028899	chr4	Taf12	0.1637915	0.237354961	0.299452572	4.901979012	0.020713513	0	437	399	373	503	383	557	538	451	556	465
ENSMUSG00000050730	chr9	Arhgap42	-0.2323835	0.237389424	0.299463362	2.646138005	0.033820549	0	107	90	93	124	82	107	80	98	90	85
ENSMUSG00000023805	chr17	Synj2	-0.2198943	0.237512	0.299590949	4.738085545	0.038428497	0	318	365	347	742	406	395	407	452	397	339
ENSMUSG00000001995	chr8	Sipa1l2	-0.2232704	0.237555275	0.299591456	3.780309186	0.037920789	0	175	218	207	262	228	295	195	218	133	192
ENSMUSG00000053460	chr6	Ggcx	0.22842869	0.237538237	0.299591456	3.532933748	0.038709826	0	156	142	123	225	148	192	208	264	148	189
ENSMUSG00000048120	chr19	Entpd1	0.18843811	0.238045305	0.300182367	4.162961349	0.026420042	0	252	197	237	317	240	411	295	230	277	349
ENSMUSG00000005907	chr5	Pex1	-0.229561	0.238146599	0.30025592	2.560242319	0.033818077	0	85	87	92	129	75	91	84	77	79	104
ENSMUSG00000027940	chr3	Tpm3	0.87941914	0.238129988	0.30025592	7.107378229	0.636634085	0	185	303	222	7758	200	5477	2532	2025	3261	1492
ENSMUSG00000014503	chr18	Pkd2l2	-0.4771495	0.238181845	0.300273269	0.407071097	0.132012925	0	16	30	16	27	16	4	19	14	25	19
ENSMUSG00000021607	chr13	Mrpl36	0.17837822	0.238343004	0.300422243	4.906834534	0.025140331	0	496	393	410	497	299	559	571	457	531	472
ENSMUSG00000028932	chr5	Psmc2	0.17671584	0.238326115	0.300422243	6.793020261	0.026304529	0	1693	1488	1258	1989	1372	2338	1991	1590	1953	1763
ENSMUSG00000049891	chr8	Gm7984	-0.4405135	0.238884073	0.301077085	0.151047825	0.08396289	0	26	11	13	19	16	11	14	11	19	13
ENSMUSG00000043719	chr9	Col6a6	0.26295183	0.239043022	0.301247318	5.281968984	0.057621032	0	459	459	480	538	659	618	528	683	475	1157
ENSMUSG00000071567	chr14	A830039N20Rik	-0.2949311	0.23906225	0.301247318	2.457125866	0.061122597	0	66	67	96	138	79	111	73	85	74	51
ENSMUSG00000048406	chr4	B330016D10Rik	-0.2713061	0.239316826	0.301540927	2.642156028	0.051387996	0	95	83	110	136	78	67	103	69	87	127
ENSMUSG00000032667	chr6	Pon2	0.18014365	0.239811132	0.302125481	5.978036922	0.027018525	0	907	874	891	1086	651	1298	1032	961	921	1275
ENSMUSG00000038346	chr6	Zfp384	0.16347601	0.23982399	0.302125481	4.548618803	0.020262257	0	334	290	274	435	314	478	403	349	375	411
ENSMUSG00000024067	chr17	Dpy30	0.17080052	0.239951186	0.302258475	4.538613024	0.022268698	0	331	340	285	393	275	462	436	319	418	370
ENSMUSG00000073563	chr18	Csnk1g3	-0.1773928	0.240067641	0.302377916	3.787920873	0.022200311	0	223	190	188	292	198	251	229	189	176	209
ENSMUSG00000061536	chr9	Sec22c	0.24050563	0.24008989	0.302378688	3.425783473	0.043040281	0	144	139	129	160	150	120	193	178	198	243
ENSMUSG00000041846	chr12	Smek1	-0.1787771	0.240585333	0.302975366	4.317233061	0.024269382	0	298	287	280	399	308	309	339	235	346	289
ENSMUSG00000078546	chr17	2210404O09Rik	0.467562	0.240610734	0.302980054	-0.033827931	0.093270653	0	11	17	5	13	7	24	18	10	13	16
ENSMUSG00000009035	chr15	Tmem184b	-0.1982803	0.240713064	0.303081603	5.425478602	0.032716015	0	616	549	677	828	735	855	733	604	439	656
ENSMUSG00000043801	chr17	Oaz1-ps	0.17193535	0.240751687	0.303102926	5.917044725	0.024515928	0	965	792	785	915	755	1270	972	888	989	1122
ENSMUSG00000025357	chr10	Dgka	-0.1935151	0.240962875	0.303341483	3.478926954	0.026321393	0	182	169	155	211	161	172	177	121	175	198
ENSMUSG00000021905	chr14	Dph3	-0.1679487	0.241039773	0.303410958	5.514769053	0.023079561	0	803	722	647	858	575	793	717	594	718	692
ENSMUSG00000031367	chrX	Ap1s2	-0.1657827	0.241251843	0.303650554	5.046296416	0.021776759	0	540	484	472	711	412	511	545	411	526	544
ENSMUSG00000052293	chr13	Taf9	-0.1988289	0.241469664	0.303897345	4.787137591	0.031929429	0	533	427	397	485	347	363	455	308	507	453
ENSMUSG00000002308	chr17	Cd320	0.18475835	0.241550807	0.303972094	3.875117175	0.024929678	0	225	177	171	235	206	302	226	232	268	236
ENSMUSG00000023026	chr15	Dip2b	0.17848086	0.241832831	0.304299599	4.018556105	0.023465379	0	232	205	220	283	188	321	321	253	223	282
ENSMUSG00000027281	chr2	Slx4ip	-0.2964371	0.242159539	0.304683266	1.747102489	0.055089115	0	53	55	44	54	58	44	57	32	59	45

ENSMUSG00000052854	chrX	Nrk	0.33299014	0.242372166	0.304923341	2.551435762	0.082739463	0	69	51	74	101	84	104	58	105	75	181
ENSMUSG00000025216	chr19	Lbx1	-0.1849539	0.242573983	0.305149773	5.615670283	0.02845214	0	740	744	673	1085	674	623	726	757	714	899
ENSMUSG00000033430	chr8	Terf2ip	-0.174297	0.242993694	0.305650245	4.187319449	0.022729947	0	281	241	269	362	280	286	247	277	276	299
ENSMUSG00000050947	chr3	Amigo1	-0.2099956	0.243109607	0.305768527	5.814506015	0.037495217	0	913	819	799	923	995	636	769	801	973	1040
ENSMUSG00000058192	chr9	Zfp846	-0.3465396	0.243230915	0.305893573	1.267002369	0.070387837	0	46	45	22	53	27	27	38	32	39	27
ENSMUSG00000063849	chr9	Ppcdc	0.2199519	0.243611674	0.306344858	2.799500938	0.032276731	0	106	94	90	101	78	131	118	97	131	124
ENSMUSG00000033450	chr17	Tagap	0.44337398	0.243699096	0.306425662	0.912981855	0.123774065	0	28	19	20	24	19	75	32	17	20	25
ENSMUSG00000040034	chr10	Nup43	0.25424781	0.243719781	0.306425662	2.420334561	0.042294654	0	79	63	68	69	73	110	98	71	105	81
ENSMUSG00000031379	chrX	Pir	0.32759512	0.243766414	0.306456724	1.611779627	0.067012079	0	43	50	38	36	25	71	45	50	61	39
ENSMUSG00000027956	chr3	Tmem144	-0.3305738	0.243869116	0.306558262	1.326760532	0.067533084	0	29	32	28	51	58	38	36	30	31	38
ENSMUSG00000021904	chr14	Sema3g	-0.2567396	0.243935042	0.306613557	3.756533501	0.05266961	0	167	166	176	354	241	309	145	199	141	212
ENSMUSG00000032656	chr18	March3	-0.3665677	0.243992561	0.306658276	1.196120835	0.086135325	0	36	38	30	58	23	54	39	19	21	24
ENSMUSG00000047613	chr4	A430005L14Rik	0.19856155	0.24426632	0.30697474	3.870435862	0.029533692	0	216	179	196	216	194	313	297	183	266	213
ENSMUSG00000008958	chr3	Vps72	-0.1584403	0.24436956	0.307076872	4.854008986	0.019863534	0	468	411	392	578	425	551	451	390	382	461
ENSMUSG00000022579	chr15	Gpihbp1	0.23142175	0.244484282	0.307193412	5.017059436	0.045020747	0	372	472	464	550	354	913	369	588	445	553
ENSMUSG00000022538	chr16	Lsg1	-0.1825371	0.244677795	0.307408923	3.850237417	0.024391865	0	252	200	201	297	191	204	255	194	202	239
ENSMUSG00000016382	chrX	Pls3	-0.1688555	0.245030503	0.30779672	4.919933899	0.022870209	0	433	479	417	696	383	507	498	422	385	514
ENSMUSG00000048616	chr11	Nog	0.34716681	0.245025643	0.30779672	1.978700275	0.083780931	0	44	42	62	60	41	137	65	48	54	51
ENSMUSG00000053841	chr4	Txlna	0.16865767	0.245130753	0.307894977	4.949202098	0.022845457	0	422	380	397	533	429	725	518	441	486	509
ENSMUSG00000096173	chr15	Gm3150	-0.3381453	0.245356356	0.30815065	0.835919804	0.05495915	0	24	32	29	31	22	24	28	18	25	25
ENSMUSG00000097571	chrX	Jpx	-0.3927804	0.245522952	0.308332175	0.324935787	0.069989089	0	15	15	17	27	22	20	11	13	14	22
ENSMUSG00000056427	chr11	Slit3	-0.2497962	0.245602037	0.30840378	3.353004636	0.048521723	0	112	131	156	200	214	215	147	105	147	147
ENSMUSG00000045414	chr9	1190002N15Rik	-0.2636066	0.245658208	0.308446601	3.344616116	0.053328209	0	181	171	138	226	110	87	203	140	151	158
ENSMUSG00000020893	chr11	Per1	-0.4619815	0.245845139	0.308653581	5.082653198	0.185906461	0	345	486	644	650	751	1367	264	149	355	296
ENSMUSG00000028540	chr4	Dph2	0.30658519	0.245873143	0.308661011	1.967171617	0.06590699	0	41	50	53	74	36	90	99	52	43	61
ENSMUSG00000046070	chr17	Igfals	-0.3598442	0.246099073	0.30891689	1.399395845	0.081502328	0	39	51	37	45	38	20	41	49	26	42
ENSMUSG00000056724	chr9	Nbeal2	0.23769144	0.246200133	0.30901599	2.512412026	0.036973098	0	65	72	81	98	66	123	92	76	91	114
ENSMUSG00000028706	chr4	Nsun4	-0.1846584	0.246400291	0.309239445	4.638812112	0.027282315	0	375	354	373	546	334	346	317	386	425	408
ENSMUSG00000041769	chr7	Ppp2r2d	-0.1610778	0.24664818	0.309522758	4.911089377	0.020888389	0	489	392	444	584	453	520	486	385	478	446
ENSMUSG00000025575	chr11	Cant1	0.18737404	0.246751157	0.309624185	4.480290174	0.027937752	0	356	303	268	352	268	570	383	298	319	383
ENSMUSG00000024045	chr17	Akap8	-0.1656434	0.24684486	0.309708727	4.834282944	0.022059282	0	390	410	407	640	412	544	425	363	421	445
ENSMUSG00000036188	chr12	Ankmy2	0.19450101	0.246862852	0.309708727	3.479858531	0.02768063	0	172	156	124	177	138	205	233	180	179	164
ENSMUSG00000034321	chr19	Exosc1	0.22455305	0.247106347	0.309958563	3.191935513	0.037251593	0	137	87	93	173	135	201	181	123	138	156
ENSMUSG00000044017	chr5	Gpr133	0.25953073	0.247102388	0.309958563	3.570609531	0.053149128	0	97	151	173	193	178	288	214	238	153	155
ENSMUSG00000022754	chr16	Tmem45a	0.25573596	0.247229234	0.310084876	2.435017354	0.043598927	0	80	82	56	69	69	97	116	92	78	86
ENSMUSG00000017718	chr11	Afmid	-0.2902338	0.247268436	0.310106215	2.734050516	0.062469451	0	139	105	88	96	103	65	76	110	97	127
ENSMUSG00000059343	chr4	Aldoart1	-0.2873255	0.247408749	0.310254345	2.315403651	0.060412969	0	77	67	76	67	104	70	65	77	53	92
ENSMUSG00000031495	chr8	Cd209d	-0.5533846	0.247457298	0.310287385	0.204403045	0.204227005	0	9	28	16	17	20	37	10	7	11	5
ENSMUSG00000040389	chr3	Wdr47	-0.2428505	0.248047779	0.310999521	2.424824932	0.038305909	0	87	84	75	100	78	69	90	63	72	99
ENSMUSG00000078317	chrX	F8a	0.21618892	0.248069738	0.310999521	3.615587758	0.035983918	0	205	157	160	157	150	219	185	241	163	254
ENSMUSG00000037254	chr2	Itih2	0.37758629	0.248194686	0.311100353	0.860648325	0.079464749	0	30	17	17	17	27	29	35	38	23	30
ENSMUSG00000058922	chr9	Gm10052	0.34233212	0.24817968	0.311100353	1.858149127	0.082333169	0	46	55	29	50	49	64	96	71	51	36
ENSMUSG00000027132	chr2	Katnbl1	0.28718797	0.248709082	0.311717167	2.351805428	0.059787659	0	59	71	49	91	66	72	142	66	82	85
ENSMUSG00000051978	chr8	Erich1	-0.3843302	0.248984559	0.31203445	0.651436696	0.079823331	0	29	28	23	25	17	11	23	17	24	27
ENSMUSG00000008200	chr2	Fnbp4	-0.1856998	0.249101963	0.312153595	3.805332915	0.02639998	0	268	205	182	244	200	271	232	163	190	211
ENSMUSG00000021400	chr13	Wrnip1	0.19192079	0.249197193	0.312244931	3.39568793	0.026193673	0	129	150	138	175	131	201	189	135	184	200
ENSMUSG00000028243	chr4	Ubxn2b	-0.3402459	0.249296702	0.312341614	1.252276605	0.069475861	0	23	40	36	48	41	30	49	26	30	28
ENSMUSG00000023000	chr15	Dhh	-0.4083047	0.249895209	0.313063413	0.466516856	0.083199565	0	16	14	19	34	25	27	14	15	11	22
ENSMUSG00000022956	chr16	Atp5o	0.17804888	0.250053105	0.313233145	9.16974085	0.02860817	0	7853	7825	7025	11173	6789	11061	8821	9952	9367	10681
ENSMUSG00000086370	chrX	Ftx	-0.4002365	0.250158821	0.313337487	0.731764117	0.093938227	0	25	21	17	35	33	31	10	18	18	32
ENSMUSG00000031673	chr8	Cdh11	0.35606967	0.250252104	0.31342624	2.681488035	0.10240357	0	107	64	83	103	56	138	151	61	48	190
ENSMUSG00000047261	chr16	Gap43	0.43268993	0.250308312	0.313468545	0.284166856	0.108350603	0	11	9	6	25	19	29	17	19	24	13
ENSMUSG00000061411	chr2	Nol4l	0.32736982	0.250485943	0.313662892	1.550137617	0.069319028	0	27	24	40	60	36	40	63	48	40	63
ENSMUSG00000051278	chr3	Zgrf1	-0.3689486	0.250598848	0.31377616	0.421843802	0.069403855	0	21	23	18	22	18	20	26	16	10	15
ENSMUSG00000020496	chr11	Rnf187	0.17257904	0.250698745	0.313845008	6.674100627	0.026373941	0	1398	1242	1250	1771	1493	1811	1629	1682	1695	2000
ENSMUSG00000031097	chr7	Tnni2	-0.1809156	0.250681933	0.313845008	13.08026328	0.029722583	0	153977	125559	122015	153355	129474	130221	132223	112692	143799	143200
ENSMUSG00000046275	chr11	Tusc5	-0.5418447	0.250850741	0.314007161	1.564616174	0.236063907	0	18	110	40	24	51	33	30	60	16	49
ENSMUSG00000001017	chr3	Chtop	-0.1671391	0.251034855	0.314209488	6.740477997	0.024751685	0	1766	1431	1465	2233	1583	1776	1816	1499	1465	1676
ENSMUSG00000018167	chr11	Stard3	0.2080391	0.251196543	0.31438371	4.213280007	0.035234738	0	252	287	250	302	184	500	336	242	268	288
ENSMUSG00000033486	chr2	Catsper2	-0.3609507	0.251275079	0.314453841	1.249025721	0.086269402	0	31	47	28	56	29	61	24	28	25	25
ENSMUSG00000029840	chr6	Mtpn	0.1953887	0.251461519	0.314658984	5.447003212	0.033154576	0	581	527	542	866	539	876	1000	488	656	812
ENSMUSG00000028331	chr4	5830415F09Rik	0.3586718	0.251517468	0.314700817	1.549862616	0.090547035	0	23	31	40	56	34	59	66	31	70	31
ENSMUSG00000037465	chr15	Klf10	-0.2529086	0.25218545	0.315508356	4.58699827	0.0557794	0	291	424	519	285	366	343	469	295	275	408
ENSMUSG00000038690	chr5	Atp5j2	0.19043367	0.252247164	0.315557319	8.495463366	0.032959626	0	5346	5227	5005	5958	3617	6706	5471	5748	7155	6235
ENSMUSG00000000148	chr5	Brat1	0.19943371	0.252748498	0.316156181	3.244489549	0.029255674	0	130	123	103	170	126	178	150	175	129	184

ENSMUSG00000038936	chr1	Sccpdh	-0.1802807	0.252978157	0.316415136	5.997746319	0.028703505	0	1185	1023	901	1032	882	968	866	968	1028	1032
ENSMUSG00000021681	chr13	Aggf1	-0.1700518	0.253129693	0.31657634	4.701610412	0.023865136	0	416	362	404	554	324	438	428	296	377	463
ENSMUSG00000044149	chrX	Nkrf	0.28515174	0.25319002	0.316623453	1.511830135	0.048088719	0	40	38	33	43	29	44	55	36	57	52
ENSMUSG00000014873	chr2	Surf2	-0.2025288	0.253293257	0.316724216	3.248285314	0.03061482	0	174	157	113	167	137	135	152	118	137	171
ENSMUSG00000038861	chr3	Pi4kb	0.15872329	0.253371028	0.316793119	4.864909246	0.020664177	0	373	392	402	481	390	554	473	454	524	493
ENSMUSG00000020780	chr11	Srp68	-0.1739431	0.253671337	0.317140228	6.458258777	0.026994751	0	1388	1174	1131	1895	1405	1303	1456	1220	1329	1422
ENSMUSG00000033961	chr7	Zfp446	-0.2907666	0.253912783	0.31741369	1.580548115	0.055857576	0	62	47	42	44	39	42	47	28	50	44
ENSMUSG00000020811	chr11	Wscd1	0.32047196	0.254135108	0.317663203	1.506272753	0.063831712	0	28	45	36	36	33	38	61	40	42	65
ENSMUSG00000052105	chr17	Mtcl1	-0.303417	0.254342253	0.317893698	2.602706126	0.070294033	0	76	84	78	164	97	94	86	128	61	62
ENSMUSG00000034235	chr14	Usp54	-0.2433022	0.254469173	0.31802389	2.512950094	0.042981864	0	92	81	85	106	87	120	85	52	86	79
ENSMUSG00000029134	chr5	Plb1	-0.3493854	0.254607173	0.318167904	1.241266089	0.078346424	0	41	43	38	46	20	52	23	25	36	26
ENSMUSG00000073062	chrX	Zxdb	-0.4141246	0.254745727	0.318312587	0.311755786	0.090790638	0	21	15	25	21	13	23	19	14	6	17
ENSMUSG00000068923	chr3	Syt11	0.21278904	0.255242899	0.318905306	2.921397207	0.031973223	0	118	89	83	123	102	144	118	126	110	156
ENSMUSG00000047676	chr3	Rpsa-ps10	-0.688251	0.255266893	0.318906775	6.343239884	0.425540504	0	1609	1390	1296	1695	1451	4406	320	259	285	203
ENSMUSG00000018661	chr11	Cog1	0.16248437	0.255586008	0.319262996	4.331964219	0.021034822	0	305	253	228	353	274	378	341	318	302	391
ENSMUSG00000028669	chr4	Pithd1	0.15899528	0.255597715	0.319262996	4.868194708	0.021154007	0	399	410	348	543	361	496	549	409	519	534
ENSMUSG00000057156	chr14	Homez	-0.2580436	0.255733367	0.319403891	2.190709283	0.046055081	0	77	69	66	104	49	69	66	67	47	82
ENSMUSG00000027984	chr3	Hadh	-0.2025651	0.256005549	0.319715266	7.774355106	0.037746905	0	2768	3893	3323	5103	2565	3753	2685	3579	3081	3478
ENSMUSG00000070476	chr2	Fam217b	-0.2387087	0.256129269	0.319841195	2.413852702	0.039281256	0	77	83	67	115	81	111	75	64	70	73
ENSMUSG00000023328	chr5	Ache	0.25352712	0.256341555	0.320077689	5.98094459	0.058447874	0	955	832	872	750	814	601	1459	1087	1031	1374
ENSMUSG00000000915	chr5	Hip1r	-0.2842682	0.25762097	0.321646478	3.0212424	0.066083171	0	112	103	106	231	118	206	82	95	122	90
ENSMUSG00000075704	chr16	Txnrd2	0.16840659	0.257649434	0.321653282	4.303736632	0.023162398	0	287	269	225	353	250	385	329	337	353	288
ENSMUSG00000025170	chr11	Rab40b	-0.2535729	0.257847742	0.3218721	4.463840478	0.056703825	0	508	328	341	348	248	221	294	311	296	506
ENSMUSG00000042379	chr13	Esm1	-0.4128628	0.257920612	0.321934311	0.988050062	0.113507357	0	36	41	27	31	23	27	25	28	40	9
ENSMUSG00000020189	chr10	Osbpl8	0.25767687	0.25812834	0.322164823	4.487039372	0.058772176	0	251	272	286	449	272	420	576	163	378	473
ENSMUSG00000019578	chr17	Ubxn6	0.16723847	0.25830197	0.322352739	5.628122992	0.024816703	0	721	712	598	865	582	1058	805	688	892	837
ENSMUSG00000024542	chr18	Cep192	0.30309557	0.25839741	0.322443054	2.227710643	0.066709164	0	67	61	67	44	59	75	106	53	100	77
ENSMUSG00000031171	chrX	Ftsj1	-0.1886061	0.258911286	0.323055454	3.701455925	0.027751508	0	251	171	198	236	168	199	207	195	204	175
ENSMUSG00000052125	chr12	F730043M19Rik	0.44240059	0.25905845	0.323210221	0.166390474	0.093865036	0	20	7	15	9	11	18	15	19	23	18
ENSMUSG00000031916	chr8	Cog8	-0.1649134	0.259091845	0.323223032	6.028042032	0.024511513	0	1120	979	944	1234	865	974	1115	863	1022	1038
ENSMUSG00000018822	chr19	Sfrp5	-0.2957614	0.259261418	0.32340571	2.998908708	0.07386114	0	97	87	171	166	124	195	104	100	62	126
ENSMUSG00000060600	chr11	Eno3	-0.2258302	0.259356485	0.323495425	12.73173741	0.047975342	0	112891	96797	91500	136959	110019	64072	105764	95220	102853	140617
ENSMUSG00000095687	chr17	Rnaset2a	-0.291729	0.259754523	0.323962986	3.298640581	0.073138964	0	170	147	145	195	142	310	113	101	103	104
ENSMUSG00000079557	chr17	March2	-0.1668477	0.259813412	0.324007518	6.439883227	0.025446751	0	1435	1322	1230	1664	1198	1346	1217	1250	1430	1408
ENSMUSG00000002661	chr17	Alkbh7	0.18284259	0.259860612	0.324037465	3.886353776	0.027199426	0	207	186	201	274	162	239	250	288	247	240
ENSMUSG00000065124	chr2	Snora65	0.42360371	0.259896014	0.324052698	0.738878173	0.117864734	0	22	25	9	28	15	35	37	17	41	14
ENSMUSG00000044894	chr11	Uqcrq	0.18899663	0.26005798	0.324225721	8.460439743	0.033547696	0	4849	4977	5106	6138	3535	6994	5238	5782	6858	5695
ENSMUSG00000030352	chr6	Tspan9	-0.2252886	0.26015801	0.324321501	5.746513873	0.046490846	0	653	603	754	1376	978	943	796	964	575	749
ENSMUSG00000001663	chr10	Gstt1	0.23047935	0.260273771	0.324436874	3.044949501	0.040521064	0	115	115	87	100	133	153	137	134	161	129
ENSMUSG00000020092	chr10	Pald1	-0.1740458	0.260634035	0.324856976	4.157848022	0.024744725	0	269	297	271	331	232	313	233	287	235	292
ENSMUSG00000049670	chr19	Morn4	0.35385637	0.260706688	0.324918555	1.747999095	0.09274225	0	46	36	17	49	63	68	42	69	52	64
ENSMUSG00000049904	chr11	Tmem17	0.29545612	0.260745129	0.324937487	1.309502482	0.053540427	0	45	31	24	32	25	43	45	43	39	41
ENSMUSG00000087408	chr8	Cers1	-0.2418217	0.261251767	0.325539826	4.812663336	0.052729578	0	475	383	368	549	487	229	475	413	358	605
ENSMUSG00000020549	chr11	Elac2	0.15960749	0.261952745	0.326355105	4.69473153	0.021656288	0	340	331	318	480	354	462	503	435	397	422
ENSMUSG00000074340	chr3	Ovgp1	0.37294681	0.261937259	0.326355105	0.813982462	0.079119768	0	22	16	26	22	19	28	22	20	40	40
ENSMUSG00000032194	chr9	Kank2	-0.1803482	0.261984679	0.326365797	5.545793652	0.029417721	0	720	618	631	935	793	762	605	802	598	790
ENSMUSG00000041460	chr6	Cacna2d4	0.55836334	0.262201108	0.3266063	1.377649796	0.25961781	0	28	41	41	26	11	10	24	41	67	95
ENSMUSG00000032298	chr9	Neil1	0.22247861	0.262282089	0.326678057	2.869244384	0.038241461	0	123	96	80	115	81	108	132	124	143	120
ENSMUSG00000029199	chr5	Lias	0.17716277	0.262348843	0.326732083	5.556309405	0.028523596	0	693	670	612	812	508	680	790	760	861	956
ENSMUSG00000055675	chr8	Kbtbd11	0.26292609	0.262409501	0.326778507	1.953529927	0.046226681	0	46	53	48	49	55	67	57	72	66	70
ENSMUSG00000019518	chr5	Ap4m1	-0.2985207	0.262528556	0.326897639	2.20432492	0.068167113	0	90	98	69	60	48	52	75	57	77	66
ENSMUSG00000016349	chr2	Eef1a2	-0.2172976	0.26334159	0.327880807	10.48088671	0.04513423	0	20426	19359	18427	32947	24464	17377	21585	22611	16378	29641
ENSMUSG00000056014	chr5	A430033K04Rik	0.36562684	0.263393019	0.327915627	1.304261656	0.093680153	0	37	42	24	25	23	29	41	59	32	52
ENSMUSG00000029229	chr5	Chic2	0.18372452	0.26367871	0.328242064	3.464825018	0.025905426	0	149	148	154	184	127	239	208	152	157	199
ENSMUSG00000029661	chr6	Col1a2	0.22539367	0.263756687	0.328309891	11.14039136	0.048654903	0	42483	28000	31115	27350	24604	47720	40495	40139	25494	45979
ENSMUSG00000078786	chr7	BC024978	-0.2110632	0.263866041	0.328416759	2.74677991	0.032012893	0	125	93	90	120	99	100	103	85	100	111
ENSMUSG00000040990	chrX	Sh3kbp1	0.20288111	0.264133901	0.328720872	5.521484577	0.037891472	0	670	735	634	663	456	788	955	531	941	796
ENSMUSG00000030718	chr7	Ppme1	0.15550534	0.26419221	0.328764164	4.988332422	0.021029669	0	409	417	401	571	437	613	546	526	447	595
ENSMUSG00000017264	chr4	Exosc10	0.16692096	0.264862674	0.329569153	4.465948206	0.023943557	0	290	277	238	452	304	416	424	335	376	349
ENSMUSG00000041215	chr16	Yeats2	-0.1990407	0.264929863	0.32962341	3.146783277	0.030386919	0	117	148	129	164	136	128	130	110	139	157
ENSMUSG00000040269	chr3	Mrps28	0.16001798	0.265021796	0.32970844	5.818380619	0.023465491	0	816	790	739	963	663	1163	997	872	981	847
ENSMUSG00000028948	chr4	Nol9	-0.1846724	0.265116286	0.329796637	3.900791565	0.028285113	0	204	191	231	299	250	242	276	179	229	209
ENSMUSG00000087993	chr10	Mir1982	0.34423971	0.265284046	0.329975955	1.489219121	0.082900065	0	52	28	39	34	22	81	34	41	43	48
ENSMUSG00000036046	chr15	5031439G07Rik	-0.1792804	0.265404899	0.3300969	7.109921771	0.030549102	0	2186	2133	2000	2573	2023	2039	2328	1580	2535	2079
ENSMUSG00000015341	chr8	Golga7	0.16453017	0.265557271	0.330257022	5.209332994	0.024256984	0	573	492	477	638	421	679	704	554	495	766

ENSMUSG00000014668	chr5	Chfr	-0.1786613	0.265611758	0.330279502	4.24235287	0.027273554	0	322	301	312	343	210	348	323	230	286	260
ENSMUSG00000026335	chr1	Pam	0.16229639	0.26562261	0.330279502	6.030189003	0.024435641	0	1003	848	833	1186	748	1337	1119	1068	934	1188
ENSMUSG00000083899	chr11	Gm12346	0.37303649	0.265857509	0.330542171	1.21108543	0.099948026	0	21	24	24	38	35	41	56	26	57	21
ENSMUSG00000027221	chr2	Chst1	0.33774278	0.265957291	0.330636817	1.946118493	0.087842697	0	29	69	46	49	49	98	45	61	46	93
ENSMUSG00000002103	chr2	Acp2	0.16703374	0.26614661	0.330842749	5.092199279	0.024790235	0	556	463	464	500	393	681	671	438	555	609
ENSMUSG00000038759	chr6	Nup205	0.19512257	0.266442657	0.331143285	3.867305248	0.031973591	0	182	208	192	260	167	285	331	185	262	203
ENSMUSG00000060671	chr3	Atp8b2	-0.1730455	0.266459458	0.331143285	4.277340036	0.025805358	0	296	254	339	340	285	364	310	221	286	308
ENSMUSG00000063972	chr2	Nr6a1	-0.3051761	0.266412289	0.331143285	1.228675352	0.059236565	0	32	34	26	40	50	41	33	28	27	34
ENSMUSG00000061607	chr17	Mdc1	0.2221305	0.266914635	0.331649977	2.987955335	0.038309031	0	105	101	84	130	117	139	178	103	149	118
ENSMUSG00000092356	chr2	Gm20532	0.19296332	0.266899528	0.331649977	3.889215089	0.031451802	0	196	228	203	268	133	325	239	254	201	266
ENSMUSG00000031787	chr8	Katnb1	-0.1839176	0.266968485	0.331668849	3.304233876	0.025917044	0	148	136	139	201	152	156	155	145	155	133
ENSMUSG00000043415	chr2	Otud1	-0.4909305	0.266977286	0.331668849	4.95765689	0.22898399	0	285	574	1105	448	209	752	802	140	201	280
ENSMUSG00000054381	chr7	Zfp747	-0.2834193	0.267011538	0.331681918	1.453873793	0.053880387	0	44	44	40	44	41	55	45	24	30	41
ENSMUSG00000056383	chr7	AI987944	-0.3424474	0.267764685	0.332587916	2.67684271	0.100753184	0	123	93	99	123	86	27	109	108	90	110
ENSMUSG00000038299	chr18	Wdr36	0.17090354	0.267880356	0.332702022	4.545867739	0.02553021	0	278	307	303	425	320	404	499	375	378	351
ENSMUSG00000040488	chr7	Ltbp4	-0.2167487	0.268800456	0.333815103	7.378039085	0.045547829	0	2206	2274	2471	3840	2642	2822	2227	3093	1516	2887
ENSMUSG00000026142	chr1	Rhbdd1	-0.1746427	0.269262805	0.33435957	3.549803872	0.024437089	0	204	163	161	205	181	182	188	149	165	207
ENSMUSG00000002012	chrX	Pnck	-0.2120074	0.269437567	0.334546858	3.867019499	0.03945315	0	298	245	144	214	248	266	194	198	209	231
ENSMUSG00000042787	chr9	Exog	0.28155471	0.269656675	0.33478917	1.825213864	0.053978283	0	47	36	44	48	53	68	61	44	78	55
ENSMUSG00000021661	chr13	Ankra2	-0.1764921	0.269698867	0.33481181	3.5751842	0.024623425	0	190	179	180	222	162	186	179	141	203	196
ENSMUSG00000033735	chr6	Spr	-0.1625909	0.270437773	0.335699291	5.06199675	0.023910793	0	507	503	448	687	489	567	607	475	508	407
ENSMUSG00000001105	chr11	Ift20	0.18042388	0.270529614	0.335775473	4.131302214	0.027967443	0	276	243	214	263	216	367	283	278	339	241
ENSMUSG00000025207	chr19	Sema4g	-0.4219046	0.270547195	0.335775473	-0.053735661	0.099246349	0	7	17	12	21	15	21	11	11	7	9
ENSMUSG00000030785	chr7	Cox6a2	0.17485822	0.270647813	0.335870523	9.389580696	0.030099801	0	9084	8280	7964	12979	9049	14497	11218	11710	10027	10746
ENSMUSG00000018405	chr11	Mrm1	0.21246986	0.270742055	0.335957646	3.14461895	0.036586499	0	105	107	103	182	112	211	161	120	155	122
ENSMUSG00000047420	chr6	Fam180a	-0.5027286	0.27079113	0.335958885	0.240566846	0.182475427	0	30	17	20	22	4	31	16	6	8	12
ENSMUSG00000078815	chr7	Cacng6	-0.1872073	0.27078767	0.335958885	7.195072579	0.034117002	0	2866	2204	2080	2554	1907	1793	2294	2215	2317	2485
ENSMUSG00000097413	chr18	A830052D11Rik	0.29494984	0.270826422	0.335972846	2.104346215	0.067146505	0	73	45	45	57	58	52	86	55	101	79
ENSMUSG00000047496	chr1	Rnf152	-0.3734694	0.27108464	0.336263329	1.207032385	0.102790474	0	55	54	27	24	22	28	36	32	31	28
ENSMUSG00000029657	chr5	Hsph1	-0.1970665	0.271824812	0.337121623	5.979014758	0.037308536	0	1178	811	786	1286	984	952	1204	1016	901	693
ENSMUSG00000040725	chr7	Hnrnpul1	-0.1585319	0.271804563	0.337121623	5.940212731	0.023810447	0	913	836	875	1222	981	983	1013	894	834	1008
ENSMUSG00000052040	chr7	Klf13	-0.1990385	0.272023793	0.337338467	5.438515465	0.037777696	0	514	598	633	995	730	988	563	523	559	695
ENSMUSG00000021124	chr12	Vti1b	0.16613541	0.272125502	0.337404721	5.631550128	0.026017322	0	733	631	602	868	651	1041	840	701	948	750
ENSMUSG00000041645	chr12	Ddx24	-0.1590734	0.272124822	0.337404721	5.720532246	0.023773131	0	828	739	678	1096	821	805	906	715	802	830
ENSMUSG00000038866	chr1	Zcchc2	0.19524095	0.272176668	0.337438226	3.305445112	0.03013906	0	139	115	124	180	124	179	180	115	176	205
ENSMUSG00000090626	chr9	Tex9	0.37483409	0.272459656	0.337759105	1.026477089	0.094578829	0	24	33	30	14	20	31	33	30	49	32
ENSMUSG00000019302	chr11	Atp6v0a1	0.17842447	0.272625005	0.337919438	6.69591931	0.030968938	0	1660	1333	1145	1593	1491	1972	1949	1450	1441	2228
ENSMUSG00000063445	chr16	Nmral1	0.24019072	0.272637349	0.337919438	2.380023098	0.042024467	0	67	63	71	85	61	102	118	60	83	89
ENSMUSG00000031310	chrX	Zmym3	-0.1616208	0.272787671	0.338052027	3.95440778	0.021441355	0	249	212	212	317	227	271	241	223	200	254
ENSMUSG00000039826	chr2	Trub2	0.15197196	0.272792699	0.338052027	4.874303605	0.020707573	0	456	401	387	501	323	549	488	493	478	500
ENSMUSG00000031145	chrX	Prickle3	-0.1922289	0.272827952	0.338065738	3.496308006	0.03074515	0	167	185	167	203	163	205	178	154	113	207
ENSMUSG00000026107	chr1	Nabp1	-0.2502637	0.273286252	0.338603604	4.566435164	0.059210821	0	482	394	306	415	312	209	335	246	448	511
ENSMUSG00000038239	chr7	Hrc	-0.2093205	0.274341397	0.339880805	10.1142137	0.043839713	0	17597	16081	14104	23013	18215	12294	15938	17191	14579	23494
ENSMUSG00000063568	chr6	Jazf1	-0.3845142	0.275235655	0.340958475	0.157483715	0.063019232	0	20	18	14	20	12	12	15	15	12	16
ENSMUSG00000056666	chr6	Retsat	-0.2026668	0.27568107	0.341479981	4.790226939	0.038418239	0	376	408	326	695	429	303	480	461	378	452
ENSMUSG00000082045	chr11	Gm11585	0.45987118	0.276136153	0.34201337	-0.130724857	0.122794971	0	19	10	6	8	6	16	18	11	21	8
ENSMUSG00000025147	chr7	Mob2	-0.1676667	0.276452021	0.342334759	5.641814343	0.027039318	0	962	729	739	846	643	820	710	701	815	780
ENSMUSG00000027340	chr2	Slc23a2	-0.1804906	0.27646912	0.342334759	3.856308322	0.028150729	0	206	234	206	304	194	234	288	160	196	228
ENSMUSG00000056978	chr7	Hamp2	1.52517553	0.276454571	0.342334759	1.450943272	2.00979102	0	21	42	6	23	6	340	0	0	0	0
ENSMUSG00000027338	chr2	Prnd	-0.4924318	0.276655895	0.342535683	3.363093569	0.234326369	0	258	278	190	105	41	72	134	222	45	208
ENSMUSG00000028677	chr4	Rnf220	0.15962653	0.277112479	0.3430706	5.78004574	0.024598184	0	773	679	649	1037	749	1243	924	846	854	883
ENSMUSG00000022545	chr16	Ercc4	0.19248976	0.277383431	0.343284409	3.037657573	0.028955326	0	108	92	99	164	105	152	138	120	133	163
ENSMUSG00000032184	chr9	Lysmd2	-0.218894	0.2773376	0.343284409	3.184410351	0.04092154	0	151	159	125	173	113	221	118	106	109	132
ENSMUSG00000036395	chr9	Glb1l2	-0.4850119	0.277379286	0.343284409	1.561484432	0.207041742	0	25	93	41	30	51	14	42	54	21	60
ENSMUSG00000048878	chr11	Hexim1	0.17350094	0.277374192	0.343284409	4.94767429	0.028323947	0	413	398	368	564	420	561	468	559	391	684
ENSMUSG00000073147	chr5	5031425E22Rik	-0.2135376	0.277452118	0.343339011	3.445296153	0.040509882	0	204	207	151	166	129	211	151	114	143	204
ENSMUSG00000064179	chr7	Tnnt1	0.99038153	0.278030894	0.34402477	7.062898444	0.937293462	0	72	264	152	7417	146	8451	499	3509	1737	678
ENSMUSG00000068606	chr18	Gm4841	0.4372148	0.278082291	0.344057905	5.267099125	0.190430966	0	977	548	489	195	171	420	408	680	856	1205
ENSMUSG00000073940	chr7	Hbb-bt	0.38116073	0.278228877	0.344208797	4.384650748	0.142988657	0	298	282	352	295	113	603	147	203	279	732
ENSMUSG00000032349	chr9	Elovl5	0.16120675	0.278482415	0.344491966	4.332676336	0.022886967	0	262	288	238	357	268	391	385	288	274	399
ENSMUSG00000049657	chr4	Zbtb5	-0.220417	0.278777569	0.344826561	2.835175601	0.037918079	0	125	90	92	165	98	101	90	104	102	131
ENSMUSG00000020122	chr11	Egfr	-0.184493	0.279421926	0.345592995	4.172154281	0.031325967	0	237	256	240	320	357	331	305	218	237	287
ENSMUSG00000028960	chr4	Ube4b	0.17003463	0.279537963	0.345705917	5.209073735	0.02771851	0	539	476	428	616	527	566	688	638	505	786
ENSMUSG00000098792	chr11	Gm27401	0.48373925	0.279853801	0.346065893	-0.038462585	0.12348702	0	9	7	15	12	9	26	24	14	11	6
ENSMUSG00000044148	chrX	1810030O07Rik	0.1695739	0.279917287	0.346113775	4.117000662	0.025492632	0	258	245	193	300	217	384	280	275	305	248

ENSMUSG00000017837	chr11	Nkiras2	0.16062527	0.280028817	0.34622105	4.903443642	0.024177309	0	485	421	362	477	353	453	552	472	494	592
ENSMUSG00000029623	chr5	Pdap1	0.16252967	0.280189564	0.34638915	6.135501522	0.026219819	0	1096	884	806	1275	907	1134	1372	1122	1216	1192
ENSMUSG00000021819	chr14	Zswim8	-0.1657421	0.280804363	0.347087802	5.169544305	0.026428149	0	498	480	496	755	609	711	505	489	456	619
ENSMUSG00000040875	chr9	Osbpl10	-0.2752649	0.28078325	0.347087802	1.903412464	0.055605834	0	69	63	46	64	53	39	49	55	50	73
ENSMUSG00000053414	chr16	Hunk	0.46335017	0.281077095	0.347394188	1.291280513	0.179731793	0	29	17	17	36	46	13	50	44	30	81
ENSMUSG00000029198	chr5	Grpel1	-0.1553932	0.281145042	0.34744744	6.264727268	0.02401198	0	1191	1188	1181	1476	1002	1287	1122	1124	1096	1306
ENSMUSG00000032033	chr9	Barx2	-0.5443286	0.281217613	0.347506398	2.891601603	0.287782307	0	48	112	165	289	57	240	25	122	70	34
ENSMUSG00000042688	chr9	Mapk6	-0.1722209	0.281409589	0.347712882	5.18634678	0.028560526	0	547	510	505	742	572	473	689	590	494	525
ENSMUSG00000026254	chr1	Eif4e2	-0.1515208	0.281463501	0.347748753	6.014072381	0.022612391	0	992	936	906	1332	922	1107	1035	939	949	963
ENSMUSG00000037211	chr3	Spry1	0.16780697	0.281518281	0.347785689	4.863504284	0.026753935	0	373	418	384	528	340	430	531	486	422	631
ENSMUSG00000029381	chr5	Shroom3	0.49042684	0.281798592	0.348101213	0.516893955	0.181244366	0	12	17	22	14	14	53	15	31	6	21
ENSMUSG00000097915	chr15	A330009N23Rik	0.41264125	0.281964969	0.348275953	0.335845421	0.105480457	0	16	23	8	20	6	32	14	18	22	20
ENSMUSG00000041607	chr18	Mbp	-0.2442273	0.282106751	0.348420285	5.156510364	0.059793774	0	302	466	769	785	546	702	680	391	413	503
ENSMUSG00000057054	chr11	Inca1	-0.3233905	0.282182417	0.348482943	1.429772989	0.080153318	0	43	48	42	54	27	64	37	33	34	20
ENSMUSG00000039529	chr18	Atp8b1	0.25978127	0.282403239	0.348724834	2.407986914	0.053044843	0	73	85	58	75	59	146	85	60	84	92
ENSMUSG00000021771	chr14	Vdac2	0.16598505	0.28276009	0.3491038	8.251210177	0.028404764	0	4187	3932	3634	6024	3842	6243	5399	5113	4172	5468
ENSMUSG00000030084	chr6	Plxna1	-0.1909974	0.282752142	0.3491038	5.704140532	0.036602586	0	946	766	731	836	824	682	896	646	636	1120
ENSMUSG00000036983	chr17	Tfb1m	-0.2234019	0.282894872	0.349239355	2.953136401	0.042640023	0	138	141	98	124	108	88	144	110	117	112
ENSMUSG00000034793	chr11	G6pc3	0.16254208	0.283141652	0.349513137	5.280496651	0.025546807	0	628	487	425	593	583	781	737	571	590	678
ENSMUSG00000017802	chr11	Fam134c	-0.1557841	0.283240746	0.34960458	6.043563494	0.024203262	0	1129	986	916	1201	939	1003	1026	882	1052	1120
ENSMUSG00000038593	chr5	Tctn1	-0.2963334	0.2833465	0.349704228	1.279008973	0.060381429	0	49	40	33	44	24	40	37	28	22	43
ENSMUSG00000031949	chr8	Adat1	0.27268149	0.283590693	0.349974705	1.335922793	0.045480231	0	34	32	23	40	33	55	46	36	38	40
ENSMUSG00000066491	chr12	Gm6265	0.3348803	0.283765182	0.350159119	0.818982668	0.074151787	0	28	24	17	25	14	39	18	26	36	30
ENSMUSG00000040028	chr8	Elavl1	0.15881764	0.283895495	0.350288995	4.915865188	0.023950792	0	440	423	360	501	394	492	660	455	441	545
ENSMUSG00000021868	chr14	Ppif	-0.1737125	0.283960166	0.350337861	5.671700013	0.029998616	0	679	829	767	1117	657	866	771	871	721	658
ENSMUSG00000032384	chr9	Csnk1g1	-0.1849582	0.284030837	0.35039412	3.0927124	0.027446278	0	140	120	126	167	116	146	153	101	114	132
ENSMUSG00000028195	chr3	Cyr61	0.40803039	0.285003477	0.351562983	5.213271149	0.170559113	0	361	570	468	567	395	1637	1087	258	338	265
ENSMUSG00000063235	chr2	Ptpmt1	0.15288658	0.28549827	0.352142249	4.982265211	0.022372928	0	477	414	440	530	363	506	543	494	547	611
ENSMUSG00000064193	chr2	Gm4735	-0.4140694	0.285591085	0.352225645	3.148787308	0.171581898	0	169	147	129	145	148	364	60	80	52	83
ENSMUSG00000027865	chr3	Gdap2	-0.215477	0.285753226	0.35239452	2.788204363	0.038503679	0	97	98	114	146	91	131	117	81	106	80
ENSMUSG00000056665	chr15	Them6	-0.2066094	0.285893209	0.352536041	2.859116645	0.034430141	0	103	109	110	142	106	92	113	118	96	119
ENSMUSG00000002833	chr17	Hdgfrp2	0.1468551	0.286038586	0.352684189	4.900148152	0.02046889	0	386	399	356	579	399	594	527	484	452	500
ENSMUSG00000025171	chr19	Ubtd1	-0.1556319	0.286368717	0.353060091	4.430625253	0.022670707	0	337	339	349	350	297	398	359	273	290	346
ENSMUSG00000042520	chr3	Ubap2l	-0.162198	0.286561624	0.353266759	6.218498687	0.026826828	0	1148	1028	947	1535	1223	1215	1244	1021	946	1324
ENSMUSG00000065954	chr8	Tacc1	0.16403325	0.286648736	0.353342983	4.830790594	0.025880646	0	340	398	337	559	374	675	503	392	402	498
ENSMUSG00000072653	chr6	Zfp783	0.35319053	0.287049341	0.35380559	1.786195335	0.103136126	0	58	54	44	21	35	47	55	67	48	86
ENSMUSG00000019916	chr10	P4ha1	-0.1623307	0.287237765	0.354006614	5.603225687	0.026546448	0	920	732	648	797	705	886	868	629	663	710
ENSMUSG00000025280	chr14	Polr3a	-0.1908012	0.287542572	0.354319783	3.230215803	0.0306891	0	126	152	139	191	130	123	173	126	137	146
ENSMUSG00000036214	chr17	Znrd1as	-0.1684117	0.287540515	0.354319783	3.382479427	0.02355725	0	178	147	148	186	153	181	159	135	160	159
ENSMUSG00000025651	chr9	Uqcrc1	-0.1800173	0.287804226	0.354610938	9.803728729	0.034284697	0	12318	14470	14680	19251	10512	13985	11861	14022	12927	15441
ENSMUSG00000027562	chr3	Car2	-0.2875792	0.287987986	0.354794852	2.909810931	0.075498262	0	78	105	104	250	90	78	98	94	128	142
ENSMUSG00000028869	chr4	Gnl2	-0.1583843	0.288004265	0.354794852	4.8520355	0.024025047	0	452	384	370	617	455	407	479	383	474	472
ENSMUSG00000047221	chr5	Fam185a	-0.1805445	0.288088875	0.354867805	3.469973245	0.027783019	0	187	173	162	228	124	182	150	165	177	163
ENSMUSG00000030347	chr6	D6Wsu163e	-0.2304667	0.288273047	0.355063374	2.780210238	0.044670025	0	118	97	91	149	93	94	145	70	107	92
ENSMUSG00000074166	chr7	AW146154	-0.2645337	0.288424629	0.355218771	1.814837587	0.051395076	0	68	45	58	71	36	48	55	39	54	56
ENSMUSG00000012705	chr8	Retn	0.63197804	0.28850524	0.355286741	2.401596616	0.397744872	0	17	131	40	13	85	19	75	141	72	197
ENSMUSG00000014907	chr8	Naf1	-0.2441168	0.288533668	0.355290445	2.464924626	0.049897179	0	90	75	70	125	81	102	90	48	98	68
ENSMUSG00000097343	chr7	9030407P20Rik	0.38437841	0.288605126	0.355347128	1.026045759	0.111807962	0	26	34	28	26	9	25	24	35	42	49
ENSMUSG00000003070	chr10	Efna2	0.39925485	0.288673305	0.355368459	0.394819801	0.109752717	0	21	11	7	17	20	40	18	21	17	15
ENSMUSG00000056310	chr5	Tyw1	0.1711886	0.288669017	0.355368459	3.533673871	0.025231951	0	151	162	142	199	150	203	188	168	229	201
ENSMUSG00000049295	chr14	Zfp219	0.18485789	0.288839785	0.355542085	4.169036584	0.032331619	0	222	223	255	331	220	429	242	316	233	341
ENSMUSG00000057378	chr2	Ryr3	0.37795766	0.288992967	0.355699314	0.920586623	0.106901688	0	25	19	25	20	24	26	20	52	22	41
ENSMUSG00000054252	chr5	Fgfr3	-0.3830636	0.289129344	0.355835832	0.923536996	0.116264455	0	15	25	27	38	44	45	20	27	15	20
ENSMUSG00000014748	chr6	Tex261	0.1533058	0.289178346	0.355864803	6.287746783	0.024183677	0	1073	1005	934	1380	1124	1467	1342	1297	1202	1403
ENSMUSG00000022672	chr16	Prkdc	-0.1872697	0.289270049	0.355946311	3.334373885	0.029881537	0	157	147	134	196	158	130	139	143	170	175
ENSMUSG00000102717	chr1	RP23-211F21.1	0.8685229	0.289421901	0.356101813	1.062237602	0.725545097	0	4	8	5	42	47	15	5	122	3	53
ENSMUSG00000079168	chr8	Cd209g	-0.7752768	0.289787393	0.356520124	0.592722667	0.561482056	0	33	25	20	15	34	73	3	6	6	1
ENSMUSG00000043284	chr11	Tmem11	0.14914183	0.290113583	0.356890013	5.397014672	0.022115641	0	637	561	596	676	494	775	735	670	690	738
ENSMUSG00000024135	chr17	Srbd1	0.22374884	0.290197054	0.356940184	2.177957205	0.03508592	0	66	58	51	69	58	86	85	61	75	81
ENSMUSG00000033576	chr15	Apol6	-0.3586559	0.290205446	0.356940184	3.973532817	0.131231989	0	96	306	249	555	149	282	152	329	203	136
ENSMUSG00000031534	chr8	Smim19	0.15574721	0.290291807	0.357014985	4.971699198	0.023764298	0	433	447	401	563	369	720	455	501	516	508
ENSMUSG00000035198	chr11	Tubg1	-0.163617	0.290447238	0.357174711	4.833772918	0.026124052	0	452	354	440	558	435	370	510	405	448	445
ENSMUSG00000028771	chr5	Ptpn12	-0.1880147	0.290490588	0.357196591	4.238109271	0.034074439	0	225	305	279	453	245	310	346	187	287	311
ENSMUSG00000032733	chr9	Snx33	0.21152081	0.290653419	0.357365373	3.004345309	0.037790026	0	113	98	120	120	92	187	112	141	107	148
ENSMUSG00000032477	chr9	Cdc25a	0.2335363	0.290697864	0.357388577	3.105257033	0.049279886	0	121	98	95	141	126	227	162	95	163	109

ENSMUSG00000082087	chr11	Gm12138	-0.3430838	0.291199327	0.357973594	0.829533425	0.074700949	0	34	28	20	36	21	13	29	23	28	25
ENSMUSG00000030231	chr6	Plekha5	-0.2746207	0.291504247	0.358316918	2.344284614	0.065437768	0	59	95	73	95	81	54	66	52	83	111
ENSMUSG00000050567	chr11	Maml1	-0.1906318	0.291712574	0.358541459	3.572173362	0.033182348	0	155	184	197	241	160	212	205	156	118	214
ENSMUSG00000028385	chr4	Snx30	0.23814257	0.291772837	0.358583993	3.261111337	0.053096843	0	151	131	99	151	116	246	172	78	186	166
ENSMUSG00000032126	chr9	Hmbs	0.16931834	0.291860298	0.358659942	4.503665803	0.027617616	0	309	332	326	366	247	502	407	317	411	321
ENSMUSG00000086863	chr6	Gm15543	0.39281898	0.291888139	0.358662619	2.641402287	0.154933966	0	33	128	87	114	35	71	69	164	141	108
ENSMUSG00000029433	chr5	Diablo	0.1522061	0.292315151	0.35915574	5.640477589	0.023690104	0	757	658	648	886	580	903	839	746	926	860
ENSMUSG00000027551	chr2	Zfp64	-0.2016882	0.292558862	0.35942358	2.884526088	0.034236873	0	139	111	110	125	93	122	115	79	114	124
ENSMUSG00000028252	chr4	Ccnc	-0.2117207	0.292600405	0.359443022	3.068158608	0.039450804	0	141	147	126	151	96	102	167	109	121	125
ENSMUSG00000040043	chr10	Rbms2	-0.144812	0.292744825	0.359582677	5.919069951	0.021566952	0	949	892	863	1154	874	1031	948	886	844	980
ENSMUSG00000040247	chr19	Tbc1d10c	0.24353422	0.292765546	0.359582677	2.424110122	0.050641856	0	92	67	75	81	43	78	103	83	99	99
ENSMUSG00000050043	chr2	Tmx2	-0.2072055	0.292910974	0.359729681	5.558820042	0.044770611	0	767	657	707	960	679	431	922	723	798	646
ENSMUSG00000026249	chr1	Serpine2	-0.1602124	0.292982343	0.359785716	6.327728683	0.026899658	0	1187	1162	1272	1710	1021	1295	1402	1197	1162	1122
ENSMUSG00000015377	chr15	Dennd6b	-0.1923418	0.293338962	0.360142806	3.287916942	0.032788448	0	152	136	136	179	162	166	130	146	172	118
ENSMUSG00000030199	chr6	Etv6	0.17242415	0.293350437	0.360142806	3.874061847	0.027636186	0	196	174	174	301	186	299	291	233	182	260
ENSMUSG00000038957	chr9	Edc3	0.16632061	0.293308158	0.360142806	4.028100301	0.02517095	0	221	226	208	256	222	353	277	232	222	325
ENSMUSG00000028626	chr4	Col9a2	-0.503176	0.293562011	0.360369773	-0.138055438	0.186893925	0	9	16	15	14	14	28	2	8	10	6
ENSMUSG00000029613	chr5	Eif2ak1	0.15971962	0.29358688	0.360369773	5.698214672	0.026352398	0	782	722	634	798	697	780	931	893	878	958
ENSMUSG00000090330	chr7	9130221H12Rik	0.24405465	0.293869218	0.360684658	2.582195485	0.05220653	0	55	74	65	115	93	125	93	113	72	117
ENSMUSG00000032024	chr9	Clmp	0.18388214	0.294052234	0.360877592	3.689051622	0.030411232	0	186	166	189	161	177	252	243	224	178	213
ENSMUSG00000020577	chr12	Tspan13	0.18734852	0.294233537	0.361068392	5.313972131	0.036407033	0	581	595	572	653	366	716	555	658	578	947
ENSMUSG00000027833	chr3	Shox2	0.29531953	0.294890677	0.361811263	1.777338933	0.070308595	0	48	50	31	42	48	37	63	60	55	80
ENSMUSG00000029103	chr5	Lrpap1	0.15716857	0.294887602	0.361811263	5.802759654	0.025606877	0	842	814	624	857	775	1160	1022	732	887	1029
ENSMUSG00000020486	chr11	Sept4	0.23440752	0.295059914	0.361987128	4.024086542	0.055335541	0	254	219	223	258	153	390	178	319	177	369
ENSMUSG00000028271	chr3	Gtf2b	0.19454673	0.295260912	0.362201923	3.776874954	0.036039173	0	194	186	176	256	140	315	272	139	250	220
ENSMUSG00000030002	chr6	Dusp11	-0.1421822	0.295518633	0.362486258	5.175691019	0.020258604	0	578	507	524	663	542	611	598	494	555	541
ENSMUSG00000076012	chr6	Mir705	0.33817692	0.296231015	0.363328184	1.043305009	0.092929141	0	18	26	18	54	15	41	34	29	24	49
ENSMUSG00000030120	chr6	Mlf2	0.16040474	0.296599134	0.36374723	7.876219117	0.027996042	0	3538	3057	2944	3817	3154	4742	3651	3653	3452	4836
ENSMUSG00000086429	chr6	Gt(ROSA)26Sor	-0.2871981	0.296624726	0.36374723	1.890635952	0.068357765	0	55	52	48	87	55	41	60	35	42	87
ENSMUSG00000022437	chr15	Samm50	0.16336943	0.29682768	0.363964174	7.42545292	0.029018793	0	2089	2234	2231	3530	2128	3202	2672	3072	2707	3141
ENSMUSG00000024112	chr17	Cacna1h	0.35096278	0.297035568	0.364123243	1.469344194	0.107020604	0	21	27	25	53	48	33	42	48	36	82
ENSMUSG00000044982	chr18	Sft2d3	-0.2710113	0.297026455	0.364123243	1.37830734	0.054446455	0	53	33	42	45	29	36	31	36	35	45
ENSMUSG00000086922	chr6	Gm13835	-0.1748627	0.29702403	0.364123243	4.289910848	0.030313975	0	377	290	252	328	286	407	266	219	321	289
ENSMUSG00000005474	chr5	Myl10	-0.4222016	0.29718019	0.364268579	1.708036208	0.169723175	0	18	64	50	109	35	88	35	32	46	21
ENSMUSG00000027363	chr2	Usp8	-0.1590356	0.297252857	0.364325698	4.598186964	0.02489557	0	364	325	321	544	361	371	413	291	340	452
ENSMUSG00000024099	chr17	Ndufv2	0.16708255	0.297337296	0.364397233	8.545129152	0.030625913	0	5215	5441	5038	6684	3968	7371	5831	5968	7071	5974
ENSMUSG00000051154	chr2	Commd3	0.16166331	0.297557158	0.364634708	5.957990746	0.027784476	0	1025	789	804	1048	712	960	1169	966	1155	1078
ENSMUSG00000037287	chr9	Tbcel	-0.1814648	0.297742512	0.364765896	4.49758999	0.033077161	0	387	384	292	428	294	263	400	331	284	437
ENSMUSG00000097658	chr11	Gm16755	0.69569163	0.297694125	0.364765896	-0.000840596	0.431249086	0	4	7	7	15	17	6	4	51	3	21
ENSMUSG00000098022	chr7	Zfp82	0.27899165	0.297734129	0.364765896	1.034637216	0.047448821	0	28	25	28	29	19	39	33	32	32	36
ENSMUSG00000002109	chr2	Ddb2	0.26730179	0.297817565	0.364822494	1.620968221	0.055477153	0	46	39	38	39	36	49	41	51	69	51
ENSMUSG00000041747	chr13	Utp15	0.20282553	0.297840917	0.364822494	2.787571102	0.034777957	0	85	86	81	118	100	144	143	89	107	113
ENSMUSG00000068732	chr3	Tmem167b	-0.1462744	0.298347071	0.365410451	4.643707519	0.020958406	0	387	376	348	463	373	379	396	335	364	456
ENSMUSG00000021024	chr12	Psma6	0.15536878	0.29843851	0.365490415	6.956157535	0.026195887	0	1958	1658	1504	2052	1584	2365	2075	1758	2368	2117
ENSMUSG00000034867	chr7	Ankrd27	0.15889106	0.298464946	0.365490763	3.841439256	0.023383211	0	187	190	162	284	187	275	240	215	257	238
ENSMUSG00000006462	chr2	A530013C23Rik	-0.2958559	0.298940109	0.366040561	1.723838756	0.075082422	0	45	52	37	68	60	71	28	30	44	63
ENSMUSG00000019850	chr10	Tnfaip3	0.20448764	0.298966836	0.366041218	3.289954422	0.039573814	0	150	89	131	205	104	195	196	118	149	193
ENSMUSG00000021360	chr13	Gcnt2	0.23883531	0.299165816	0.366252754	2.613873709	0.051094104	0	68	84	65	117	79	159	108	69	114	85
ENSMUSG00000062861	chr7	Zfp28	-0.2853236	0.299356331	0.366453891	1.92533577	0.068382248	0	63	60	74	61	41	59	72	55	52	32
ENSMUSG00000020389	chr11	Cdkl3	0.3410262	0.299456658	0.366544601	0.819468582	0.089391444	0	10	29	20	31	18	23	25	31	37	32
ENSMUSG00000020798	chr11	Spns3	-0.4445768	0.299672766	0.366777002	0.504868512	0.157486762	0	21	31	20	19	19	46	8	11	12	15
ENSMUSG00000028423	chr4	Nfx1	-0.1401834	0.299789803	0.366888116	5.052261045	0.019969214	0	550	509	458	581	480	623	520	444	447	548
ENSMUSG00000036073	chr4	Galt	-0.1901277	0.300046927	0.367170637	4.759055488	0.03753211	0	332	392	369	682	400	588	421	410	343	305
ENSMUSG00000103104	chr17	Riok2	-0.1760776	0.300192756	0.367316929	4.014621557	0.029990427	0	289	262	214	302	205	204	269	200	271	283
ENSMUSG00000030763	chr7	Lcmt1	0.14435813	0.300234509	0.367335858	4.647489061	0.020274855	0	379	317	329	398	338	498	444	361	413	429
ENSMUSG00000022000	chr14	Zc3h13	-0.1923525	0.300351675	0.367407348	3.978950264	0.03645601	0	232	201	212	387	231	211	269	210	178	328
ENSMUSG00000038807	chr11	Rap1gap2	-0.1790753	0.300398094	0.367407348	4.679615053	0.033069921	0	367	396	386	496	374	420	342	431	257	506
ENSMUSG00000039069	chr2	Mtg2	-0.1530039	0.300371171	0.367407348	3.903467654	0.02137895	0	254	212	202	282	217	244	230	198	241	235
ENSMUSG00000050192	chr3	Eif5a2	0.31336817	0.300384567	0.367407348	0.733442393	0.060889281	0	20	17	26	26	13	33	32	26	24	24
ENSMUSG00000047767	chr7	Atg16l2	-0.2496162	0.300469527	0.367462557	2.336131746	0.054121972	0	86	71	67	103	74	109	59	59	90	52
ENSMUSG00000043162	chr6	Pyurf	-0.1631234	0.300574143	0.367558336	5.424342496	0.028023784	0	745	654	671	793	512	557	729	648	643	706
ENSMUSG00000057093	chr7	C030039L03Rik	0.40916691	0.300718186	0.367702307	0.062597444	0.096804606	0	15	13	6	10	14	21	22	7	17	19
ENSMUSG00000041849	chr15	Card6	-0.275836	0.300872564	0.367858888	1.736143191	0.05937381	0	38	51	40	77	58	45	37	54	42	58
ENSMUSG00000020178	chr10	Adora2a	-0.3013588	0.301430105	0.368508322	1.637556052	0.074557415	0	53	61	44	60	29	68	35	41	25	52
ENSMUSG00000022678	chr16	Nde1	-0.1385764	0.302082934	0.369274126	4.999235088	0.019338782	0	536	451	440	635	439	547	495	476	467	492

ENSMUSG00000020015	chr10	Cdk17	-0.1824623	0.30220885	0.369331138	3.483524207	0.031190739	0	190	176	176	221	118	166	173	150	145	214
ENSMUSG00000029314	chr5	Agpat9	-0.2488656	0.302166478	0.369331138	2.555297889	0.056571453	0	87	102	70	116	92	149	83	74	65	64
ENSMUSG00000086158	chr9	Ccpg1os	-0.233672	0.302188231	0.369331138	2.136058201	0.044799007	0	76	84	53	80	52	85	61	60	56	60
ENSMUSG00000040746	chr11	Rnf167	-0.1645339	0.302356304	0.369479034	5.163409075	0.028677243	0	577	578	512	662	485	827	455	462	498	535
ENSMUSG00000030701	chr7	Plekhb1	0.18313943	0.302636346	0.369788912	5.049796911	0.035571341	0	412	372	401	542	566	468	552	492	601	744
ENSMUSG00000031639	chr8	Tlr3	0.24987741	0.302689474	0.369804823	1.762508242	0.047772181	0	42	50	42	57	32	75	51	55	44	66
ENSMUSG00000087578	chr6	Ccdc142os	0.32760925	0.302702288	0.369804823	0.559430494	0.06533165	0	23	20	16	14	15	27	24	28	20	23
ENSMUSG00000022234	chr15	Cct5	0.16471333	0.303765469	0.371071252	7.485807573	0.03036042	0	2813	2228	2133	2987	2441	2937	3495	2706	3481	2787
ENSMUSG00000020589	chr12	Fam49a	0.1941715	0.303858844	0.371152876	3.273499031	0.034465699	0	134	132	126	135	131	160	159	173	124	215
ENSMUSG00000039754	chr5	Alkbh4	0.22448009	0.304046525	0.371349666	2.395658188	0.042790522	0	58	55	63	101	78	112	92	68	93	89
ENSMUSG00000026816	chr2	Gtf3c5	0.15902789	0.304104422	0.371387924	3.854953681	0.023649208	0	198	211	156	236	208	270	247	219	252	248
ENSMUSG00000031770	chr8	Herpud1	-0.1549107	0.304202481	0.371475219	6.559303004	0.026506565	0	1588	1464	1321	1710	1310	1557	1401	1191	1669	1459
ENSMUSG00000014232	chr16	Cluap1	0.17699878	0.304345356	0.371617219	3.218906279	0.027333432	0	114	124	129	153	121	174	154	153	168	145
ENSMUSG00000001053	chr11	N4bp3	0.25730239	0.304423183	0.371647311	2.992575807	0.064974338	0	111	119	127	112	60	161	88	159	107	181
ENSMUSG00000097316	chr1	Gm10516	-0.2760884	0.304420975	0.371647311	1.651268763	0.062142068	0	60	45	51	53	37	32	52	33	43	63
ENSMUSG00000029591	chr5	Ung	-0.2017947	0.304950749	0.372258858	3.499838135	0.039402595	0	146	186	171	263	136	162	209	189	156	129
ENSMUSG00000073125	chrX	Xlr3b	-0.5358505	0.305120805	0.372433919	0.563956238	0.247793455	0	60	13	9	28	12	12	17	9	37	14
ENSMUSG00000035152	chr11	Ap2b1	0.14887547	0.305405973	0.372749444	5.752585807	0.023982282	0	742	678	622	1017	767	1132	989	760	825	942
ENSMUSG00000101941	chr9	Gm28979	-0.5363695	0.305458771	0.372781329	-0.134688167	0.223528519	0	17	6	23	12	11	1	19	14	6	12
ENSMUSG00000020677	chr11	Ddx52	0.16622486	0.305699552	0.373042603	4.156630721	0.027646659	0	310	236	237	293	172	317	349	264	304	296
ENSMUSG00000028187	chr3	Rpf1	0.16773487	0.305734625	0.373052831	3.636263331	0.026324067	0	179	172	148	212	155	253	251	184	207	171
ENSMUSG00000025176	chr19	Hoga1	0.36659443	0.305978382	0.373317666	0.441990097	0.084881716	0	17	22	14	12	14	23	15	25	18	32
ENSMUSG00000028076	chr3	Cd1d1	0.40109125	0.30639709	0.373795891	1.441389375	0.152483071	0	13	66	30	27	27	45	35	66	33	60
ENSMUSG00000023262	chr9	Acy1	0.21845586	0.306584689	0.373992111	2.945901201	0.046122448	0	97	97	81	154	99	210	148	96	115	105
ENSMUSG00000026121	chr1	Sema4c	0.2016543	0.306839606	0.374270407	3.757413176	0.040799701	0	188	170	219	200	146	278	252	258	137	249
ENSMUSG00000032018	chr9	Sc5d	-0.2457399	0.307514961	0.375061445	3.481216752	0.061580996	0	180	178	174	223	141	90	227	128	222	150
ENSMUSG00000049241	chr5	Hcar1	0.75844063	0.30798448	0.375601317	-0.10127837	0.533221189	0	1	27	5	2	8	4	7	37	7	26
ENSMUSG00000026189	chr1	Pecr	0.17281313	0.308525372	0.37622813	4.2582722	0.030938205	0	283	286	200	332	237	271	321	272	359	418
ENSMUSG00000038611	chr7	Phrf1	0.15783427	0.308611544	0.376300379	4.287438267	0.02506293	0	231	239	232	363	306	387	370	282	301	338
ENSMUSG00000000131	chr7	Xpo6	0.1618138	0.309280952	0.377050818	4.527694328	0.026845604	0	367	295	297	317	324	529	357	358	339	407
ENSMUSG00000030411	chr7	Nova2	-0.2692501	0.309278665	0.377050818	1.795033865	0.063484882	0	43	41	62	77	51	69	45	33	37	67
ENSMUSG00000029504	chr5	Ddx51	0.17642953	0.309641888	0.377424997	3.413639703	0.029286516	0	137	141	127	169	160	184	188	203	152	182
ENSMUSG00000041945	chr1	Mfsd9	0.42806063	0.309637211	0.377424997	0.571212345	0.148505421	0	20	22	25	9	8	40	33	21	10	25
ENSMUSG00000062070	chrX	Pgk1	-0.1931905	0.309812916	0.377600533	9.986346517	0.043262401	0	17084	15719	14510	18419	14782	10632	15845	13253	15832	21395
ENSMUSG00000043542	chr3	Zc2hc1a	-0.2082733	0.310004526	0.377801121	2.681757765	0.039392727	0	87	103	91	137	88	113	96	74	71	127
ENSMUSG00000035390	chr7	Brsk1	0.33072228	0.310102315	0.377872375	0.864288074	0.08829352	0	20	28	19	29	16	42	16	38	21	37
ENSMUSG00000048280	chr13	Zfp738	-0.3036479	0.310117068	0.377872375	1.476011553	0.076189133	0	42	43	41	57	37	20	53	40	47	32
ENSMUSG00000022130	chr14	Tgds	0.19970893	0.310272371	0.377980134	2.735699555	0.034959926	0	100	83	90	114	68	136	108	96	127	104
ENSMUSG00000022377	chr15	Asap1	0.15723474	0.310243399	0.377980134	4.02763478	0.024381819	0	223	204	189	296	233	285	321	223	257	312
ENSMUSG00000034663	chr5	Bmp2k	-0.1806586	0.31028664	0.377980134	3.760612784	0.033086624	0	183	186	192	297	213	294	208	134	180	226
ENSMUSG00000032519	chr9	Slc25a38	-0.1786003	0.310771579	0.378537876	3.835271799	0.03205718	0	274	244	176	237	187	193	230	179	249	230
ENSMUSG00000031755	chr8	Bbs2	-0.2565993	0.311094685	0.378898416	2.044521787	0.057599718	0	58	57	62	100	52	56	43	49	61	89
ENSMUSG00000029916	chr6	Agk	-0.2064358	0.311318298	0.379137725	2.862801845	0.040246619	0	120	107	110	147	90	101	145	72	112	114
ENSMUSG00000096687	chr10	AA474331	0.23720774	0.311520181	0.379350532	2.006001904	0.04493281	0	57	57	48	52	50	66	67	58	62	91
ENSMUSG00000091898	chr14	Tnnc1	1.10150633	0.311862411	0.379734192	6.355041863	1.304330465	0	13	55	24	4630	31	6154	266	1872	833	334
ENSMUSG00000028455	chr4	Stoml2	0.15070784	0.312052868	0.379932998	5.781269491	0.025453134	0	667	760	751	1077	650	977	972	902	985	865
ENSMUSG00000000563	chr3	Atp5f1	-0.1597331	0.313238447	0.381343252	9.404195032	0.02996473	0	10406	10796	10800	13378	8070	10495	10170	9912	10934	10590
ENSMUSG00000036873	chr3	2410004B18Rik	-0.1565109	0.31330951	0.381372255	3.946719069	0.024377892	0	240	234	202	287	239	257	291	195	231	210
ENSMUSG00000060152	chr5	Pop5	0.14734094	0.313316846	0.381372255	4.335599022	0.022260021	0	283	255	253	360	272	333	372	329	367	314
ENSMUSG00000032688	chr18	Malt1	0.31215121	0.313589909	0.381636766	2.36519808	0.095760918	0	67	68	69	60	65	131	134	39	48	113
ENSMUSG00000033628	chr18	Pik3c3	-0.1484498	0.313602735	0.381636766	4.322189874	0.022493495	0	363	321	242	358	276	345	299	285	278	336
ENSMUSG00000100599	chr15	1700120C14Rik	0.15823391	0.313616074	0.381636766	4.728967755	0.026898432	0	419	336	306	458	347	540	428	350	547	412
ENSMUSG00000054302	chr12	Eapp	-0.1444274	0.313658397	0.381655037	4.215275487	0.020832214	0	300	288	263	363	236	330	290	233	292	291
ENSMUSG00000037762	chr10	Slc16a9	-0.2442591	0.314290571	0.382390965	2.296882281	0.054979173	0	69	81	66	84	85	61	62	71	56	108
ENSMUSG00000020964	chr12	Sel1l	-0.1507124	0.314394363	0.38248395	5.952751508	0.025777566	0	943	889	815	1262	961	1023	1106	855	753	1067
ENSMUSG00000022185	chr14	Acin1	0.15355409	0.314676766	0.382794193	5.758957609	0.026693035	0	654	636	696	1098	762	1172	853	864	844	931
ENSMUSG00000031808	chr8	Slc27a1	0.20967108	0.314875779	0.383002949	5.601339393	0.050634602	0	339	787	663	1006	580	840	795	696	914	996
ENSMUSG00000028274	chr4	Rngtt	-0.1688524	0.315163498	0.383252854	3.484871769	0.026953757	0	170	169	151	242	149	168	183	182	136	181
ENSMUSG00000039990	chr7	Edrf1	-0.1639086	0.315137276	0.383252854	3.623360658	0.026229112	0	201	166	152	242	203	230	185	161	197	169
ENSMUSG00000059363	chr19	Fxn	0.148708	0.315135471	0.383252854	3.994372929	0.021673699	0	230	216	207	270	196	316	248	228	268	302
ENSMUSG00000085218	chr2	BB218582	-0.328741	0.315474471	0.383597634	1.664689758	0.098812557	0	30	50	60	86	31	52	47	24	63	35
ENSMUSG00000056228	chr8	Cars2	-0.1632658	0.315720055	0.383862852	4.044616695	0.027248276	0	274	257	224	322	218	316	236	237	274	199
ENSMUSG00000004788	chr12	Eif2b2	0.15002582	0.315772117	0.383892755	5.425320233	0.025155692	0	663	489	519	726	632	745	700	686	696	852
ENSMUSG00000022941	chr16	Ripply3	0.34421188	0.315849815	0.383953816	0.904828895	0.092352351	0	30	21	21	23	19	32	22	41	17	47
ENSMUSG00000090035	chr10	Galnt4	0.20630061	0.315877627	0.383954229	2.490472005	0.035738889	0	71	71	64	102	74	118	108	69	87	102

ENSMUSG00000022441	chr15	Efcab6	-0.4283531	0.316173754	0.384280754	1.833805129	0.189910544	0	40	84	70	45	50	16	66	90	29	33
ENSMUSG00000034278	chr2	Dnajc17	0.20399579	0.316637699	0.384811172	2.613306814	0.037775888	0	92	66	73	108	78	107	98	120	86	111
ENSMUSG00000071757	chr15	Zhx2	-0.1788897	0.317096367	0.385335086	5.2465732	0.036304033	0	622	523	488	771	605	561	524	699	388	717
ENSMUSG00000010755	chr7	Cars	-0.1456643	0.317414124	0.385639921	5.305113786	0.023631053	0	645	579	477	770	625	661	627	516	652	602
ENSMUSG00000039263	chr2	Npepl1	-0.150863	0.317429998	0.385639921	6.201632823	0.026306702	0	1064	1065	1051	1577	1047	1415	1037	1030	1180	1035
ENSMUSG00000084159	chr4	Gm12696	0.42917946	0.317402739	0.385639921	-0.183249234	0.101612734	0	8	5	14	15	6	12	17	14	18	9
ENSMUSG00000029098	chr5	Acox3	0.14698394	0.317508384	0.385701623	4.646120658	0.023052277	0	345	379	279	444	322	476	417	362	371	522
ENSMUSG00000028809	chr4	Srrm1	0.15952672	0.317698229	0.385898701	5.697727906	0.029199838	0	653	585	623	1033	781	1114	845	844	710	972
ENSMUSG00000021884	chr14	Hacl1	-0.2198226	0.318059387	0.386303814	2.83023064	0.047884028	0	102	128	95	136	100	87	86	83	125	145
ENSMUSG00000040855	chrX	Reps2	-0.2250014	0.318341386	0.386612308	2.269084372	0.045257264	0	69	96	73	82	56	79	66	60	63	87
ENSMUSG00000050973	chr7	Gdpgp1	-0.3365031	0.318368707	0.386612308	0.651249792	0.080463423	0	30	13	22	37	20	15	30	19	19	21
ENSMUSG00000039461	chr9	Tcta	-0.1444208	0.318846809	0.387159253	4.832388876	0.022724126	0	485	467	412	501	353	514	411	381	473	424
ENSMUSG00000032842	chr17	Abcc10	0.24870101	0.318987075	0.387262862	1.964682755	0.052919578	0	43	59	40	58	56	85	49	72	57	72
ENSMUSG00000103041	chr3	RP24-372I24.4	-0.349806	0.318987555	0.387262862	0.736048077	0.105353294	0	38	28	23	16	22	31	14	13	22	32
ENSMUSG00000083179	chr4	Gm12693	0.27393881	0.319024438	0.387273998	1.428534284	0.056921286	0	23	29	34	47	40	53	48	40	51	37
ENSMUSG00000027722	chr3	Spata5	0.1894673	0.319100326	0.387332478	2.959823372	0.034812636	0	99	99	101	145	92	134	104	149	135	140
ENSMUSG00000036442	chr8	Thap11	0.14048264	0.319283342	0.387520971	4.702092404	0.021180765	0	387	357	293	457	349	488	402	399	432	500
ENSMUSG00000039033	chr2	Tasp1	-0.2019866	0.319336911	0.387552333	2.494070129	0.037759295	0	93	88	76	100	82	115	78	64	88	76
ENSMUSG00000041779	chr1	Tram2	0.16666908	0.319379853	0.387570793	3.773051031	0.027940531	0	189	194	162	217	187	289	225	236	164	261
ENSMUSG00000032599	chr9	Ip6k2	0.17484073	0.319925172	0.388198837	3.67583491	0.030952681	0	217	189	170	178	128	282	211	203	195	209
ENSMUSG00000030823	chr7	9130019O22Rik	-0.2672511	0.32006981	0.388340626	1.423946409	0.057275192	0	50	41	37	39	40	36	54	35	28	37
ENSMUSG00000029076	chr4	Sdf4	0.14291943	0.320344712	0.388606691	6.771668571	0.024128108	0	1542	1532	1312	1857	1492	2234	1839	1634	1714	1972
ENSMUSG00000079071	chr2	Gm14085	-0.9723087	0.320330221	0.388606691	1.496375624	1.033834216	0	55	41	43	91	41	155	4	1	0	2
ENSMUSG00000020770	chr11	Unk	0.17797827	0.320496144	0.388696436	3.09812916	0.029998801	0	138	106	94	157	100	189	135	123	130	159
ENSMUSG00000035172	chr11	Plekhh3	-0.1521302	0.320502127	0.388696436	4.773989635	0.025419148	0	440	349	434	580	350	455	369	397	368	522
ENSMUSG00000052056	chr2	Zfp217	0.17685506	0.320461855	0.388696436	3.334006125	0.030852159	0	155	142	103	161	136	192	193	146	129	208
ENSMUSG00000037514	chr2	Pank2	0.1453016	0.321044115	0.389319961	4.559196776	0.022758138	0	324	305	307	432	299	450	348	335	447	433
ENSMUSG00000028102	chr3	Pex11b	-0.1417507	0.321265933	0.389515811	4.47578724	0.021359546	0	395	328	308	419	286	372	366	272	330	385
ENSMUSG00000029185	chr5	Fam114a1	0.14850059	0.321274634	0.389515811	4.371813742	0.023245331	0	334	264	295	316	241	398	385	305	356	325
ENSMUSG00000041444	chr9	Arhgap32	-0.2377723	0.32128923	0.389515811	2.442685027	0.054776204	0	96	85	63	104	82	85	68	79	49	119
ENSMUSG00000029106	chr5	Add1	-0.1453651	0.321681211	0.389957204	6.352062508	0.024938748	0	1221	1221	1168	1587	1198	1421	1107	1112	1293	1401
ENSMUSG00000050428	chr7	Fbxo46	0.24713838	0.321771499	0.390032825	1.968724036	0.053726699	0	45	48	44	60	60	99	55	65	48	71
ENSMUSG00000002228	chr3	Ppm1j	-0.1555957	0.321818795	0.390056324	5.550883724	0.027961417	0	759	731	676	883	628	609	688	649	826	821
ENSMUSG00000035354	chr7	Uvrag	0.16783693	0.321997311	0.39023885	3.497897763	0.027326778	0	151	154	151	172	152	199	175	155	217	219
ENSMUSG00000020000	chr10	Moxd1	-0.4247674	0.322283025	0.390514006	-0.091210003	0.106429433	0	9	10	20	21	10	16	17	9	9	6
ENSMUSG00000034566	chr11	Atp5h	0.169112	0.322305009	0.390514006	8.577018512	0.034804828	0	5076	5447	5157	7367	3982	9182	5583	6404	5894	6098
ENSMUSG00000073755	chr4	5730409E04Rik	-0.1578167	0.322308176	0.390514006	4.774170432	0.027872634	0	519	403	332	456	425	397	394	360	460	488
ENSMUSG00000021639	chr13	Gtf2h2	-0.1708672	0.322365645	0.390549779	3.623362225	0.029654526	0	230	183	160	225	167	166	193	156	223	196
ENSMUSG00000034684	chr9	Sema3f	0.27877951	0.322756879	0.390989871	3.431897342	0.088240319	0	93	121	124	267	131	396	131	155	128	165
ENSMUSG00000027894	chr3	Slc6a17	-0.436624	0.322967657	0.3912113	0.012876677	0.126237844	0	9	14	8	33	14	19	9	16	10	7
ENSMUSG00000021385	chr13	Ippk	-0.1901192	0.323344347	0.391633642	2.967206745	0.035178243	0	120	112	102	176	108	100	147	93	120	127
ENSMUSG00000026333	chr1	Gin1	-0.2501032	0.323390809	0.391655975	1.753624189	0.054796994	0	64	55	39	62	44	49	58	34	37	66
ENSMUSG00000071645	chr19	Tut1	0.18323982	0.323487735	0.391739415	3.231305559	0.0330758	0	139	99	106	187	123	192	163	140	120	195
ENSMUSG00000019810	chr10	Fuca2	-0.1469058	0.323845119	0.392138224	4.918941761	0.024406993	0	512	460	442	556	392	518	553	324	437	520
ENSMUSG00000048503	chr9	Tmem136	-0.3576773	0.324067044	0.392339881	1.122518925	0.114552203	0	38	41	36	47	12	24	17	35	40	29
ENSMUSG00000073791	chr4	Efcab7	0.3660205	0.324067801	0.392339881	0.165189252	0.074146763	0	9	13	14	13	15	15	25	18	17	16
ENSMUSG00000027435	chr2	Cd93	0.16535383	0.324464201	0.392785767	6.615490799	0.033002031	0	1216	1316	1440	1905	1056	2264	1913	1365	1288	1716
ENSMUSG00000062611	chr14	Rps3a2	0.31234613	0.324499842	0.392794889	4.255281807	0.115444017	0	266	258	241	316	185	880	252	208	266	166
ENSMUSG00000018848	chr11	Rars	0.16001764	0.324685113	0.392985116	5.947130424	0.030489888	0	1013	797	700	980	842	1031	1230	914	1204	911
ENSMUSG00000030787	chr7	Lyve1	0.40563793	0.324745908	0.393024663	2.739737424	0.186296099	0	95	40	64	121	103	310	140	37	83	63
ENSMUSG00000034121	chr11	Mks1	0.28000597	0.32492973	0.393213084	1.168401226	0.060757689	0	32	25	22	36	28	61	29	33	36	32
ENSMUSG00000027573	chr2	Gid8	-0.1368501	0.324982842	0.393243307	5.028830459	0.020940444	0	567	475	437	616	451	522	487	441	554	523
ENSMUSG00000020538	chr11	Srebf1	-0.1969838	0.325237823	0.39348371	5.17473834	0.046200126	0	451	571	538	697	601	816	442	533	311	671
ENSMUSG00000087440	chr3	4930577N17Rik	-0.3535083	0.325221553	0.39348371	0.177002876	0.089144471	0	16	17	14	19	18	20	11	8	9	25
ENSMUSG00000047193	chr9	Dync2h1	-0.230494	0.325666318	0.393968014	2.066866537	0.048781973	0	61	74	58	67	65	57	72	41	70	66
ENSMUSG00000022680	chr16	Pdxdc1	-0.1645991	0.325703929	0.39397941	5.458391596	0.0318216	0	721	645	651	907	553	506	702	644	700	803
ENSMUSG00000000805	chr11	Car4	-0.2790519	0.325916315	0.394202199	2.84689006	0.087284898	0	78	136	116	136	109	207	72	90	55	109
ENSMUSG00000047084	chr7	Ngrn	-0.1598401	0.325992775	0.39426056	4.793047197	0.02929247	0	462	447	406	538	327	644	377	365	370	394
ENSMUSG00000028688	chr4	Toe1	0.18742922	0.326037517	0.394280552	2.923647945	0.033501943	0	94	106	97	128	95	111	131	135	115	154
ENSMUSG00000019813	chr10	Cep57l1	-0.2706882	0.326350459	0.39459071	1.460441351	0.060140712	0	39	52	39	49	35	30	36	36	53	38
ENSMUSG00000073403	chr17	Gm10499	-0.9449127	0.326335968	0.39459071	1.637786925	1.021095656	0	94	26	53	44	71	171	1	6	4	0
ENSMUSG00000051113	chr7	Fam71e1	-0.3186866	0.326580843	0.394835109	0.50633271	0.07470872	0	27	25	20	21	14	31	15	15	16	18
ENSMUSG00000081476	chr2	Itpa-ps1	-0.341286	0.32683134	0.39510378	0.445873563	0.083315669	0	31	16	22	20	14	14	25	14	20	16
ENSMUSG00000029769	chr6	Ccdc136	0.19628978	0.327144618	0.395448294	3.026403222	0.039235531	0	98	96	109	170	91	193	105	131	138	135
ENSMUSG00000022378	chr15	Fam49b	-0.1483837	0.327593156	0.395956236	5.527644715	0.025961729	0	725	658	638	947	658	691	828	537	782	729

ENSMUSG00000097729	chr12	2310015A10Rik	-0.1497637	0.327793395	0.396163999	3.858214315	0.023157919	0	223	230	208	271	196	261	187	217	212	237
ENSMUSG00000040003	chr5	Magi2	-0.2922915	0.327873996	0.396227148	1.017828509	0.066472771	0	40	30	21	39	27	25	29	17	29	40
ENSMUSG00000000223	chrX	Drp2	-0.2278508	0.328015865	0.39636432	3.521035373	0.058086422	0	136	154	187	230	204	193	176	236	93	153
ENSMUSG00000035109	chr2	Shc4	-0.2930845	0.32806304	0.396387054	0.996190844	0.062412615	0	23	27	37	36	30	22	29	28	23	35
ENSMUSG00000027944	chr3	Hax1	0.14389113	0.328101266	0.396398971	4.797030993	0.02335769	0	421	387	365	477	315	530	541	355	501	454
ENSMUSG00000058126	chr14	Tpm3-rs7	0.76454548	0.328138856	0.396410118	4.431312959	0.696813076	0	210	212	216	396	173	2188	60	47	64	48
ENSMUSG00000027531	chr3	Impa1	0.15204268	0.3287799	0.397150206	4.259457322	0.02519182	0	295	267	229	305	246	352	410	272	323	281
ENSMUSG00000071359	chr10	Tbpl1	0.15839302	0.329255467	0.397690296	4.033627561	0.027299795	0	258	185	201	299	209	355	297	280	219	254
ENSMUSG00000028138	chr3	Adh5	-0.1512145	0.329587649	0.39805712	5.834796433	0.027530787	0	986	848	784	1056	798	724	947	785	943	989
ENSMUSG00000022365	chr15	Derl1	0.14262977	0.329841062	0.39831595	6.543989738	0.024903715	0	1440	1289	1143	1509	1215	1602	1728	1345	1528	1795
ENSMUSG00000024213	chr17	Nudt3	0.14115624	0.329858958	0.39831595	7.056065353	0.024644948	0	1900	1835	1701	2310	1695	2246	2311	2105	2371	2325
ENSMUSG00000052374	chr13	Actn2	0.29471019	0.330704862	0.399302907	10.05403117	0.109416473	0	6576	9861	11749	35869	11215	25251	14682	23836	15424	16207
ENSMUSG00000052605	chr7	Isoc2b	0.19868064	0.33084522	0.399437872	2.506099356	0.035981576	0	89	82	70	76	66	107	96	94	95	92
ENSMUSG00000025264	chrX	Tsr2	0.16721179	0.331237034	0.399876375	3.348685155	0.027825274	0	142	139	119	158	146	207	207	148	160	150
ENSMUSG00000024560	chr18	Cxxc1	-0.1460913	0.332032619	0.400802201	4.260134729	0.023733646	0	294	252	256	352	334	363	290	252	272	306
ENSMUSG00000006906	chr6	Stambp	0.16263622	0.332067574	0.400809777	3.39596786	0.026740663	0	149	161	143	169	109	210	177	167	172	172
ENSMUSG00000086534	chr17	Gm16758	0.49527878	0.332368947	0.401138894	-0.017689127	0.208392889	0	20	8	7	9	9	3	10	18	20	30
ENSMUSG00000000402	chrX	Egfl6	-0.3902325	0.332546373	0.401318376	1.749802257	0.169706595	0	118	47	38	45	26	81	48	18	29	59
ENSMUSG00000004610	chr7	Etfb	0.16796934	0.332798734	0.401588249	7.744981368	0.035738259	0	2555	2925	2688	4546	2544	4951	3123	3717	3651	3108
ENSMUSG00000082456	chr11	Gm11598	0.33980808	0.333347675	0.402215929	0.274251584	0.077111952	0	21	14	9	15	12	26	17	20	12	24
ENSMUSG00000018574	chr11	Acadvl	-0.1869841	0.333389295	0.402231422	8.376023831	0.044500818	0	3687	5192	4988	8946	4095	5684	4301	5291	5451	4522
ENSMUSG00000021497	chr13	Txndc15	-0.1466257	0.333500444	0.402296065	5.033776205	0.02544638	0	594	509	482	551	413	474	526	405	522	604
ENSMUSG00000084846	chr3	A730011C13Rik	0.4114386	0.333497433	0.402296065	0.151459749	0.13820724	0	21	15	7	9	10	38	11	11	15	18
ENSMUSG00000015839	chr2	Nfe2l2	-0.1477779	0.333559665	0.402332777	5.111663611	0.025951863	0	488	510	520	781	430	647	584	374	519	567
ENSMUSG00000002846	chr16	Timmdc1	-0.1553368	0.333700141	0.402445222	4.907187107	0.028313294	0	415	519	452	629	347	402	503	481	450	459
ENSMUSG00000057594	chr11	Arl16	0.22033352	0.33371048	0.402445222	2.306482901	0.046461494	0	86	56	73	66	49	88	99	69	84	84
ENSMUSG00000029455	chr5	Aldh2	-0.1622028	0.333876454	0.40261064	7.127373709	0.033239349	0	1625	2049	1882	3412	2176	2704	2094	1862	1954	2213
ENSMUSG00000067722	chr17	BC003965	-0.1406263	0.334021035	0.402750236	5.106956753	0.023435711	0	586	517	556	600	419	639	566	479	512	478
ENSMUSG00000028759	chr4	Hp1bp3	-0.1378697	0.335125375	0.404012097	6.237194337	0.023600089	0	1174	1122	1105	1526	985	1308	1211	1031	1018	1311
ENSMUSG00000076431	chr13	Sox4	-0.2702221	0.335121072	0.404012097	3.787251413	0.088264277	0	322	216	225	217	132	136	205	221	104	346
ENSMUSG00000031823	chr8	Zdhhc7	0.13271014	0.33527179	0.404153747	5.153006668	0.020703504	0	469	466	475	639	477	712	578	554	529	666
ENSMUSG00000040370	chr6	Lyrm5	-0.1403689	0.335508122	0.404403753	5.086169393	0.023244778	0	559	573	473	630	415	511	527	556	494	530
ENSMUSG00000032051	chr9	Fdx1	-0.1517369	0.335761574	0.40467435	4.540948554	0.026554665	0	297	385	354	510	285	428	364	355	329	317
ENSMUSG00000083863	chr2	Gm13341	-0.2930941	0.335953482	0.40487073	1.035334773	0.075261399	0	27	30	25	49	29	26	20	33	19	43
ENSMUSG00000033396	chr2	Spg11	-0.2128571	0.336138222	0.40505844	2.731932011	0.04759438	0	95	97	102	125	102	77	110	65	117	124
ENSMUSG00000058620	chr2	Adra2b	-0.3734176	0.336251491	0.40516	0.376772344	0.104459105	0	20	10	11	37	23	15	17	12	24	15
ENSMUSG00000034379	chr16	Wdr5b	-0.2444741	0.336291435	0.405173198	1.697969555	0.052940009	0	61	46	50	60	36	46	34	43	49	61
ENSMUSG00000038481	chr10	Cdk19	-0.1696016	0.336577952	0.405483446	3.847197588	0.032960987	0	264	227	235	220	172	288	216	153	209	241
ENSMUSG00000036322	chr17	H2-Ea-ps	1.32388091	0.33668938	0.405582724	2.59946281	1.988178548	0	53	66	32	46	49	756	0	1	0	0
ENSMUSG00000033075	chr15	Senp1	-0.1627653	0.33689313	0.40579319	3.37922043	0.027297497	0	149	154	136	217	158	164	181	119	170	160
ENSMUSG00000025269	chrX	Apex2	-0.177231	0.337385138	0.406350801	2.764830289	0.030386719	0	95	96	106	131	100	107	107	85	105	108
ENSMUSG00000051730	chr2	Mettl5	-0.205944	0.337809778	0.406827183	3.096480068	0.045964815	0	157	115	126	163	114	82	161	108	137	148
ENSMUSG00000001632	chr6	Brpf1	0.15210677	0.337970311	0.406985445	4.014604981	0.025408671	0	232	191	218	268	222	362	299	228	253	245
ENSMUSG00000001134	chrX	Uxt	0.15082032	0.338542614	0.407633535	4.077386134	0.025415089	0	276	203	225	279	202	343	321	238	292	250
ENSMUSG00000025940	chr1	Tmem70	-0.1695221	0.338566835	0.407633535	5.816446027	0.036181195	0	797	868	804	1234	771	590	952	785	916	1051
ENSMUSG00000022312	chr15	Eif3h	-0.1426468	0.338617261	0.40765913	6.823536782	0.026048809	0	1924	1856	1560	1961	1529	2029	1766	1433	1803	1780
ENSMUSG00000032125	chr9	Robo4	-0.1679281	0.338914474	0.407913468	4.016647331	0.032492796	0	262	240	213	309	245	291	196	269	176	306
ENSMUSG00000032332	chr9	Col12a1	-0.1880154	0.338916084	0.407913468	5.67770189	0.044893964	0	1138	610	709	1031	606	1021	916	683	477	845
ENSMUSG00000042099	chr17	Kank3	-0.1619881	0.33890158	0.407913468	4.194767754	0.03053582	0	265	289	272	384	231	395	206	243	253	316
ENSMUSG00000069089	chr13	Cdk7	-0.1479256	0.339382887	0.40844013	4.214045294	0.025154802	0	308	312	262	306	250	335	342	251	256	249
ENSMUSG00000000127	chr17	Fer	-0.1827952	0.340441433	0.40967879	3.132961132	0.035478251	0	145	128	136	160	116	116	129	111	171	131
ENSMUSG00000039354	chr1	Smarcal1	-0.1448643	0.340581185	0.409811678	4.479173559	0.024404251	0	363	287	284	449	361	339	328	291	352	411
ENSMUSG00000018372	chr11	Cep95	0.20865663	0.340714688	0.409936884	2.22894358	0.040673267	0	72	72	49	74	49	93	75	65	86	81
ENSMUSG00000035203	chr7	Epn1	-0.1457871	0.340743902	0.409936884	7.174890992	0.027581629	0	2088	1853	2070	3105	2262	2651	2192	2069	1883	2446
ENSMUSG00000031925	chr9	Maml2	-0.2014193	0.340903755	0.410063631	2.424509316	0.039772591	0	74	74	80	112	80	96	82	72	55	96
ENSMUSG00000032381	chr9	Fam96a	-0.1418593	0.340907937	0.410063631	5.322128881	0.024719735	0	610	590	525	920	517	764	667	515	597	569
ENSMUSG00000020107	chr10	Anapc16	0.1429651	0.340969764	0.410102704	5.366135678	0.025117924	0	663	579	548	591	513	860	690	588	722	676
ENSMUSG00000048332	chr3	Lhfp	-0.1471564	0.341089621	0.410211561	4.427134994	0.02558733	0	390	314	341	371	257	414	376	266	293	320
ENSMUSG00000027167	chr2	Elp4	0.20108489	0.341407222	0.410522872	2.328931215	0.040313646	0	73	58	55	102	56	75	90	84	86	91
ENSMUSG00000073436	chr17	Eme2	-0.1743308	0.341386639	0.410522872	3.170056964	0.031701234	0	171	140	107	162	123	135	127	144	138	134
ENSMUSG00000004843	chr16	Chmp2b	-0.1481372	0.341809592	0.410971341	4.847788182	0.026464996	0	485	427	395	593	364	381	461	399	400	579
ENSMUSG00000028683	chr4	Eif2b3	0.13846023	0.342227188	0.411438037	4.13985103	0.021601574	0	246	219	218	327	238	310	305	258	321	303
ENSMUSG00000074215	chr8	Gm10643	0.38543726	0.342409132	0.411621369	0.251700121	0.117199103	0	12	19	17	13	7	11	19	19	15	34
ENSMUSG00000038893	chr11	Fam117a	0.23521868	0.342715562	0.411954304	2.707724063	0.061468505	0	96	90	87	95	69	82	113	112	77	181
ENSMUSG00000103114	chr1	RP23-103B18.8	0.54349781	0.342765429	0.411978813	-0.123995527	0.273691679	0	15	3	14	11	5	1	11	21	17	25

ENSMUSG00000029767	chr6	Calu	0.15166183	0.342827441	0.411982487	7.597471429	0.03027761	0	2695	2604	2634	3558	2248	4034	3830	2901	3290	2625
ENSMUSG00000061374	chr7	Fiz1	-0.1417826	0.342817601	0.411982487	4.248833849	0.023305277	0	264	270	270	378	298	384	302	231	267	294
ENSMUSG00000084830	chrX	Gm14539	0.17083359	0.343339366	0.412562203	4.588411025	0.035779337	0	391	329	382	345	222	466	411	344	491	356
ENSMUSG00000038150	chr11	Ormdl3	0.13658249	0.343542654	0.412770987	5.29615254	0.023122376	0	551	609	490	663	470	729	619	664	602	735
ENSMUSG00000024381	chr18	Bin1	0.16036525	0.343784155	0.413025647	9.667214886	0.034304083	0	13066	10017	9874	13624	10740	12166	12816	13620	16274	14652
ENSMUSG00000041671	chr6	Pyroxd1	-0.1568141	0.344099769	0.413333767	3.336118115	0.02631712	0	170	153	145	178	137	173	160	118	171	150
ENSMUSG00000047227	chr12	Gm527	-0.3113322	0.344092589	0.413333767	0.614132306	0.067033933	0	34	20	19	23	20	19	17	24	20	22
ENSMUSG00000038623	chr7	Tm6sf1	0.1902383	0.344189015	0.413337853	4.627944908	0.045569587	0	244	360	395	447	268	292	419	432	437	543
ENSMUSG00000038975	chr3	Rabggtb	0.1365133	0.344191895	0.413337853	5.957083117	0.02384573	0	971	840	784	1104	725	1302	1052	927	1030	1010
ENSMUSG00000055866	chr1	Per2	-0.3075313	0.3441684	0.413337853	2.927374636	0.117944947	0	167	143	153	74	67	137	172	52	117	75
ENSMUSG00000028015	chr3	Ctso	-0.1719483	0.344264387	0.413389387	3.364274435	0.033096332	0	140	176	164	181	139	163	152	109	183	176
ENSMUSG00000032076	chr9	Cadm1	0.32017393	0.344299525	0.413396062	2.81790029	0.125334531	0	137	64	61	89	105	279	79	76	69	144
ENSMUSG00000000194	chr2	Gpr107	-0.1379417	0.344711762	0.413784384	5.450146715	0.023984142	0	642	612	618	823	706	712	723	550	704	706
ENSMUSG00000016918	chr1	Sulf1	-0.1568599	0.344691919	0.413784384	4.27702084	0.029748418	0	302	291	308	350	260	422	263	255	215	349
ENSMUSG00000031840	chr8	Rab3a	-0.1493942	0.344702133	0.413784384	5.298175967	0.028172523	0	569	662	505	730	606	579	598	581	496	785
ENSMUSG00000002108	chr2	Nr1h3	0.16534749	0.344806246	0.413862254	3.729609427	0.030687789	0	177	146	193	232	176	316	229	157	205	240
ENSMUSG00000059743	chr3	Fdps	0.15610028	0.344896872	0.413935481	4.852897748	0.030277593	0	447	364	367	439	402	452	526	517	568	391
ENSMUSG00000020363	chr11	Gfpt2	0.19649774	0.344934515	0.413945112	3.324373422	0.042735306	0	133	132	142	129	142	252	191	165	114	148
ENSMUSG00000031255	chrX	Sytl4	-0.3086137	0.345261993	0.414302534	0.235304905	0.059601558	0	15	17	19	22	14	20	14	12	16	15
ENSMUSG00000021047	chr12	Nova1	-0.2315453	0.345599769	0.41467225	2.147720382	0.055398027	0	62	60	66	78	79	63	50	82	49	78
ENSMUSG00000024330	chr17	Col11a2	-0.2359892	0.346044437	0.415170148	5.513619111	0.073528353	0	1143	660	668	751	455	1293	704	420	509	574
ENSMUSG00000029576	chr5	Radil	-0.2671328	0.346457432	0.415629963	1.108081329	0.063334899	0	27	39	33	27	37	37	32	31	23	28
ENSMUSG00000071141	chr6	Rpl36a-ps3	0.24334755	0.347157989	0.416434646	2.07801076	0.062821407	0	67	54	41	66	52	79	96	46	91	51
ENSMUSG00000031982	chr8	Arv1	0.27532556	0.347451629	0.416751113	1.053406164	0.063696866	0	22	18	32	33	26	41	38	30	40	25
ENSMUSG00000033233	chr3	Trim45	-0.2521078	0.347519566	0.41679683	1.755711175	0.062039346	0	33	54	58	66	52	69	40	36	54	45
ENSMUSG00000004637	chr8	Wwox	-0.1887015	0.347555607	0.416804287	2.872108488	0.039206625	0	106	113	96	132	123	101	111	84	102	153
ENSMUSG00000025421	chr18	Hdhd2	-0.1372486	0.34769355	0.416898169	5.645997809	0.024130376	0	765	696	717	976	753	727	825	728	800	792
ENSMUSG00000043505	chr6	Gimap5	-0.273037	0.347686479	0.416898169	1.122293498	0.068898282	0	34	39	39	41	15	32	34	28	26	32
ENSMUSG00000002635	chr7	Pdcd2l	-0.1443468	0.348220093	0.41738628	3.72871163	0.023201842	0	212	205	204	230	174	205	227	170	199	219
ENSMUSG00000012609	chr12	Ttll5	-0.1948955	0.348176664	0.41738628	2.542514264	0.03729768	0	88	85	86	120	77	74	89	89	75	106
ENSMUSG00000022681	chr16	Ntan1	0.14010577	0.348196491	0.41738628	4.53349796	0.02355474	0	335	313	342	379	262	445	395	333	433	367
ENSMUSG00000024382	chr18	Ercc3	0.15333992	0.34819605	0.41738628	3.933025443	0.027287257	0	221	192	183	268	208	318	258	206	305	218
ENSMUSG00000035828	chr15	Pim3	0.1728355	0.348397905	0.417563598	4.440436866	0.036914573	0	226	375	257	346	301	545	409	293	320	321
ENSMUSG00000079562	chr5	Maea	-0.133939	0.348620777	0.417794887	6.080366804	0.023409872	0	1061	919	966	1367	979	1053	1129	946	991	1142
ENSMUSG00000025925	chr1	Terf1	0.21241607	0.348673612	0.417822379	2.340661931	0.045357263	0	58	81	54	88	61	109	91	85	84	64
ENSMUSG00000097388	chr7	Gm3200	0.37952172	0.34894971	0.418117382	0.223591543	0.113663358	0	15	11	12	15	14	13	16	19	10	38
ENSMUSG00000022817	chr16	Itgb5	0.1695372	0.348998454	0.418127715	6.30736108	0.038265991	0	1019	1192	941	1380	1026	2245	1180	1108	1062	1344
ENSMUSG00000049643	chr7	2310022A10Rik	0.13851572	0.349018169	0.418127715	6.53947609	0.025503032	0	1299	1131	1171	1778	1257	1865	1422	1492	1609	1565
ENSMUSG00000101225	chr7	1700008J07Rik	-0.2368118	0.349844498	0.419081744	1.817320351	0.053193442	0	65	55	47	60	47	39	62	55	39	59
ENSMUSG00000009535	chr18	Rnmt	-0.1425317	0.350064068	0.419308829	4.903142319	0.025668839	0	576	413	401	508	429	560	500	344	478	444
ENSMUSG00000020289	chr11	Nprl3	0.14754367	0.350171752	0.419401868	4.001493645	0.025377248	0	193	193	210	290	239	281	261	268	243	310
ENSMUSG00000031353	chrX	Rbbp7	-0.1353122	0.351085929	0.420460749	6.866226086	0.024609356	0	1930	1775	1568	2356	1524	1785	1999	1656	1675	1955
ENSMUSG00000029397	chr5	Rchy1	-0.1283896	0.351132265	0.42048021	5.261335137	0.020893795	0	624	580	533	688	548	597	586	557	577	663
ENSMUSG00000028649	chr4	Macf1	-0.1476787	0.351346359	0.42070054	6.415597387	0.029243436	0	1153	1185	1277	1800	1294	1489	1417	1394	1021	1288
ENSMUSG00000027522	chr2	Stx16	-0.1294334	0.351409197	0.420739736	5.041948723	0.021116728	0	561	522	460	541	460	557	524	484	440	559
ENSMUSG00000062352	chr12	Itgb1bp1	0.14734669	0.351495656	0.420807203	4.462704169	0.026582637	0	306	277	259	409	308	524	397	272	361	346
ENSMUSG00000022052	chr14	Ppp2r2a	-0.1342059	0.351876516	0.421227082	5.886220035	0.023638039	0	915	822	799	1201	889	874	965	858	945	940
ENSMUSG00000031913	chr8	Vps4a	-0.132593	0.352095161	0.421452721	6.21622649	0.023385731	0	1211	1079	1063	1408	1035	1253	1160	1006	1217	1148
ENSMUSG00000026389	chr1	Steap3	-0.1479106	0.352393534	0.421737628	5.983607122	0.029323796	0	887	1019	892	1050	1058	1203	933	935	756	1091
ENSMUSG00000089718	chr9	2310075C17Rik	-0.2656326	0.352388774	0.421737628	2.04930357	0.079841057	0	51	87	84	57	43	57	76	53	68	43
ENSMUSG00000039246	chr1	Lyplal1	-0.3048295	0.352883307	0.422251464	1.652940983	0.104572391	0	64	56	51	44	32	83	31	38	47	24
ENSMUSG00000063019	chr2	Manbal	0.16064868	0.352862729	0.422251464	4.600872721	0.032392099	0	416	290	292	337	352	591	389	348	322	453
ENSMUSG00000049354	chr11	Dcaf7	-0.1350077	0.35307445	0.422444012	5.876612902	0.024092679	0	827	865	777	1198	925	904	1014	865	834	943
ENSMUSG00000031391	chrX	L1cam	0.2929284	0.353174582	0.422527646	1.622183883	0.090086649	0	35	30	24	58	52	75	71	37	54	30
ENSMUSG00000039159	chr6	Ube2h	-0.1446731	0.353339661	0.422688959	6.225892719	0.028151538	0	1231	1130	973	1435	1095	1334	1109	1280	886	1187
ENSMUSG00000024422	chr17	Dhx16	0.13575387	0.353795667	0.423198241	4.278642391	0.022011689	0	304	231	257	352	233	395	323	263	322	354
ENSMUSG00000025203	chr19	Scd2	-0.182745	0.353999565	0.423405899	6.083721192	0.045573992	0	1150	1060	1109	978	996	1156	933	1185	605	1310
ENSMUSG00000025995	chr1	Wdr75	0.1587679	0.354474074	0.42393716	3.798236429	0.0301579	0	183	156	177	255	203	260	260	213	269	183
ENSMUSG00000042406	chr15	Atf4	0.1591101	0.354614452	0.424068759	7.53453475	0.03499478	0	2646	2474	2298	3126	2507	4623	3172	2592	3297	2394
ENSMUSG00000032301	chr9	Psma4	0.14395091	0.354806346	0.424261935	6.767378134	0.028353979	0	1706	1539	1425	1786	1253	1985	1970	1502	2129	1742
ENSMUSG00000075289	chr19	Carns1	0.16443868	0.354860364	0.424290226	5.212122133	0.03607189	0	644	463	421	638	445	460	608	597	704	796
ENSMUSG00000055254	chr13	Ntrk2	-0.2322953	0.35502094	0.424445908	2.972992876	0.066095966	0	80	139	91	131	174	125	128	97	77	158
ENSMUSG00000099210	chr7	Mir7051	0.24024401	0.355165632	0.424582574	2.026017998	0.058177672	0	42	53	50	62	61	108	77	56	61	50
ENSMUSG00000039810	chr10	Zc3h10	0.17417477	0.355268646	0.424669398	2.90488127	0.032529879	0	116	83	107	132	80	161	131	110	109	130
ENSMUSG00000039096	chr11	Rsad1	-0.2023172	0.355338785	0.424685772	2.701893875	0.04480356	0	114	122	99	104	68	94	105	89	109	86

ENSMUSG00000059834	chr3	Sclt1	-0.2402314	0.355343118	0.424685772	1.604058185	0.051823662	0	36	42	53	73	34	51	45	35	44	44
ENSMUSG00000000359	chr2	Rem1	0.24818264	0.355908344	0.425324926	2.240467873	0.071590448	0	61	64	50	84	56	151	79	73	59	51
ENSMUSG00000042216	chr5	Sgsm1	0.35228093	0.356003689	0.425402492	-0.013899752	0.07236289	0	14	13	9	10	10	18	13	17	11	20
ENSMUSG00000046447	chr4	Camk2n1	0.19407601	0.356040771	0.425410431	2.989497709	0.043850118	0	130	94	101	119	98	152	122	166	88	152
ENSMUSG00000040046	chr7	Tph1	-0.3306809	0.356292428	0.425674729	1.153431453	0.118924869	0	52	31	42	18	28	18	39	24	30	41
ENSMUSG00000029097	chr5	Trmt44	-0.2834918	0.356367071	0.425727514	0.913446423	0.069938717	0	32	27	24	33	28	43	29	16	25	18
ENSMUSG00000034126	chr12	Pomt2	-0.1580597	0.356612075	0.425983792	3.360818856	0.028567075	0	154	135	176	187	144	199	146	140	128	175
ENSMUSG00000049516	chr7	Spty2d1	-0.1829481	0.356676111	0.426023872	3.230224602	0.040048419	0	130	122	156	176	148	144	177	103	104	186
ENSMUSG00000029017	chr5	Pmpcb	-0.140397	0.356993558	0.426366601	6.309165725	0.026897212	0	1173	1238	1161	1687	979	1233	1135	1108	1217	1456
ENSMUSG00000029550	chr5	Sppl3	0.14535952	0.357059283	0.426372227	5.234373839	0.02781709	0	529	514	473	664	483	897	594	560	458	744
ENSMUSG00000038781	chr17	Stap2	0.21556566	0.357039289	0.426372227	2.45735472	0.051050098	0	70	96	63	73	65	134	77	95	87	79
ENSMUSG00000005718	chr16	Tfap4	0.24465011	0.357277347	0.426545222	1.698748123	0.05960953	0	57	34	50	39	31	65	57	60	45	49
ENSMUSG00000021276	chr12	Cinp	0.13564061	0.357295715	0.426545222	4.368667473	0.022234189	0	305	303	279	318	248	422	375	279	350	337
ENSMUSG00000033730	chr14	Egr3	-0.5091137	0.357267875	0.426545222	-0.360441421	0.229160519	0	5	20	19	6	6	12	17	6	2	8
ENSMUSG00000038702	chr1	Dsel	-0.1944467	0.357528863	0.426787102	2.836379944	0.043614063	0	113	115	104	134	93	96	125	89	75	152
ENSMUSG00000049882	chr12	Vcpkmt	-0.275069	0.357757302	0.42702332	2.347384036	0.092695395	0	100	102	63	68	68	143	80	39	53	61
ENSMUSG00000030747	chr7	Dgat2	-0.3190742	0.357896567	0.427153068	4.871736317	0.140450747	0	138	918	444	565	332	364	338	629	396	354
ENSMUSG00000030862	chr7	Cpxm2	-0.273367	0.357970233	0.427204507	4.818149893	0.103242934	0	634	480	483	408	268	928	442	238	257	279
ENSMUSG00000028214	chr4	Gem	0.26418261	0.35801883	0.427226022	2.20148376	0.07975244	0	71	61	66	66	38	90	95	64	36	118
ENSMUSG00000025047	chr19	Pdcd11	0.16460394	0.358575961	0.427817794	3.952487113	0.033896992	0	184	166	163	301	271	305	279	245	251	247
ENSMUSG00000038013	chr11	Wipf2	-0.146197	0.358555115	0.427817794	3.49412931	0.024812815	0	166	163	172	209	162	186	171	150	147	213
ENSMUSG00000044636	chr15	Csrnp2	0.24155277	0.358923801	0.428196248	1.903364849	0.062018439	0	59	32	57	60	39	78	52	64	44	83
ENSMUSG00000078941	chr13	Ak6	-0.1455678	0.359215014	0.428507088	5.522007967	0.028646257	0	818	700	627	847	603	711	789	515	836	705
ENSMUSG00000030894	chr7	Tpp1	0.14958915	0.359318926	0.428594462	6.021390095	0.030732087	0	906	833	769	1133	947	1201	1323	744	1009	1338
ENSMUSG00000025645	chr9	Ccdc51	0.16814865	0.359589701	0.428880838	2.907825044	0.03186086	0	101	109	92	138	81	119	122	133	121	140
ENSMUSG00000032192	chr9	Gnb5	-0.1975191	0.359628489	0.428890499	3.256094313	0.046341611	0	119	154	151	202	128	95	143	172	138	161
ENSMUSG00000097656	chr6	Gm26712	0.14849157	0.359810919	0.429071451	4.623249712	0.02859408	0	390	336	363	374	264	362	476	425	414	416
ENSMUSG00000054690	chr3	Emcn	-0.1523395	0.360199511	0.429498197	4.14660823	0.029145656	0	278	305	246	338	217	365	224	285	222	269
ENSMUSG00000032121	chr9	Tmem218	0.22887798	0.360986891	0.430364079	2.077440748	0.058099822	0	44	65	41	80	53	56	77	62	94	69
ENSMUSG00000038692	chr11	Hoxb4	0.49929961	0.360987271	0.430364079	-0.224228844	0.215040684	0	17	8	12	4	3	23	19	14	11	3
ENSMUSG00000000093	chr11	Tbx2	0.21633149	0.361283905	0.430680984	2.530696271	0.052204306	0	94	67	90	91	48	107	110	102	66	112
ENSMUSG00000019505	chr11	Ubb	0.14676757	0.361390401	0.430771194	8.556233441	0.030802438	0	5415	5055	4409	6428	5335	6212	6647	5990	5329	8154
ENSMUSG00000030417	chr7	Pdcd5	0.13153254	0.361540176	0.430876226	5.715074198	0.023548273	0	792	704	655	886	693	1005	879	758	987	847
ENSMUSG00000030556	chr7	Lrrc28	-0.1400447	0.361537609	0.430876226	3.948314394	0.023522478	0	256	250	225	274	191	230	242	231	218	267
ENSMUSG00000023964	chr6	Calcr	-0.4478856	0.361571865	0.43087725	0.137387483	0.182642261	0	12	13	18	15	25	2	16	8	22	19
ENSMUSG00000040331	chr7	Nsmce4a	0.12981596	0.361654669	0.430939181	4.948960893	0.021904054	0	475	431	423	514	348	636	518	439	543	497
ENSMUSG00000019863	chr10	Qrsl1	-0.1545222	0.361724263	0.430971507	4.218173847	0.030103604	0	247	244	312	399	257	257	302	325	262	273
ENSMUSG00000020451	chr11	Limk2	-0.1488004	0.361743471	0.430971507	4.205391597	0.028262413	0	328	285	251	286	276	373	244	291	253	261
ENSMUSG00000000296	chr10	Tpd52l1	-0.1678089	0.362450139	0.431776606	3.833563467	0.034895832	0	225	239	169	284	203	172	193	212	270	230
ENSMUSG00000036199	chr8	Ndufa13	0.13752899	0.362816503	0.432176208	8.491375139	0.027189867	0	5317	5120	4529	6364	4304	7357	5664	5500	6329	5978
ENSMUSG00000095832	chr3	Supt20	0.17852816	0.363477532	0.432926707	2.932263358	0.036168069	0	112	116	101	104	88	173	122	131	105	122
ENSMUSG00000036398	chr17	Ppp1r11	0.1476497	0.363578325	0.433009857	5.183221297	0.029635841	0	561	485	460	621	440	894	575	571	610	473
ENSMUSG00000074698	chr2	Csnk2a1	-0.132496	0.364234321	0.433754164	6.753408483	0.024876051	0	1813	1609	1499	2115	1405	1702	1855	1620	1549	1660
ENSMUSG00000055531	chr10	Cpsf6	-0.1308825	0.364310603	0.433808042	4.642716041	0.02226966	0	395	347	381	477	340	432	464	305	337	411
ENSMUSG00000019845	chr10	Tube1	0.3504757	0.365446481	0.435123532	0.244847743	0.084565398	0	11	17	12	10	18	24	24	14	21	14
ENSMUSG00000045827	chr13	Serpinb9	-0.1963138	0.366034127	0.435786094	2.817259252	0.045389628	0	108	111	126	135	72	85	103	102	102	133
ENSMUSG00000075040	chr2	Zfp408	0.20288677	0.366433345	0.436224228	2.227447487	0.044570689	0	72	73	50	77	45	103	74	81	67	74
ENSMUSG00000061897	chr2	Gm14292	-0.291135	0.366558978	0.436336622	1.039893995	0.079902666	0	33	28	29	29	38	15	30	26	33	37
ENSMUSG00000018239	chr11	Zcchc10	0.17409619	0.366647767	0.436399968	2.752369384	0.033462284	0	90	77	95	114	87	116	119	109	92	137
ENSMUSG00000059040	chr18	Eno1b	-0.8501651	0.366674644	0.436399968	4.197401446	0.995361161	0	406	313	284	392	348	1120	6	16	5	23
ENSMUSG00000081249	chr11	Gm11517	0.32526016	0.366843922	0.436527089	0.466196757	0.089825254	0	21	11	15	14	21	15	30	22	27	19
ENSMUSG00000081413	chr2	Gm14088	0.33280443	0.366824612	0.436527089	0.093375143	0.080417704	0	15	17	9	15	6	25	18	13	13	17
ENSMUSG00000019826	chr10	Zbtb24	0.20200422	0.368017019	0.437885737	2.072167505	0.040970157	0	59	61	40	63	59	77	78	70	64	67
ENSMUSG00000045237	chrX	1110012L19Rik	-0.1505554	0.368416036	0.438323191	3.790924977	0.028442276	0	226	212	195	229	208	185	253	173	237	211
ENSMUSG00000092868	chr15	Mir5113	-0.2968853	0.368461558	0.438340036	1.434552635	0.097964395	0	29	58	34	52	39	28	55	41	18	47
ENSMUSG00000032399	chr9	Rpl4	0.13409964	0.368563355	0.438423819	9.123878271	0.026541419	0	8109	7438	6811	9747	7615	10426	10292	8290	9506	9208
ENSMUSG00000065399	chr18	Mir133a-1	0.31506934	0.368689385	0.438499093	1.597028407	0.124334115	0	75	34	23	41	21	28	57	45	61	69
ENSMUSG00000087174	chrX	5530601H04Rik	-0.2714912	0.368673642	0.438499093	1.277926657	0.077130771	0	36	48	38	35	29	55	20	28	30	39
ENSMUSG00000055013	chr1	Agap1	-0.1597992	0.369412131	0.439321302	4.892142453	0.035756511	0	410	379	432	588	517	615	447	430	278	534
ENSMUSG00000022774	chr16	Ncbp2	0.12706267	0.369468915	0.439351447	4.548562012	0.020799485	0	352	333	303	377	291	435	458	338	363	396
ENSMUSG00000092564	chr17	BC051226	0.29085554	0.369551694	0.439412496	0.851050352	0.074826473	0	27	30	22	17	15	29	36	31	30	24
ENSMUSG00000022983	chr16	Scaf4	0.14552001	0.369623366	0.439460329	3.750341129	0.025912549	0	157	167	179	250	193	253	270	181	204	241
ENSMUSG00000047446	chr12	Arl4a	0.14757594	0.369655895	0.439461619	4.079376933	0.028591113	0	238	233	229	322	174	300	230	290	315	299
ENSMUSG00000056367	chr5	Actr3b	0.36854879	0.369701285	0.439478196	-0.03937287	0.108836385	0	7	11	16	16	5	24	18	16	11	9
ENSMUSG00000023232	chr4	Serinc2	-0.1571602	0.370695725	0.440622848	6.484056409	0.036130711	0	1755	1281	1176	1318	1430	1187	1358	1426	1333	1558

ENSMUSG00000000827	chr2	Tpd52l2	-0.130715	0.371067068	0.441026732	5.631954554	0.024173005	0	795	775	688	935	668	826	768	611	847	810
ENSMUSG00000048489	chr6	8430408G22Rik	0.39679141	0.37151535	0.441521984	2.846260625	0.219141303	0	50	91	102	92	110	405	79	43	63	99
ENSMUSG00000017713	chr11	Tha1	0.15879936	0.372077171	0.442152074	3.136160666	0.029380211	0	136	115	120	136	102	190	146	137	147	128
ENSMUSG00000017314	chr11	Mpp2	-0.2586817	0.372913922	0.443108738	1.389000193	0.065277015	0	31	52	36	51	33	29	52	38	29	37
ENSMUSG00000033543	chr9	Gtf2a2	0.12870516	0.373348848	0.443587818	4.730036006	0.022400593	0	418	397	329	461	284	510	491	376	438	445
ENSMUSG00000101166	chr7	Gm28496	0.34372572	0.373414779	0.443628438	0.496051423	0.116717626	0	18	22	19	12	12	9	31	24	26	26
ENSMUSG00000011158	chr12	Brf1	0.12960095	0.373506236	0.443699376	4.260565627	0.021666475	0	284	233	249	335	257	391	283	307	314	332
ENSMUSG00000061535	chr5	C1qtnf7	0.35191551	0.373933962	0.444169731	0.537782765	0.121510549	0	14	12	24	19	17	26	18	43	13	20
ENSMUSG00000021765	chr13	Fst	-0.2196215	0.374795678	0.445130892	2.847270235	0.06476299	0	97	123	82	96	159	135	101	71	90	143
ENSMUSG00000031951	chr8	Tmem231	0.30182217	0.374826061	0.445130892	1.002975853	0.090864261	0	34	22	27	21	20	18	36	35	31	48
ENSMUSG00000045100	chr6	Slc25a26	-0.148931	0.374838685	0.445130892	4.069301348	0.02902285	0	306	288	219	314	185	249	273	266	253	244
ENSMUSG00000024436	chr17	Mrps18b	0.13154465	0.37496782	0.445246411	4.320353037	0.023141091	0	254	237	257	415	264	339	363	315	333	343
ENSMUSG00000047875	chr4	Gpr157	0.14627885	0.375220843	0.445509005	5.511658224	0.031135497	0	549	502	654	911	625	662	870	747	729	882
ENSMUSG00000032251	chr9	Irak1bp1	0.2779242	0.375416201	0.445703094	1.036248063	0.078078186	0	27	32	29	27	14	28	28	30	46	39
ENSMUSG00000001062	chr8	Vps9d1	-0.1327534	0.375506311	0.445772208	4.31167432	0.02330219	0	318	298	299	350	270	342	274	276	350	293
ENSMUSG00000029436	chr5	Mmp17	-0.2986237	0.375677977	0.445938118	0.601417853	0.084759859	0	14	16	26	28	30	26	26	13	15	23
ENSMUSG00000032370	chr9	Lactb	-0.1264596	0.375761279	0.44599912	4.478247014	0.021259318	0	384	302	285	421	337	369	368	282	344	372
ENSMUSG00000023106	chr5	Denr	0.12891963	0.375815979	0.446026166	5.639755068	0.024074505	0	699	664	614	939	647	812	949	767	871	834
ENSMUSG00000003039	chr8	Fam32a	0.16000438	0.376019425	0.44619184	4.617298315	0.03567089	0	347	338	323	381	323	703	385	315	326	410
ENSMUSG00000051864	chr15	Tbc1d22a	0.1231213	0.376007329	0.44619184	4.799568624	0.020631003	0	401	346	347	520	375	586	452	392	460	482
ENSMUSG00000029227	chr5	Fip1l1	0.13108753	0.376097798	0.44624695	4.572190392	0.023603692	0	303	286	281	504	330	420	431	377	369	424
ENSMUSG00000027430	chr2	Dtd1	0.16461394	0.376529453	0.446721191	3.103887543	0.03276477	0	117	91	132	142	112	136	158	141	128	167
ENSMUSG00000021149	chr13	Gtpbp4	0.12364482	0.377073253	0.447256178	5.256663596	0.021714251	0	558	484	485	698	505	649	735	583	655	619
ENSMUSG00000031112	chrX	Stk26	-0.482804	0.377076384	0.447256178	0.677815087	0.287214802	0	0	27	30	37	34	16	33	11	22	19
ENSMUSG00000035967	chrX	Ddx26b	-0.1818925	0.377069528	0.447256178	3.389050834	0.043153037	0	192	159	159	164	141	163	163	108	220	137
ENSMUSG00000033788	chr6	Dysf	-0.1489609	0.377123813	0.447274474	6.456341588	0.033231938	0	1319	1031	1241	1733	1553	1236	1355	1238	1538	1391
ENSMUSG00000055932	chr8	Fto	0.15445991	0.377440998	0.447612676	6.499087843	0.035947504	0	1192	1094	1124	1719	1280	1194	1528	1541	1399	2073
ENSMUSG00000035754	chr10	Wdr18	0.11980506	0.378110927	0.448369109	5.02520845	0.020108475	0	467	443	364	612	446	609	553	512	546	539
ENSMUSG00000019782	chr10	Rwdd1	-0.1323636	0.378157818	0.448386669	5.721485171	0.025608743	0	868	768	755	1040	691	834	892	702	933	732
ENSMUSG00000035877	chr2	Zhx3	-0.1399648	0.378434724	0.448676935	4.794162394	0.027625089	0	372	410	356	584	448	496	358	435	345	517
ENSMUSG00000003575	chr8	Crtc1	-0.141597	0.378990169	0.449297362	3.801676609	0.025864889	0	190	186	194	277	235	232	193	208	191	250
ENSMUSG00000004815	chr5	Dgkq	-0.1910498	0.379052387	0.449333007	2.383661411	0.042933063	0	63	86	78	102	76	96	75	56	90	73
ENSMUSG00000085172	chr18	Gm6542	-0.2610827	0.379517804	0.449846563	0.888157538	0.057990436	0	23	31	28	38	21	25	22	21	32	28
ENSMUSG00000022663	chr16	Atg3	0.15100689	0.379691695	0.450014512	4.526468047	0.032137639	0	349	352	284	360	271	361	473	269	466	401
ENSMUSG00000022177	chr14	Haus4	0.16221956	0.380178327	0.450514863	3.161896613	0.033594386	0	137	131	100	165	93	207	154	145	125	134
ENSMUSG00000032547	chr9	Ryk	-0.1260066	0.38016159	0.450514863	5.957403877	0.023499051	0	1007	865	829	1231	913	951	978	935	949	1018
ENSMUSG00000027395	chr2	Polr1b	0.14988414	0.380230365	0.450538329	3.775371741	0.02968991	0	175	154	164	259	211	227	260	219	183	278
ENSMUSG00000025352	chr10	Gdf11	0.20657255	0.38028701	0.450567248	3.692978741	0.06038597	0	280	153	125	165	160	152	248	192	213	312
ENSMUSG00000034951	chr7	Cog7	0.13159894	0.380326773	0.450576162	4.256870658	0.023343497	0	253	247	226	345	283	328	319	343	287	340
ENSMUSG00000038007	chr4	Acer2	-0.256539	0.380432073	0.45066271	1.523391856	0.073695977	0	34	59	36	53	41	38	43	32	27	66
ENSMUSG00000082809	chr2	Gm14150	-0.5951162	0.380606562	0.450831199	0.593336344	0.475822973	0	25	23	28	27	20	74	4	7	9	1
ENSMUSG00000000794	chr3	Kcnn3	-0.3221406	0.38089697	0.451136954	1.585326021	0.127590477	0	53	43	26	84	39	24	35	76	27	42
ENSMUSG00000002944	chr5	Cd36	-0.2247394	0.3809952	0.45121506	7.893163231	0.078314816	0	2505	3887	3473	6474	3136	2405	4548	1825	4548	4576
ENSMUSG00000083477	chr5	Gm5555	-0.3323657	0.381117091	0.451321172	0.189596412	0.087455439	0	17	10	20	24	14	12	12	11	23	15
ENSMUSG00000078247	chr17	Airn	-0.1973813	0.381422052	0.45164404	2.222397231	0.045988714	0	67	75	76	70	70	73	52	70	68	82
ENSMUSG00000039457	chr16	Ppl	-0.2964635	0.381671473	0.451901094	0.864652137	0.087911621	0	25	28	21	31	34	23	28	15	40	18
ENSMUSG00000031467	chr8	Agpat5	0.1216729	0.381796599	0.45201095	5.166134783	0.021194237	0	552	468	468	607	461	606	699	546	550	646
ENSMUSG00000005378	chr5	Wbscr22	0.13044378	0.382023508	0.45224128	4.188997723	0.022821851	0	248	264	227	326	228	339	319	257	347	284
ENSMUSG00000052906	chr8	Ubxn8	0.18188902	0.382188526	0.45239831	2.453246092	0.037162549	0	73	83	70	86	61	95	110	79	97	83
ENSMUSG00000039128	chr2	Cdc123	0.12447269	0.38241325	0.45262598	5.225748341	0.022607044	0	514	460	467	751	493	671	733	580	610	583
ENSMUSG00000097368	chr5	Gm10390	-0.2759189	0.382626197	0.452839676	1.054863721	0.070501555	0	29	31	22	57	24	23	24	32	33	31
ENSMUSG00000041571	chr7	Sepw1	0.13440586	0.38294691	0.453180865	9.789961328	0.028373616	0	13523	11147	10591	15855	12048	18024	15038	13180	15579	13980
ENSMUSG00000024246	chr17	Thumpd2	0.22464843	0.38314906	0.453367991	1.532786716	0.054129352	0	46	36	40	48	21	62	47	48	40	47
ENSMUSG00000035696	chr4	Rnf38	-0.1404989	0.383169913	0.453367991	3.663733555	0.02513036	0	182	200	183	259	162	192	215	193	158	217
ENSMUSG00000032375	chr9	Aph1b	-0.2001603	0.383225841	0.45339578	2.134297357	0.045313318	0	73	43	68	92	66	62	75	59	62	66
ENSMUSG00000001440	chr11	Kpnb1	0.13617661	0.383464602	0.453639857	6.962512578	0.028700381	0	1672	1561	1569	2236	1825	2031	2586	1909	2152	1954
ENSMUSG00000038077	chr6	Kcna6	-0.3827373	0.383825453	0.454028315	0.478608316	0.148088613	0	13	13	13	51	21	31	13	12	23	11
ENSMUSG00000029863	chr6	Casp2	0.16187352	0.383858722	0.454029239	3.096438286	0.032132005	0	124	126	113	130	98	188	127	132	115	169
ENSMUSG00000093290	chr7	Mir3572	0.29261875	0.383994794	0.454151751	0.401246346	0.070739326	0	23	10	12	19	16	25	16	21	24	21
ENSMUSG00000016239	chrX	Lonrf3	0.4257307	0.384149365	0.454296118	0.317443999	0.195702588	0	13	21	16	7	12	23	41	4	23	15
ENSMUSG00000082922	chr7	Gm6939	0.2755925	0.38431733	0.4544563	0.876471504	0.070539453	0	31	14	22	32	17	45	27	24	23	35
ENSMUSG00000074676	chr2	Foxs1	0.28540959	0.384565986	0.454711863	1.729706692	0.103096889	0	25	52	39	51	46	88	49	79	36	34
ENSMUSG00000092176	chr17	Gm20460	-0.129649	0.384763786	0.454907256	4.552566734	0.023812503	0	361	352	297	415	388	384	408	330	294	410
ENSMUSG00000058145	chr7	Adamts17	0.27461389	0.385295431	0.455497288	1.773765704	0.092140481	0	47	41	60	35	35	62	55	59	29	91
ENSMUSG00000025260	chrX	Hsd17b10	0.12600716	0.385508862	0.455711059	5.618569619	0.023842266	0	687	694	567	898	663	987	817	685	898	800

ENSMUSG00000048429	chr9	1810026J23Rik	-0.152028	0.38600953	0.456264309	6.563958809	0.036083383	0	1673	1500	1353	1588	1272	1151	1452	1400	1291	1994
ENSMUSG00000030287	chr6	Itpr2	-0.1467171	0.386721199	0.457066848	3.412541377	0.027369815	0	167	169	153	193	142	203	165	171	133	145
ENSMUSG00000026353	chr1	Ubxn4	-0.132591	0.387009764	0.457369225	5.736570276	0.02673406	0	956	798	734	1015	662	775	887	696	927	850
ENSMUSG00000080904	chr11	Gm11966	0.21242945	0.387053401	0.45738212	2.139275267	0.051505526	0	50	69	69	52	51	81	62	77	74	80
ENSMUSG00000027472	chr2	Pdrg1	0.13642255	0.387360753	0.457706619	6.295346539	0.028949113	0	1284	1147	1031	1211	883	1242	1377	1261	1446	1349
ENSMUSG00000038151	chr10	Prdm1	0.26583614	0.387483147	0.457773834	1.16048912	0.08200014	0	23	29	31	49	13	36	48	36	25	43
ENSMUSG00000091994	chr10	E130317F20Rik	-0.274442	0.387471153	0.457773834	1.271216264	0.093288999	0	52	41	28	19	43	36	30	29	31	44
ENSMUSG00000021288	chr12	Klc1	0.13824338	0.38765428	0.457937301	6.303296825	0.029785087	0	1204	1007	923	1308	1150	1583	1229	1519	1150	1252
ENSMUSG00000099041	chr2	Gm28035	-0.1556304	0.387742182	0.458002429	4.26424607	0.034984249	0	249	273	330	405	249	387	220	270	340	259
ENSMUSG00000027667	chr3	Zfp639	0.14174859	0.38786665	0.458110733	4.034785546	0.028095117	0	238	202	238	291	187	237	291	247	312	300
ENSMUSG00000000916	chr5	Nsun5	0.16589447	0.387958061	0.458130552	2.621197561	0.030632735	0	86	74	77	101	85	121	105	92	103	100
ENSMUSG00000059734	chr19	Ndufs8	-0.132087	0.387962358	0.458130552	7.182301178	0.027554184	0	2155	2296	2203	2893	1808	2658	1973	2195	2280	2198
ENSMUSG00000064369	chrMT	mt-Te	0.63762674	0.387981769	0.458130552	2.153492606	0.612201956	0	30	22	22	118	72	5	14	226	18	147
ENSMUSG00000048109	chr3	Rbm15	-0.1622875	0.388406755	0.458593631	3.191683645	0.034509946	0	129	128	141	194	122	195	151	130	113	110
ENSMUSG00000026098	chr1	Pms1	-0.2668271	0.388463792	0.45862223	1.273544904	0.073763983	0	53	24	22	52	38	30	41	25	36	38
ENSMUSG00000050565	chr1	Tor1aip2	-0.1268141	0.388631289	0.458781223	6.217757065	0.024988517	0	1193	1103	1083	1363	1037	1089	1228	1029	1102	1351
ENSMUSG00000056380	chrX	Gpr50	-0.3933131	0.38871669	0.458843282	-0.084658813	0.158790371	0	22	19	13	4	10	9	9	12	8	20
ENSMUSG00000090031	chr1	4732440D04Rik	-0.3784535	0.389074163	0.459226459	-0.196330517	0.107239886	0	18	13	15	12	5	13	10	15	6	9
ENSMUSG00000026806	chr2	Ddx31	0.19350332	0.389111237	0.459231435	2.839937599	0.049317586	0	117	95	86	106	84	175	148	76	126	94
ENSMUSG00000022332	chr15	Khdrbs3	-0.2504131	0.389166439	0.459257803	2.978131279	0.088217126	0	66	131	107	267	81	107	106	150	116	92
ENSMUSG00000026890	chr2	Lhx6	-0.2427613	0.389263052	0.459333031	1.205403137	0.06245942	0	40	29	35	34	37	29	41	21	29	44
ENSMUSG00000078440	chr10	Dohh	0.12143947	0.389377104	0.459428823	5.364122236	0.022201588	0	603	540	535	733	529	751	732	672	711	621
ENSMUSG00000015568	chr8	Lpl	0.22823293	0.389447471	0.459473059	8.866906311	0.083895938	0	2916	6883	5139	12949	5255	6180	10206	6271	8220	10221
ENSMUSG00000025949	chr1	Pikfyve	0.1702814	0.389956276	0.460034516	3.317419441	0.04020049	0	128	137	92	205	137	176	230	117	169	163
ENSMUSG00000030691	chr7	Fchsd2	-0.1679542	0.390010648	0.460059826	3.227376647	0.03926115	0	145	141	124	199	126	197	147	116	86	174
ENSMUSG00000025371	chr11	Chmp6	0.11914874	0.390483768	0.460579048	4.91316575	0.020739751	0	424	410	373	547	398	556	525	408	557	509
ENSMUSG00000028292	chr4	Rars2	0.14067852	0.390541991	0.460608849	4.044408927	0.027975095	0	271	201	211	269	209	258	305	286	300	244
ENSMUSG00000025980	chr1	Hspd1	-0.1392189	0.390911171	0.460929468	7.789995204	0.031205044	0	3254	3333	2983	4951	2958	3565	4201	3267	3283	2851
ENSMUSG00000034520	chr11	Gjc1	0.17244667	0.390907662	0.460929468	2.865555707	0.03725014	0	111	108	98	124	63	159	123	110	105	126
ENSMUSG00000041476	chrX	Smpx	-0.1516537	0.390912778	0.460929468	8.174468016	0.037167864	0	5066	4426	4346	5391	3473	3361	4477	4192	4856	5302
ENSMUSG00000034930	chr6	Rtkn	0.13942698	0.391080979	0.461088895	4.234159023	0.027973382	0	254	235	211	338	291	279	317	324	292	382
ENSMUSG00000073775	chr4	Kti12	0.12511033	0.391370496	0.461391316	4.478335087	0.022428215	0	309	298	290	413	278	447	407	387	318	331
ENSMUSG00000104394	chr1	RP23-306B14.3	-0.2932685	0.391781138	0.46183647	0.316209637	0.07254111	0	14	20	15	29	15	16	20	20	10	16
ENSMUSG00000020349	chr11	Ppp2ca	-0.1323087	0.391876549	0.461909981	7.183184022	0.02809929	0	2106	2109	2104	3289	1846	2612	2456	1933	2312	2024
ENSMUSG00000029815	chr6	Malsu1	-0.1253609	0.392007468	0.462025331	4.749237651	0.023028768	0	447	454	349	501	337	447	456	333	442	417
ENSMUSG00000039316	chr17	Rftn1	0.14406891	0.392535094	0.462608185	5.08177206	0.031881721	0	434	393	387	634	550	593	688	588	403	625
ENSMUSG00000019846	chr10	Lama4	-0.1461968	0.392881743	0.462977677	5.972850981	0.03393315	0	800	963	981	1313	871	1227	880	1070	677	1020
ENSMUSG00000058454	chr7	Dhcr7	0.14056841	0.393018692	0.463100012	3.79906796	0.026611531	0	205	175	190	192	206	243	220	236	216	264
ENSMUSG00000046546	chr16	Fam43a	0.13385248	0.393176023	0.463246341	4.082606664	0.025329775	0	223	257	205	323	196	355	252	278	243	314
ENSMUSG00000022313	chr15	Utp23	0.18849869	0.393274213	0.463322971	2.411109895	0.042257304	0	89	57	80	80	55	111	96	81	81	84
ENSMUSG00000030562	chr7	Nox4	0.35184914	0.393466671	0.463510637	1.226116723	0.157209472	0	26	42	39	27	9	66	41	42	14	42
ENSMUSG00000074207	chr3	Adh1	0.22105051	0.393537261	0.463554721	4.545323385	0.076481672	0	276	435	298	346	235	837	270	251	376	355
ENSMUSG00000026123	chr1	Plekhb2	-0.1284132	0.393887375	0.463928026	5.970956069	0.026020839	0	858	917	928	1364	846	1050	966	768	1022	1092
ENSMUSG00000004561	chr14	Mettl17	0.17502264	0.393924304	0.463932424	3.485581074	0.043389892	0	133	159	146	195	143	298	186	201	147	133
ENSMUSG00000042303	chr15	Sgsm3	-0.135292	0.394006428	0.463990043	3.485898894	0.023858502	0	182	151	156	208	168	187	155	159	177	184
ENSMUSG00000010911	chr2	Apip	0.14286633	0.394342553	0.464346745	4.496614883	0.03075873	0	307	343	309	402	235	368	390	375	461	316
ENSMUSG00000022215	chr14	Fitm1	0.13687405	0.394634808	0.464651734	7.826533291	0.030665165	0	3408	3227	2909	3556	2952	3647	3547	3795	3473	4911
ENSMUSG00000023830	chr17	Igf2r	-0.1419626	0.3947754	0.464778114	6.92200991	0.032763072	0	1674	1592	1685	2522	2035	1900	1845	1754	1461	2473
ENSMUSG00000029781	chr6	Fkbp9	0.12710604	0.395061276	0.465075504	6.82227447	0.026114672	0	1789	1478	1429	1761	1567	2029	2013	1898	1659	2038
ENSMUSG00000052488	chr8	Cherp	0.12408619	0.395246978	0.465254928	4.511176921	0.022599813	0	305	284	276	449	316	396	373	368	345	450
ENSMUSG00000040195	chr10	Tmem194	0.18358611	0.395618685	0.465653254	2.375642732	0.04086335	0	67	85	65	82	54	88	110	76	80	86
ENSMUSG00000036197	chr15	Gxylt1	0.15662854	0.395695928	0.465704951	3.50658148	0.033500599	0	123	165	160	212	135	255	216	138	193	173
ENSMUSG00000010663	chr19	Fads1	0.15546057	0.396049461	0.466081784	4.795929512	0.037248274	0	347	419	361	467	354	770	516	383	387	355
ENSMUSG00000035086	chr11	Becn1	-0.1185606	0.396963235	0.467112324	5.81111482	0.022215077	0	965	802	762	1083	754	1000	946	736	864	854
ENSMUSG00000062038	chr5	Gm10108	-0.2633467	0.396991999	0.467112324	1.347808749	0.079659121	0	44	39	53	30	28	30	39	30	47	33
ENSMUSG00000028521	chr4	Slc35d1	-0.1546253	0.397098681	0.467198516	3.06585278	0.031361295	0	154	114	122	144	113	145	137	107	140	109
ENSMUSG00000029778	chr6	Adcyap1r1	0.19233582	0.397421564	0.467539038	2.89569118	0.051821472	0	108	106	85	102	104	99	123	175	105	127
ENSMUSG00000031378	chrX	Abcd1	0.12044294	0.398657914	0.468924345	5.391911013	0.022707809	0	571	629	538	744	515	822	643	686	637	779
ENSMUSG00000031996	chr9	Aplp2	-0.1412091	0.398666218	0.468924345	7.830954463	0.033263479	0	3540	3595	3151	3850	3552	3900	3352	3290	2593	4630
ENSMUSG00000005950	chr11	P2rx5	-0.1620359	0.39892345	0.469187422	4.230595967	0.039985735	0	277	244	271	423	268	403	251	265	335	185
ENSMUSG00000029310	chr5	Nudt9	0.11835499	0.399418459	0.469730089	5.617453483	0.022206913	0	745	633	632	863	636	988	844	796	776	764
ENSMUSG00000029500	chr5	Pgam5	0.11578961	0.399523861	0.469814512	4.967811021	0.020439272	0	424	418	420	588	391	563	586	511	444	546
ENSMUSG00000024346	chr18	Pfdn1	0.12415418	0.399617224	0.469884766	6.637432827	0.025356729	0	1551	1423	1259	1718	1162	1686	1651	1566	1692	1861
ENSMUSG00000030322	chr6	Mbd4	-0.2180216	0.39997768	0.470269038	1.335245234	0.052672984	0	38	38	35	49	33	58	32	28	29	36
ENSMUSG00000020877	chr11	Scrn2	0.14782532	0.400750668	0.471138235	3.36396535	0.028981351	0	140	133	135	170	140	152	193	143	167	218

ENSMUSG00000074766	chr2	Ism1	0.43732551	0.401338895	0.471790092	0.702728765	0.263131449	0	29	13	10	25	18	87	17	16	17	8
ENSMUSG00000083844	chr11	2210015D19Rik	0.16011284	0.401843196	0.472343188	5.098012005	0.041658001	0	474	434	467	609	425	357	647	488	679	749
ENSMUSG00000028556	chr4	Dock7	-0.1366237	0.402063753	0.472562695	4.087639192	0.027303516	0	274	216	260	348	227	230	328	230	256	267
ENSMUSG00000021687	chr13	Scamp1	-0.1163117	0.402193505	0.472675448	5.075357454	0.021077726	0	543	495	470	617	480	594	606	426	534	480
ENSMUSG00000071291	chr13	Zfp58	-0.2148928	0.402608997	0.473123967	1.602454466	0.053332753	0	41	46	57	46	41	40	57	40	40	43
ENSMUSG00000046658	chr5	Zfp316	-0.1855207	0.402842716	0.473358819	2.836101077	0.047852406	0	100	91	78	154	137	109	95	104	86	143
ENSMUSG00000054034	chrX	Tceal5	0.16181784	0.402906749	0.47339426	5.63189856	0.043378014	0	975	649	548	692	605	748	977	1039	693	772
ENSMUSG00000051413	chr2	Plagl2	0.16145885	0.403118069	0.473602735	3.226564621	0.036310099	0	137	122	104	193	103	182	158	101	166	195
ENSMUSG00000033029	chr15	1700088E04Rik	0.36090113	0.403328685	0.473810347	0.140631636	0.112994672	0	13	13	17	12	8	18	7	24	15	25
ENSMUSG00000054737	chrX	Zfp182	0.27925887	0.403425838	0.473884646	0.702002374	0.072500355	0	24	18	22	18	18	24	23	29	36	21
ENSMUSG00000036580	chr3	Spg20	-0.1232606	0.403496194	0.473927457	4.938175246	0.023429813	0	483	404	407	684	423	441	473	439	490	538
ENSMUSG00000032324	chr9	Tspan3	-0.1328432	0.404076387	0.47456904	7.053484665	0.029821596	0	2071	2090	1934	2484	1774	1799	2035	2121	1819	2525
ENSMUSG00000092241	chr17	Gm20522	0.25406528	0.404183922	0.474655448	1.155398953	0.082901331	0	31	29	18	50	18	29	30	47	43	35
ENSMUSG00000022471	chr15	Xrcc6	0.12668229	0.404360422	0.474782934	4.705429408	0.024981882	0	374	378	328	430	338	386	495	422	483	414
ENSMUSG00000029364	chr5	Wsb2	-0.1189526	0.404344708	0.474782934	6.841995689	0.023800927	0	1943	1623	1650	2044	1623	1996	1769	1675	1594	1956
ENSMUSG00000036403	chr5	Cep135	-0.2490032	0.404545828	0.474960727	0.957029577	0.068066735	0	31	32	33	22	27	26	29	18	30	33
ENSMUSG00000003809	chr8	Gcdh	-0.1362989	0.405210103	0.475700664	4.989873459	0.029741923	0	498	523	441	576	431	392	496	410	589	563
ENSMUSG00000032504	chr9	Pdcd6ip	0.12285882	0.405293428	0.475718565	5.952976078	0.025023553	0	881	761	763	1260	796	1224	1150	863	907	1152
ENSMUSG00000042992	chr6	Loh12cr1	-0.129066	0.405280519	0.475718565	4.103922497	0.024128319	0	284	263	197	358	239	264	265	270	244	286
ENSMUSG00000020251	chr10	Glt8d2	-0.2131137	0.40537526	0.475757721	1.754556213	0.053538749	0	53	55	41	60	51	33	55	49	54	53
ENSMUSG00000041632	chr13	Mrps27	-0.1177846	0.405428911	0.475757721	5.298279947	0.022127046	0	556	607	583	814	501	674	629	555	613	603
ENSMUSG00000060098	chr8	Prmt7	-0.13077	0.405427351	0.475757721	5.233516838	0.02752187	0	558	496	431	819	643	603	631	524	621	540
ENSMUSG00000039703	chr11	Nploc4	-0.1224872	0.405565117	0.475877599	6.496223687	0.025189411	0	1447	1264	1346	1704	1251	1381	1314	1303	1432	1606
ENSMUSG00000039607	chr9	Rbms3	-0.1429198	0.405758576	0.476064629	3.500164418	0.028762877	0	194	173	163	196	148	162	172	188	142	202
ENSMUSG00000024754	chr19	Tmem2	0.12549605	0.405822242	0.476099358	4.290238458	0.023932964	0	309	246	240	373	230	391	318	349	270	330
ENSMUSG00000090115	chr17	Usp49	-0.1775301	0.405956416	0.476216793	2.634810577	0.041964089	0	100	65	108	120	89	88	107	92	79	100
ENSMUSG00000059708	chrX	Akap17b	-0.2275719	0.406039013	0.476273709	1.898062609	0.067456959	0	48	57	55	69	60	60	71	23	55	65
ENSMUSG00000062761	chr5	Zfp512	0.12006583	0.40665626	0.476957695	4.067177939	0.020862041	0	231	230	221	294	214	295	287	266	284	281
ENSMUSG00000078607	chr11	1810010H24Rik	-0.3207081	0.406727521	0.477001244	0.196903519	0.101224514	0	21	12	21	15	15	8	14	15	12	25
ENSMUSG00000026975	chr2	Dph7	0.17991292	0.406877966	0.477137645	2.384281727	0.042979126	0	80	78	50	81	67	113	82	91	82	74
ENSMUSG00000031708	chr8	Tecr	0.1560258	0.40719017	0.477463698	8.271770023	0.042191504	0	5446	4074	3755	4365	4018	7624	4844	5718	3737	4825
ENSMUSG00000032607	chr9	Amt	0.35980347	0.408061528	0.478445295	0.07456142	0.133731186	0	7	24	12	12	5	12	15	22	19	16
ENSMUSG00000035572	chr4	Dcaf10	-0.1338921	0.408544041	0.478970851	3.991272376	0.027134883	0	269	210	212	299	243	312	229	229	181	286
ENSMUSG00000075528	chr11	Aarsd1	0.12382096	0.408733985	0.479153345	4.954587653	0.024887832	0	418	383	378	626	419	561	529	499	588	444
ENSMUSG00000097061	chr12	9330151L19Rik	-0.211575	0.408996042	0.479420337	1.882314476	0.058105764	0	62	57	50	42	69	52	58	45	52	63
ENSMUSG00000021774	chr14	Ube2e1	-0.1942131	0.409456238	0.479919523	5.81924484	0.064913368	0	1039	803	744	1058	845	432	922	677	832	1413
ENSMUSG00000054321	chr18	Taf4b	-0.2419886	0.409767123	0.480243632	1.314936376	0.070978181	0	35	41	36	46	33	36	61	23	28	30
ENSMUSG00000066900	chr5	Suds3	-0.1240833	0.409837361	0.480285675	5.932271748	0.025886827	0	885	874	899	1353	776	1064	1013	869	985	830
ENSMUSG00000020397	chr11	Med7	0.13313559	0.409923302	0.480346111	3.517343239	0.024702435	0	188	150	145	192	132	200	223	168	176	202
ENSMUSG00000031565	chr8	Fgfr1	0.13004901	0.410196412	0.480625843	6.210676555	0.028913156	0	958	982	882	1367	1091	1484	1155	1305	973	1407
ENSMUSG00000027428	chr2	Rbbp9	-0.1800976	0.410719501	0.481198403	2.877603004	0.046748502	0	107	129	111	144	83	80	122	99	100	151
ENSMUSG00000059277	chr7	R74862	0.24126146	0.410796861	0.481248695	0.913694857	0.059267602	0	20	28	19	36	18	35	24	34	29	33
ENSMUSG00000002885	chr8	Cd97	0.13702246	0.41103962	0.481492728	5.555522203	0.031770456	0	581	546	603	926	695	857	859	811	552	944
ENSMUSG00000042229	chr1	Rabif	0.13316255	0.411227218	0.481672109	3.599846984	0.025357283	0	162	161	170	225	139	199	232	162	211	222
ENSMUSG00000034810	chr2	Scn7a	0.20740706	0.411866841	0.482380874	2.909781016	0.063211114	0	86	116	112	105	87	221	127	106	70	134
ENSMUSG00000057388	chr17	Mrpl18	-0.126233	0.412362524	0.482920952	6.197634525	0.027330089	0	1089	1074	1053	1604	937	1239	1210	1169	1121	966
ENSMUSG00000033985	chr4	Tesk2	-0.2132987	0.412714535	0.483292697	1.354974438	0.049519401	0	35	42	33	53	33	52	38	35	29	31
ENSMUSG00000055546	chr11	Timd4	-0.3848881	0.412881218	0.483447377	0.441185756	0.199948396	0	19	19	21	21	23	43	26	10	5	6
ENSMUSG00000036977	chr8	Anapc10	-0.1876853	0.413185324	0.48376293	2.308398037	0.047642189	0	82	78	62	105	60	82	94	44	79	72
ENSMUSG00000043924	chr4	Ncmap	-0.2195596	0.413326972	0.483888236	1.965491293	0.062822437	0	38	49	69	85	63	52	75	58	44	56
ENSMUSG00000045999	chr17	AY036118	0.72739327	0.413428052	0.483925498	4.022482717	0.893388094	0	56	65	35	288	464	45	47	1059	5	390
ENSMUSG00000048833	chr12	Slc39a9	-0.1281054	0.413426868	0.483925498	4.190207032	0.025565262	0	258	267	267	377	250	388	287	224	279	247
ENSMUSG00000048706	chr4	Lurap1l	-0.1911423	0.4134767	0.483941911	2.060704468	0.047405022	0	47	75	61	82	57	61	75	59	48	66
ENSMUSG00000022863	chr16	Btg3	-0.2461649	0.413745551	0.484216029	1.303683182	0.073603989	0	34	36	42	53	26	19	45	33	35	42
ENSMUSG00000045104	chr19	Gm5514	-0.4603055	0.41379964	0.484238781	0.484153397	0.314664729	0	4	34	14	39	21	32	2	27	17	9
ENSMUSG00000028013	chr3	Ppa2	0.12289149	0.413905677	0.484322316	5.274010649	0.025418444	0	515	525	519	762	454	803	610	693	610	565
ENSMUSG00000028970	chr5	Abcb1b	-0.2128819	0.414235782	0.484634538	2.409582649	0.065012555	0	93	83	75	111	57	90	102	44	102	56
ENSMUSG00000038762	chr17	Abcf1	0.11998286	0.414241857	0.484634538	6.701987506	0.025270493	0	1455	1290	1260	2067	1423	1869	1789	1696	1735	1743
ENSMUSG00000026564	chr1	Dusp27	-0.1595118	0.414585921	0.484996471	6.730068565	0.044995298	0	1564	1091	1311	2709	1820	1546	1388	1633	1461	2137
ENSMUSG00000074364	chr7	Ehd2	-0.1286949	0.414916202	0.485342219	6.705074602	0.029199102	0	1520	1580	1479	2013	1531	1909	1425	1636	1241	1947
ENSMUSG00000026617	chr1	Bpnt1	-0.126369	0.415485194	0.485967116	4.026419567	0.024276159	0	241	276	224	291	224	248	267	253	252	238
ENSMUSG00000001911	chr8	Nfix	-0.1695672	0.415708142	0.486160351	7.987452113	0.051656001	0	3387	3117	3321	5771	4586	3316	3629	4412	2643	5437
ENSMUSG00000016252	chr2	Atp5e	0.12932087	0.415752346	0.486160351	8.564626785	0.030078304	0	5518	5573	5138	6638	4161	8411	6188	5438	6465	5955
ENSMUSG00000024487	chr18	Yipf5	-0.1230024	0.41575476	0.486160351	3.916034057	0.022873273	0	239	208	215	276	225	260	272	179	233	231
ENSMUSG00000027671	chr3	Actl6a	0.13060377	0.415929958	0.486324529	4.024299446	0.026708323	0	243	201	188	315	212	292	334	222	288	244

ENSMUSG00000037235	chr5	Mxd4	-0.1291086	0.41647152	0.486917012	5.99712116	0.029274697	0	1058	1007	1021	1014	827	1265	868	888	844	1139
ENSMUSG00000003123	chr7	Lipe	0.2428915	0.416788209	0.487222312	4.577360284	0.10340816	0	160	525	231	357	334	356	271	617	280	553
ENSMUSG00000004056	chr7	Akt2	-0.12631	0.416802373	0.487222312	7.624311275	0.028626746	0	2921	2993	2579	3710	3134	2847	3033	3047	3236	3151
ENSMUSG00000028251	chr4	Tstd3	0.1398933	0.417614338	0.48810984	4.127128518	0.031437457	0	289	272	229	260	177	253	336	259	306	327
ENSMUSG00000097868	chr2	A330069E16Rik	-0.2733442	0.417631473	0.48810984	0.631722859	0.079231164	0	35	14	17	29	22	27	20	12	23	24
ENSMUSG00000036655	chr12	Colec11	0.31241873	0.418112396	0.48863106	0.195766187	0.091294749	0	17	11	12	12	15	26	9	23	15	19
ENSMUSG00000022096	chr14	Hr	-0.1744798	0.418330629	0.488845223	5.579760308	0.053916924	0	510	695	699	1115	782	488	772	803	555	1019
ENSMUSG00000035958	chr13	Tdp2	-0.1584992	0.418392494	0.488876641	2.945788329	0.036488944	0	138	111	105	157	90	136	155	98	98	101
ENSMUSG00000032827	chr6	Ppp1r9a	-0.1834197	0.41854251	0.489003507	2.258101416	0.047672128	0	63	71	83	72	76	75	64	78	56	83
ENSMUSG00000056366	chr10	Fabp3-ps1	-0.2025389	0.418571047	0.489003507	5.330873891	0.072718146	0	360	622	541	1259	521	829	513	769	523	402
ENSMUSG00000082284	chrX	H3f3a-ps1	-0.3142302	0.418619958	0.489019771	0.143499114	0.101492005	0	19	14	17	18	13	11	15	7	26	12
ENSMUSG00000027993	chr3	Trim2	-0.1669707	0.418857138	0.489255943	2.340444171	0.037058017	0	83	78	73	83	71	83	86	62	61	90
ENSMUSG00000001052	chr3	Sec24b	-0.1266013	0.419317716	0.489753	4.503797022	0.026519557	0	294	320	297	449	397	416	385	274	309	390
ENSMUSG00000079671	chr1	2610203C22Rik	-0.3623104	0.419415023	0.489825717	0.694566757	0.181359051	0	20	28	24	41	14	56	12	12	20	9
ENSMUSG00000026080	chr1	Chst10	0.49614221	0.419742696	0.490167439	0.315523541	0.350899753	0	19	13	18	10	7	77	8	10	9	7
ENSMUSG00000002728	chr2	Naa20	-0.128027	0.419804371	0.490198504	5.169496032	0.028104186	0	630	537	482	708	452	597	717	435	584	472
ENSMUSG00000061759	chr10	1700052N19Rik	-0.1264791	0.420151663	0.490563044	4.154228793	0.025339668	0	329	247	224	314	262	279	292	232	308	268
ENSMUSG00000005510	chr2	Ndufs3	-0.1267341	0.420621955	0.491030107	8.096005812	0.029421683	0	4344	4391	4321	5029	3199	4761	3786	4144	4254	4387
ENSMUSG00000026869	chr2	Psmd5	0.12254556	0.42062123	0.491030107	4.491805692	0.024586834	0	344	313	253	409	287	405	444	275	407	380
ENSMUSG00000020718	chr11	Polg2	0.18012475	0.420721993	0.49110587	2.028751005	0.042584455	0	59	46	47	70	55	65	64	55	72	87
ENSMUSG00000042207	chr1	Kdm5b	-0.1315552	0.420883251	0.491253074	4.119437024	0.027661286	0	255	249	228	365	257	303	236	279	200	330
ENSMUSG00000083044	chr4	Gm12416	0.32314541	0.42100166	0.491350246	0.354750241	0.136454209	0	16	17	5	17	21	22	13	31	10	28
ENSMUSG00000020844	chr11	Nxn	0.11824767	0.421195161	0.491503256	5.655377624	0.024558821	0	665	669	697	982	606	1017	764	822	819	856
ENSMUSG00000056673	chrY	Kdm5d	-0.8589153	0.421203098	0.491503256	2.84410131	1.256868944	0	266	205	184	0	0	1	108	84	106	103
ENSMUSG00000023030	chr15	Slc11a2	-0.1104676	0.421516079	0.49182741	5.014039993	0.020428453	0	543	452	414	592	492	511	534	453	478	553
ENSMUSG00000066632	chr12	Pgk1-rs7	-0.2154681	0.421665758	0.491960985	2.508493287	0.070316898	0	94	92	73	108	80	53	57	76	119	111
ENSMUSG00000040564	chr7	Apoc1	0.61116269	0.421749206	0.492017271	1.149919463	0.609450414	0	4	77	19	0	17	29	17	77	19	62
ENSMUSG00000057666	chr6	Gapdh	0.16905602	0.42198192	0.492247668	12.41958753	0.053055506	0	73971	65308	62852	106123	79260	58922	97373	86460	88095	140368
ENSMUSG00000038860	chr2	Garnl3	-0.2996952	0.422346146	0.492631425	0.257195897	0.082473009	0	17	24	14	19	14	14	17	22	9	16
ENSMUSG00000032869	chr2	Psmf1	0.12433917	0.422583746	0.492867431	4.194411067	0.024713393	0	272	218	219	324	267	330	306	265	262	392
ENSMUSG00000019437	chr11	Tlcd1	0.33165348	0.422678183	0.492895309	2.657349754	0.191897339	0	56	84	55	112	103	67	50	255	48	125
ENSMUSG00000019814	chr10	Ltv1	0.11853003	0.422664679	0.492895309	4.522482353	0.023372342	0	310	317	260	451	309	385	420	345	421	368
ENSMUSG00000021629	chr13	Slc30a5	0.12503233	0.422766259	0.492956886	4.121241917	0.024803105	0	241	232	230	314	219	318	379	224	259	300
ENSMUSG00000091373	chr17	Gm8810	0.5636826	0.422829748	0.492989785	1.713675372	0.538907426	0	25	44	33	65	24	272	12	11	19	13
ENSMUSG00000033697	chr15	Arhgap39	0.19241849	0.422919114	0.493052848	2.585055814	0.056229947	0	82	63	71	116	80	141	85	102	57	131
ENSMUSG00000025035	chr19	Arl3	-0.1283552	0.42305783	0.493173428	5.606072165	0.029300583	0	897	790	628	792	662	680	760	657	754	936
ENSMUSG00000004791	chr12	Pgf	-0.2590705	0.423110517	0.49319371	1.120568571	0.080734783	0	30	29	32	49	28	53	31	31	15	24
ENSMUSG00000019779	chr10	Frk	-0.2236658	0.423586638	0.493682999	1.01472683	0.052866075	0	28	30	29	35	30	37	35	18	25	29
ENSMUSG00000061013	chr18	Mkx	-0.2685763	0.423600925	0.493682999	1.389820558	0.10903789	0	72	34	33	37	27	61	49	21	28	29
ENSMUSG00000002845	chr16	Tmem39a	0.15927412	0.424565444	0.494765834	3.43928326	0.039680846	0	180	120	140	154	156	268	203	150	171	139
ENSMUSG00000025495	chr7	Ptdss2	-0.1154171	0.424644906	0.494817176	4.190198652	0.020985789	0	294	272	234	334	272	305	278	277	283	276
ENSMUSG00000031935	chr9	Med17	0.12366111	0.424902362	0.495075899	3.584998739	0.022583931	0	186	143	152	221	150	225	225	177	183	204
ENSMUSG00000078580	chr7	E430018J23Rik	0.22891694	0.425041505	0.495196738	1.307992312	0.064968838	0	47	32	23	28	30	55	36	30	44	43
ENSMUSG00000042292	chr15	Mkl1	-0.1482081	0.425108853	0.495233919	5.510302295	0.039674166	0	745	508	594	929	801	601	610	621	685	1000
ENSMUSG00000020228	chr10	Helb	-0.1402629	0.425695024	0.495875451	3.254405027	0.029134748	0	144	157	138	187	113	153	164	150	138	125
ENSMUSG00000040749	chrX	Siah1b	-0.1956887	0.425938132	0.496117287	1.653026144	0.047293154	0	52	37	54	50	46	51	52	34	43	51
ENSMUSG00000034105	chr8	Tldc1	0.19211937	0.42606089	0.496179669	2.223274396	0.052610127	0	62	64	68	76	46	80	58	62	86	110
ENSMUSG00000098715	chr6	Gm28053	-0.284696	0.426062693	0.496179669	0.311591425	0.076999539	0	19	16	21	25	11	13	13	13	19	24
ENSMUSG00000008206	chr8	Cers4	-0.1823884	0.42635764	0.496440422	2.394205764	0.047006227	0	90	76	71	91	78	85	75	100	71	59
ENSMUSG00000026087	chr1	Mrpl30	-0.1255465	0.426335508	0.496440422	6.324272249	0.028873398	0	1309	1245	1184	1498	997	1155	1258	1230	1409	1155
ENSMUSG00000028737	chr4	Aldh4a1	-0.1823743	0.42829527	0.498655006	6.347052008	0.062403368	0	1263	1364	1142	1485	1175	574	1360	1156	1480	1569
ENSMUSG00000032537	chr9	Ephb1	0.24366533	0.428462182	0.4987738	1.630713343	0.080495819	0	41	44	47	45	25	51	42	68	30	71
ENSMUSG00000056962	chr11	Jmjd6	0.12805245	0.428468678	0.4987738	4.736529473	0.028710545	0	352	322	357	529	345	614	467	430	421	339
ENSMUSG00000005846	chr16	Rsl1d1	-0.1256012	0.429195023	0.499577717	5.844057696	0.028872461	0	954	813	784	1223	729	808	1102	705	971	887
ENSMUSG00000024858	chr19	Adrbk1	0.13739749	0.429404048	0.499779395	6.305071183	0.035277181	0	954	1024	953	1557	1154	1964	1381	1043	1338	1089
ENSMUSG00000038319	chr5	Kcnh2	-0.1946716	0.429649293	0.500023193	3.467889083	0.064546685	0	200	186	182	189	112	96	154	230	152	187
ENSMUSG00000053094	chr5	Tmem248	0.11466741	0.429898087	0.500271079	5.521895493	0.0237118	0	699	576	559	819	637	803	858	608	771	862
ENSMUSG00000030108	chr6	Slc6a13	-0.3026418	0.430282472	0.500676698	0.651929953	0.108919455	0	16	16	20	31	36	19	19	23	11	34
ENSMUSG00000029617	chr5	Ccz1	-0.1146123	0.430654226	0.501067554	5.036480983	0.023142198	0	550	506	438	623	426	575	585	402	552	456
ENSMUSG00000024990	chr19	Rbp4	-0.3170217	0.430736604	0.501121683	1.688629641	0.165412967	0	25	80	38	38	69	101	29	36	31	34
ENSMUSG00000026887	chr2	Mrrf	0.11805493	0.4308309	0.501189667	4.364955521	0.02377768	0	275	250	277	404	268	315	362	328	374	354
ENSMUSG00000048349	chr14	Pou4f1	-0.2318323	0.431138364	0.501505599	1.268174596	0.065494313	0	38	34	28	54	32	26	42	22	32	50
ENSMUSG00000001156	chr6	Mxd1	0.1916721	0.431206071	0.501542614	2.776355412	0.056588986	0	117	92	91	83	80	189	109	97	74	125
ENSMUSG00000057147	chr2	Dph6	-0.1823025	0.431293565	0.501602634	2.244015733	0.046802836	0	66	78	65	104	56	70	100	57	60	67
ENSMUSG00000050490	chr10	Gm8394	0.24515446	0.431623466	0.501944546	0.877793849	0.073541034	0	31	24	13	28	21	29	29	21	27	46

ENSMUSG00000044339	chr5	Alkbh2	0.32371246	0.431946874	0.502278852	1.473517533	0.160681361	0	35	40	44	29	24	121	38	30	35	23
ENSMUSG00000025736	chr17	Jmjd8	-0.1377292	0.432164708	0.502490347	3.958911177	0.031872622	0	279	201	193	273	257	199	242	248	217	288
ENSMUSG00000020876	chr11	Snx11	0.13786377	0.432292389	0.502596991	3.965120981	0.031671327	0	257	260	173	211	191	339	260	228	267	236
ENSMUSG00000068015	chr14	Lrch1	0.16455942	0.432355064	0.502628047	2.41744804	0.037681756	0	67	67	64	102	69	121	93	71	73	96
ENSMUSG00000034258	chr12	Mfsd7c	-0.3904673	0.432519935	0.502777893	0.213350611	0.209933859	0	34	17	10	11	15	4	13	14	10	32
ENSMUSG00000078919	chr2	Dpm1	-0.1178117	0.432768428	0.503024912	5.359518751	0.025368385	0	679	686	568	721	519	714	754	499	643	608
ENSMUSG00000001420	chr3	Tmem79	-0.2553068	0.433442747	0.503766805	0.950157459	0.083102629	0	32	34	33	29	18	17	31	30	20	36
ENSMUSG00000012422	chr13	Tmem167	0.12591515	0.433730888	0.504052008	4.947018367	0.0284921	0	546	399	361	481	401	659	579	402	552	439
ENSMUSG00000017715	chr11	Pgs1	0.11739514	0.433760268	0.504052008	4.952761802	0.024395034	0	437	409	458	507	388	655	517	404	575	481
ENSMUSG00000086503	chrX	Xist	-1.4237457	0.433838463	0.50410096	5.334826648	3.264970918	0	1	1	3	2067	2442	1971	1	4	0	2
ENSMUSG00000079442	chr2	St6galnac4	0.13301195	0.43454572	0.504880787	5.352588618	0.03307398	0	481	448	491	914	605	897	708	681	551	659
ENSMUSG00000040918	chr1	Slc19a2	-0.2168957	0.434687444	0.505003468	1.852595332	0.070380555	0	38	66	69	64	41	46	77	39	49	53
ENSMUSG00000044405	chr2	Adig	0.43927379	0.43478641	0.505076458	1.062811932	0.333151691	0	3	48	21	19	30	11	23	56	22	70
ENSMUSG00000036572	chrX	Upf3b	-0.1406201	0.435679575	0.506071953	3.931894937	0.034086063	0	311	212	200	281	185	223	283	160	246	268
ENSMUSG00000028975	chr4	Pex14	0.11991469	0.436241101	0.506682093	4.609313202	0.025614104	0	301	346	320	460	315	408	391	450	335	476
ENSMUSG00000022241	chr15	Tars	0.11075939	0.436331002	0.506741957	5.482906225	0.022686494	0	642	591	540	806	627	772	849	656	745	761
ENSMUSG00000029603	chr5	Dtx1	0.3357016	0.436366037	0.506741957	0.313017693	0.138790869	0	16	8	20	11	17	37	13	22	21	9
ENSMUSG00000056214	chr18	Pard6g	0.220895	0.436401416	0.506741957	1.430180811	0.068138136	0	56	35	26	37	23	53	42	47	33	51
ENSMUSG00000019998	chr10	Stx7	0.11217086	0.436719643	0.507027225	5.115298598	0.022871283	0	479	467	449	627	459	534	691	486	563	657
ENSMUSG00000020153	chr10	Ndufs7	0.12605636	0.436686722	0.507027225	8.001674468	0.031221598	0	3152	3497	3284	5356	3183	5798	4065	4135	3936	3993
ENSMUSG00000042535	chr15	Gtpbp1	-0.1229985	0.436932825	0.507232591	4.923515439	0.027593604	0	406	352	457	639	504	551	452	474	384	507
ENSMUSG00000032580	chr9	Rbm5	-0.1197592	0.436985126	0.507251173	5.371854879	0.026962159	0	629	593	601	706	658	908	591	526	609	624
ENSMUSG00000039693	chr4	Msantd3	0.12099983	0.437268211	0.507537623	3.623219872	0.022988153	0	188	150	167	203	162	225	223	193	205	191
ENSMUSG00000024176	chr17	Sox8	0.20680948	0.437717347	0.508016745	1.941672517	0.062365167	0	56	57	38	64	43	70	70	70	33	83
ENSMUSG00000079316	chrX	Rab9	-0.1272438	0.43776349	0.50802811	3.970654686	0.027706461	0	253	212	217	291	238	247	240	225	184	322
ENSMUSG00000031812	chr8	Map1lc3b	-0.1179876	0.437928941	0.508177921	7.424829272	0.027319338	0	2896	2641	2218	3258	2353	3325	2565	2287	2830	2481
ENSMUSG00000028093	chr3	Acp6	-0.1237358	0.438151221	0.508393646	4.00197545	0.025495811	0	255	225	239	325	199	281	213	260	254	231
ENSMUSG00000002265	chr7	Peg3	0.21116573	0.438318642	0.508545687	6.664875365	0.087842353	0	1835	1275	1015	1015	1725	1170	1434	2104	1209	2901
ENSMUSG00000003423	chr7	Pih1d1	0.13706592	0.438403594	0.508553236	5.469333568	0.035722586	0	693	591	529	777	559	1234	655	621	672	643
ENSMUSG00000022261	chr15	Sdc2	-0.119323	0.438434312	0.508553236	5.687451566	0.027092901	0	807	677	632	970	905	922	851	726	664	879
ENSMUSG00000025129	chr11	Ppp1r27	-0.1623586	0.438432351	0.508553236	6.766483812	0.051753064	0	1394	1360	1300	3202	1567	2330	1288	1740	1683	1347
ENSMUSG00000054855	chr15	Rnd1	0.25365475	0.438643622	0.508753798	0.816526246	0.086307115	0	14	14	18	37	29	41	34	25	20	26
ENSMUSG00000054405	chr4	Dnajc8	0.11012225	0.439723663	0.509964145	5.422881712	0.022696948	0	639	557	561	802	526	890	795	651	637	669
ENSMUSG00000070934	chr4	Rraga	-0.1118771	0.440527077	0.510853504	5.374462885	0.023486947	0	639	590	595	790	593	613	766	576	571	723
ENSMUSG00000028565	chr4	Nfia	-0.1219426	0.441129405	0.511509546	5.343917446	0.028189165	0	615	630	506	764	633	715	564	728	496	658
ENSMUSG00000026269	chr1	Rnpepl1	-0.1151608	0.441524045	0.511924676	6.047377892	0.025752483	0	955	926	847	1338	1071	1262	937	966	941	1086
ENSMUSG00000035062	chrX	Zc4h2	0.24940161	0.441860256	0.512229507	1.082566553	0.087123952	0	40	22	31	32	11	35	48	28	28	38
ENSMUSG00000052560	chr15	Cpne8	0.23203882	0.441842493	0.512229507	1.861050415	0.087059373	0	40	32	49	86	38	108	68	53	41	43
ENSMUSG00000052763	chr6	Zfp212	-0.1315311	0.441915484	0.512251041	3.313084017	0.028003191	0	159	149	147	193	120	157	159	128	129	195
ENSMUSG00000074506	chr3	Gm10705	-0.30496	0.44244212	0.512818964	0.153304613	0.095538421	0	13	16	11	24	18	14	24	11	16	7
ENSMUSG00000024427	chr18	Spry4	-0.1717985	0.442649973	0.513017334	3.290958641	0.051446571	0	141	124	196	198	106	232	159	130	116	113
ENSMUSG00000047731	chr19	Wbp1l	-0.1178938	0.442751971	0.513092997	6.030690641	0.02715727	0	918	872	837	1393	1076	1168	951	916	912	1182
ENSMUSG00000029179	chr5	Zcchc4	0.16158159	0.442879196	0.513197881	2.522831087	0.041893416	0	90	75	57	112	66	82	113	80	99	110
ENSMUSG00000017550	chr11	Atad5	0.25771563	0.442983647	0.513276359	1.178244604	0.099251422	0	24	23	22	43	34	26	67	30	40	26
ENSMUSG00000027254	chr2	Map1a	-0.1666855	0.443220494	0.513465652	3.957445039	0.05080462	0	243	194	211	365	219	262	185	351	163	214
ENSMUSG00000097164	chr10	Cep83os	0.21984203	0.443193095	0.513465652	1.486506484	0.070262019	0	55	37	23	42	28	36	49	49	39	61
ENSMUSG00000049115	chr13	Agtr1a	-0.1631484	0.443277815	0.513489494	2.467733427	0.041087405	0	86	97	79	86	75	80	73	83	75	105
ENSMUSG00000023911	chr17	Flywch2	-0.3096884	0.44363204	0.513857235	0.059946669	0.096694527	0	17	11	10	26	13	15	7	11	11	23
ENSMUSG00000024120	chr17	Lrpprc	-0.130895	0.444687422	0.515036994	6.580248251	0.034241786	0	1253	1392	1431	2208	1249	1245	1536	1662	1479	1459
ENSMUSG00000038685	chr2	Rtel1	0.14267247	0.444856022	0.515189572	3.337720109	0.034558733	0	150	122	119	155	158	195	178	139	205	138
ENSMUSG00000022779	chr16	Top3b	-0.1160682	0.445700156	0.516124399	3.89403015	0.023141474	0	232	203	189	282	239	283	238	200	195	246
ENSMUSG00000020863	chr11	Luc7l3	-0.1118447	0.445920784	0.516337107	5.491377004	0.024260224	0	786	690	609	777	607	799	753	586	737	653
ENSMUSG00000015053	chr6	Gata2	-0.2125343	0.446092828	0.516493527	2.291252576	0.077830342	0	57	52	62	125	91	126	76	50	53	62
ENSMUSG00000014470	chr8	Rnf166	-0.1195175	0.446505891	0.516928954	4.8365843	0.026942767	0	446	449	433	549	338	423	403	367	449	587
ENSMUSG00000061474	chr13	Mrps36	-0.1050893	0.446633362	0.5170337	5.121144714	0.020712448	0	565	547	471	672	436	623	566	537	474	532
ENSMUSG00000035530	chr11	Eif1	0.12984529	0.446687716	0.517053795	8.738311717	0.034727065	0	5879	5351	4966	8381	6066	10723	6807	6340	6528	6350
ENSMUSG00000052676	chrX	Zmat1	-0.263274	0.447074851	0.517459058	0.544550952	0.082255506	0	26	21	15	21	25	15	25	11	26	22
ENSMUSG00000038324	chr2	Trpc4ap	-0.1120693	0.447237719	0.5176047	7.036179451	0.025511894	0	1886	1825	1740	2722	2037	2414	1915	1850	1969	2171
ENSMUSG00000030790	chr7	Adm	0.19382277	0.447377118	0.51772316	1.859999071	0.053239165	0	54	44	44	50	50	90	54	63	42	58
ENSMUSG00000004462	chr16	Tbccd1	-0.1385557	0.447484263	0.517804277	2.990410414	0.029831654	0	130	127	97	150	109	128	112	124	104	140
ENSMUSG00000034430	chr6	Zxdc	0.11211996	0.447710034	0.518022638	4.070695651	0.022032272	0	243	210	199	322	229	291	297	246	266	317
ENSMUSG00000027678	chr2	Ncoa3	0.13961262	0.447983862	0.518296561	4.544976929	0.037089154	0	289	283	289	447	347	634	431	294	331	326
ENSMUSG00000024845	chr19	Tmem134	0.11399338	0.448107401	0.518396576	6.085708536	0.025916526	0	954	1002	879	1121	888	1529	1101	1029	1081	1043
ENSMUSG00000031584	chr8	Gsr	-0.1245286	0.448513105	0.518822973	4.758341633	0.029690812	0	462	454	385	524	282	531	485	313	413	378
ENSMUSG00000089875	chr13	Etohd2	-0.2572561	0.448741904	0.519044678	0.839559798	0.086884818	0	40	23	20	32	21	28	15	36	20	24

ENSMUSG00000020823	chr11	Sec14l1	0.11110452	0.448789998	0.519057349	6.270377039	0.024820741	0	1202	1066	1032	1267	951	1507	1267	1284	1092	1399
ENSMUSG00000037363	chr8	Letm2	-0.1925392	0.448846778	0.519080064	1.694267828	0.050782589	0	45	56	50	52	43	39	48	41	45	64
ENSMUSG00000046605	chr11	B3gntl1	0.21680885	0.448897776	0.519096088	1.582318442	0.067572291	0	41	46	41	53	18	60	55	46	33	59
ENSMUSG00000013523	chr2	Bcas1	-0.3113151	0.449703167	0.519984402	0.311432926	0.109170418	0	8	16	21	24	23	13	21	22	9	16
ENSMUSG00000050666	chr14	Vstm4	0.16825296	0.449817786	0.520073906	3.288292514	0.052170125	0	156	128	122	152	118	202	131	195	89	219
ENSMUSG00000085436	chr2	Zfp335os	0.20124938	0.449990208	0.520230221	1.812316575	0.06268245	0	59	31	41	56	48	47	50	57	77	62
ENSMUSG00000017734	chr2	Dbndd2	-0.1247601	0.450462083	0.520692961	4.739992552	0.029935855	0	425	404	354	578	330	605	415	346	405	323
ENSMUSG00000028647	chr4	Mycbp	-0.1199208	0.450464983	0.520692961	3.669926507	0.02397769	0	218	184	164	246	171	195	205	179	216	189
ENSMUSG00000030849	chr7	Fgfr2	-0.2842636	0.450779716	0.521013672	0.476165822	0.113798733	0	22	12	20	28	22	41	15	13	10	16
ENSMUSG00000025184	chr19	R3hcc1l	0.12255556	0.451006174	0.521232307	3.59502241	0.02477308	0	155	167	169	195	164	252	191	168	213	197
ENSMUSG00000022122	chr14	Ednrb	-0.1763541	0.452219446	0.522579104	3.606699782	0.059999159	0	143	196	197	297	134	300	220	140	165	111
ENSMUSG00000040177	chr7	2310057M21Rik	0.1340731	0.452246298	0.522579104	3.329528038	0.030922866	0	151	122	151	170	112	227	161	169	145	149
ENSMUSG00000092118	chr7	Fancf	0.28872005	0.452584449	0.522926608	0.505999254	0.109570691	0	14	20	6	24	23	16	28	18	19	35
ENSMUSG00000031865	chr6	Dctn1	-0.120094	0.452692757	0.523008512	7.159661098	0.030121225	0	2213	1842	1912	2887	2284	2137	2022	2228	2032	2737
ENSMUSG00000020070	chr10	Rufy2	-0.182795	0.452937734	0.523248286	2.090763051	0.053068272	0	79	75	49	63	60	66	59	45	60	88
ENSMUSG00000058886	chr7	Deaf1	0.11739198	0.453257947	0.523574929	3.736995712	0.023778376	0	187	163	175	237	184	271	188	215	213	237
ENSMUSG00000049892	chr11	Rasd1	0.35047709	0.453316351	0.523599117	0.271208897	0.167075612	0	7	24	10	15	14	32	14	30	6	17
ENSMUSG00000099034	chr15	2810039B14Rik	0.32710266	0.453373759	0.523622152	0.485422267	0.148914621	0	35	11	12	9	16	14	36	23	21	21
ENSMUSG00000047759	chr11	Hs3st3a1	-0.3333687	0.453426991	0.523640359	-0.212124181	0.142860609	0	8	10	14	21	9	19	19	6	4	6
ENSMUSG00000020758	chr11	Itgb4	-0.2074766	0.453767447	0.523990237	2.421081215	0.078229682	0	43	72	96	112	94	126	88	67	50	71
ENSMUSG00000024210	chr17	Ip6k3	0.12214361	0.453969756	0.52413747	6.26728153	0.030915462	0	1004	920	1125	1422	1031	1511	1296	1351	923	1485
ENSMUSG00000029141	chr5	Slc4a1ap	0.11198289	0.453969954	0.52413747	4.039830949	0.022398621	0	238	252	191	289	203	303	267	251	255	311
ENSMUSG00000007030	chr17	Vwa7	-0.1580803	0.454162728	0.524316727	3.298746206	0.044561932	0	176	145	104	200	145	106	162	164	173	136
ENSMUSG00000044469	chr17	Tnfaip8l1	0.24159932	0.454344168	0.524482869	1.667538978	0.099569827	0	48	35	61	43	20	71	32	68	47	51
ENSMUSG00000042644	chr17	Itpr3	-0.1878278	0.454434445	0.524543756	2.817247783	0.064091223	0	98	90	113	161	93	194	98	71	67	110
ENSMUSG00000029659	chr5	Medag	0.12392225	0.454602176	0.52469403	4.115257769	0.028291045	0	254	268	223	268	210	379	320	258	289	224
ENSMUSG00000030695	chr7	Aldoa	-0.1264646	0.455717393	0.525937761	13.94996489	0.034450657	0	234340	209261	195291	334132	266242	228848	238442	239113	221954	305255
ENSMUSG00000060739	chr13	Nsa2	0.11887321	0.455940202	0.526151454	5.408680517	0.028648651	0	717	618	576	617	483	704	737	593	809	753
ENSMUSG00000026639	chr1	Lamb3	-0.2434115	0.456063381	0.526250149	0.849069821	0.077266812	0	22	35	27	29	22	17	25	34	25	23
ENSMUSG00000053093	chr14	Myh7	-1.0082271	0.456313885	0.526495736	7.694951185	1.958376799	0	10	102	19	25327	31	8372	44	960	2306	125
ENSMUSG00000015134	chr7	Aldh1a3	0.23451476	0.456418196	0.526572619	1.709495658	0.093563073	0	30	55	45	43	40	46	40	90	47	50
ENSMUSG00000023249	chr9	Parp3	0.14217253	0.456546081	0.526676685	5.724327343	0.042299933	0	916	723	724	743	608	612	936	917	1071	928
ENSMUSG00000004035	chr3	Gstm7	-0.2275513	0.456861875	0.526997489	1.734280652	0.090483236	0	36	48	52	74	49	90	31	48	44	30
ENSMUSG00000040740	chr4	Slc25a34	-0.2561939	0.457122419	0.527254513	3.62467871	0.134328372	0	46	201	174	433	173	207	139	156	252	150
ENSMUSG00000027947	chr3	Il6ra	0.23685437	0.45720551	0.527306834	1.745293132	0.0890576	0	25	51	42	47	53	56	71	26	63	71
ENSMUSG00000035125	chr6	Gcfc2	0.21506991	0.457701098	0.52783485	1.244833362	0.063800727	0	32	33	20	33	36	29	50	33	42	42
ENSMUSG00000000934	chr15	Top1mt	-0.1272977	0.458818359	0.529079652	3.291048205	0.028461621	0	145	128	153	180	145	173	167	149	142	123
ENSMUSG00000027905	chr3	Ddx20	-0.127192	0.45887166	0.52909746	3.229193843	0.027920301	0	170	141	118	149	139	153	143	137	137	152
ENSMUSG00000022761	chr16	Lztr1	0.1084813	0.459303039	0.529551169	5.007229352	0.023258207	0	488	515	427	484	373	652	542	460	541	528
ENSMUSG00000040463	chr11	Mybbp1a	-0.1150902	0.459565478	0.529810041	6.087186722	0.027915261	0	945	886	864	1481	1126	1167	1191	991	902	1082
ENSMUSG00000026688	chr1	Mgst3	-0.1686035	0.459898399	0.530150118	6.526407827	0.061467515	0	1198	1549	1552	1905	1084	2420	1177	1460	1268	805
ENSMUSG00000020720	chr11	Psmd12	-0.1104193	0.459977191	0.530153491	6.707653173	0.026017541	0	1761	1542	1348	2151	1348	1603	1748	1410	1690	1743
ENSMUSG00000022635	chr15	Zcrb1	-0.1106336	0.459958908	0.530153491	5.913169914	0.025564064	0	967	903	750	1225	842	964	1075	830	1005	842
ENSMUSG00000079184	chr14	Mphosph8	-0.1143982	0.460155201	0.530314925	3.980985112	0.023614028	0	271	236	205	297	209	240	237	253	251	242
ENSMUSG00000035799	chr12	Twist1	0.24465802	0.460278725	0.530401588	1.622148886	0.097600869	0	69	36	35	29	30	62	79	37	33	53
ENSMUSG00000092367	chr7	Gm20479	0.28176098	0.460306301	0.530401588	0.056413696	0.082991263	0	7	12	9	15	18	19	21	11	16	15
ENSMUSG00000032193	chr9	Ldlr	-0.1381018	0.460449445	0.53052279	4.4452999	0.038615706	0	368	291	363	342	313	327	471	329	316	236
ENSMUSG00000030602	chr7	Pak4	0.11482429	0.460648717	0.530708637	4.542310349	0.025805639	0	294	288	315	465	309	537	409	338	313	388
ENSMUSG00000020439	chr11	Smtn	-0.1197543	0.46076419	0.530797916	7.082474767	0.031000855	0	2009	1982	1780	2788	2013	2167	1853	2489	1782	2253
ENSMUSG00000025036	chr19	Sfxn2	-0.1848789	0.460865401	0.530870752	2.418658248	0.062821665	0	100	93	71	50	91	91	83	63	78	86
ENSMUSG00000057554	chr13	Lgals8	-0.1085372	0.461112944	0.531112123	4.745246571	0.023218964	0	465	414	384	497	311	425	431	343	438	463
ENSMUSG00000007888	chr8	Crlf1	0.27162402	0.461232678	0.53120505	2.064300732	0.141161625	0	33	57	31	94	63	171	49	52	47	52
ENSMUSG00000081087	chr2	Rps15a-ps7	-0.3322192	0.46126964	0.53120505	4.213255919	0.236862639	0	289	296	249	409	296	939	134	125	103	108
ENSMUSG00000036353	chr3	P2ry12	0.30146367	0.461924587	0.531915467	0.380968929	0.123585061	0	18	8	20	11	20	15	16	18	35	21
ENSMUSG00000020681	chr11	Ace	0.1362335	0.46224839	0.532200634	6.153017842	0.039859405	0	903	1034	1109	920	995	1357	1075	1151	878	1644
ENSMUSG00000034926	chr4	Dhcr24	0.222341	0.462234101	0.532200634	3.422265622	0.101708994	0	114	123	127	202	166	209	245	198	220	52
ENSMUSG00000064105	chr19	Cnnm2	0.21221186	0.462355026	0.532279559	1.652235614	0.076536292	0	31	29	39	79	35	57	53	54	31	70
ENSMUSG00000030008	chr6	Pradc1	-0.1261656	0.462400048	0.532287544	3.321883321	0.028695839	0	171	171	128	164	132	158	146	159	135	172
ENSMUSG00000044139	chr7	Prss53	-0.2047953	0.462503154	0.532362385	1.168243131	0.059551951	0	36	30	28	32	42	45	30	24	34	29
ENSMUSG00000047963	chr5	Stbd1	0.12339304	0.462759032	0.532613047	7.32187488	0.033393744	0	3049	2019	1743	2501	2101	2793	2443	2522	2799	3035
ENSMUSG00000028836	chr4	Slc30a2	-0.2556273	0.463103795	0.532965962	2.229748191	0.126762829	0	64	55	125	92	34	99	37	76	82	45
ENSMUSG00000007877	chr11	Tcap	-0.1872226	0.463383575	0.533200135	10.83465762	0.077902336	0	28344	32075	30381	33840	20186	56721	24172	22445	23243	15619
ENSMUSG00000027663	chr3	Zmat3	-0.121339	0.463368299	0.533200135	3.88925714	0.027514196	0	212	200	216	290	225	204	265	247	189	240
ENSMUSG00000071014	chr4	Ndufb6	0.10828859	0.463440808	0.533222091	6.87185197	0.025558493	0	1707	1687	1669	2093	1265	2140	1997	1916	1872	1981
ENSMUSG00000020149	chr11	Rab1	-0.1167175	0.463828089	0.533623755	7.015982657	0.029845582	0	1915	1838	1738	2762	1857	1885	2533	1554	1970	2212

ENSMUSG00000022570	chr15	Tsta3	-0.1105904	0.464240061	0.534053757	4.331500934	0.023752586	0	311	304	270	363	299	321	302	251	370	326
ENSMUSG00000026839	chr2	Upp2	-0.2822445	0.464315114	0.534094517	0.287839205	0.086252593	0	23	19	16	21	11	27	13	17	15	9
ENSMUSG00000039254	chr2	Pomt1	-0.126302	0.464351923	0.534094517	3.932278821	0.03085807	0	231	205	191	283	267	201	261	209	210	301
ENSMUSG00000003234	chr16	Abcf3	0.1025909	0.464593706	0.53432864	5.866499938	0.022407637	0	886	798	710	1047	760	1108	931	910	1011	962
ENSMUSG00000091471	chr19	Gm20538	0.11690423	0.464848481	0.534577666	7.83147252	0.030364827	0	2933	3201	3255	4384	2608	4687	3414	3531	4147	3574
ENSMUSG00000048696	chr10	Mex3d	-0.1429883	0.465090459	0.534780764	2.619256318	0.034456096	0	94	78	100	101	95	110	101	80	83	95
ENSMUSG00000101174	chr2	Hoxd4	-0.3555578	0.465101616	0.534780764	-0.183778513	0.141912206	0	16	16	15	11	5	11	5	6	20	12
ENSMUSG00000038187	chr7	Btbd10	-0.1332827	0.465196758	0.534846157	3.176693478	0.032678891	0	142	148	123	156	125	148	177	94	129	151
ENSMUSG00000040289	chr3	Hey1	-0.1726637	0.465457171	0.53510154	2.341180338	0.04837771	0	68	82	64	107	72	76	64	94	56	88
ENSMUSG00000036461	chr14	Elf1	-0.1327443	0.465865226	0.5355266	3.067158858	0.030501599	0	127	119	133	169	99	136	135	96	138	140
ENSMUSG00000089902	chr2	Gm13625	0.21525885	0.466208652	0.535877303	1.081252383	0.062960724	0	33	21	28	37	19	26	46	30	33	39
ENSMUSG00000028618	chr4	Tmem59	0.11348701	0.466390088	0.536041766	6.625088368	0.028266452	0	1530	1446	1282	1578	1209	2222	1734	1352	1351	1791
ENSMUSG00000026494	chr1	Kif26b	-0.2493599	0.467506403	0.537280609	1.630690752	0.106701565	0	41	28	40	83	53	60	33	52	18	60
ENSMUSG00000014786	chr8	Slc9a5	0.20712781	0.468199787	0.538033237	1.276686453	0.057750341	0	42	35	26	30	25	51	43	39	38	30
ENSMUSG00000067586	chr13	S1pr3	-0.1254421	0.468261589	0.538060015	3.875116298	0.030662562	0	273	220	217	259	164	265	236	249	171	216
ENSMUSG00000045917	chr4	6330416G13Rik	-0.12439	0.468563001	0.538362093	3.869467951	0.029986035	0	209	182	229	303	209	192	259	179	233	269
ENSMUSG00000002307	chr17	Daxx	0.11595111	0.468809733	0.538601301	3.759281888	0.02448666	0	199	174	199	205	177	261	220	211	188	263
ENSMUSG00000003662	chr2	Ciao1	0.10568864	0.468938798	0.538634681	5.143521564	0.023659975	0	545	498	461	629	406	534	650	615	548	621
ENSMUSG00000028755	chr4	Cda	0.28282467	0.468908695	0.538634681	0.262948094	0.095040606	0	11	14	12	25	11	29	19	24	14	10
ENSMUSG00000097392	chr5	D930016D06Rik	0.16440703	0.468954408	0.538634681	2.262039898	0.046970117	0	54	60	64	92	60	60	82	84	83	91
ENSMUSG00000052712	chr17	BC004004	0.10438829	0.469296901	0.538983769	6.446547096	0.024129371	0	1386	1141	1080	1499	1161	1555	1553	1339	1451	1470
ENSMUSG00000034135	chr9	Sik3	-0.1131038	0.469604729	0.53929299	5.21546197	0.027239324	0	506	515	485	783	596	535	585	554	497	733
ENSMUSG00000050777	chr1	Tmem37	0.16678576	0.470708392	0.540516021	5.030006886	0.061467421	0	428	507	524	537	287	904	311	611	418	589
ENSMUSG00000036904	chr18	Fzd8	0.16542375	0.470755361	0.540525544	2.411191518	0.047180447	0	59	68	74	94	70	108	91	86	55	111
ENSMUSG00000020400	chr11	Tnip1	-0.1132655	0.470984583	0.540744313	5.695991356	0.028195059	0	895	780	670	919	741	769	808	764	664	1056
ENSMUSG00000048921	chr7	Zfp689	-0.2550965	0.471522698	0.541317663	0.363399182	0.078125227	0	10	23	17	23	21	20	21	10	17	19
ENSMUSG00000033022	chr18	Cdo1	-0.4266019	0.471792002	0.541582342	3.249958989	0.403542507	0	34	398	102	43	188	30	89	207	72	245
ENSMUSG00000045996	chr15	Polr2k	-0.134074	0.472194474	0.541999833	3.640549315	0.035664493	0	226	218	159	204	154	181	232	141	225	182
ENSMUSG00000082431	chr1	Tdpx-ps1	-0.3282112	0.47266852	0.542499403	-0.024665343	0.138892998	0	18	11	21	15	6	24	6	10	7	16
ENSMUSG00000021902	chr14	Phf7	-0.1452101	0.473008353	0.542800291	2.593055018	0.037728323	0	83	82	83	121	95	99	74	76	97	113
ENSMUSG00000035342	chr19	Lzts2	0.11972743	0.472986645	0.542800291	4.68963865	0.030403206	0	291	332	350	496	372	594	388	451	338	423
ENSMUSG00000031955	chr8	Bcar1	0.10856092	0.473285115	0.543073298	4.061646242	0.023309092	0	236	208	202	307	240	286	270	287	259	299
ENSMUSG00000037139	chr4	Myom3	0.34450026	0.473742482	0.543553479	5.941123877	0.272281143	0	136	609	739	2403	449	1444	766	2091	707	492
ENSMUSG00000036646	chr2	Man1b1	0.09699304	0.473849903	0.5436321	4.961914907	0.019479569	0	443	429	404	537	423	617	521	426	504	564
ENSMUSG00000042699	chr1	Dhx9	0.11439059	0.473969074	0.543724188	5.738460242	0.029334727	0	750	713	603	1038	739	807	1171	779	891	867
ENSMUSG00000074807	chr2	Gm10762	0.166058	0.474135132	0.543870043	2.994913924	0.055875981	0	105	107	95	159	91	78	153	120	129	194
ENSMUSG00000054226	chr6	Tprkb	-0.1121605	0.474278756	0.543990143	4.749966607	0.026984097	0	490	402	374	444	358	532	418	305	463	396
ENSMUSG00000048218	chr15	Amigo2	0.2213918	0.474666733	0.54439047	1.608777719	0.087905894	0	25	35	31	60	51	92	53	34	39	43
ENSMUSG00000023353	chr5	Agap3	0.10210764	0.47485875	0.544521323	5.160145876	0.022310601	0	438	492	477	657	502	727	572	504	560	665
ENSMUSG00000039850	chr11	Endov	-0.1446939	0.474836798	0.544521323	2.835133066	0.038758472	0	106	83	109	141	111	107	109	82	102	146
ENSMUSG00000041889	chr1	Shisa4	0.10541402	0.475052981	0.544699357	7.694688239	0.025774831	0	3132	2715	2716	3571	2746	3584	3354	3498	3392	3650
ENSMUSG00000015217	chrX	Hmgb3	0.13231888	0.475107217	0.544716855	3.457534059	0.033741279	0	142	161	152	191	127	200	227	199	160	139
ENSMUSG00000021484	chr13	Lman2	0.10258559	0.475626656	0.545222945	6.694060401	0.024074138	0	1484	1322	1343	1819	1471	1941	1914	1550	1649	1708
ENSMUSG00000040877	chr12	Wdr25	-0.1537422	0.475612253	0.545222945	2.270918156	0.039367246	0	74	65	66	97	69	103	73	54	63	74
ENSMUSG00000082029	chr2	H3f3c	-0.3050334	0.475710402	0.545274221	0.251189912	0.167541927	0	18	28	16	8	16	13	9	7	28	21
ENSMUSG00000004187	chr15	Kifc2	-0.1962213	0.47623639	0.545832359	1.672535425	0.067570599	0	53	57	55	41	35	60	31	49	50	43
ENSMUSG00000044348	chrX	Slc25a53	0.24508848	0.476631324	0.546240212	0.589508816	0.077591895	0	24	17	16	16	20	27	14	21	27	33
ENSMUSG00000034570	chr11	Inpp5j	-0.3059841	0.476891193	0.546466546	1.74858007	0.191957416	0	14	42	44	133	46	74	38	62	39	22
ENSMUSG00000070425	chr7	Trpc2	0.16560007	0.476907016	0.546466546	2.08349909	0.047011533	0	55	54	59	81	42	90	83	58	48	79
ENSMUSG00000001802	chr7	Lrp3	0.14537014	0.477066889	0.546560114	3.110737151	0.041479693	0	128	107	101	146	121	103	148	164	130	179
ENSMUSG00000081228	chr5	Gm16089	0.18468538	0.477054899	0.546560114	1.589771769	0.054538418	0	39	41	35	38	46	53	42	57	38	60
ENSMUSG00000030678	chr7	Maz	-0.1053617	0.477381292	0.546875486	6.347009632	0.025479112	0	1132	1137	1122	1629	1277	1484	1267	1081	1321	1257
ENSMUSG00000040913	chr19	Fbxw4	0.10833479	0.477720218	0.547218897	4.57404098	0.025017953	0	270	344	277	487	336	473	396	364	394	384
ENSMUSG00000097047	chr17	1110020A21Rik	0.20106161	0.477839433	0.547310598	0.940927415	0.056606678	0	26	18	26	35	20	33	24	32	34	33
ENSMUSG00000079658	chr1	Tceb1	0.10719099	0.477881493	0.547313918	6.327939588	0.026512779	0	1337	1052	988	1425	982	1372	1355	1242	1490	1314
ENSMUSG00000037300	chr8	Ttc13	0.10411914	0.477924735	0.547318592	4.583044296	0.022706532	0	358	325	282	398	348	382	457	356	408	411
ENSMUSG00000026648	chr2	Dclre1c	0.25458303	0.478094953	0.547443975	1.290683135	0.109163493	0	34	25	41	31	25	54	32	17	66	38
ENSMUSG00000068290	chr2	Ddrgk1	0.10134111	0.478112561	0.547443975	6.031822457	0.023333995	0	929	881	786	1154	952	1258	1095	965	1091	1122
ENSMUSG00000058013	chr5	Sept11	-0.1020647	0.478171227	0.547466295	6.278253436	0.023957726	0	1221	1162	1029	1367	1187	1356	1263	1114	1061	1327
ENSMUSG00000069171	chr13	Nr2f1	0.24775058	0.478744331	0.548077553	0.330217943	0.070167096	0	13	16	17	20	11	18	15	17	21	29
ENSMUSG00000027087	chr2	Itgav	-0.1135753	0.479195283	0.54854888	5.157519702	0.028706887	0	591	497	516	688	473	477	751	473	545	540
ENSMUSG00000006599	chr7	Gtf2h1	-0.1065123	0.479357311	0.548689417	4.416778824	0.023892369	0	368	296	306	392	282	423	336	260	356	303
ENSMUSG00000029387	chr5	Gtf2h3	-0.1216517	0.479793132	0.549143298	3.507251214	0.028196917	0	173	173	141	252	145	163	205	146	164	203
ENSMUSG00000075389	chr11	2810410L24Rik	-0.1920019	0.480055674	0.549398796	1.389870616	0.057344331	0	35	29	44	48	42	51	34	41	26	39
ENSMUSG00000064284	chr15	Cdpf1	0.12781397	0.480228732	0.549551851	4.011412371	0.034778949	0	253	204	234	260	187	235	248	240	360	271

ENSMUSG00000022125	chr14	Cln5	0.15112466	0.480762316	0.550117417	3.843124154	0.049130392	0	240	244	174	207	137	249	353	144	242	243
ENSMUSG00000030922	chr7	Lyrm1	-0.1418585	0.481255942	0.550637171	2.561924103	0.037124079	0	82	86	97	115	73	93	104	68	79	107
ENSMUSG00000033326	chr4	Kdm4a	-0.1122967	0.481462751	0.5508287	4.987704103	0.028072052	0	489	393	402	645	530	540	464	531	379	567
ENSMUSG00000033335	chr9	Dnm2	0.10493545	0.481519073	0.550848045	5.757794093	0.025259483	0	724	645	730	1044	755	1149	883	715	908	942
ENSMUSG00000048076	chr11	Arf1	0.10396648	0.481610496	0.550872702	7.802273335	0.025842962	0	3204	2998	2833	4050	2996	4250	4225	3085	3725	3651
ENSMUSG00000057497	chr6	Fam136a	-0.1216108	0.481619458	0.550872702	4.206058144	0.031174704	0	338	271	236	370	221	257	323	237	350	261
ENSMUSG00000019842	chr10	Traf3ip2	0.17957078	0.481786968	0.550974116	1.944085816	0.056244871	0	47	48	65	55	43	50	78	56	74	63
ENSMUSG00000036661	chr15	Dennd3	-0.1842327	0.481784702	0.550974116	2.146547126	0.061042985	0	56	50	59	119	64	95	64	51	44	79
ENSMUSG00000040605	chr16	Bace2	0.16562609	0.48249799	0.551742097	2.384996475	0.049730093	0	63	66	86	85	57	122	96	87	69	68
ENSMUSG00000028277	chr4	Ube2j1	0.09602254	0.482656711	0.551878442	5.153691901	0.020410248	0	523	482	452	645	463	704	606	520	610	559
ENSMUSG00000003868	chr7	Ruvbl2	0.10859276	0.482931277	0.552147212	4.659068511	0.026046426	0	357	298	309	516	342	496	471	438	319	411
ENSMUSG00000026260	chr1	Ndufa10	-0.1124301	0.483022412	0.552206236	8.334109538	0.03055118	0	4410	4881	4772	7270	3937	5881	4630	5117	4406	5305
ENSMUSG00000050174	chr3	Nudt6	0.1541818	0.483801967	0.553009094	3.110128568	0.049308142	0	98	127	131	145	98	91	170	147	153	164
ENSMUSG00000094130	chr14	Rpp14	-0.121634	0.48380382	0.553009094	3.331249896	0.028419316	0	142	138	161	207	128	184	158	128	171	138
ENSMUSG00000033579	chr8	Fa2h	-0.2646828	0.484114288	0.553318719	0.667098493	0.114027629	0	12	17	22	39	30	39	25	17	12	17
ENSMUSG00000038160	chr10	Atg5	-0.1141669	0.484635424	0.553869056	4.040961654	0.027736315	0	229	279	263	278	210	252	255	207	280	287
ENSMUSG00000074754	chr2	Gm561	-0.1211558	0.484845162	0.55406345	4.197688237	0.032123404	0	263	355	289	306	196	313	298	243	309	263
ENSMUSG00000024462	chr17	Gabbr1	-0.1366558	0.485211456	0.554436703	3.121732871	0.036744249	0	177	119	135	134	102	166	124	132	116	131
ENSMUSG00000013089	chr16	Etv5	-0.1243153	0.485412309	0.554620866	4.508216599	0.035115026	0	275	310	366	397	397	318	386	258	364	446
ENSMUSG00000021139	chr12	Gm20498	-0.1064037	0.485848314	0.555073656	5.51451787	0.026293301	0	826	727	619	797	556	704	678	634	750	815
ENSMUSG00000039956	chr16	Mrap	0.44248265	0.485969404	0.555121242	0.023608784	0.339944635	0	4	30	14	1	5	14	10	28	15	16
ENSMUSG00000042121	chr5	Ssh1	-0.1263569	0.485950854	0.555121242	3.393733205	0.032472723	0	144	152	165	216	135	220	163	149	111	175
ENSMUSG00000052751	chr6	Repin1	-0.0970759	0.486290026	0.55544209	4.488177858	0.019779179	0	335	332	311	461	292	371	351	342	321	376
ENSMUSG00000022889	chr16	Mrpl39	0.10171581	0.486418782	0.555543752	4.960508697	0.023253834	0	470	455	450	514	339	511	516	475	547	567
ENSMUSG00000041879	chr1	Ipo9	-0.096526	0.486503051	0.555594594	5.250108461	0.021271278	0	579	530	515	741	566	695	646	479	536	656
ENSMUSG00000038648	chr6	Creb3l2	-0.1002022	0.486738223	0.555817747	4.661652571	0.022001402	0	404	337	330	491	387	457	413	386	317	418
ENSMUSG00000032135	chr9	Mcam	-0.1093663	0.486865446	0.555872189	5.716777182	0.028273688	0	882	793	740	887	742	911	685	913	685	921
ENSMUSG00000039321	chr11	Uts2r	0.27714676	0.486840127	0.555872189	1.301277787	0.155026076	0	27	31	23	41	35	101	39	14	22	40
ENSMUSG00000030327	chr6	Necap1	0.10414359	0.488047737	0.557176538	4.336797311	0.022976313	0	318	265	279	329	250	425	379	261	323	322
ENSMUSG00000051124	chr6	Gimap9	-0.2302512	0.488104485	0.557195808	0.690698415	0.082734939	0	29	29	19	32	12	32	18	27	16	19
ENSMUSG00000002608	chr7	Ccdc97	0.10671253	0.488260086	0.557327913	5.561008559	0.026808871	0	655	598	552	843	736	915	818	798	606	861
ENSMUSG00000037257	chr9	Aagab	0.10386248	0.488445939	0.557494524	4.530237774	0.023315474	0	380	340	303	336	283	462	375	329	366	420
ENSMUSG00000097121	chr12	D130020L05Rik	0.24866808	0.48863284	0.557662303	0.474335199	0.070869203	0	24	13	14	20	15	25	17	23	16	31
ENSMUSG00000033272	chr18	Slc35a4	-0.0980254	0.489027763	0.558067294	6.193219524	0.023047754	0	1155	1026	1078	1391	991	1201	1183	1111	1072	1191
ENSMUSG00000025868	chr13	Higd2a	0.1078864	0.489074394	0.558075092	6.513354009	0.028384072	0	1307	1269	1192	1747	1078	2038	1366	1568	1278	1507
ENSMUSG00000002052	chr11	Supt6	0.10506737	0.489312631	0.558301358	5.64644089	0.02623927	0	682	651	605	962	710	991	813	830	652	958
ENSMUSG00000020717	chr11	Pecam1	-0.1184326	0.489459782	0.558423666	6.511326249	0.034400252	0	1314	1505	1385	1781	1104	1833	1165	1438	1041	1697
ENSMUSG00000021235	chr12	Coq6	-0.1030955	0.48992569	0.558909595	4.730681496	0.023844288	0	373	428	410	538	302	474	377	391	389	453
ENSMUSG00000021007	chr12	Spata7	-0.194229	0.490029991	0.558982954	1.32743777	0.060731103	0	36	47	43	35	27	46	28	34	37	37
ENSMUSG00000027954	chr3	Efna1	0.11757348	0.491402861	0.560503255	3.695487366	0.029384275	0	180	210	172	223	134	224	239	236	176	213
ENSMUSG00000005899	chr16	Smpd4	-0.1102049	0.49157608	0.560609326	3.492773983	0.023978788	0	156	182	148	211	165	194	186	166	148	182
ENSMUSG00000057103	chr6	Cml1	0.25186362	0.491536345	0.560609326	0.761865886	0.099638184	0	19	28	26	16	16	19	22	25	41	31
ENSMUSG00000021257	chr12	Angel1	0.13118552	0.492789518	0.561947316	3.41192673	0.036170515	0	172	155	104	152	161	155	185	186	182	184
ENSMUSG00000021087	chr12	Rtn1	-0.2521597	0.492840537	0.561959643	0.46251075	0.108451792	0	23	20	20	14	23	26	20	24	6	18
ENSMUSG00000039376	chr14	Synpo2l	-0.112637	0.492966653	0.562057591	8.139898904	0.032072663	0	4478	3274	3750	6144	4401	4688	3989	4358	3904	5188
ENSMUSG00000003435	chr7	Supt5	-0.1062321	0.493432505	0.562496957	6.105063629	0.027644668	0	1028	886	841	1559	1062	1169	1017	1065	966	1188
ENSMUSG00000018548	chr11	Trim37	-0.125952	0.493425322	0.562496957	3.030260233	0.031696671	0	120	139	105	162	103	122	149	104	134	119
ENSMUSG00000033249	chr8	Hsf4	0.15187795	0.494189838	0.563314344	2.394391064	0.043879698	0	86	59	50	92	77	83	90	84	98	84
ENSMUSG00000036327	chr2	Qsox2	0.1459585	0.494238875	0.563324296	2.814722639	0.042743878	0	88	98	83	125	96	131	152	84	135	92
ENSMUSG00000031024	chr7	St5	-0.1285896	0.494665346	0.563764403	3.969656603	0.037689749	0	227	240	243	325	183	320	260	254	140	247
ENSMUSG00000048310	chr8	Pskh1	-0.1013531	0.49472874	0.563790678	4.284276715	0.023095201	0	252	296	286	357	299	356	315	254	261	348
ENSMUSG00000001441	chr11	Npepps	-0.1012522	0.495280738	0.564373713	6.206321784	0.025333312	0	1029	987	1039	1671	1027	1281	1161	1090	1098	1182
ENSMUSG00000027227	chr2	Sord	0.11328549	0.495701938	0.564807621	4.955868239	0.031011715	0	447	494	365	551	365	388	550	517	552	596
ENSMUSG00000032657	chr3	Fam189b	-0.1253445	0.496195684	0.565324112	4.024251476	0.035982794	0	250	212	208	275	303	195	270	242	247	301
ENSMUSG00000032925	chr14	Itgbl1	-0.1433544	0.496246608	0.565336045	3.961026185	0.048719458	0	309	276	255	230	132	326	267	206	181	230
ENSMUSG00000001444	chr11	Tbx21	0.28468806	0.496429643	0.565498466	0.820068293	0.151498663	0	9	29	28	20	22	13	44	21	24	45
ENSMUSG00000051223	chr1	Bzw1	-0.1052281	0.496955285	0.566051105	6.527465818	0.028004998	0	1533	1422	1245	1673	1249	1478	1834	1108	1400	1454
ENSMUSG00000022771	chr16	Ppil2	0.09374911	0.497035702	0.566096567	4.991973098	0.020382478	0	473	473	399	513	422	624	495	486	519	553
ENSMUSG00000091705	chr17	H2-Q2	0.6880773	0.497413801	0.566481037	0.833096879	1.088076275	0	18	17	21	19	16	173	1	1	3	1
ENSMUSG00000025525	chrX	Apool	-0.1064439	0.497872152	0.566956832	5.227252495	0.027376825	0	571	610	548	706	456	511	520	587	627	673
ENSMUSG00000102070	chr1	Gm28661	-0.1238559	0.49817051	0.56725037	3.558353091	0.032748316	0	188	195	179	215	130	179	150	187	212	177
ENSMUSG00000026860	chr2	Sh3glb2	0.10608109	0.499048093	0.568203352	4.943424329	0.026920657	0	513	463	369	450	394	496	489	450	501	659
ENSMUSG00000054057	chr2	A930004D18Rik	-0.2346337	0.499318275	0.568464664	0.268887812	0.071389669	0	10	21	19	22	15	20	16	17	15	13
ENSMUSG00000025027	chr19	Xpnpep1	-0.0984583	0.500307492	0.569544474	5.59978264	0.023990551	0	730	680	610	1026	714	934	740	745	646	762
ENSMUSG00000031119	chrX	Gpc4	0.11628012	0.500508911	0.569727361	4.950910911	0.03344643	0	338	375	370	666	478	577	446	518	424	657

ENSMUSG00000021186	chr12	Fbln5	0.14480759	0.50077556	0.569984464	4.571958321	0.051549297	0	369	315	328	383	278	759	337	311	253	413
ENSMUSG00000034758	chr10	Tle6	-0.1850028	0.50092646	0.570063367	1.288011924	0.054160396	0	38	41	32	38	34	29	37	26	40	45
ENSMUSG00000049076	chr16	Acap2	-0.1068545	0.500898073	0.570063367	4.066722792	0.02580379	0	271	238	231	341	214	288	301	180	261	286
ENSMUSG00000025154	chr19	Arhgap19	0.10109489	0.501178904	0.570219232	4.323233646	0.022903981	0	255	255	289	338	289	383	332	264	335	374
ENSMUSG00000031990	chr9	Jam3	0.13569326	0.501185822	0.570219232	3.957902085	0.044170612	0	194	243	209	299	158	274	276	333	155	276
ENSMUSG00000074797	chr2	Itpa	0.10671319	0.501123984	0.570219232	4.603674905	0.026954699	0	377	364	336	368	283	398	453	340	474	378
ENSMUSG00000026851	chr2	BC005624	0.10102242	0.50139523	0.570411049	4.922343303	0.024303489	0	425	421	419	499	402	682	493	388	534	472
ENSMUSG00000058503	chr5	Fam133b	-0.1364754	0.501616842	0.570616717	2.832016946	0.039419936	0	96	109	97	112	127	116	124	78	116	112
ENSMUSG00000002409	chr7	Dyrk1b	-0.1280204	0.501775047	0.570750228	6.292973092	0.042496962	0	1293	1115	1034	1480	1182	1002	981	1297	979	1829
ENSMUSG00000021559	chr13	Dapk1	0.16137302	0.501831893	0.570765186	3.497726992	0.059064173	0	135	169	115	162	197	315	169	126	132	240
ENSMUSG00000042828	chr7	Trim72	-0.1161634	0.501869875	0.570765186	8.096650776	0.035545527	0	4214	3129	3255	6363	4549	4349	4259	4526	3999	4228
ENSMUSG00000024533	chr18	Spire1	-0.1100122	0.502097807	0.570977946	3.572456764	0.026007305	0	194	151	153	222	192	188	218	152	182	186
ENSMUSG00000037214	chr8	Thap1	-0.1904919	0.502412415	0.571289229	1.126580232	0.064309733	0	33	25	38	42	26	38	24	20	33	43
ENSMUSG00000054728	chr13	Phactr1	0.16153737	0.502583963	0.571437802	1.870734259	0.048128313	0	46	43	49	65	46	68	46	58	51	82
ENSMUSG00000029135	chr5	Fosl2	0.16779469	0.503204172	0.572096438	4.854173076	0.07176479	0	284	335	556	480	351	960	444	348	306	492
ENSMUSG00000018599	chr11	Mief2	-0.1123837	0.503561841	0.572414309	6.62496375	0.032923003	0	1371	1390	1495	2265	1209	1385	1436	1727	1513	1614
ENSMUSG00000031667	chr8	Aktip	-0.0960262	0.503606636	0.572414309	5.39389889	0.022880098	0	685	615	567	796	575	623	694	632	599	757
ENSMUSG00000053580	chr11	Tanc2	-0.1228349	0.503602636	0.572414309	3.863417006	0.035501324	0	217	205	223	247	223	270	192	266	148	253
ENSMUSG00000036833	chr2	Pnpla7	-0.1061068	0.503679475	0.572450545	5.09170655	0.028270028	0	492	556	412	644	525	759	467	426	447	603
ENSMUSG00000025494	chr7	Sigirr	0.18885355	0.50380872	0.572550876	1.760139486	0.06924173	0	38	40	50	63	37	96	61	50	36	44
ENSMUSG00000010045	chr9	Tmem115	0.09554838	0.503950651	0.572665607	4.452336849	0.020999132	0	301	270	276	395	329	419	376	333	319	395
ENSMUSG00000008859	chr13	Rala	-0.0951027	0.504572964	0.573326158	5.266233567	0.022321366	0	563	567	564	778	497	656	672	552	614	534
ENSMUSG00000043671	chr7	Dpy19l3	0.15206966	0.505131036	0.573913614	3.023000357	0.053340362	0	112	105	77	162	115	163	121	177	80	146
ENSMUSG00000078584	chr4	AU022252	0.1151278	0.505193111	0.573937483	4.218725651	0.031452792	0	278	255	252	271	257	245	308	276	341	393
ENSMUSG00000022040	chr14	Ephx2	-0.1453664	0.505295361	0.574006987	4.390570762	0.052408373	0	214	390	301	523	231	257	274	394	329	343
ENSMUSG00000027931	chr3	Npr1	0.11583059	0.505497501	0.574143281	4.090573242	0.031401359	0	234	233	242	293	208	420	218	267	233	310
ENSMUSG00000028023	chr3	Pitx2	-0.1784122	0.505463804	0.574143281	3.136524398	0.075499858	0	109	142	155	163	115	85	134	206	82	147
ENSMUSG00000054237	chr19	Fra10ac1	0.11656199	0.50564159	0.574260268	3.733082041	0.031795643	0	204	200	171	238	134	209	242	234	243	183
ENSMUSG00000049872	chr10	Fam26e	-0.2106075	0.505910669	0.574519176	1.198503392	0.084661598	0	45	28	41	46	15	47	33	20	30	36
ENSMUSG00000002416	chr6	Ndufb2	-0.1047528	0.506139396	0.574732223	7.29165671	0.029289966	0	2638	2455	2464	2690	1818	2556	2487	2194	2675	2387
ENSMUSG00000032892	chr11	Rangrf	-0.0971296	0.506323251	0.574894285	4.690656664	0.022657025	0	358	384	365	515	365	486	409	419	354	361
ENSMUSG00000006587	chr8	Snai3	-0.1503843	0.506372663	0.574903683	2.425630629	0.044846717	0	75	88	58	137	62	95	82	69	73	89
ENSMUSG00000095438	chr18	Gm21747	-0.2034	0.506529724	0.575035288	2.833711522	0.100506128	0	163	130	96	98	69	73	97	69	188	99
ENSMUSG00000051498	chr5	Tlr6	0.17833683	0.506656124	0.575132065	1.574180758	0.055415874	0	42	43	44	35	33	62	53	35	56	42
ENSMUSG00000029518	chr5	Rab35	0.09150816	0.506762343	0.575205921	5.063838761	0.020859008	0	453	439	420	693	426	655	531	513	562	550
ENSMUSG00000037149	chr12	Ddx1	-0.100074	0.507319303	0.575791342	6.795871297	0.026601997	0	1819	1615	1432	2154	1576	1700	1845	1526	1944	1711
ENSMUSG00000045064	chr12	Zc2hc1c	-0.2504488	0.507484989	0.575932619	0.324834221	0.088169421	0	11	25	12	33	12	17	20	14	16	17
ENSMUSG00000044881	chr7	Coa4	0.13852904	0.507555228	0.575965562	2.678440023	0.038114009	0	90	93	90	104	68	148	116	82	101	94
ENSMUSG00000038195	chr11	Rilp	0.11549519	0.507740031	0.576128496	5.325960792	0.034626529	0	550	571	574	675	487	492	640	668	691	881
ENSMUSG00000019809	chr10	Pex3	-0.110873	0.508437509	0.576873082	3.532560998	0.027696124	0	196	181	176	190	140	196	168	142	178	218
ENSMUSG00000047710	chr8	Champ1	0.10647703	0.50937849	0.577893804	3.52006859	0.024515278	0	155	160	132	212	159	221	203	147	192	202
ENSMUSG00000011877	chr11	Git1	-0.1043479	0.509555599	0.5780397	5.317848783	0.028027504	0	506	505	530	906	654	701	622	596	530	688
ENSMUSG00000059183	chr9	Mtfmt	0.13785048	0.509589807	0.5780397	2.44899319	0.038661233	0	73	83	59	88	75	83	86	97	88	100
ENSMUSG00000016181	chr1	Diexf	-0.1154332	0.509648322	0.578059159	3.168231169	0.027987973	0	140	109	123	188	132	158	143	138	129	127
ENSMUSG00000053333	chr1	Dis3l2	0.10714927	0.509739476	0.57811563	3.962744027	0.026993756	0	215	227	177	271	221	247	226	258	254	321
ENSMUSG00000009545	chr7	Kcnq1	0.24168424	0.509868768	0.578215344	0.323338417	0.089803223	0	13	12	22	16	13	34	15	20	16	15
ENSMUSG00000022475	chr15	Hdac7	0.0961056	0.509951298	0.578262015	4.497491665	0.022369301	0	293	321	300	455	264	460	364	319	353	409
ENSMUSG00000038457	chr8	Tmem255b	0.18603988	0.510360037	0.578678556	1.724326467	0.070448916	0	41	49	45	61	27	91	40	47	57	43
ENSMUSG00000032872	chr9	Cyb5r4	-0.1066076	0.510571078	0.578870884	5.029979576	0.028886017	0	536	464	482	654	395	397	600	447	559	544
ENSMUSG00000090077	chr2	Lime1	0.12338347	0.510880218	0.579174393	3.214398757	0.032653533	0	136	146	115	129	122	196	145	146	161	132
ENSMUSG00000030725	chr7	Lipt2	0.14310919	0.511139693	0.579421554	2.523738488	0.041873099	0	99	77	67	78	75	117	82	85	109	89
ENSMUSG00000040506	chr2	Ambra1	-0.1004784	0.511486287	0.579767424	4.410247821	0.024221541	0	330	281	263	437	330	328	300	321	326	388
ENSMUSG00000028560	chr4	Usp1	-0.1208085	0.511549597	0.579792164	3.799608443	0.034623575	0	196	205	201	301	178	172	284	160	231	232
ENSMUSG00000038503	chr7	Mesdc2	-0.0938492	0.511637369	0.579844621	5.060076164	0.022278492	0	462	470	431	693	517	636	575	471	481	472
ENSMUSG00000037216	chr1	Lipt1	0.15338121	0.512008062	0.580217682	2.500215517	0.051956145	0	72	83	62	111	66	99	61	116	96	100
ENSMUSG00000020430	chr11	Pes1	0.10312092	0.512087452	0.580260599	5.273847543	0.027725164	0	629	526	438	708	489	928	642	539	622	556
ENSMUSG00000028826	chr4	Tmem57	-0.0955677	0.512173701	0.580311281	4.48386338	0.022570534	0	326	330	351	413	293	419	396	262	326	366
ENSMUSG00000072258	chr1	Taf1a	-0.1527093	0.512951666	0.581145629	2.18323306	0.049502676	0	65	73	55	80	73	75	61	46	90	70
ENSMUSG00000016496	chr19	Cd274	0.20530139	0.513070622	0.581233283	1.774637759	0.096126594	0	29	49	39	70	43	52	85	36	31	87
ENSMUSG00000020072	chr10	Pbld1	0.24105355	0.513330975	0.581481091	0.560094042	0.088947395	0	30	22	9	18	13	26	29	25	19	20
ENSMUSG00000031783	chr8	Polr2c	-0.0947888	0.513543456	0.581551614	5.528115528	0.023614433	0	787	683	585	911	601	852	775	571	735	718
ENSMUSG00000034194	chr14	R3hcc1	0.09653527	0.513559675	0.581551614	4.171413552	0.022032883	0	278	241	247	295	226	294	321	278	314	299
ENSMUSG00000037119	chr15	D15Ertd621e	-0.1166729	0.51347114	0.581551614	3.919886309	0.033739975	0	198	259	206	280	220	247	315	149	221	253
ENSMUSG00000073002	chr6	Vamp5	-0.1368209	0.513524171	0.581551614	6.438069378	0.051681411	0	1401	1451	1195	1682	1059	2437	1121	1239	1078	953
ENSMUSG00000025077	chr19	Dclre1a	0.14855991	0.513715604	0.581681057	2.182079564	0.042800931	0	69	64	68	68	42	78	89	65	72	75

ENSMUSG00000007656	chr9	Arpp19	0.09205405	0.513951065	0.581900525	5.845729272	0.022606904	0	846	852	759	1004	687	1058	1003	911	969	890
ENSMUSG00000030123	chr6	Plxnd1	-0.1154067	0.514445572	0.582413229	6.36144895	0.036687834	0	1146	1145	1197	1804	1130	1925	1117	1146	896	1432
ENSMUSG00000027937	chr3	Jtb	0.09020594	0.514648422	0.582595687	5.803309304	0.021656083	0	805	783	757	996	691	1088	926	816	954	917
ENSMUSG00000025199	chr19	Chuk	-0.1086338	0.514715959	0.582624949	3.787538799	0.027450543	0	200	202	194	297	175	214	256	159	238	210
ENSMUSG00000029165	chr5	Agbl5	-0.160004	0.515069746	0.582978196	1.629929576	0.047356949	0	34	49	44	61	46	44	53	37	50	45
ENSMUSG00000042857	chr13	Gm9776	0.24159364	0.515205899	0.583085079	0.016619301	0.077186156	0	17	10	9	11	13	17	14	20	11	16
ENSMUSG00000032846	chr13	Zswim6	0.20178657	0.515340862	0.583190599	1.70112809	0.08890012	0	50	35	38	68	29	58	86	23	45	64
ENSMUSG00000027108	chr2	Ola1	-0.1154917	0.515653199	0.583449572	5.869099391	0.03643357	0	1026	862	856	1046	733	646	1022	920	807	1151
ENSMUSG00000037315	chrX	Jade3	-0.2505802	0.515631033	0.583449572	0.225782985	0.090209102	0	7	21	13	25	19	17	19	11	17	14
ENSMUSG00000069939	chr11	Gm12070	0.26483441	0.515704724	0.583460635	0.877860638	0.138654717	0	24	20	16	29	27	8	31	26	34	52
ENSMUSG00000002771	chr7	Grin2d	0.22894072	0.516336791	0.584087648	0.222105345	0.069476748	0	9	12	16	18	16	24	17	15	14	22
ENSMUSG00000022973	chr16	Synj1	0.11663524	0.516342508	0.584087648	3.446066953	0.031940097	0	120	160	155	218	123	239	180	138	177	188
ENSMUSG00000025856	chr5	Pdgfa	0.08928339	0.516616737	0.58435056	4.800112281	0.020055446	0	397	378	365	482	381	481	498	465	404	485
ENSMUSG00000036160	chr2	Surf6	-0.1158479	0.516830472	0.584545009	3.324797053	0.030810531	0	140	140	160	189	138	127	176	135	153	183
ENSMUSG00000025488	chr7	Cox8b	-0.1063822	0.516972594	0.584657801	8.397834169	0.032080368	0	5481	5571	4869	6059	4081	5986	4754	4869	6123	4722
ENSMUSG00000075268	chr19	Gm10819	0.21015771	0.517013864	0.584657801	1.324975608	0.089714678	0	32	21	47	30	32	25	52	42	39	49
ENSMUSG00000043024	chr6	Gm16433	-0.271607	0.517102542	0.58471077	0.510544216	0.121530487	0	18	12	8	50	22	23	20	15	18	20
ENSMUSG00000028034	chr3	Fubp1	0.10156067	0.517179161	0.584750098	4.687869541	0.026659242	0	352	358	297	493	356	465	556	339	437	377
ENSMUSG00000059810	chr4	Rgs3	-0.1073513	0.517247346	0.584779883	3.499719848	0.026453421	0	152	154	184	225	152	204	175	163	142	199
ENSMUSG00000024187	chr17	Itfg3	0.10506777	0.517814722	0.585373984	6.210830846	0.030740602	0	999	980	855	1550	992	1397	1060	1255	1013	1545
ENSMUSG00000092252	chr5	Gm20499	-0.2010674	0.517905102	0.585428802	0.774510575	0.073321496	0	27	27	21	21	29	35	25	15	17	30
ENSMUSG00000064342	chrMT	mt-Ti	0.13033126	0.5180645	0.585561621	5.815454669	0.047406248	0	792	815	840	942	607	748	847	1253	670	1232
ENSMUSG00000018882	chr11	Mrpl45	-0.0969377	0.518139863	0.585599444	6.036615607	0.025728207	0	973	1005	976	1325	797	1018	1026	981	1103	1024
ENSMUSG00000022035	chr14	Ccdc25	0.08809342	0.518208475	0.585629631	4.878921635	0.02000288	0	453	397	359	534	383	505	511	465	508	471
ENSMUSG00000022828	chr16	Gtf2e1	-0.1212231	0.518380925	0.585729793	3.253717739	0.033348199	0	151	129	140	179	133	110	164	133	154	172
ENSMUSG00000048747	chr4	E130114P18Rik	-0.3050484	0.518379619	0.585729793	-0.173846728	0.158561091	0	16	17	11	8	10	23	6	15	8	4
ENSMUSG00000064339	chrMT	mt-Rnr2	-0.1538819	0.518867157	0.586231801	9.055084292	0.067903101	0	5217	6326	7246	15807	8318	6733	6114	8240	8322	11463
ENSMUSG00000018169	chr15	Mfng	0.14999997	0.51895489	0.586236141	2.478786019	0.049929768	0	78	90	69	81	65	115	77	105	61	111
ENSMUSG00000087177	chr10	E130307A14Rik	-0.1194234	0.518923812	0.586236141	2.887636268	0.03088331	0	135	102	103	133	93	144	103	101	105	119
ENSMUSG00000072381	chr3	Gm10355	-0.2276831	0.51900304	0.58624315	0.291013736	0.081421431	0	15	21	21	19	12	22	9	13	17	22
ENSMUSG00000059401	chrX	Mamld1	-0.1556364	0.519816453	0.587114494	1.716517975	0.041921763	0	53	48	43	61	44	45	49	39	56	55
ENSMUSG00000001986	chrX	Gria3	0.20350204	0.520355565	0.58767591	1.133293973	0.071657305	0	24	27	28	25	37	27	34	32	38	49
ENSMUSG00000050608	chr4	Minos1	0.10287024	0.520540105	0.587836822	7.06039331	0.030189629	0	2002	2000	1908	2321	1376	2716	2076	2237	2238	2005
ENSMUSG00000055401	chr4	Fbxo6	0.09378314	0.520908107	0.588204872	4.519884962	0.022177149	0	328	328	313	395	282	412	390	292	409	426
ENSMUSG00000035781	chr10	R3hdm4	0.09393126	0.521156726	0.588438068	7.088288201	0.0251519	0	2026	1836	1660	2391	1906	2679	2190	2219	1958	2445
ENSMUSG00000078490	chr4	C030017K20Rik	-0.2076095	0.521578901	0.588867171	0.734830121	0.067031486	0	30	24	17	27	25	23	26	30	20	17
ENSMUSG00000046667	chr4	Rbm12b1	0.1758998	0.522193083	0.589512967	1.35413982	0.056476189	0	29	32	35	43	31	57	42	32	50	30
ENSMUSG00000033594	chr8	Spata2l	0.20336771	0.52241474	0.589715565	0.903146324	0.070694298	0	17	17	26	29	31	33	29	23	26	42
ENSMUSG00000036693	chr5	Nop14	-0.0964988	0.522465276	0.58972498	4.180673255	0.023097636	0	285	221	257	352	276	286	297	237	297	305
ENSMUSG00000005078	chr12	Jkamp	0.10667332	0.523074427	0.59036487	3.833272269	0.027577171	0	208	225	174	207	193	224	243	197	256	275
ENSMUSG00000020532	chr11	Acaca	-0.2551864	0.523364585	0.590644658	3.81484616	0.183166438	0	87	358	188	203	272	49	227	314	189	233
ENSMUSG00000060038	chr8	Dhps	0.11669295	0.523479564	0.590726717	3.977335385	0.036063771	0	191	207	176	364	200	331	261	222	311	204
ENSMUSG00000015488	chr2	Cacfd1	-0.0870858	0.523654235	0.590876117	5.765936247	0.021003486	0	817	781	748	1055	780	952	847	790	801	916
ENSMUSG00000025200	chr19	Cwf19l1	0.14306435	0.523748996	0.590935333	2.293553001	0.041189023	0	67	73	63	74	60	109	68	62	80	93
ENSMUSG00000009210	chr11	2310007L24Rik	0.17978841	0.524183253	0.591377554	2.575890928	0.078850076	0	89	91	87	55	77	61	94	90	134	122
ENSMUSG00000030541	chr7	Idh2	-0.1579648	0.524579384	0.591747216	7.370815114	0.073126917	0	1674	2652	2131	5308	1738	3738	1838	2896	2267	2045
ENSMUSG00000059824	chr7	Dbp	-0.1489889	0.524595593	0.591747216	6.71812507	0.064947169	0	2064	1913	2067	1284	787	1892	1823	1414	1446	1604
ENSMUSG00000020462	chr11	Cfap36	0.1276493	0.52473617	0.591858019	3.315553178	0.03946009	0	208	133	111	151	99	166	190	150	159	173
ENSMUSG00000024966	chr19	Stip1	0.09606755	0.52519479	0.592279705	6.762725129	0.026777631	0	1667	1321	1328	2012	1526	1903	2057	1806	1699	1671
ENSMUSG00000045410	chr13	Akr1e1	-0.1001362	0.525194288	0.592279705	4.171783203	0.025772978	0	309	286	255	293	232	284	273	228	321	304
ENSMUSG00000022505	chr16	Emp2	0.10170892	0.525913417	0.593042272	4.162868484	0.026572261	0	204	243	240	358	242	378	314	282	231	307
ENSMUSG00000050164	chr15	Mchr1	0.2237291	0.526090205	0.593193764	2.372975169	0.131336375	0	57	80	112	66	28	78	47	101	130	82
ENSMUSG00000049488	chr4	Tmem67	0.18417758	0.526182473	0.593249939	1.039354589	0.055629963	0	26	28	26	24	29	34	27	31	38	37
ENSMUSG00000048537	chr9	Phldb1	-0.0910703	0.52680275	0.593901366	5.424586488	0.022918252	0	616	585	599	960	571	750	658	622	625	738
ENSMUSG00000028016	chr3	Ints12	-0.122244	0.526921957	0.593987843	3.360869357	0.037260537	0	159	155	128	206	145	121	182	129	142	220
ENSMUSG00000030278	chr6	Cidec	0.39025164	0.527051308	0.594085739	3.366793596	0.436536571	0	35	336	62	41	154	39	101	324	75	386
ENSMUSG00000027552	chr3	E2f5	0.18801435	0.52721942	0.594227308	1.244805763	0.070533445	0	29	34	32	42	20	35	60	28	41	31
ENSMUSG00000025650	chr9	Col7a1	0.1530806	0.527296695	0.59426648	3.435085289	0.060789679	0	211	143	155	113	121	186	143	162	145	287
ENSMUSG00000031558	chr5	Slit2	0.2564599	0.52767303	0.594642659	0.254537385	0.119202743	0	14	15	19	17	7	33	10	12	13	28
ENSMUSG00000058447	chr7	Gm26920	0.17050702	0.527733902	0.594663309	1.180922194	0.043140277	0	29	31	30	36	24	41	36	34	37	37
ENSMUSG00000033439	chr3	Trmt13	-0.1808245	0.528168939	0.595105538	1.394287354	0.062363388	0	43	35	27	60	36	56	47	33	30	27
ENSMUSG00000022450	chr15	Ndufa6	-0.0975754	0.528772435	0.59573749	7.469710143	0.028334305	0	2797	2718	2646	3363	2161	3008	2490	2467	3152	2838
ENSMUSG00000003235	chr16	Eif2b5	0.09489916	0.529115473	0.596027875	5.903065121	0.026171846	0	837	764	720	1172	843	983	1028	918	1135	953
ENSMUSG00000039983	chr2	Ccdc32	0.12253254	0.529081572	0.596027875	3.148176901	0.035457223	0	142	146	106	127	100	187	168	119	115	161
ENSMUSG00000020115	chr10	Tbk1	0.10922413	0.529202192	0.596077518	3.701133528	0.029809612	0	175	207	170	233	142	285	232	149	218	217

ENSMUSG00000018820	chr19	Zfyve27	0.09385959	0.529859837	0.596770173	4.011168742	0.022268675	0	244	236	183	295	202	321	268	249	241	274
ENSMUSG00000035027	chr10	Map2k2	0.09418368	0.531101563	0.598120504	7.398064846	0.026662295	0	2621	2092	2109	2847	2474	3083	2833	2804	2465	3033
ENSMUSG00000032120	chr9	C2cd2l	0.11253431	0.531759046	0.5988127	3.816432855	0.032496877	0	187	171	195	243	203	310	290	196	156	245
ENSMUSG00000002997	chr12	Prkar2b	0.27105492	0.53228076	0.59935191	2.618030745	0.208511036	0	28	202	54	46	64	73	110	137	70	143
ENSMUSG00000028703	chr4	Lrrc41	0.09192649	0.532722969	0.599801515	4.454234267	0.022587671	0	269	292	284	424	311	406	385	284	376	392
ENSMUSG00000085479	chr11	9430073C21Rik	0.40508773	0.533158264	0.600243265	3.009785246	0.484126922	0	46	125	114	161	69	199	11	404	14	88
ENSMUSG00000021215	chr13	Net1	-0.1130649	0.533206216	0.600248899	5.171182509	0.037538457	0	633	634	487	592	428	704	561	564	336	673
ENSMUSG00000040174	chr2	Alkbh3	0.08617524	0.533551935	0.60058971	5.061904254	0.021035219	0	517	446	427	621	409	554	596	576	524	539
ENSMUSG00000020264	chr11	Slc36a2	-0.2858006	0.534530352	0.601642603	1.703876779	0.216510148	0	15	88	45	45	59	24	42	76	19	67
ENSMUSG00000024563	chr18	Smad2	-0.1049291	0.5352936	0.602415582	3.784288039	0.029149517	0	196	200	182	271	209	299	198	159	233	193
ENSMUSG00000028955	chr4	Vamp3	-0.0892754	0.535303314	0.602415582	6.136769492	0.02378139	0	1138	1095	971	1347	869	1176	1205	962	1091	1131
ENSMUSG00000033423	chr4	Eri3	0.0893085	0.535495492	0.602583333	6.096653642	0.023854428	0	1040	963	831	1191	917	1269	1074	1163	1060	1179
ENSMUSG00000020963	chr12	Tshr	-0.3077944	0.536268356	0.60340444	-0.155809651	0.221338137	0	9	21	5	6	21	24	12	6	4	12
ENSMUSG00000023723	chr11	Mrps23	0.09149058	0.536622244	0.603749876	6.470584886	0.025469287	0	1379	1306	1195	1532	993	1662	1448	1438	1428	1483
ENSMUSG00000024002	chr17	Brd4	-0.0957898	0.536661757	0.603749876	5.225358528	0.026700668	0	510	495	463	797	626	621	631	585	467	643
ENSMUSG00000026434	chr1	Nucks1	0.09685523	0.536862813	0.603927453	6.389219755	0.028576863	0	1351	1210	1134	1352	974	1388	1747	1305	1282	1338
ENSMUSG00000018001	chr5	Cyth3	-0.0927526	0.537232264	0.604294416	4.327564517	0.023254715	0	322	319	266	397	241	378	324	249	335	297
ENSMUSG00000074781	chr10	Ube2n	-0.0936918	0.53804493	0.605159822	5.920616819	0.026527838	0	1054	890	791	1073	845	914	1150	777	979	957
ENSMUSG00000026740	chr2	Dnajc1	0.09185026	0.538938826	0.606116443	4.024678126	0.022047129	0	259	207	218	267	213	283	290	256	256	275
ENSMUSG00000038070	chr4	Cntln	-0.1369314	0.53922989	0.606394991	2.105817532	0.041198862	0	65	68	58	80	56	62	86	50	59	69
ENSMUSG00000005312	chr13	Ubqln1	-0.0876114	0.539917145	0.607118997	5.920632546	0.023222391	0	879	831	803	1280	886	1072	1052	856	847	974
ENSMUSG00000044172	chr17	Ptx4	-0.2237911	0.540531178	0.607760558	1.378859989	0.11606041	0	52	22	31	71	28	71	38	24	34	22
ENSMUSG00000063458	chr14	1700112E06Rik	0.16479455	0.541640815	0.608959217	1.554766597	0.057934426	0	33	41	30	47	46	52	45	32	46	69
ENSMUSG00000049555	chr9	Tmie	-0.2875077	0.541959268	0.609268238	-0.072585147	0.160042997	0	11	8	18	21	10	30	6	6	7	13
ENSMUSG00000093157	chr6	Mir3098	0.23038586	0.542645291	0.609990395	0.131607166	0.078016319	0	18	7	14	20	8	16	19	18	16	16
ENSMUSG00000061650	chr11	Med9	0.08984894	0.542899703	0.6102273	4.411852197	0.022248677	0	332	316	288	320	264	408	364	319	360	332
ENSMUSG00000029627	chr5	Zkscan14	-0.1155964	0.542969806	0.610257017	3.245076358	0.034500801	0	164	139	149	165	108	130	151	126	132	195
ENSMUSG00000020156	chr10	Mum1	0.08669855	0.543291847	0.610569866	4.652219832	0.021523455	0	364	357	342	448	302	463	361	397	429	453
ENSMUSG00000022837	chr16	Iqcb1	-0.1466884	0.543418083	0.61066263	1.972374715	0.048378848	0	73	43	50	75	58	63	63	42	69	58
ENSMUSG00000032330	chr9	Cox7a2	0.09684575	0.543876997	0.611129194	7.54611996	0.03014639	0	2632	2942	2574	3273	2057	3124	2775	3095	3351	3351
ENSMUSG00000031480	chr8	Thsd1	-0.1498164	0.543967061	0.611181256	2.246660513	0.058053771	0	54	76	86	86	59	114	58	66	58	65
ENSMUSG00000025020	chr19	Slit1	0.19507107	0.544210584	0.611405717	1.406424016	0.093202032	0	47	28	32	46	24	35	28	62	56	35
ENSMUSG00000097354	chr6	2310001H17Rik	0.12176074	0.544744646	0.611956529	4.128679881	0.043226542	0	306	296	235	223	169	399	244	220	330	294
ENSMUSG00000031734	chr8	Irx3	0.24025963	0.544896588	0.612078019	0.728913323	0.131118659	0	16	16	32	25	15	33	14	40	13	35
ENSMUSG00000067786	chr2	Nnat	-0.3804365	0.545498569	0.612704975	0.728015047	0.409045418	0	12	65	11	9	28	23	10	21	3	54
ENSMUSG00000028989	chr4	Angptl7	-0.3822175	0.545747024	0.61293478	4.752113561	0.465295968	0	806	392	428	347	269	1578	243	49	115	66
ENSMUSG00000028676	chr4	Srsf10	-0.110598	0.54607939	0.613258784	4.599744398	0.036974381	0	308	297	345	556	380	475	453	268	418	291
ENSMUSG00000045934	chr3	Mtmr11	0.1525955	0.547214406	0.614484054	2.404933414	0.05919656	0	84	82	71	87	42	145	83	68	73	81
ENSMUSG00000023186	chr9	Vwa5a	-0.1046068	0.547976728	0.615290653	5.266848175	0.034432711	0	711	543	550	685	479	653	715	375	721	569
ENSMUSG00000036093	chr2	Arl5a	-0.0940927	0.548248886	0.615546789	4.885391384	0.026680017	0	500	435	420	548	368	371	538	414	467	527
ENSMUSG00000043190	chr13	Rfesd	-0.1250597	0.548561672	0.615848496	3.363241501	0.043446601	0	220	154	145	168	104	128	171	150	179	161
ENSMUSG00000027001	chr2	Dusp19	-0.1319347	0.549122755	0.616428886	2.835690888	0.044691027	0	123	113	94	130	88	88	107	98	147	102
ENSMUSG00000028165	chr3	Cisd2	-0.1022548	0.549670125	0.616982607	4.795259625	0.031827674	0	374	334	404	640	406	357	550	388	436	439
ENSMUSG00000032085	chr9	Tagln	0.12500732	0.549704309	0.616982607	5.250560318	0.050234793	0	342	477	390	804	712	898	618	636	542	555
ENSMUSG00000034022	chr15	Cpsf1	-0.0908489	0.550310656	0.617563974	4.655542439	0.024603018	0	324	389	310	555	369	466	392	314	406	414
ENSMUSG00000042055	chr7	Wdr11	-0.0814738	0.55030761	0.617563974	4.691860821	0.019518738	0	371	389	366	489	359	482	413	374	379	398
ENSMUSG00000036898	chr5	Zfp157	0.16049737	0.550362644	0.617572727	1.722593178	0.051440249	0	51	49	49	39	33	55	62	44	51	62
ENSMUSG00000043243	chr8	Fam129c	-0.299369	0.550746627	0.617953987	-0.206275492	0.172296116	0	17	8	16	14	6	26	4	7	12	6
ENSMUSG00000040265	chr1	Dnm3	-0.1533498	0.550999668	0.618188276	1.983941862	0.054569189	0	47	61	50	91	55	91	58	43	58	49
ENSMUSG00000078676	chr11	Casc3	0.08695506	0.551099735	0.618250914	4.928156866	0.023047615	0	414	424	398	581	387	682	437	473	453	519
ENSMUSG00000098488	chr2	Pla2g4b	-0.1906648	0.551933837	0.619136953	0.946730417	0.080056404	0	35	30	27	19	30	22	24	23	36	32
ENSMUSG00000047409	chr9	Ctdspl	0.11320479	0.552203579	0.619389825	3.433725745	0.035942399	0	145	166	110	209	141	251	177	190	140	152
ENSMUSG00000015850	chr3	Adamtsl4	0.12935266	0.552487217	0.619658241	4.016010372	0.051738932	0	178	185	205	371	222	461	259	219	169	286
ENSMUSG00000063229	chr7	Ldha	0.11999956	0.552545948	0.619674384	11.74666776	0.048874325	0	51566	41524	40173	63947	49629	37824	57229	55702	56109	83570
ENSMUSG00000081453	chr16	Gm6767	0.24657466	0.552590399	0.61967451	-0.015180374	0.081028758	0	11	14	9	9	15	11	18	15	17	15
ENSMUSG00000021271	chr12	Zfp839	-0.1151458	0.553125255	0.620224532	3.01666723	0.034549127	0	120	125	119	150	104	106	110	128	143	133
ENSMUSG00000024594	chr18	Prrc1	-0.0962318	0.553319125	0.620392145	5.298500975	0.029765088	0	536	597	538	812	556	882	670	566	471	535
ENSMUSG00000058835	chr2	Abi1	0.09118078	0.553426474	0.620462731	4.491866552	0.025114329	0	352	296	290	434	257	407	455	274	352	408
ENSMUSG00000046574	chr7	Prr12	-0.1165509	0.553574514	0.620529148	4.605898262	0.04303721	0	373	294	276	549	409	437	326	368	240	540
ENSMUSG00000087598	chr7	Zfp111	-0.1406718	0.553564871	0.620529148	1.706849454	0.042707687	0	45	50	51	57	42	65	49	40	48	43
ENSMUSG00000032555	chr9	Topbp1	-0.1165602	0.553949874	0.620900107	3.762360759	0.041173955	0	212	236	191	231	170	207	318	136	207	191
ENSMUSG00000029279	chr5	Brdt	0.14632311	0.554031404	0.620941692	1.546432606	0.049937246	0	45	40	31	42	39	39	45	52	50	52
ENSMUSG00000038194	chr7	Lhb	-0.2219456	0.554329175	0.621225608	0.570886301	0.095552903	0	29	13	32	23	12	17	21	24	19	21
ENSMUSG00000011096	chr7	Akt1s1	-0.0880076	0.554944324	0.621865128	6.68647268	0.025952314	0	1532	1383	1414	1962	1618	1865	1474	1472	1476	1883
ENSMUSG00000020849	chr11	Ywhae	-0.087042	0.555547279	0.622490882	8.758915311	0.025980488	0	6834	6064	5758	8322	6374	7634	7237	6155	6027	7352

ENSMUSG00000004937	chr10	Sgta	0.08490991	0.555883685	0.622817892	6.666269364	0.024232708	0	1457	1290	1309	1948	1378	1882	1645	1513	1741	1752
ENSMUSG00000027099	chr2	Mtx2	-0.1024187	0.556303637	0.623238448	4.728906629	0.032812814	0	327	353	444	653	293	411	411	399	436	415
ENSMUSG00000076435	chr11	Acsf2	0.1592136	0.556388551	0.623283616	2.297795864	0.069703385	0	72	85	45	79	57	78	82	108	45	98
ENSMUSG00000002910	chr8	Arrdc2	0.26931631	0.556557436	0.623422836	3.108827171	0.23726105	0	64	89	102	88	212	441	78	52	136	84
ENSMUSG00000040323	chr1	Gm15429	0.17088738	0.55683164	0.623679997	1.035880757	0.049356094	0	25	28	29	34	19	41	34	28	28	36
ENSMUSG00000030037	chr6	Mrpl53	0.08385574	0.557415565	0.624233969	5.737292727	0.023113809	0	818	774	714	894	650	965	883	867	908	840
ENSMUSG00000035834	chr13	Polr3g	0.15842852	0.557399023	0.624233969	1.337222068	0.05654892	0	40	21	31	51	28	38	41	36	48	43
ENSMUSG00000057541	chr5	Pus7	-0.1013737	0.557810124	0.624625775	3.501737779	0.028725878	0	221	158	146	185	153	192	194	170	169	157
ENSMUSG00000009630	chr8	Ppp2cb	0.08299658	0.558412168	0.625249837	4.8942868	0.021430963	0	431	414	417	536	352	619	544	389	469	483
ENSMUSG00000033039	chr15	Micall1	0.09757889	0.5588037	0.625638109	4.426176988	0.030080986	0	263	272	255	464	304	428	345	349	256	436
ENSMUSG00000002396	chr8	Ocel1	-0.1730316	0.558856856	0.625647503	2.931924541	0.093596218	0	96	106	108	173	115	264	92	82	70	84
ENSMUSG00000028247	chr4	Coq3	-0.0858502	0.559096163	0.625841198	4.986478721	0.023269374	0	445	441	494	656	402	501	538	454	536	467
ENSMUSG00000031465	chr8	Angpt2	-0.144838	0.559119433	0.625841198	2.000627455	0.055817045	0	52	63	52	77	60	88	58	33	53	73
ENSMUSG00000047793	chr1	Sned1	0.12173283	0.559544009	0.626266282	3.648046631	0.043982385	0	190	152	152	154	224	302	210	155	216	182
ENSMUSG00000085287	chr17	4833418N02Rik	-0.180329	0.559715796	0.62640839	1.992849781	0.094763939	0	66	63	57	60	57	40	53	38	47	119
ENSMUSG00000022803	chr16	Popdc2	0.09187549	0.559995773	0.626621371	6.120565189	0.028760773	0	1101	860	807	1187	1058	1082	1221	1132	1255	1131
ENSMUSG00000038296	chr7	Galnt18	-0.1232642	0.559987293	0.626621371	2.961273884	0.041282829	0	121	103	138	158	79	147	110	130	92	121
ENSMUSG00000023147	chr16	Wrb	0.11399624	0.56010475	0.626693138	3.19669826	0.036224365	0	137	110	119	145	134	157	176	101	183	152
ENSMUSG00000051346	chr10	Spryd4	-0.0864923	0.560517441	0.627104688	5.27175099	0.024341014	0	639	534	601	746	449	596	575	594	593	685
ENSMUSG00000030664	chr7	Sox6os	-0.1949426	0.560647937	0.627198747	1.285468971	0.092401269	0	59	28	29	37	31	32	28	24	32	61
ENSMUSG00000036206	chr1	Sh3bp4	-0.1177353	0.560691267	0.627198747	3.104903073	0.038274047	0	113	125	127	182	115	164	89	125	126	162
ENSMUSG00000035139	chr13	Secisbp2	-0.0934515	0.560941332	0.627428256	3.477432829	0.025746546	0	172	153	148	192	180	202	196	136	157	184
ENSMUSG00000022751	chr16	Nit2	-0.0933352	0.561063204	0.627514352	4.454320377	0.027194621	0	356	322	334	378	283	276	341	342	360	392
ENSMUSG00000021650	chr13	Ptcd2	0.08610824	0.562311163	0.628859791	4.890011123	0.024413794	0	417	444	375	585	333	484	508	479	549	451
ENSMUSG00000024457	chr17	Trim26	-0.0854316	0.562439416	0.628952895	4.210896652	0.022195749	0	310	287	262	326	227	322	325	266	242	307
ENSMUSG00000028300	chr4	3110043O21Rik	-0.0869541	0.563001778	0.62952531	4.106414347	0.023053623	0	309	242	220	302	241	334	264	221	253	290
ENSMUSG00000042210	chr9	Abhd14a	0.09986216	0.563041384	0.62952531	3.466099995	0.028923489	0	164	139	136	200	150	249	159	187	147	185
ENSMUSG00000041623	chr11	D11Wsu47e	-0.1234127	0.563460322	0.629892934	2.319966759	0.040257651	0	88	78	67	92	55	101	67	63	69	83
ENSMUSG00000068079	chr2	Tcf15	0.13120791	0.563420674	0.629892934	2.992894248	0.050483026	0	79	108	125	144	101	107	124	160	106	167
ENSMUSG00000022962	chr16	Gart	-0.0829987	0.563778731	0.630198476	5.565382315	0.023174847	0	706	674	647	926	681	764	890	631	744	720
ENSMUSG00000101841	chr11	Gm11993	-0.2397254	0.565675991	0.632268686	0.171227686	0.116374351	0	24	6	13	19	19	16	10	17	9	23
ENSMUSG00000020705	chr11	Ddx42	0.07764795	0.566329061	0.632948017	5.242993775	0.020057102	0	577	504	480	693	495	693	676	593	537	673
ENSMUSG00000078908	chr8	Mon1b	-0.1089512	0.566617833	0.633220121	2.689637429	0.032845807	0	103	98	98	99	88	104	103	82	97	112
ENSMUSG00000023235	chr8	Ccl25	0.17801411	0.567084593	0.633691075	1.607947814	0.084782787	0	47	35	50	32	37	28	65	45	49	65
ENSMUSG00000022103	chr14	Gfra2	0.14356163	0.567166556	0.633731995	2.223421155	0.056348196	0	42	61	79	73	64	71	95	78	60	85
ENSMUSG00000003208	chr17	Ccdc94	-0.113292	0.567356029	0.633893026	2.567954777	0.032215272	0	93	96	71	106	84	97	88	80	88	103
ENSMUSG00000041559	chr1	Fmod	-0.1611973	0.567500944	0.634004252	7.95309953	0.094688662	0	6016	2879	3252	4768	2774	8049	4142	2034	2470	3012
ENSMUSG00000040648	chr1	Ppip5k2	-0.1284929	0.567747581	0.634229093	2.256049204	0.042263468	0	76	63	61	99	66	66	93	54	67	84
ENSMUSG00000031059	chrX	Ndufb11	-0.0920712	0.568139813	0.634572583	8.15006971	0.030917272	0	4262	4493	4342	5606	3239	5492	4155	4081	4737	4005
ENSMUSG00000085622	chr12	3110056K07Rik	0.16095019	0.568145874	0.634572583	0.862993437	0.048793903	0	21	27	22	29	20	33	32	25	28	28
ENSMUSG00000019891	chr10	Dcbld1	-0.1693621	0.568354605	0.634754992	1.768620831	0.079475077	0	47	46	53	69	45	93	55	45	30	33
ENSMUSG00000064372	chrMT	mt-Tp	0.39417041	0.568634382	0.63501671	0.995153624	0.512618903	0	12	5	32	59	18	1	12	72	41	39
ENSMUSG00000006998	chr16	Psmd2	0.08579781	0.569082793	0.635466692	7.968062776	0.026938762	0	3580	3338	3084	4696	3487	4782	4186	3632	4520	3939
ENSMUSG00000029307	chr5	Dmp1	-0.1982903	0.569214342	0.635562806	0.512282505	0.097028732	0	30	14	20	13	25	31	18	17	14	20
ENSMUSG00000039910	chr10	Cited2	-0.1339713	0.56935523	0.635636523	5.063864849	0.063453925	0	448	554	438	742	444	316	446	370	837	595
ENSMUSG00000048930	chr6	Tada3	0.08497774	0.569416805	0.635636523	3.951124829	0.021513552	0	214	203	203	279	213	323	248	222	236	267
ENSMUSG00000097767	chr5	Miat	-0.2639367	0.569379287	0.635636523	-0.159981442	0.12735633	0	18	14	15	8	7	7	8	8	16	18
ENSMUSG00000026594	chr1	Ralgps2	0.15888859	0.570239124	0.636503633	2.426957985	0.077518981	0	84	83	67	71	62	103	82	129	41	96
ENSMUSG00000029592	chr5	Usp30	-0.09095	0.570859848	0.637145603	3.651402807	0.024680271	0	197	166	154	252	193	243	176	179	176	214
ENSMUSG00000040339	chr3	Fam102b	-0.0992054	0.571154264	0.637423301	4.03258034	0.033085551	0	254	278	232	274	210	363	280	164	224	267
ENSMUSG00000015709	chr7	Arnt2	0.17710556	0.571216554	0.637441916	1.563747834	0.08540668	0	56	40	32	32	36	27	61	55	43	57
ENSMUSG00000027223	chr2	Mapk8ip1	0.13923868	0.571610777	0.637830915	4.345318909	0.068317978	0	297	262	239	299	325	185	276	326	337	593
ENSMUSG00000006021	chr7	Kptn	-0.093209	0.571898734	0.638101285	3.570809776	0.025977256	0	187	185	180	193	155	184	206	182	187	167
ENSMUSG00000074829	chr9	2010315B03Rik	0.1719151	0.572157983	0.638339584	1.797407911	0.084414978	0	67	44	36	46	41	31	79	45	66	67
ENSMUSG00000052395	chr14	Rft1	0.1138372	0.573382138	0.639654276	2.833277771	0.037670473	0	104	102	91	130	77	137	129	95	85	153
ENSMUSG00000021192	chr12	Golga5	-0.0849788	0.574050495	0.640336516	4.472962328	0.023601518	0	354	314	297	425	310	295	380	323	363	382
ENSMUSG00000057092	chr7	Fxyd3	-0.2304685	0.574085328	0.640336516	-0.136944635	0.089700507	0	11	9	12	15	16	18	7	15	8	11
ENSMUSG00000027661	chr2	Slc2a10	-0.1480087	0.574991543	0.641296131	1.785820901	0.060927225	0	47	34	45	74	62	70	61	48	38	42
ENSMUSG00000022463	chr15	Srebf2	-0.0878072	0.575132594	0.641383078	5.096456365	0.027084421	0	490	479	435	659	559	565	654	552	484	438
ENSMUSG00000039887	chr3	Alg14	-0.1120667	0.575161285	0.641383078	2.849339504	0.037183387	0	133	110	99	120	86	104	140	91	98	124
ENSMUSG00000031494	chr8	Cd209a	0.23924594	0.57536221	0.641555947	0.583006682	0.129174059	0	19	17	18	13	25	22	29	28	33	8
ENSMUSG00000049502	chr16	Dtx3l	-0.1160041	0.575677788	0.641856623	3.66732665	0.044470255	0	187	210	192	223	161	121	189	193	227	246
ENSMUSG00000032584	chr9	Mst1r	0.1816303	0.576303817	0.642503363	0.872322076	0.078679916	0	29	18	16	23	32	47	24	25	25	28
ENSMUSG00000044080	chr3	S100a1	-0.0959706	0.576964861	0.643172418	6.597878091	0.034707707	0	1534	1477	1489	1827	1141	2211	1196	1371	1551	1350
ENSMUSG00000104348	chr1	RP23-59N15.4	0.16680119	0.576995978	0.643172418	1.107409031	0.072933578	0	24	31	27	44	18	25	43	28	45	33

ENSMUSG00000042570	chr10	Mier2	0.08866811	0.577140737	0.643282474	4.057224564	0.025035422	0	252	210	222	281	228	375	291	236	224	276
ENSMUSG00000046947	chr6	Adck2	-0.0869507	0.577233799	0.643283595	7.141116783	0.028639919	0	2342	2145	2238	2426	1653	2313	2249	1969	2425	2197
ENSMUSG00000052833	chr7	Sae1	0.10185042	0.577222738	0.643283595	5.738778475	0.038403416	0	797	750	637	939	717	1468	910	771	760	648
ENSMUSG00000054426	chr3	A930005H10Rik	-0.1221718	0.577469374	0.643443512	3.093335702	0.049230262	0	134	129	109	165	119	236	102	102	108	120
ENSMUSG00000087385	chr4	AA415398	0.15730934	0.577449703	0.643443512	1.067547864	0.054762825	0	25	21	22	37	34	33	32	36	31	37
ENSMUSG00000035517	chr4	Tdrd7	0.09160101	0.578086402	0.644060147	4.085414476	0.02801503	0	242	221	197	318	244	281	297	199	317	329
ENSMUSG00000100691	chr8	2010320M18Rik	0.10664287	0.57811495	0.644060147	3.399360311	0.036559688	0	205	146	134	149	112	239	172	151	163	163
ENSMUSG00000093904	chr8	Tomm20	-0.0833815	0.578166387	0.644066111	5.673746407	0.025331503	0	697	695	768	1102	676	859	877	706	838	758
ENSMUSG00000045176	chr11	2310047M10Rik	-0.0864713	0.578212958	0.644066653	4.733755444	0.026355151	0	399	359	339	494	442	577	363	393	374	402
ENSMUSG00000022878	chr16	Adipoq	0.34225316	0.578630883	0.644480811	3.523106003	0.437664054	0	37	372	50	53	203	35	152	376	96	353
ENSMUSG00000037552	chr7	Plekhg2	-0.1014722	0.578923165	0.644703598	3.450149756	0.032661598	0	153	132	164	243	150	244	172	140	136	168
ENSMUSG00000073131	chrX	Vma21	-0.0835791	0.578896961	0.644703598	4.942565488	0.024584677	0	476	396	434	617	438	496	448	486	392	608
ENSMUSG00000061143	chr3	Maml3	-0.1138063	0.578976172	0.644711256	2.417660726	0.034963968	0	80	71	79	92	81	94	73	83	78	81
ENSMUSG00000024360	chr18	Etf1	-0.0841178	0.579335184	0.645059634	6.701380189	0.026802093	0	1620	1390	1328	2256	1467	1813	1843	1385	1695	1517
ENSMUSG00000003477	chr6	Inmt	-0.2435346	0.579524062	0.645218537	0.685776928	0.174032498	0	18	46	18	11	24	10	24	18	23	36
ENSMUSG00000032571	chr9	Pik3r4	-0.081189	0.579701665	0.645364861	3.865885505	0.020679491	0	213	213	195	281	209	256	237	200	205	253
ENSMUSG00000031371	chrX	Haus7	0.09168518	0.579867426	0.64549798	4.073251069	0.027947844	0	295	249	186	255	218	330	284	226	305	266
ENSMUSG00000057130	chr18	Txnl4a	0.0788907	0.580345271	0.645978457	4.446100821	0.02093095	0	343	328	275	361	264	377	395	331	359	355
ENSMUSG00000020530	chr11	Ggnbp2	-0.0833484	0.580843885	0.646453027	5.311903478	0.02537675	0	649	625	566	721	480	600	712	503	670	655
ENSMUSG00000030553	chr7	Pgpep1l	0.14573934	0.580864132	0.646453027	1.831565248	0.058622818	0	48	38	58	51	46	69	48	75	50	51
ENSMUSG00000056536	chr1	Pign	-0.1082359	0.580970271	0.646519667	2.716836524	0.032265297	0	98	98	92	129	84	114	125	88	83	99
ENSMUSG00000008153	chr6	Clstn3	0.25104043	0.581035196	0.646540438	0.635460705	0.190011932	0	9	31	11	18	27	14	21	50	17	22
ENSMUSG00000026077	chr1	Npas2	-0.2617804	0.581338328	0.646826246	0.864976274	0.209907718	0	9	21	12	46	51	46	14	30	14	23
ENSMUSG00000004328	chr7	Hif3a	-0.3223635	0.58141695	0.646862226	-0.158022842	0.247575168	0	18	9	8	11	17	33	11	4	2	8
ENSMUSG00000027822	chr3	Slc33a1	-0.1018855	0.581518018	0.64691684	3.254616571	0.032971034	0	144	139	130	162	149	131	192	112	145	163
ENSMUSG00000081669	chr6	Npm3-ps1	-0.2503272	0.581558613	0.64691684	-0.017559147	0.146052485	0	13	8	15	19	15	28	9	8	16	4
ENSMUSG00000074218	chr7	Cox7a1	0.10246004	0.582066406	0.647430171	7.874597399	0.041259664	0	2913	3556	3613	4761	2181	3538	3643	4091	4508	3882
ENSMUSG00000041890	chr5	Git2	-0.0847972	0.582129026	0.647448294	4.570466771	0.025330853	0	308	375	325	510	311	501	358	295	346	389
ENSMUSG00000021286	chr12	Zfyve21	-0.0916312	0.582258829	0.64747225	3.632167628	0.02776982	0	169	183	180	236	177	280	187	160	171	181
ENSMUSG00000060279	chr7	Ap2a1	0.08423345	0.582251508	0.64747225	6.34330499	0.027185885	0	1112	1041	1038	1481	1204	1395	1378	1403	1105	1528
ENSMUSG00000062866	chr10	Phactr2	0.08919433	0.582289548	0.64747225	4.511152958	0.028135426	0	298	307	305	409	320	381	346	411	290	479
ENSMUSG00000024299	chr17	Adamts10	-0.0996378	0.582422365	0.647568415	3.856346143	0.035325369	0	256	231	213	179	211	298	211	211	178	241
ENSMUSG00000025161	chr11	Slc16a3	-0.1235965	0.582606999	0.647722172	8.129853224	0.060231626	0	4618	3622	3806	5308	4434	2291	4669	3779	4591	6397
ENSMUSG00000043773	chr9	1700048O20Rik	0.28752876	0.583016892	0.648126319	-0.074440444	0.215207277	0	20	18	7	9	1	25	15	16	12	6
ENSMUSG00000026435	chr1	Slc45a3	-0.1656832	0.583092727	0.648159068	1.421794144	0.076466354	0	40	30	30	58	45	68	39	25	39	28
ENSMUSG00000028427	chr4	Aqp7	-0.1133869	0.583210069	0.648237946	3.376913119	0.043722574	0	153	187	130	178	145	154	113	192	134	208
ENSMUSG00000029524	chr5	Sirt4	-0.0980967	0.583660654	0.648687181	3.232115276	0.028399267	0	165	134	123	178	118	169	124	149	128	162
ENSMUSG00000031283	chrX	Chrdl1	-0.1494771	0.583722675	0.648704525	2.373514625	0.077651747	0	73	90	68	89	75	149	90	44	50	68
ENSMUSG00000040310	chr2	Alx4	-0.1554348	0.583960816	0.648917577	1.034845063	0.061825411	0	31	32	31	29	27	37	32	23	18	40
ENSMUSG00000034820	chr19	Cpsf7	-0.0765095	0.584450462	0.649358428	4.50690383	0.020104431	0	332	313	320	454	319	383	370	307	338	404
ENSMUSG00000038583	chr10	Pln	-0.1844353	0.584433519	0.649358428	0.672183708	0.064556631	0	21	19	20	38	20	23	30	23	20	16
ENSMUSG00000014813	chr14	Stc1	-0.1798148	0.584784802	0.649668097	0.625237639	0.071180622	0	22	19	24	26	21	36	20	12	17	25
ENSMUSG00000050373	chr2	Snx21	-0.0802889	0.584822147	0.649668097	4.70912709	0.022896401	0	398	367	396	503	336	502	343	413	392	418
ENSMUSG00000040213	chr3	Ccbl2	-0.1152071	0.584925714	0.649731503	2.863535008	0.043319633	0	96	143	94	138	85	138	101	78	112	136
ENSMUSG00000019577	chr6	Pdk4	0.2093181	0.585350294	0.650151451	7.840665865	0.174841107	0	774	2508	1620	8617	3349	3195	4053	5392	3675	3441
ENSMUSG00000030772	chr7	Dkk3	-0.1539992	0.58566378	0.650396264	3.035579693	0.087500809	0	205	116	103	92	110	189	113	82	71	182
ENSMUSG00000082319	chrX	Gm8822	-0.3550489	0.585650692	0.650396264	2.040431687	0.474416776	0	57	81	63	89	44	247	17	7	15	21
ENSMUSG00000018983	chr4	E2f2	0.16897993	0.585857997	0.650560255	3.930626623	0.108454617	0	437	194	189	102	121	246	301	285	216	254
ENSMUSG00000028433	chr4	Ubap2	-0.1106897	0.586379996	0.651088172	6.407957151	0.048580064	0	1104	1106	964	1792	1627	1163	1231	1409	970	1875
ENSMUSG00000031485	chr8	Prosc	-0.078163	0.586547448	0.651222365	5.016485076	0.022302948	0	473	484	458	654	414	494	624	437	469	541
ENSMUSG00000042015	chr13	Wdr41	-0.0765116	0.586628667	0.65124295	4.794283346	0.020966963	0	393	384	375	558	413	478	467	355	463	437
ENSMUSG00000059689	chr6	Zfp637	-0.0820668	0.586659183	0.65124295	4.477781195	0.023775358	0	385	315	279	445	288	384	366	255	366	395
ENSMUSG00000022820	chr16	Ndufb4	0.08174537	0.587159298	0.651694595	6.181321396	0.026103477	0	1109	1106	1016	1230	789	1374	1253	1030	1248	1190
ENSMUSG00000098413	chr19	Mir6990	-0.2574903	0.587145226	0.651694595	-0.006271015	0.111240078	0	14	12	9	25	12	4	16	15	11	18
ENSMUSG00000021189	chr12	Atxn3	0.10897698	0.587277001	0.651773475	3.20813842	0.038589929	0	118	113	142	194	94	210	174	111	139	146
ENSMUSG00000039738	chr16	Slx4	0.11336758	0.587430474	0.651892037	2.605990432	0.040370653	0	66	87	68	127	83	130	107	87	97	87
ENSMUSG00000035923	chr10	Myf6	-0.0884749	0.587850635	0.652306508	5.947598643	0.030723763	0	1047	770	905	1080	919	910	935	975	797	1254
ENSMUSG00000042364	chr13	Snx18	0.0818991	0.588424076	0.652890988	4.416963373	0.023239336	0	283	283	317	359	291	462	356	317	289	371
ENSMUSG00000028879	chr4	Stx12	0.07817211	0.588740537	0.653190263	5.307721071	0.023288902	0	531	545	510	768	526	685	734	555	710	627
ENSMUSG00000027963	chr3	Extl2	-0.0919363	0.589225117	0.653675999	3.850767026	0.029120416	0	232	228	196	252	191	179	273	211	210	254
ENSMUSG00000021234	chr12	Fam161b	-0.2269195	0.589284061	0.653689502	0.103764943	0.090184263	0	11	16	13	30	8	11	18	13	15	14
ENSMUSG00000040136	chr7	Abcc8	-0.16176	0.589591451	0.653978581	1.160087734	0.072200322	0	44	31	25	30	35	32	40	41	23	26
ENSMUSG00000028416	chr4	Bag1	0.07980709	0.589665623	0.654007816	7.171901232	0.025761466	0	2174	2000	1807	2702	1820	2948	2138	2239	2382	2407
ENSMUSG00000032187	chr9	Smarca4	-0.0889474	0.589711398	0.654007816	6.040875337	0.031316332	0	963	760	825	1453	1098	984	1195	940	947	1134
ENSMUSG00000036764	chr10	Dnajc12	-0.1140896	0.589837023	0.654095234	3.2535505	0.045249596	0	168	110	121	191	144	106	136	125	176	191

ENSMUSG00000001910	chr8	Nacc1	-0.0832117	0.590122036	0.654359376	5.341242737	0.026620201	0	587	476	549	817	681	623	689	615	584	690
ENSMUSG00000000826	chr2	Dnajc5	-0.0788221	0.590528377	0.654758	5.987414317	0.024474801	0	890	819	887	1323	959	1101	1037	959	891	1047
ENSMUSG00000038732	chr13	Mboat1	0.14193949	0.590658456	0.654850276	2.20966324	0.062359053	0	70	60	53	62	71	102	91	89	52	52
ENSMUSG00000026275	chr1	Ppp1r7	0.07575908	0.591492366	0.655626658	4.616313413	0.020765376	0	373	323	309	436	334	459	459	346	409	376
ENSMUSG00000029334	chr5	Prkg2	0.24136615	0.59149664	0.655626658	0.374837787	0.151324019	0	5	14	19	31	12	29	33	19	9	14
ENSMUSG00000066191	chr4	Anks6	0.14059562	0.591499466	0.655626658	1.266920301	0.051667628	0	30	31	20	42	39	41	39	37	38	40
ENSMUSG00000028073	chr3	Pear1	0.10439293	0.591741543	0.655842966	3.960079801	0.03997856	0	199	191	211	302	212	371	206	262	163	316
ENSMUSG00000022354	chr15	Ndufb9	0.08604532	0.591901721	0.655958833	8.710357005	0.030718904	0	5748	6208	6120	7882	4478	8182	6268	6712	7159	6884
ENSMUSG00000040557	chr5	Wbscr27	0.2052776	0.591939955	0.655958833	1.48194039	0.133579558	0	67	37	26	31	23	59	29	65	22	58
ENSMUSG00000099233	chr16	Gm27883	0.12315858	0.592026536	0.656002764	2.745499937	0.051520485	0	109	64	84	101	109	84	124	117	99	133
ENSMUSG00000023307	chr19	March5	-0.0831286	0.592137576	0.656073788	5.817566941	0.02742801	0	867	788	730	1130	824	781	971	786	789	1137
ENSMUSG00000032435	chr9	Dync1li1	0.07540742	0.592689914	0.656633709	5.374126211	0.021958923	0	643	510	562	725	564	733	744	650	600	742
ENSMUSG00000032178	chr9	Ilf3	-0.0809294	0.592952704	0.65687278	4.719619629	0.024572565	0	390	327	372	502	420	418	498	354	425	386
ENSMUSG00000056832	chr6	Ttc26	0.18720577	0.593099468	0.65698329	0.710916215	0.081363494	0	25	16	21	18	24	19	37	18	31	26
ENSMUSG00000101609	chr7	Kcnq1ot1	0.19296938	0.593691754	0.657587253	1.256827288	0.107608224	0	39	40	29	12	33	31	39	41	43	42
ENSMUSG00000024790	chr19	Sac3d1	-0.0890853	0.594217739	0.658117689	3.581639551	0.027073739	0	213	158	155	212	173	184	172	166	180	236
ENSMUSG00000045140	chr11	Pigw	-0.1370607	0.594370834	0.658235085	2.023735579	0.057109123	0	66	62	59	77	45	38	76	63	63	64
ENSMUSG00000025766	chr3	D3Ertd751e	-0.16635	0.594484347	0.658308631	1.575322999	0.079867377	0	42	48	42	53	40	23	66	36	54	39
ENSMUSG00000027193	chr2	Api5	0.08439045	0.594932793	0.658753028	5.141520745	0.027938463	0	518	456	461	624	489	645	698	424	690	505
ENSMUSG00000052949	chr11	Rnf157	-0.133942	0.595101802	0.658887966	5.47346077	0.07399893	0	830	609	551	764	696	317	774	489	776	1077
ENSMUSG00000041482	chr18	Piezo2	-0.1626973	0.595721647	0.659522001	1.630532792	0.090932369	0	54	42	41	64	35	83	31	38	22	59
ENSMUSG00000037921	chr8	Ddx60	-0.1917345	0.595880912	0.65964607	0.704153766	0.10280525	0	30	27	25	23	14	29	16	16	14	41
ENSMUSG00000000959	chr14	Oxa1l	-0.0829811	0.596070519	0.659803704	6.046008418	0.028254397	0	992	1043	1028	1210	785	1324	895	1051	920	1053
ENSMUSG00000021411	chr13	Pxdc1	0.15588007	0.596149391	0.65983875	2.316068607	0.086881809	0	60	74	54	102	56	176	61	62	63	64
ENSMUSG00000061904	chr10	Slc25a3	0.08931063	0.596460019	0.660130284	9.735340881	0.034029048	0	10365	11799	11740	18354	10070	17127	12891	15269	12013	14476
ENSMUSG00000049422	chr10	Chchd10	0.08936498	0.596550224	0.660177839	8.679184671	0.033992037	0	5318	5349	5048	8550	5648	8705	6140	7342	5239	7173
ENSMUSG00000015337	chr2	Endog	0.07941062	0.596650959	0.660196204	5.091383154	0.025066221	0	412	476	437	686	468	603	523	634	512	567
ENSMUSG00000021379	chr13	Id4	-0.1730056	0.596661294	0.660196204	0.831625207	0.081563611	0	22	29	24	28	27	38	19	28	12	31
ENSMUSG00000041313	chr5	Slc7a1	0.12444242	0.596869812	0.660374643	3.234779864	0.056736163	0	131	107	99	207	129	226	210	131	140	90
ENSMUSG00000020238	chr10	Ncln	0.08273882	0.597057303	0.660477866	5.755099996	0.027852317	0	763	645	673	978	847	1099	1058	750	861	779
ENSMUSG00000029205	chr5	Chrna9	0.40520807	0.597057625	0.660477866	0.978321037	0.59630058	0	13	3	6	29	64	130	13	8	11	19
ENSMUSG00000051510	chr11	Mafg	-0.0794371	0.597377835	0.660727494	6.073350896	0.026099354	0	1077	999	969	1195	903	1360	1077	844	1115	969
ENSMUSG00000063808	chr7	Gpatch1	-0.1267197	0.597346598	0.660727494	2.688686885	0.055123762	0	81	107	68	139	101	70	110	75	114	123
ENSMUSG00000015224	chr4	Cyp2j9	0.19046531	0.597991188	0.661353553	0.476005289	0.08226415	0	12	15	21	18	21	22	14	19	23	32
ENSMUSG00000033707	chr15	Lrrc24	-0.0779875	0.598075834	0.661394829	4.876692779	0.023289464	0	408	432	455	597	359	481	434	493	441	467
ENSMUSG00000001520	chr6	Nrip2	-0.1589209	0.598544406	0.661721738	1.868241603	0.082476602	0	30	58	42	96	56	75	37	59	40	62
ENSMUSG00000011254	chr11	Thg1l	0.1170241	0.598438472	0.661721738	2.682255998	0.044018236	0	104	77	75	109	86	168	110	83	86	94
ENSMUSG00000024260	chr18	Sap130	-0.0879859	0.598537269	0.661721738	3.468436751	0.026483544	0	173	148	134	232	161	193	202	131	164	181
ENSMUSG00000096255	chr17	Dynlt1b	0.17332629	0.598560834	0.661721738	1.92519961	0.094683563	0	39	53	73	29	55	73	66	75	42	62
ENSMUSG00000022091	chr14	Sorbs3	0.09721371	0.598813642	0.661948862	5.178376101	0.03869856	0	548	511	411	706	448	984	487	583	418	611
ENSMUSG00000056267	chr9	Cep70	0.14303212	0.599046526	0.662153927	1.448736544	0.055091715	0	38	38	28	47	34	49	31	35	55	53
ENSMUSG00000009741	chr9	Ubp1	0.07721057	0.599805232	0.662940128	4.634799281	0.022702258	0	332	366	349	443	305	504	469	367	378	362
ENSMUSG00000051811	chr7	Cox6b2	0.23520846	0.600355067	0.663495368	-0.154938377	0.120631517	0	12	7	15	8	10	21	8	20	10	9
ENSMUSG00000026750	chr2	Psmb7	-0.0822599	0.60066814	0.663788876	7.832411947	0.029258486	0	3915	3366	3159	4181	2884	3465	3578	3017	4064	3915
ENSMUSG00000003848	chr8	Nob1	0.07975789	0.601134728	0.664212634	4.05927519	0.023184613	0	233	221	213	303	232	341	295	250	267	239
ENSMUSG00000075271	chr2	Ttc30a1	0.17855333	0.601146652	0.664212634	0.737562599	0.065424302	0	16	21	25	24	21	29	25	25	34	20
ENSMUSG00000097944	chr8	A130014A01Rik	-0.1660694	0.601730708	0.664805405	0.710351453	0.070260495	0	16	24	25	36	19	25	26	13	22	31
ENSMUSG00000048776	chr6	Pthlh	-0.1945158	0.601925842	0.664968427	0.249661866	0.073975106	0	16	14	17	23	15	20	17	21	8	15
ENSMUSG00000020585	chr12	Laptm4a	-0.0792652	0.602116013	0.665125941	8.50744705	0.027515129	0	6181	5690	4977	6310	4681	6012	5980	5421	5108	6394
ENSMUSG00000032553	chr9	Srprb	0.07523227	0.602382273	0.665367473	5.254748239	0.023066322	0	556	490	483	701	541	653	705	523	696	611
ENSMUSG00000014859	chr8	E2f4	0.0892681	0.602495125	0.665439534	4.672235714	0.032450474	0	304	297	316	556	381	522	481	364	445	329
ENSMUSG00000031984	chr8	2810004N23Rik	0.08056249	0.602776218	0.665697386	4.649545665	0.025943233	0	339	356	371	448	297	384	442	423	458	375
ENSMUSG00000036634	chr7	Mag	0.15897318	0.603343376	0.666271098	0.978853146	0.066658282	0	23	23	23	34	27	39	46	26	18	31
ENSMUSG00000033955	chr2	Tnks1bp1	-0.0837792	0.603507913	0.666400142	5.06552822	0.028710444	0	420	445	465	775	485	666	504	533	389	566
ENSMUSG00000048970	chrX	C1galt1c1	-0.0976776	0.603607182	0.6664571	3.544404233	0.034411685	0	222	166	134	208	162	161	219	141	210	178
ENSMUSG00000024400	chr18	Wdr33	-0.0703568	0.603660845	0.6664637	4.953378472	0.019455102	0	457	440	415	626	432	532	478	448	448	557
ENSMUSG00000038368	chr4	Focad	-0.0984906	0.603832368	0.666600409	3.589830039	0.034759658	0	174	159	148	274	175	139	211	169	202	214
ENSMUSG00000044986	chr15	Tst	-0.102649	0.603920037	0.666644534	4.799525559	0.044142187	0	454	550	394	390	329	343	412	455	365	599
ENSMUSG00000040667	chr11	Nup88	-0.07394	0.604004289	0.66668488	5.226324881	0.022163876	0	562	521	528	714	533	542	616	546	629	625
ENSMUSG00000023110	chr14	Prmt5	0.08140463	0.604359879	0.667009881	5.28124126	0.027685471	0	565	491	455	678	618	634	726	619	704	557
ENSMUSG00000046618	chr2	Olfml2a	-0.1165955	0.604394185	0.667009881	3.136429953	0.052169394	0	148	105	148	163	109	100	134	154	97	191
ENSMUSG00000082424	chr2	Gm13292	0.26662263	0.604449969	0.667018774	0.114249182	0.211043793	0	11	17	10	10	16	7	10	41	11	14
ENSMUSG00000039318	chr1	Rab3gap2	-0.0717355	0.604502776	0.667024379	4.809075685	0.020319741	0	424	394	378	553	393	488	516	358	420	449
ENSMUSG00000025610	chr16	Map3k7cl	-0.1264451	0.604669873	0.667076397	4.49666597	0.068151399	0	609	314	298	269	242	406	501	280	242	340
ENSMUSG00000028811	chr4	Yars	-0.0764241	0.604634612	0.667076397	5.472530885	0.024319276	0	732	662	590	795	610	740	733	648	768	622

ENSMUSG00000047905	chr6	Gm8566	0.18842557	0.604693108	0.667076397	0.468650242	0.066200508	0	14	12	19	20	22	22	25	23	20	19
ENSMUSG00000060126	chr14	Tpt1	-0.080892	0.605077339	0.667447584	10.25423702	0.029284201	0	20962	17690	16260	22767	16201	25079	19984	16540	18278	17593
ENSMUSG00000090083	chr17	Rnf8	0.07645361	0.605198551	0.667528604	4.465786493	0.023262832	0	317	297	281	432	279	349	348	379	326	435
ENSMUSG00000019295	chr5	Tmem129	-0.0820162	0.60529534	0.667582676	3.727822145	0.024194757	0	220	216	155	246	173	244	212	176	212	200
ENSMUSG00000063455	chr6	D630045J12Rik	0.19793379	0.605400971	0.667646491	0.547010865	0.100077908	0	16	7	19	34	18	30	30	20	13	24
ENSMUSG00000028139	chr3	Riiad1	0.12920239	0.605963807	0.668214468	1.73066177	0.053367406	0	45	42	43	49	47	56	40	49	72	54
ENSMUSG00000028393	chr4	Alad	-0.110725	0.6066668	0.668936899	5.544719181	0.053666193	0	619	691	575	1098	672	1324	670	576	668	473
ENSMUSG00000050914	chr8	Ankrd37	-0.1430078	0.607271054	0.669550351	1.384169273	0.05587605	0	50	45	28	44	28	35	42	31	38	47
ENSMUSG00000021890	chr14	Eaf1	-0.072707	0.60758417	0.669842735	4.827625333	0.021353465	0	383	442	389	545	405	468	507	376	465	436
ENSMUSG00000003444	chr7	Med29	0.08342276	0.60773882	0.669960384	3.955616061	0.026232777	0	227	241	226	237	177	294	228	250	269	250
ENSMUSG00000038253	chr6	Hoxa5	0.15498737	0.608134672	0.670291023	1.142203684	0.0735575	0	21	21	38	41	26	28	35	41	29	45
ENSMUSG00000044991	chr2	1110034G24Rik	0.12631955	0.608088666	0.670291023	2.071625889	0.053057277	0	67	65	59	58	40	90	70	49	80	60
ENSMUSG00000032316	chr9	Clk3	0.07172483	0.608766042	0.670934011	5.042663456	0.020876476	0	520	478	427	503	446	642	578	478	531	526
ENSMUSG00000068267	chr2	Cenpb	0.08017131	0.609713183	0.671924889	7.359788217	0.029171414	0	2311	2182	2037	3244	2213	2395	2798	2470	2919	3143
ENSMUSG00000048058	chr2	Ldlrad3	0.10250185	0.611714887	0.674077684	3.277032021	0.040659414	0	138	102	139	196	119	201	146	170	102	194
ENSMUSG00000025354	chr10	Dnajc14	0.07063213	0.61213004	0.674481981	5.024252682	0.020814074	0	472	467	428	600	400	676	514	427	527	585
ENSMUSG00000031578	chr8	Mak16	0.09119265	0.612364166	0.674686762	3.730928492	0.032330479	0	191	170	175	244	173	276	298	155	204	184
ENSMUSG00000032067	chr9	Pts	0.09043188	0.612463934	0.674690308	3.272289274	0.029056309	0	142	141	145	151	107	193	158	121	163	172
ENSMUSG00000042506	chr11	Usp22	0.07478071	0.612439581	0.674690308	4.715613353	0.022996116	0	396	375	369	464	299	561	444	403	347	449
ENSMUSG00000046768	chr12	Rhoj	-0.0874154	0.613273831	0.675529245	4.35027225	0.032220073	0	287	315	257	395	307	428	260	325	220	383
ENSMUSG00000097577	chr14	6230400D17Rik	-0.1630812	0.613710476	0.67595694	0.798519346	0.081862343	0	28	29	21	28	21	35	28	14	33	15
ENSMUSG00000001909	chr8	Trmt1	0.06994841	0.613824697	0.676029469	4.53975314	0.019785004	0	330	291	305	433	329	434	396	353	362	393
ENSMUSG00000037606	chr7	Osbpl5	0.08027017	0.613876717	0.676033488	4.714238993	0.027569812	0	414	348	267	471	400	417	413	420	400	540
ENSMUSG00000093769	chr3	Hist2h3c1	-0.17103	0.614415527	0.676573543	1.92738263	0.11310773	0	43	57	43	90	61	25	79	51	35	92
ENSMUSG00000021185	chr12	9030617O03Rik	-0.1324739	0.614834106	0.676924224	2.800251765	0.070626486	0	70	141	129	120	70	82	133	124	88	102
ENSMUSG00000027513	chr2	Pck1	0.41364677	0.61487136	0.676924224	3.622682399	0.767844775	0	20	412	56	28	222	24	66	571	27	406
ENSMUSG00000028036	chr3	Ptgfr	-0.2003048	0.614879295	0.676924224	0.560041149	0.128539222	0	26	31	17	25	9	28	19	8	32	16
ENSMUSG00000046380	chr15	Jrk	-0.1437831	0.614957191	0.676956655	1.461987824	0.069802807	0	44	38	46	54	25	25	50	35	44	49
ENSMUSG00000084093	chr1	Gm16418	0.11807075	0.615913943	0.677956467	2.179697659	0.042556269	0	66	47	67	73	61	82	63	64	73	93
ENSMUSG00000021113	chr12	Snapc1	0.09131655	0.615963628	0.677957762	3.10815522	0.030623123	0	101	107	122	169	117	137	151	129	153	144
ENSMUSG00000020123	chr10	Avpr1a	0.18676381	0.616329643	0.678307197	0.769016008	0.08879163	0	16	19	28	25	21	44	36	14	22	23
ENSMUSG00000037096	chr3	Gm9762	-0.1392427	0.616822228	0.678795863	1.269648449	0.052797659	0	38	30	26	55	32	38	29	31	33	47
ENSMUSG00000020069	chr10	Hnrnph3	-0.0774466	0.61773005	0.679721658	4.054369777	0.02432438	0	252	223	232	309	247	309	294	227	264	219
ENSMUSG00000054499	chr7	Dedd2	-0.112736	0.617760768	0.679721658	2.774492147	0.049156667	0	102	75	119	141	86	129	79	123	81	115
ENSMUSG00000049792	chr12	Bag5	-0.0795346	0.617932222	0.679856785	3.90391301	0.02541495	0	219	184	205	313	224	281	238	173	226	269
ENSMUSG00000027170	chr2	Eif3m	-0.0827668	0.617994522	0.679871807	6.198016033	0.031826466	0	1314	1047	1011	1329	931	938	1336	1051	1287	1167
ENSMUSG00000028412	chr4	Slc44a1	-0.0717049	0.618060514	0.679890889	5.185207719	0.0228355	0	584	557	502	675	459	647	569	470	503	715
ENSMUSG00000025436	chr10	Xrcc6bp1	0.1396228	0.618250996	0.6800469	1.246496268	0.055794756	0	33	25	26	43	33	55	41	35	35	27
ENSMUSG00000066152	chr4	Slc31a2	-0.0934714	0.61880917	0.6806073	3.184781268	0.036695489	0	140	139	149	141	116	163	146	89	144	172
ENSMUSG00000092260	chr8	Zfp963	0.126317	0.619368916	0.681169339	1.803751242	0.052442696	0	47	53	44	58	38	43	54	51	69	68
ENSMUSG00000027582	chr2	Zgpat	-0.0787874	0.619427236	0.681179877	4.252015974	0.026275495	0	336	299	245	285	274	319	285	285	329	281
ENSMUSG00000041161	chr4	Otud3	0.14943929	0.619572017	0.681285485	2.599669086	0.093781962	0	86	66	77	104	87	36	125	122	92	127
ENSMUSG00000031684	chr8	Slc10a7	0.10228099	0.619914631	0.681608597	2.589774775	0.035579747	0	78	83	64	114	87	112	108	80	84	117
ENSMUSG00000059772	chr7	Slx1b	0.1030074	0.620202716	0.681871708	2.627510522	0.036396365	0	106	81	74	102	73	136	91	91	86	111
ENSMUSG00000074071	chr7	Fam169b	0.19581537	0.620304448	0.681929912	0.669668292	0.107967697	0	29	12	19	14	26	39	24	28	22	15
ENSMUSG00000037172	chr6	E330009J07Rik	0.18059019	0.620366437	0.681944417	2.039924976	0.129201473	0	55	69	38	61	54	104	67	24	35	125
ENSMUSG00000028099	chr3	Polr3c	0.07478134	0.621077679	0.682618878	4.440953754	0.024513614	0	311	286	254	421	306	326	357	391	337	388
ENSMUSG00000100783	chr5	2310047D07Rik	-0.1305912	0.621077018	0.682618878	2.441217559	0.065608469	0	105	78	58	115	63	72	97	63	119	60
ENSMUSG00000039828	chr15	Wdr70	0.09109622	0.621296282	0.682805444	4.044823082	0.036531598	0	282	227	179	298	204	205	273	240	292	364
ENSMUSG00000026620	chr1	Mark1	0.13469888	0.621719636	0.683216987	1.82282796	0.072269413	0	46	45	34	86	37	62	35	61	52	81
ENSMUSG00000079477	chr6	Rab7	0.07836418	0.621771413	0.683220164	7.830278824	0.029865496	0	3169	2934	2910	4083	3409	4686	4263	2714	3614	3967
ENSMUSG00000020612	chr11	Prkar1a	0.07892605	0.622282744	0.683728273	7.999689195	0.030461922	0	3048	3385	3433	4949	3792	4690	4144	3695	3753	5270
ENSMUSG00000048647	chr2	Exd1	-0.1889484	0.622441278	0.683832932	0.535034419	0.092025713	0	24	19	9	29	25	19	17	12	27	26
ENSMUSG00000066043	chr4	Phactr4	-0.0769642	0.622475856	0.683832932	3.827443254	0.023725675	0	199	193	211	287	192	272	238	217	184	211
ENSMUSG00000020392	chr11	Cdkn2aipnl	0.08685939	0.622645336	0.683965355	4.050888136	0.031831273	0	268	234	202	268	216	326	335	171	293	269
ENSMUSG00000048376	chr13	F2r	-0.1149166	0.622729584	0.684004139	3.683256629	0.058705781	0	184	219	194	304	102	313	236	156	129	179
ENSMUSG00000001403	chr2	Ube2c	0.31558875	0.622862482	0.684096349	6.961818317	0.481098935	0	789	858	415	2790	3516	748	533	6086	374	3027
ENSMUSG00000031921	chr8	Terf2	0.07531147	0.623177606	0.68438867	4.034182474	0.024039173	0	244	224	210	317	194	296	237	280	247	301
ENSMUSG00000002578	chr10	Ikzf4	0.2570616	0.624114533	0.685363771	-0.130572201	0.19187829	0	9	20	10	4	9	13	27	15	10	5
ENSMUSG00000031980	chr8	Agt	-0.0939205	0.624380866	0.685602371	3.838811955	0.038050223	0	204	193	176	291	233	179	227	210	179	325
ENSMUSG00000019837	chr10	Gtf3c6	-0.0784383	0.624864371	0.686079382	4.068624284	0.02636174	0	257	238	254	293	230	285	323	232	269	214
ENSMUSG00000032942	chr7	Ucp3	0.11407451	0.625011017	0.686186486	6.015651445	0.064155333	0	578	863	730	1495	1024	693	1202	913	1478	1136
ENSMUSG00000000326	chr16	Comt	0.09236846	0.6254225	0.686517461	5.538578393	0.041354784	0	626	669	638	796	611	481	847	893	761	875
ENSMUSG00000050106	chr11	Tmc8	-0.2101695	0.625459848	0.686517461	0.546174365	0.142599003	0	18	27	10	28	24	45	22	14	12	10
ENSMUSG00000090996	chr2	Gm20458	-0.0744726	0.625403047	0.686517461	4.972073992	0.025336995	0	484	468	396	641	420	677	503	433	486	401

ENSMUSG00000024800	chr19	Rpp30	-0.0925739	0.625563682	0.68654704	3.185979538	0.034445436	0	140	136	141	149	121	130	180	108	157	134
ENSMUSG00000045377	chr11	Tmem88	0.10306709	0.625585043	0.68654704	3.619375004	0.046931707	0	161	146	164	238	170	248	157	257	121	246
ENSMUSG00000020078	chr10	Vps26a	-0.0761609	0.62564124	0.686554803	5.39922395	0.027512677	0	671	578	565	752	649	656	806	481	707	704
ENSMUSG00000030835	chr7	Nomo1	-0.0819942	0.626433285	0.687369992	5.983434682	0.032647208	0	813	795	758	1399	1117	968	1135	916	912	1078
ENSMUSG00000033282	chr8	Rpgrip1l	-0.1354384	0.626790881	0.68770838	1.692721746	0.058776586	0	59	43	44	52	44	30	54	51	48	57
ENSMUSG00000043153	chr12	Ispd	-0.1508707	0.626960132	0.687786092	1.536296835	0.076594593	0	41	29	36	51	60	30	37	42	54	50
ENSMUSG00000049588	chr11	Ccdc69	0.13537075	0.626954005	0.687786092	3.580071927	0.084428303	0	226	181	156	166	109	90	190	171	282	265
ENSMUSG00000020955	chr12	Ap4s1	-0.0724462	0.627157149	0.687948223	5.334873807	0.024689533	0	645	637	511	762	531	701	627	500	735	644
ENSMUSG00000030619	chr7	Eed	-0.0796639	0.627886105	0.688693784	4.16102069	0.027914241	0	297	230	253	351	237	337	334	216	301	228
ENSMUSG00000048175	chr15	Asb8	0.07545933	0.628312531	0.689107427	6.967224027	0.028519318	0	1946	1835	1663	2127	1507	1943	2123	2056	1773	2567
ENSMUSG00000054517	chr11	Trim65	-0.1109037	0.628379633	0.689126942	2.540287226	0.047821446	0	76	80	64	121	102	84	90	68	113	91
ENSMUSG00000019464	chr8	Ptger1	0.26161467	0.628645223	0.689364115	-0.155190817	0.215301583	0	7	4	5	21	16	27	9	17	3	13
ENSMUSG00000075028	chr2	Prdm11	-0.1631124	0.62874941	0.68942427	0.717944136	0.086977014	0	20	22	25	32	21	44	15	23	20	16
ENSMUSG00000014609	chr11	Chrne	-0.1066929	0.628876894	0.689466749	4.940911175	0.05631805	0	522	491	435	417	467	525	349	302	425	832
ENSMUSG00000020387	chr11	Jade2	0.15286382	0.628886814	0.689466749	2.309991984	0.095894149	0	44	60	62	93	82	145	54	58	48	119
ENSMUSG00000039842	chr8	Mcph1	-0.1097767	0.628985809	0.689471958	2.314792389	0.041578029	0	69	65	62	119	66	87	78	77	57	83
ENSMUSG00000057969	chr9	Sema3b	-0.0909741	0.628990231	0.689471958	4.603786961	0.038989554	0	444	309	376	478	266	553	308	426	288	346
ENSMUSG00000008348	chr5	Ubc	-0.0877249	0.629222073	0.689665303	7.40265397	0.039117479	0	2371	2513	1979	2949	3109	2972	2670	3043	1864	2834
ENSMUSG00000029446	chr5	Psph	-0.0828841	0.629265308	0.689665303	3.398279681	0.028345889	0	168	136	168	175	148	154	157	160	161	192
ENSMUSG00000025155	chr11	Dus1l	-0.0672369	0.629437556	0.689799991	4.839674526	0.020430992	0	448	390	432	535	373	459	460	420	476	454
ENSMUSG00000020528	chr11	Prpsap2	0.09822968	0.629531023	0.689848328	2.608655211	0.033990491	0	95	77	84	101	73	93	117	96	97	100
ENSMUSG00000030400	chr7	Ercc2	0.07411871	0.629832794	0.690124902	3.98954828	0.023970359	0	203	210	207	317	215	258	298	235	272	255
ENSMUSG00000047911	chr14	Npm2	0.19532642	0.63002269	0.690277681	0.00082027	0.076752769	0	10	13	8	18	12	16	9	15	15	21
ENSMUSG00000052031	chr17	Tagap1	-0.0843248	0.630071005	0.690277681	3.431671592	0.027081098	0	167	143	139	222	153	155	173	157	189	168
ENSMUSG00000001029	chr11	Icam2	-0.1116306	0.630300409	0.690420763	3.388565002	0.057738765	0	160	185	179	190	88	276	133	124	130	162
ENSMUSG00000075394	chr15	Hoxc4	-0.1067385	0.63028815	0.690420763	2.211408671	0.036257636	0	67	63	61	88	70	74	64	73	63	80
ENSMUSG00000047248	chr7	C2cd3	0.09956525	0.630396426	0.690471822	3.183015948	0.041846163	0	119	130	105	151	138	113	170	142	124	206
ENSMUSG00000027881	chr3	Prpf38b	0.07644314	0.630656218	0.690702242	4.579269236	0.0269072	0	350	258	323	442	357	470	445	393	301	391
ENSMUSG00000027998	chr3	Plrg1	0.07006441	0.630870622	0.690882919	4.652916656	0.022546698	0	371	363	342	442	305	386	445	360	452	446
ENSMUSG00000010554	chr11	Mettl16	-0.0738095	0.631232873	0.691225467	3.976364293	0.023609558	0	210	213	223	296	251	275	277	220	241	231
ENSMUSG00000025139	chr7	Tollip	-0.0691083	0.631331879	0.691279719	5.743080249	0.02348842	0	796	826	679	1059	740	1052	899	671	814	850
ENSMUSG00000019961	chr10	Tmpo	-0.0770865	0.631484086	0.691392211	5.245708286	0.028919207	0	671	515	497	662	548	555	774	467	631	579
ENSMUSG00000026270	chr1	Capn10	0.09733788	0.631792307	0.691649142	2.726426796	0.036520456	0	110	85	94	96	80	106	118	101	120	101
ENSMUSG00000037434	chr1	Slc30a1	0.07871043	0.631859779	0.691649142	4.044157467	0.027206271	0	245	224	232	306	186	335	335	197	244	274
ENSMUSG00000058966	chr7	Fam57b	0.12310848	0.631867218	0.691649142	5.207638331	0.077161444	0	354	388	432	962	557	357	632	622	498	1010
ENSMUSG00000004558	chr14	Ndrg2	0.07631202	0.631954063	0.691690029	10.57402782	0.030391424	0	20927	20904	20467	29062	19800	24956	22458	22747	27194	30182
ENSMUSG00000022120	chr14	Rnf219	-0.1106328	0.632174249	0.691876844	2.275046036	0.045611426	0	77	62	53	110	68	75	97	55	65	80
ENSMUSG00000022537	chr16	Tmem44	-0.131815	0.632502296	0.692181669	2.171750358	0.069946826	0	93	67	78	66	36	93	53	61	54	83
ENSMUSG00000015697	chr3	Setdb1	0.06830924	0.632854191	0.692509966	4.268854504	0.020195933	0	283	256	267	339	250	389	327	271	311	309
ENSMUSG00000025939	chr1	Ube2w	0.08584844	0.632901387	0.692509966	3.375770435	0.030144447	0	147	146	139	213	105	219	176	156	132	185
ENSMUSG00000029166	chr5	Mapre3	0.07813886	0.633207636	0.692790818	5.992407581	0.030908124	0	1158	816	692	1022	918	1082	946	1008	1027	1261
ENSMUSG00000006221	chr4	Hspb7	-0.1799485	0.633551267	0.693112525	8.566989509	0.16927464	0	2762	3141	7899	14781	3022	9486	4943	5438	6760	2510
ENSMUSG00000097445	chr9	Gm26631	0.45092499	0.633766269	0.69329347	1.279533935	0.96358908	0	7	7	4	60	71	6	4	129	1	67
ENSMUSG00000027999	chr3	Pla2g12a	0.12564369	0.633822706	0.693300942	4.963328378	0.081334623	0	288	371	353	992	314	831	418	480	595	335
ENSMUSG00000030509	chr7	Asb7	-0.096742	0.634005721	0.693446858	3.155813083	0.038322937	0	138	138	125	160	116	101	134	134	136	185
ENSMUSG00000005936	chr17	Kctd20	-0.0678449	0.634228925	0.693610984	5.753662649	0.022989581	0	821	778	685	1044	794	1069	802	734	841	865
ENSMUSG00000027030	chr2	Stk39	0.1229188	0.634255036	0.693610984	2.550691051	0.064617077	0	51	81	108	96	70	148	92	90	90	71
ENSMUSG00000024454	chr18	Hdac3	-0.0688202	0.634640351	0.693946152	6.010963413	0.023964421	0	1056	1011	840	1191	828	1217	949	897	997	1087
ENSMUSG00000103400	chr1	RP24-229G16.1	0.21776702	0.634660827	0.693946152	0.181136317	0.115128631	0	10	11	9	11	27	24	14	13	17	21
ENSMUSG00000034748	chr10	Sirt6	0.10646668	0.634768447	0.69400953	2.258511478	0.043104308	0	61	64	74	76	58	104	69	84	66	72
ENSMUSG00000039007	chr15	Cpq	-0.0769455	0.634875901	0.694072716	4.721609398	0.028713369	0	436	439	356	395	367	356	440	397	377	512
ENSMUSG00000018189	chr1	Uchl5	0.07496631	0.634943997	0.694092867	4.746239534	0.027255059	0	369	357	349	509	364	359	527	377	484	483
ENSMUSG00000020776	chr11	Fbf1	-0.0777871	0.635061331	0.694166836	3.480430822	0.024671531	0	198	138	147	205	159	186	177	162	170	182
ENSMUSG00000021495	chr13	Fam193b	0.09343482	0.635185159	0.694247891	3.678359496	0.038642115	0	213	183	175	169	165	303	158	175	237	201
ENSMUSG00000002981	chr7	Clptm1	0.06816717	0.63588991	0.694915038	6.122487658	0.023762223	0	1037	930	855	1237	1009	1203	1208	1128	1037	1235
ENSMUSG00000029782	chr6	Tmem209	0.08363766	0.635894993	0.694915038	3.440337574	0.030863995	0	170	146	125	179	156	176	238	141	176	172
ENSMUSG00000049305	chr9	Ccdc71	0.07213134	0.636252638	0.69519716	4.138236037	0.023284085	0	225	232	237	327	252	294	307	234	294	337
ENSMUSG00000058444	chr9	Map2k5	0.07340798	0.636206879	0.69519716	4.165964221	0.024650672	0	317	226	210	310	236	327	277	292	259	339
ENSMUSG00000043909	chr2	Trp53bp1	0.07349784	0.636402795	0.695252518	4.185266992	0.025361331	0	285	236	203	337	258	300	305	332	287	281
ENSMUSG00000097660	chr7	Gm26762	-0.3912771	0.636401187	0.695252518	0.375209154	0.642223953	0	9	8	3	45	38	6	1	40	2	31
ENSMUSG00000034936	chr11	Arl4d	0.11901069	0.637092412	0.695897112	2.544763401	0.058378633	0	67	87	85	89	77	108	122	120	64	70
ENSMUSG00000079511	chr6	Ccdc142	0.06675476	0.637056137	0.695897112	5.782539503	0.022626379	0	844	810	735	932	677	987	907	884	928	874
ENSMUSG00000022095	chr14	Fam160b2	0.06768373	0.637960902	0.696736857	5.507001888	0.023175427	0	653	590	608	833	625	790	719	772	662	843
ENSMUSG00000085881	chr13	Gm15912	0.18392251	0.637952247	0.696736857	0.823642275	0.094591859	0	23	30	24	12	23	21	28	25	36	32
ENSMUSG00000068250	chr6	Amn1	-0.1117464	0.638036571	0.696765051	1.619110072	0.040313256	0	49	45	43	52	39	53	53	43	36	47

ENSMUSG00000032306	chr9	Mpi	0.07112849	0.638226289	0.696917776	6.055680008	0.02642766	0	922	952	940	1311	739	1162	994	1092	1065	1234
ENSMUSG00000052914	chr4	Cyp2j6	-0.0983644	0.638389734	0.697041791	2.449765946	0.035797484	0	93	71	84	98	66	86	97	73	73	93
ENSMUSG00000024589	chr18	Nedd4l	0.08156962	0.6387121	0.697339295	4.954637173	0.033344397	0	466	436	354	482	487	426	577	471	421	698
ENSMUSG00000025137	chr11	Pcyt2	0.06890687	0.639814658	0.698488491	5.058498547	0.024091813	0	461	484	462	634	387	545	509	590	585	529
ENSMUSG00000040669	chr6	Phc1	-0.0938191	0.640185553	0.69883881	3.507889066	0.039422013	0	161	121	135	232	220	184	184	166	142	215
ENSMUSG00000020653	chr12	Klf11	-0.1263316	0.64062036	0.699258837	3.419789703	0.081341195	0	102	196	182	146	180	273	133	168	80	184
ENSMUSG00000085379	chr11	2310058D17Rik	-0.1642131	0.64075101	0.699346827	0.575392282	0.076065743	0	27	23	23	20	14	26	18	18	28	15
ENSMUSG00000025499	chr7	Hras	0.07965402	0.641566566	0.700182284	6.824388369	0.034368787	0	2009	1561	1407	1644	1534	1589	1836	1806	1926	2298
ENSMUSG00000022438	chr15	Parvb	0.07460862	0.641818126	0.700347449	6.317491772	0.029938535	0	967	1215	1016	1579	1042	1378	1366	1416	1030	1476
ENSMUSG00000039849	chr2	Pcif1	-0.0652663	0.641815082	0.700347449	4.702040056	0.020569031	0	398	363	363	535	331	510	415	354	370	430
ENSMUSG00000026342	chr1	Slc35f5	0.06703425	0.642377952	0.700870637	4.401619671	0.021468932	0	275	286	298	409	269	374	367	296	366	354
ENSMUSG00000033227	chr1	Wnt6	0.20679814	0.642397886	0.700870637	0.158288932	0.13168249	0	8	14	12	24	11	37	16	11	7	17
ENSMUSG00000038383	chr2	Pigu	0.0663311	0.642598369	0.701034643	4.646361305	0.021562272	0	368	350	310	443	346	425	424	378	459	390
ENSMUSG00000029701	chr6	Rbm28	0.06505527	0.642760018	0.701156261	4.819608768	0.02086376	0	412	382	375	480	396	489	482	457	488	424
ENSMUSG00000032718	chr6	Mansc1	-0.1515348	0.643178862	0.701558399	1.029890585	0.084098786	0	29	41	17	32	31	22	29	31	22	44
ENSMUSG00000028893	chr4	Sesn2	0.11601331	0.643664738	0.702033586	2.054169587	0.052378739	0	69	50	63	66	40	73	91	64	48	67
ENSMUSG00000025277	chr14	Abhd6	-0.1270719	0.64388307	0.702216916	1.597263322	0.060993107	0	35	52	37	72	33	48	54	29	53	43
ENSMUSG00000015806	chr5	Qdpr	0.08521739	0.643975347	0.702262754	6.25808937	0.039663101	0	1442	1039	909	1074	1029	975	1375	1278	1184	1577
ENSMUSG00000002900	chr12	Lamb1	0.08155098	0.644464432	0.702741274	6.624227207	0.036538566	0	1260	1382	1368	1665	1433	1836	1415	1826	1129	2077
ENSMUSG00000026307	chr1	Scly	0.07800326	0.644548292	0.702777885	3.829181002	0.027653422	0	202	203	170	245	202	336	241	175	220	221
ENSMUSG00000039031	chr10	Arhgap18	-0.0793699	0.645721779	0.704002464	4.044821048	0.031059925	0	267	300	243	274	168	286	236	225	260	296
ENSMUSG00000062270	chr9	Morf4l1	0.07422333	0.645958964	0.704206121	6.887551937	0.030661425	0	1845	1723	1518	2013	1494	1741	2051	1608	2388	2080
ENSMUSG00000030759	chr7	Far1	0.08030677	0.646188435	0.704401339	3.925467175	0.030995216	0	217	183	182	295	222	333	311	174	235	224
ENSMUSG00000039349	chr1	C130074G19Rik	-0.0880248	0.646252817	0.704416579	4.864002801	0.04160295	0	504	510	457	396	334	460	371	484	353	627
ENSMUSG00000022111	chr14	Uchl3	0.07701242	0.646446051	0.704572254	4.243305756	0.029821058	0	284	269	231	331	252	290	350	249	401	281
ENSMUSG00000004980	chr6	Hnrnpa2b1	0.07117228	0.646847879	0.704955237	8.984707485	0.028807105	0	6698	6903	6210	10490	6891	9115	9513	8010	7828	7916
ENSMUSG00000056459	chr12	Zbtb25	-0.1219004	0.647235308	0.705322469	2.090604652	0.06233281	0	66	69	56	92	42	40	66	59	73	83
ENSMUSG00000022724	chr16	Mina	0.07452895	0.647306915	0.705324727	4.243303742	0.028220883	0	269	253	255	371	228	264	399	270	333	305
ENSMUSG00000055900	chr4	Tmem69	-0.0717152	0.647338314	0.705324727	4.149845374	0.024082933	0	268	254	256	371	209	258	305	271	279	286
ENSMUSG00000046879	chr11	Irgm1	0.07257371	0.647526915	0.705475223	4.143333908	0.026137671	0	244	273	240	326	197	261	291	262	306	345
ENSMUSG00000001445	chr11	Mrpl10	0.06774096	0.647641638	0.705545213	5.366864512	0.024466422	0	562	622	624	722	464	728	693	687	649	675
ENSMUSG00000102805	chr3	RP24-559D1.1	0.06612492	0.647841051	0.705707446	4.495543517	0.021562962	0	316	305	324	410	282	410	440	321	353	354
ENSMUSG00000042709	chr11	Atpaf2	0.06598194	0.648016472	0.705843521	4.706833854	0.022037537	0	356	379	333	460	365	441	407	433	380	508
ENSMUSG00000043384	chrX	Gprasp1	-0.0741182	0.648432511	0.706241644	4.279675814	0.026833671	0	289	254	231	388	320	285	297	319	322	303
ENSMUSG00000096974	chr4	Gm26881	-0.1096996	0.648586405	0.706354211	2.033400243	0.050753048	0	66	60	49	71	61	98	58	56	43	60
ENSMUSG00000037990	chr10	Sh3rf3	0.15638959	0.649091317	0.706849014	0.58471185	0.082405807	0	25	9	17	31	16	37	22	18	20	22
ENSMUSG00000018841	chr11	Rad51d	-0.0919274	0.649183594	0.706894422	2.658685847	0.036445734	0	108	87	100	96	82	112	88	79	97	115
ENSMUSG00000030671	chr7	Pde3b	-0.1285821	0.650311899	0.708067864	2.048034313	0.074803563	0	42	97	47	61	62	59	70	55	47	83
ENSMUSG00000060073	chr12	Psma3	-0.0678171	0.651348508	0.709141291	7.245595415	0.026509596	0	2579	2139	2125	2685	2039	2553	2618	1953	2573	2409
ENSMUSG00000021037	chr12	Ahsa1	0.06775482	0.651685732	0.709453169	6.801476655	0.026342787	0	1758	1474	1442	2044	1428	2025	2157	1588	1892	1660
ENSMUSG00000068706	chr15	Gm10250	0.07413482	0.651855186	0.709582372	5.070133128	0.030194189	0	471	478	459	704	349	812	484	529	467	532
ENSMUSG00000090877	chr17	Hspa1b	-0.1586283	0.652474031	0.710200706	1.291982356	0.108972048	0	18	27	27	68	46	52	44	20	36	29
ENSMUSG00000030738	chr7	Eif3c	0.06911504	0.652628413	0.710313425	7.154478919	0.027801634	0	1974	1779	1655	3000	2066	2576	2396	2026	2462	2455
ENSMUSG00000086610	chr5	Gm15408	0.14665698	0.65296778	0.710627448	1.76079964	0.099624058	0	46	51	46	64	26	23	57	56	69	71
ENSMUSG00000028101	chr3	Pias3	0.07404473	0.653313777	0.710948638	3.416275592	0.024782679	0	158	161	145	187	117	204	180	149	163	191
ENSMUSG00000006378	chr15	Gcat	0.10555724	0.653614348	0.711220346	2.876599761	0.053961199	0	91	89	92	121	123	115	120	106	175	90
ENSMUSG00000028772	chr4	Zcchc17	-0.0654023	0.654191065	0.711792473	5.486220531	0.023773245	0	783	649	624	771	578	713	694	664	722	768
ENSMUSG00000042272	chr2	Sestd1	0.07240911	0.654260655	0.711812775	3.935600997	0.025930668	0	223	173	208	299	207	289	276	181	241	292
ENSMUSG00000029632	chr6	Ndufa4	-0.0742743	0.655469695	0.71307266	8.754397039	0.033030484	0	6813	6924	6563	7969	4803	7874	6379	6176	7804	6069
ENSMUSG00000041115	chrX	Iqsec2	0.07724321	0.655614694	0.713174888	4.359816127	0.03301682	0	243	284	313	465	198	368	311	335	366	326
ENSMUSG00000032452	chr9	Clstn2	-0.1538446	0.655691682	0.713182714	0.57227772	0.087749413	0	18	14	31	28	16	15	29	21	16	24
ENSMUSG00000034387	chr6	Ssu2	-0.1600209	0.655749004	0.713182714	0.75506072	0.081139059	0	22	27	25	30	19	37	14	29	15	26
ENSMUSG00000037296	chr8	Lsm1	0.07640874	0.655774976	0.713182714	3.174335697	0.026745501	0	135	117	112	163	121	157	178	126	147	139
ENSMUSG00000098470	chr6	C1rb	0.30946169	0.656423933	0.713832935	0.902365521	0.473289172	0	22	19	20	32	22	128	3	6	14	15
ENSMUSG00000097993	chr1	Ptprv	-0.279395	0.656592248	0.713960418	0.825453329	0.408294444	0	58	21	26	19	9	89	13	8	6	12
ENSMUSG00000026504	chr1	Sdccag8	0.09277886	0.657357965	0.714737429	2.958952861	0.040651279	0	131	116	114	94	90	155	112	133	124	120
ENSMUSG00000070509	chr7	Rgma	-0.0881128	0.657480109	0.714814625	5.741470854	0.0455288	0	668	735	766	1132	821	765	638	1074	617	1102
ENSMUSG00000016534	chrX	Lamp2	-0.0760192	0.657968492	0.715289953	6.671069328	0.03461078	0	1487	1466	1459	1945	1442	1463	1806	1247	1320	2298
ENSMUSG00000047712	chr10	Ust	0.11793526	0.658382993	0.715684896	1.692006609	0.050189421	0	35	50	42	51	43	66	62	51	36	50
ENSMUSG00000020520	chr11	Galnt10	0.07555374	0.658536261	0.715740165	4.219118809	0.03007002	0	246	213	280	307	289	312	316	313	234	376
ENSMUSG00000073535	chr1	Gm5532	-0.3047386	0.658498033	0.715740165	-0.172490228	0.28413014	0	3	9	15	36	3	10	4	20	10	10
ENSMUSG00000020331	chr10	Hcn2	-0.1630956	0.659035047	0.71622658	0.88851441	0.101360193	0	37	33	15	28	23	17	30	24	18	44
ENSMUSG00000030499	chr7	Kctd15	-0.0907208	0.659152259	0.716298263	5.672332554	0.04888356	0	945	730	658	823	740	467	836	766	844	1075
ENSMUSG00000029108	chr5	Pcdh7	0.08934416	0.65992351	0.717080624	2.993034256	0.036774817	0	136	105	96	107	117	119	129	123	128	159
ENSMUSG00000005686	chr7	Ampd3	-0.0861285	0.660028386	0.717138827	3.531052315	0.036834835	0	177	162	124	286	147	200	153	213	164	172

ENSMUSG00000022335	chr15	Zfat	-0.1181496	0.660151686	0.717217037	1.644147076	0.055250105	0	52	36	61	46	36	48	52	40	49	46
ENSMUSG00000013833	chr10	Med16	-0.0680402	0.660327226	0.717351986	4.978278291	0.026315094	0	485	416	413	585	498	513	436	450	440	670
ENSMUSG00000097616	chr6	1110019D14Rik	0.12267673	0.66097182	0.717996437	1.451496789	0.066269241	0	37	31	44	40	33	34	40	33	60	54
ENSMUSG00000066306	chr7	Numa1	-0.0665125	0.661095071	0.718074509	6.009594368	0.026384762	0	978	898	841	1269	940	1324	909	1006	842	1072
ENSMUSG00000030979	chr7	Uros	0.06880595	0.661483753	0.718440856	4.339238634	0.025947299	0	308	292	290	334	237	303	304	348	363	352
ENSMUSG00000028621	chr4	Cyb5rl	-0.085336	0.661690013	0.718609032	3.111416081	0.035346209	0	128	124	105	155	141	113	127	118	144	171
ENSMUSG00000038188	chr11	Scarf1	0.08875158	0.661790594	0.71866242	3.291679554	0.042212987	0	98	143	127	213	125	228	149	131	119	196
ENSMUSG00000034453	chr10	Polr3b	0.06145441	0.661869195	0.718691933	4.338290367	0.019567284	0	282	290	272	356	267	386	359	296	322	317
ENSMUSG00000034248	chr14	Slc25a37	-0.065988	0.662419096	0.719233164	4.569896626	0.024379407	0	397	376	338	368	311	412	354	325	420	373
ENSMUSG00000021127	chr12	Zfp36l1	0.07382079	0.662759302	0.719546648	5.256691296	0.031581978	0	595	560	586	578	432	859	710	454	507	702
ENSMUSG00000027959	chr3	Sass6	0.15100385	0.663233952	0.720006037	1.291926529	0.088255416	0	40	20	32	29	41	38	57	34	45	25
ENSMUSG00000004934	chr10	Pias4	0.06606054	0.66464197	0.721478537	4.053952385	0.023146324	0	261	214	190	309	233	326	290	255	231	280
ENSMUSG00000040435	chr7	Ppp1r15a	0.07709059	0.665133449	0.721955971	4.220725409	0.033425263	0	275	264	246	364	206	470	347	263	229	262
ENSMUSG00000021748	chr14	Pdhb	0.07343817	0.665192136	0.721963601	8.487491462	0.034325029	0	5033	5590	5450	6584	3505	6107	5485	6093	6178	6051
ENSMUSG00000028773	chr4	Fabp3	-0.1105207	0.665418094	0.72209669	8.502617886	0.077835284	0	3343	5897	5099	10173	4269	8760	4560	6811	4893	3474
ENSMUSG00000031351	chrX	Zfp185	-0.1265708	0.665407243	0.72209669	1.928297452	0.07665133	0	66	50	50	74	48	89	79	33	30	62
ENSMUSG00000020898	chr11	Ctc1	0.06713374	0.665611961	0.722250991	4.078862187	0.023828152	0	231	232	224	309	228	354	289	267	213	286
ENSMUSG00000019792	chr10	Trmt11	-0.1031454	0.665800963	0.722399989	2.140316836	0.048785177	0	72	58	57	93	54	54	95	56	63	69
ENSMUSG00000026828	chr2	Galnt5	0.14323706	0.665920199	0.722473273	0.997618483	0.089333606	0	37	19	26	37	15	22	27	43	34	32
ENSMUSG00000014504	chr18	Srp19	0.05945627	0.666045794	0.722497363	4.94980626	0.020287255	0	461	454	384	554	400	506	581	448	482	550
ENSMUSG00000071001	chr4	Hrct1	0.16697889	0.665998567	0.722497363	1.128595187	0.119478004	0	21	42	28	23	28	59	14	33	39	34
ENSMUSG00000033429	chr7	Mcee	0.06497652	0.666375366	0.722798767	4.839679906	0.024858929	0	403	467	374	538	307	472	483	427	526	466
ENSMUSG00000037007	chr5	Zfp113	-0.0976136	0.666810349	0.723214453	2.377182502	0.041518392	0	94	64	61	100	74	90	76	91	70	72
ENSMUSG00000097042	chr8	Gm17491	-0.1491957	0.667944694	0.724388535	0.544326119	0.07807971	0	24	26	19	20	15	34	18	21	13	18
ENSMUSG00000060166	chr16	Zdhhc8	-0.0646298	0.668080198	0.724479271	5.191822532	0.025180313	0	548	473	516	705	541	615	591	528	447	739
ENSMUSG00000027679	chr3	Dnajc19	-0.065668	0.66819744	0.724550192	5.266426774	0.026037633	0	682	612	496	657	478	639	684	512	673	552
ENSMUSG00000031712	chr8	Il15	0.12658893	0.668397813	0.724711236	1.795756445	0.087010479	0	48	50	51	73	20	36	64	48	68	67
ENSMUSG00000036139	chr15	Hoxc9	-0.073642	0.668661221	0.724940596	3.302366961	0.027706414	0	141	143	132	174	153	168	141	143	131	194
ENSMUSG00000031627	chr8	Irf2	-0.068908	0.668968192	0.725217146	4.001991113	0.026516571	0	219	218	232	332	220	341	258	214	194	272
ENSMUSG00000021930	chr14	Spryd7	-0.0800606	0.669184893	0.725395802	4.807982267	0.038612926	0	456	409	382	516	377	271	496	408	500	519
ENSMUSG00000062397	chr15	Zfp706	0.06378009	0.669470791	0.725649431	6.033779263	0.025387914	0	1003	843	821	1142	959	1405	1124	920	925	1125
ENSMUSG00000048581	chr3	E130311K13Rik	-0.1187117	0.669792952	0.725942327	1.665404263	0.058300959	0	47	38	51	70	33	37	46	43	60	51
ENSMUSG00000074170	chr7	Plekhf1	0.09049591	0.669860821	0.725959587	3.367095661	0.044055597	0	143	162	132	175	124	279	120	126	155	190
ENSMUSG00000000579	chr17	Dynlt1c	0.11629079	0.669930695	0.725979018	1.341039172	0.049881805	0	43	32	29	38	30	56	40	39	37	33
ENSMUSG00000092981	chr17	Mir5125	-0.1254455	0.670021505	0.726021131	0.89883899	0.070753401	0	32	23	22	24	33	40	27	25	17	28
ENSMUSG00000057337	chr10	Chst3	-0.1467091	0.670343191	0.726313391	0.974740961	0.097534481	0	16	21	35	55	20	41	23	30	21	28
ENSMUSG00000039485	chr10	Tspyl4	-0.119335	0.670502663	0.726429862	1.52853563	0.053359028	0	55	45	26	50	39	42	41	36	46	51
ENSMUSG00000030880	chr7	Polr3e	-0.0663254	0.670602768	0.726482	3.917935408	0.024221745	0	262	223	198	276	188	283	241	199	195	286
ENSMUSG00000027357	chr2	Crls1	-0.0690858	0.670940101	0.726791107	4.062511853	0.02654217	0	259	257	201	316	237	275	260	208	317	261
ENSMUSG00000036086	chr1	Zranb3	0.10347407	0.671108303	0.726916968	3.035702287	0.056890269	0	110	113	102	128	124	207	152	68	155	110
ENSMUSG00000022843	chr16	Clcn2	-0.1186495	0.671162844	0.726919707	1.4360174	0.063151356	0	45	48	45	38	23	37	41	35	40	49
ENSMUSG00000048439	chr5	Nupl2	-0.086958	0.671698372	0.727443351	2.756091587	0.037364641	0	101	92	101	140	79	91	132	87	102	113
ENSMUSG00000036309	chr11	Skp1a	-0.0642833	0.671803107	0.727500405	7.346760704	0.027070269	0	2851	2286	1967	3130	2235	2532	2774	2316	2497	2864
ENSMUSG00000047735	chr6	Samd9l	-0.0869234	0.672376539	0.728064965	2.983330613	0.041073865	0	98	124	141	142	91	129	133	86	116	156
ENSMUSG00000036615	chr3	Rfxap	-0.0676048	0.672435026	0.728071888	4.002168839	0.025554363	0	235	243	178	300	259	258	257	232	229	293
ENSMUSG00000017300	chr2	Tnnc2	0.06644382	0.672845921	0.728460345	13.48003043	0.029688097	0	186426	155321	137378	186717	164590	187301	184213	179814	188256	213082
ENSMUSG00000030530	chr7	Furin	0.0653834	0.673110983	0.728690867	5.993486765	0.02742346	0	809	785	860	1194	990	1314	1018	975	879	1152
ENSMUSG00000061330	chr13	Gm11361	0.22936735	0.673235013	0.728768689	2.496299874	0.331303884	0	75	73	56	109	68	373	30	42	37	32
ENSMUSG00000024130	chr17	Abca3	-0.0853359	0.673344014	0.728830231	4.41071505	0.045975435	0	272	307	308	437	306	603	280	237	243	347
ENSMUSG00000046417	chr11	Lrrc75a	0.08532507	0.673404865	0.728839649	3.070893503	0.041220696	0	123	85	106	170	120	193	119	127	99	164
ENSMUSG00000026399	chr1	Cd55	-0.1027024	0.674076975	0.72940977	5.628548265	0.069195818	0	772	658	694	1061	661	417	615	588	1125	1099
ENSMUSG00000032612	chr9	Usp4	-0.0631341	0.674034385	0.72940977	6.505222034	0.02607124	0	1407	1296	1187	1711	1324	1300	1505	1324	1465	1631
ENSMUSG00000038965	chr16	Ube2l3	0.06244531	0.674088193	0.72940977	7.183231876	0.025855004	0	2355	2093	1770	2434	1936	2606	2521	1986	2308	2735
ENSMUSG00000032679	chr2	Cd59a	0.0738994	0.674167379	0.729438979	5.785540525	0.035581175	0	912	823	748	884	624	732	850	769	1053	1186
ENSMUSG00000028029	chr3	Aimp1	0.06382714	0.6743995	0.729577166	6.314078958	0.026702159	0	1330	1176	1004	1327	957	1374	1416	1168	1419	1245
ENSMUSG00000059013	chr2	Sh2d3c	-0.0937235	0.674368831	0.729577166	3.348842879	0.053561225	0	124	194	167	146	133	258	136	120	114	180
ENSMUSG00000018166	chr10	Erbb3	0.0987969	0.674781642	0.729934073	3.470223784	0.059700625	0	103	144	170	228	148	214	162	265	121	157
ENSMUSG00000041491	chr19	Cep78	0.12319157	0.674952171	0.730062035	1.649839259	0.072069764	0	37	54	28	62	36	40	61	37	70	47
ENSMUSG00000038412	chr9	Higd1a	0.06286162	0.675010576	0.730068705	6.255807839	0.026045966	0	1080	1051	1104	1438	913	1212	1279	1211	1355	1282
ENSMUSG00000029629	chr6	Phf14	-0.062133	0.675820153	0.730887756	4.366554744	0.021687553	0	338	267	268	446	261	350	318	310	319	341
ENSMUSG00000025731	chr17	0610011F06Rik	0.06290716	0.675960268	0.730982723	4.676438283	0.02361413	0	384	355	351	384	367	418	390	413	411	486
ENSMUSG00000041530	chr4	Ago1	0.06206458	0.676310255	0.731304613	4.17267993	0.022249546	0	240	231	265	356	222	352	312	276	267	291
ENSMUSG00000015837	chr11	Sqstm1	0.06452524	0.676493717	0.731446401	8.573217038	0.028458937	0	6184	5661	4517	6577	4867	7761	6040	5158	6357	6630
ENSMUSG00000022664	chr16	Slc35a5	0.10607801	0.676844058	0.731747922	2.422827408	0.055524074	0	66	107	66	75	59	81	101	63	93	106
ENSMUSG00000058638	chr7	Zfp110	-0.0761454	0.677032073	0.731747922	3.581202744	0.032048758	0	152	189	176	237	155	198	169	143	238	193

ENSMUSG00000079225	chr9	Gm9531	0.10131857	0.67691731	0.731747922	2.225290843	0.052083408	0	74	71	58	78	47	103	94	47	78	66
ENSMUSG00000101795	chr1	Gm5835	0.10419396	0.676955795	0.731747922	2.240092284	0.050787751	0	69	63	56	77	65	86	49	66	89	99
ENSMUSG00000104300	chr9	DHX30	0.05531496	0.677034371	0.731747922	4.923515808	0.018787698	0	455	403	389	574	400	548	497	471	471	530
ENSMUSG00000028607	chr4	Cpt2	-0.0727192	0.677705075	0.732416187	6.151082327	0.035281339	0	843	1033	989	1750	901	1423	948	1180	1044	1054
ENSMUSG00000083829	chr5	Gm2199	-0.1787316	0.67812203	0.732810136	-0.188799083	0.118456259	0	10	15	15	10	9	6	6	16	13	16
ENSMUSG00000019326	chr11	Aoc3	-0.1081295	0.678652472	0.733269961	4.163456601	0.076621345	0	193	311	204	328	334	240	243	316	138	463
ENSMUSG00000021572	chr13	Cep72	-0.1537457	0.678618862	0.733269961	-0.095595368	0.099576877	0	21	14	10	8	10	17	12	7	15	12
ENSMUSG00000061950	chr17	Ppp4r1	0.06454479	0.678920887	0.733503271	4.515683545	0.025546594	0	322	271	282	457	338	455	456	296	328	378
ENSMUSG00000059173	chr2	Pde1a	0.12466099	0.679098621	0.733638581	1.240236421	0.052615201	0	26	36	29	32	35	43	39	39	38	31
ENSMUSG00000038982	chr13	Bloc1s5	0.06651539	0.679659877	0.734188162	3.630662594	0.024786445	0	182	191	157	223	143	210	196	170	215	234
ENSMUSG00000024855	chr19	Pacs1	0.07884584	0.680054354	0.734557512	3.859142097	0.038463828	0	129	171	218	329	207	254	250	215	219	271
ENSMUSG00000025037	chrX	Maoa	0.08021292	0.680137205	0.73459023	3.353836015	0.035622379	0	166	161	121	162	121	136	205	133	180	192
ENSMUSG00000026456	chr1	Cyb5r1	0.0627526	0.680513062	0.734939383	6.883324897	0.027196613	0	1956	1660	1480	1983	1523	1945	1837	2010	1740	2287
ENSMUSG00000020412	chr11	Ascc2	0.05969745	0.681085245	0.735500493	4.827037253	0.022755799	0	409	365	333	534	430	438	512	444	442	515
ENSMUSG00000039164	chr2	Naif1	-0.0810219	0.681422681	0.735808035	2.706846078	0.033502608	0	98	102	104	108	77	126	95	90	95	104
ENSMUSG00000039929	chr16	Urb1	-0.0956519	0.681790364	0.736148187	2.850272827	0.05436684	0	93	96	92	156	113	191	104	102	73	97
ENSMUSG00000091803	chr12	Cox16	0.06418176	0.682136613	0.736465145	5.311370578	0.027464775	0	709	602	485	643	448	673	608	581	693	747
ENSMUSG00000019923	chr10	Zwint	-0.0621461	0.682761335	0.737082684	5.245692272	0.025792603	0	663	572	458	648	537	727	624	461	655	567
ENSMUSG00000025157	chr19	Zdhhc16	0.05795171	0.682879489	0.737153297	4.323370398	0.01998966	0	300	253	276	345	278	354	350	301	327	325
ENSMUSG00000033720	chr6	Sfxn5	-0.1003246	0.683527156	0.737795454	2.250879902	0.052657107	0	61	98	69	73	54	70	73	58	84	80
ENSMUSG00000027854	chr3	Sike1	-0.060615	0.683880248	0.738119573	4.725485821	0.024098577	0	475	377	367	395	375	512	411	386	399	402
ENSMUSG00000020806	chr11	Rhbdf2	-0.0898658	0.684009014	0.738201543	3.914536992	0.054394702	0	195	224	215	266	244	454	210	153	190	202
ENSMUSG00000013973	chr1	Dedd	0.05737496	0.684076015	0.738216847	4.975168422	0.021567846	0	486	399	391	586	437	594	455	527	497	534
ENSMUSG00000032579	chr9	Hemk1	0.07631646	0.684473829	0.738589117	3.694481288	0.036035975	0	181	190	189	210	157	229	176	224	269	168
ENSMUSG00000047789	chr13	Slc38a9	-0.0756289	0.684770169	0.73885184	3.173557171	0.031528185	0	137	138	104	158	143	165	148	98	142	159
ENSMUSG00000037362	chr15	Nov	-0.135716	0.68514272	0.739196747	3.696321585	0.127402155	0	311	201	192	204	95	345	121	105	105	352
ENSMUSG00000025933	chr1	Tmem14a	-0.1248068	0.685331103	0.739342917	0.800888993	0.056583689	0	30	29	20	29	18	23	29	25	24	25
ENSMUSG00000011658	chr7	Fuz	-0.0657474	0.68538969	0.739349051	4.272094854	0.026696631	0	353	265	252	350	248	276	289	324	280	356
ENSMUSG00000044847	chr11	Lsm11	0.0813308	0.685494644	0.739405197	2.364974007	0.035503795	0	77	63	55	101	71	96	90	78	72	87
ENSMUSG00000051483	chr16	Cbr1	-0.0585906	0.685864423	0.739746965	4.275176211	0.021315042	0	326	283	250	337	267	380	293	288	275	308
ENSMUSG00000029683	chr6	Lmod2	0.16732257	0.686652394	0.740539691	6.010266085	0.203160483	0	168	909	974	2218	479	1958	827	1315	883	604
ENSMUSG00000055319	chr7	Sec23ip	-0.058343	0.686942258	0.740795139	4.741156684	0.021683949	0	417	352	322	553	397	439	473	395	397	426
ENSMUSG00000021108	chr12	Prkch	-0.0867215	0.687050616	0.740854826	3.41420612	0.048920077	0	114	163	158	255	130	205	201	91	153	195
ENSMUSG00000091586	chr17	Cyp4f17	-0.1633209	0.687223549	0.740984132	0.131111807	0.106093466	0	10	13	16	18	19	13	11	7	18	26
ENSMUSG00000045968	chr1	Teddm2	-0.1390252	0.687469574	0.741192222	1.492333002	0.116225163	0	34	46	36	24	64	39	39	26	37	70
ENSMUSG00000079049	chr13	Serpinb1c	-0.1527284	0.68767115	0.74135236	0.494045926	0.105268696	0	38	15	18	20	10	16	26	16	21	20
ENSMUSG00000045625	chr16	Pigz	-0.1481253	0.687884031	0.74152466	0.754508161	0.109240303	0	27	33	20	19	22	32	9	22	33	25
ENSMUSG00000026848	chr2	Tor1b	0.05887826	0.688339982	0.741958938	5.232634715	0.023533473	0	547	536	442	672	544	769	650	481	653	585
ENSMUSG00000021737	chr14	Psmd6	0.074233	0.688558517	0.742088169	6.736404028	0.040398673	0	1785	1464	1356	1833	1313	1229	1932	1453	2060	2196
ENSMUSG00000026914	chr2	Psmd14	-0.0708538	0.688566068	0.742088169	5.761482134	0.035799773	0	958	744	693	980	766	697	994	631	1084	889
ENSMUSG00000023008	chr15	Fmnl3	0.0688628	0.6887334	0.742211273	4.163172223	0.031427328	0	232	268	208	407	202	413	316	253	240	279
ENSMUSG00000019873	chr10	Reep3	0.06119965	0.689171325	0.742625939	4.698354443	0.02476669	0	366	349	353	493	333	446	515	312	384	511
ENSMUSG00000085493	chr5	Gm15469	0.36412974	0.689672424	0.743108612	-0.257489278	0.730246553	0	2	6	2	16	21	3	2	38	0	20
ENSMUSG00000004562	chr14	Arhgef40	-0.060386	0.689760911	0.743146661	4.553285876	0.024106246	0	341	321	324	457	340	484	361	378	289	363
ENSMUSG00000054931	chr13	Zkscan4	-0.1954713	0.690268735	0.743636463	-0.167871085	0.129686845	0	9	20	17	8	6	8	12	15	9	14
ENSMUSG00000026941	chr2	Mamdc4	-0.0573245	0.690744342	0.744091485	5.683690511	0.023452321	0	703	762	700	983	756	1023	811	731	761	795
ENSMUSG00000035095	chr14	Fam167a	-0.1593	0.691197406	0.744522154	0.783829276	0.132823026	0	28	13	18	34	33	34	46	12	14	19
ENSMUSG00000046962	chr16	Zbtb21	0.08714577	0.692024036	0.745355112	2.31576739	0.040774887	0	71	51	67	97	67	100	70	65	82	93
ENSMUSG00000022099	chr14	Dmtn	-0.1178367	0.692217817	0.745439727	1.198582727	0.064550809	0	30	37	28	44	30	50	23	37	35	25
ENSMUSG00000035878	chr9	Hykk	-0.1316474	0.692262608	0.745439727	0.749773673	0.066629985	0	25	22	21	27	26	16	28	23	20	34
ENSMUSG00000056899	chr12	Immp2l	-0.1007489	0.692162715	0.745439727	2.31041742	0.057036237	0	67	82	72	90	62	46	78	76	92	85
ENSMUSG00000027823	chr3	Gmps	0.05701004	0.692385787	0.745514928	5.187966989	0.023053135	0	512	517	456	746	450	623	731	528	565	582
ENSMUSG00000021754	chr13	Map3k1	-0.0787227	0.692523283	0.745605531	3.505420279	0.038542223	0	109	182	164	238	170	193	221	132	164	187
ENSMUSG00000082488	chr13	1700119I11Rik	-0.4045043	0.69265769	0.745692796	-0.306815113	0.996292728	0	2	3	1	36	20	2	0	31	0	12
ENSMUSG00000029557	chr5	Ftsj2	0.07838517	0.692819042	0.745809053	3.022051252	0.03698452	0	113	91	135	136	103	123	125	146	139	133
ENSMUSG00000023495	chr9	Pcbp4	0.06623527	0.693015685	0.745963279	5.626448402	0.032238382	0	671	670	709	971	591	1085	755	914	707	656
ENSMUSG00000032867	chr5	Fbxw8	0.05932978	0.693202143	0.746106519	5.57208053	0.025663492	0	652	625	561	972	685	953	752	819	687	746
ENSMUSG00000028776	chr4	Tinagl1	0.06876879	0.694304709	0.747235686	4.810678573	0.033272301	0	336	370	322	517	488	582	479	427	322	544
ENSMUSG00000031505	chr8	Carkd	0.05541426	0.694612387	0.747509257	4.741369497	0.020721306	0	357	366	373	494	360	530	444	366	455	428
ENSMUSG00000020752	chr11	Recql5	-0.0653415	0.695974869	0.748860172	3.142054683	0.026904026	0	137	121	131	143	128	166	145	114	136	136
ENSMUSG00000037347	chrX	Chst7	-0.1080266	0.695926984	0.748860172	1.783881068	0.069120845	0	43	53	55	61	44	92	44	50	33	45
ENSMUSG00000025776	chr1	Crispld1	-0.1030546	0.696183521	0.748969355	1.71416828	0.049126856	0	40	34	55	65	50	53	56	45	42	53
ENSMUSG00000047067	chr1	Dusp28	-0.056969	0.696159002	0.748969355	4.436380364	0.021919565	0	335	330	303	397	274	387	342	336	269	394
ENSMUSG00000004748	chr11	Mtfp1	-0.0701417	0.696501309	0.749253564	5.729526489	0.036740784	0	637	783	834	1201	631	716	946	972	737	813
ENSMUSG00000046598	chr16	Bdh1	0.2555781	0.696637829	0.749342746	2.210766988	0.478126499	0	8	58	74	178	9	119	23	153	77	18

ENSMUSG00000025024	chr19	Smndc1	0.06040255	0.697186578	0.749817592	4.321573424	0.02495168	0	261	257	283	390	266	367	396	329	261	306
ENSMUSG00000030213	chr6	Atf7ip	-0.0633381	0.697149368	0.749817592	5.143192107	0.029212928	0	482	479	454	764	528	539	536	508	460	776
ENSMUSG00000032594	chr9	Ip6k1	-0.0625447	0.697268616	0.749848121	5.402305153	0.029323853	0	666	632	602	787	532	983	560	584	549	727
ENSMUSG00000017858	chr2	Ift52	-0.0631262	0.697530532	0.750072072	4.061966454	0.027340897	0	316	263	204	264	213	320	274	214	250	273
ENSMUSG00000034902	chr10	Pip5k1c	0.06331958	0.698348685	0.750894077	5.435927177	0.029762196	0	604	531	580	815	627	930	718	530	566	901
ENSMUSG00000024761	chr19	Gm16437	-0.1321323	0.698632306	0.75114125	0.776945965	0.068519804	0	28	25	25	35	12	31	19	20	27	27
ENSMUSG00000021431	chr13	Snrnp48	0.07296552	0.698918084	0.751390703	2.819319962	0.032597553	0	101	102	75	139	91	144	122	94	115	108
ENSMUSG00000027224	chr2	Duoxa1	-0.2113472	0.699197013	0.751632756	0.72641001	0.300722772	0	8	26	27	27	32	75	12	12	6	16
ENSMUSG00000022684	chr16	Bfar	0.05856537	0.699357369	0.751747315	5.686890384	0.026038134	0	865	810	661	847	571	924	856	851	783	864
ENSMUSG00000021144	chr12	Mta1	-0.0571974	0.699568477	0.751916406	4.775951295	0.023413382	0	369	390	339	557	429	547	434	412	360	440
ENSMUSG00000031816	chr8	Mthfsd	-0.071185	0.699863115	0.752175245	3.455141497	0.031849952	0	196	176	140	180	135	182	174	166	197	141
ENSMUSG00000020492	chr11	Ska2	0.0938984	0.700033423	0.752300432	2.423487299	0.056127183	0	82	76	54	98	70	91	139	69	78	66
ENSMUSG00000029148	chr5	Nrbp1	0.05960919	0.700286629	0.752456825	6.220198047	0.027784389	0	1096	1035	949	1452	941	1462	1164	1040	1440	1100
ENSMUSG00000057110	chr2	Cntrl	-0.0672888	0.700267043	0.752456825	3.340305518	0.027674206	0	156	155	147	163	138	186	166	167	143	135
ENSMUSG00000071041	chr8	Gm15210	0.09045755	0.700425851	0.752548562	2.25269677	0.048893405	0	67	60	46	86	77	100	91	74	53	75
ENSMUSG00000008690	chr15	Ncaph2	0.0554923	0.70099626	0.753099515	5.957456805	0.023764874	0	869	906	755	1142	874	1212	1073	961	982	941
ENSMUSG00000024513	chr18	Mbd2	-0.0589429	0.701046415	0.753099515	5.016353123	0.025842757	0	440	460	426	661	479	562	605	350	540	536
ENSMUSG00000032403	chr9	2300009A05Rik	-0.0736259	0.701389872	0.753410564	3.266672213	0.035791889	0	113	140	168	185	120	162	139	166	120	168
ENSMUSG00000021054	chr12	Sgpp1	0.05987629	0.701943092	0.753888931	4.404264961	0.024906115	0	292	288	336	369	250	386	398	304	278	397
ENSMUSG00000031948	chr8	Kars	0.05744213	0.701918133	0.753888931	6.49320118	0.026191258	0	1310	1169	1056	1700	1365	1644	1556	1441	1485	1357
ENSMUSG00000024906	chr19	Mus81	-0.0561448	0.702029392	0.753923681	4.750036529	0.023038748	0	466	369	356	433	402	461	391	426	394	471
ENSMUSG00000032409	chr9	Atr	0.07365682	0.70285055	0.754747544	3.048725342	0.033127166	0	115	114	97	148	119	142	164	103	153	121
ENSMUSG00000049755	chr11	Zfp672	-0.064834	0.702955305	0.75480204	4.616506098	0.030607056	0	409	324	368	458	306	294	385	401	387	467
ENSMUSG00000032212	chr9	Sltm	0.05550208	0.703195647	0.754944105	4.840247164	0.022809662	0	415	349	359	580	400	549	546	376	468	445
ENSMUSG00000066270	chr9	Gm10157	-0.0993713	0.703167333	0.754944105	1.390988903	0.051362508	0	36	37	33	49	38	60	33	38	33	34
ENSMUSG00000019777	chr10	Hdac2	0.05563939	0.703741269	0.755471847	6.074190809	0.024595081	0	1087	904	849	1238	862	1071	1215	976	1137	1193
ENSMUSG00000014773	chr17	Dll1	-0.0862923	0.704294708	0.756007898	3.036714863	0.048868113	0	96	120	103	178	128	90	127	147	110	161
ENSMUSG00000036285	chr5	Noa1	0.05469401	0.704500578	0.756112738	4.222677951	0.021222424	0	262	279	227	358	238	307	335	296	290	313
ENSMUSG00000061877	chr7	BC048679	-0.2268472	0.704495366	0.756112738	0.580100057	0.302502948	0	4	17	14	66	16	24	11	33	26	6
ENSMUSG00000029456	chr5	Acad10	0.10510655	0.705366395	0.756867619	1.59458663	0.055314225	0	46	49	34	48	31	57	39	61	40	47
ENSMUSG00000031399	chrX	Fam3a	0.05600955	0.705271683	0.756867619	4.193869961	0.022105696	0	297	257	212	337	233	347	297	247	318	308
ENSMUSG00000043644	chr11	0610009L18Rik	-0.0642097	0.705341409	0.756867619	3.50846492	0.027191057	0	192	182	147	188	147	187	158	165	171	218
ENSMUSG00000039474	chr5	Wfs1	-0.0780573	0.705528005	0.756982911	6.34389145	0.049800556	0	833	1230	1187	1959	1086	1351	1292	1675	856	1235
ENSMUSG00000024999	chr19	Noc3l	0.07413605	0.705769826	0.757086202	2.90960993	0.039042232	0	107	100	84	149	101	100	159	111	132	114
ENSMUSG00000029641	chr5	Rasl11a	-0.1776436	0.705681342	0.757086202	-0.043852384	0.125183724	0	10	13	4	25	16	18	15	12	5	15
ENSMUSG00000048997	chr3	Atxn7l2	0.07789349	0.705786786	0.757086202	2.945451435	0.040017248	0	121	93	100	145	94	112	115	110	113	186
ENSMUSG00000021972	chr14	Hmbox1	-0.056175	0.707838247	0.759228498	4.037340257	0.021628545	0	234	244	220	332	216	303	243	237	245	280
ENSMUSG00000052371	chr2	Hoxd3os1	-0.1245958	0.708329846	0.759697485	0.893503344	0.061291162	0	30	28	20	38	20	31	22	21	23	39
ENSMUSG00000039046	chr2	Usp6nl	-0.0704972	0.708483527	0.759804003	2.94089567	0.032052785	0	101	115	104	152	107	119	153	112	103	115
ENSMUSG00000023153	chr4	Tmem52	0.06095782	0.708611758	0.759883214	6.469952325	0.030880393	0	1185	1080	1148	1670	1390	1800	1430	1405	1090	1699
ENSMUSG00000026638	chr1	Irf6	-0.1668578	0.709275121	0.76053622	0.412165987	0.110854063	0	22	11	18	33	13	11	13	27	23	17
ENSMUSG00000020305	chr11	Asb3	0.07052072	0.709919372	0.761113664	2.868516291	0.030155001	0	106	115	101	118	81	138	122	104	112	126
ENSMUSG00000035107	chr16	Dcbld2	0.07802879	0.709922562	0.761113664	3.593807731	0.044077581	0	144	163	171	209	177	298	241	182	161	128
ENSMUSG00000028849	chr4	Map7d1	-0.0635167	0.710089886	0.761234659	7.921188399	0.034571304	0	3497	3142	3109	5231	3654	3232	3708	4115	3555	4619
ENSMUSG00000024831	chr19	Ighmbp2	-0.0867828	0.710508829	0.761625356	2.419924755	0.04580364	0	83	78	63	107	73	81	69	95	62	106
ENSMUSG00000028717	chr4	Tal1	-0.1095302	0.710992216	0.762085069	1.313056172	0.078379994	0	33	49	36	35	28	62	33	29	38	25
ENSMUSG00000009894	chr11	Snap47	0.05823509	0.712199838	0.763320931	4.679482442	0.027451909	0	346	296	335	549	357	380	401	395	443	498
ENSMUSG00000015599	chr17	Ttbk1	0.15634292	0.712962455	0.764079693	0.96486624	0.169393749	0	20	30	19	33	27	8	36	45	16	50
ENSMUSG00000043822	chr10	Adamtsl5	-0.0842997	0.713142254	0.764213782	5.220540448	0.060139657	0	306	512	566	1067	473	877	581	571	450	491
ENSMUSG00000033904	chr7	Ccp110	-0.1026088	0.713235627	0.764255243	1.84813748	0.063247025	0	65	45	51	55	51	40	64	42	75	51
ENSMUSG00000062444	chr7	Ap3b2	-0.1768579	0.713627041	0.764557418	-0.034366372	0.131773966	0	12	11	4	21	20	7	18	11	10	19
ENSMUSG00000070343	chr3	Gm10288	0.09817029	0.713614392	0.764557418	3.567393152	0.074509214	0	159	206	163	158	148	412	165	128	169	139
ENSMUSG00000074971	chr2	Fibin	0.08325897	0.713772199	0.76465432	4.087516925	0.054624401	0	344	241	222	206	196	422	249	236	171	361
ENSMUSG00000060568	chr1	Fam78b	-0.1126539	0.713854074	0.764683416	1.55863575	0.076478729	0	32	40	51	74	25	55	61	33	33	41
ENSMUSG00000050248	chr5	Evc2	0.06892853	0.714307015	0.765051333	3.217038964	0.035287612	0	97	138	141	183	111	164	162	164	125	151
ENSMUSG00000053293	chr5	Pom121	0.06084156	0.714263182	0.765051333	4.297313437	0.028638049	0	238	233	246	380	332	387	367	302	280	298
ENSMUSG00000040151	chr3	Hs2st1	0.05380149	0.714497237	0.765196428	4.531474098	0.022137067	0	366	352	285	393	288	404	397	320	343	456
ENSMUSG00000031683	chr8	Lsm6	0.06030844	0.714616626	0.765265647	5.670469042	0.030609983	0	837	782	598	765	706	1162	875	787	688	752
ENSMUSG00000042408	chr4	Zmym6	-0.1007743	0.715387549	0.766032515	2.572320955	0.076725056	0	103	95	85	113	56	60	81	58	126	132
ENSMUSG00000040483	chr11	Xaf1	0.09789651	0.715612396	0.766214575	3.351940495	0.076306308	0	171	149	143	168	96	346	135	132	91	168
ENSMUSG00000049957	chr11	Ccdc137	-0.0749547	0.715690736	0.766239753	2.920470251	0.038560469	0	85	121	115	143	105	128	133	110	128	92
ENSMUSG00000031483	chr8	Erlin2	0.05509072	0.715781613	0.766257047	4.189159519	0.023090521	0	260	258	223	325	260	275	316	285	277	352
ENSMUSG00000035640	chr10	Dos	0.11830392	0.71587137	0.766257047	0.831072009	0.074976905	0	19	16	20	31	32	39	26	30	18	28
ENSMUSG00000041625	chr14	Ggact	-0.0954373	0.715842995	0.766257047	2.774125331	0.06533873	0	88	133	79	110	104	59	112	103	120	131
ENSMUSG00000007338	chr19	Mrpl49	0.05285414	0.716041667	0.766380635	4.946470039	0.02277943	0	454	458	437	529	368	501	513	458	576	497

ENSMUSG00000018593	chr11	Sparc	-0.0678898	0.716196495	0.766487649	10.5667085	0.041750846	0	29659	22910	23235	21789	17197	32304	24532	23018	17671	24313
ENSMUSG00000022329	chr15	Stk3	-0.0753465	0.716872715	0.767093872	2.638054705	0.038014219	0	103	94	89	105	75	81	106	81	104	112
ENSMUSG00000047786	chr17	Lix1	-0.1306038	0.71685415	0.767093872	0.850454507	0.072921551	0	29	19	27	38	19	22	22	34	19	33
ENSMUSG00000029670	chr6	Ing3	-0.0720542	0.717858541	0.768089953	2.676525416	0.036080627	0	97	99	87	113	83	108	102	81	78	133
ENSMUSG00000054733	chr14	Msra	-0.0519629	0.718073344	0.76826097	4.523576841	0.021068431	0	326	347	324	450	296	428	360	331	378	339
ENSMUSG00000030560	chr7	Ctsc	0.06299542	0.718321095	0.76846721	6.057983715	0.034884304	0	1028	1137	929	875	819	1387	1151	843	1200	995
ENSMUSG00000002812	chr11	Flii	-0.0592456	0.718441905	0.768537625	6.456230052	0.031276332	0	1182	1103	1040	2027	1408	1684	1434	1338	1198	1381
ENSMUSG00000022394	chr15	L3mbtl2	-0.0651678	0.718740322	0.768736733	3.471251433	0.030355651	0	131	166	159	213	167	173	204	170	135	194
ENSMUSG00000022833	chr16	Ccdc14	-0.0965317	0.718763246	0.768736733	1.558894962	0.055448758	0	47	54	39	52	26	40	52	40	48	42
ENSMUSG00000029338	chr5	Antxr2	-0.0531385	0.718793048	0.768736733	4.785831077	0.023543783	0	410	433	407	443	378	416	455	412	389	528
ENSMUSG00000027887	chr3	Sypl2	-0.0719206	0.719029922	0.768931225	10.21538645	0.047810009	0	19055	15975	15419	20227	19746	12722	20499	18042	16404	26577
ENSMUSG00000031489	chr8	Adrb3	0.28240515	0.719656941	0.769542877	0.533903659	0.643437453	0	2	48	9	2	24	2	18	42	12	43
ENSMUSG00000032850	chr5	Rnft2	-0.1378377	0.720060931	0.769915964	0.864787924	0.096706428	0	38	23	16	30	26	13	27	35	27	28
ENSMUSG00000072964	chrX	Bhlhb9	-0.0838374	0.720794496	0.770641362	3.261924368	0.05670221	0	179	135	115	153	142	99	169	112	217	147
ENSMUSG00000029650	chr5	Slc46a3	-0.0764158	0.720924739	0.770721651	2.909626971	0.04461421	0	113	144	111	102	89	118	102	103	112	153
ENSMUSG00000061126	chr17	Cyp4f39	-0.1750792	0.722138214	0.771959896	1.737198129	0.245230625	0	42	25	16	94	83	15	51	64	25	88
ENSMUSG00000035211	chr7	Xrra1	-0.172885	0.722473798	0.772259564	0.121587249	0.154740176	0	17	15	7	11	25	11	7	12	16	28
ENSMUSG00000043432	chr7	Leng9	0.08858084	0.722808909	0.772558681	1.863119823	0.04155816	0	44	49	53	60	47	59	63	62	49	62
ENSMUSG00000063281	chr18	Zfp35	-0.064096	0.722907415	0.772604881	3.146067258	0.028862272	0	126	120	128	180	115	159	143	104	155	138
ENSMUSG00000019796	chr10	Lrp11	0.09500162	0.723149167	0.772804157	2.235959432	0.061632282	0	61	80	55	72	61	56	69	65	75	121
ENSMUSG00000021619	chr13	Atg10	-0.0725138	0.723481123	0.773040686	2.978434842	0.037822126	0	105	122	126	168	77	134	136	92	124	134
ENSMUSG00000039220	chr17	Ppp1r10	-0.0738444	0.723475171	0.773040686	4.46270192	0.047244723	0	239	210	293	620	356	414	334	305	296	405
ENSMUSG00000001946	chr9	Esam	0.0622473	0.723580126	0.773087366	5.183981807	0.034723175	0	485	571	440	715	451	919	467	584	461	619
ENSMUSG00000004865	chr17	Srpk1	0.05250103	0.723846121	0.773133405	4.359917254	0.022604463	0	291	276	283	381	267	373	373	286	372	293
ENSMUSG00000023032	chr15	Slc4a8	-0.1581566	0.723819431	0.773133405	1.008022672	0.172875367	0	6	32	34	33	41	57	22	27	19	23
ENSMUSG00000024423	chr18	Impact	0.05938375	0.72389981	0.773133405	3.487375194	0.025300268	0	148	163	144	212	146	205	185	138	190	210
ENSMUSG00000051339	chr5	2900026A02Rik	0.06983966	0.723749214	0.773133405	5.54674975	0.045127825	0	542	471	584	1071	769	899	716	841	516	938
ENSMUSG00000092541	chr9	Gm20537	-0.0612078	0.723728707	0.773133405	3.706691996	0.027661615	0	179	165	170	307	178	221	235	183	210	185
ENSMUSG00000002129	chr11	Sf3a1	0.05332688	0.723959389	0.773137955	4.862179327	0.024609166	0	378	344	398	611	407	588	552	400	435	447
ENSMUSG00000041696	chr9	Rasl12	-0.0761814	0.724096286	0.773225068	2.738143813	0.042336928	0	98	120	81	117	85	123	104	118	71	105
ENSMUSG00000022687	chr16	Boc	-0.0766103	0.724442737	0.773535923	3.376439396	0.049403798	0	203	137	175	173	97	234	148	131	114	199
ENSMUSG00000033712	chr14	Ccar2	-0.0507629	0.724749619	0.773804482	4.530464607	0.02107234	0	340	324	302	453	332	374	348	325	373	424
ENSMUSG00000038836	chr6	Agbl3	-0.1291295	0.724887824	0.773892921	0.565155933	0.068288968	0	19	20	24	29	14	16	18	20	26	25
ENSMUSG00000030731	chr7	Syt3	0.16011426	0.725112349	0.774073495	-0.077807487	0.100883558	0	5	9	8	19	17	19	11	11	12	18
ENSMUSG00000023456	chr6	Tpi1	-0.0688573	0.725548806	0.774446831	11.39342625	0.046063023	0	42681	36714	37918	50149	38112	27494	42473	38088	48409	56281
ENSMUSG00000031642	chr8	Sh3rf1	-0.0992008	0.725712586	0.774446831	1.990728518	0.073583403	0	62	40	62	74	59	80	82	61	28	55
ENSMUSG00000047171	chr8	Helt	-0.1985179	0.725794547	0.774446831	-0.092388469	0.169590928	0	9	18	10	23	6	11	20	15	13	2
ENSMUSG00000048482	chr2	Bdnf	0.18857301	0.725688123	0.774446831	0.074730193	0.182200339	0	7	23	5	25	6	22	10	12	26	10
ENSMUSG00000055334	chr9	Snupn	-0.0640204	0.725783968	0.774446831	3.286785607	0.030323871	0	168	143	124	185	118	134	151	147	174	159
ENSMUSG00000073591	chr18	Pcdhb22	0.09945888	0.725638592	0.774446831	1.815077036	0.05568314	0	53	42	45	48	54	86	60	43	40	61
ENSMUSG00000028672	chr4	Hmgcl	0.05457837	0.726506803	0.775088479	5.615049549	0.027173936	0	768	756	616	794	633	1100	736	644	831	784
ENSMUSG00000058793	chr2	Cds2	0.05604855	0.726473902	0.775088479	5.667725623	0.029280926	0	574	741	668	1082	677	1025	715	778	783	934
ENSMUSG00000050953	chr10	Gja1	0.07178732	0.726774605	0.775315005	4.477649791	0.045338129	0	298	322	332	384	272	630	419	288	223	329
ENSMUSG00000031556	chr8	Tm2d2	0.04994036	0.728062074	0.776629183	5.377303803	0.022518318	0	658	591	562	709	516	827	657	611	588	777
ENSMUSG00000024082	chr17	Ndufaf7	0.05353672	0.728323017	0.77684824	4.214227102	0.025063701	0	259	275	245	375	207	273	343	285	305	323
ENSMUSG00000026917	chr2	Wdr5	-0.0488411	0.72883923	0.777339521	5.086989708	0.021257187	0	507	471	425	699	485	646	577	436	550	521
ENSMUSG00000025532	chr5	Crcp	0.05791464	0.729539885	0.778027427	4.084294119	0.028245582	0	292	228	221	272	215	306	323	217	316	242
ENSMUSG00000097290	chr16	1300002E11Rik	-0.0798495	0.730157376	0.778567139	2.477895828	0.044788717	0	82	99	67	92	76	102	64	92	93	80
ENSMUSG00000098972	chr2	Mir8093	0.15372177	0.730157329	0.778567139	-0.065194878	0.103404691	0	16	15	4	16	8	13	18	10	19	11
ENSMUSG00000092071	chr7	A230065N10Rik	0.19708413	0.730779237	0.779170783	-0.268164073	0.162224319	0	12	6	13	13	5	3	18	6	16	18
ENSMUSG00000056851	chr15	Pcbp2	0.05482399	0.731473062	0.779851057	7.27460011	0.030095799	0	2128	2016	1859	3083	2305	2465	2783	2278	2167	3207
ENSMUSG00000006435	chr19	Neurl1a	-0.0554141	0.731800565	0.78014071	7.406716618	0.030803006	0	2614	2290	2426	3191	2383	2682	2388	3012	2243	3209
ENSMUSG00000032902	chr3	Slc16a1	-0.0719187	0.731926417	0.780148575	5.454106425	0.050215789	0	401	714	730	1087	460	689	813	717	663	584
ENSMUSG00000036537	chrX	Rnf113a1	-0.1071836	0.731959484	0.780148575	0.902209669	0.056303409	0	30	21	24	33	27	31	29	32	19	26
ENSMUSG00000071659	chr19	Hnrnpul2	0.05002362	0.731975405	0.780148575	6.622709144	0.024788418	0	1359	1298	1254	1922	1415	1708	1814	1407	1565	1695
ENSMUSG00000024747	chr19	Aldh1a7	0.1719589	0.73291402	0.781089397	2.290249724	0.271478723	0	47	98	72	85	33	12	37	68	104	186
ENSMUSG00000040040	chr14	Ift88	-0.0851952	0.734749475	0.782985792	1.945394612	0.049101001	0	57	40	68	71	50	63	57	44	64	68
ENSMUSG00000032604	chr9	Qars	0.04909581	0.735270549	0.783481336	6.481983049	0.024285363	0	1419	1266	1093	1520	1241	1617	1556	1278	1385	1597
ENSMUSG00000031070	chr7	Mrgprf	0.07748424	0.735434753	0.783596563	2.787676752	0.047861407	0	99	67	78	128	121	108	110	105	94	152
ENSMUSG00000025377	chr11	Enthd2	0.06086297	0.735636755	0.783752042	2.952992055	0.027498354	0	115	95	103	135	108	127	132	118	129	128
ENSMUSG00000021103	chr12	Mnat1	-0.0582147	0.735780906	0.783845868	3.697803937	0.028572735	0	212	196	199	242	132	212	232	168	217	200
ENSMUSG00000024287	chr18	Thoc1	0.06696979	0.735880003	0.783891686	3.451581708	0.041218621	0	164	131	152	205	139	208	229	145	207	115
ENSMUSG00000055745	chr15	Ldoc1l	-0.0630618	0.736237119	0.784212329	3.187350965	0.036114006	0	153	137	114	126	147	139	127	130	141	180
ENSMUSG00000005897	chr10	Nr2c1	-0.0615717	0.736575986	0.784461232	3.070164273	0.028250173	0	129	112	106	182	108	152	133	129	108	141
ENSMUSG00000010051	chr9	Hyal1	-0.0710788	0.736583053	0.784461232	2.533646507	0.038674263	0	74	84	74	109	92	90	97	68	83	115

ENSMUSG00000027628	chr2	Aar2	-0.0499174	0.736747177	0.784576238	4.917614939	0.023258192	0	492	437	350	580	435	520	446	515	412	519
ENSMUSG00000048495	chr1	Tyw5	0.09761188	0.736909268	0.784637364	1.300833819	0.053241479	0	32	34	30	34	37	49	46	28	43	32
ENSMUSG00000057406	chr5	Whsc1	-0.0632512	0.736916861	0.784637364	4.120190189	0.036848555	0	265	216	232	352	258	315	320	221	338	184
ENSMUSG00000034457	chrX	Eda2r	0.07843664	0.737012757	0.78467969	3.859810038	0.058018081	0	270	210	207	240	120	414	165	190	196	261
ENSMUSG00000027875	chr3	Hmgcs2	0.16025989	0.73710836	0.784721697	0.199845795	0.109987124	0	7	12	17	22	14	27	11	10	14	27
ENSMUSG00000021806	chr14	Nid2	0.05760822	0.737211795	0.784772035	5.248372807	0.032393748	0	541	561	541	545	549	623	620	599	463	859
ENSMUSG00000073643	chr1	Wdfy1	0.0543209	0.737744025	0.785278789	4.323804076	0.027451781	0	295	319	274	363	210	312	407	294	276	369
ENSMUSG00000024486	chr18	Hbegf	-0.0647964	0.738188838	0.785651828	4.639789869	0.042318485	0	465	362	352	411	298	620	456	341	242	350
ENSMUSG00000037355	chr5	Uvssa	-0.0794297	0.738206912	0.785651828	2.014696078	0.045241491	0	58	58	71	63	48	80	60	51	52	70
ENSMUSG00000038697	chr8	Taf5l	-0.0532607	0.738480969	0.785883654	3.689709481	0.024630553	0	187	180	199	243	163	244	241	163	185	197
ENSMUSG00000084319	chr6	Tpt1-ps3	-0.0516416	0.738549098	0.785896314	7.275244749	0.028215263	0	2737	2173	2026	2753	2073	3234	2476	2013	2459	2307
ENSMUSG00000028684	chr4	Urod	-0.0481579	0.739881659	0.787254364	5.708014004	0.023452495	0	795	782	680	1026	691	985	735	811	828	829
ENSMUSG00000009828	chr9	Ick	0.06715591	0.740000279	0.787320638	3.268840711	0.038311035	0	112	121	144	171	143	188	152	138	109	214
ENSMUSG00000103988	chr3	Dnajc19	-0.0518673	0.74021094	0.787484821	5.24848707	0.027070739	0	675	609	492	642	457	632	681	503	672	549
ENSMUSG00000030216	chr6	Wbp11	-0.0512853	0.74027443	0.787492421	5.17391168	0.026000011	0	519	469	425	785	560	572	622	519	492	686
ENSMUSG00000024896	chr19	Minpp1	0.04969245	0.740534651	0.78769508	4.33709868	0.022569383	0	322	269	259	351	272	373	361	253	364	322
ENSMUSG00000052684	chr4	Jun	-0.0748486	0.740634019	0.78769508	6.190446782	0.060230849	0	853	1021	1565	1450	688	1771	1265	721	975	1168
ENSMUSG00000093677	chr15	Gm20712	0.09285344	0.740578684	0.78769508	1.752983781	0.060739365	0	28	41	46	83	40	60	62	49	46	57
ENSMUSG00000047264	chr8	Zfp358	0.05297213	0.741266137	0.788307375	4.711255443	0.02758568	0	348	322	329	491	421	534	362	459	368	447
ENSMUSG00000027012	chr2	Dync1i2	0.04662458	0.741452156	0.78838522	5.901860642	0.022637783	0	922	880	740	1080	768	1000	1081	880	943	1049
ENSMUSG00000028954	chr5	Nub1	0.04809285	0.741395874	0.78838522	5.322643886	0.023384172	0	626	563	455	754	544	784	635	555	588	769
ENSMUSG00000060224	chr19	Pyroxd2	0.12087925	0.741613857	0.788497167	1.975292514	0.121201225	0	71	52	51	40	53	135	41	65	30	59
ENSMUSG00000019880	chr10	Rspo3	0.16888696	0.742080917	0.788933736	0.958204349	0.268276358	0	8	13	20	82	13	62	16	15	34	31
ENSMUSG00000022179	chr14	4931414P19Rik	-0.0826357	0.742146465	0.788943408	1.717114821	0.04403801	0	48	51	37	55	51	44	51	49	50	56
ENSMUSG00000049521	chr15	Cdc42ep1	-0.0578424	0.742457682	0.78921422	4.358176231	0.032466328	0	292	324	268	437	245	424	292	352	215	356
ENSMUSG00000050271	chr8	D8Ertd82e	-0.0723308	0.742519628	0.789220042	2.605410257	0.046244203	0	76	91	69	138	87	135	100	76	66	103
ENSMUSG00000029647	chr5	Pan3	0.06976173	0.742878391	0.789541323	3.697455927	0.045270144	0	146	210	188	240	152	364	209	153	164	203
ENSMUSG00000000171	chr9	Sdhd	-0.0517515	0.743040288	0.789653339	8.385476023	0.029583882	0	4773	5075	5055	6927	3740	5680	5406	5320	5119	5233
ENSMUSG00000038112	chr9	AW551984	0.07961511	0.743406523	0.789982479	3.943047299	0.064141455	0	360	111	168	241	228	281	264	175	237	333
ENSMUSG00000025579	chr11	Gaa	0.05418963	0.743625744	0.790114699	7.430574709	0.032426603	0	2763	2267	1984	2921	2663	2460	3095	2766	2561	3421
ENSMUSG00000027860	chr3	Vangl1	-0.0750752	0.743644015	0.790114699	2.164217473	0.043916308	0	52	65	64	88	65	96	71	50	58	75
ENSMUSG00000032606	chr9	Nicn1	-0.0622557	0.74409842	0.790537402	3.724454538	0.037092376	0	222	210	197	203	159	158	216	175	219	275
ENSMUSG00000030298	chr6	Sec13	0.04825939	0.744451267	0.790852152	5.941564137	0.024996345	0	888	754	796	1161	912	1028	1140	881	1046	995
ENSMUSG00000041229	chrX	Phf8	-0.0554735	0.744582974	0.790931948	3.621758349	0.028811427	0	161	178	171	247	173	252	218	153	143	220
ENSMUSG00000074001	chr9	Klhl40	-0.0552345	0.745038043	0.791355198	7.391419722	0.033971275	0	2743	1967	2304	3518	2333	2973	2449	2270	3332	2384
ENSMUSG00000027374	chr2	Mrps5	-0.0508772	0.745145122	0.791408786	5.039693742	0.026024881	0	459	483	485	674	401	473	517	519	601	500
ENSMUSG00000021532	chr13	Fastkd3	-0.0608153	0.746394264	0.792675246	3.168838778	0.03211075	0	139	153	109	169	108	135	174	126	118	157
ENSMUSG00000051379	chr2	Flrt3	0.13892185	0.746752635	0.79299558	0.155142571	0.081512055	0	12	16	14	18	10	17	24	9	12	23
ENSMUSG00000025474	chr7	Tubgcp2	-0.0482182	0.746864749	0.793054379	4.243043274	0.021768433	0	302	290	237	343	256	293	305	281	320	307
ENSMUSG00000024472	chr18	Dcp2	-0.0522009	0.747089474	0.793232735	4.054519425	0.025786321	0	224	222	216	343	254	308	296	260	230	230
ENSMUSG00000021631	chr17	Mrps36-ps1	-0.1166795	0.747235708	0.793326102	1.029852833	0.075090824	0	28	22	24	55	23	42	26	34	27	21
ENSMUSG00000025316	chr8	Banp	-0.0706875	0.747290936	0.793326102	2.980263796	0.047114209	0	156	133	93	95	109	159	121	94	130	118
ENSMUSG00000022881	chr16	Rfc4	-0.0722107	0.747506194	0.793494346	2.640514459	0.045912884	0	95	74	112	110	75	89	121	84	108	83
ENSMUSG00000061315	chr10	Naca	-0.0574864	0.747790225	0.793735565	8.677145362	0.038087724	0	5477	5178	4667	8540	7426	7432	6263	6706	5056	7358
ENSMUSG00000050017	chr5	Pitpnb	-0.0440354	0.74788025	0.793770836	4.937995515	0.019828272	0	471	409	434	586	418	567	526	463	413	493
ENSMUSG00000029569	chr6	Tmem168	-0.0524441	0.7481984	0.793927632	3.974346066	0.027856047	0	208	251	215	283	225	303	302	171	229	256
ENSMUSG00000030966	chr7	Trim21	-0.0794643	0.748095645	0.793927632	1.828412434	0.047982363	0	51	50	50	66	46	49	74	41	45	64
ENSMUSG00000094568	chr8	Gm1815	0.1111293	0.74815769	0.793927632	0.686345424	0.072650403	0	27	16	20	23	20	15	31	22	28	29
ENSMUSG00000073415	chr17	Gm10501	-0.0929486	0.748746084	0.794448471	1.090456553	0.048866516	0	35	25	30	35	29	31	29	34	28	36
ENSMUSG00000030978	chr7	Rrm1	-0.0542315	0.748819278	0.794465819	5.296475957	0.032109938	0	598	623	541	726	493	584	861	483	666	545
ENSMUSG00000028687	chr4	Mutyh	-0.106875	0.748876829	0.794466568	1.059151304	0.092879409	0	46	30	32	18	23	33	31	23	41	26
ENSMUSG00000086784	chr7	Isoc2a	-0.0520617	0.749153136	0.794699372	4.835487506	0.02963549	0	436	494	377	457	382	671	381	377	413	459
ENSMUSG00000025193	chr19	Cutc	-0.0615956	0.749265684	0.794758439	3.684068791	0.036950995	0	193	213	188	240	138	163	249	149	227	228
ENSMUSG00000029016	chr4	Clcn6	0.06058316	0.749456929	0.794900966	3.166555154	0.033218077	0	125	124	113	160	125	218	148	113	138	128
ENSMUSG00000032913	chr3	Lrig2	-0.0590099	0.749804676	0.795209452	3.365417692	0.03129615	0	175	116	131	182	170	191	150	171	145	157
ENSMUSG00000015467	chr17	Egfl8	0.11136973	0.750316832	0.79569224	1.299497759	0.079970102	0	25	22	30	39	50	61	40	32	30	37
ENSMUSG00000038742	chr9	Angptl6	0.0958006	0.750838854	0.796185419	2.032669419	0.087589435	0	63	52	26	81	67	43	59	67	92	69
ENSMUSG00000021039	chr12	Snw1	-0.0461729	0.751042311	0.796337359	5.782336034	0.023936792	0	944	855	706	954	702	909	974	734	845	960
ENSMUSG00000056328	chr11	Myh1	-0.0811117	0.751096098	0.796337359	12.37578383	0.078202111	0	38056	70821	81475	147472	78135	88774	76156	115218	65629	72033
ENSMUSG00000018217	chr11	Pmp22	-0.0622702	0.751245797	0.796435656	6.551518334	0.045503372	0	931	1230	1716	1885	1362	2141	1688	1104	1285	1358
ENSMUSG00000039536	chr2	Stau1	-0.0481688	0.751508838	0.79665409	5.396435006	0.025412596	0	598	554	543	870	639	663	638	667	600	800
ENSMUSG00000033128	chr15	Gga1	-0.0449124	0.751918833	0.79702826	5.744121548	0.022706606	0	783	694	762	1067	761	1034	840	736	784	926
ENSMUSG00000034168	chr12	Irf2bpl	0.05037083	0.752369108	0.797445067	5.255445774	0.028019108	0	560	514	500	616	584	638	607	674	478	764
ENSMUSG00000021250	chr12	Fos	-0.1839377	0.752649881	0.797621682	4.576066463	0.396378499	0	209	370	1003	132	67	376	926	96	227	231
ENSMUSG00000063821	chr14	Dupd1	0.07209124	0.752597119	0.797621682	6.109047186	0.061137391	0	1469	1077	881	786	736	753	1303	1086	1110	1479

ENSMUSG00000020423	chr1	Btg2	-0.1177412	0.752811087	0.79773203	5.686707475	0.164930324	0	634	639	1625	702	296	1646	933	375	608	586
ENSMUSG00000047881	chr5	Rell1	-0.0473798	0.753128397	0.798007769	3.895835646	0.022188712	0	217	222	191	279	212	289	247	202	195	260
ENSMUSG00000022414	chr15	Tab1	-0.0511767	0.753321053	0.798151394	4.535159524	0.026819284	0	341	294	346	508	280	373	311	377	387	394
ENSMUSG00000025270	chrX	Alas2	-0.1132957	0.75365415	0.798443784	2.661731862	0.146676258	0	101	78	126	124	53	154	44	49	57	195
ENSMUSG00000022637	chr16	Cblb	0.04824338	0.753815836	0.798554546	3.900580191	0.023401031	0	225	190	180	312	191	284	278	200	222	252
ENSMUSG00000029104	chr5	Htt	-0.0493864	0.753901404	0.798584662	4.25145262	0.025937295	0	259	259	238	342	333	353	343	250	295	283
ENSMUSG00000097756	chr7	A730056A06Rik	0.13904709	0.754744199	0.799416819	0.205251756	0.132408479	0	10	20	20	14	8	18	7	14	19	30
ENSMUSG00000000884	chr16	Gnb1l	0.09236902	0.754802157	0.799417623	1.390885075	0.056409567	0	45	27	44	36	27	51	46	34	41	39
ENSMUSG00000023932	chr17	Cdc5l	0.04371513	0.755114867	0.799688216	5.570783428	0.022165662	0	702	670	588	944	605	856	821	758	754	738
ENSMUSG00000025422	chr10	Agap2	0.08880219	0.755370922	0.799898773	1.193442886	0.061673901	0	22	38	27	50	21	37	40	34	29	42
ENSMUSG00000027349	chr2	Fam98b	0.04441403	0.756540358	0.801076449	4.416327581	0.021481745	0	313	289	270	424	274	346	407	331	332	342
ENSMUSG00000034110	chr5	Kctd7	-0.0707736	0.758168488	0.802611402	2.596397523	0.043770047	0	95	95	93	104	65	97	71	106	86	110
ENSMUSG00000042202	chr4	Slc35e2	-0.0633123	0.758071287	0.802611402	2.571736492	0.040332405	0	82	83	84	98	94	101	105	73	69	120
ENSMUSG00000045822	chr2	Zswim3	-0.0926099	0.758175743	0.802611402	0.9481217	0.049710194	0	26	26	26	35	26	29	33	20	28	33
ENSMUSG00000060475	chr17	Wtap	0.04328046	0.758219687	0.802611402	4.564957122	0.020210539	0	359	323	318	448	290	439	425	315	378	402
ENSMUSG00000024940	chr19	Ltbp3	-0.0566547	0.758612302	0.802966187	6.305775551	0.039726993	0	1161	1030	1006	1554	1273	1913	1001	1258	878	1335
ENSMUSG00000028681	chr4	Ptch2	0.11918405	0.758790437	0.803093915	1.146304233	0.138787004	0	15	27	33	42	32	30	39	28	13	69
ENSMUSG00000040350	chr11	Trim7	-0.0565089	0.75894977	0.803201725	6.033885295	0.039000637	0	1051	917	886	1196	925	771	869	1168	1001	1378
ENSMUSG00000056598	chr11	Lrrc48	0.09810318	0.759450532	0.803670829	0.958810494	0.072796734	0	28	20	26	38	20	18	35	29	38	32
ENSMUSG00000038216	chr11	Pnmt	0.14835997	0.760518415	0.804739958	0.213541595	0.142142155	0	13	19	18	13	9	39	7	15	13	16
ENSMUSG00000039428	chr7	Tmem135	-0.0506863	0.76058935	0.804754089	4.701971641	0.029275375	0	374	391	312	520	379	333	438	367	396	540
ENSMUSG00000059288	chr13	Cdyl	0.06825478	0.760865061	0.804984867	2.382209893	0.043152159	0	70	69	58	117	62	100	90	74	61	103
ENSMUSG00000001707	chr13	Eef1e1	0.06083041	0.761167964	0.805244377	3.392929371	0.038974237	0	170	112	110	221	154	162	231	139	170	164
ENSMUSG00000015994	chr8	Fnta	-0.0442182	0.761303156	0.805326439	6.021153761	0.024037539	0	1026	915	862	1279	854	1235	1054	851	1090	999
ENSMUSG00000074406	chr7	Zfp628	0.06406253	0.761592531	0.805571575	2.973879956	0.042336205	0	103	89	97	153	124	145	113	135	88	166
ENSMUSG00000058440	chr6	Nrf1	-0.0537326	0.762014713	0.805957138	3.573754941	0.0320056	0	156	160	151	238	193	260	203	138	188	163
ENSMUSG00000052593	chr12	Adam17	0.04425222	0.762081791	0.805967091	5.358393643	0.023304149	0	575	579	563	771	525	860	757	541	607	651
ENSMUSG00000024182	chr17	Axin1	-0.0467549	0.763445881	0.807287556	4.389597469	0.024536609	0	287	315	259	441	290	418	328	260	356	320
ENSMUSG00000025420	chr18	Katnal2	-0.1430693	0.763432304	0.807287556	0.084592033	0.183089303	0	22	17	8	8	17	8	13	12	7	33
ENSMUSG00000020611	chr11	Gna13	-0.0451525	0.763763892	0.807562729	5.211581131	0.025160928	0	508	558	510	712	515	666	709	436	495	687
ENSMUSG00000000552	chr15	Zfp385a	0.10335853	0.76416957	0.807930548	4.855128295	0.138528871	0	178	218	201	933	624	527	443	405	338	744
ENSMUSG00000016831	chr14	Tox4	-0.046998	0.764779322	0.808514055	5.621820661	0.027555552	0	795	697	592	908	737	666	808	719	842	893
ENSMUSG00000064181	chr10	Rab3ip	-0.051602	0.765128573	0.808822096	3.918079627	0.02767413	0	184	215	200	353	201	242	227	246	243	240
ENSMUSG00000070371	chr7	Prss36	0.06530747	0.765346469	0.808991245	2.668258997	0.042202075	0	92	103	69	102	87	100	87	111	88	133
ENSMUSG00000028799	chr4	Zfp362	-0.0535077	0.766116843	0.809744309	3.755518653	0.031681114	0	197	174	174	278	200	257	186	228	148	257
ENSMUSG00000059554	chr10	Ccdc28a	-0.0714293	0.766567181	0.810159024	2.481351903	0.051040603	0	105	102	63	75	69	105	72	70	95	94
ENSMUSG00000019831	chr10	Wasf1	0.11898633	0.767351979	0.810895314	0.464059626	0.096515249	0	23	16	13	23	15	16	28	28	9	25
ENSMUSG00000036446	chr10	Lum	-0.0579268	0.767437917	0.810895314	6.560436894	0.04504906	0	1458	1511	1379	1400	1343	972	1583	1383	1511	2047
ENSMUSG00000042901	chr1	Aida	-0.0438203	0.767417695	0.810895314	4.79407785	0.023232077	0	455	397	355	523	369	488	437	323	490	491
ENSMUSG00000027361	chr2	Gabpb1	0.05330893	0.768136325	0.811571914	3.110978825	0.027123701	0	125	108	124	169	101	150	156	119	131	154
ENSMUSG00000034442	chr12	Trmt5	-0.0617714	0.7683032	0.811686864	2.629673226	0.041127102	0	71	103	90	104	91	95	103	102	75	109
ENSMUSG00000033157	chr16	Abhd10	-0.0497352	0.768644538	0.811924727	3.196910853	0.026479292	0	138	136	129	142	136	161	154	122	145	145
ENSMUSG00000050394	chrX	Armcx6	0.08004153	0.76860005	0.811924727	1.878245873	0.066928567	0	86	39	42	50	40	62	66	61	58	50
ENSMUSG00000041361	chr9	Myzap	0.07624477	0.769265266	0.812518997	2.425223074	0.064487356	0	95	88	67	88	44	84	91	119	64	78
ENSMUSG00000064307	chr7	Lrrc51	0.10756904	0.76943659	0.812638539	1.273946956	0.104182996	0	40	36	29	40	20	73	25	44	21	33
ENSMUSG00000061313	chr8	Ddhd2	-0.0476112	0.769723716	0.812880357	3.954938836	0.027412236	0	194	226	238	258	241	272	230	194	267	275
ENSMUSG00000032336	chr9	Nptn	0.0483648	0.770226333	0.813349696	6.559942569	0.031878097	0	1520	1320	1219	1595	1249	1326	1837	1212	1492	1967
ENSMUSG00000022656	chr16	Pvrl3	0.06116526	0.770945965	0.814048111	2.876752669	0.040570336	0	87	84	88	159	114	139	130	126	89	119
ENSMUSG00000037379	chr5	Spon2	-0.0853912	0.771047688	0.814094016	3.223559562	0.089422208	0	150	93	115	225	137	189	99	202	59	182
ENSMUSG00000030870	chr7	Ubfd1	0.04082338	0.771471389	0.814479841	5.359475336	0.021399558	0	627	552	563	736	535	840	684	575	640	667
ENSMUSG00000062198	chr12	2700097O09Rik	-0.071578	0.771569536	0.814521931	2.251148556	0.051766108	0	68	87	73	73	51	86	72	60	91	60
ENSMUSG00000066892	chr9	Fbxl12	0.06466594	0.77170305	0.814601346	2.334095629	0.038794315	0	75	74	73	83	53	87	69	79	81	94
ENSMUSG00000041147	chr5	Brca2	0.10693855	0.771838764	0.814683073	0.911113618	0.065173086	0	23	27	26	26	23	38	40	25	27	19
ENSMUSG00000001855	chr2	Nup214	-0.0490783	0.772217403	0.814904393	4.131014333	0.029609069	0	211	229	225	368	293	344	303	254	212	292
ENSMUSG00000018541	chr11	Cwc25	-0.0511019	0.772177869	0.814904393	3.177478016	0.028461131	0	128	124	129	174	124	182	154	110	116	160
ENSMUSG00000032105	chr9	Pdzd3	-0.1534032	0.772223367	0.814904393	0.439053047	0.212510411	0	18	19	20	32	9	43	16	15	20	2
ENSMUSG00000103235	chr9	DHX30	0.03845718	0.772737445	0.815385317	4.935280687	0.018760974	0	466	409	394	574	408	547	499	472	472	533
ENSMUSG00000024678	chr19	Ms4a4d	-0.0551453	0.773010491	0.815584497	2.91385625	0.035015693	0	113	123	92	123	110	128	152	91	98	128
ENSMUSG00000037509	chr1	Arhgef4	0.13055504	0.773101275	0.815584497	0.178204182	0.111040818	0	14	8	21	15	13	12	14	14	29	16
ENSMUSG00000037643	chr3	Prkci	0.07016709	0.773081962	0.815584497	2.72912056	0.052093997	0	101	96	87	106	82	123	170	72	97	86
ENSMUSG00000028163	chr3	Nfkb1	0.04248811	0.773382335	0.815791565	4.808876894	0.022919205	0	381	358	377	565	383	559	524	347	439	459
ENSMUSG00000029869	chr6	Ephb6	-0.1179437	0.773414298	0.815791565	0.846716698	0.105368926	0	10	21	26	43	31	21	27	34	20	28
ENSMUSG00000016487	chr6	Ppfibp1	-0.0488984	0.773659625	0.815988749	4.632992736	0.02975079	0	354	319	307	599	327	361	428	366	332	496
ENSMUSG00000016510	chr5	Mtif3	-0.0454208	0.773905382	0.816186359	4.19777495	0.025001456	0	299	281	267	316	216	290	281	248	336	307
ENSMUSG00000025173	chr11	Wdr45b	-0.0411521	0.774273574	0.816513052	4.761210107	0.021721864	0	424	450	376	462	326	474	459	381	432	429

ENSMUSG00000074217	chr8	2210011C24Rik	-0.0825613	0.774807139	0.817014077	2.465231353	0.07935754	0	134	49	72	69	86	68	79	75	89	116
ENSMUSG00000049950	chr2	Rpp38	-0.0694813	0.775014158	0.817170719	2.04006461	0.045974623	0	64	60	57	65	57	52	79	62	67	56
ENSMUSG00000049551	chr5	Fzd9	0.05867019	0.77517532	0.817278989	4.148815473	0.048079865	0	233	251	171	423	235	210	252	361	294	331
ENSMUSG00000030401	chr7	Rtn2	-0.0442971	0.775276055	0.817323538	9.785153788	0.028784157	0	14825	13089	10639	15010	13097	14913	14661	12846	12784	15845
ENSMUSG00000029328	chr5	Hnrnpdl	-0.0464816	0.775533987	0.817533791	6.314327841	0.030577666	0	1408	1095	1002	1544	1013	1363	1516	1047	1396	1063
ENSMUSG00000022013	chr14	Dnajc15	0.04165999	0.776257527	0.818234799	5.449089471	0.023717236	0	686	652	604	713	537	781	698	691	739	693
ENSMUSG00000075592	chr14	Nynrin	0.06049013	0.777471744	0.819452873	2.728548454	0.039016067	0	89	87	75	132	95	135	109	98	74	130
ENSMUSG00000028958	chr5	Tmub1	0.04322769	0.777682145	0.819612824	3.903255028	0.022090721	0	219	189	203	271	209	273	261	207	259	231
ENSMUSG00000054414	chr3	Slc30a7	0.04641838	0.777865885	0.819744655	3.581253937	0.024902573	0	167	172	147	236	153	231	232	149	179	198
ENSMUSG00000054072	chr18	Ilgp1	0.08172474	0.778170805	0.82000416	2.843290866	0.084758092	0	107	118	109	94	77	77	99	121	79	215
ENSMUSG00000020198	chr10	Ap3d1	0.04344797	0.778581843	0.82037544	5.503098418	0.02653205	0	575	556	586	876	736	825	789	612	702	836
ENSMUSG00000080811	chrX	Gm14513	-0.3124606	0.779388846	0.821163853	2.907793606	1.360620009	0	126	133	110	148	91	585	2	1	3	1
ENSMUSG00000055725	chr5	Paqr3	0.09417526	0.780082159	0.821832373	0.843589275	0.054261143	0	26	23	19	27	25	31	25	20	30	35
ENSMUSG00000036120	chr8	Rfxank	0.05281399	0.780223293	0.821919103	3.215012363	0.029365575	0	141	128	131	140	126	184	136	135	166	141
ENSMUSG00000039611	chr4	Tmem246	0.0438183	0.780552667	0.822204106	5.399221697	0.028189284	0	652	527	546	811	571	634	601	774	703	749
ENSMUSG00000003228	chr19	Grk5	-0.0567043	0.780942366	0.822486394	2.873191078	0.036453672	0	95	115	93	128	115	157	124	82	104	115
ENSMUSG00000049044	chr2	Rapgef4	-0.1270657	0.780997205	0.822486394	0.264056162	0.106246458	0	10	8	17	31	19	13	14	22	17	17
ENSMUSG00000074203	chr8	G430095P16Rik	-0.1207736	0.780924221	0.822486394	0.102395864	0.14584077	0	19	15	15	13	11	26	3	8	18	20
ENSMUSG00000038256	chr3	Bcl9	-0.0635633	0.781115709	0.822549213	2.800554631	0.050978614	0	76	98	94	160	99	153	108	101	65	125
ENSMUSG00000058586	chr15	Serhl	-0.0437285	0.781437076	0.822825629	4.737163799	0.026137801	0	428	427	386	478	293	509	382	426	440	375
ENSMUSG00000057604	chr6	Lmcd1	0.07369497	0.781508318	0.822838651	6.97284806	0.084048459	0	995	1176	1493	4431	1510	2668	1866	2090	2020	1875
ENSMUSG00000040997	chr14	Abhd4	0.04819449	0.781913251	0.823202982	5.065076531	0.03290315	0	479	487	462	592	426	857	463	497	383	604
ENSMUSG00000001507	chr11	Itga3	0.06397683	0.782150753	0.823380701	3.005131552	0.050259265	0	92	103	91	165	129	137	178	126	131	86
ENSMUSG00000001642	chr6	Akr1b3	0.04528645	0.782199883	0.823380701	7.359599744	0.031720274	0	2787	2138	2095	2880	2168	2313	2801	2944	2405	3067
ENSMUSG00000026632	chr1	Tatdn3	0.05296711	0.782769726	0.823856441	3.181311104	0.03517825	0	163	144	106	136	104	148	138	138	170	147
ENSMUSG00000099647	chr7	Gm5776	0.08204894	0.782718554	0.823856441	1.640095631	0.065787997	0	56	52	37	48	24	46	56	43	62	43
ENSMUSG00000002221	chr5	Paxip1	-0.0518769	0.783221969	0.82427035	3.256329788	0.031542198	0	140	140	137	199	106	152	169	107	157	174
ENSMUSG00000035235	chr14	Trim13	-0.0715835	0.7840047	0.825031977	3.23025856	0.066927458	0	151	156	125	173	105	76	125	173	140	214
ENSMUSG00000041438	chr8	Cirh1a	0.04019755	0.784541734	0.825534955	4.365056441	0.021515843	0	269	283	284	388	285	340	362	278	329	390
ENSMUSG00000023175	chr10	Bsg	-0.0455392	0.785054044	0.826011843	9.199503169	0.03329882	0	9293	9048	6963	9447	9490	9647	9137	8875	7957	11700
ENSMUSG00000040459	chr8	Arglu1	-0.0369438	0.785798715	0.826733126	5.199389611	0.01994235	0	581	518	477	664	527	650	627	503	581	597
ENSMUSG00000027496	chr2	Aurka	0.07270546	0.785908062	0.82678593	3.141445127	0.072850988	0	202	124	83	95	121	180	191	135	131	93
ENSMUSG00000034875	chr7	Nudt19	0.04556532	0.786421047	0.827263326	4.991868818	0.031822429	0	413	423	405	643	457	384	553	488	584	601
ENSMUSG00000024078	chr17	Ttc27	0.05012735	0.787867205	0.828722214	3.292953546	0.028430803	0	146	126	133	163	139	164	192	128	173	147
ENSMUSG00000074811	chr19	Hps6	0.06351686	0.788066315	0.828869267	2.283777073	0.043497886	0	50	70	74	95	58	76	92	67	76	85
ENSMUSG00000035601	chr4	Trmt10b	-0.0682837	0.788570506	0.82933715	1.808987595	0.053416233	0	52	54	47	52	51	63	76	37	50	45
ENSMUSG00000045435	chr5	Tmem60	0.04551911	0.788791636	0.829507292	3.906196064	0.027036999	0	241	235	217	237	158	300	268	204	208	261
ENSMUSG00000028532	chr4	Cachd1	-0.0649265	0.789187211	0.82983554	2.107970961	0.040462696	0	61	52	49	93	67	68	64	62	65	75
ENSMUSG00000051515	chr7	Fam181b	-0.1085299	0.789237668	0.82983554	0.811397805	0.137673678	0	29	29	21	29	18	42	8	13	24	43
ENSMUSG00000051985	chr1	Igfn1	-0.1079953	0.789281899	0.82983554	4.099037269	0.18671018	0	153	344	76	507	278	524	233	214	70	334
ENSMUSG00000002279	chr17	Lmf1	0.04834593	0.789431272	0.829899291	3.812008981	0.031901969	0	197	198	166	254	207	294	240	240	145	243
ENSMUSG00000021248	chr12	Tmed10	-0.0417005	0.789461296	0.829899291	6.820832519	0.028506757	0	1772	1513	1421	2195	1678	1954	2152	1309	1763	1962
ENSMUSG00000001943	chr9	Vsig2	0.13143029	0.7897253	0.830005191	0.059211494	0.103015838	0	15	12	18	9	10	28	13	9	16	13
ENSMUSG00000025902	chr1	Sox17	0.06234594	0.789706688	0.830005191	2.228101807	0.048839511	0	69	41	67	99	60	101	66	65	75	75
ENSMUSG00000053012	chr6	Krcc1	0.04205563	0.789740199	0.830005191	4.324932446	0.026945082	0	286	276	243	431	246	289	382	277	361	337
ENSMUSG00000014778	chr8	Fhod1	0.0411974	0.789855425	0.830063871	5.608928686	0.027187196	0	820	583	671	904	616	802	784	726	939	765
ENSMUSG00000015312	chr10	Gadd45b	0.0693875	0.790850901	0.830997149	4.709940834	0.076891491	0	512	413	472	298	174	447	577	415	260	490
ENSMUSG00000021493	chr13	Pdlim7	0.04175524	0.790862412	0.830997149	8.811215562	0.029498208	0	7792	5993	5553	6925	6566	7986	7655	6472	7230	7918
ENSMUSG00000021253	chr12	Tgfb3	0.05210251	0.790973692	0.831051595	5.35342994	0.04419364	0	639	521	466	796	584	902	524	843	413	712
ENSMUSG00000002968	chr7	Med25	0.04301959	0.791139036	0.831162833	5.48253859	0.029764525	0	657	498	569	854	708	746	662	742	641	901
ENSMUSG00000000031	chr7	H19	-0.0623491	0.793262025	0.833057498	12.06089822	0.067718957	0	72170	60328	55222	87925	52980	54179	43572	65722	53900	123885
ENSMUSG00000005951	chr11	Shpk	-0.1062355	0.793300103	0.833057498	0.665126874	0.092805285	0	27	21	23	15	25	25	16	28	14	32
ENSMUSG00000033917	chr7	Gde1	0.03636881	0.793253048	0.833057498	5.300031664	0.020706784	0	586	543	546	698	519	692	662	572	599	729
ENSMUSG00000037949	chr9	Ano10	-0.0382533	0.793274596	0.833057498	5.350489634	0.02324804	0	649	580	541	756	554	634	641	616	584	802
ENSMUSG00000055720	chr9	Ubl7	-0.0387113	0.793129046	0.833057498	5.488440344	0.023808892	0	669	610	542	944	649	797	736	690	610	781
ENSMUSG00000098907	chr9	Mir7082	0.07456798	0.793265657	0.833057498	1.208022638	0.051378486	0	31	33	25	46	25	44	43	31	25	41
ENSMUSG00000101856	chr5	1700096K18Rik	-0.1049476	0.793476959	0.833180614	0.794100277	0.109654169	0	35	25	18	35	13	16	19	24	22	45
ENSMUSG00000025265	chrX	Fgd1	0.06005658	0.793634617	0.833283555	2.342420298	0.042610877	0	68	60	63	99	73	107	83	78	55	92
ENSMUSG00000009406	chrX	Elk1	-0.0412899	0.793876636	0.83347505	3.80774837	0.023878411	0	227	210	173	230	206	214	228	200	220	254
ENSMUSG00000028976	chr4	Slc2a5	0.16516981	0.794218845	0.833711419	-0.221820883	0.30733196	0	6	16	20	5	3	4	8	17	6	28
ENSMUSG00000034300	chr18	Fam53c	-0.0378429	0.794221082	0.833711419	5.114162246	0.022630239	0	490	464	502	654	499	605	503	578	470	624
ENSMUSG00000000339	chr3	Rtca	-0.0405836	0.7942875	0.83371852	4.507274246	0.024996855	0	389	328	327	367	292	330	390	337	393	363
ENSMUSG00000039735	chr3	Fnbp1l	0.05553734	0.794830384	0.834225702	2.901813232	0.041151587	0	126	96	98	140	81	104	147	89	116	157
ENSMUSG00000010054	chr9	Tusc2	0.03716016	0.794943281	0.834260451	5.205099753	0.022296557	0	609	507	473	653	470	692	575	543	660	570
ENSMUSG00000066357	chr9	Wdr6	0.04340811	0.794982877	0.834260451	4.080243404	0.027791255	0	265	268	228	269	199	305	254	311	225	294

ENSMUSG00000027333	chr2	Smox	0.05408868	0.795940172	0.835202331	5.573577395	0.050332444	0	769	726	758	685	507	476	844	821	746	1028
ENSMUSG00000002763	chr17	Pex6	0.04124154	0.796590961	0.835759723	4.850368087	0.02729041	0	341	429	381	573	397	668	470	436	396	426
ENSMUSG00000041153	chr4	Osgin2	0.05525538	0.796549664	0.835759723	2.701064341	0.039271871	0	84	80	103	116	83	119	88	118	87	118
ENSMUSG00000043342	chr2	Hoxd9	0.06556935	0.79691335	0.836035204	2.540763447	0.058251297	0	81	80	57	128	75	111	81	74	65	149
ENSMUSG00000050668	chr17	Gpatch11	0.04066163	0.797316345	0.836395199	3.849894027	0.023448185	0	227	202	197	244	180	263	251	201	256	213
ENSMUSG00000074024	chr7	4632427E13Rik	0.14036915	0.79739358	0.83641344	-0.039107837	0.140429243	0	20	13	7	6	13	21	7	8	19	18
ENSMUSG00000098134	chr12	Rnf113a2	0.05346382	0.798249143	0.837195002	2.655934068	0.037491633	0	105	95	63	107	83	98	103	87	112	113
ENSMUSG00000104049	chr12	AC120402.1	0.05346396	0.798258485	0.837195002	2.655934068	0.037496158	0	105	95	63	107	83	98	103	87	112	113
ENSMUSG00000034255	chr11	Arhgap27	-0.0576865	0.798502668	0.837388256	2.940633143	0.050236376	0	89	103	93	181	116	198	111	92	95	117
ENSMUSG00000026820	chr2	Ptges2	-0.0401499	0.798566146	0.837391991	5.522009304	0.027252317	0	626	690	690	942	539	840	698	804	669	670
ENSMUSG00000028107	chr3	Tars2	0.03624305	0.798735747	0.837506999	4.922769235	0.021826748	0	394	461	383	604	396	575	462	478	503	479
ENSMUSG00000047749	chr6	Zc3hav1l	-0.082364	0.798953699	0.837672685	1.338160216	0.082516069	0	23	33	33	43	51	26	39	37	34	54
ENSMUSG00000026049	chr1	Tex30	-0.073867	0.799117543	0.83778162	1.543043296	0.059023911	0	45	42	35	54	38	44	67	26	44	42
ENSMUSG00000060227	chr2	Casc4	0.04612386	0.799395134	0.83800978	3.129523402	0.030409606	0	133	118	132	139	108	128	139	141	150	154
ENSMUSG00000016087	chr9	Fli1	0.05062615	0.800026091	0.838608314	3.235567316	0.035996807	0	137	150	140	174	83	193	173	122	142	147
ENSMUSG00000049184	chr8	Purg	-0.0736733	0.800231283	0.838760493	1.56846212	0.057401071	0	33	35	43	61	46	54	44	29	39	62
ENSMUSG00000022226	chr14	Mcpt2	-0.3105966	0.800433901	0.838909951	2.089405759	1.637508882	0	32	54	80	92	79	329	0	0	0	2
ENSMUSG00000028407	chr4	Toporsos	-0.0487524	0.800761964	0.83912793	3.239299409	0.036101748	0	181	133	124	141	124	199	117	143	146	145
ENSMUSG00000029708	chr6	Gcc1	-0.0456568	0.800716545	0.83912793	3.36049456	0.026962403	0	144	140	144	221	127	210	172	129	152	158
ENSMUSG00000038155	chr19	Gstp2	-0.0450104	0.800998998	0.83931339	4.085172652	0.031635275	0	272	244	171	334	263	323	206	259	287	279
ENSMUSG00000023572	chr2	Ccndbp1	0.04314912	0.80151308	0.8397891	4.861108224	0.031591822	0	480	481	349	477	338	707	386	434	426	464
ENSMUSG00000067825	chr6	Pex26	-0.0539097	0.801779319	0.84000508	2.536826386	0.040671102	0	89	103	73	89	75	94	105	65	87	106
ENSMUSG00000019996	chr10	Map7	-0.1042434	0.801853903	0.84002025	0.690601389	0.100746667	0	30	16	23	20	25	10	29	24	28	25
ENSMUSG00000051232	chr11	Tmem199	0.04295831	0.801915164	0.840021461	3.712955778	0.027804281	0	212	174	167	244	162	232	253	144	225	228
ENSMUSG00000103171	chr3	DNAJC19	-0.0394025	0.802803876	0.840889378	5.21501312	0.027342834	0	662	593	482	619	440	625	668	495	662	530
ENSMUSG00000057315	chr5	Arhgap24	0.04568598	0.803358097	0.841406832	3.636024251	0.036006084	0	160	156	152	302	151	180	230	210	161	238
ENSMUSG00000055413	chr17	H2-Q5	-0.1378851	0.803661385	0.841598345	1.734883729	0.353877135	0	47	60	47	56	38	192	14	18	14	26
ENSMUSG00000091937	chr1	Gm3646	0.11987956	0.80364858	0.841598345	0.193078325	0.165619681	0	30	17	13	8	4	14	15	14	25	18
ENSMUSG00000037710	chr10	Cisd1	-0.0362525	0.804094043	0.841943615	7.069274813	0.024889817	0	1967	1908	1920	2563	1797	2446	2104	2122	2133	2002
ENSMUSG00000044864	chr3	Ankrd50	-0.0409994	0.804111575	0.841943615	3.896721111	0.025122345	0	222	202	199	313	191	266	204	243	201	276
ENSMUSG00000050549	chr3	5730508B09Rik	-0.0695025	0.804317077	0.842040741	1.960086899	0.051281398	0	65	45	47	94	42	55	73	49	61	62
ENSMUSG00000051906	chr8	Cd209f	-0.1302384	0.804324835	0.842040741	2.13181992	0.315523479	0	58	78	59	49	79	239	31	28	36	16
ENSMUSG00000052456	chr8	Asna1	-0.0352253	0.804401072	0.842057478	5.406797218	0.02209585	0	720	570	586	779	546	787	712	625	644	650
ENSMUSG00000017309	chr11	Cd300lg	-0.0415981	0.804606637	0.842209583	4.661939815	0.029536747	0	349	385	324	490	363	342	350	395	399	533
ENSMUSG00000023051	chr15	Tarbp2	0.03611629	0.804795164	0.842286017	4.612059811	0.021136355	0	372	360	311	390	350	463	434	377	360	381
ENSMUSG00000034480	chrX	Diap2	0.05906152	0.804800191	0.842286017	2.566017315	0.054078358	0	84	67	73	108	92	103	121	53	119	89
ENSMUSG00000032480	chr9	Dhx30	0.03289765	0.804971642	0.842402371	4.94147608	0.018725676	0	471	413	397	576	408	548	501	473	474	533
ENSMUSG00000090266	chr11	Mettl23	-0.0386052	0.805623531	0.843021449	4.794865514	0.025416201	0	429	391	398	517	357	380	428	416	517	471
ENSMUSG00000079614	chr18	Seh1l	0.03514668	0.805699853	0.843038193	4.79500059	0.021858517	0	433	389	343	523	358	432	531	400	466	452
ENSMUSG00000038628	chr2	Polr3k	-0.0426214	0.805781555	0.843060564	4.312358432	0.03016022	0	361	297	227	360	255	255	383	297	308	339
ENSMUSG00000036504	chr2	Phpt1	-0.0354881	0.80591345	0.843135443	5.678445868	0.023455143	0	698	763	691	966	742	1031	819	733	764	791
ENSMUSG00000027893	chr3	Ahcyl1	0.037423	0.806406007	0.843587602	5.376192857	0.02514468	0	534	581	661	718	542	771	776	533	651	711
ENSMUSG00000030930	chr7	Chst15	-0.0498192	0.807245439	0.844402534	3.491437033	0.041332836	0	138	149	193	210	152	204	162	202	112	214
ENSMUSG00000019854	chr10	Reps1	0.03579322	0.808018707	0.84514814	4.428680821	0.021995077	0	291	276	268	411	335	405	330	344	330	362
ENSMUSG00000063902	chr7	Gm7964	-0.0459458	0.808219541	0.845294941	3.568999651	0.031578923	0	147	181	136	259	175	166	222	181	166	207
ENSMUSG00000029439	chr5	Sfswap	-0.0372481	0.808396241	0.845389827	3.967957869	0.022941472	0	251	214	218	276	213	273	243	195	271	272
ENSMUSG00000052928	chr18	Ctif	-0.0427772	0.808431242	0.845389827	4.363802991	0.031986618	0	320	261	249	417	312	332	310	355	227	423
ENSMUSG00000053600	chr17	Zfp472	-0.0719864	0.808672245	0.84557858	1.41469152	0.083558062	0	37	44	34	36	41	56	30	19	55	44
ENSMUSG00000078202	chr2	Nrarp	-0.0556833	0.809000005	0.845858014	3.22314061	0.053549037	0	128	145	157	162	106	143	150	198	84	159
ENSMUSG00000027394	chr2	Ttl	-0.0391916	0.809513555	0.84626834	3.817360559	0.023188948	0	226	206	186	270	173	219	221	233	221	227
ENSMUSG00000031431	chrX	Tsc22d3	0.07091175	0.80945426	0.84626834	7.338201427	0.102235359	0	2253	2325	2819	2017	2120	6385	2323	1474	2053	1743
ENSMUSG00000017221	chr11	Psmd3	0.03453048	0.809798595	0.846503004	6.922374376	0.023982309	0	1854	1575	1562	2312	1667	2381	2042	1830	1860	1927
ENSMUSG00000089083	chr6	Rnu7	-0.1213109	0.810327321	0.846992345	0.138233417	0.120924336	0	11	21	10	20	14	10	24	7	23	12
ENSMUSG00000024620	chr18	Pdgfrb	0.04139056	0.810535809	0.847083561	5.898312949	0.034195167	0	830	797	790	1206	785	1224	941	1047	608	1136
ENSMUSG00000081600	chr11	Gm12286	-0.0916268	0.81048773	0.847083561	1.042513945	0.089090588	0	33	20	31	37	28	19	36	27	20	51
ENSMUSG00000027198	chr2	Ext2	-0.0336624	0.810614491	0.847102447	5.312999142	0.021506771	0	581	568	509	745	591	771	625	597	582	632
ENSMUSG00000029089	chr5	Pacrgl	0.08027253	0.810779819	0.847148531	1.417787792	0.06457346	0	47	35	35	34	32	64	44	36	25	47
ENSMUSG00000029710	chr5	Ephb4	0.04015555	0.810766636	0.847148531	4.79297166	0.0301029	0	370	388	380	533	366	650	357	467	350	475
ENSMUSG00000031302	chrX	Nlgn3	0.13122708	0.810853982	0.847162686	-0.113425943	0.097855053	0	10	13	7	9	17	17	15	16	12	8
ENSMUSG00000021969	chr14	Zdhhc20	-0.0870104	0.811051335	0.847305536	4.476905876	0.154237642	0	359	382	330	340	275	1038	191	183	203	218
ENSMUSG00000031303	chrX	Map3k15	0.1342346	0.811312517	0.847515041	1.378026398	0.30948549	0	12	14	18	57	76	22	21	86	23	54
ENSMUSG00000030470	chr7	Csrp3	0.13590199	0.811439767	0.847584618	6.283098547	0.380431841	0	312	458	1858	2801	379	3800	1051	1210	542	282
ENSMUSG00000028078	chr3	Dclk2	-0.0903798	0.811685755	0.847778201	0.699741701	0.073467886	0	30	22	20	24	19	29	29	26	11	24
ENSMUSG00000020160	chr11	Meis1	0.0543364	0.812504564	0.848570004	2.296801253	0.058603969	0	74	63	50	123	49	66	67	83	91	88
ENSMUSG00000037138	chr1	Aff3	-0.0621003	0.812804188	0.848819498	1.659676268	0.058920002	0	43	35	45	53	54	78	42	40	38	47

ENSMUSG00000064371	chrMT	mt-Tt	0.06912507	0.813733586	0.849663101	1.053948436	0.063360789	0	26	26	27	47	18	26	36	37	29	34
ENSMUSG00000079492	chr17	Gm11127	0.30276934	0.813730278	0.849663101	1.917864743	1.705478844	0	32	57	48	61	42	359	0	0	1	0
ENSMUSG00000070002	chr8	Ell	0.03823333	0.813969031	0.849845448	3.944308136	0.023958774	0	226	196	206	251	239	314	227	236	230	260
ENSMUSG00000039244	chr5	E130309D02Rik	0.04728147	0.814420493	0.850189782	3.505101007	0.037597337	0	116	139	169	242	163	239	185	132	166	219
ENSMUSG00000101013	chr5	A630072M18Rik	0.06491486	0.814371202	0.850189782	1.546164522	0.054757304	0	31	37	41	60	36	58	32	48	49	46
ENSMUSG00000043290	chr7	Zfp784	0.07237349	0.815315459	0.851060487	1.970856561	0.071733219	0	45	62	71	70	28	75	57	70	44	72
ENSMUSG00000039670	chr11	Oxld1	-0.0446415	0.816448698	0.852179761	3.504736209	0.032266736	0	163	179	158	242	117	176	212	140	197	178
ENSMUSG00000004768	chr1	Rab23	0.05502746	0.816713225	0.852328556	2.70452255	0.050947395	0	93	96	58	153	77	132	137	73	89	106
ENSMUSG00000024169	chr17	Ift140	-0.0499015	0.816665721	0.852328556	2.366348741	0.038533755	0	78	71	55	107	74	88	83	60	86	88
ENSMUSG00000013936	chr5	Myl2	-0.2563756	0.816981197	0.852472854	6.586759016	1.371880125	0	12	387	172	8688	145	5874	35	617	1000	62
ENSMUSG00000020167	chr10	Tcf3	-0.0327715	0.816988092	0.852472854	4.503516165	0.020620155	0	329	326	349	405	290	404	397	317	334	374
ENSMUSG00000025577	chr11	Cbx2	0.08206599	0.817080931	0.852472854	1.353604937	0.079098794	0	38	35	40	37	25	47	49	44	17	48
ENSMUSG00000041202	chr4	Pla2g2d	-0.1225673	0.817095475	0.852472854	0.183852216	0.206616227	0	12	18	13	13	21	35	13	14	1	18
ENSMUSG00000085779	chr10	Atcayos	0.06312954	0.817193507	0.852511492	6.866530353	0.088104721	0	2614	2213	1525	1192	847	1312	2183	1605	1983	2609
ENSMUSG00000022677	chr16	Fopnl	-0.0362147	0.81790099	0.853185866	5.743047427	0.027845497	0	918	783	801	879	640	764	935	792	908	892
ENSMUSG00000020519	chr11	Sap30l	-0.0397582	0.818492097	0.853738752	4.089924685	0.029373841	0	250	231	227	373	212	385	231	236	277	240
ENSMUSG00000020453	chr11	Patz1	0.03948662	0.818819863	0.854016896	3.492459736	0.024971188	0	151	174	146	209	141	238	186	159	157	187
ENSMUSG00000025218	chr19	Poll	0.03801073	0.81902048	0.854098659	4.094914641	0.028151437	0	301	252	204	272	217	243	277	279	296	300
ENSMUSG00000038042	chr13	Ptpdc1	-0.050727	0.81901798	0.854098659	2.170126647	0.04449695	0	64	67	67	71	61	67	58	62	68	96
ENSMUSG00000022428	chr15	Cby1	-0.0388517	0.819496702	0.854404035	3.522268104	0.026802542	0	180	171	163	200	144	193	152	183	200	184
ENSMUSG00000028024	chr3	Enpep	-0.0658946	0.819496715	0.854404035	3.072538711	0.08223788	0	123	134	99	134	138	64	156	90	204	140
ENSMUSG00000064354	chrMT	mt-Co2	-0.0531676	0.819441235	0.854404035	3.831752102	0.05397744	0	156	248	195	325	161	152	182	244	267	272
ENSMUSG00000012296	chr17	Tjap1	0.03651539	0.819716251	0.854569173	4.664858927	0.025554444	0	366	311	373	424	376	576	402	351	354	422
ENSMUSG00000042662	chr2	Dusp15	-0.0962224	0.819798888	0.854591576	-0.126500899	0.121214283	0	9	8	16	11	16	19	20	8	10	6
ENSMUSG00000024982	chr19	Zdhhc6	0.03389042	0.820004202	0.85474185	4.54810351	0.022029821	0	331	297	305	416	364	444	420	356	328	380
ENSMUSG00000038486	chr3	Sv2a	-0.098449	0.820223557	0.854842986	0.556373508	0.113456375	0	15	17	22	41	11	40	19	18	15	15
ENSMUSG00000041133	chrX	Smc1a	0.03360366	0.820192315	0.854842986	5.67051006	0.024474665	0	703	735	655	969	696	905	913	675	913	796
ENSMUSG00000024392	chr17	Bag6	-0.0358692	0.820458135	0.855023704	7.141542092	0.02921272	0	2078	1785	1679	2906	2275	2665	2166	2247	1917	2406
ENSMUSG00000096393	chr9	Gm590	-0.1106101	0.820736233	0.855249746	0.22106246	0.126487439	0	6	17	12	32	15	29	11	17	11	14
ENSMUSG00000021990	chr14	Spata13	-0.0554078	0.820947387	0.855406	2.857280943	0.060898548	0	104	102	139	123	71	152	90	129	69	133
ENSMUSG00000013997	chr1	Nit1	-0.0346381	0.821626665	0.855922352	4.586888288	0.024231604	0	415	350	323	383	325	359	373	385	401	401
ENSMUSG00000028089	chr3	Chd1l	-0.0396964	0.821622119	0.855922352	3.992551188	0.028339827	0	232	196	204	366	213	229	259	220	277	284
ENSMUSG00000036298	chr15	Slc2a13	-0.0908586	0.821610165	0.855922352	0.616469263	0.101241218	0	18	27	20	19	23	16	36	27	12	20
ENSMUSG00000045598	chr7	Zfp553	0.05036599	0.821937853	0.856182711	2.933998706	0.04341193	0	101	90	95	136	128	116	132	125	87	165
ENSMUSG00000028344	chr4	Invs	-0.0740675	0.822146641	0.856336373	1.516780789	0.084681505	0	35	43	48	41	40	31	38	31	71	45
ENSMUSG00000099835	chr1	Gm29668	-0.0994602	0.822235763	0.856365379	0.10465045	0.078042212	0	12	14	15	17	15	14	12	14	10	25
ENSMUSG00000041187	chr7	Prkd2	0.05118402	0.82247354	0.856549195	3.18969231	0.046353983	0	90	139	149	172	109	200	117	167	131	133
ENSMUSG00000031661	chr8	Nkd1	-0.0818857	0.823291875	0.857337549	1.474208793	0.0938417	0	32	41	23	65	45	80	33	27	34	40
ENSMUSG00000031232	chrX	Magt1	-0.036484	0.823496825	0.857487083	5.244285166	0.029379266	0	494	484	496	782	611	632	772	497	616	533
ENSMUSG00000045854	chr4	Lyrm2	0.04209747	0.823883639	0.857825951	3.628626289	0.034885527	0	219	180	174	183	139	159	219	190	221	219
ENSMUSG00000008845	chr6	Cd163	0.09029008	0.824575123	0.85841802	3.09629132	0.171285858	0	89	143	106	96	159	404	80	77	84	94
ENSMUSG00000054604	chr16	Cggbp1	0.03203599	0.824522382	0.85841802	4.885407565	0.021691912	0	443	404	390	575	372	605	551	373	436	484
ENSMUSG00000021514	chr13	Zfp369	0.05327343	0.825328942	0.859138782	1.905041358	0.046861599	0	49	53	48	61	53	69	46	71	53	61
ENSMUSG00000016984	chr11	Etaa1	-0.0700692	0.825725973	0.859488061	1.538806474	0.086457857	0	34	35	51	49	42	49	70	22	50	32
ENSMUSG00000018765	chr11	Fxr2	-0.0334877	0.826330336	0.860053081	6.601005828	0.026832534	0	1488	1273	1197	1893	1493	1514	1527	1406	1560	1810
ENSMUSG00000072694	chr5	1500011B03Rik	0.07874632	0.826608969	0.86027902	2.219605051	0.106698747	0	76	70	63	52	62	168	57	41	64	60
ENSMUSG00000079605	chr17	Zbtb9	-0.0480747	0.826800163	0.86041393	2.459644334	0.038450494	0	97	64	76	106	67	114	79	71	84	86
ENSMUSG00000019256	chr12	Ahr	-0.081115	0.827178	0.860743036	1.245666595	0.082244984	0	38	25	19	71	25	34	41	32	30	41
ENSMUSG00000073678	chr1	Pgap1	-0.0570816	0.82731748	0.860760001	2.500242527	0.06074264	0	64	82	88	101	84	66	114	54	91	119
ENSMUSG00000087080	chr11	Gm12199	0.09181502	0.827312816	0.860760001	1.889672843	0.17549037	0	87	66	29	23	48	23	94	52	55	76
ENSMUSG00000053286	chr1	Trmt1l	-0.0335532	0.827515393	0.860901827	4.012686879	0.021818098	0	249	229	211	293	227	258	268	253	258	252
ENSMUSG00000003778	chr18	Brd8	-0.0338292	0.827849836	0.861185657	4.166395931	0.024229821	0	281	249	259	332	227	356	300	216	309	265
ENSMUSG00000021763	chr13	BC067074	0.06930455	0.829072729	0.862393603	2.069886054	0.088704699	0	63	71	35	62	64	92	49	91	34	75
ENSMUSG00000080850	chr4	Gm12439	0.03573882	0.82931359	0.862579946	4.501124352	0.029508606	0	335	268	255	430	376	319	409	364	367	394
ENSMUSG00000031250	chrX	Tnmd	0.0632976	0.829413592	0.862619762	5.667320071	0.100210562	0	1395	592	725	631	344	1417	983	489	718	709
ENSMUSG00000030498	chr7	Gas2	-0.06281	0.829861917	0.863021814	2.123985719	0.069058034	0	95	55	54	70	49	63	85	35	75	82
ENSMUSG00000020361	chr11	Hspa4	0.03224169	0.830542047	0.863664855	7.021215416	0.026644998	0	1757	1701	1617	2673	1896	2272	2385	2045	1986	2023
ENSMUSG00000030643	chr7	Rab30	-0.0599872	0.830687416	0.863751754	1.803661792	0.060076249	0	62	51	54	47	40	56	46	64	60	41
ENSMUSG00000056592	chr7	Zfp658	0.09574847	0.831044267	0.864058523	0.66811192	0.10858874	0	18	21	21	26	19	53	24	11	18	20
ENSMUSG00000025204	chr19	Ndufb8	-0.0345197	0.831202787	0.864094774	8.545450528	0.031139487	0	5022	5596	5529	7846	4420	7034	5362	5408	6541	5794
ENSMUSG00000053838	chr11	Nudcd3	-0.0380801	0.83119558	0.864094774	6.497745604	0.036820466	0	1304	1232	1213	1755	1334	989	1588	1465	1512	1651
ENSMUSG00000040102	chr6	Klhl42	-0.0415834	0.831499962	0.864339417	2.608238504	0.039301334	0	77	96	94	95	86	123	102	84	71	104
ENSMUSG00000024160	chr17	Spsb3	0.03759545	0.832060897	0.864793864	4.978427839	0.035047262	0	389	407	420	611	489	361	589	496	512	623
ENSMUSG00000079481	chrX	Nhsl2	-0.0574556	0.832015509	0.864793864	2.465740938	0.06864264	0	72	62	57	125	99	143	81	68	53	94
ENSMUSG00000026277	chr1	Stk25	0.03107442	0.83220329	0.864877542	6.079940501	0.02455208	0	1090	987	852	1170	884	1100	1069	1107	1086	1194

ENSMUSG00000032290	chr9	Ptpn9	0.03643172	0.833758804	0.866429701	3.599427469	0.025715779	0	175	164	174	217	154	251	227	143	182	197
ENSMUSG00000039196	chr4	Orm1	0.15574802	0.834155464	0.866777454	0.32353742	0.512830802	0	0	43	16	2	15	9	13	30	20	24
ENSMUSG00000034449	chr11	Dhrs11	0.03550701	0.834518875	0.867090611	4.928545263	0.032451365	0	404	446	446	631	327	445	410	455	568	618
ENSMUSG00000041268	chr9	Dmxl2	-0.047748	0.834613576	0.867124542	2.444953789	0.044348144	0	75	71	75	99	83	88	89	52	98	102
ENSMUSG00000005069	chr6	Pex5	0.02848102	0.835103162	0.867568705	5.165631691	0.020215293	0	520	522	471	685	455	643	561	567	540	640
ENSMUSG00000024079	chr17	Eif2ak2	0.04243962	0.83540359	0.867816306	3.177821911	0.036124231	0	147	108	130	153	117	122	180	114	164	158
ENSMUSG00000002345	chr8	2310045N01Rik	0.04661631	0.835501479	0.867853488	3.413185669	0.047794689	0	149	158	120	169	172	272	161	186	108	154
ENSMUSG00000051456	chr13	Hspb3	0.03493962	0.835797484	0.868096435	5.194884025	0.03153	0	671	556	432	558	463	594	539	698	513	657
ENSMUSG00000047757	chrX	Fancb	0.10685327	0.836431264	0.868690149	0.352446276	0.124336512	0	17	25	19	10	10	24	21	8	28	17
ENSMUSG00000040713	chr1	Creg1	-0.0361971	0.836710233	0.868915308	5.843391938	0.035924343	0	869	861	736	1002	849	1131	978	513	881	1177
ENSMUSG00000028795	chr4	Ccdc28b	-0.0451947	0.836811867	0.868956285	4.584451883	0.052759262	0	470	385	304	313	316	257	387	343	532	376
ENSMUSG00000022350	chr15	E430025E21Rik	0.02955898	0.837049117	0.869138072	4.983764115	0.021235398	0	467	457	410	542	446	580	587	417	531	492
ENSMUSG00000043929	chrX	Klhl15	-0.0589524	0.837452547	0.86949237	1.508069402	0.061087127	0	39	36	44	57	32	56	59	40	25	39
ENSMUSG00000022210	chr14	Dhrs4	-0.0364273	0.837754619	0.869741387	4.891399241	0.033010101	0	334	456	416	724	340	560	402	458	505	456
ENSMUSG00000061731	chr15	Ext1	-0.0326139	0.837844118	0.869769694	4.265015758	0.02719658	0	296	284	296	328	233	367	373	211	275	330
ENSMUSG00000025809	chr8	Itgb1	0.03090757	0.837932739	0.869797086	8.290176172	0.02705976	0	4907	4265	4339	5803	3854	6507	5320	4358	4803	4985
ENSMUSG00000001158	chr6	Snrnp27	-0.0314292	0.839127855	0.870915963	5.619214684	0.026462746	0	818	743	663	884	595	817	846	695	902	690
ENSMUSG00000028862	chr4	Map3k6	0.10661271	0.839135257	0.870915963	1.233377622	0.216484359	0	35	25	23	39	37	113	19	16	29	18
ENSMUSG00000029388	chr5	Eif2b1	-0.0307685	0.839712738	0.871450599	5.261855372	0.024459037	0	523	537	508	814	525	556	682	540	631	675
ENSMUSG00000040957	chr18	Cables1	-0.0609982	0.839804685	0.87148131	1.57434974	0.077649646	0	27	47	38	52	52	79	40	31	43	38
ENSMUSG00000021548	chr13	Ccnh	-0.0313044	0.840259609	0.871842373	4.13795432	0.023030511	0	274	274	221	308	240	265	303	247	300	294
ENSMUSG00000038168	chr16	Leprel1	0.06997696	0.840277387	0.871842373	2.112679052	0.115001311	0	49	57	53	105	47	156	68	42	34	61
ENSMUSG00000071180	chr13	Smim15	-0.036116	0.840600074	0.872112437	3.996899597	0.032752176	0	220	229	261	331	164	336	293	185	225	251
ENSMUSG00000026821	chr2	Ralgds	0.028197	0.840762518	0.872216222	5.079401328	0.020041044	0	501	495	493	566	425	650	549	488	492	610
ENSMUSG00000030222	chr6	Rerg	-0.0878186	0.841161839	0.872565714	0.373359652	0.131738223	0	23	19	23	9	14	19	24	23	6	21
ENSMUSG00000015672	chr13	Mrpl32	-0.0295927	0.841817605	0.873077675	4.446992171	0.021246978	0	327	333	314	416	250	357	374	331	325	365
ENSMUSG00000020743	chr11	Mif4gd	-0.0307	0.841905254	0.873077675	5.131482312	0.025283654	0	468	512	418	693	551	632	510	599	469	611
ENSMUSG00000025889	chr6	Snca	0.13433435	0.841904622	0.873077675	0.025014267	0.399875825	0	13	5	21	18	6	29	1	2	11	35
ENSMUSG00000042429	chr1	Adora1	0.11963826	0.841774856	0.873077675	2.212012976	0.40345388	0	36	74	35	82	95	24	20	179	10	139
ENSMUSG00000041459	chr4	Tardbp	-0.0302804	0.842045683	0.873158515	6.599458833	0.026678038	0	1560	1401	1227	1762	1358	1729	1767	1299	1664	1375
ENSMUSG00000048967	chr8	Yjefn3	-0.0487074	0.84228779	0.87334477	2.7313078	0.052983189	0	95	104	78	123	95	167	82	95	110	72
ENSMUSG00000032583	chr9	Mon1a	0.03552236	0.842842518	0.873855122	3.356324439	0.026912683	0	118	147	152	182	144	175	167	155	171	167
ENSMUSG00000009733	chr15	Tfcp2	-0.0355947	0.843145467	0.874104373	3.201380095	0.029886032	0	124	144	126	147	139	151	136	158	136	148
ENSMUSG00000099312	chrX	Gm27733	0.34137916	0.843300019	0.874199753	0.463065099	2.751562747	0	0	0	0	42	41	122	0	0	0	0
ENSMUSG00000054580	chr2	Pla2r1	0.05118182	0.844105737	0.874970095	1.866949753	0.051327094	0	50	53	53	58	43	45	61	66	48	71
ENSMUSG00000026782	chr1	Abi2	0.03546461	0.844657301	0.875354007	3.382066799	0.0303422	0	166	141	150	189	115	145	204	147	168	186
ENSMUSG00000030727	chr7	Rabep2	0.15232013	0.844664005	0.875354007	6.049666983	0.697763054	0	308	333	153	1429	2441	280	154	3016	104	1886
ENSMUSG00000031691	chr8	Tnpo2	0.02947831	0.844564052	0.875354007	5.116914513	0.024203514	0	549	487	426	667	440	777	608	463	522	505
ENSMUSG00000045932	chr19	Ifit2	-0.065616	0.845043561	0.875682421	2.437300724	0.112396814	0	97	71	94	95	47	50	98	56	53	168
ENSMUSG00000025978	chr1	Rftn2	0.04682385	0.845382793	0.875969003	2.796095298	0.050226593	0	111	102	92	119	77	182	92	110	74	114
ENSMUSG00000019948	chr10	Actr6	-0.0464735	0.846619477	0.877150868	2.176334795	0.042530227	0	71	57	62	80	63	55	77	63	71	86
ENSMUSG00000064368	chrMT	mt-Nd6	-0.102149	0.846648913	0.877150868	6.66217902	0.327018372	0	650	718	1064	3976	1835	334	542	3453	947	2375
ENSMUSG00000060121	chr12	Gemin2	0.03999229	0.846799118	0.877241456	2.660507782	0.038254357	0	98	95	71	99	91	93	126	87	108	98
ENSMUSG00000033819	chr15	Ppp1r16a	-0.0286605	0.847211746	0.877603866	4.580578677	0.022445235	0	382	313	324	423	349	423	326	358	400	416
ENSMUSG00000028452	chr4	Vcp	0.02895898	0.848069798	0.878362494	8.949791622	0.02722896	0	7917	6627	6278	9105	6693	8088	8593	7818	7309	8937
ENSMUSG00000034994	chr10	Eef2	-0.0318169	0.848061849	0.878362494	10.18574415	0.032983177	0	16408	16194	13971	23261	18380	22460	17868	18271	14152	21747
ENSMUSG00000040260	chr17	Daam2	-0.0445404	0.849751476	0.880039024	3.664973481	0.055946261	0	213	159	150	241	192	235	157	266	104	247
ENSMUSG00000015536	chr13	Mocs2	0.03223578	0.850187374	0.880359987	5.159321814	0.032134522	0	579	543	441	596	464	461	642	453	674	702
ENSMUSG00000029480	chr5	Dhx37	0.04152716	0.8501564	0.880359987	2.747553925	0.042406209	0	93	76	72	146	103	135	130	94	101	88
ENSMUSG00000036854	chr7	Hspb6	-0.045089	0.850320476	0.88043258	9.349702962	0.068061333	0	5571	7479	9184	19483	9191	11139	11604	12419	8575	8428
ENSMUSG00000025504	chr7	Eps8l2	-0.0740931	0.850398092	0.880447717	1.031269741	0.079299923	0	28	23	20	43	34	25	19	39	33	35
ENSMUSG00000026003	chr1	Acadl	-0.039483	0.850479293	0.880466563	8.170490519	0.051984367	0	2626	4244	3920	8023	3529	5415	3773	4732	4335	4932
ENSMUSG00000022362	chr15	9130401M01Rik	0.03142308	0.850639168	0.880566848	3.733571983	0.024858929	0	197	168	205	229	171	231	254	189	218	196
ENSMUSG00000031652	chr8	N4bp1	-0.0306521	0.851278999	0.881163923	4.942246016	0.028790814	0	388	411	389	668	472	694	471	450	385	495
ENSMUSG00000018433	chr11	Nol11	-0.0307443	0.851947247	0.881742477	3.959024753	0.025813974	0	216	216	196	333	213	292	297	185	217	265
ENSMUSG00000061979	chr5	Wbscr16	0.03077775	0.851964111	0.881742477	4.487595892	0.028116972	0	326	304	328	417	275	452	388	300	424	280
ENSMUSG00000035778	chr2	Ggta1	0.03817872	0.852283476	0.882007691	4.119363405	0.042386856	0	203	249	240	365	223	402	357	155	245	292
ENSMUSG00000103653	chr1	Wl1-1003N17.1	0.04519523	0.852700278	0.882373692	3.678033807	0.061311105	0	209	152	136	264	180	396	129	173	189	180
ENSMUSG00000003346	chr10	Abhd17a	-0.0264812	0.853171958	0.882796423	5.774567555	0.022850521	0	838	759	746	1005	766	996	774	774	879	1005
ENSMUSG00000069049	chrY	Eif2s3y	-0.2146864	0.853605417	0.883179547	4.801126706	1.496864334	0	721	737	665	1	1	1	526	478	570	465
ENSMUSG00000017286	chr11	Glod4	0.02752917	0.854144988	0.883541585	4.9275571	0.024052752	0	476	452	362	540	412	458	532	417	566	519
ENSMUSG00000026991	chr2	Pkp4	-0.0290562	0.854108229	0.883541585	3.790754162	0.024025288	0	189	191	188	272	197	286	222	176	187	247
ENSMUSG00000102827	chr18	RP23-56B11.5	0.07335654	0.854140939	0.883541585	0.446322886	0.074781104	0	25	15	17	21	12	24	19	22	25	13
ENSMUSG00000020088	chr10	Sar1a	-0.0266411	0.854981877	0.884341823	7.176462465	0.024812944	0	2257	2143	1962	2643	1888	2637	2430	1973	2424	2250
ENSMUSG00000035234	chr5	Fam175a	-0.0387081	0.855790353	0.885112557	2.17446863	0.037964516	0	73	65	65	74	54	75	76	56	62	86

ENSMUSG00000026755	chr2	Arpc5l	-0.0288699	0.856163697	0.885433167	6.362714778	0.028859259	0	1313	1143	1114	1648	1017	1406	1530	1142	1454	1104
ENSMUSG00000039253	chr11	Fn3krp	-0.039203	0.856346669	0.885556866	2.50501438	0.037795554	0	86	77	78	94	83	85	77	92	81	111
ENSMUSG00000019478	chr8	Rab4a	-0.0349338	0.856523319	0.885674009	4.392430174	0.039356185	0	368	253	304	351	295	270	305	351	265	488
ENSMUSG00000021226	chr12	Acot2	0.04360547	0.85678971	0.885687352	2.597753745	0.059887005	0	51	96	71	158	69	92	93	99	101	104
ENSMUSG00000038909	chr11	Kat7	-0.0265377	0.856606144	0.885687352	4.872406067	0.022536419	0	435	372	398	555	439	476	533	440	381	534
ENSMUSG00000041354	chr17	Rgl2	-0.0261975	0.856767495	0.885687352	4.995965886	0.023077869	0	475	507	451	550	404	654	471	402	515	546
ENSMUSG00000056698	chr6	Elmod3	0.03609156	0.85673232	0.885687352	3.075656218	0.033547515	0	124	139	104	158	90	166	116	120	121	167
ENSMUSG00000027077	chr2	Smtnl1	-0.067644	0.857235962	0.886083115	5.070396952	0.16143961	0	172	373	553	1244	340	649	279	808	581	307
ENSMUSG00000020173	chr11	Cobl	0.02836054	0.857487431	0.886277498	5.434317823	0.027687604	0	646	582	525	787	648	717	592	699	649	895
ENSMUSG00000048285	chr12	Frmd6	-0.0265434	0.857552234	0.886278934	4.867231814	0.023746432	0	429	440	392	514	409	645	444	444	374	460
ENSMUSG00000053279	chr19	Aldh1a1	-0.0468915	0.857664389	0.886329303	5.095995377	0.07866482	0	329	763	681	465	297	413	600	428	678	604
ENSMUSG00000043411	chr4	Usp48	0.02738137	0.857765499	0.886368253	4.493257147	0.022886149	0	309	300	282	436	334	471	372	289	351	376
ENSMUSG00000035441	chr11	Myo1d	0.04705292	0.858222592	0.886775022	3.291573826	0.06658555	0	139	155	129	182	107	261	195	98	77	190
ENSMUSG00000027835	chr3	Pdcd10	-0.0392521	0.858348523	0.886839577	3.440687363	0.048426861	0	175	152	152	211	126	177	232	86	204	171
ENSMUSG00000031107	chrX	Rbmx2	-0.0501698	0.859508654	0.887972572	1.55899425	0.058457134	0	55	37	39	48	35	65	57	32	31	44
ENSMUSG00000038646	chr7	Fam103a1	-0.0420134	0.859939407	0.888351922	3.300471226	0.049377731	0	165	140	127	188	120	100	188	110	185	197
ENSMUSG00000048402	chr1	Gli2	-0.052534	0.860527307	0.888893544	1.409979008	0.076476204	0	31	37	28	48	48	53	42	46	19	44
ENSMUSG00000000078	chr13	Klf6	0.03596136	0.860840805	0.889069241	5.41679616	0.046307156	0	494	624	685	739	578	1094	730	379	716	661
ENSMUSG00000028116	chr3	Myoz2	0.09305526	0.860776579	0.889069241	6.907334972	0.331468241	0	268	1059	1229	5817	1103	5192	866	1931	1421	956
ENSMUSG00000038152	chr13	5033430I15Rik	-0.0584635	0.86088824	0.889069241	1.61769177	0.054023487	0	36	39	42	68	41	43	49	59	38	45
ENSMUSG00000071984	chr17	Fndc1	0.03565464	0.861250088	0.889377216	6.508173951	0.04819521	0	1454	1136	1215	1498	1365	2087	1228	1524	819	1935
ENSMUSG00000028405	chr4	Aco1	0.02616962	0.862279783	0.890374751	4.821279359	0.023891043	0	369	487	353	505	366	467	478	473	407	490
ENSMUSG00000024269	chr18	Tpgs2	0.03167348	0.862500191	0.890470759	3.150269405	0.027880139	0	125	110	111	166	135	173	147	126	147	131
ENSMUSG00000039166	chr10	Akap7	0.0285436	0.862456712	0.890470759	3.345483796	0.024285656	0	157	147	122	195	125	204	161	143	149	175
ENSMUSG00000038797	chr7	Zscan2	-0.0536732	0.862573167	0.89048032	0.665867404	0.059245398	0	28	22	19	25	17	24	20	25	18	30
ENSMUSG00000097867	chr16	1110054M08Rik	0.03022333	0.862929202	0.890782076	4.003440009	0.029016061	0	258	224	186	266	238	350	258	267	221	221
ENSMUSG00000021692	chr13	Dimt1	-0.0502121	0.8633771	0.891178608	1.807120852	0.059139813	0	62	42	53	64	36	62	67	32	63	48
ENSMUSG00000003199	chr17	Mpnd	-0.0260226	0.863627311	0.891371044	5.662221112	0.026100663	0	816	813	713	778	654	997	794	731	819	756
ENSMUSG00000099881	chr8	2810013P06Rik	-0.0394647	0.864497848	0.892203657	2.717250537	0.039087053	0	103	108	92	115	70	88	103	97	103	127
ENSMUSG00000020471	chr11	Pold2	0.0264779	0.865018887	0.892659098	4.62022942	0.025381171	0	355	352	302	435	363	370	395	355	478	409
ENSMUSG00000063889	chr18	Crem	-0.0286226	0.865066888	0.892659098	3.400689043	0.027450002	0	157	146	170	186	126	181	170	134	158	204
ENSMUSG00000000399	chr6	Ndufa9	-0.0280304	0.86554633	0.893087893	8.173560031	0.032358372	0	3750	4203	4172	6538	3356	5508	4167	4798	4230	4634
ENSMUSG00000015971	chr14	Actr8	0.02533337	0.865911514	0.893332791	4.667759974	0.023192243	0	407	353	341	450	321	422	395	339	477	449
ENSMUSG00000072847	chr11	A530017D24Rik	-0.0408002	0.8658768	0.893332791	2.226992724	0.042401848	0	69	69	50	94	65	62	77	70	67	90
ENSMUSG00000022323	chr15	Hrsp12	-0.0400532	0.866565773	0.893941781	2.726555995	0.04864161	0	119	101	63	123	88	76	113	97	110	124
ENSMUSG00000021621	chr13	Zcchc9	0.02826093	0.866954212	0.894276482	3.502771543	0.024250807	0	154	147	165	211	152	197	191	163	159	217
ENSMUSG00000055963	chr4	Triqk	0.07175673	0.867074764	0.894334826	0.399782548	0.111867685	0	24	11	22	21	9	17	23	30	11	18
ENSMUSG00000001054	chr11	Rmnd5b	0.0266125	0.867564472	0.894773895	3.874112514	0.024807643	0	192	225	171	305	191	295	218	224	218	247
ENSMUSG00000034083	chr6	Ccdc174	0.03053087	0.867978751	0.895135111	3.164285175	0.030190308	0	161	127	96	158	113	162	151	116	144	159
ENSMUSG00000024011	chr17	Pi16	0.05753303	0.868116697	0.895211315	5.465895432	0.138809599	0	539	694	563	749	661	1885	336	756	378	415
ENSMUSG00000035495	chr4	Tstd2	0.03026694	0.868505364	0.895546035	3.95236324	0.034209163	0	204	190	181	295	265	250	199	282	244	285
ENSMUSG00000027173	chr2	Depdc7	-0.0576424	0.868725119	0.895706548	1.534328649	0.073402212	0	45	50	34	59	25	51	43	36	62	29
ENSMUSG00000053581	chr5	Zfand2a	0.02913998	0.869393722	0.896329792	3.861708645	0.028167131	0	237	203	207	236	178	260	254	162	270	247
ENSMUSG00000006445	chr4	Epha2	0.04893691	0.870360523	0.89724688	2.243327584	0.074327109	0	61	81	58	91	49	76	129	73	55	50
ENSMUSG00000037243	chr11	Zfp692	0.03921798	0.870411649	0.89724688	2.562676707	0.044895336	0	104	84	76	81	77	98	96	92	115	75
ENSMUSG00000039063	chr2	Echdc3	-0.0361007	0.870501931	0.897273765	3.140191198	0.03883239	0	146	160	103	138	107	117	138	129	159	154
ENSMUSG00000070327	chr11	Rnf213	0.03055021	0.870566248	0.897273885	4.766195253	0.036844237	0	353	384	423	501	338	417	591	312	339	594
ENSMUSG00000045268	chr4	Zfp691	-0.0321704	0.870697811	0.897277143	3.481126542	0.031079386	0	175	164	153	208	135	140	174	188	181	202
ENSMUSG00000099143	chr7	Gm27483	0.1142392	0.870691088	0.897277143	1.757948336	0.495664855	0	42	36	12	84	66	9	13	145	9	89
ENSMUSG00000002372	chr17	Ranbp3	0.02379706	0.870836434	0.897353831	5.622561805	0.023082703	0	708	655	659	870	737	950	863	652	812	785
ENSMUSG00000009907	chr1	Vps4b	-0.025796	0.870987507	0.897443335	4.629728845	0.026734726	0	357	372	329	475	327	486	421	255	429	418
ENSMUSG00000039233	chr13	Tbce	-0.0279655	0.871070784	0.897462976	4.309844046	0.029873575	0	355	290	264	340	236	332	350	234	388	290
ENSMUSG00000050088	chr17	1600012H06Rik	0.03003921	0.871220143	0.897550695	4.06929482	0.032246472	0	284	226	253	242	214	245	283	236	243	369
ENSMUSG00000044086	chr6	Lmod3	0.02798191	0.871865989	0.898149853	7.483234418	0.035784868	0	2187	2497	2375	4058	2273	3099	2594	3517	2513	2937
ENSMUSG00000100863	chr4	Gm12669	-0.0325889	0.872381431	0.898614599	2.881741363	0.034988547	0	110	105	104	121	104	147	132	110	110	87
ENSMUSG00000007603	chr17	Dus3l	0.02531185	0.872590939	0.898744717	4.168215983	0.022787868	0	278	283	240	297	219	363	280	281	257	294
ENSMUSG00000083396	chr7	Gm15542	-0.0610292	0.872636363	0.898744717	0.94337357	0.089331454	0	23	27	19	41	28	44	41	18	26	16
ENSMUSG00000071528	chr19	Usmg5	-0.0287871	0.872877402	0.898926724	7.405477835	0.038100432	0	2748	2797	2730	2864	1599	2885	2658	2371	3207	2543
ENSMUSG00000032392	chr9	Parp16	-0.0375005	0.873609808	0.899614698	2.808573617	0.048847221	0	99	97	126	133	66	95	106	113	95	144
ENSMUSG00000022085	chr14	Pebp4	-0.0877354	0.874741536	0.900713748	-0.049935903	0.135864396	0	15	15	6	17	12	4	14	8	19	21
ENSMUSG00000056763	chr1	Cspp1	-0.0439149	0.874951939	0.900864026	1.862323393	0.047892461	0	60	43	49	69	46	48	67	42	64	61
ENSMUSG00000032239	chr9	Rp9	-0.0239804	0.875224198	0.901077966	4.766803839	0.023876537	0	436	368	372	510	358	579	382	418	432	389
ENSMUSG00000024769	chr19	Cdc42bpg	-0.0344948	0.87540982	0.901202685	2.812724066	0.041453277	0	96	92	111	118	101	96	121	114	83	142
ENSMUSG00000034292	chr1	Traf3ip1	-0.0391174	0.875658273	0.901392061	2.376409842	0.040478955	0	78	62	70	112	65	92	91	56	88	83
ENSMUSG00000039205	chr2	Ciz1	0.02386937	0.876261575	0.901946662	4.677562354	0.023651147	0	361	310	358	464	389	459	362	392	400	485

ENSMUSG00000057409	chr17	Zfp53	-0.0473479	0.876360826	0.901982392	1.093655805	0.073647265	0	36	40	21	32	23	45	30	22	40	25
ENSMUSG00000004895	chr3	Prcc	-0.022187	0.876516505	0.902076191	5.244536681	0.021512131	0	546	500	496	761	552	742	575	557	568	630
ENSMUSG00000039725	chr2	2810408M09Rik	-0.0278756	0.876610014	0.902105998	3.267520697	0.025284079	0	159	132	116	182	130	190	147	138	148	148
ENSMUSG00000021395	chr13	Spin1	-0.0236286	0.876688206	0.902120039	4.4153585	0.021602348	0	332	304	275	429	267	358	353	326	286	398
ENSMUSG00000026797	chr2	Stxbp1	0.03480795	0.876822707	0.9021256	2.838175556	0.040922233	0	100	96	85	146	95	146	132	117	71	118
ENSMUSG00000028037	chr3	Ifi44	0.07982831	0.876815457	0.9021256	0.835633888	0.185861533	0	35	10	25	28	22	22	29	14	11	65
ENSMUSG00000030825	chr7	Hsd17b14	0.07550131	0.877072491	0.902316167	0.468761206	0.123479539	0	24	17	7	20	23	38	19	16	9	25
ENSMUSG00000002342	chr8	Tmem161a	-0.0249515	0.877285582	0.902451125	6.225910023	0.029414436	0	1122	1059	945	1431	1082	1004	1176	1213	1181	1442
ENSMUSG00000050323	chr4	Ndufaf6	0.02982446	0.877332816	0.902451125	3.869310869	0.036776383	0	219	201	193	232	218	163	242	229	247	306
ENSMUSG00000064138	chr13	Fam172a	0.03255673	0.877414631	0.902468861	3.454574065	0.03672306	0	186	164	147	173	127	168	191	116	206	216
ENSMUSG00000036864	chr7	Proser3	-0.0472161	0.877492878	0.902482925	1.443774255	0.068151798	0	37	32	31	56	42	42	28	32	41	66
ENSMUSG00000024817	chr19	Uhrf2	0.02857125	0.877875172	0.902765441	4.03425989	0.031841387	0	246	229	205	305	220	399	288	176	232	265
ENSMUSG00000098954	chr4	Mir7658	-0.0585789	0.877896759	0.902765441	0.273572002	0.07501734	0	23	18	16	15	10	21	15	15	13	23
ENSMUSG00000093571	chr7	Gm24757	0.04851398	0.878335758	0.903150424	1.739298054	0.063376685	0	61	52	45	39	36	65	66	37	57	43
ENSMUSG00000017344	chr11	Vtn	0.02573141	0.878616953	0.903373099	5.091533536	0.031686525	0	446	484	450	713	440	662	426	646	431	632
ENSMUSG00000073422	chr17	H2-Ke6	-0.0261756	0.878957812	0.903657083	5.062414186	0.032120558	0	411	518	486	685	419	779	413	457	559	503
ENSMUSG00000024847	chr19	Aip	0.02218813	0.879270548	0.903912114	5.83722302	0.023503083	0	985	778	692	955	807	1058	923	856	855	1013
ENSMUSG00000097666	chr18	A330094K24Rik	-0.047594	0.879877683	0.904469733	1.886066028	0.072047491	0	65	52	63	44	43	39	50	67	58	70
ENSMUSG00000026843	chr2	Fubp3	0.02613327	0.88061514	0.905030426	3.510706076	0.026678311	0	158	179	147	205	145	184	232	157	161	197
ENSMUSG00000036782	chrX	Klhl13	-0.0405147	0.880617399	0.905030426	3.324646638	0.068124891	0	108	129	126	234	160	106	138	180	114	254
ENSMUSG00000059482	chr4	2610301B20Rik	0.03807444	0.880507162	0.905030426	2.348416184	0.047048071	0	91	72	70	84	49	90	109	69	74	70
ENSMUSG00000071604	chr19	Fam189a2	0.02157491	0.880744344	0.905094335	4.961877085	0.021469225	0	446	408	377	583	488	547	490	458	496	565
ENSMUSG00000028194	chr3	Ddah1	0.03472213	0.881484373	0.905721629	3.662623057	0.055870516	0	118	177	236	277	123	257	181	240	146	213
ENSMUSG00000040852	chr17	Plekhh2	-0.0431551	0.881421787	0.905721629	2.051971216	0.057422566	0	72	57	68	68	39	76	56	79	46	66
ENSMUSG00000001569	chr5	Nom1	-0.02429	0.881766549	0.905944959	3.930050296	0.024022271	0	239	230	185	265	217	226	270	246	215	264
ENSMUSG00000049097	chr3	Ankrd34a	-0.0648375	0.882694397	0.906831586	1.197494684	0.115086434	0	33	35	26	42	30	10	40	39	31	51
ENSMUSG00000030051	chr6	Aplf	-0.0333732	0.883025949	0.907044441	2.21212839	0.045757852	0	58	63	61	81	76	83	69	49	87	77
ENSMUSG00000047246	chr13	Hist1h2be	-0.0323883	0.883096287	0.907044441	3.963427146	0.0469411	0	271	213	195	286	206	141	280	259	235	323
ENSMUSG00000049659	chr11	Aftph	-0.0208689	0.883034247	0.907044441	4.564088214	0.019481267	0	335	330	332	457	319	414	377	333	369	418
ENSMUSG00000020740	chr11	Gga3	0.02552465	0.883212954	0.907097608	4.047893087	0.028417254	0	231	203	199	309	273	349	271	265	217	256
ENSMUSG00000031906	chr8	Smpd3	0.07486757	0.883616276	0.907445152	0.550324522	0.122029228	0	14	19	14	19	30	20	25	30	8	29
ENSMUSG00000026974	chr2	Zmynd19	-0.0243208	0.883787971	0.907488111	4.093697102	0.024258824	0	292	226	219	324	220	249	307	259	275	278
ENSMUSG00000091475	chr17	2810468N07Rik	-0.0498823	0.88376545	0.907488111	0.799816214	0.078497913	0	33	25	30	18	15	28	27	24	20	31
ENSMUSG00000026176	chr1	Ctdsp1	-0.0228344	0.884010078	0.907582814	6.607600412	0.028274929	0	1269	1362	1215	1958	1546	1986	1435	1473	1387	1643
ENSMUSG00000048087	chr16	Gm4737	-0.0590253	0.883970715	0.907582814	0.709558777	0.092834491	0	25	21	18	22	28	13	26	17	35	29
ENSMUSG00000007107	chr1	Atp1a4	-0.0628262	0.884116059	0.907624948	0.160145944	0.112644674	0	15	12	11	16	21	16	15	9	9	31
ENSMUSG00000025509	chr7	Pnpla2	-0.0275589	0.884367285	0.907816171	7.375238498	0.042165408	0	1745	2608	2313	3941	2065	3430	2190	2625	2073	3175
ENSMUSG00000036009	chr10	Mettl25	0.04200936	0.885128799	0.908531147	1.767228201	0.046769388	0	49	56	43	62	32	69	60	45	47	52
ENSMUSG00000020216	chr10	Jsrp1	0.02168714	0.885274203	0.908613664	8.557055504	0.026845928	0	5931	4901	5114	6857	5114	6443	5865	5955	6297	6347
ENSMUSG00000052563	chr11	D930048N14Rik	-0.0584286	0.885387637	0.908663359	0.174305632	0.11284114	0	23	21	13	13	6	21	10	20	15	14
ENSMUSG00000035171	chr19	1110059E24Rik	0.02845778	0.885526047	0.908738677	3.175516017	0.035156535	0	147	128	146	141	93	169	162	151	121	132
ENSMUSG00000038210	chr6	Hoxa11	0.0530811	0.885733429	0.908884758	0.764146608	0.087678125	0	30	20	23	31	12	17	23	21	32	37
ENSMUSG00000011958	chr9	Bnip2	-0.0213174	0.886032416	0.909124811	6.386270326	0.025258654	0	1346	1186	1166	1515	1070	1622	1375	1176	1391	1221
ENSMUSG00000026535	chr1	Ifi202b	-0.1984275	0.88619231	0.909135918	2.913353635	2.036448623	0	104	121	129	114	111	622	0	0	0	0
ENSMUSG00000028221	chr4	Tmem55a	0.02093126	0.886238391	0.909135918	4.900161117	0.023194229	0	417	405	390	601	403	439	584	439	479	500
ENSMUSG00000047187	chr4	Rab2a	-0.0213114	0.88615776	0.909135918	7.039715512	0.025614187	0	2183	1884	1683	2436	1723	2065	2259	1839	2174	2311
ENSMUSG00000026442	chr1	Nfasc	-0.0805503	0.886410286	0.909186319	0.604811085	0.213528393	0	18	4	30	32	23	54	14	16	16	13
ENSMUSG00000048240	chr10	Gng7	-0.0496973	0.886417629	0.909186319	1.106028809	0.090503239	0	16	37	32	27	39	31	31	33	23	45
ENSMUSG00000038550	chr3	Ciart	0.07792142	0.886806085	0.909518004	1.241110545	0.227774345	0	36	40	57	10	13	82	31	22	26	32
ENSMUSG00000016427	chrX	Ndufa1	-0.0225004	0.886962321	0.909565687	6.844973919	0.02898857	0	1754	1833	1622	2172	1284	2360	1813	1683	1887	1584
ENSMUSG00000039706	chr5	Ldb2	0.03507534	0.886982738	0.909565687	2.606518198	0.046690686	0	74	89	85	122	72	90	108	81	74	142
ENSMUSG00000048782	chr7	Insc	-0.0550091	0.888273831	0.91078958	1.053147133	0.105036706	0	33	15	39	42	20	44	48	20	20	26
ENSMUSG00000090625	chr2	Gm20721	-0.1227798	0.88830658	0.91078958	3.259296949	0.854601992	0	53	82	33	279	304	21	6	422	5	250
ENSMUSG00000020785	chr11	Camkk1	-0.0530904	0.888641637	0.911066279	1.23016806	0.07825487	0	44	27	23	45	31	48	43	38	31	18
ENSMUSG00000037722	chr14	Gnpnat1	0.03024244	0.888993352	0.911360015	2.780032434	0.03702702	0	99	87	91	137	87	109	142	83	120	103
ENSMUSG00000028551	chr4	Cdkn2c	0.03730145	0.889182331	0.91148689	3.025014862	0.056719365	0	127	170	99	84	99	137	162	128	112	124
ENSMUSG00000031217	chrX	Efnb1	0.03437851	0.889338266	0.911555073	3.430653446	0.061593879	0	120	136	157	213	161	187	155	204	84	253
ENSMUSG00000045409	chr17	Trim39	0.02815056	0.889379291	0.911555073	3.078500557	0.029570055	0	122	116	124	129	119	162	137	103	142	145
ENSMUSG00000091971	chr17	Hspa1a	-0.0601176	0.889522589	0.911635088	1.718800269	0.153115288	0	17	39	38	108	47	92	61	28	44	32
ENSMUSG00000056305	chr6	Usp39	-0.0206067	0.889741565	0.911792646	4.474289243	0.022748064	0	312	296	291	403	356	424	377	283	368	347
ENSMUSG00000028614	chr4	Ndc1	0.02460074	0.890156538	0.912151021	4.038531462	0.031323962	0	239	232	220	313	207	306	332	213	297	197
ENSMUSG00000020952	chr12	Scfd1	0.02758112	0.890340664	0.912272809	4.051556456	0.04066482	0	277	252	218	276	192	252	313	185	370	233
ENSMUSG00000021567	chr13	Nkd2	0.04909922	0.890507735	0.912377106	1.371734941	0.103941793	0	28	34	32	56	32	84	45	23	24	33
ENSMUSG00000036158	chr15	Prickle1	-0.0292031	0.890835513	0.912646029	2.836760014	0.035356391	0	103	113	96	132	86	128	100	100	92	150
ENSMUSG00000038671	chr2	Arfrp1	-0.0206109	0.891907116	0.913676893	5.039147808	0.024108385	0	522	477	460	616	394	706	519	477	524	440

ENSMUSG00000014313	chr15	Cox6c	0.02415361	0.892348198	0.913976841	8.771293713	0.037958756	0	6315	6816	6537	8373	4430	8853	6434	6487	8313	5861
ENSMUSG00000024683	chr19	Mrpl16	0.0196015	0.892363775	0.913976841	5.264400323	0.022981362	0	567	563	565	723	430	642	624	589	653	635
ENSMUSG00000037242	chr4	Clic4	0.02207061	0.892396105	0.913976841	6.389345805	0.030364308	0	1032	1138	1097	1776	1203	1762	1521	1031	1170	1473
ENSMUSG00000032294	chr9	Pkm	0.0269483	0.892842657	0.914300189	11.77731208	0.047924127	0	55617	45812	42444	65518	50899	38581	56074	52241	55882	85200
ENSMUSG00000071856	chr18	Mcc	0.04200968	0.892791576	0.914300189	1.619033843	0.071948608	0	34	28	59	46	47	41	53	55	39	55
ENSMUSG00000024891	chr19	Slc29a2	0.03104799	0.893382837	0.914719307	2.800846946	0.049956149	0	79	80	92	151	107	110	130	138	94	89
ENSMUSG00000056019	chr8	Zfp709	0.05445775	0.893372403	0.914719307	0.848816469	0.091804991	0	20	36	19	32	16	17	39	23	24	36
ENSMUSG00000033373	chr12	Fntb	0.01845493	0.893511948	0.914784483	5.35404851	0.02037495	0	605	581	543	755	544	749	666	644	637	655
ENSMUSG00000045466	chr6	Zfp956	0.03383376	0.893739969	0.914950909	2.761847099	0.053367353	0	109	108	101	84	82	79	117	103	100	149
ENSMUSG00000021537	chr13	Cetn3	-0.0264913	0.894761921	0.915930023	3.952036654	0.03818055	0	255	250	210	284	161	209	284	172	308	267
ENSMUSG00000046844	chr8	Vat1l	0.07150632	0.894913129	0.916017716	0.242866855	0.12952899	0	5	15	17	24	16	20	31	14	8	16
ENSMUSG00000062944	chr7	9130023H24Rik	-0.0527949	0.895058185	0.916099098	1.500016523	0.09343749	0	62	25	34	62	26	27	57	47	35	49
ENSMUSG00000068742	chr2	Cry2	-0.0236009	0.895363584	0.91634457	5.099794776	0.036253955	0	654	555	511	473	354	580	530	482	463	723
ENSMUSG00000029359	chr5	Tesc	-0.0773041	0.895713765	0.916509353	0.009030028	0.206721322	0	4	16	9	18	20	29	3	12	9	18
ENSMUSG00000034445	chr19	Cyb561a3	-0.0330908	0.895721326	0.916509353	2.279494117	0.038964963	0	76	78	61	84	58	72	95	66	69	80
ENSMUSG00000085028	chr2	Slc2a4rg-ps	0.04549327	0.89565855	0.916509353	1.088583545	0.063706277	0	25	28	30	33	30	51	29	23	38	26
ENSMUSG00000026019	chr1	Wdr12	0.01968286	0.89650878	0.917239273	4.522457724	0.022929795	0	368	292	299	420	318	377	447	320	383	352
ENSMUSG00000096952	chr8	Gm26572	0.05385539	0.896565949	0.917239273	0.978304474	0.079625757	0	30	28	26	21	28	24	22	28	32	47
ENSMUSG00000050619	chr2	Zscan29	-0.0323965	0.896711196	0.91732072	2.612730376	0.044481337	0	89	91	81	101	88	69	104	83	112	113
ENSMUSG00000020774	chr11	Aspa	-0.0438831	0.896795476	0.917339792	1.840923331	0.081623194	0	49	61	56	68	29	29	64	59	58	65
ENSMUSG00000048796	chr3	Cyb561d1	0.02557104	0.897375644	0.917866071	2.998404558	0.031949451	0	144	104	103	126	103	141	110	127	130	139
ENSMUSG00000038520	chr7	Tbc1d17	0.02004045	0.898030548	0.918468711	5.37375599	0.026306341	0	719	639	499	731	484	891	624	576	640	689
ENSMUSG00000031681	chr8	Smad1	0.02282697	0.898353442	0.918731721	4.17447277	0.029529793	0	258	320	256	285	201	318	304	289	226	342
ENSMUSG00000096917	chr8	2500002B13Rik	-0.0252587	0.898496753	0.91881105	2.379227526	0.035506229	0	79	75	62	82	82	87	81	73	82	88
ENSMUSG00000062526	chr18	Mppe1	-0.0298366	0.898756732	0.919009664	2.59991558	0.035489864	0	89	86	98	111	64	111	90	88	86	106
ENSMUSG00000043953	chr9	Ccrl2	-0.0408619	0.898880749	0.919069233	2.374466483	0.107920384	0	99	94	75	71	41	123	85	41	42	126
ENSMUSG00000054793	chr7	Cadm4	0.02795213	0.899516641	0.919652127	2.420848817	0.0482807	0	56	85	67	112	69	104	81	96	82	67
ENSMUSG00000027091	chr2	Zc3h15	0.01865125	0.900542238	0.920633335	5.709161115	0.025389873	0	864	678	603	1061	700	884	937	725	900	844
ENSMUSG00000002249	chr17	Tead3	-0.0264654	0.900699722	0.920726983	2.872792771	0.032477922	0	94	103	102	150	96	137	97	110	104	136
ENSMUSG00000036552	chr17	Ermard	-0.0306874	0.900978482	0.920877232	2.53749944	0.055454976	0	98	98	55	87	88	133	76	62	100	92
ENSMUSG00000067235	chr17	H2-Q10	0.08710473	0.90097586	0.920877232	2.179939048	0.477829891	0	43	70	80	69	51	322	16	16	25	18
ENSMUSG00000086003	chr11	B230206L02Rik	0.05929095	0.901112379	0.920946735	0.442256017	0.105179681	0	19	20	20	15	15	10	16	23	19	34
ENSMUSG00000027341	chr2	Tmem230	0.01891802	0.901324503	0.921096172	4.436465105	0.021140778	0	358	303	281	367	285	383	403	288	315	388
ENSMUSG00000026240	chr1	Cops7b	-0.0191494	0.901555183	0.921264549	3.887746837	0.023586531	0	213	196	231	239	215	250	263	207	235	236
ENSMUSG00000055067	chr1	Smyd3	0.02514071	0.901749443	0.921395688	2.668415006	0.034326563	0	109	96	68	110	79	109	99	93	94	119
ENSMUSG00000037152	chr3	Ndufc1	0.01884394	0.901992212	0.92157637	7.347093008	0.027291817	0	2545	2604	2305	2770	1819	3045	2672	2398	2609	2670
ENSMUSG00000035759	chr10	Bbs10	0.0393401	0.90255533	0.922084305	0.775946172	0.058250501	0	24	24	19	36	15	26	26	22	31	26
ENSMUSG00000062937	chr4	Mtap	0.0239715	0.902639668	0.922103063	4.244989747	0.039329388	0	331	264	212	302	280	228	417	252	342	305
ENSMUSG00000021076	chr12	Actr10	0.01782162	0.902793327	0.922192628	5.723239198	0.023615446	0	867	728	725	942	651	876	883	752	933	881
ENSMUSG00000061461	chr5	Smim20	-0.0187034	0.903310563	0.922653543	6.136156474	0.026567533	0	1183	1054	996	1233	808	1245	1140	1018	1229	1059
ENSMUSG00000032582	chr9	Rbm6	-0.0175673	0.903682089	0.922965571	4.823578029	0.0218194	0	450	377	421	516	354	583	468	387	444	417
ENSMUSG00000023068	chr10	Nus1	-0.0194055	0.903801468	0.923020045	5.250976132	0.02777941	0	525	539	556	811	446	770	714	432	583	607
ENSMUSG00000026878	chr2	Rab14	0.01768416	0.904202437	0.923362067	6.49870053	0.024749351	0	1341	1298	1130	1771	1195	1560	1735	1293	1289	1564
ENSMUSG00000041577	chr1	Prelp	-0.0255237	0.904330722	0.923425599	5.485047024	0.051940059	0	766	583	544	889	605	1366	670	507	498	657
ENSMUSG00000090110	chrX	Mtcp1	-0.0327799	0.905641693	0.924696691	1.450188495	0.044568148	0	42	37	34	54	31	43	51	37	33	47
ENSMUSG00000026753	chr2	Ppp6c	0.01691526	0.905837221	0.924828768	6.01358354	0.022935374	0	973	861	868	1240	860	1199	1141	965	1006	993
ENSMUSG00000005267	chr11	Zfp287	0.05564149	0.906151439	0.925014427	0.704175616	0.075053802	0	18	21	19	23	28	29	14	27	23	32
ENSMUSG00000057177	chr7	Gsk3a	0.01775646	0.906125143	0.925014427	6.392067805	0.025986839	0	1113	1088	1096	1706	1249	1538	1362	1342	1202	1454
ENSMUSG00000037972	chr16	Snn	-0.024916	0.906381856	0.925182064	3.151995981	0.039599652	0	136	143	125	154	101	157	119	150	98	187
ENSMUSG00000053754	chr14	Chd8	0.01664135	0.906637272	0.925375193	5.126469052	0.021094103	0	501	474	425	657	530	583	561	521	546	648
ENSMUSG00000001847	chr5	Rac1	-0.0175956	0.90709084	0.92576176	7.397016309	0.026603556	0	2503	2389	2208	3254	2333	3244	2978	2084	2794	2640
ENSMUSG00000097617	chr9	Gm10687	-0.0409822	0.90714849	0.92576176	1.138581502	0.081305438	0	39	31	24	40	24	22	23	33	36	52
ENSMUSG00000058806	chr10	Col13a1	0.04011782	0.907292878	0.925841506	1.435438032	0.089696717	0	57	26	28	62	21	37	53	51	32	39
ENSMUSG00000051359	chr15	Ncald	0.02205554	0.907747266	0.926237555	3.22416098	0.036765698	0	145	110	108	173	148	159	156	183	122	135
ENSMUSG00000046792	chr7	Zfp787	-0.020188	0.908055572	0.9264845	4.512721029	0.029090108	0	319	306	301	452	334	324	315	386	335	473
ENSMUSG00000016756	chr13	Cmah	-0.0410623	0.908700403	0.927074738	1.382506518	0.10103413	0	29	31	40	42	44	72	44	37	16	34
ENSMUSG00000061576	chr5	Dpp6	-0.0622166	0.908793499	0.92710204	0.91074708	0.214537104	0	53	26	22	18	14	11	24	48	13	42
ENSMUSG00000061062	chr17	Gm10093	0.05795189	0.909282182	0.927532864	1.678419242	0.195323114	0	52	40	49	58	26	151	33	26	25	31
ENSMUSG00000028128	chr3	F3	-0.0315789	0.909774521	0.927899635	2.815978549	0.071516116	0	74	118	98	94	128	79	164	119	83	111
ENSMUSG00000033068	chr2	Entpd6	-0.0244451	0.909732146	0.927899635	3.380717341	0.037378034	0	185	130	123	175	160	197	203	134	179	122
ENSMUSG00000026051	chr1	1500015O10Rik	0.04544078	0.910717194	0.928793309	3.213376451	0.165006095	0	273	111	129	63	82	325	169	98	94	94
ENSMUSG00000041119	chr17	Pde9a	0.05703949	0.910977829	0.928991327	1.04754751	0.10728625	0	34	35	32	28	12	58	30	18	31	27
ENSMUSG00000024526	chr18	Cidea	-0.0680165	0.911625466	0.92942266	1.950602281	0.375117721	0	7	159	57	18	33	58	40	105	48	43
ENSMUSG00000070972	chr4	Dnajc25	0.01894084	0.911549095	0.92942266	3.537968072	0.025040657	0	163	181	147	225	140	217	217	173	153	188
ENSMUSG00000085419	chr11	Gm11734	-0.062019	0.911666804	0.92942266	-0.040843711	0.111915051	0	21	8	15	11	9	12	16	6	13	21

ENSMUSG00000089671	chr15	Gm16537	-0.082956	0.911514777	0.92942266	1.07345088	0.378041138	0	18	17	10	59	52	21	7	78	8	38
ENSMUSG00000040771	chr17	Oard1	-0.0204426	0.912604184	0.930310436	3.625361168	0.032102379	0	213	186	175	211	133	231	195	134	228	207
ENSMUSG00000021072	chr12	Tmx1	-0.017167	0.913065099	0.930675468	4.263522601	0.024594073	0	269	258	256	372	281	380	359	222	303	296
ENSMUSG00000024253	chr17	Dync2li1	0.03302221	0.913095451	0.930675468	2.273095901	0.062877177	0	90	70	58	76	53	131	58	76	65	62
ENSMUSG00000051390	chr17	Zbtb22	-0.0172047	0.913205901	0.930720169	4.257963747	0.021717398	0	286	244	289	370	242	329	291	288	320	313
ENSMUSG00000021764	chr13	Ndufs4	0.01798768	0.913497909	0.930949889	7.368680294	0.032276092	0	2284	2703	2472	3060	1748	2877	2506	2642	2985	2506
ENSMUSG00000048142	chr5	Nat8l	-0.0611619	0.913703529	0.931091543	1.167672335	0.24309906	0	11	73	27	17	29	17	22	47	28	54
ENSMUSG00000017897	chr2	Eya2	-0.0376643	0.913795932	0.931117814	1.182398118	0.092522127	0	27	31	38	42	24	68	22	31	26	28
ENSMUSG00000023243	chr14	Kcnk5	0.06883876	0.914376968	0.931574027	0.128625825	0.084816466	0	10	12	17	10	20	18	19	14	15	15
ENSMUSG00000028104	chr3	Polr3gl	-0.0157393	0.914328254	0.931574027	5.112703214	0.021628143	0	571	521	465	631	405	604	568	472	594	564
ENSMUSG00000024975	chr19	Pdcd4	-0.0178984	0.914978757	0.932119185	4.076976718	0.029152164	0	253	265	258	274	201	328	262	259	194	324
ENSMUSG00000030663	chr7	1110004F10Rik	0.01595796	0.915658174	0.932743341	5.380161338	0.024070127	0	644	569	547	743	578	648	817	552	680	715
ENSMUSG00000036356	chr8	Csgalnact1	-0.0234304	0.915772598	0.932791912	2.652133022	0.037205222	0	100	97	92	116	60	116	108	87	98	91
ENSMUSG00000041592	chr11	Sdk2	0.04583482	0.915850057	0.932802828	0.816510763	0.085028231	0	31	15	22	34	19	33	27	31	12	33
ENSMUSG00000028578	chr4	Caap1	-0.0365257	0.918142687	0.935069751	1.134134404	0.0509015	0	37	26	34	35	24	37	35	26	37	32
ENSMUSG00000055897	chr2	Ppp4r1l-ps	0.02293835	0.918835647	0.935707301	3.166887145	0.033753999	0	138	146	120	130	116	193	128	137	115	160
ENSMUSG00000020359	chr11	Phykpl	0.01667101	0.918914591	0.935719513	4.085337129	0.028697732	0	218	231	226	355	229	229	276	266	308	296
ENSMUSG00000015016	chr8	Acsf3	0.01552199	0.919470046	0.936216914	4.261434204	0.024667255	0	263	268	263	393	237	304	274	318	295	369
ENSMUSG00000022791	chr16	Tnk2	-0.0190502	0.919825433	0.936374117	5.972004359	0.03917656	0	830	821	892	1352	850	732	918	1129	985	1268
ENSMUSG00000053646	chr9	Plxnb1	-0.0336174	0.919812195	0.936374117	1.720876094	0.080432761	0	41	37	50	56	54	52	39	62	27	76
ENSMUSG00000075467	chr2	Dnlz	-0.0146213	0.91976592	0.936374117	5.05352485	0.020794235	0	479	452	468	630	456	623	510	546	517	489
ENSMUSG00000032470	chr9	Mras	0.02097978	0.920556625	0.937050211	3.512353976	0.041209579	0	117	121	171	229	198	210	169	183	153	215
ENSMUSG00000024826	chr19	Dpf2	-0.0150862	0.920915054	0.937126062	5.690622872	0.025168712	0	774	710	679	955	749	933	821	872	644	920
ENSMUSG00000037013	chr18	Ss18	-0.0169777	0.920832538	0.937126062	4.272581491	0.027697294	0	274	284	256	405	235	424	340	229	309	270
ENSMUSG00000037017	chr5	Zscan21	-0.0180713	0.920966404	0.937126062	3.962654515	0.027823253	0	233	213	208	292	217	219	216	233	281	300
ENSMUSG00000043998	chr12	Mgat2	-0.0192055	0.920962008	0.937126062	3.732884249	0.036053132	0	193	180	185	251	182	207	277	123	222	246
ENSMUSG00000100214	chr7	6230415J03Rik	-0.0393413	0.920757616	0.937126062	0.199306076	0.096161446	0	17	19	17	10	13	20	19	15	7	22
ENSMUSG00000024613	chr18	Tcof1	0.0167894	0.921685549	0.937789548	4.778842887	0.031924566	0	351	332	324	636	413	504	525	338	492	392
ENSMUSG00000021391	chr13	Cenpp	0.03735698	0.922963565	0.939021532	0.259689886	0.092732884	0	14	14	14	21	16	15	27	24	11	11
ENSMUSG00000032462	chr9	Pik3cb	-0.0184013	0.923294542	0.939289891	3.241932133	0.03448318	0	120	140	159	168	112	196	166	109	126	168
ENSMUSG00000027425	chr2	Csrp2bp	-0.015999	0.92345081	0.939380487	4.183333034	0.024552521	0	234	221	282	371	251	297	312	272	262	323
ENSMUSG00000026510	chr1	Trp53bp2	-0.0152027	0.924557398	0.940401	3.511203146	0.023625153	0	152	165	161	204	162	189	177	169	173	208
ENSMUSG00000037210	chr5	Fam193a	-0.0161922	0.92458859	0.940401	3.949107538	0.023525773	0	224	207	187	303	233	270	241	260	214	258
ENSMUSG00000026021	chr1	Sumo1	-0.0153222	0.92473196	0.940478379	5.26025564	0.027735982	0	617	607	539	673	430	578	690	478	689	667
ENSMUSG00000025584	chr7	Pde8a	0.01981762	0.92590712	0.941605029	3.192969045	0.040421327	0	102	152	118	198	105	199	153	100	130	168
ENSMUSG00000038074	chr6	Fkbp14	0.01550827	0.927131582	0.94278165	3.953793206	0.021957316	0	236	243	206	247	203	277	274	223	235	255
ENSMUSG00000039347	chr6	Atp6v0e2	0.01372314	0.927596283	0.94318557	5.732534551	0.024374356	0	854	768	718	874	710	833	906	736	898	977
ENSMUSG00000002748	chr5	Baz1b	-0.0131022	0.927950926	0.943477531	5.770020003	0.022549974	0	763	734	714	1098	792	971	976	772	788	933
ENSMUSG00000000384	chr11	Tbrg4	-0.0143684	0.928078996	0.943539103	5.624648105	0.026268531	0	656	623	673	1080	694	940	800	815	721	723
ENSMUSG00000092085	chr1	Gm17224	0.07895212	0.928495397	0.943893779	3.280416062	0.843635439	0	50	79	26	205	336	24	9	470	6	257
ENSMUSG00000056919	chr9	Cep162	-0.0244044	0.928867653	0.944203529	2.067538594	0.062471386	0	85	49	59	68	45	92	74	50	71	44
ENSMUSG00000027242	chr2	Wdr76	0.04686714	0.929111878	0.944383098	1.142573165	0.077034363	0	36	26	35	27	27	27	48	20	39	39
ENSMUSG00000054715	chr7	Zscan22	0.02815039	0.929832982	0.945047324	1.766821334	0.059759628	0	44	40	48	71	41	45	77	35	51	63
ENSMUSG00000032757	chr6	Bet1	-0.0154795	0.930030451	0.945179289	4.15407715	0.026022268	0	323	240	239	332	199	274	329	248	289	295
ENSMUSG00000020922	chr11	Lsm12	-0.0129298	0.930334321	0.945350623	5.374256106	0.024056551	0	651	578	571	724	570	899	681	591	616	594
ENSMUSG00000032551	chr9	1110059G10Rik	0.01936585	0.930282748	0.945350623	2.910476352	0.039613284	0	132	124	93	114	83	133	135	96	139	105
ENSMUSG00000055694	chr8	Gdf1	0.01983576	0.930632708	0.945585076	4.213534944	0.055220661	0	309	199	234	336	289	167	358	319	250	409
ENSMUSG00000010021	chr11	Kif19a	-0.0440727	0.930803958	0.945690326	0.591374797	0.067830939	0	13	19	25	31	17	20	24	20	19	28
ENSMUSG00000029427	chr5	Zcchc8	0.01512274	0.930933546	0.945753234	3.561563197	0.024671924	0	193	156	162	210	147	205	209	160	209	176
ENSMUSG00000001280	chr15	Sp1	0.01279507	0.931112484	0.945866265	5.058101203	0.020603322	0	472	494	483	605	412	671	564	441	491	573
ENSMUSG00000028233	chr4	Tgs1	-0.0164749	0.931706285	0.946335958	3.403665486	0.02672952	0	147	127	149	221	146	166	186	147	159	192
ENSMUSG00000039481	chr17	Nrtn	0.04766692	0.931710273	0.946335958	0.823030155	0.149170202	0	22	13	21	46	21	60	22	21	24	11
ENSMUSG00000041765	chr14	Ubac2	-0.013184	0.931815977	0.946374544	4.774246002	0.022262649	0	351	393	400	535	367	471	395	440	424	481
ENSMUSG00000066894	chr5	Vsig10	-0.0216158	0.932083508	0.946577468	2.68574171	0.041203609	0	89	94	106	116	69	138	83	103	88	101
ENSMUSG00000037166	chr7	Ppp1r14a	0.04021275	0.93221277	0.946639953	1.191376497	0.079966138	0	30	28	28	26	44	49	34	43	24	29
ENSMUSG00000021707	chr13	Dhfr	0.02622815	0.93306327	0.947434776	2.775931252	0.073204107	0	95	93	126	119	63	121	174	60	118	85
ENSMUSG00000032898	chr5	Fbxo21	-0.015667	0.935270223	0.94960673	3.835090424	0.027580237	0	178	216	194	297	183	221	211	246	205	262
ENSMUSG00000010651	chr9	Acaa1b	0.07395091	0.936118209	0.95039867	0.248557179	0.459979797	0	18	14	6	23	16	69	2	6	3	13
ENSMUSG00000029447	chr5	Cct6a	-0.0127614	0.936649567	0.95086906	6.526314875	0.028550469	0	1444	1205	1099	1850	1347	1336	1765	1338	1479	1549
ENSMUSG00000030612	chr7	Mrpl46	-0.0123465	0.937265237	0.951424967	4.634216246	0.02293939	0	400	371	351	443	288	429	409	334	446	391
ENSMUSG00000071361	chr14	Mcpt9	0.1099465	0.938104741	0.952207993	0.231787641	1.445131806	0	10	14	16	14	18	96	0	0	0	0
ENSMUSG00000050505	chr14	Pcdh20	-0.0497562	0.938214853	0.952250602	0.368874038	0.142690749	0	11	18	19	15	24	5	23	19	17	29
ENSMUSG00000066551	chr5	Hmgb1	0.01210816	0.938344234	0.95231276	6.786595615	0.027833147	0	1716	1633	1502	1970	1377	1944	2214	1405	1824	1684
ENSMUSG00000017670	chr2	Elmo2	0.01237907	0.938451694	0.952352663	4.601876966	0.021827565	0	347	367	330	433	317	454	438	295	367	440
ENSMUSG00000091421	chr3	Gm4202	-0.0385297	0.939789271	0.953640809	0.614078082	0.099755587	0	23	28	13	23	19	14	36	13	27	23

ENSMUSG00000020483	chr11	Dynll2	0.01511154	0.940168136	0.953955994	8.070297481	0.048053599	0	4172	3831	3188	4639	4073	2751	4621	4687	3904	5902
ENSMUSG00000029918	chr6	Mrps33	0.01214038	0.940544942	0.954269046	3.85921558	0.024427822	0	222	196	221	276	158	252	236	226	239	225
ENSMUSG00000026276	chr1	Sept2	-0.0112167	0.940797255	0.954455752	6.636437006	0.025901849	0	1596	1516	1332	1756	1243	1751	1867	1364	1608	1506
ENSMUSG00000078773	chr4	Rad54b	0.03824286	0.941452464	0.955051146	0.719657188	0.089212653	0	24	25	18	27	18	19	41	12	29	25
ENSMUSG00000052135	chr4	Foxo6	0.0198087	0.942651986	0.956198589	3.781474556	0.080098812	0	145	189	182	260	232	104	243	328	170	254
ENSMUSG00000038563	chr7	Eftud1	0.01553493	0.942811776	0.956291268	3.20348839	0.027911492	0	142	134	120	146	129	177	152	130	118	173
ENSMUSG00000026707	chr2	Nsun6	0.03365429	0.94294239	0.956354343	1.011821155	0.056552066	0	32	27	19	42	21	43	30	28	24	32
ENSMUSG00000031347	chrX	Cetn2	-0.012907	0.943200245	0.95654645	4.616043051	0.032445029	0	462	391	346	373	249	355	429	362	376	458
ENSMUSG00000035184	chr14	Fam124a	-0.0187391	0.94352944	0.956810873	1.603933222	0.064709927	0	50	50	47	36	33	58	48	56	39	35
ENSMUSG00000027175	chr2	Tcp11l1	0.02058817	0.944303167	0.957526015	2.216682507	0.051932499	0	67	67	61	95	48	103	74	63	83	50
ENSMUSG00000078994	chr13	Zfp429	-0.0326542	0.944994711	0.958157725	0.773295776	0.096561959	0	20	33	26	21	18	32	33	21	30	12
ENSMUSG00000063268	chr15	Parp10	-0.0137657	0.945318555	0.958416549	3.422697037	0.043859187	0	164	168	159	170	129	240	135	161	109	225
ENSMUSG00000027630	chr3	Tbl1xr1	0.01085587	0.94547563	0.958506267	5.307658332	0.025058028	0	657	628	520	677	453	730	743	543	548	689
ENSMUSG00000004994	chr8	Ccdc130	0.01594285	0.945570785	0.958533205	2.701707064	0.044305322	0	91	104	71	117	91	162	94	97	87	88
ENSMUSG00000025867	chr13	Cplx2	-0.0204857	0.946070038	0.958969745	1.942656657	0.086583905	0	56	59	50	47	63	66	62	84	26	63
ENSMUSG00000020108	chr10	Ddit4	0.02560187	0.947000187	0.959842962	4.103740148	0.144932779	0	232	184	358	208	249	742	175	179	128	238
ENSMUSG00000014177	chr11	Tvp23b	-0.0138131	0.947349114	0.960126992	3.371195964	0.038072561	0	170	145	138	212	109	252	149	115	145	181
ENSMUSG00000049265	chr5	Kcnk3	-0.0385875	0.947462792	0.960172575	0.834071742	0.264135672	0	13	56	19	16	19	16	14	57	12	32
ENSMUSG00000001700	chr18	Gramd3	0.01328905	0.947560313	0.960201779	3.633455573	0.028841926	0	221	197	163	190	138	229	189	180	178	235
ENSMUSG00000030243	chr6	Recql	0.01689987	0.947683825	0.960257314	2.769820702	0.043764903	0	98	86	101	99	107	100	133	102	124	88
ENSMUSG00000040843	chr1	Tiprl	0.00912353	0.948394391	0.960907642	4.771795286	0.021111691	0	433	384	336	536	347	503	442	427	450	404
ENSMUSG00000029036	chr4	Atad3a	-0.010124	0.949140727	0.961594114	4.907549815	0.023853949	0	389	453	417	582	402	605	475	495	444	415
ENSMUSG00000002428	chr3	Hltf	0.01741316	0.949323635	0.961681054	2.738747861	0.049535195	0	97	102	96	101	86	108	128	87	139	74
ENSMUSG00000047037	chr7	Nipa1	0.02133183	0.94936416	0.961681054	1.819797461	0.06033353	0	50	44	42	57	58	39	63	47	73	56
ENSMUSG00000053091	chr7	Lins	0.01580803	0.94978381	0.96203642	2.523001976	0.041150659	0	97	82	79	78	77	80	100	91	98	90
ENSMUSG00000028982	chr4	Slc25a33	0.01174556	0.950953239	0.963151132	3.992291323	0.030755158	0	237	274	226	283	155	277	245	208	252	317
ENSMUSG00000031922	chr9	Cep57	0.02363667	0.951066296	0.963195837	2.303464031	0.062143045	0	83	71	91	60	46	72	100	62	83	79
ENSMUSG00000035372	chr19	1810055G02Rik	-0.012644	0.951237371	0.96329929	3.388343109	0.030911012	0	152	120	145	206	155	161	208	130	174	169
ENSMUSG00000056486	chr2	Chn1	0.02236512	0.951456041	0.963450922	1.924112475	0.056981304	0	64	52	50	60	45	77	46	67	38	75
ENSMUSG00000041375	chr7	Ccdc9	-0.0098933	0.952116755	0.963980279	4.612845823	0.024639648	0	348	326	313	506	343	548	383	346	365	352
ENSMUSG00000047635	chr5	2810006K23Rik	-0.0133636	0.952105497	0.963980279	3.041820342	0.035509995	0	134	112	117	141	103	102	141	144	128	139
ENSMUSG00000037447	chr1	Arid5a	-0.014153	0.952329361	0.96412569	3.307533119	0.052608032	0	175	128	143	154	129	288	137	135	124	122
ENSMUSG00000031586	chr8	Rbpms	0.01364276	0.952476769	0.964205079	3.590673427	0.037574479	0	195	212	147	204	128	291	189	170	141	198
ENSMUSG00000020311	chr11	Erlec1	0.00853244	0.952627156	0.964264166	4.969725707	0.021568169	0	479	443	437	585	384	475	520	468	542	543
ENSMUSG00000040836	chr1	Gpr161	0.02403173	0.952673125	0.964264166	1.394786074	0.049142248	0	28	42	35	41	38	54	42	34	39	38
ENSMUSG00000030534	chr7	Vps33b	-0.0154663	0.953561689	0.965093647	2.183971373	0.041412296	0	74	69	61	75	52	80	80	50	80	70
ENSMUSG00000031904	chr8	Slc7a6	-0.0143771	0.953677316	0.96514078	3.09828105	0.035341772	0	125	123	102	172	115	174	180	111	108	118
ENSMUSG00000103715	chr9	RP23-58N8.6	-0.0274794	0.954244744	0.965645105	1.377905708	0.05575804	0	33	40	28	50	36	28	45	36	44	46
ENSMUSG00000026279	chr1	Thap4	0.00912566	0.955037116	0.966376972	4.603968947	0.027897299	0	286	295	356	528	348	363	409	378	400	425
ENSMUSG00000036435	chr5	Exoc1	0.01059219	0.955307557	0.966580642	3.89312237	0.025487305	0	225	240	197	254	178	287	274	191	246	214
ENSMUSG00000062554	chr4	Gm12751	0.06013655	0.955805805	0.967014762	-0.013739356	0.105664479	0	17	9	9	15	13	26	20	8	8	11
ENSMUSG00000034893	chr14	Cog3	0.01084903	0.956449459	0.96759592	4.083662296	0.027982805	0	270	224	234	287	233	343	327	192	282	245
ENSMUSG00000023944	chr17	Hsp90ab1	0.008573	0.957544558	0.968633667	10.19287262	0.030955981	0	18106	16071	13813	22782	16765	24308	19829	18979	15921	17143
ENSMUSG00000035048	chr9	Anapc13	-0.0080784	0.957614361	0.968634168	5.282763869	0.023598065	0	648	572	519	673	490	793	587	547	658	584
ENSMUSG00000059602	chr10	Syn3	0.05974886	0.957855949	0.96880842	-0.01061859	0.685379657	0	7	6	2	21	28	7	1	30	0	33
ENSMUSG00000075296	chr19	Aldh3b2	0.0676116	0.957959114	0.96884265	-0.662478311	0.425186276	0	1	17	5	4	9	1	5	15	2	19
ENSMUSG00000027015	chr2	Cybrd1	0.03613645	0.958031932	0.968846185	1.48139048	0.163911338	0	66	29	45	27	26	89	58	19	21	40
ENSMUSG00000038156	chr7	Spon1	0.02077709	0.958340526	0.969088141	2.922688997	0.123572794	0	123	127	75	76	139	139	100	164	38	174
ENSMUSG00000027122	chr2	Arl14ep	-0.0118569	0.958490988	0.969170167	2.875368528	0.037990627	0	109	121	109	131	71	143	137	105	99	105
ENSMUSG00000028952	chr4	Zbtb48	0.02435171	0.958683434	0.96929463	1.451058663	0.065864567	0	31	51	33	53	26	57	39	36	51	32
ENSMUSG00000037072	chr3	Sep15	0.0082609	0.958907701	0.969381124	6.640444457	0.028372077	0	1656	1483	1418	1663	1176	1680	1960	1305	1627	1605
ENSMUSG00000062421	chr11	Arf2	-0.008628	0.958881587	0.969381124	4.700572006	0.027105222	0	377	354	354	491	364	496	489	297	472	362
ENSMUSG00000035671	chr8	Zswim4	-0.0116575	0.959042437	0.969447208	3.55682072	0.029997063	0	175	170	156	224	150	160	213	216	159	193
ENSMUSG00000050640	chr5	Tmem150c	0.02865276	0.959138228	0.969473919	0.157683714	0.094862964	0	11	9	18	26	10	18	10	21	16	16
ENSMUSG00000036880	chr18	Acaa2	-0.0102302	0.959866096	0.970139467	7.646487366	0.047572879	0	1982	3284	2734	4891	2353	4164	2551	3539	3075	2949
ENSMUSG00000041353	chrX	Tmem29	-0.022409	0.959971381	0.970175719	1.507357616	0.064810377	0	31	44	30	61	40	44	52	29	58	37
ENSMUSG00000025971	chr1	9430016H08Rik	-0.009392	0.960975305	0.971120091	4.163614387	0.025637957	0	216	230	244	399	256	298	320	265	261	306
ENSMUSG00000029467	chr5	Atp2a2	-0.0256314	0.961357243	0.97143582	7.579587387	0.325546174	0	1043	1070	1000	12306	1068	4779	2055	4040	2465	2115
ENSMUSG00000021266	chr12	Wars	0.0074466	0.961477648	0.971487247	5.100003669	0.025524633	0	500	409	434	671	538	500	622	539	570	554
ENSMUSG00000068966	chr2	Zbtb34	-0.0087073	0.96180411	0.971746855	3.032410385	0.036373298	0	103	131	123	129	112	152	140	103	99	167
ENSMUSG00000027695	chr3	Pld1	-0.0117221	0.962185698	0.972062116	2.474766602	0.044233652	0	66	83	66	117	78	121	106	68	71	80
ENSMUSG00000020962	chr12	Gtf2a1	0.00933716	0.962538554	0.972277789	4.093295429	0.033012319	0	282	247	219	318	200	248	343	196	244	364
ENSMUSG00000025544	chr14	Tm9sf2	-0.0073206	0.962607883	0.972277789	6.494395066	0.026391565	0	1432	1261	1078	1771	1235	1473	1708	1283	1241	1648
ENSMUSG00000061981	chr11	Flot2	0.00712244	0.962565158	0.972277789	6.636989445	0.025637441	0	1403	1422	1246	1849	1484	1698	1526	1415	1699	1799
ENSMUSG00000047656	chr19	Trpt1	-0.010911	0.963161037	0.972766199	3.522971063	0.031775395	0	165	177	140	226	148	170	187	220	145	198

ENSMUSG00000051669	chr16	AU021092	0.03276965	0.963471175	0.973009115	0.328408964	0.096302701	0	15	18	19	19	12	15	18	9	31	20
ENSMUSG00000051022	chr5	Hs3st1	-0.0079651	0.963643865	0.973068538	0.535203828	0.064471682	0	13	23	22	20	20	28	21	19	21	19
ENSMUSG00000090125	chr4	Pou3f1	0.03086106	0.963669264	0.973068538	0.244230285	0.117117692	0	8	10	19	29	13	21	25	12	8	22
ENSMUSG00000039130	chr6	Zc3hc1	0.00709965	0.963814644	0.973145027	4.284402733	0.022010708	0	283	265	265	375	258	369	274	327	295	319
ENSMUSG00000020534	chr11	Shmt1	-0.0123486	0.964208875	0.973472747	3.661787353	0.063423861	0	184	191	144	216	201	110	316	147	225	216
ENSMUSG00000016494	chr1	Cd34	0.00796652	0.964426023	0.973548607	7.052684474	0.036175747	0	2096	2103	2139	2074	1392	2453	1782	2398	1889	2316
ENSMUSG00000043372	chr11	Hexim2	0.01512826	0.964392373	0.973548607	1.756961543	0.058125139	0	42	50	41	63	46	50	34	56	54	72
ENSMUSG00000071661	chr19	Zbtb3	-0.0270696	0.964492989	0.973548607	0.629228731	0.058466909	0	26	20	17	31	14	24	27	22	18	24
ENSMUSG00000070424	chr7	Art5	0.01273367	0.964747169	0.973734848	4.285733192	0.080090801	0	303	345	247	386	172	648	177	237	308	249
ENSMUSG00000098661	chr7	Mir7052	-0.0266786	0.965839939	0.974767402	0.485032778	0.087916358	0	23	11	24	18	19	27	22	25	16	13
ENSMUSG00000021752	chr14	Kctd6	0.01151892	0.966724987	0.975590182	2.770812763	0.037943395	0	98	79	101	125	95	128	143	79	97	106
ENSMUSG00000020257	chr9	Wdr82	-0.0062331	0.967534477	0.976336596	5.229411669	0.02263324	0	557	518	522	719	489	707	720	482	598	553
ENSMUSG00000078853	chr11	Igtp	-0.013369	0.96764966	0.97638233	4.185622888	0.11287036	0	391	348	339	131	110	248	287	359	251	311
ENSMUSG00000059430	chr6	Actg2	0.04995333	0.967821321	0.976485041	0.250813985	0.160904151	0	5	22	9	11	29	23	22	17	13	14
ENSMUSG00000022364	chr15	Tbc1d31	0.01494921	0.967975609	0.976499719	2.089789456	0.044334853	0	65	53	53	67	67	62	73	69	75	58
ENSMUSG00000079343	chr6	C1s2	-0.0357067	0.967951311	0.976499719	1.987075689	0.814743082	0	45	82	52	52	52	303	1	13	10	8
ENSMUSG00000031960	chr8	Aars	-0.0061887	0.96872751	0.977187707	6.592270921	0.026291573	0	1402	1184	1215	1993	1462	1642	1693	1468	1482	1565
ENSMUSG00000035049	chr19	Rrp12	0.00678266	0.96884552	0.977236214	5.168990213	0.030155434	0	495	397	459	708	616	637	582	626	467	621
ENSMUSG00000034850	chr2	Tmem127	-0.0056565	0.969768976	0.978097078	5.883726894	0.024668311	0	794	859	870	1067	806	1250	931	820	928	898
ENSMUSG00000001018	chr3	Snapin	-0.006298	0.969888193	0.97814673	5.954899529	0.028621437	0	1082	958	786	1014	778	877	1092	943	1012	1101
ENSMUSG00000031634	chr8	Ufsp2	-0.0061892	0.970156792	0.978347018	5.136217483	0.025605911	0	630	508	474	573	429	553	630	474	635	559
ENSMUSG00000021013	chr12	Ttc8	-0.0117378	0.970369184	0.9784906	1.990226539	0.063841405	0	52	51	68	49	63	56	64	43	62	89
ENSMUSG00000047921	chr15	Trappc9	-0.0062457	0.971405796	0.979465219	5.336070299	0.027743856	0	583	498	503	788	648	682	619	709	530	736
ENSMUSG00000028967	chr4	Errfi1	0.01074135	0.971628772	0.979619371	4.93232648	0.081372734	0	345	493	532	434	418	1039	543	339	307	332
ENSMUSG00000038705	chr2	Gmeb2	0.00872183	0.971810248	0.979715164	3.214823624	0.028468004	0	161	140	108	158	115	172	153	118	151	159
ENSMUSG00000054770	chr1	Kctd18	0.01102637	0.971863984	0.979715164	2.346718304	0.041007461	0	81	66	75	85	61	92	73	94	76	70
ENSMUSG00000062906	chr15	Hdac10	-0.0078884	0.972325162	0.980109373	3.040036327	0.039072369	0	107	122	125	126	120	155	131	87	160	129
ENSMUSG00000026893	chr2	Gca	-0.0211536	0.97243235	0.980146727	0.835686712	0.086468783	0	31	16	28	31	19	16	22	28	35	32
ENSMUSG00000020105	chr10	Lrig3	-0.0087311	0.972590321	0.980235258	2.228671439	0.053115082	0	70	60	54	91	68	111	73	48	53	92
ENSMUSG00000027079	chr2	Clp1	-0.0126219	0.97310583	0.980684098	2.384599178	0.043230802	0	79	76	73	83	69	85	109	72	85	63
ENSMUSG00000025825	chr5	Iscu	0.00506512	0.973176765	0.98068487	6.191789646	0.024107705	0	1109	1080	999	1348	910	1372	1153	1054	1258	1137
ENSMUSG00000044122	chr11	Proca1	0.0355287	0.973422856	0.980862137	0.385765792	0.203966762	0	31	24	13	4	13	16	10	29	15	27
ENSMUSG00000002688	chr12	Prkd1	-0.0150547	0.973768971	0.981140159	1.145689121	0.056974679	0	29	32	24	47	26	47	31	37	24	31
ENSMUSG00000042167	chr13	Papd4	-0.0074997	0.974274704	0.981578955	3.07935314	0.043698366	0	107	137	130	147	100	122	161	84	153	160
ENSMUSG00000083097	chr2	Gm14494	-0.0221355	0.974577861	0.981813609	1.038751592	0.075647322	0	28	35	20	40	23	26	42	19	41	28
ENSMUSG00000055371	chr2	Stam2	-0.0053446	0.974912289	0.982079728	3.955622176	0.03016245	0	255	227	236	239	186	269	289	167	250	287
ENSMUSG00000000120	chr11	Ngfr	-0.0148084	0.975144921	0.982243273	1.99305617	0.097588164	0	61	59	38	68	63	33	60	64	43	112
ENSMUSG00000022529	chr16	Zfp263	0.00805489	0.97526233	0.982290741	3.369025522	0.03076143	0	153	158	143	201	109	213	183	123	137	188
ENSMUSG00000052305	chr7	Hbb-bs	-0.0102671	0.975610803	0.982570914	7.565513927	0.13353209	0	3417	2876	3709	2456	1516	5991	1423	1301	2676	4479
ENSMUSG00000046997	chr9	Spsb4	-0.0200067	0.975788228	0.982678792	1.22814548	0.062374188	0	40	28	22	52	27	38	47	36	24	35
ENSMUSG00000033909	chr11	Usp36	0.00570823	0.975947184	0.982768055	4.260762186	0.027798167	0	239	236	250	391	308	395	316	300	286	265
ENSMUSG00000038845	chr11	Phb	0.00470595	0.976503781	0.983257698	6.918643648	0.030463568	0	1680	1764	1680	2463	1478	1709	2052	2082	2097	1862
ENSMUSG00000036091	chr9	Hyal3	-0.009617	0.976943832	0.983629925	1.52305617	0.041847563	0	33	41	39	49	43	50	45	38	44	47
ENSMUSG00000042826	chr11	Fgf11	-0.0077273	0.977439106	0.984057697	4.216751121	0.05054305	0	310	278	229	311	251	227	258	452	229	314
ENSMUSG00000037773	chr2	Pced1a	-0.0079902	0.977563854	0.984112398	2.67664206	0.042829104	0	112	89	93	86	84	98	90	83	114	125
ENSMUSG00000057738	chr2	Sptan1	-0.0045049	0.978067881	0.984548884	6.385948688	0.028219944	0	1141	1067	1084	1696	1283	1697	1356	1327	1091	1366
ENSMUSG00000080374	chr2	Gm22953	-0.0441345	0.978596872	0.985010435	0.164419675	0.492850315	0	4	15	5	23	29	6	3	39	2	28
ENSMUSG00000039683	chr5	Sdk1	-0.0156314	0.97905733	0.985331983	1.529799256	0.055003255	0	34	42	39	52	40	42	45	51	29	57
ENSMUSG00000053963	chr1	6330403A02Rik	-0.0177749	0.979056962	0.985331983	0.86865195	0.168555596	0	19	27	23	30	28	36	11	10	57	24
ENSMUSG00000026110	chr1	Mgat4a	-0.008533	0.979749548	0.985957639	2.833650729	0.043053932	0	75	98	84	160	112	146	109	84	115	120
ENSMUSG00000020307	chr10	Cdc34	0.00394894	0.980044617	0.986183567	7.919940482	0.028745903	0	4317	3330	3133	4107	3139	3960	3770	3652	4189	4173
ENSMUSG00000017707	chr2	Serinc3	-0.0038857	0.980450376	0.986520839	7.540937484	0.029859878	0	2729	2778	2660	3247	2455	4199	2805	2328	2671	3339
ENSMUSG00000015222	chr1	Map2	-0.0203455	0.980937763	0.98694019	1.425935871	0.084976703	0	37	28	42	56	31	24	54	42	54	31
ENSMUSG00000039556	chrX	Ppp1r3f	-0.0120424	0.981023673	0.986955576	1.586985883	0.06545043	0	38	49	34	50	44	39	41	30	59	65
ENSMUSG00000026814	chr2	Eng	0.00445538	0.981417867	0.987281084	5.615157587	0.034508226	0	595	646	600	1035	790	951	801	727	546	1004
ENSMUSG00000032440	chr9	Tgfbr2	0.00425143	0.981546041	0.987338957	5.733323128	0.027858754	0	765	812	821	911	632	999	869	723	692	1088
ENSMUSG00000026387	chr1	Sctr	0.00991132	0.981866332	0.987590058	2.565184529	0.083877315	0	102	86	105	87	48	133	46	110	95	90
ENSMUSG00000053483	chr1	Usp21	0.00546164	0.981950329	0.987603468	4.245182256	0.023352264	0	269	262	281	306	275	401	284	279	281	303
ENSMUSG00000032485	chr9	Scap	0.00418431	0.982245264	0.987829014	4.628904595	0.026950152	0	328	331	335	499	350	413	367	354	339	547
ENSMUSG00000025607	chr6	Copg2	0.00373526	0.982430013	0.987943723	4.671288333	0.027175872	0	462	347	333	427	319	357	416	437	414	435
ENSMUSG00000029084	chr5	Cd38	0.00547201	0.984088381	0.989540198	3.150312912	0.04681687	0	117	135	144	171	87	163	140	158	86	171
ENSMUSG00000006289	chr14	Osgep	-0.0033918	0.985655226	0.99104442	5.265238345	0.023809358	0	526	563	452	806	541	777	601	582	594	581
ENSMUSG00000019951	chr10	Uhrf1bp1l	-0.0046044	0.985968083	0.991216367	3.478430276	0.038148121	0	144	138	157	254	141	237	194	106	176	196
ENSMUSG00000032109	chr9	Nlrx1	0.00374989	0.985957675	0.991216367	4.690460589	0.022765218	0	419	351	323	432	384	462	411	369	359	508
ENSMUSG00000031158	chrX	Timm17b	-0.0029186	0.986106006	0.991283719	4.893713226	0.023916724	0	536	445	363	472	388	566	447	406	501	501

ENSMUSG00000059741	chr9	Myl3	-0.0196567	0.986544033	0.991652719	6.70710225	1.479275351	0	3	241	143	9041	103	5469	50	1419	1740	54
ENSMUSG00000020638	chr12	Cmpk2	0.00905792	0.987094963	0.9920638	2.245495579	0.059990913	0	76	55	64	95	56	68	92	66	44	110
ENSMUSG00000089917	chr2	Uckl1	-0.0031096	0.987052549	0.9920638	4.414980856	0.025281712	0	363	326	278	360	256	413	293	279	367	384
ENSMUSG00000002486	chr5	Tchp	-0.0095708	0.987568922	0.992468775	2.452667947	0.047346383	0	86	80	50	111	77	114	76	96	69	81
ENSMUSG00000041837	chr9	Pdcd7	0.00396692	0.987665267	0.992494231	3.616880317	0.033153939	0	193	159	148	268	149	300	199	159	168	178
ENSMUSG00000020021	chr10	Fgd6	0.00605788	0.988210757	0.992828232	2.440716159	0.055132175	0	87	67	78	100	64	105	106	50	61	118
ENSMUSG00000026473	chr1	Glul	-0.0034317	0.988206476	0.992828232	7.682714578	0.065581342	0	2802	3620	2666	2216	3635	5362	2406	3029	2353	3829
ENSMUSG00000078173	chr3	Lenep	0.00386532	0.988076235	0.992828232	2.594056498	0.041916442	0	72	83	79	129	81	109	102	111	83	77
ENSMUSG00000028622	chr4	Mrpl37	-0.0023341	0.98877919	0.993327915	6.573779547	0.025307576	0	1344	1384	1350	1791	1245	1745	1416	1568	1548	1469
ENSMUSG00000053950	chr18	Adnp2	-0.0041067	0.988959611	0.993437758	2.885655999	0.031984106	0	109	85	102	145	104	110	138	104	115	125
ENSMUSG00000020380	chr11	Rad50	-0.0064977	0.989308609	0.993716912	2.972888331	0.030167051	0	123	112	93	152	101	122	137	103	115	154
ENSMUSG00000025510	chr7	Cd151	-0.0019788	0.990381661	0.994710308	6.631650976	0.028562453	0	1639	1593	1291	1511	1308	1878	1405	1541	1628	1629
ENSMUSG00000037104	chr17	Socs5	0.00236028	0.990439943	0.994710308	3.930160957	0.025448573	0	213	218	203	319	184	279	285	203	260	211
ENSMUSG00000027236	chr2	Eif3j1	0.00282865	0.99057143	0.994729865	5.736037301	0.064633798	0	852	715	669	1076	685	403	1132	744	1128	882
ENSMUSG00000040705	chr7	A930016O22Rik	-0.0084415	0.990601764	0.994729865	6.162580694	0.552876021	0	482	525	258	1984	2204	429	192	3038	110	1819
ENSMUSG00000028736	chr4	Pax7	-0.006214	0.99071754	0.994774649	2.698807529	0.064752686	0	101	83	96	106	88	79	111	156	68	98
ENSMUSG00000093242	chr2	Gm24574	0.01361624	0.991023876	0.995010754	1.694239532	0.316699598	0	19	47	60	95	16	64	136	13	26	21
ENSMUSG00000050069	chr1	Grem2	-0.0046312	0.991186158	0.995102202	4.644752471	0.143119518	0	481	345	261	348	408	104	370	279	460	803
ENSMUSG00000021973	chr14	Micu2	-0.0021024	0.991556834	0.995402838	5.874317557	0.029082711	0	1039	823	796	1078	654	1086	886	756	1116	938
ENSMUSG00000037470	chr1	Uggt1	-0.0020842	0.991939705	0.995715673	5.636471202	0.027952092	0	714	633	587	990	798	834	859	657	897	802
ENSMUSG00000027580	chr2	Helz2	-0.0013138	0.992268968	0.995974656	3.346126864	0.037170765	0	123	120	141	197	169	198	197	120	123	190
ENSMUSG00000057143	chr7	Trim12c	0.00484654	0.992883076	0.996519488	3.395213693	0.041728298	0	166	195	164	138	102	170	160	157	172	190
ENSMUSG00000021520	chr13	Uqcrb	0.00137016	0.993074847	0.996640389	8.275466996	0.028065168	0	4923	4693	4216	5786	3569	5816	4960	4637	5207	4690
ENSMUSG00000056174	chr4	Col8a2	0.00651326	0.993416387	0.996911569	3.031353583	0.085596153	0	186	95	81	154	90	201	179	55	101	137
ENSMUSG00000030876	chr7	Mettl9	-0.0020887	0.994896601	0.998325309	4.331978898	0.025687131	0	275	275	299	381	266	297	403	269	345	317
ENSMUSG00000054874	chr19	Pcnxl3	0.00228462	0.994996737	0.99835411	4.358405314	0.023581485	0	288	279	260	397	301	448	334	288	265	345
ENSMUSG00000027282	chr2	Mtch2	0.00096477	0.995111314	0.998397395	7.024708012	0.025459158	0	1828	1939	1850	2577	1559	2199	2189	1915	2176	2138
ENSMUSG00000014243	chr11	Zswim7	-0.0022809	0.995960448	0.999177605	4.164301398	0.028530924	0	283	265	251	322	210	284	283	235	368	278
ENSMUSG00000073609	chr1	D2hgdh	0.00216238	0.996383806	0.999530583	3.842229507	0.099066259	0	196	204	193	247	216	63	279	234	266	301
ENSMUSG00000001767	chr2	Crnkl1	-0.0010525	0.996666772	0.999742683	4.331336546	0.023814831	0	334	298	284	327	245	357	346	249	354	331
ENSMUSG00000003810	chr4	Mast2	-2.602E-06	1	1	6.34135969	0.035497868	0	1009	914	1074	1784	1312	1281	1243	1374	1121	1578
ENSMUSG00000016386	chr2	Mpped2	-0.0055265	1	1	0.655178589	0.220220603	0	10	10	20	66	9	22	19	16	40	19
ENSMUSG00000019080	chr15	Mfsd3	0.00266854	1	1	3.37686416	0.026693512	0	168	161	122	157	152	179	169	158	153	180
ENSMUSG00000021023	chr12	1110008L16Rik	0.00097141	1	1	3.061712307	0.03030833	0	140	112	102	147	113	132	125	144	116	153
ENSMUSG00000023066	chr18	Rttn	0.00049446	1	1	1.306774873	0.070392131	0	25	32	36	41	40	43	48	19	44	39
ENSMUSG00000024235	chr18	Map3k8	-0.0147279	1	1	1.00119096	0.0754055	0	45	18	26	32	20	38	27	21	34	33
ENSMUSG00000024352	chr18	Spata24	-0.0100092	1	1	0.825662577	0.113713924	0	38	31	19	23	12	35	23	18	40	18
ENSMUSG00000024778	chr19	Fas	0.00653902	1	1	2.10477159	0.042283819	0	70	59	53	69	59	93	78	60	53	60
ENSMUSG00000026113	chr1	Inpp4a	-2.01E-05	0.998511644	1	4.269673037	0.034864138	0	258	243	236	456	260	235	341	275	342	364
ENSMUSG00000027438	chr2	Napb	-7.338E-05	1	1	2.779823644	0.051451433	0	141	96	98	82	80	101	98	99	119	132
ENSMUSG00000027478	chr2	Dnmt3b	0.0047368	1	1	0.474047799	0.068899766	0	14	19	24	18	18	18	18	21	20	26
ENSMUSG00000027864	chr3	Ptgfrn	-8.859E-05	1	1	5.802379817	0.02953944	0	867	734	777	982	788	1064	933	931	597	1042
ENSMUSG00000029864	chr6	Gstk1	0.00091282	0.997425338	1	4.477552607	0.023081268	0	304	362	289	423	279	404	344	335	394	330
ENSMUSG00000030806	chr7	Stx1b	-0.0053734	1	1	0.752850156	0.094643415	0	16	26	20	22	31	25	18	31	16	37
ENSMUSG00000031068	chr7	Glrx3	0.00048007	0.998541701	1	6.737837445	0.02597939	0	1631	1602	1518	1857	1332	2040	1825	1559	1771	1522
ENSMUSG00000031284	chrX	Pak3	-0.0049819	1	1	0.032343361	0.231608593	0	15	23	18	5	4	27	12	7	6	23
ENSMUSG00000031381	chrX	Piga	0.01073865	1	1	1.443351084	0.066739053	0	38	41	33	48	33	54	66	34	31	29
ENSMUSG00000035504	chr10	Reep6	0.01306449	1	1	0.782788205	0.103297116	0	22	20	21	27	28	13	19	38	23	36
ENSMUSG00000037185	chr15	Krt80	0.01862324	1	1	0.522376464	0.119673496	0	9	20	11	27	30	24	27	11	28	18
ENSMUSG00000037845	chr9	Fdxacb1	-0.0009732	1	1	2.592131567	0.038534387	0	101	87	84	77	86	96	101	89	98	97
ENSMUSG00000038233	chr9	Fam198a	0.00510172	1	1	1.300022415	0.067244052	0	38	28	39	32	35	28	43	27	42	51
ENSMUSG00000040183	chr4	Ankrd6	-0.0188896	1	1	0.823923254	0.068439412	0	20	30	24	34	16	39	28	22	26	19
ENSMUSG00000040710	chr1	St8sia4	0.00382085	1	1	2.862724693	0.072916427	0	98	120	131	115	65	104	120	63	115	187
ENSMUSG00000041012	chr9	Cmtm8	0.0005782	1	1	1.285918399	0.076310763	0	26	31	41	53	23	47	28	50	31	32
ENSMUSG00000041995	chr13	Zbed3	0.00536488	1	1	2.446767231	0.051903223	0	90	91	74	83	57	83	94	92	56	111
ENSMUSG00000042138	chr9	Msantd2	-0.0025585	1	1	1.486727174	0.04928795	0	45	35	44	43	32	62	45	34	38	41
ENSMUSG00000047342	chr11	Zfp286	-0.0060328	1	1	0.588764384	0.092275674	0	29	18	20	22	14	19	12	31	25	24
ENSMUSG00000050295	chr13	Foxc1	0.02426205	1	1	0.245769253	0.074610967	0	16	14	10	17	21	13	21	17	15	21
ENSMUSG00000050605	chr7	Zfp61	0.00769013	1	1	1.742394594	0.045337734	0	56	56	34	56	38	57	56	48	47	56
ENSMUSG00000052137	chr4	Rbm12b2	0.0075529	1	1	1.932635477	0.054515182	0	58	49	49	68	51	78	78	32	51	67
ENSMUSG00000053025	chr7	Sv2b	-0.0474056	1	1	-0.306544877	0.211571953	0	4	4	11	30	5	16	6	16	8	8
ENSMUSG00000053647	chr5	Gper1	-0.0037261	1	1	0.775713632	0.074591388	0	22	12	25	40	21	21	30	22	26	30
ENSMUSG00000053965	chr3	Pde5a	-0.0057081	1	1	2.400110909	0.037575206	0	79	72	66	97	72	98	90	87	59	87
ENSMUSG00000062590	chr1	Armc9	-0.0018684	1	1	1.657394466	0.0440274	0	43	45	43	50	44	60	42	47	39	60
ENSMUSG00000064128	chr14	Cenpj	-0.0084148	1	1	1.797011643	0.06307998	0	47	53	54	68	30	45	59	38	70	60

ENSMUSG00000066057	chr17	Gm1976	0.0057595	1	1	0.765147934	0.080260705	0	31	27	21	19	18	29	19	28	17	36
ENSMUSG00000070720	chr4	Tmem200b	-0.0073294	1	1	1.19090768	0.057496068	0	32	28	25	49	29	42	23	30	37	44
ENSMUSG00000074623	chr2	Gm826	-0.0165225	1	1	-0.354089265	0.180712701	0	8	16	2	17	7	19	6	14	10	4
ENSMUSG00000079507	chr17	H2-Q1	0.01950753	1	1	0.334398971	0.478038579	0	10	12	25	24	12	77	3	8	4	6
ENSMUSG00000086427	chr6	Hoxa11os	-0.0244021	1	1	0.264181208	0.093159559	0	22	10	16	26	8	16	18	10	21	22
ENSMUSG00000097210	chr7	Fam160a2	-0.0097508	1	1	1.041838722	0.052987739	0	36	26	26	35	22	32	38	29	33	25
ENSMUSG00000097885	chr3	5031434O11Rik	-0.008804	1	1	0.632132033	0.070715433	0	27	22	18	21	18	35	17	17	18	30
ENSMUSG00000104435	chr1	RP24-288J3.2	0.0297096	1	1	-0.257796671	0.774366626	0	5	1	2	21	25	3	3	38	0	12

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Table S8. RNA sequencing analysis and differential expression data of D2-mdx vs D2-WT mice at 6 months of age. Raw reads were mapped to chromosomes and gene identifiers and subsequent differential analysis was completed (n = 5 per group).

Ensembl ID	Chromosome	Gene Name	Start	End	Length	logFC_D2-mdx.6mo_D2-WT.6mo	logCPM_D2-mdx.6mo_D2-WT.6mo	P-value_D2-mdx.6mo_D2-WT.6mo	FDR_D2-mdx.6mo_D2-WT.6mo	Tgw.Disp	UpDown.Tgw	D2-WT.6mo_Rep1_raw	D2-WT.6mo_Rep2_raw	D2-WT.6mo_Rep3_raw	D2-WT.6mo_Rep4_raw	D2-WT.6mo_Rep5_raw	D2-mdx.6mo_Rep1_raw	D2-mdx.6mo_Rep2_raw	D2-mdx.6mo_Rep3_raw	D2-mdx.6mo_Rep4_raw	D2-mdx.6mo_Rep5_raw
ENSMUSG00000028238	chr4	Atp6v0d2	2E+07	2E+07	2716	7.184145742	3.989373155	1.035E-73	1.45166E-69	0.08183	1	2	2	7	0	5	398	800	380	765	884
ENSMUSG00000030789	chr7	Itgax	1.3E+08	1.3E+08	4045	6.95781205	4.98182892	4.396E-72	3.08317E-68	0.0924	1	5	5	9	6	13	690	1367	662	1619	2135
ENSMUSG00000044303	chr4	Cdkn2a	8.9E+07	8.9E+07	1172	7.225575065	3.395567523	2.476E-65	1.15767E-61	0.08465	1	0	1	2	2	5	409	255	389	578	450
ENSMUSG00000029304	chr5	Spp1	1E+08	1E+08	1648	3.907592086	5.379840904	4.734E-64	1.66004E-60	0.0476	1	58	35	126	101	84	1667	1948	1268	1567	1577
ENSMUSG00000050335	chr14	Lgals3	4.7E+07	4.7E+07	1858	5.084725483	6.997155703	1.069E-62	2.99902E-59	0.07669	1	83	71	118	76	222	4756	4989	3021	6293	6794
ENSMUSG00000009214	chr2	Tmem8c	2.7E+07	2.7E+07	1511	6.426076029	3.853443639	2.178E-59	5.0926E-56	0.09409	1	4	0	14	7	0	577	395	500	623	785
ENSMUSG00000049723	chr9	Mmp12	7344381	7344437	7237	7.831258821	6.160321996	3.07E-59	6.15122E-56	0.14367	1	4	1	14	6	25	1634	4056	1471	3350	4315
ENSMUSG00000038642	chr3	Ctss	9.6E+07	9.6E+07	1358	4.281451607	6.74186555	2.545E-57	3.96623E-54	0.06518	1	118	123	139	118	303	5577	4030	2738	4255	4722
ENSMUSG00000079471	chr17	Gm7325	4.6E+07	4.6E+07	976	7.182971455	2.472465819	2.265E-57	3.96623E-54	0.07642	1	1	2	2	0	0	218	168	187	245	268
ENSMUSG00000046805	chr19	Mpeg1	1.2E+07	1.2E+07	4335	4.087394824	5.661868386	2.015E-56	2.82645E-53	0.05925	1	59	69	97	52	154	2221	2606	1254	1698	2206
ENSMUSG00000056888	chr10	Glipr1	1.1E+08	1.1E+08	1543	5.40218968	2.982620566	4.809E-56	6.13183E-53	0.06949	1	2	2	8	6	9	266	314	224	309	440
ENSMUSG00000072812	chr12	Ahnak2	1.1E+08	1.1E+08	14163	3.139485619	5.327474297	1.586E-53	1.85324E-50	0.03962	1	94	81	146	141	162	2258	1278	1048	1394	1554
ENSMUSG00000000290	chr10	Itgb2	7.8E+07	7.8E+07	3052	4.23940881	5.093588312	8.459E-53	9.12643E-50	0.06612	1	34	35	48	42	105	1128	1517	717	1647	1735
ENSMUSG00000040751	chr5	Lat2	1.3E+08	1.3E+08	1505	4.394238959	3.564341495	1.628E-48	1.63134E-45	0.06814	1	14	10	13	8	36	550	374	323	489	573
ENSMUSG00000026796	chr2	Fam129b	3.3E+07	3.3E+07	4672	3.021320685	5.631832604	2.315E-48	2.16431E-45	0.04257	1	143	119	170	148	246	1701	1751	1301	2181	2155
ENSMUSG00000001020	chr3	S100a4	9.1E+07	9.1E+07	587	3.737908572	5.778916678	2.226E-47	1.95175E-44	0.06208	1	104	71	146	82	190	3368	1385	1740	1945	2155
ENSMUSG00000028111	chr3	Ctsk	9.5E+07	9.5E+07	1482	4.656748969	6.484244342	4.411E-47	3.63962E-44	0.08989	1	101	80	71	62	204	2842	3981	2201	4287	4536
ENSMUSG00000026253	chr1	Chrng	8.7E+07	8.7E+07	4163	5.814172139	3.197333079	9.841E-47	7.66816E-44	0.10177	1	1	1	6	5	11	399	187	316	395	507
ENSMUSG00000038147	chr1	Cd84	1.7E+08	1.7E+08	6272	4.51661744	3.775949985	2.878E-46	2.1243E-43	0.07683	1	10	14	10	12	40	552	688	305	535	633
ENSMUSG00000023992	chr17	Trem2	4.8E+07	4.8E+07	4946	5.389033403	4.576871137	1.474E-45	1.03364E-42	0.10952	1	12	6	10	9	50	835	889	621	1265	1179
ENSMUSG00000044811	chr11	AF251705	1.1E+08	1.1E+08	1275	5.047423751	2.535815881	2.107E-44	1.4075E-41	0.07887	1	2	2	4	3	14	267	197	171	207	285
ENSMUSG00000032122	chr9	Slc37a2	3.7E+07	3.7E+07	5079	3.602354368	3.661040995	3.911E-44	2.49323E-41	0.05466	1	26	31	25	16	43	521	553	313	527	483
ENSMUSG00000034652	chr11	Cd300a	1.1E+08	1.1E+08	4738	3.688928364	3.521773008	1.5E-43	9.14827E-41	0.05772	1	20	17	23	20	44	435	456	244	475	584
ENSMUSG00000020120	chr11	Plek	1.7E+07	1.7E+07	4486	3.037219504	4.167317362	1.722E-43	1.00651E-40	0.04353	1	52	46	41	62	89	708	744	458	663	721
ENSMUSG00000001131	chrX	Timp1	2.1E+07	2.1E+07	888	5.390722873	4.479327796	3.564E-43	1.99956E-40	0.11504	1	12	12	32	9	14	1524	509	1119	616	593
ENSMUSG00000030144	chr6	Clec4d	1.2E+08	1.2E+08	1336	5.464234313	2.253489812	1.309E-42	7.06337E-40	0.08596	1	0	1	1	6	7	161	202	128	207	226
ENSMUSG00000079293	chr6	Clec7a	1.3E+08	1.3E+08	2287	3.797901797	3.026836595	6.748E-42	3.50528E-39	0.05871	1	18	13	19	13	17	298	361	194	269	424
ENSMUSG00000042436	chr11	Mfap4	6.1E+07	6.1E+07	1922	3.045020649	5.573674319	1.154E-41	5.78198E-39	0.05046	1	166	123	178	152	147	2475	1163	1358	1684	2116
ENSMUSG00000056737	chr6	Capg	7.3E+07	7.3E+07	2529	3.146321712	5.790941348	9.571E-41	4.62907E-38	0.05515	1	145	106	165	140	311	2322	1800	1300	2459	2474
ENSMUSG00000021728	chr13	Emb	1.2E+08	1.2E+08	2253	3.771677557	3.855480723	5.548E-40	2.59368E-37	0.0685	1	20	23	46	39	19	791	359	487	502	605
ENSMUSG00000031760	chr8	Mt3	9.4E+07	9.4E+07	538	4.047367834	2.207562531	1.293E-38	5.84937E-36	0.06117	1	5	5	9	9	10	247	186	108	160	177
ENSMUSG00000039062	chr7	Anpep	8E+07	8E+07	3879	3.222958721	6.243278133	3.3E-38	1.44657E-35	0.06181	1	173	177	186	219	350	2964	2482	1621	3406	3818
ENSMUSG00000053687	chr8	Dpep2	1.1E+08	1.1E+08	4540	4.356280318	2.892519837	4.193E-38	1.78211E-35	0.08236	1	11	7	10	4	19	234	296	170	333	399
ENSMUSG00000026600	chr1	Soat1	1.6E+08	1.6E+08	9791	2.631867303	4.211487669	1.128E-36	4.65441E-34	0.04064	1	69	74	84	57	97	701	679	420	757	734
ENSMUSG00000050390	chr4	C77080	1.3E+08	1.3E+08	5770	2.898104654	4.015948649	1.59E-36	6.37348E-34	0.04898	1	34	34	83	55	89	548	640	390	738	611
ENSMUSG00000025473	chr7	Adam8	1.4E+08	1.4E+08	4638	3.712638408	3.058328539	8.318E-36	3.24062E-33	0.07034	1	6	11	21	19	32	376	259	230	300	405
ENSMUSG00000009687	chr7	Fxyd5	3.1E+07	3.1E+07	4185	2.571658873	4.973518366	1.204E-35	4.49627E-33	0.04268	1	102	78	185	128	209	1536	817	881	1144	1173
ENSMUSG00000015745	chr3	Plekho1	9.6E+07	9.6E+07	2172	2.571358361	5.143360446	1.218E-35	4.49627E-33	0.04304	1	115	85	205	135	254	1641	1060	893	1201	1487
ENSMUSG00000024300	chr17	Myo1f	3.4E+07	3.4E+07	4914	3.80428424	3.89364701	2.629E-35	9.45648E-33	0.08105	1	18	21	16	28	67	611	550	341	621	739
ENSMUSG00000031394	chrX	Opn1mw	7.4E+07	7.4E+07	1562	-3.97262968	2.637532663	3.317E-35	1.16323E-32	0.07992	-1	178	136	165	204	191	29	23	5	11	11
ENSMUSG00000027797	chr3	Dclk1	5.5E+07	5.5E+07	12991	2.956367628	3.90041424	4.071E-35	1.39258E-32	0.05225	1	50	34	48	47	77	741	383	511	481	564
ENSMUSG00000030047	chr6	Arhgap25	8.7E+07	8.7E+07	4250	3.215703885	3.22417144	1.319E-34	4.40483E-32	0.05749	1	30	18	24	27	35	316	352	211	353	488
ENSMUSG00000001473	chr18	Tubb6	6.7E+07	6.7E+07	1757	2.90443497	5.673045624	2.119E-34	6.91168E-32	0.05738	1	143	80	296	192	236	2398	1459	1739	1995	1598
ENSMUSG00000031880	chr8	Rrad	1E+08	1E+08	1575	4.374559752	5.47801206	2.3E-34	7.31845E-32	0.11251	1	33	23	114	84	71	2304	866	2099	1499	1727
ENSMUSG00000044734	chr13	Serpinb1a	3.3E+07	3.3E+07	1943	3.295845109	5.013882368	2.348E-34	7.31845E-32	0.06904	1	100	81	82	68	109	2035	969	1154	1145	717
ENSMUSG00000045103	chrX	Dmd	8.3E+07	8.3E+07	23801	-4.26117502	6.371106254	2.953E-34	9.00444E-32	0.10996	-1	2569	1829	3267	2925	1082	210	306	87	139	130
ENSMUSG00000005087	chr2	Cd44	1E+08	1E+08	6776	2.622268104	4.889539637	4.333E-34	1.29303E-31	0.04646	1	96	59	147	117	229	1276	1033	840	936	1165
ENSMUSG00000042254	chr9	Cilp	6.5E+07	6.5E+07	4252	2.68604239	7.291717351	7.719E-34	2.25569E-31	0.05142	1	495	536	789	567	800	8395	4603	4095	5824	5427
ENSMUSG00000018774	chr11	Cd68	7E+07	7E+07	1257	4.317190042	5.920780297	1.085E-33	3.10611E-31	0.11302	1	56	80	50	55	197	2127	2222	1391	3062	3180
ENSMUSG00000037280	chr15	Galnt6	1E+08	1E+08	3871	4.765465535	2.261757673	1.419E-33	3.98122E-31	0.10232	1	5	0	6	3	11	145	228	100	225	228
ENSMUSG00000000682	chr4	Cd52	1.3E+08	1.3E+08	1187	4.374569404	2.846110656	2.177E-33	5.98754E-31	0.09926	1	7	3	11	7	22	343	174	181	272	423
ENSMUSG00000061451	chr19	Tmem151a	5070859	5071111	4807	7.002715029	1.208034057	3.019E-33	8.14251E-31	0.10754	1	0	0	1	0	1	84	60	86	109	89
ENSMUSG00000091345	chr9	Col6a5	1.1E+08	1.1E+08	9405	4.995540159	1.904662165	3.648E-33	9.65315E-31	0.09705	1	1	4	5	0	6	185	117	147	139	114
ENSMUSG00000020901	chr11	Pik3r5	6.8E+07	6.8E+07	5550	3.055999921	2.794708382	4.846E-32	1.2587E-29	0.05421	1	15	15	30	20	31	244	267	168	260	313
ENSMUSG00000026956	chr2	Uap1l1	2.5E+07	2.5E+07	4071	3.013394468	3.579396767	6.545E-32	1.66908E-29	0.05931	1	21	25	41	38	76	441	417	333	507	462
ENSMUSG00000001864	chr2	Aif1l	3.2E+07	3.2E+07	4032	3.358372461	4.634456455	8.412E-32	2.10701E-29	0.07668	1	49	57	56	68	99	771	522	943	963	1315
ENSMUSG00000030218	chr6	Mgp	1.4E+08	1.4E+08	598	3.393406718	6.933183507	1.047E-31	2.57609E-29	0.08266	1	287	267	387	367	272	5747	2236	4707	4331	5595
ENSMUSG00000026414	chr1	Tnnt2	1.4E+08	1.4E+08	7752	3.826366086	4.240845389	1.425E-31	3.44585E-29	0.09553	1	22	18	84	49	20	848	557	651	578	951

ENSMUSG00000062760	chr15	1810041L15Rik	8.4E+07	8.4E+07	6551	3.304265717	2.807229585	5.57E-31	1.32407E-28	0.06491	1	24	15	18	10	27	292	265	164	327	241
ENSMUSG00000024672	chr19	Ms4a7	1.1E+07	1.1E+07	4453	4.030322053	3.468115782	8.03E-31	1.87714E-28	0.1002	1	10	20	12	13	39	787	329	298	379	369
ENSMUSG00000006731	chr10	B4galnt1	1.3E+08	1.3E+08	2474	3.808595686	2.678201765	1.384E-30	3.18131E-28	0.08566	1	13	3	10	11	27	272	196	185	219	327
ENSMUSG00000089929	chr9	Bcl2a1b	8.9E+07	8.9E+07	817	4.643562453	1.977684208	1.698E-30	3.84094E-28	0.09918	1	4	6	3	2	6	137	128	106	129	243
ENSMUSG00000023043	chr15	Krt18	1E+08	1E+08	1400	6.294710738	3.159766997	2.391E-30	5.32392E-28	0.18656	1	3	3	3	4	3	98	202	412	454	526
ENSMUSG00000024737	chr19	Slc15a3	1.1E+07	1.1E+07	5491	3.893682836	3.382389086	2.689E-30	5.89413E-28	0.09822	1	8	7	26	21	40	291	407	242	450	599
ENSMUSG00000025877	chr13	Hk3	5.5E+07	5.5E+07	3682	3.576096607	3.548758467	3.989E-30	8.60721E-28	0.08475	1	22	26	13	19	53	424	431	264	518	575
ENSMUSG00000061086	chr11	Myl4	1E+08	1E+08	4637	4.330978855	5.74573431	6.299E-30	1.33858E-27	0.12907	1	66	21	160	112	42	2929	1320	1866	1705	2682
ENSMUSG00000001270	chr12	Ckb	1.1E+08	1.1E+08	1478	3.343001637	5.667489229	7.386E-30	1.54612E-27	0.08425	1	100	97	135	105	266	1482	1581	1075	2737	2707
ENSMUSG00000040613	chr6	Apobec1	1.2E+08	1.2E+08	2391	2.518896637	3.52017819	1.301E-29	2.68345E-27	0.04565	1	45	31	52	44	86	523	401	270	376	443
ENSMUSG00000018920	chr11	Cxcl16	7E+07	7E+07	3021	2.528314824	4.05122738	4.875E-29	9.91024E-27	0.04948	1	49	47	86	65	129	756	482	394	578	712
ENSMUSG00000022952	chr16	Runx1	9.3E+07	9.3E+07	11827	2.935301415	3.409695808	7.335E-29	1.46975E-26	0.06246	1	41	18	36	36	54	373	342	407	315	427
ENSMUSG00000072945	chrX	Ripply1	1.4E+08	1.4E+08	811	5.794799844	0.901109768	1.074E-28	2.12075E-26	0.09521	1	1	1	1	1	0	74	50	63	68	84
ENSMUSG00000040907	chr7	Atp1a3	2.5E+07	2.5E+07	5972	4.428032086	3.228934348	2.313E-28	4.5058E-26	0.12648	1	20	6	4	9	22	255	390	170	517	500
ENSMUSG00000028843	chr4	Sh3bgrl3	1.3E+08	1.3E+08	821	2.774446643	5.166213767	2.623E-28	5.03887E-26	0.06372	1	111	80	136	107	278	1395	936	914	1596	1617
ENSMUSG00000075330	chr16	A930003A15Rik	2E+07	2E+07	746	4.049580766	2.269101145	3.842E-28	7.28132E-26	0.09722	1	8	4	12	8	8	175	113	185	260	148
ENSMUSG00000031375	chrX	Bgn	7.3E+07	7.3E+07	6099	2.545684367	7.946607792	4.728E-28	8.84109E-26	0.05719	1	871	597	1352	1066	1761	12823	7315	6785	8650	8299
ENSMUSG00000029322	chr5	Plac8	1E+08	1E+08	1592	4.402573837	2.285736776	4.026E-27	7.34321E-25	0.11793	1	3	4	4	6	15	359	149	131	188	117
ENSMUSG00000071714	chr15	Csf2rb2	7.8E+07	7.8E+07	4612	2.51540233	3.711172817	4.031E-27	7.34321E-25	0.05099	1	47	57	65	49	69	430	519	264	477	606
ENSMUSG00000003363	chr7	Pld3	2.8E+07	2.8E+07	2924	2.511333732	5.94118231	7.856E-27	1.41274E-24	0.05772	1	239	171	321	292	384	1812	1875	1274	3034	2840
ENSMUSG00000087410	chr11	2310065F04Rik	6.7E+07	6.7E+07	2916	-3.22744642	6.279375562	1.576E-26	2.79845E-24	0.09173	-1	2406	2032	2137	1853	1810	217	584	173	327	267
ENSMUSG00000031827	chr8	Cotl1	1.2E+08	1.2E+08	1628	3.060878027	5.143852707	2.129E-26	3.73212E-24	0.08174	1	86	90	77	73	251	1507	1161	801	1616	1484
ENSMUSG00000076609	chr6	Igkc	7.1E+07	7.1E+07	323	3.838861969	2.759435903	2.29E-26	3.965E-24	0.10515	1	4	8	9	15	30	398	275	126	232	279
ENSMUSG00000024803	chr19	Ankrd1	3.6E+07	3.6E+07	1765	4.209736854	6.857425737	2.382E-26	4.07441E-24	0.14345	1	193	155	244	214	65	4537	2254	6019	4045	4774
ENSMUSG00000076612	chr12	Ighg2c	1.1E+08	1.1E+08	1326	8.724538175	2.155656004	3.097E-26	5.23413E-24	0.25458	1	0	0	1	0	0	549	96	70	114	107
ENSMUSG00000040659	chr4	Efhd2	1.4E+08	1.4E+08	2381	2.307089728	4.916558504	6.178E-26	1.03162E-23	0.04954	1	100	103	161	137	282	1262	842	736	1154	1203
ENSMUSG00000030579	chr7	Tyrobp	3E+07	3E+07	564	3.358352227	4.732202604	8.293E-26	1.36846E-23	0.09695	1	57	74	38	38	142	1351	751	712	1217	978
ENSMUSG00000022488	chr15	Nckap1l	1E+08	1E+08	4717	2.934957657	4.237112609	1.186E-25	1.93411E-23	0.07545	1	54	62	35	45	127	871	702	469	644	764
ENSMUSG00000031838	chr8	Ifi30	7.1E+07	7.1E+07	980	2.226019734	4.736980878	1.207E-25	1.94631E-23	0.04663	1	122	75	163	122	247	1085	704	669	1119	950
ENSMUSG00000052336	chr9	Cx3cr1	1.2E+08	1.2E+08	3742	3.448195413	2.496168689	1.485E-25	2.36619E-23	0.08697	1	14	10	17	4	25	292	162	193	176	205
ENSMUSG00000034361	chr8	Cpne2	9.5E+07	9.5E+07	3198	2.631046153	4.945811641	2.23E-25	3.51372E-23	0.06468	1	135	105	147	69	190	915	785	1000	1286	1361
ENSMUSG00000006519	chr8	Cyba	1.2E+08	1.2E+08	758	3.365092427	5.441723721	3.177E-25	4.95062E-23	0.10209	1	54	76	97	106	267	1538	1248	1030	2257	2116
ENSMUSG00000031444	chr8	F10	1.3E+07	1.3E+07	2731	5.150590363	0.982275085	3.574E-25	5.50837E-23	0.11463	1	1	1	2	0	3	57	85	36	102	84
ENSMUSG00000039208	chr11	Metrnl	1.2E+08	1.2E+08	1586	2.255008228	4.226024114	3.85E-25	5.80644E-23	0.04752	1	78	60	117	77	167	749	481	512	738	682
ENSMUSG00000053063	chr6	Clec12a	1.3E+08	1.3E+08	5139	3.667512154	3.488496132	3.81E-25	5.80644E-23	0.11065	1	21	12	17	12	64	636	312	272	425	506
ENSMUSG00000027848	chr3	Olfml3	1E+08	1E+08	4014	2.121352844	4.819470506	4.352E-25	6.49327E-23	0.0442	1	126	113	249	110	215	1431	836	723	962	814
ENSMUSG00000021998	chr14	Lcp1	7.5E+07	7.5E+07	9504	3.133540372	5.640814481	4.418E-25	6.52289E-23	0.09102	1	87	129	102	115	347	2257	1864	1258	1735	2209
ENSMUSG00000027386	chr2	Fbln7	1.3E+08	1.3E+08	3228	3.214666229	3.880877096	4.536E-25	6.62746E-23	0.08927	1	51	39	28	41	48	764	245	417	648	647
ENSMUSG00000060429	chr15	Sntb1	5.6E+07	5.6E+07	2869	-3.97481797	1.572687929	6.348E-25	9.17874E-23	0.10228	-1	55	65	77	129	91	7	12	6	6	5
ENSMUSG00000003882	chr15	Il7r	9506161	9508358	3208	4.573867424	1.86187603	7.735E-25	1.10701E-22	0.12985	1	0	3	6	3	9	100	220	64	156	153
ENSMUSG00000030342	chr6	Cd9	1.3E+08	1.3E+08	2044	1.905720027	5.659110284	1.416E-24	2.00678E-22	0.03753	1	306	262	335	284	408	2042	1467	1145	1747	1888
ENSMUSG00000031740	chr8	Mmp2	9.3E+07	9.3E+07	3038	2.268067326	7.897287528	1.508E-24	2.11482E-22	0.05344	1	1122	843	1375	1016	1947	10954	6525	6715	8083	8566
ENSMUSG00000028581	chr4	Laptm5	1.3E+08	1.3E+08	3788	3.452934343	5.96627379	1.567E-24	2.1762E-22	0.11147	1	91	118	99	116	385	2557	2061	1379	2957	3002
ENSMUSG00000034116	chr17	Vav1	5.7E+07	5.7E+07	3688	3.126451763	2.357510756	1.977E-24	2.71838E-22	0.07569	1	12	9	14	11	32	254	145	131	193	202
ENSMUSG00000047230	chrX	Cldn2	1.4E+08	1.4E+08	3325	5.326057085	0.931872922	2.823E-24	3.8436E-22	0.12409	1	1	0	4	1	0	56	54	78	68	84
ENSMUSG00000072620	chr11	Slfn2	8.3E+07	8.3E+07	1664	2.776183603	3.008451489	2.955E-24	3.98474E-22	0.06638	1	22	21	30	23	58	409	231	194	310	293
ENSMUSG00000020388	chr11	Pdlim4	5.4E+07	5.4E+07	2560	2.22042134	3.826246334	3.139E-24	4.19327E-22	0.04681	1	56	45	90	75	117	560	358	372	558	536
ENSMUSG00000004473	chr7	Clec11a	4.4E+07	4.4E+07	1952	2.832701862	3.654380608	3.495E-24	4.58181E-22	0.07329	1	47	33	54	43	54	779	245	344	545	362
ENSMUSG00000063632	chr12	Sox11	2.7E+07	2.7E+07	8311	5.330626526	1.44571355	3.483E-24	4.58181E-22	0.15324	1	0	1	1	2	5	84	64	120	76	152
ENSMUSG00000028599	chr4	Tnfrsf1b	1.5E+08	1.5E+08	3818	2.227621198	4.170124176	3.772E-24	4.89913E-22	0.04833	1	65	68	93	83	174	683	593	418	649	715
ENSMUSG00000034845	chr8	Plvap	7.1E+07	7.1E+07	2015	2.2952775	5.464587402	4.158E-24	5.34993E-22	0.05449	1	152	172	306	216	296	1804	1021	1078	2168	1507
ENSMUSG00000021190	chr12	Lgmn	1E+08	1E+08	2323	2.16262923	6.861720251	4.494E-24	5.73021E-22	0.0497	1	578	454	789	534	897	5554	3263	3455	3870	3462
ENSMUSG00000040552	chr6	C3ar1	1.2E+08	1.2E+08	4305	3.096707208	3.827335545	4.944E-24	6.2469E-22	0.08805	1	19	38	29	40	98	693	560	377	461	527
ENSMUSG00000027107	chr2	Chrna1	7.4E+07	7.4E+07	4386	2.655524241	6.179354482	6.334E-24	7.93273E-22	0.07245	1	274	202	479	316	243	2060	1819	2698	2683	3253
ENSMUSG00000060512	chr5	0610040J01Rik	6.4E+07	6.4E+07	1870	-3.41466069	2.104449815	7.714E-24	9.57486E-22	0.0914	-1	89	67	212	127	115	8	23	10	19	15
ENSMUSG00000040690	chr4	Col16a1	1.3E+08	1.3E+08	6750	1.96020044	4.730539489	1.084E-23	1.33399E-21	0.04003	1	146	137	166	156	204	1248	639	661	990	829
ENSMUSG00000017400	chr11	Stac2	9.8E+07	9.8E+07	3139	3.565411196	2.085395238	1.152E-23	1.40493E-21	0.09487	1	7	6	6	8	21	130	171	88	192	198
ENSMUSG00000001750	chr19	Tcirg1	3896050	3896192	4470	2.161421351	4.292157179	2.087E-23	2.52289E-21	0.04761	1	89	76	105	95	178	749	575	383	750	870
ENSMUSG00000063193	chr11	Cd300lb	1.1E+08	1.1E+08	2917	3.347638342	2.606430476	2.554E-23	3.06146E-21	0.09347	1	16	12	9	8	35	208	252	143	226	288
ENSMUSG00000048612	chr19	Myof	3.8E+07	3.8E+07	7109	1.931085345	4.429547921	2.619E-23	3.11272E-21	0.03857	1	110	93	134	129	214	843	894	445	646	727
ENSMUSG00000026442	chr1	Nfasc	1.3E+08	1.3E+08	14145	3.250942695	1.896948533	3.219E-23	3.79463E-21	0.07716	1	6	9	10	16	9	204	119	98	131	117
ENSMUSG00000056515	chr17	Rab31	6.6E+07	6.6E+07	3476	1.713257878	4.540825875	4.834E-23	5.65029E-21	0.0314	1	154	109	196	137	233	936	669	548	703	829
ENSMUSG00000004266	chr6	Ptpn6	1.2E+08	1.2E+08	2802	2.925262339	3.257434389	5.546E-23	6.42847E-21	0.08003	1	26	28	25	18	69	479	299	235	379	341
ENSMUSG00000046841	chr10	Ckap4	8.5E+07	8.5E+07	2954	2.071360956	4.855234395	5.993E-23	6.88962E-21	0.04673	1	165	96	203	143	249	1421	702	882	932	855
ENSMUSG00000021665	chr13	Hexb	9.7E+07	9.7E+07	1904	2.083800714	5.113435841	8.665E-23	9.86204E-21	0.04794	1	198	135	209	123	348	1466	1039	888	1210	1182
ENSMUSG00000043157	chr14	Arl11	6.1E+07	6.1E+07	1482	3.637569387	1.431571298	8.719E-23	9.86204E-21	0.0864	1	3	5	4	4	12	118	108	53	117	93
ENSMUSG00000047986	chr8	Palm3	8.4E+07	8.4E+07	3612	4.350552865	1.072532868	1.17E-22	1.3124E-20	0.10284	1	6	2	3	0	2	88	94	38	91	74

ENSMUSG00000004267	chr6	Eno2	1.2E+08	1.2E+08	4705	2.673941626	2.450029578	1.219E-22	1.35609E-20	0.06243	1	20	11	26	21	32	234	138	141	213	222
ENSMUSG00000006360	chr12	Crip1	1.1E+08	1.1E+08	445	2.333129991	6.513246598	1.228E-22	1.35609E-20	0.06101	1	344	264	493	462	791	4206	2211	2327	3469	3618
ENSMUSG00000025044	chr8	Msr1	4E+07	4E+07	3998	3.536060624	2.88794776	1.351E-22	1.47977E-20	0.11136	1	12	12	8	18	37	402	260	296	206	191
ENSMUSG00000040345	chr10	Arhgap9	1.3E+08	1.3E+08	1811	3.006712375	2.763928031	1.361E-22	1.47977E-20	0.08262	1	19	14	25	11	44	328	182	149	285	289
ENSMUSG00000069372	chr18	Ctxn3	5.7E+07	5.7E+07	1472	2.145458115	5.346975113	1.972E-22	2.12782E-20	0.05167	1	190	213	231	200	278	1462	2118	1054	1019	1208
ENSMUSG00000004707	chr1	Ly9	1.7E+08	1.7E+08	3307	4.161178647	2.020207873	2.034E-22	2.16238E-20	0.13153	1	3	6	4	0	18	203	132	105	149	175
ENSMUSG00000035279	chr7	Ssc5d	4925844	4925979	4284	1.91556488	5.287345083	2.035E-22	2.16238E-20	0.04167	1	211	176	272	219	369	1808	950	955	1372	1320
ENSMUSG00000005142	chr8	Man2b1	8.5E+07	8.5E+07	4325	2.226462569	5.586179661	2.9E-22	3.05821E-20	0.05631	1	191	179	233	230	464	1620	1547	1045	1905	2093
ENSMUSG00000079523	chr6	Tmsb10	7.3E+07	7.3E+07	1276	2.873708118	5.639825909	3.812E-22	3.98982E-20	0.09042	1	143	102	162	123	409	2544	1110	1483	2035	1877
ENSMUSG00000026480	chr1	Ncf2	1.5E+08	1.5E+08	8478	2.960861375	3.2417968	4.204E-22	4.36764E-20	0.08593	1	13	25	24	31	69	421	351	208	354	390
ENSMUSG00000024245	chr17	Tmem178	8.1E+07	8.1E+07	1696	4.415079751	1.859084397	4.883E-22	5.03567E-20	0.14913	1	2	0	9	4	9	82	132	76	167	224
ENSMUSG00000020098	chr10	Pcbd1	6.1E+07	6.1E+07	809	3.925498465	2.179039539	5.025E-22	5.14466E-20	0.12275	1	10	10	2	3	14	198	109	150	215	160
ENSMUSG00000020689	chr11	Itgb3	1E+08	1E+08	5901	2.495457825	3.293675089	8.257E-22	8.39221E-20	0.06309	1	42	29	41	52	55	276	304	215	409	489
ENSMUSG00000030220	chr6	Arhgdib	1.4E+08	1.4E+08	1839	1.937540762	4.790080335	8.901E-22	8.98149E-20	0.04345	1	112	113	209	161	290	1195	739	702	935	957
ENSMUSG00000026547	chr1	Tagln2	1.7E+08	1.7E+08	2082	2.307504272	6.096811336	9.057E-22	9.07413E-20	0.06218	1	221	203	407	306	671	2986	2030	1693	2478	2645
ENSMUSG00000039126	chr19	Prune2	1.7E+07	1.7E+07	12512	2.594754685	5.057290969	1.053E-21	1.04764E-19	0.07556	1	85	77	298	167	114	1085	1782	879	1035	1104
ENSMUSG00000031304	chrX	Il2rg	1E+08	1E+08	2387	2.665417911	2.844347608	1.105E-21	1.09108E-19	0.06982	1	27	12	29	27	53	339	198	167	270	292
ENSMUSG00000032322	chr9	Pstpip1	5.6E+07	5.6E+07	3830	3.868503539	2.298883423	1.15E-21	1.12779E-19	0.13123	1	4	1	8	9	26	194	139	142	190	249
ENSMUSG00000037405	chr9	Icam1	2.1E+07	2.1E+07	2540	2.114725758	3.480343234	1.162E-21	1.13164E-19	0.04672	1	54	47	61	56	95	450	302	268	408	426
ENSMUSG00000000957	chr14	Mmp14	5.4E+07	5.4E+07	2597	2.206838467	5.738554822	1.187E-21	1.14843E-19	0.05722	1	252	209	247	233	507	2565	1394	1372	1895	1886
ENSMUSG00000021943	chr14	Gdf10	3.4E+07	3.4E+07	2507	2.271995523	3.665502864	1.236E-21	1.18749E-19	0.05494	1	55	53	68	42	109	644	408	334	373	404
ENSMUSG00000101389	chr19	Ms4a4a	1.1E+07	1.1E+07	836	3.468803198	2.447503182	1.597E-21	1.52362E-19	0.10751	1	10	14	6	7	28	327	183	155	180	164
ENSMUSG00000030329	chr6	Pianp	1.2E+08	1.2E+08	2753	2.175299841	4.301297007	1.808E-21	1.71361E-19	0.05354	1	85	54	123	101	192	728	582	390	824	826
ENSMUSG00000015340	chrX	Cybb	9435252	9438343	5808	2.857970783	4.848526377	2.096E-21	1.97304E-19	0.09048	1	51	110	83	69	210	1240	1161	530	1144	1242
ENSMUSG00000046402	chr9	Rbp1	9.8E+07	9.8E+07	2652	2.816034935	3.075659193	2.673E-21	2.49968E-19	0.08013	1	29	26	19	31	48	363	179	228	354	368
ENSMUSG00000025534	chr5	Gusb	1.3E+08	1.3E+08	4548	1.987047091	5.341349476	3.519E-21	3.26865E-19	0.04783	1	208	138	266	212	446	1484	1305	853	1507	1586
ENSMUSG00000049382	chr15	Krt8	1E+08	1E+08	1805	6.139763589	2.083737937	4.168E-21	3.84613E-19	0.24578	1	0	3	1	1	3	48	90	236	169	228
ENSMUSG00000052837	chr8	Junb	8.5E+07	8.5E+07	1840	2.303699767	4.822779317	4.269E-21	3.91396E-19	0.06194	1	118	95	139	189	177	787	627	908	1271	1132
ENSMUSG00000026395	chr1	Ptprc	1.4E+08	1.4E+08	18313	2.34876652	3.625435872	5.178E-21	4.71613E-19	0.06057	1	40	50	51	56	106	498	507	260	343	526
ENSMUSG00000031762	chr8	Mt2	9.4E+07	9.4E+07	556	4.740082742	5.854781368	5.383E-21	4.87121E-19	0.21839	1	36	19	58	49	178	3776	981	3325	1727	1218
ENSMUSG00000058715	chr1	Fcer1g	1.7E+08	1.7E+08	874	3.402135967	4.711190361	5.905E-21	5.3088E-19	0.12542	1	55	57	27	37	166	1377	689	744	1094	1037
ENSMUSG00000026358	chr1	Rgs1	1.4E+08	1.4E+08	6947	4.41339275	1.581916516	6.061E-21	5.4147E-19	0.14862	1	4	0	2	5	8	63	138	91	84	172
ENSMUSG00000026981	chr2	Il1rn	2.4E+07	2.4E+07	5535	3.797458449	2.422141662	6.188E-21	5.49325E-19	0.13559	1	2	1	18	9	26	218	256	123	215	198
ENSMUSG00000043613	chr9	Mmp3	7445822	7446008	1798	4.317193425	4.920782388	9.173E-21	8.09196E-19	0.18756	1	30	51	9	25	96	1438	590	1316	1239	1185
ENSMUSG00000032359	chr9	Ctsh	9E+07	9E+07	4499	2.003016657	4.783563584	9.951E-21	8.72335E-19	0.04881	1	137	134	160	126	274	1406	742	618	945	893
ENSMUSG00000002111	chr2	Spi1	9.1E+07	9.1E+07	2695	3.321254118	3.531067979	1.109E-20	9.60313E-19	0.11642	1	15	30	20	15	78	518	367	296	485	485
ENSMUSG00000021508	chr13	Cxcl14	5.6E+07	5.6E+07	1823	2.397254953	6.830676581	1.103E-20	9.60313E-19	0.07085	1	579	330	557	339	1011	4097	3711	3750	4257	3629
ENSMUSG00000089672	chr10	Gp49a	5.1E+07	5.1E+07	2107	2.842734688	2.969838229	1.302E-20	1.12025E-18	0.08512	1	25	13	22	27	58	290	251	171	267	423
ENSMUSG00000038059	chr18	Smim3	6E+07	6E+07	1984	2.625902097	2.335850174	1.547E-20	1.3233E-18	0.06748	1	11	11	35	18	31	208	150	146	182	179
ENSMUSG00000036606	chr15	Plxnb2	8.9E+07	8.9E+07	7119	1.699935819	5.26236811	1.627E-20	1.3832E-18	0.03635	1	204	226	292	241	402	1469	1173	865	1313	1263
ENSMUSG00000031595	chr8	Pdgfrl	4.1E+07	4.1E+07	3126	2.232011716	3.68454932	1.825E-20	1.54232E-18	0.05691	1	67	49	66	48	109	688	339	297	416	458
ENSMUSG00000033192	chr8	Lpcat2	9.3E+07	9.3E+07	3377	3.243749634	1.52418802	2.394E-20	2.01027E-18	0.08519	1	6	5	13	7	8	134	88	62	79	149
ENSMUSG00000007888	chr8	Crlf1	7E+07	7E+07	1644	2.398635183	3.171055263	2.545E-20	2.12476E-18	0.06367	1	25	22	71	49	53	327	244	248	315	395
ENSMUSG00000094686	chr4	Ccl21a	4.3E+07	4.3E+07	870	2.355243647	4.587444779	3.164E-20	2.62575E-18	0.06664	1	86	138	87	133	118	1085	702	539	730	1125
ENSMUSG00000034993	chr11	Vat1	1E+08	1E+08	2766	2.265188797	6.261384858	3.64E-20	3.00332E-18	0.0654	1	261	254	431	356	758	2913	2220	1677	3296	3110
ENSMUSG00000005054	chr10	Cstb	7.8E+07	7.8E+07	599	2.377292825	4.735098208	4.874E-20	3.99772E-18	0.06972	1	99	71	123	95	284	1074	684	692	1027	1117
ENSMUSG00000022441	chr15	Efcab6	8.4E+07	8.4E+07	6408	-4.96318538	1.321058293	5.123E-20	4.17763E-18	0.18698	-1	91	24	132	43	89	1	9	3	2	0
ENSMUSG00000029819	chr6	Npy	5E+07	5E+07	566	5.828037233	0.610395771	5.316E-20	4.30983E-18	0.15941	1	0	1	1	1	0	46	41	23	94	73
ENSMUSG00000038451	chr6	Spsb2	1.2E+08	1.2E+08	1658	2.592662202	2.922656573	6.449E-20	5.19819E-18	0.07347	1	36	21	29	23	51	339	163	216	302	290
ENSMUSG00000031443	chr8	F7	1.3E+07	1.3E+07	1859	5.702866057	0.063750876	6.571E-20	5.26621E-18	0.10557	1	1	0	1	0	0	51	41	18	42	30
ENSMUSG00000030729	chr7	Pgm2l1	1E+08	1E+08	7036	-1.93215553	4.391076156	9.325E-20	7.43153E-18	0.04727	-1	480	479	550	477	459	184	262	122	188	150
ENSMUSG00000067591	chr6	Klra3	1.3E+08	1.3E+08	1238	6.170439942	-0.17306859	9.455E-20	7.49224E-18	0.10155	1	0	0	0	1	0	28	27	29	31	32
ENSMUSG00000028874	chr4	Fgr	1.3E+08	1.3E+08	3863	3.627368536	0.977241942	9.539E-20	7.51623E-18	0.09202	1	4	2	2	4	8	86	51	48	89	71
ENSMUSG00000005958	chr16	Ephb3	2.1E+07	2.1E+07	6289	2.697939148	2.847846201	1.054E-19	8.25576E-18	0.08009	1	34	15	26	25	43	318	145	239	264	277
ENSMUSG00000043895	chr9	S1pr2	2.1E+07	2.1E+07	2815	2.176991748	3.22541804	1.059E-19	8.25576E-18	0.05443	1	42	32	41	53	86	415	295	232	332	291
ENSMUSG00000030742	chr7	Lat	1.3E+08	1.3E+08	1239	4.291793725	0.996321356	1.347E-19	1.0435E-17	0.13028	1	1	2	3	2	5	62	53	38	81	126
ENSMUSG00000058672	chr13	Tubb2a	3.4E+07	3.4E+07	1584	1.844803934	4.748608849	1.666E-19	1.28416E-17	0.0446	1	142	119	185	146	306	1136	686	737	895	859
ENSMUSG00000021238	chr12	Aldh6a1	8.4E+07	8.4E+07	3340	-2.13762759	6.974940063	1.7E-19	1.30279E-17	0.06132	-1	3439	2309	3514	3209	2852	1002	1545	635	720	974
ENSMUSG00000045136	chr13	Tubb2b	3.4E+07	3.4E+07	1922	2.51847012	2.736365274	1.733E-19	1.3207E-17	0.07045	1	23	17	48	20	42	368	185	175	236	191
ENSMUSG00000087366	chr4	Junos	9.5E+07	9.5E+07	4117	-2.09714489	3.104851257	1.979E-19	1.50059E-17	0.05201	-1	215	148	212	243	227	74	89	35	72	71
ENSMUSG00000031387	chrX	Renbp	7.4E+07	7.4E+07	2494	2.528982755	3.077424606	2.104E-19	1.58693E-17	0.07362	1	22	28	27	38	71	341	256	189	330	353
ENSMUSG00000087591	chrX	Gm14635	1.2E+07	1.2E+07	1614	7.851273988	-0.06455543	2.524E-19	1.89341E-17	0.14289	1	0	0	0	0	0	29	19	39	34	39
ENSMUSG00000060063	chr5	Alox5ap	1.5E+08	1.5E+08	852	2.456955493	3.739570849	2.656E-19	1.97347E-17	0.07407	1	45	38	47	62	121	757	352	326	489	418
ENSMUSG00000100838	chr9	Gm29094	8.9E+07	8.9E+07	664	2.645657912	2.171774655	2.659E-19	1.97347E-17	0.07098	1	15	14	15	17	29	160	137	110	144	222
ENSMUSG00000054342	chr7	Kcnn4	2.4E+07	2.4E+07	2034	3.176676629	1.462648578	3.076E-19	2.27091E-17	0.08883	1	6	5	11	6	11	91	69	67	115	138
ENSMUSG00000052889	chr7	Prkcb	1.2E+08	1.2E+08	4749	3.295108297	1.966555153	7.356E-19	5.40153E-17	0.11003	1	9	5	7	6	26	177	114	76	162	182
ENSMUSG00000050022	chr5	Amz1	1.4E+08	1.4E+08	6697	3.917605699	1.96378535	7.644E-19	5.58399E-17	0.15407	1	3	1	17	1	15	125	149	83	181	188

ENSMUSG00000006369	chr15	Fbln1	8.5E+07	8.5E+07	4368	2.233886814	6.088439113	9.95E-19	7.23095E-17	0.06893	1	273	284	286	347	615	3216	1509	1699	2556	2682
ENSMUSG00000023947	chr17	Nfkbie	4.6E+07	4.6E+07	2422	2.580900267	2.201534703	1.164E-18	8.41577E-17	0.06996	1	18	18	14	19	25	203	114	128	168	169
ENSMUSG00000033220	chr15	Rac2	7.9E+07	7.9E+07	3036	3.098404952	3.95340524	1.227E-18	8.82277E-17	0.11875	1	35	38	26	26	121	752	390	381	603	737
ENSMUSG00000009185	chr11	Ccl8	8.2E+07	8.2E+07	511	5.825600993	5.218737584	1.409E-18	1.00843E-16	0.33477	1	8	17	6	3	66	3923	648	926	1515	849
ENSMUSG00000062593	chr10	Lilrb4	5.1E+07	5.1E+07	1491	2.691694612	3.051217345	1.472E-18	1.04806E-16	0.08706	1	17	32	23	26	66	341	309	192	252	372
ENSMUSG00000006219	chr4	Fblim1	1.4E+08	1.4E+08	4457	2.291348408	2.719423769	1.507E-18	1.06763E-16	0.06081	1	27	24	25	32	57	242	222	148	234	262
ENSMUSG00000074677	chr3	Sirpb1c	1.6E+07	1.6E+07	3682	4.819041684	0.472835059	1.59E-18	1.12074E-16	0.1437	1	0	0	4	0	2	85	32	42	52	34
ENSMUSG00000079592	chr9	C1qtnf5	4.4E+07	4.4E+07	1398	2.419053368	3.844901747	1.65E-18	1.1573E-16	0.07603	1	54	37	68	57	133	654	281	418	600	511
ENSMUSG00000042045	chr9	Sln	5.4E+07	5.4E+07	515	6.035155021	5.508612501	1.736E-18	1.21106E-16	0.35615	1	7	2	49	48	3	978	864	2317	1869	2706
ENSMUSG00000033825	chr17	Tpsb2	2.5E+07	2.5E+07	1081	3.497128219	4.627969875	1.913E-18	1.32825E-16	0.1505	1	47	68	22	63	88	1672	317	680	1088	971
ENSMUSG00000021457	chr13	Syk	5.3E+07	5.3E+07	9362	2.340254305	3.532213954	2.527E-18	1.74626E-16	0.07124	1	33	31	60	47	125	435	391	280	420	451
ENSMUSG00000079227	chr9	Ccr5	1.2E+08	1.2E+08	3704	3.311786733	2.449533774	2.59E-18	1.7809E-16	0.12488	1	10	5	9	10	42	272	232	149	152	196
ENSMUSG00000042485	chr14	Mustn1	3.1E+07	3.1E+07	1177	2.33486336	7.26215084	2.619E-18	1.79219E-16	0.07726	1	1036	404	1007	671	764	8136	3155	4574	5357	5275
ENSMUSG00000034739	chr9	Mfrp	4.4E+07	4.4E+07	4325	2.397281159	3.848281701	2.645E-18	1.80091E-16	0.07573	1	58	37	68	57	134	654	281	418	600	511
ENSMUSG00000015950	chr5	Ncf1	1.3E+08	1.3E+08	3663	2.964312999	3.349348274	2.836E-18	1.92136E-16	0.10929	1	27	25	25	13	86	409	411	223	387	427
ENSMUSG00000053318	chr1	Slamf8	1.7E+08	1.7E+08	3079	4.30335411	0.873603437	3.046E-18	2.05386E-16	0.1437	1	0	0	0	3	9	70	56	59	57	82
ENSMUSG00000033777	chrX	Tlr13	1.1E+08	1.1E+08	4086	2.824510946	2.193886454	3.36E-18	2.24407E-16	0.08947	1	6	9	19	14	37	169	187	106	163	178
ENSMUSG00000055541	chr7	Lair1	4007073	4009834	3760	2.968521648	1.924109663	3.36E-18	2.24407E-16	0.09098	1	13	12	8	6	22	206	109	90	125	142
ENSMUSG00000043740	chr17	B430306N03Rik	4.8E+07	4.8E+07	6937	4.092890447	0.374549159	3.63E-18	2.41293E-16	0.09843	1	1	1	0	3	4	60	36	28	54	45
ENSMUSG00000029470	chr5	P2rx4	1.2E+08	1.2E+08	3309	2.29665634	4.30397726	3.67E-18	2.42785E-16	0.07183	1	101	63	82	58	208	873	593	426	699	821
ENSMUSG00000026288	chr1	Inpp5d	8.8E+07	8.8E+07	7602	1.984340204	3.336047644	3.796E-18	2.49942E-16	0.05044	1	54	38	64	59	92	489	269	213	326	370
ENSMUSG00000028047	chr3	Thbs3	8.9E+07	8.9E+07	4823	2.052330802	4.52506671	4.253E-18	2.78763E-16	0.05848	1	89	112	102	144	223	1177	612	536	787	750
ENSMUSG00000052688	chr1	5430435G22Rik	1.3E+08	1.3E+08	4624	2.010991295	3.142106557	4.34E-18	2.83147E-16	0.05053	1	47	37	51	59	66	297	384	168	315	289
ENSMUSG00000092463	chrX	Gm20489	1E+08	1E+08	1350	2.518114821	2.068374547	5.451E-18	3.53978E-16	0.07001	1	15	10	19	14	34	190	124	92	149	162
ENSMUSG00000069516	chr10	Lyz2	1.2E+08	1.2E+08	1266	2.65428351	8.275266655	5.61E-18	3.62606E-16	0.09955	1	1022	1152	870	759	2623	16224	11128	7651	11775	9319
ENSMUSG00000020592	chr12	Sdc1	8771323	8771701	3809	2.060629247	3.789389673	5.752E-18	3.70111E-16	0.05718	1	79	64	73	52	132	568	342	363	477	527
ENSMUSG00000027346	chr2	Gpcpd1	1.3E+08	1.3E+08	7289	-2.24422583	7.360098	5.804E-18	3.71715E-16	0.07347	-1	4396	2805	5489	4059	3814	1108	2175	762	920	1029
ENSMUSG00000056069	chr15	Fam105a	2.8E+07	2.8E+07	2830	2.794788623	2.266199346	6.182E-18	3.94137E-16	0.08937	1	12	15	16	9	37	239	134	136	149	182
ENSMUSG00000087006	chr2	Gm13889	9.4E+07	9.4E+07	1392	2.49595311	3.954125406	6.637E-18	4.21227E-16	0.08463	1	40	39	106	59	121	699	305	548	657	437
ENSMUSG00000029163	chr5	Emilin1	3.1E+07	3.1E+07	4938	1.719973673	4.540473717	7.114E-18	4.49471E-16	0.04235	1	120	137	188	162	206	1075	558	511	884	681
ENSMUSG00000060572	chr4	Mfap2	1.4E+08	1.4E+08	1211	2.567674435	3.486317811	8.777E-18	5.52026E-16	0.0866	1	60	36	38	26	80	553	236	285	473	417
ENSMUSG00000018507	chr11	Trpv2	6.3E+07	6.3E+07	4485	2.63924386	3.0703749	9.365E-18	5.8641E-16	0.08904	1	13	32	30	30	68	380	271	177	305	354
ENSMUSG00000026459	chr1	Myog	1.3E+08	1.3E+08	1495	2.819515052	5.306325986	9.495E-18	5.918E-16	0.10985	1	93	135	182	218	94	1387	693	1596	1268	1960
ENSMUSG00000042359	chr2	Osbpl6	7.6E+07	7.6E+07	10063	-1.65803058	4.828309371	9.536E-18	5.918E-16	0.04061	-1	659	556	690	619	680	285	422	190	279	247
ENSMUSG00000024965	chr19	Fermt3	6998958	6999520	2587	2.822597333	2.951857377	1.02E-17	6.30428E-16	0.10065	1	10	26	31	17	60	339	221	184	306	330
ENSMUSG00000034226	chr2	Rhov	1.2E+08	1.2E+08	1703	5.402941327	0.226156392	1.043E-17	6.41341E-16	0.14621	1	0	0	0	3	0	25	42	30	63	41
ENSMUSG00000031849	chr8	Comp	7E+07	7E+07	2425	2.611331937	6.308699811	1.084E-17	6.63839E-16	0.09786	1	367	192	384	201	589	5161	1804	1763	1975	3753
ENSMUSG00000025268	chrX	Maged2	1.5E+08	1.5E+08	3239	1.598200767	5.327392979	1.119E-17	6.82106E-16	0.03821	1	315	204	318	265	409	1828	1132	922	1307	1094
ENSMUSG00000001555	chr11	Fkbp10	1E+08	1E+08	2935	2.017531428	4.065901082	1.128E-17	6.84896E-16	0.05721	1	77	61	118	87	167	855	370	469	549	515
ENSMUSG00000037902	chr2	Sirpa	1.3E+08	1.3E+08	4911	2.349247184	6.0397137	1.173E-17	7.09111E-16	0.08073	1	259	242	240	222	694	2731	1908	1667	2515	2568
ENSMUSG00000023349	chr6	Clec4n	1.2E+08	1.2E+08	1420	3.383807191	1.571767632	1.202E-17	7.23742E-16	0.11237	1	4	10	7	5	10	147	87	121	86	76
ENSMUSG00000030605	chr7	Mfge8	7.9E+07	7.9E+07	2125	2.343471113	7.274811288	1.26E-17	7.55404E-16	0.08112	1	557	442	1026	790	1171	3655	5205	2947	7241	7823
ENSMUSG00000007041	chr17	Clic1	3.5E+07	3.5E+07	1799	1.963179196	5.374968419	1.285E-17	7.67016E-16	0.05736	1	200	186	270	184	462	2040	1016	1041	1425	1339
ENSMUSG00000021423	chr13	Ly86	3.7E+07	3.7E+07	997	3.198186997	3.313332616	1.383E-17	8.22076E-16	0.13039	1	25	23	16	15	67	669	210	295	320	346
ENSMUSG00000046223	chr7	Plaur	2.4E+07	2.4E+07	1396	3.130994225	2.38918939	1.603E-17	9.46555E-16	0.11876	1	11	6	15	7	43	196	164	135	204	241
ENSMUSG00000073982	chr7	Rhog	1E+08	1E+08	1356	1.714531918	4.850084729	1.606E-17	9.46555E-16	0.04386	1	170	109	225	219	317	1024	742	613	1193	1001
ENSMUSG00000028583	chr4	Pdpn	1.4E+08	1.4E+08	1817	2.054251401	3.781759194	1.798E-17	1.05519E-15	0.05857	1	79	68	72	58	119	522	361	479	413	441
ENSMUSG00000071715	chr15	Ncf4	7.8E+07	7.8E+07	2021	3.588403747	2.884140539	1.866E-17	1.09074E-15	0.15688	1	13	8	4	11	50	292	252	191	285	358
ENSMUSG00000026100	chr1	Mstn	5.3E+07	5.3E+07	2705	-3.30062376	5.037726937	1.944E-17	1.13155E-15	0.14777	-1	1026	1161	580	699	697	131	282	70	89	69
ENSMUSG00000042607	chr6	Asb4	5383386	5383405	3932	-2.13127085	4.069580863	2.125E-17	1.23177E-15	0.06529	-1	428	313	412	562	303	134	202	93	115	104
ENSMUSG00000067071	chr1	Hes6	9.1E+07	9.1E+07	1808	1.725960715	4.064507186	2.249E-17	1.29828E-15	0.0427	1	109	68	172	111	134	556	401	457	578	614
ENSMUSG00000026251	chr1	Chrnd	8.7E+07	8.7E+07	3288	2.34644667	3.452450043	2.271E-17	1.30542E-15	0.07561	1	43	26	105	63	39	338	347	328	340	486
ENSMUSG00000054958	chr4	Nt5c1a	1.2E+08	1.2E+08	1220	-4.41135652	2.38962138	2.419E-17	1.38472E-15	0.21713	-1	135	130	217	209	49	8	27	5	4	5
ENSMUSG00000018983	chr4	E2f2	1.4E+08	1.4E+08	4882	2.361292957	2.637490438	2.503E-17	1.42716E-15	0.06928	1	31	28	26	19	43	259	210	173	248	154
ENSMUSG00000046186	chr9	Cd109	7.9E+07	7.9E+07	6900	2.263314855	3.378331902	2.598E-17	1.4752E-15	0.07063	1	45	28	74	28	103	503	349	237	341	347
ENSMUSG00000083679	chr4	Gm12892	1.2E+08	1.2E+08	1146	4.058119979	1.455645864	2.747E-17	1.55386E-15	0.16598	1	1	1	2	8	10	73	70	63	157	135
ENSMUSG00000020695	chr11	Mrc2	1.1E+08	1.1E+08	6674	1.649113594	4.948794084	2.773E-17	1.56207E-15	0.04127	1	186	154	231	214	354	1326	733	715	1118	959
ENSMUSG00000002603	chr7	Tgfb1	2.6E+07	2.6E+07	2558	2.253378748	4.230708257	2.799E-17	1.57043E-15	0.07353	1	58	45	119	88	204	633	499	513	781	732
ENSMUSG00000006411	chr1	Pvrl4	1.7E+08	1.7E+08	3746	3.523232962	0.506319944	3.07E-17	1.71575E-15	0.08991	1	3	0	3	3	6	59	51	28	56	48
ENSMUSG00000024696	chr19	Lpxn	1.3E+07	1.3E+07	1675	3.051963568	1.825083687	3.397E-17	1.89049E-15	0.10698	1	8	2	7	16	23	178	123	99	112	113
ENSMUSG00000024601	chr18	Isoc1	5.9E+07	5.9E+07	2563	-1.74319558	4.710181715	3.439E-17	1.9067E-15	0.04631	-1	658	480	696	528	657	277	396	190	196	191
ENSMUSG00000076036	chr7	Gm22133	4.5E+07	4.5E+07	109	2.801148561	8.143226306	3.536E-17	1.95283E-15	0.11511	1	870	661	687	731	2596	11814	7144	7734	12210	12203
ENSMUSG00000004933	chr10	Matk	8.1E+07	8.1E+07	4594	3.830089857	1.770347532	3.578E-17	1.96781E-15	0.15389	1	2	9	2	4	14	101	124	59	170	175
ENSMUSG00000040212	chr7	Emp3	4.6E+07	4.6E+07	972	2.317935978	4.6935917	3.609E-17	1.97733E-15	0.07886	1	85	110	102	88	272	1158	618	655	996	1022
ENSMUSG00000020773	chr11	Trim47	1.2E+08	1.2E+08	2735	1.626955862	4.435725675	3.731E-17	2.03639E-15	0.03982	1	123	85	191	179	239	776	625	469	831	675
ENSMUSG00000064267	chr5	Hvcn1	1.2E+08	1.2E+08	3563	3.139121266	3.679885608	4.276E-17	2.32443E-15	0.13217	1	44	37	10	27	71	370	493	266	593	637
ENSMUSG00000033467	chr5	Crlf2	1.1E+08	1.1E+08	1325	2.140178198	3.347806617	4.555E-17	2.46661E-15	0.06349	1	37	39	52	63	92	359	261	248	463	354

ENSMUSG00000021280	chr12	Exoc3l4	1.1E+08	1.1E+08	2922	2.644288449	3.442814948	4.932E-17	2.65025E-15	0.09668	1	52	30	51	16	78	368	311	380	505	300
ENSMUSG00000021702	chr13	Thbs4	9.3E+07	9.3E+07	3289	2.281481276	8.929485506	4.919E-17	2.65025E-15	0.08045	1	2141	1407	4192	3047	2101	25975	10754	13966	13906	19427
ENSMUSG00000048865	chr1	Arhgap30	1.7E+08	1.7E+08	8591	2.522294049	3.332242659	5.382E-17	2.88133E-15	0.08788	1	25	34	30	39	97	495	363	256	264	384
ENSMUSG00000024781	chr19	Lipa	3.4E+07	3.4E+07	2969	2.18773328	5.242475141	5.641E-17	3.00837E-15	0.07322	1	202	143	174	118	407	1226	1509	702	1418	1627
ENSMUSG00000037012	chr10	Hk1	6.2E+07	6.2E+07	8532	1.657453568	4.755065258	6.822E-17	3.62427E-15	0.04268	1	130	112	253	190	328	1080	752	603	947	867
ENSMUSG00000047878	chr15	A4galt	8.3E+07	8.3E+07	2171	2.358981626	2.752789045	7.255E-17	3.83995E-15	0.07418	1	30	17	34	25	60	307	159	177	214	284
ENSMUSG00000050967	chr1	Creg2	4E+07	4E+07	6091	4.517587275	0.290671327	7.284E-17	3.84082E-15	0.11732	1	3	3	0	0	0	38	45	24	49	54
ENSMUSG00000032089	chr9	Il10ra	4.5E+07	4.5E+07	3498	2.623512274	2.929411446	7.378E-17	3.87586E-15	0.09192	1	33	25	17	22	59	406	223	174	216	327
ENSMUSG00000037868	chr10	Egr2	6.8E+07	6.8E+07	3398	3.115867497	1.976717769	7.969E-17	4.1704E-15	0.11238	1	10	10	7	19	11	95	144	88	143	225
ENSMUSG00000020644	chr12	Id2	2.5E+07	2.5E+07	1270	2.378164326	3.442913173	8.902E-17	4.63803E-15	0.07993	1	64	39	41	38	77	487	234	334	289	500
ENSMUSG00000030257	chr6	Srgap3	1.1E+08	1.1E+08	9852	2.060871382	2.473089117	8.928E-17	4.63803E-15	0.0531	1	36	20	35	34	32	233	167	122	172	213
ENSMUSG00000054871	chr9	Tmem158	1.2E+08	1.2E+08	1732	2.976346781	2.756747814	1.089E-16	5.63452E-15	0.1175	1	27	13	15	16	42	205	125	236	299	312
ENSMUSG00000056978	chr7	Hamp2	3.1E+07	3.1E+07	437	4.502917517	4.257460571	1.172E-16	6.04494E-15	0.25383	1	6	11	21	49	37	179	409	1026	782	1097
ENSMUSG00000073490	chr1	AI607873	1.7E+08	1.7E+08	3481	2.187822487	3.070976193	1.197E-16	6.15171E-15	0.06705	1	33	31	56	26	84	398	261	192	258	306
ENSMUSG00000044042	chr2	Fmn1	1.1E+08	1.1E+08	15397	2.714101737	1.644106383	1.493E-16	7.64211E-15	0.08335	1	17	7	12	6	17	136	113	93	74	113
ENSMUSG00000021886	chr12	Gpr65	9.8E+07	9.8E+07	2049	3.478756876	0.786415035	1.513E-16	7.71602E-15	0.10407	1	5	1	1	5	7	84	53	46	42	72
ENSMUSG00000029333	chr5	Rasgef1b	9.9E+07	9.9E+07	3261	2.727002961	1.373523624	1.567E-16	7.96077E-15	0.07673	1	8	8	11	5	16	90	88	54	93	113
ENSMUSG00000025232	chr9	Hexa	6E+07	6E+07	1865	1.598191303	6.878947253	1.815E-16	9.19085E-15	0.04248	1	826	627	1012	795	1192	4351	3403	2571	4260	3808
ENSMUSG00000035004	chr7	Igsf6	1.2E+08	1.2E+08	2133	2.815711065	2.073548152	1.839E-16	9.27848E-15	0.09777	1	12	13	10	7	34	181	166	93	130	169
ENSMUSG00000063821	chr14	Dupd1	2.2E+07	2.2E+07	1093	1.792019375	5.915159403	2.056E-16	1.0337E-14	0.05249	1	442	345	397	296	536	1941	1569	1656	2013	2380
ENSMUSG00000063011	chr17	Msln	2.6E+07	2.6E+07	2114	3.533855816	1.869507938	2.274E-16	1.13899E-14	0.14817	1	2	5	17	15	3	183	73	120	131	150
ENSMUSG00000061132	chr19	Blnk	4.1E+07	4.1E+07	5991	2.637963698	2.797134489	2.424E-16	1.21E-14	0.096	1	27	22	20	12	62	275	247	157	256	282
ENSMUSG00000019102	chr11	Aldh3a1	6.1E+07	6.1E+07	1942	4.210894876	0.784454169	2.482E-16	1.23434E-14	0.16578	1	1	0	4	2	5	44	30	51	86	89
ENSMUSG00000050708	chr7	Ftl1	4.5E+07	4.5E+07	1340	2.452164074	9.269621802	2.703E-16	1.33975E-14	0.09632	1	2456	1839	2185	1950	6425	25307	16829	15983	25762	24259
ENSMUSG00000001025	chr3	S100a6	9.1E+07	9.1E+07	719	2.274405641	7.192105923	3.253E-16	1.60658E-14	0.08415	1	656	538	807	565	1287	8872	2807	4151	4721	4725
ENSMUSG00000049719	chr9	Prss46	1.1E+08	1.1E+08	1346	8.132912022	0.196868454	3.276E-16	1.61211E-14	0.24429	1	0	0	0	0	0	15	38	18	43	88
ENSMUSG00000029810	chr6	Tmem176b	4.9E+07	4.9E+07	2049	2.496672246	5.800528344	3.941E-16	1.9326E-14	0.09954	1	180	200	172	156	580	2508	1429	1417	2195	2269
ENSMUSG00000026228	chr1	Htr2b	8.6E+07	8.6E+07	2131	4.548459083	0.073090305	4.071E-16	1.98958E-14	0.12387	1	0	1	2	2	0	42	38	13	38	49
ENSMUSG00000016256	chr2	Ctsz	1.7E+08	1.7E+08	1441	2.257311605	6.697971832	4.139E-16	2.01554E-14	0.08346	1	448	309	501	382	1180	3720	3008	2331	4258	4518
ENSMUSG00000026979	chr2	Psd4	2.4E+07	2.4E+07	11786	2.788478764	1.588997487	4.639E-16	2.2512E-14	0.08966	1	8	10	9	6	21	112	94	68	95	146
ENSMUSG00000038843	chr19	Gcnt1	1.7E+07	1.7E+07	5571	3.319565432	0.724946932	6.032E-16	2.91733E-14	0.09848	1	6	3	4	1	6	83	57	37	39	67
ENSMUSG00000025492	chr7	Ifitm3	1.4E+08	1.4E+08	678	2.141466828	6.416793246	6.613E-16	3.18754E-14	0.07663	1	321	333	434	424	927	3962	1974	2347	3520	2581
ENSMUSG00000034708	chr11	Grn	1E+08	1E+08	3474	2.369031382	7.30560938	6.657E-16	3.19772E-14	0.09268	1	528	466	684	600	1758	6609	4343	3566	7095	6031
ENSMUSG00000097328	chr11	Tnfsf12	7E+07	7E+07	1515	1.66151338	4.317935502	8.204E-16	3.9272E-14	0.04491	1	122	89	158	122	245	682	538	415	777	716
ENSMUSG00000024501	chr18	Dpysl3	4.3E+07	4.3E+07	6265	1.644548286	5.14659233	8.889E-16	4.24093E-14	0.04581	1	214	193	253	228	416	1730	892	835	1104	1027
ENSMUSG00000028859	chr4	Csf3r	1.3E+08	1.3E+08	3609	2.547555498	1.793560186	9.018E-16	4.28765E-14	0.082	1	15	7	18	10	24	193	91	75	121	113
ENSMUSG00000003812	chr8	Dnase2a	8.5E+07	8.5E+07	5389	1.449376211	4.384663945	9.699E-16	4.59579E-14	0.03438	1	150	132	193	160	205	765	505	446	684	756
ENSMUSG00000022548	chr16	Apod	3.1E+07	3.1E+07	2577	2.137494459	7.204118208	1.032E-15	4.87263E-14	0.07767	1	654	748	686	635	1376	7361	3412	3411	4800	6191
ENSMUSG00000038390	chr6	Gpr162	1.2E+08	1.2E+08	2676	3.323075075	0.348616171	1.045E-15	4.92077E-14	0.08608	1	4	0	3	4	4	56	40	29	45	41
ENSMUSG00000035277	chrX	Arx	9.3E+07	9.3E+07	4391	3.393428362	0.468243399	1.062E-15	4.97991E-14	0.09746	1	2	1	7	2	4	36	53	38	55	47
ENSMUSG00000022048	chr14	Dpysl2	6.7E+07	6.7E+07	4520	1.830140703	4.499937547	1.082E-15	5.05804E-14	0.05538	1	112	90	145	151	266	1065	509	586	686	797
ENSMUSG00000038894	chr8	Irs2	1.1E+07	1.1E+07	4024	-2.43169518	2.666669837	1.129E-15	5.26283E-14	0.08785	-1	163	108	199	162	180	37	81	15	44	32
ENSMUSG00000017057	chrX	Il13ra1	3.6E+07	3.6E+07	3712	1.989189852	3.6958875	1.305E-15	6.05899E-14	0.06271	1	72	63	77	61	116	717	344	378	341	342
ENSMUSG00000015027	chr8	Galns	1.2E+08	1.2E+08	2585	2.15467501	2.567809317	1.311E-15	6.06642E-14	0.06619	1	20	23	47	32	40	229	149	118	240	247
ENSMUSG00000027339	chr2	Rassf2	1.3E+08	1.3E+08	11993	1.62225438	3.963008079	1.336E-15	6.16228E-14	0.04201	1	108	96	95	109	158	648	430	364	477	504
ENSMUSG00000026321	chr1	Tnfrsf11a	1.1E+08	1.1E+08	5985	2.479363881	1.62739103	1.379E-15	6.34379E-14	0.0725	1	13	12	12	14	15	153	76	78	101	107
ENSMUSG00000022440	chr15	C1qtnf6	7.9E+07	7.9E+07	2402	1.907444486	3.547894839	1.461E-15	6.69693E-14	0.05756	1	45	51	108	56	118	552	318	276	416	340
ENSMUSG00000052974	chr7	Cyp2f2	2.7E+07	2.7E+07	2025	3.694311651	4.017972142	1.541E-15	7.03923E-14	0.19666	1	47	43	6	16	50	905	271	498	604	800
ENSMUSG00000078794	chr7	Dact3	1.7E+07	1.7E+07	2828	2.135927761	2.909453386	1.562E-15	7.11444E-14	0.06768	1	36	32	37	42	58	384	161	185	268	250
ENSMUSG00000038034	chr1	Igsf8	1.7E+08	1.7E+08	5217	1.620930648	4.34032965	1.617E-15	7.33798E-14	0.04377	1	132	88	172	133	239	635	502	492	749	744
ENSMUSG00000032020	chr9	Ubash3b	4.1E+07	4.1E+07	7326	2.232226556	2.58473218	1.636E-15	7.4039E-14	0.07089	1	36	28	23	27	37	313	181	164	169	172
ENSMUSG00000024600	chr18	Slc27a6	5.9E+07	5.9E+07	2485	4.543925783	0.081729631	1.68E-15	7.57503E-14	0.12524	1	0	2	1	2	0	29	40	17	43	50
ENSMUSG00000021306	chr13	Gpr137b	1.3E+07	1.3E+07	2978	2.432858008	3.187714377	1.747E-15	7.8532E-14	0.09052	1	48	31	31	27	74	247	357	164	345	462
ENSMUSG00000102947	chr2	AL772372.1	9.4E+07	9.4E+07	747	2.457411497	2.992305804	1.84E-15	8.24575E-14	0.09237	1	18	21	63	31	56	365	174	261	337	210
ENSMUSG00000052373	chr11	Mpp3	1E+08	1E+08	9385	-1.62192375	4.612436051	1.944E-15	8.68472E-14	0.0452	-1	478	462	641	406	813	199	333	199	243	256
ENSMUSG00000025402	chr10	Nab2	1.3E+08	1.3E+08	2941	1.767441661	3.869814865	1.958E-15	8.72055E-14	0.05085	1	83	70	123	83	145	542	335	365	645	417
ENSMUSG00000023367	chr6	Tmem176a	4.9E+07	4.9E+07	1119	2.414492551	4.127343502	2.029E-15	9.00517E-14	0.0945	1	58	69	61	52	178	836	366	438	702	691
ENSMUSG00000028931	chr4	Kcnab2	1.5E+08	1.5E+08	5578	2.783301504	1.982231991	2.212E-15	9.78612E-14	0.10447	1	4	11	14	11	34	147	129	101	159	146
ENSMUSG00000020241	chr10	Col6a2	7.7E+07	7.7E+07	8326	1.833555323	7.689667194	2.316E-15	1.02162E-13	0.05992	1	1132	1058	1315	1393	1939	8824	4727	4928	8725	6278
ENSMUSG00000030117	chr6	Gdf3	1.2E+08	1.2E+08	2125	5.581576262	0.392054294	2.444E-15	1.0697E-13	0.21403	1	1	1	1	0	0	92	14	44	50	32
ENSMUSG00000040711	chr11	Sh3pxd2b	3.2E+07	3.2E+07	9709	1.728615282	4.272145753	2.443E-15	1.0697E-13	0.04993	1	107	118	123	101	222	807	506	449	685	615
ENSMUSG00000075702	chr11	Selm	3514684	3515073	1481	1.659068628	4.41570826	2.448E-15	1.0697E-13	0.04654	1	154	98	153	143	231	933	458	476	766	724
ENSMUSG00000026271	chr1	Gpr35	9.3E+07	9.3E+07	4839	3.164384047	0.379399152	2.544E-15	1.10793E-13	0.07976	1	2	3	5	2	5	46	42	29	51	45
ENSMUSG00000000794	chr3	Kcnn3	9E+07	9E+07	7391	2.416201178	2.208426919	2.558E-15	1.1107E-13	0.08128	1	21	14	36	26	9	193	147	130	161	142
ENSMUSG00000031146	chrX	Plp2	7667941	7668506	1334	1.758325181	5.439768075	2.776E-15	1.20178E-13	0.05454	1	259	212	260	224	561	1708	1221	1052	1463	1481
ENSMUSG00000024411	chr18	Aqp4	1.5E+07	1.5E+07	5082	-3.4104328	3.462039531	2.816E-15	1.21548E-13	0.17484	-1	262	83	660	445	151	33	70	25	45	23
ENSMUSG00000040747	chr3	Cd53	1.1E+08	1.1E+08	1742	2.177001914	3.324447367	2.9E-15	1.24763E-13	0.07504	1	45	48	38	35	103	463	359	263	291	301

ENSMUSG00000022831	chr16	Hcls1	3.7E+07	3.7E+07	2525	2.318255295	3.758955154	2.938E-15	1.26006E-13	0.08728	1	29	61	58	56	137	602	355	322	525	516
ENSMUSG00000074419	chr7	Gm15448	3816781	3817004	2176	4.361793645	0.143605037	3.22E-15	1.37685E-13	0.12042	1	1	3	0	0	2	54	26	26	31	50
ENSMUSG00000022490	chr15	Ppp1r1a	1E+08	1E+08	1295	-2.64957096	5.440927423	3.351E-15	1.4286E-13	0.11837	-1	1557	964	804	1126	979	296	89	158	357	343
ENSMUSG00000027750	chr3	Postn	5.4E+07	5.4E+07	7833	2.23791849	5.879265707	3.492E-15	1.48414E-13	0.0873	1	266	180	440	183	552	3785	1920	1645	1474	1356
ENSMUSG00000036067	chr2	Slc2a6	2.7E+07	2.7E+07	3211	2.969925158	0.756585036	3.756E-15	1.59161E-13	0.08758	1	1	3	6	8	8	67	61	33	65	57
ENSMUSG00000020810	chr11	Cygb	1.2E+08	1.2E+08	2331	1.900607576	5.822904672	3.804E-15	1.60691E-13	0.06433	1	298	254	363	310	607	2188	1081	1597	1864	2407
ENSMUSG00000020634	chr12	Ubxn2a	4879032	4880771	2820	-2.87247299	6.466561198	3.822E-15	1.60979E-13	0.13788	-1	2682	2056	2997	2499	1173	405	1007	226	314	300
ENSMUSG00000099233	chr16	Gm27883	2E+07	2E+07	102	3.376663726	0.615337629	3.926E-15	1.64866E-13	0.10828	1	3	2	6	3	4	63	43	56	60	32
ENSMUSG00000026193	chr1	Fn1	7.2E+07	7.2E+07	11685	1.933912214	8.314337467	4.042E-15	1.6924E-13	0.06753	1	1608	1559	1687	1641	3565	15929	10266	7398	9762	9618
ENSMUSG00000039519	chr3	Cyp7b1	1.8E+07	1.8E+07	2166	3.807411782	0.269834772	4.154E-15	1.73321E-13	0.10849	1	2	3	4	0	1	53	27	29	49	44
ENSMUSG00000050503	chr9	Fbxl22	6.7E+07	6.7E+07	3935	2.651300742	3.555075187	4.164E-15	1.73321E-13	0.11169	1	64	39	50	51	29	614	222	435	514	246
ENSMUSG00000031837	chr8	Necab2	1.2E+08	1.2E+08	2096	6.292650177	-0.04635087	4.208E-15	1.74616E-13	0.18459	1	0	1	0	0	0	16	34	15	46	54
ENSMUSG00000003283	chr2	Hck	1.5E+08	1.5E+08	2092	2.987961298	1.806513358	4.235E-15	1.75223E-13	0.12133	1	8	4	8	8	30	196	96	92	110	123
ENSMUSG00000020143	chr11	Dock2	3.4E+07	3.4E+07	11425	2.436224118	2.944205003	4.617E-15	1.90446E-13	0.0925	1	20	28	26	27	79	290	285	151	273	332
ENSMUSG00000034685	chr11	Fam171a2	1E+08	1E+08	3119	2.473629976	2.110521791	4.914E-15	2.02111E-13	0.08787	1	17	8	30	13	31	167	94	117	193	153
ENSMUSG00000021203	chr12	Otub2	1E+08	1E+08	3695	-1.94600919	3.963756487	5.225E-15	2.14303E-13	0.0648	-1	549	266	381	341	292	141	195	85	121	129
ENSMUSG00000061068	chr14	Mcpt4	5.6E+07	5.6E+07	990	2.90335996	5.128312249	5.746E-15	2.34968E-13	0.13939	1	99	156	57	105	168	2295	494	1049	1380	1182
ENSMUSG00000024978	chr19	Gpam	5.5E+07	5.5E+07	3832	-2.84925234	7.047864566	5.973E-15	2.42849E-13	0.13805	-1	3401	2703	5776	4023	1535	639	1426	405	465	459
ENSMUSG00000027646	chr2	Src	1.6E+08	1.6E+08	4371	1.728355489	3.369572127	5.963E-15	2.42849E-13	0.04814	1	60	58	70	61	108	339	296	230	397	356
ENSMUSG00000033590	chr9	Myo5c	7.5E+07	7.5E+07	6733	-1.93687198	3.37124407	6.043E-15	2.44976E-13	0.06238	-1	230	231	313	195	251	68	130	55	81	110
ENSMUSG00000022372	chr15	Sla	6.7E+07	6.7E+07	9186	2.574539677	2.037039306	6.155E-15	2.4878E-13	0.09168	1	18	16	10	11	29	212	117	105	109	159
ENSMUSG00000045763	chr15	Basp1	2.5E+07	2.5E+07	1847	2.099075397	2.697457217	6.422E-15	2.58829E-13	0.06735	1	39	23	29	29	62	302	168	165	210	220
ENSMUSG00000022357	chr15	Klhl38	5.8E+07	5.8E+07	2212	-2.51583119	5.583379175	6.441E-15	2.58877E-13	0.11027	-1	1420	993	1358	1672	512	318	486	164	329	207
ENSMUSG00000060716	chr12	Plekhh1	7.9E+07	7.9E+07	6432	3.092231848	1.657536834	6.483E-15	2.59811E-13	0.12632	1	9	6	16	13	3	86	72	108	151	121
ENSMUSG00000039323	chr1	Igfbp2	7.3E+07	7.3E+07	1847	6.253071482	0.928795446	6.803E-15	2.71845E-13	0.32517	1	0	0	2	0	1	25	18	74	79	144
ENSMUSG00000039960	chr8	Rhou	1.2E+08	1.2E+08	3806	-1.67513575	5.322195969	6.845E-15	2.7276E-13	0.05126	-1	920	466	1608	905	857	515	499	241	331	423
ENSMUSG00000024173	chr17	Tpsab1	2.5E+07	2.5E+07	2094	3.945035996	1.716566689	7.449E-15	2.95988E-13	0.19705	1	3	5	11	8	1	251	42	91	93	136
ENSMUSG00000059498	chr1	Fcgr3	1.7E+08	1.7E+08	1736	2.585931878	4.604877719	8.119E-15	3.21671E-13	0.11348	1	67	122	50	65	203	1328	747	486	842	986
ENSMUSG00000000278	chr11	Scpep1	8.9E+07	8.9E+07	2097	1.572827165	5.051267304	9.199E-15	3.6344E-13	0.04519	1	224	181	236	187	445	1273	985	658	1101	1156
ENSMUSG00000059089	chr1	Fcgr4	1.7E+08	1.7E+08	1256	4.496196665	0.563583601	9.3E-15	3.66393E-13	0.18833	1	1	0	1	2	4	114	23	26	51	53
ENSMUSG00000040322	chr3	Slc25a24	1.1E+08	1.1E+08	3431	1.768102297	3.563139915	9.351E-15	3.67396E-13	0.0523	1	80	65	75	53	127	518	422	252	353	345
ENSMUSG00000015143	chr12	Actn1	8E+07	8E+07	3805	1.361133008	4.190803486	9.627E-15	3.77185E-13	0.03201	1	128	102	176	150	223	636	599	387	516	577
ENSMUSG00000025283	chrX	Sat1	1.6E+08	1.6E+08	2774	1.537017359	4.937153815	1.069E-14	4.17772E-13	0.04323	1	210	171	244	192	378	1415	781	702	804	1039
ENSMUSG00000021699	chr13	Pde4d	1.1E+08	1.1E+08	12006	-2.95293606	5.919180512	1.137E-14	4.4293E-13	0.14966	-1	1830	1350	2282	1700	757	261	689	143	193	183
ENSMUSG00000020399	chr11	Havcr2	4.6E+07	4.6E+07	2721	3.574923857	0.315195175	1.15E-14	4.46883E-13	0.10099	1	1	5	1	1	4	52	46	35	34	39
ENSMUSG00000049625	chr13	Tifab	5.6E+07	5.6E+07	3498	2.86813934	1.551555197	1.174E-14	4.54954E-13	0.1061	1	5	13	7	7	17	164	80	80	89	92
ENSMUSG00000024679	chr19	Ms4a6d	1.2E+07	1.2E+07	1735	3.050900648	2.554771369	1.215E-14	4.69611E-13	0.13984	1	10	23	7	14	36	307	222	213	166	133
ENSMUSG00000031147	chrX	Magix	7673164	7675191	2910	-1.36256904	4.777972083	1.28E-14	4.93089E-13	0.03408	-1	584	382	883	622	546	323	341	252	341	324
ENSMUSG00000033684	chr1	Qsox1	1.6E+08	1.6E+08	8291	1.482958858	5.427567136	1.292E-14	4.9659E-13	0.04108	1	292	245	337	330	519	1744	1071	1021	1431	1288
ENSMUSG00000025351	chr10	Cd63	1.3E+08	1.3E+08	1031	1.604884815	7.415288954	1.517E-14	5.81333E-13	0.04938	1	1272	904	1428	1105	1716	7054	4148	4250	5804	5336
ENSMUSG00000036242	chr14	3632451O06Rik	5E+07	5E+07	3663	1.972906604	3.146047367	1.667E-14	6.36972E-13	0.06407	1	71	45	45	38	62	427	282	223	267	243
ENSMUSG00000094439	chr4	Gm21969	1.4E+08	1.4E+08	4402	-1.66623678	4.45092795	1.773E-14	6.75875E-13	0.05125	-1	511	367	599	559	458	218	360	141	208	166
ENSMUSG00000058818	chr7	Pirb	3711409	3712830	4471	2.725436662	3.982378916	1.816E-14	6.9041E-13	0.12656	1	50	54	21	39	146	791	461	400	567	616
ENSMUSG00000023169	chr15	Slc38a1	9.7E+07	9.7E+07	8391	2.666211699	1.402355153	1.863E-14	7.06169E-13	0.08929	1	6	11	6	10	17	91	74	72	90	112
ENSMUSG00000024349	chr18	Tmem173	3.6E+07	3.6E+07	2302	2.11970742	3.380665735	1.883E-14	7.11863E-13	0.07626	1	50	48	43	48	100	437	206	299	388	381
ENSMUSG00000062312	chr11	Erbb2	9.8E+07	9.8E+07	5210	1.597617412	3.287904393	2.177E-14	8.20981E-13	0.04265	1	61	45	100	67	95	363	250	235	314	333
ENSMUSG00000002233	chr3	Rhoc	1E+08	1E+08	1292	1.708994579	6.061811639	2.223E-14	8.36023E-13	0.05588	1	408	271	550	423	781	2475	1472	1635	2379	2587
ENSMUSG00000028327	chr4	Stra6l	4.6E+07	4.6E+07	9567	4.629015029	0.135862449	2.261E-14	8.47888E-13	0.16565	1	1	1	1	0	2	26	48	16	29	69
ENSMUSG00000006576	chr1	Slc4a3	7.6E+07	7.6E+07	8599	1.504931557	3.751840947	2.327E-14	8.70243E-13	0.03942	1	91	68	149	120	102	469	412	329	350	475
ENSMUSG00000029468	chr5	P2rx7	1.2E+08	1.2E+08	5408	1.916402531	2.932546788	2.361E-14	8.80562E-13	0.06025	1	40	37	48	30	84	310	250	183	226	259
ENSMUSG00000014609	chr11	Chrne	7.1E+07	7.1E+07	1690	1.886640116	5.589205891	2.382E-14	8.83911E-13	0.06711	1	379	246	244	207	450	1381	1394	1398	2040	1466
ENSMUSG00000030798	chr7	Cd37	4.5E+07	4.5E+07	3538	3.227157806	3.375369224	2.381E-14	8.83911E-13	0.16878	1	18	22	10	17	85	360	327	210	458	568
ENSMUSG00000028572	chr4	Hook1	9.6E+07	9.6E+07	8318	-1.96515741	4.412774312	2.445E-14	9.0466E-13	0.07105	-1	533	494	555	522	367	186	313	98	145	173
ENSMUSG00000084883	chr12	Ccdc85c	1.1E+08	1.1E+08	1547	-2.99042139	1.968047703	2.581E-14	9.52661E-13	0.13631	-1	92	55	173	150	60	15	36	11	12	16
ENSMUSG00000027995	chr3	Tlr2	8.4E+07	8.4E+07	3014	2.149666556	2.619782626	2.665E-14	9.81048E-13	0.0735	1	22	32	26	28	57	290	179	159	176	210
ENSMUSG00000036908	chr19	Unc93b1	3935186	3935352	2841	2.290763642	5.19222347	2.685E-14	9.83333E-13	0.09673	1	168	131	107	120	424	1775	912	865	1389	1380
ENSMUSG00000049103	chr9	Ccr2	1.2E+08	1.2E+08	6393	2.582347339	3.118780852	2.681E-14	9.83333E-13	0.11089	1	34	33	24	21	71	545	198	259	237	281
ENSMUSG00000056124	chr18	B4galt6	2.1E+07	2.1E+07	5808	1.744341232	3.004306341	2.754E-14	1.00585E-12	0.04996	1	52	36	67	63	56	371	247	172	205	276
ENSMUSG00000027078	chr2	Ube2l6	8.5E+07	8.5E+07	1996	1.808871686	3.586194758	2.773E-14	1.01012E-12	0.05747	1	60	52	85	78	130	630	299	237	387	396
ENSMUSG00000036390	chr6	Gadd45a	6.7E+07	6.7E+07	1764	2.173894903	5.634549995	2.785E-14	1.01188E-12	0.0882	1	358	206	351	219	205	1781	910	2042	1601	1731
ENSMUSG00000048163	chr5	Selplg	1.1E+08	1.1E+08	2604	2.764388625	3.475327701	2.798E-14	1.01407E-12	0.12941	1	28	32	19	28	109	529	282	261	431	491
ENSMUSG00000085939	chr18	Cd63-ps	5E+07	5E+07	875	1.798584226	3.421844514	2.928E-14	1.05842E-12	0.05621	1	74	46	82	55	104	450	229	302	356	349
ENSMUSG00000079419	chr19	Ms4a6c	1.1E+07	1.1E+07	2050	2.657866225	2.674598537	2.999E-14	1.08146E-12	0.11528	1	17	15	19	20	61	381	205	179	221	134
ENSMUSG00000024912	chr19	Fosl1	5447703	5448055	1707	5.202330814	0.01459725	3.09E-14	1.10861E-12	0.20071	1	1	0	0	0	2	34	22	58	23	27
ENSMUSG00000054520	chr5	Sh3bp2	3.5E+07	3.5E+07	4277	2.172756477	3.473980282	3.089E-14	1.10861E-12	0.08272	1	41	43	69	30	127	458	339	336	395	310
ENSMUSG00000093938	chr11	Evi2b	8E+07	8E+07	1858	2.764016451	2.038459956	3.582E-14	1.28174E-12	0.11649	1	6	11	14	11	36	237	102	105	132	142
ENSMUSG00000046311	chr11	Zfp62	4.9E+07	4.9E+07	6060	-1.75353644	4.187067047	3.642E-14	1.2997E-12	0.05706	-1	434	262	603	496	340	187	277	111	133	163

ENSMUSG00000060961	chr5	Slc4a4	8.9E+07	8.9E+07	10815	-2.01628717	3.917345187	3.653E-14	1.30048E-12	0.07429	-1	323	371	270	506	269	171	139	84	115	118
ENSMUSG00000022014	chr14	Epsti1	7.8E+07	7.8E+07	2317	2.798580395	1.560322445	3.75E-14	1.33045E-12	0.10786	1	6	12	6	6	22	142	88	76	83	116
ENSMUSG00000042717	chr6	Ppp1r3a	1.5E+07	1.5E+07	7120	-2.27563423	7.804964565	3.756E-14	1.33045E-12	0.0982	-1	5952	4319	7194	6211	3956	1511	3213	924	1191	1226
ENSMUSG00000026177	chr1	Slc11a1	7.4E+07	7.4E+07	3705	2.661983745	3.511108103	3.795E-14	1.34079E-12	0.12144	1	30	56	28	21	91	382	424	214	501	507
ENSMUSG00000034786	chr17	Gpsm3	3.5E+07	3.5E+07	1343	2.653767681	3.183533372	3.809E-14	1.34242E-12	0.12084	1	22	17	38	23	95	383	190	229	382	410
ENSMUSG00000032013	chr9	Trim29	4.3E+07	4.3E+07	2830	4.909365605	-0.20444078	4.197E-14	1.47543E-12	0.16048	1	0	0	1	1	1	17	27	14	37	48
ENSMUSG00000042129	chr6	Rassf4	1.2E+08	1.2E+08	6344	1.782178054	3.661109433	4.308E-14	1.51065E-12	0.05698	1	69	62	80	62	159	567	400	253	396	420
ENSMUSG00000047592	chr5	Nxpe5	1.4E+08	1.4E+08	4473	2.851589792	2.080635878	4.414E-14	1.54395E-12	0.12402	1	17	11	9	11	26	274	119	146	99	99
ENSMUSG00000051439	chr18	Cd14	3.7E+07	3.7E+07	1572	2.527075761	3.826258755	4.442E-14	1.54984E-12	0.11293	1	64	54	23	38	131	611	423	325	596	536
ENSMUSG00000023827	chr17	Agpat4	1.2E+07	1.2E+07	2701	1.905404261	3.039641738	4.496E-14	1.56496E-12	0.06226	1	37	31	49	53	92	350	210	194	270	300
ENSMUSG00000052957	chr13	Gas1	6E+07	6E+07	2961	1.747714551	5.730118057	4.534E-14	1.57403E-12	0.05953	1	264	246	400	339	632	2777	1300	1355	1399	1690
ENSMUSG00000032220	chr9	Myo1e	7E+07	7E+07	4944	1.355493788	4.437277007	4.704E-14	1.62909E-12	0.03437	1	158	142	194	203	213	726	560	458	658	809
ENSMUSG00000032565	chr9	Nudt16	1.1E+08	1.1E+08	2573	1.639851213	3.478950515	4.774E-14	1.64912E-12	0.04728	1	91	50	69	73	123	429	351	251	335	366
ENSMUSG00000038037	chr16	Socs1	1.1E+07	1.1E+07	1220	2.428513808	1.586645463	5.061E-14	1.74422E-12	0.08299	1	8	11	17	7	25	123	121	75	101	77
ENSMUSG00000032334	chr9	Loxl1	5.8E+07	5.8E+07	3338	1.905783321	6.010853959	5.092E-14	1.75043E-12	0.07071	1	318	287	345	345	793	3048	1514	1669	2380	1937
ENSMUSG00000006403	chr1	Adamts4	1.7E+08	1.7E+08	4810	2.814427859	1.486558123	5.212E-14	1.78724E-12	0.10991	1	8	9	6	8	18	107	63	91	132	76
ENSMUSG00000044006	chr8	Cilp2	7E+07	7E+07	4314	2.136751717	4.25403862	5.253E-14	1.79718E-12	0.08436	1	109	77	168	71	111	1257	326	491	574	596
ENSMUSG00000022575	chr15	Gsdmd	7.6E+07	7.6E+07	1776	1.83708905	3.21755641	5.282E-14	1.80247E-12	0.05871	1	46	47	67	56	88	431	228	189	257	396
ENSMUSG00000035385	chr11	Ccl2	8.2E+07	8.2E+07	1138	3.027175973	2.111102185	5.847E-14	1.99054E-12	0.144	1	8	7	24	11	21	258	119	194	79	98
ENSMUSG00000062382	chr13	Gm10116	7.4E+07	7.4E+07	922	2.184963708	3.492964356	6.105E-14	2.07347E-12	0.08559	1	52	46	50	32	127	447	282	319	446	374
ENSMUSG00000015355	chr1	Cd48	1.7E+08	1.7E+08	1189	2.530685376	2.239980549	6.396E-14	2.16698E-12	0.10206	1	16	16	8	19	42	236	146	98	162	174
ENSMUSG00000033713	chr12	Foxn3	9.9E+07	9.9E+07	4651	-2.4021806	4.158266409	6.489E-14	2.19322E-12	0.10676	-1	475	368	649	554	174	106	182	57	118	135
ENSMUSG00000021185	chr12	9030617O03Rik	1E+08	1E+08	4434	-1.66351608	3.696436896	6.956E-14	2.34204E-12	0.05127	-1	238	201	478	313	281	127	189	79	121	132
ENSMUSG00000053199	chr9	Arhgap20	5.2E+07	5.2E+07	12685	-1.97021769	4.81360286	6.963E-14	2.34204E-12	0.07526	-1	591	471	974	805	559	192	464	131	182	231
ENSMUSG00000024909	chr19	Efemp2	5473973	5474323	2648	1.8733639	4.097732177	7.285E-14	2.44436E-12	0.06587	1	81	84	125	77	193	867	381	446	627	450
ENSMUSG00000047036	chr9	Zfp445	1.2E+08	1.2E+08	2961	-2.76016363	3.34127171	7.638E-14	2.55694E-12	0.13451	-1	324	304	251	219	159	63	107	39	27	37
ENSMUSG00000003206	chr17	Ebi3	5.6E+07	5.6E+07	1170	3.4374427	0.634865212	8.341E-14	2.78547E-12	0.12805	1	5	3	0	3	6	83	30	36	53	63
ENSMUSG00000001506	chr11	Col1a1	9.5E+07	9.5E+07	6563	2.02150282	8.728197975	8.438E-14	2.80441E-12	0.08126	1	2217	1989	2324	1679	4595	21467	11769	9650	17678	10847
ENSMUSG00000018008	chr15	Cyth4	7.9E+07	7.9E+07	2791	2.430265385	4.274801853	8.436E-14	2.80441E-12	0.10927	1	59	82	43	62	209	924	561	449	671	784
ENSMUSG00000067212	chr17	H2-T23	3.6E+07	3.6E+07	2889	2.144931792	5.606129459	8.666E-14	2.87347E-12	0.08964	1	211	179	254	214	531	2926	1050	844	1476	2175
ENSMUSG00000029675	chr5	Eln	1.3E+08	1.3E+08	2583	1.581265042	5.337368309	8.879E-14	2.93729E-12	0.04979	1	169	248	323	331	467	1736	1384	895	1206	1097
ENSMUSG00000030844	chr7	Rgs10	1.3E+08	1.3E+08	1711	2.277907007	3.323980129	8.947E-14	2.95264E-12	0.0924	1	60	42	25	32	92	516	332	217	339	314
ENSMUSG00000024663	chr19	Rab3il1	1E+07	1E+07	4543	1.78627774	4.207350459	9.325E-14	3.07032E-12	0.06071	1	107	91	101	99	231	822	426	463	617	619
ENSMUSG00000041449	chr12	Serpina3h	1E+08	1E+08	1434	3.390903671	1.063331106	1.03E-13	3.38421E-12	0.1487	1	2	2	7	10	4	156	65	47	53	51
ENSMUSG00000027068	chr2	Dhrs9	6.9E+07	6.9E+07	4281	2.909277597	0.779238749	1.17E-13	3.83573E-12	0.09599	1	3	5	3	7	9	61	74	34	44	73
ENSMUSG00000030148	chr6	Clec4a2	1.2E+08	1.2E+08	2860	2.608757805	2.581658286	1.174E-13	3.83697E-12	0.11329	1	19	31	11	17	41	339	171	162	194	175
ENSMUSG00000030323	chr6	Ift122	1.2E+08	1.2E+08	7953	1.481389447	4.40452408	1.217E-13	3.97075E-12	0.04287	1	180	120	188	110	248	747	678	449	786	561
ENSMUSG00000014846	chr8	Tppp3	1.1E+08	1.1E+08	1848	1.656636465	6.500659956	1.243E-13	4.01899E-12	0.05613	1	602	407	668	629	1048	4197	2778	1463	2799	3370
ENSMUSG00000019539	chr7	Rcn3	4.5E+07	4.5E+07	1604	1.860800227	5.319655761	1.244E-13	4.01899E-12	0.06906	1	228	214	213	186	460	2037	883	931	1515	1165
ENSMUSG00000032997	chr1	Chpf	7.5E+07	7.5E+07	3856	1.85134081	4.236098422	1.241E-13	4.01899E-12	0.06624	1	81	78	119	105	249	728	431	445	692	738
ENSMUSG00000057719	chr18	Sh3rf2	4.2E+07	4.2E+07	5307	-1.9604727	4.991623404	1.235E-13	4.01899E-12	0.07622	-1	959	700	804	731	481	182	382	199	246	329
ENSMUSG00000036905	chr4	C1qb	1.4E+08	1.4E+08	1088	2.826292865	5.983694671	1.302E-13	4.18695E-12	0.1504	1	160	191	115	134	601	3970	1391	1807	2260	2143
ENSMUSG00000041120	chr4	Nbl1	1.4E+08	1.4E+08	2033	1.863723929	5.725942691	1.301E-13	4.18695E-12	0.06987	1	264	221	308	387	567	1993	1090	1131	1796	2617
ENSMUSG00000030793	chr7	Pycard	1.3E+08	1.3E+08	1405	2.618222044	2.092738215	1.327E-13	4.25887E-12	0.11119	1	11	14	18	8	37	235	95	105	165	136
ENSMUSG00000091089	chr14	A930018M24Rik	5.1E+07	5.1E+07	1422	-2.3364742	4.16151074	1.349E-13	4.31998E-12	0.10397	-1	620	280	758	360	247	151	211	86	79	92
ENSMUSG00000004885	chr3	Crabp2	8.8E+07	8.8E+07	1322	4.443353399	0.177768909	1.369E-13	4.37411E-12	0.17854	1	0	0	0	4	2	52	21	35	23	60
ENSMUSG00000029718	chr5	Pcolce	1.4E+08	1.4E+08	3823	1.926602907	7.031122933	1.378E-13	4.39236E-12	0.07525	1	644	649	688	702	1459	6143	2825	3299	5170	4067
ENSMUSG00000022253	chr15	Nadk2	9071260	9071765	4345	-1.55585357	5.092559173	1.445E-13	4.58449E-12	0.04907	-1	830	486	1110	865	570	363	516	263	312	342
ENSMUSG00000069515	chr10	Lyz1	1.2E+08	1.2E+08	1264	2.647739628	3.842777507	1.443E-13	4.58449E-12	0.12922	1	51	41	29	31	149	671	614	361	304	608
ENSMUSG00000026725	chr1	Tnn	1.6E+08	1.6E+08	5817	4.677486689	-0.40677356	1.461E-13	4.62687E-12	0.13489	1	0	0	3	0	0	17	23	16	32	32
ENSMUSG00000026630	chr1	Batf3	1.9E+08	1.9E+08	1597	3.462076903	0.280527933	1.497E-13	4.72942E-12	0.11816	1	3	1	3	1	5	60	24	32	32	53
ENSMUSG00000028082	chr3	Sh3d19	8.6E+07	8.6E+07	8888	1.500405496	4.504377922	1.501E-13	4.73037E-12	0.04441	1	163	152	157	141	272	797	625	510	639	884
ENSMUSG00000018819	chr7	Lsp1	1.4E+08	1.4E+08	5174	1.824545909	6.039177605	1.582E-13	4.9755E-12	0.06767	1	462	402	308	320	644	2878	1644	1552	2122	2467
ENSMUSG00000097993	chr1	Ptprv	1.4E+08	1.4E+08	6987	3.853007056	0.624987359	1.647E-13	5.16719E-12	0.17083	1	4	2	3	0	4	63	22	34	53	95
ENSMUSG00000027792	chr3	Bche	7.4E+07	7.4E+07	6741	-1.65304558	3.383654259	1.715E-13	5.36998E-12	0.05079	-1	226	176	259	179	364	140	104	94	90	89
ENSMUSG00000053040	chr9	Aph1c	6.7E+07	6.7E+07	5205	2.502927121	1.97737549	1.941E-13	6.06414E-12	0.09981	1	19	14	17	8	27	116	159	60	155	182
ENSMUSG00000068196	chr16	Col8a1	5.8E+07	5.8E+07	5108	1.767422098	4.48071061	1.985E-13	6.18826E-12	0.06212	1	132	88	175	131	257	1137	749	669	487	505
ENSMUSG00000054428	chr4	Atpif1	1.3E+08	1.3E+08	1441	1.317158581	4.896672368	2.135E-13	6.63995E-12	0.03514	1	256	202	262	225	333	1046	709	727	989	885
ENSMUSG00000007617	chr13	Homer1	9.3E+07	9.3E+07	10502	-2.16795482	5.726011138	2.255E-13	6.99623E-12	0.09497	-1	1415	1109	1636	1319	926	331	829	236	289	337
ENSMUSG00000036887	chr4	C1qa	1.4E+08	1.4E+08	1040	2.66452646	6.400749346	2.416E-13	7.48145E-12	0.13881	1	239	263	180	224	870	4949	1871	2213	3364	2865
ENSMUSG00000040133	chr2	Gpr176	1.2E+08	1.2E+08	3899	2.932960208	0.64998006	2.44E-13	7.53941E-12	0.10619	1	0	2	7	6	10	56	61	43	55	42
ENSMUSG00000025531	chrX	Chm	1.1E+08	1.1E+08	6780	-2.18407414	4.149547089	2.512E-13	7.72604E-12	0.0939	-1	491	399	510	445	284	150	249	51	105	129
ENSMUSG00000090877	chr17	Hspa1b	3.5E+07	3.5E+07	2803	2.151785226	2.009257887	2.508E-13	7.72604E-12	0.07456	1	10	14	26	33	25	146	134	104	113	154
ENSMUSG00000026833	chr2	Olfm1	2.8E+07	2.8E+07	3553	1.434346279	4.309266099	2.57E-13	7.88704E-12	0.0414	1	116	83	208	179	245	749	527	445	602	663
ENSMUSG00000041515	chr8	Irf8	1.2E+08	1.2E+08	7055	1.589454464	3.474074275	2.712E-13	8.30658E-12	0.04744	1	63	63	91	80	119	492	270	245	335	376
ENSMUSG00000011008	chr3	Mcoln2	1.5E+08	1.5E+08	3288	2.944111174	0.55026816	2.815E-13	8.60165E-12	0.10231	1	4	0	5	3	11	62	47	33	48	51
ENSMUSG00000029816	chr6	Gpnmb	4.9E+07	4.9E+07	3798	2.576384235	3.496251521	2.884E-13	8.79431E-12	0.12537	1	31	11	60	77	74	284	402	211	423	663

ENSMUSG00000031264	chrX	Btk	1.3E+08	1.3E+08	3149	2.819858493	1.950647143	2.891E-13	8.79446E-12	0.12842	1	10	15	5	8	30	199	129	111	93	139
ENSMUSG00000011256	chr11	Adam19	4.6E+07	4.6E+07	7115	1.544957318	4.174782327	2.908E-13	8.82707E-12	0.04701	1	133	128	137	94	191	759	521	378	487	647
ENSMUSG00000019841	chr10	Rev3l	4E+07	4E+07	13293	-1.42399326	4.676433314	2.931E-13	8.87986E-12	0.04178	-1	526	520	678	540	489	333	403	200	247	264
ENSMUSG00000030707	chr7	Coro1a	1.3E+08	1.3E+08	2783	2.600967617	4.274999123	2.942E-13	8.89321E-12	0.12981	1	37	79	56	42	202	941	466	522	721	771
ENSMUSG00000021262	chr12	Evl	1.1E+08	1.1E+08	2695	1.789533344	3.580448251	3.324E-13	1.00262E-11	0.0624	1	53	40	115	63	149	404	362	261	412	464
ENSMUSG00000061119	chr7	Prcp	9.3E+07	9.3E+07	2956	1.753173176	3.929858627	3.337E-13	1.00429E-11	0.06081	1	79	75	97	77	204	680	409	362	528	444
ENSMUSG00000061878	chr11	Sphk1	1.2E+08	1.2E+08	4774	2.734578582	1.210687762	3.348E-13	1.00569E-11	0.10741	1	3	4	9	13	14	76	53	75	86	90
ENSMUSG00000027457	chr2	Snph	1.5E+08	1.5E+08	7861	-2.6098384	1.189770655	3.495E-13	1.04741E-11	0.10271	-1	43	38	101	74	39	14	14	8	17	12
ENSMUSG00000059456	chr14	Ptk2b	6.6E+07	6.6E+07	7398	2.022103156	3.429959452	3.594E-13	1.07494E-11	0.07848	1	45	48	63	37	131	351	338	227	396	459
ENSMUSG00000049866	chr1	Arl4c	8.9E+07	8.9E+07	5492	2.299294025	2.469730551	3.834E-13	1.14415E-11	0.09537	1	16	9	29	27	63	234	171	141	188	193
ENSMUSG00000028289	chr4	Epha7	2.9E+07	2.9E+07	9884	-3.12430191	0.72302703	3.854E-13	1.14763E-11	0.13799	-1	41	43	32	61	35	12	10	2	3	8
ENSMUSG00000036103	chr18	Colec12	9707648	9707759	3322	1.424309374	4.525153932	3.864E-13	1.14822E-11	0.04148	1	170	160	186	148	271	979	805	527	581	587
ENSMUSG00000004552	chr1	Ctse	1.3E+08	1.3E+08	3170	2.638454581	1.838214609	4.153E-13	1.23158E-11	0.11148	1	11	14	5	11	29	163	103	75	120	153
ENSMUSG00000030351	chr6	Tspan11	1.3E+08	1.3E+08	4380	2.086186508	2.125481966	4.197E-13	1.24196E-11	0.07286	1	16	14	31	36	25	181	107	99	169	151
ENSMUSG00000022303	chr15	Dcstamp	4E+07	4E+07	1993	5.251822736	-0.32729347	4.266E-13	1.25962E-11	0.18525	1	0	0	0	1	1	10	27	16	35	41
ENSMUSG00000059149	chr1	Mfsd4	1.3E+08	1.3E+08	7187	-1.76441953	3.72991219	4.516E-13	1.33072E-11	0.06214	-1	303	191	519	261	308	109	198	89	135	92
ENSMUSG00000027035	chr2	Cers6	6.9E+07	6.9E+07	8875	1.942118914	2.507541282	4.541E-13	1.33517E-11	0.06536	1	29	36	29	28	47	214	174	170	163	175
ENSMUSG00000039976	chr11	Tbc1d16	1.2E+08	1.2E+08	7119	-1.65457449	5.526257432	4.552E-13	1.33578E-11	0.05825	-1	976	1058	1063	1156	831	419	639	321	506	418
ENSMUSG00000057924	chr8	Gm10033	6.9E+07	6.9E+07	654	-3.204138	1.006093972	4.667E-13	1.36649E-11	0.15502	-1	58	58	65	50	30	8	18	6	4	4
ENSMUSG00000090778	chr8	Gm3235	9.2E+07	9.2E+07	695	-2.01374703	2.589632398	4.728E-13	1.38158E-11	0.07485	-1	147	91	205	145	146	53	78	26	62	30
ENSMUSG00000024030	chr17	Abcg1	3.1E+07	3.1E+07	4066	2.597259425	2.599504339	4.803E-13	1.40057E-11	0.12365	1	12	5	33	31	53	227	221	112	293	207
ENSMUSG00000015085	chr2	Entpd2	2.5E+07	2.5E+07	2128	1.516742967	4.182024252	4.908E-13	1.42817E-11	0.04649	1	123	110	139	121	214	610	415	399	660	677
ENSMUSG00000027883	chr3	Gpsm2	1.1E+08	1.1E+08	3909	1.820533256	2.568245197	5.197E-13	1.5092E-11	0.05842	1	27	32	47	30	58	246	157	151	170	207
ENSMUSG00000022226	chr14	Mcpt2	5.6E+07	5.6E+07	971	3.173729483	5.135801416	5.22E-13	1.51286E-11	0.19069	1	80	147	52	109	97	3286	447	810	1272	965
ENSMUSG00000042363	chr11	Lgalsl	2.1E+07	2.1E+07	4115	-1.68613339	6.293532876	5.297E-13	1.53182E-11	0.06127	-1	1932	1349	2244	1865	1583	835	1286	490	688	602
ENSMUSG00000054675	chr5	Tmem119	1.1E+08	1.1E+08	2315	2.063780679	3.328200916	5.329E-13	1.53792E-11	0.08156	1	64	55	46	48	67	557	190	262	356	296
ENSMUSG00000053931	chr3	Cnn3	1.2E+08	1.2E+08	2003	1.46391439	5.407922459	5.48E-13	1.57822E-11	0.04598	1	294	208	402	291	553	1785	1031	1109	1134	1360
ENSMUSG00000006589	chr8	Aprt	1.2E+08	1.2E+08	866	1.290027064	4.743997443	6.016E-13	1.72918E-11	0.03499	1	206	146	265	255	314	859	626	615	936	864
ENSMUSG00000022769	chr16	Sdf2l1	1.7E+07	1.7E+07	1108	1.915744938	3.283390824	6.471E-13	1.85613E-11	0.07048	1	48	65	44	47	92	469	268	227	304	313
ENSMUSG00000031983	chr8	2310022B05Rik	1.2E+08	1.2E+08	3297	1.198512075	5.188412775	6.561E-13	1.87794E-11	0.03079	1	278	208	466	318	437	1281	1019	713	1167	1102
ENSMUSG00000062082	chr16	Cd200r4	4.5E+07	4.5E+07	2045	3.83196916	-0.14574249	6.615E-13	1.88976E-11	0.1232	1	2	0	0	2	3	44	31	22	33	16
ENSMUSG00000047180	chr1	Neurl3	3.6E+07	3.6E+07	3217	2.317128388	2.735194136	6.662E-13	1.89926E-11	0.09927	1	19	31	26	23	65	334	168	135	205	296
ENSMUSG00000043336	chr16	Filip1l	5.7E+07	5.7E+07	5335	-1.96295896	6.153102922	6.722E-13	1.91255E-11	0.08241	-1	1870	1396	2042	2045	987	638	990	406	445	560
ENSMUSG00000047810	chr19	Ccdc88b	6844623	6845119	4959	2.417466642	1.691414076	6.75E-13	1.91656E-11	0.09424	1	11	11	21	7	24	135	80	61	109	156
ENSMUSG00000027408	chr2	Cpxm1	1.3E+08	1.3E+08	2432	2.336378024	4.222096429	6.784E-13	1.92216E-11	0.10965	1	103	87	46	48	169	788	430	586	805	546
ENSMUSG00000027935	chr3	Rab13	9E+07	9E+07	1651	1.837615348	4.503838827	7.083E-13	2.00308E-11	0.07044	1	138	107	159	70	288	978	587	625	731	712
ENSMUSG00000035357	chr6	Pdzrn3	1E+08	1E+08	7256	-1.72447546	6.20518528	7.18E-13	2.02643E-11	0.06466	-1	1571	1360	2303	1872	1388	723	1205	478	561	615
ENSMUSG00000006390	chr4	Elovl1	1.2E+08	1.2E+08	2726	1.769042016	4.191694519	7.283E-13	2.05123E-11	0.06474	1	83	81	123	92	263	712	498	468	634	582
ENSMUSG00000019876	chr10	Pkib	5.8E+07	5.8E+07	11800	2.830159831	0.450779474	7.462E-13	2.09754E-11	0.08506	1	4	4	3	4	7	54	45	23	47	53
ENSMUSG00000020961	chr12	Ston2	9.2E+07	9.2E+07	6915	-3.02990775	3.872123268	7.507E-13	2.10575E-11	0.17651	-1	492	319	495	467	137	56	161	38	45	36
ENSMUSG00000027365	chr2	Trpm7	1.3E+08	1.3E+08	11315	-1.54662984	5.20183751	7.544E-13	2.11191E-11	0.05182	-1	771	622	1138	884	721	455	608	262	252	389
ENSMUSG00000052353	chr7	Cemip	8.4E+07	8.4E+07	12232	7.038118996	-0.73834049	7.579E-13	2.11765E-11	0.16837	1	0	0	0	0	0	14	27	20	8	23
ENSMUSG00000071713	chr15	Csf2rb	7.8E+07	7.8E+07	4764	2.162065491	3.655743895	7.838E-13	2.18547E-11	0.09355	1	48	58	45	41	155	467	504	254	441	463
ENSMUSG00000036202	chr2	Rif1	5.2E+07	5.2E+07	10527	-2.03307483	3.967136296	7.889E-13	2.19548E-11	0.0851	-1	419	301	495	404	247	142	224	70	72	140
ENSMUSG00000026360	chr1	Rgs2	1.4E+08	1.4E+08	3627	1.403340779	4.427662586	8.023E-13	2.22832E-11	0.0416	1	165	90	215	178	264	915	611	402	749	588
ENSMUSG00000039652	chr19	Cpeb3	3.7E+07	3.7E+07	7414	-1.5695037	5.091426477	8.187E-13	2.26695E-11	0.05339	-1	659	653	948	831	717	317	607	221	286	364
ENSMUSG00000055782	chr15	Abcd2	9.1E+07	9.1E+07	5527	-1.83998315	5.467552181	8.194E-13	2.26695E-11	0.07302	-1	1271	801	797	629	1704	471	569	301	336	333
ENSMUSG00000018752	chr11	Tnfsf12Tnfsf13	7E+07	7E+07	2235	1.453969784	4.062499048	8.498E-13	2.34626E-11	0.04345	1	120	86	143	108	226	581	468	332	576	573
ENSMUSG00000044934	chr13	Zfp367	6.4E+07	6.4E+07	5454	-1.42766158	4.333894218	8.665E-13	2.38781E-11	0.04325	-1	475	351	500	414	455	247	349	153	196	194
ENSMUSG00000075470	chr15	Alg10b	9E+07	9E+07	3727	-2.25751362	3.607387306	8.756E-13	2.40818E-11	0.10269	-1	358	285	359	272	198	75	172	67	61	61
ENSMUSG00000052776	chr5	Oas1a	1.2E+08	1.2E+08	1885	2.955543189	1.631641757	8.867E-13	2.4338E-11	0.14042	1	4	10	6	8	22	180	102	46	140	84
ENSMUSG00000035133	chr12	Arhgap5	5.3E+07	5.3E+07	5197	-3.19169155	4.52915726	8.949E-13	2.45148E-11	0.19698	-1	647	562	836	718	294	72	271	36	47	61
ENSMUSG00000102037	chr9	Bcl2a1a	8.9E+07	8.9E+07	819	3.646118651	-0.01351666	9.087E-13	2.48452E-11	0.12565	1	0	0	2	4	3	36	28	16	32	50
ENSMUSG00000038463	chr1	Olfml2b	1.7E+08	1.7E+08	3095	1.634845886	4.516486643	9.122E-13	2.4892E-11	0.05684	1	148	123	152	131	292	1178	536	524	697	672
ENSMUSG00000034854	chr10	Mfsd12	8.1E+07	8.1E+07	3971	2.0188686	4.291411409	9.208E-13	2.50778E-11	0.08476	1	88	80	96	73	260	628	716	336	823	766
ENSMUSG00000022505	chr16	Emp2	1E+07	1E+07	3440	1.192331135	4.542669378	9.414E-13	2.5589E-11	0.02988	1	188	146	272	207	266	910	584	465	687	723
ENSMUSG00000020300	chr11	Cpeb4	3.2E+07	3.2E+07	6369	-2.01935697	6.038121985	9.55E-13	2.58963E-11	0.08803	-1	1535	1176	2112	1974	1099	482	1031	334	375	503
ENSMUSG00000031765	chr8	Mt1	9.4E+07	9.4E+07	540	2.966751021	5.815250879	9.564E-13	2.58963E-11	0.1766	1	93	56	263	117	532	2995	1172	2335	1970	1597
ENSMUSG00000029561	chr5	Oasl2	1.1E+08	1.1E+08	3879	2.11034631	2.933283871	9.696E-13	2.62043E-11	0.08601	1	42	26	42	36	69	421	229	103	329	218
ENSMUSG00000033209	chr5	Ttc28	1.1E+08	1.1E+08	12315	-1.32100624	4.829622041	1E-12	2.69854E-11	0.03786	-1	542	436	829	709	558	369	471	223	300	333
ENSMUSG00000006356	chr12	Crip2	1.1E+08	1.1E+08	1437	1.619917721	6.142248249	1.045E-12	2.81263E-11	0.05807	1	381	332	594	462	928	2682	1616	1785	2315	2580
ENSMUSG00000003949	chr11	Hlf	9E+07	9E+07	6681	-2.01529417	3.086674075	1.053E-12	2.82901E-11	0.08036	-1	196	122	229	128	383	86	90	64	49	56
ENSMUSG00000091562	chr16	Crybg3	6E+07	6E+07	2870	-4.16417303	1.07488889	1.088E-12	2.91851E-11	0.26444	-1	41	48	112	76	22	5	14	0	2	2
ENSMUSG00000027199	chr2	Gatm	1.2E+08	1.2E+08	3001	1.516807086	3.894428264	1.147E-12	3.06933E-11	0.04713	1	130	84	108	104	147	728	422	345	385	403
ENSMUSG00000028378	chr4	Ptgr1	5.9E+07	5.9E+07	2296	1.995356912	2.85662835	1.18E-12	3.15223E-11	0.07631	1	48	31	28	33	74	319	205	176	277	199
ENSMUSG00000072501	chr15	Phf20l1	6.7E+07	6.7E+07	6670	-1.62447152	5.453077176	1.197E-12	3.19164E-11	0.05833	-1	1046	818	1169	1087	782	443	712	276	346	470
ENSMUSG00000078771	chr11	Evi2a	8E+07	8E+07	2297	1.717683402	3.581530377	1.222E-12	3.2529E-11	0.05946	1	88	75	59	69	117	548	316	294	346	380

ENSMUSG00000076441	chr2	Ass1	3.1E+07	3.1E+07	2414	1.737390506	2.712331275	1.25E-12	3.31999E-11	0.05628	1	37	30	62	49	47	201	186	167	177	280
ENSMUSG00000020437	chr11	Myo1g	6506548	6506832	6957	2.520353622	2.646415168	1.253E-12	3.32223E-11	0.11938	1	16	26	12	20	62	278	208	126	205	272
ENSMUSG00000058126	chr14	Tpm3-rs7	1.1E+08	1.1E+08	2106	1.703295113	5.097895306	1.274E-12	3.37052E-11	0.0637	1	165	112	320	224	455	1474	729	857	1099	1251
ENSMUSG00000073889	chr4	Il11ra1	4.2E+07	4.2E+07	4471	1.445349365	6.41318109	1.293E-12	3.41417E-11	0.04704	1	624	485	856	665	859	3626	1838	1954	2650	2888
ENSMUSG00000037966	chr13	Ninj1	4.9E+07	4.9E+07	1570	1.34934833	4.673282868	1.296E-12	3.41635E-11	0.03948	1	137	163	305	179	322	887	676	595	833	775
ENSMUSG00000012017	chr16	Scarf2	1.8E+07	1.8E+07	3302	1.945519483	3.718762627	1.339E-12	3.52361E-11	0.07839	1	76	42	73	63	164	586	268	337	508	440
ENSMUSG00000030515	chr7	Tarsl2	6.6E+07	6.6E+07	4095	-1.57084947	5.627961608	1.355E-12	3.55809E-11	0.05501	-1	1252	851	1322	1150	941	510	801	391	488	389
ENSMUSG00000022464	chr15	Slc38a4	9.7E+07	9.7E+07	3952	-2.01632763	5.99126777	1.373E-12	3.59912E-11	0.08899	-1	1392	1494	1746	1123	1825	418	1046	356	441	363
ENSMUSG00000032717	chr17	Mdfi	4.8E+07	4.8E+07	3092	2.978219901	0.581443315	1.451E-12	3.79626E-11	0.1043	1	4	6	4	3	5	64	32	49	54	43
ENSMUSG00000019997	chr10	Ctgf	2.5E+07	2.5E+07	2861	1.47335954	4.920572813	1.463E-12	3.82182E-11	0.04798	1	168	118	435	249	294	1102	977	635	791	1123
ENSMUSG00000042349	chr1	Ikbke	1.3E+08	1.3E+08	9018	2.161736107	1.703190699	1.505E-12	3.92243E-11	0.07529	1	13	16	12	19	24	159	92	78	95	103
ENSMUSG00000070034	chr1	Sp110	8.6E+07	8.6E+07	6781	2.009389745	2.751228087	1.558E-12	4.05462E-11	0.07808	1	39	25	39	31	66	375	159	126	207	249
ENSMUSG00000059182	chr6	Skap2	5.2E+07	5.2E+07	1638	1.662873091	3.900228903	1.579E-12	4.1012E-11	0.05758	1	99	102	90	72	166	657	417	390	417	444
ENSMUSG00000063594	chr7	Gng8	1.7E+07	1.7E+07	920	3.431097811	0.060823142	1.606E-12	4.16447E-11	0.11537	1	2	1	2	2	4	52	23	22	25	48
ENSMUSG00000061436	chr6	Hipk2	3.9E+07	3.9E+07	8836	-2.45350578	4.761620187	1.628E-12	4.21394E-11	0.12676	-1	691	535	1190	689	353	123	388	83	154	135
ENSMUSG00000031875	chr8	Cmtm3	1E+08	1E+08	1616	1.78418076	4.330230822	1.648E-12	4.25659E-11	0.06822	1	124	99	85	112	263	838	513	476	735	652
ENSMUSG00000027520	chr1	Zdbf2	6.3E+07	6.3E+07	12659	2.565404771	2.012544531	1.681E-12	4.33495E-11	0.11644	1	13	11	18	33	8	155	91	131	150	146
ENSMUSG00000032575	chr9	Manf	1.1E+08	1.1E+08	3524	1.631456752	5.102305461	1.718E-12	4.42136E-11	0.05912	1	220	143	249	273	404	1711	649	930	1019	1051
ENSMUSG00000030786	chr7	Itgam	1.3E+08	1.3E+08	6377	2.221727886	3.745017682	1.761E-12	4.52402E-11	0.10207	1	48	64	37	46	159	632	484	315	402	450
ENSMUSG00000034584	chr9	Exph5	5.3E+07	5.3E+07	10519	-4.1687142	-0.26599525	1.773E-12	4.54715E-11	0.18169	-1	23	18	22	33	14	0	7	0	1	0
ENSMUSG00000038271	chr6	Iffo1	1.3E+08	1.3E+08	5691	1.331736932	4.369143165	1.805E-12	4.6197E-11	0.0381	1	164	155	177	143	235	656	554	444	642	744
ENSMUSG00000040455	chr4	Usp45	2.2E+07	2.2E+07	6226	-1.7020764	3.909657968	1.835E-12	4.68768E-11	0.06198	-1	346	324	411	352	254	171	225	77	128	144
ENSMUSG00000036896	chr4	C1qc	1.4E+08	1.4E+08	1931	2.668164251	6.190530176	1.919E-12	4.89501E-11	0.15046	1	177	221	155	189	802	4192	1652	1817	3029	2527
ENSMUSG00000007480	chr18	Mc5r	6.8E+07	6.8E+07	1162	-3.24703333	0.751168949	1.946E-12	4.95301E-11	0.16154	-1	59	48	23	50	35	11	9	3	7	3
ENSMUSG00000073433	chr17	Arhgdig	2.6E+07	2.6E+07	3252	2.739438167	1.770456086	1.951E-12	4.95832E-11	0.13018	1	9	8	22	18	7	132	51	96	153	146
ENSMUSG00000060519	chr1	Tor3a	1.6E+08	1.6E+08	3892	1.277105303	4.461351161	1.987E-12	5.039E-11	0.03561	1	176	103	227	205	279	844	596	517	604	652
ENSMUSG00000053158	chr7	Fes	8E+07	8E+07	2762	1.843483445	3.410737911	2.049E-12	5.18872E-11	0.06995	1	46	62	67	47	125	458	262	263	330	387
ENSMUSG00000056529	chr4	Ptafr	1.3E+08	1.3E+08	3637	2.287925116	3.790212086	2.078E-12	5.25182E-11	0.10873	1	51	65	38	36	162	586	434	341	500	497
ENSMUSG00000026875	chr2	Traf1	3.5E+07	3.5E+07	5051	2.436804118	1.282504022	2.12E-12	5.34896E-11	0.09286	1	5	8	13	9	19	96	69	54	62	118
ENSMUSG00000024659	chr19	Anxa1	2E+07	2E+07	2608	2.025175709	6.659039771	2.146E-12	5.40384E-11	0.0915	1	478	522	383	380	1256	3844	3332	2419	3426	3814
ENSMUSG00000068335	chr6	Dok1	8.3E+07	8.3E+07	1977	2.129829323	3.232733952	2.186E-12	5.49455E-11	0.09221	1	45	42	37	32	105	483	222	213	283	376
ENSMUSG00000060594	chr9	Layn	5.1E+07	5.1E+07	1786	2.13179552	1.420558695	2.214E-12	5.55524E-11	0.07006	1	6	12	21	15	17	108	91	66	82	78
ENSMUSG00000021712	chr13	Trim23	1E+08	1E+08	5747	-1.68655968	4.651072794	2.24E-12	5.61082E-11	0.06338	-1	684	442	735	570	422	271	418	175	177	201
ENSMUSG00000052414	chr15	Gm28047	1E+08	1E+08	1611	-2.17947623	2.417317643	2.282E-12	5.70525E-11	0.09272	-1	132	116	168	144	84	45	64	22	25	46
ENSMUSG00000058914	chr15	C1qtnf3	1.1E+07	1.1E+07	2557	2.030692472	2.651531557	2.291E-12	5.71851E-11	0.08101	1	33	14	55	39	47	343	173	171	134	205
ENSMUSG00000022871	chr16	Fetub	2.3E+07	2.3E+07	1913	3.546499446	-0.24228976	2.397E-12	5.97214E-11	0.11446	1	0	0	3	1	4	37	28	12	29	29
ENSMUSG00000029919	chr6	Hpgds	6.5E+07	6.5E+07	3586	2.400202169	2.588522613	2.552E-12	6.34578E-11	0.11042	1	22	31	10	20	54	258	201	145	198	220
ENSMUSG00000027748	chr3	Trpc4	5.4E+07	5.4E+07	3472	3.700733979	0.156992191	2.847E-12	7.06722E-11	0.15722	1	0	1	5	4	0	23	34	24	45	57
ENSMUSG00000031165	chrX	Was	8081453	8081989	2381	2.354026146	1.553297102	2.862E-12	7.09343E-11	0.09252	1	9	11	12	8	29	139	113	57	90	89
ENSMUSG00000042821	chr2	Snai1	1.7E+08	1.7E+08	1621	2.2336844	1.711262623	2.869E-12	7.09599E-11	0.08709	1	14	9	13	12	36	140	94	83	116	99
ENSMUSG00000103847	chr16	RP23-123L9.5	3.2E+07	3.2E+07	519	3.67633333	0.154182326	2.942E-12	7.26473E-11	0.14698	1	0	2	2	3	3	28	71	22	34	29
ENSMUSG00000033316	chr5	Galnt9	1.1E+08	1.1E+08	2997	4.268333789	-0.40422488	2.997E-12	7.38662E-11	0.12938	1	1	1	2	0	0	33	20	10	23	35
ENSMUSG00000025911	chr1	Adhfe1	9547948	9548151	3780	-1.6278631	5.005613341	3.045E-12	7.46869E-11	0.0603	-1	908	658	480	588	914	416	260	265	338	343
ENSMUSG00000048546	chr15	Tob2	8.2E+07	8.2E+07	3994	-1.24051712	5.09204555	3.039E-12	7.46869E-11	0.03516	-1	589	489	958	908	700	479	529	309	397	392
ENSMUSG00000052026	chr18	Slc6a7	6.1E+07	6.1E+07	3342	3.218978304	1.145156469	3.046E-12	7.46869E-11	0.16366	1	4	3	1	5	17	121	51	45	67	104
ENSMUSG00000062661	chr2	Ncs1	3.1E+07	3.1E+07	4653	1.444027242	3.484589267	3.089E-12	7.56214E-11	0.04307	1	77	61	89	95	130	398	331	280	368	287
ENSMUSG00000029661	chr6	Col1a2	4504814	4504865	12136	1.861164622	9.256687518	3.228E-12	7.88853E-11	0.07994	1	3361	3035	4003	2566	7343	32477	16824	14020	21387	16172
ENSMUSG00000038250	chr8	Usp38	8.1E+07	8.1E+07	4684	-1.28911568	4.796112927	3.244E-12	7.91217E-11	0.03777	-1	526	483	787	577	594	402	476	238	273	293
ENSMUSG00000034218	chr9	Atm	5.3E+07	5.3E+07	10338	-2.31236152	2.75825982	3.483E-12	8.48113E-11	0.10993	-1	194	157	181	172	117	52	93	21	31	43
ENSMUSG00000060131	chr2	Atp8b4	1.3E+08	1.3E+08	6660	2.695951282	0.580253902	3.569E-12	8.67494E-11	0.09414	1	3	2	5	8	9	73	55	36	40	38
ENSMUSG00000027864	chr3	Ptgfrn	1E+08	1E+08	5902	1.256768321	5.453362644	3.611E-12	8.76285E-11	0.0366	1	337	263	435	354	591	1669	1240	878	1387	1263
ENSMUSG00000056602	chr5	Fry	1.5E+08	1.5E+08	10729	-1.34752638	5.585065502	3.68E-12	8.91546E-11	0.04237	-1	820	798	1292	1316	957	601	697	410	517	585
ENSMUSG00000001525	chr17	Tubb5	3.6E+07	3.6E+07	3327	1.490090247	6.651151104	3.767E-12	9.0955E-11	0.05224	1	653	520	901	778	1211	4110	2471	2635	3522	2528
ENSMUSG00000037416	chr18	Dmxl1	5E+07	5E+07	21860	-1.92337748	4.78906797	3.768E-12	9.0955E-11	0.08373	-1	695	516	962	695	401	225	442	158	150	230
ENSMUSG00000042246	chr7	Tmc7	1.2E+08	1.2E+08	5761	-3.10808077	1.549302416	3.794E-12	9.14272E-11	0.17461	-1	86	22	111	87	102	12	31	4	6	10
ENSMUSG00000021182	chr12	Ccdc88c	1E+08	1E+08	6313	-1.77476081	4.714645648	3.834E-12	9.22389E-11	0.0717	-1	660	586	584	630	494	205	446	150	229	210
ENSMUSG00000047045	chrX	Tmem164	1.4E+08	1.4E+08	6851	1.680988951	3.300375856	3.909E-12	9.38845E-11	0.05907	1	61	52	58	55	125	444	290	215	299	299
ENSMUSG00000001493	chr11	Meox1	1E+08	1E+08	2228	1.712085989	2.92906585	3.922E-12	9.40332E-11	0.05878	1	44	42	64	49	65	360	164	196	243	222
ENSMUSG00000026430	chr1	Rassf5	1.3E+08	1.3E+08	3839	2.422931769	1.500277175	3.984E-12	9.53598E-11	0.09869	1	13	9	7	10	24	136	68	71	78	114
ENSMUSG00000034591	chr10	Slc41a2	8.3E+07	8.3E+07	5349	1.985205152	2.029106528	4.198E-12	1.00303E-10	0.07015	1	23	22	15	25	32	157	131	113	130	112
ENSMUSG00000047466	chr18	8030462N17Rik	7.8E+07	7.8E+07	3418	-2.56228358	3.839202215	4.215E-12	1.00555E-10	0.13994	-1	369	316	518	418	190	62	204	53	60	54
ENSMUSG00000045777	chr7	Ifitm10	1.4E+08	1.4E+08	4789	2.245089165	1.93395665	4.263E-12	1.01517E-10	0.0925	1	14	13	17	13	41	138	93	104	159	126
ENSMUSG00000050721	chr9	Plekho2	6.6E+07	6.6E+07	3271	1.615097109	4.836552491	4.298E-12	1.02181E-10	0.05985	1	107	136	216	259	367	910	879	563	1015	1099
ENSMUSG00000029994	chr6	Anxa4	8.7E+07	8.7E+07	4545	1.479275217	5.497163437	4.407E-12	1.04579E-10	0.05113	1	308	228	385	261	667	1787	1411	930	1262	1550
ENSMUSG00000035274	chr9	Tpbg	8.6E+07	8.6E+07	3828	2.462275624	1.559123844	4.431E-12	1.0499E-10	0.10317	1	15	11	5	13	19	135	62	83	102	103
ENSMUSG00000038668	chr4	Lpar1	5.8E+07	5.8E+07	4289	1.261117398	4.315157133	4.551E-12	1.07641E-10	0.03537	1	142	140	189	175	234	762	509	459	504	658
ENSMUSG00000052430	chr3	Bmpr1b	1.4E+08	1.4E+08	5962	-1.89495369	2.539145448	4.578E-12	1.08098E-10	0.07237	-1	148	130	154	140	95	51	60	42	43	56

ENSMUSG00000015396	chr13	Cd83	4.4E+07	4.4E+07	2143	2.285474432	2.85515368	4.631E-12	1.09173E-10	0.10752	1	26	27	31	18	84	256	219	153	234	360
ENSMUSG00000025888	chr9	Casp1	5298517	5298723	1497	2.360101165	2.559135624	4.643E-12	1.09277E-10	0.11081	1	28	19	12	20	63	278	163	158	179	216
ENSMUSG00000027239	chr2	Mdk	9.2E+07	9.2E+07	1324	2.735574982	1.562304344	4.668E-12	1.09342E-10	0.13055	1	16	7	9	3	20	129	58	98	114	95
ENSMUSG00000044244	chr9	Il20rb	1E+08	1E+08	4206	2.218737513	2.083571872	4.67E-12	1.09342E-10	0.09044	1	20	26	27	13	20	113	127	142	156	137
ENSMUSG00000078915	chr13	Hsp25-ps1	4.5E+07	4.5E+07	594	1.902577266	3.502810793	4.66E-12	1.09342E-10	0.07838	1	36	36	111	100	86	425	243	274	453	428
ENSMUSG00000037112	chr9	Sik2	5.1E+07	5.1E+07	9539	-1.85470973	4.024802725	4.741E-12	1.10834E-10	0.07685	-1	392	298	280	223	743	187	177	97	137	139
ENSMUSG00000020988	chr12	L2hgdh	7E+07	7E+07	3338	-1.38079882	5.490155851	4.846E-12	1.13091E-10	0.0449	-1	1071	720	1263	1010	806	554	709	384	487	453
ENSMUSG00000042063	chr12	Zfp386	1.2E+08	1.2E+08	8753	-1.32999039	4.254245758	5.074E-12	1.18221E-10	0.04003	-1	426	323	523	340	442	239	314	181	179	207
ENSMUSG00000078598	chr4	Skint5	1.1E+08	1.1E+08	4590	3.69062716	-0.45131972	5.088E-12	1.18344E-10	0.11072	1	0	0	4	2	0	22	27	19	20	24
ENSMUSG00000033863	chr19	Klf9	2.3E+07	2.3E+07	3263	-2.20016347	5.887691403	5.222E-12	1.21265E-10	0.1104	-1	1607	1013	2124	1570	1022	409	968	279	293	272
ENSMUSG00000057606	chr14	Colq	3.2E+07	3.2E+07	3803	1.515736367	4.257581047	5.33E-12	1.23573E-10	0.05193	1	119	82	257	134	179	489	719	355	745	618
ENSMUSG00000020814	chr11	Mxra7	1.2E+08	1.2E+08	2391	1.574339607	4.073104175	5.44E-12	1.259E-10	0.0553	1	101	97	131	112	198	754	328	449	506	542
ENSMUSG00000087523	chr11	Gm12319	7.1E+07	7.1E+07	357	-1.38518483	4.997803019	5.593E-12	1.29246E-10	0.04496	-1	683	672	667	687	670	344	450	259	450	326
ENSMUSG00000021477	chr13	Ctsl	6.4E+07	6.4E+07	1971	1.502745745	7.886122788	5.76E-12	1.32872E-10	0.05439	1	1782	1326	2034	1414	2893	7938	6258	5240	7590	9218
ENSMUSG00000037649	chr17	H2-DMa	3.4E+07	3.4E+07	1641	2.125634773	3.625857441	5.798E-12	1.33531E-10	0.09791	1	66	57	50	41	129	710	257	263	350	514
ENSMUSG00000017204	chr11	Gsdma	9.9E+07	9.9E+07	2726	4.914570075	-0.1905765	5.917E-12	1.36047E-10	0.20771	1	3	0	0	0	0	31	16	35	44	15
ENSMUSG00000000881	chrX	Dlg3	1E+08	1E+08	5844	1.594418281	2.4893455	5.992E-12	1.37291E-10	0.04815	1	39	27	48	39	54	167	172	130	180	197
ENSMUSG00000003873	chr7	Bax	4.5E+07	4.5E+07	869	1.276114	4.259000567	6E-12	1.37291E-10	0.03653	1	144	140	178	156	218	633	451	438	625	627
ENSMUSG00000039476	chr2	Prrx2	3.1E+07	3.1E+07	1961	2.689388229	2.669280297	5.999E-12	1.37291E-10	0.14282	1	15	32	13	30	29	362	90	179	257	223
ENSMUSG00000034021	chr5	Pds5b	1.5E+08	1.5E+08	9397	-1.51120772	5.121754962	6.077E-12	1.38814E-10	0.05382	-1	901	673	855	725	640	420	586	260	285	337
ENSMUSG00000032393	chr9	Dpp8	6.5E+07	6.5E+07	4968	-1.66313578	6.793886159	6.352E-12	1.44862E-10	0.06608	-1	2734	2271	2986	2551	1860	1175	1697	771	977	934
ENSMUSG00000031007	chrX	Atp6ap2	1.3E+07	1.3E+07	2618	1.092804486	5.069008867	6.425E-12	1.46293E-10	0.02776	1	296	234	365	338	383	1131	962	797	841	963
ENSMUSG00000038024	chr4	Dennd4c	8.7E+07	8.7E+07	8482	-2.48712252	4.421940919	6.561E-12	1.4916E-10	0.13687	-1	588	462	739	569	337	151	321	71	62	85
ENSMUSG00000025899	chr9	Alkbh8	3335478	3335594	3581	-2.01891665	2.772807189	6.876E-12	1.56058E-10	0.08649	-1	180	147	200	170	107	62	94	32	47	48
ENSMUSG00000022292	chr15	Rrm2b	3.8E+07	3.8E+07	6437	-1.70306279	4.561914151	6.941E-12	1.57283E-10	0.06767	-1	581	435	722	533	426	242	427	133	168	198
ENSMUSG00000030116	chr6	Mfap5	1.2E+08	1.2E+08	3589	1.894779611	5.697729238	7.136E-12	1.60912E-10	0.08436	1	254	182	245	310	725	2321	1197	1440	1750	1713
ENSMUSG00000038056	chr5	Kmt2c	2.5E+07	2.5E+07	20291	-1.39129332	5.102835252	7.134E-12	1.60912E-10	0.04602	-1	744	596	848	850	665	492	590	240	307	368
ENSMUSG00000073016	chrX	Uprt	1E+08	1E+08	2304	-2.75205575	1.451862061	7.12E-12	1.60912E-10	0.14066	-1	72	56	103	85	36	16	29	8	13	7
ENSMUSG00000026786	chr2	Apbb1ip	2.3E+07	2.3E+07	7414	2.057198333	2.580258276	7.324E-12	1.64723E-10	0.08687	1	19	19	27	37	73	254	186	142	170	225
ENSMUSG00000046230	chr19	Vps13a	1.7E+07	1.7E+07	9656	-1.73824184	4.282014029	7.328E-12	1.64723E-10	0.06957	-1	417	342	622	545	317	202	329	115	142	153
ENSMUSG00000017724	chr11	Etv4	1E+08	1E+08	3104	1.782999238	2.397632391	7.369E-12	1.65364E-10	0.06118	1	31	31	53	29	29	194	136	123	192	174
ENSMUSG00000033182	chr6	Kbtbd12	8.9E+07	8.9E+07	7153	-2.54976164	5.899755742	7.428E-12	1.66167E-10	0.14661	-1	1674	1280	1981	1693	906	306	904	182	253	201
ENSMUSG00000047798	chr11	Cd300lf	1.2E+08	1.2E+08	5149	4.137392214	-0.29626956	7.428E-12	1.66167E-10	0.1631	1	0	0	3	2	0	46	13	25	20	26
ENSMUSG00000054196	chr15	Cthrc1	3.9E+07	3.9E+07	1480	3.131912717	1.292225828	7.564E-12	1.68944E-10	0.1721	1	9	1	7	5	14	176	47	76	75	53
ENSMUSG00000029217	chr5	Tec	7.3E+07	7.3E+07	3632	1.793416893	2.683423555	7.968E-12	1.77674E-10	0.06446	1	50	36	35	49	36	204	196	133	237	238
ENSMUSG00000035614	chr12	Fam179b	6.5E+07	6.5E+07	6434	-1.79568104	3.537256427	7.98E-12	1.77674E-10	0.07197	-1	272	210	318	348	187	110	176	76	81	96
ENSMUSG00000031101	chrX	Sash3	4.8E+07	4.8E+07	2677	2.488285928	1.890656322	8.177E-12	1.81758E-10	0.11593	1	15	14	6	13	32	158	88	120	105	143
ENSMUSG00000063488	chr9	Zkscan7	1.2E+08	1.2E+08	2228	-2.7655685	1.344080448	8.455E-12	1.87636E-10	0.14251	-1	71	65	57	89	35	18	23	6	9	12
ENSMUSG00000025764	chr3	Jade1	4.2E+07	4.2E+07	8492	-1.51691852	5.020753144	8.491E-12	1.88148E-10	0.0549	-1	737	655	730	756	656	286	554	211	322	380
ENSMUSG00000073412	chr17	Lst1	3.5E+07	3.5E+07	415	2.72101563	1.52662608	8.511E-12	1.88278E-10	0.13364	1	10	8	8	6	22	147	45	61	117	123
ENSMUSG00000014496	chr14	Ankrd28	3.2E+07	3.2E+07	5229	-1.64767874	5.50753596	8.586E-12	1.89639E-10	0.06502	-1	1040	727	1499	1153	795	456	770	325	312	429
ENSMUSG00000031963	chr9	Bmper	2.3E+07	2.3E+07	3793	1.859402082	3.824848646	8.721E-12	1.92331E-10	0.0781	1	85	60	85	52	187	650	429	426	405	351
ENSMUSG00000035232	chrX	Pdk3	9.4E+07	9.4E+07	2561	2.325837716	1.381920972	8.815E-12	1.94106E-10	0.09352	1	8	8	25	6	16	121	68	75	79	78
ENSMUSG00000097644	chr7	Gm26862	9.3E+07	9.3E+07	2191	2.659740652	0.975118556	8.901E-12	1.9568E-10	0.10899	1	7	7	8	2	13	87	41	54	80	59
ENSMUSG00000022225	chr14	Cma1	5.6E+07	5.6E+07	1074	3.053748932	5.162425952	9.01E-12	1.97772E-10	0.20028	1	105	165	33	96	130	2857	481	937	1352	1120
ENSMUSG00000043091	chr15	Tuba1c	9.9E+07	9.9E+07	1977	2.141688433	3.406311617	9.314E-12	2.04128E-10	0.10164	1	33	28	67	37	144	458	298	320	327	346
ENSMUSG00000049775	chrX	Tmsb4x	1.7E+08	1.7E+08	1371	1.667346322	8.34798383	9.526E-12	2.08435E-10	0.06784	1	1998	1463	2764	1863	4071	15877	7350	8691	9641	9866
ENSMUSG00000078439	chr10	Smim24	8.1E+07	8.1E+07	1058	2.994404228	0.458832258	9.91E-12	2.165E-10	0.11801	1	2	4	5	5	4	53	24	34	44	68
ENSMUSG00000023927	chr17	Satb1	5.2E+07	5.2E+07	19027	-1.61941085	6.026056012	1.025E-11	2.23671E-10	0.06373	-1	1602	1147	1830	1474	1299	546	1121	421	678	568
ENSMUSG00000009471	chr7	Myod1	4.6E+07	4.6E+07	1854	1.555683435	5.452426596	1.028E-11	2.23919E-10	0.05839	1	254	213	342	451	430	1279	1026	1475	1318	1436
ENSMUSG00000005580	chr16	Adcy9	4287529	4289089	5197	-3.11490085	4.309294222	1.033E-11	2.24555E-10	0.20815	-1	531	435	808	589	291	81	248	36	43	31
ENSMUSG00000084939	chr4	Gm830	9.5E+07	9.5E+07	3502	3.73157885	2.712286812	1.039E-11	2.25548E-10	0.262	1	20	22	4	3	12	171	92	315	252	332
ENSMUSG00000017697	chr2	Ada	1.6E+08	1.6E+08	2002	2.781220047	1.254271753	1.045E-11	2.26454E-10	0.13625	1	6	2	6	6	24	126	64	55	79	82
ENSMUSG00000020733	chr11	Slc9a3r1	1.2E+08	1.2E+08	1925	1.919671373	2.823720345	1.06E-11	2.29456E-10	0.07904	1	22	24	52	43	86	279	201	147	228	289
ENSMUSG00000002204	chr7	Napsa	4.5E+07	4.5E+07	2158	2.735922971	0.517839113	1.07E-11	2.31326E-10	0.10173	1	5	2	3	6	9	41	35	39	51	61
ENSMUSG00000022500	chr16	Litaf	1.1E+07	1.1E+07	2642	1.600308404	4.704807559	1.083E-11	2.33439E-10	0.06099	1	146	123	187	143	405	1127	660	629	810	828
ENSMUSG00000034330	chr8	Plcg2	1.2E+08	1.2E+08	4296	1.778283198	2.03163033	1.083E-11	2.33439E-10	0.05898	1	26	16	25	28	40	169	124	80	125	140
ENSMUSG00000028459	chr4	Cd72	4.3E+07	4.3E+07	3422	2.737847747	1.185664155	1.141E-11	2.45449E-10	0.1268	1	3	7	13	4	15	114	49	38	90	96
ENSMUSG00000062901	chr16	Klhl24	2E+07	2E+07	6683	-1.97513825	6.45885233	1.144E-11	2.45694E-10	0.09362	-1	2270	1374	3262	2552	1142	802	1273	491	556	616
ENSMUSG00000031659	chr8	Adcy7	8.8E+07	8.8E+07	6330	1.339996729	3.981746673	1.161E-11	2.49048E-10	0.04074	1	94	98	148	155	180	593	561	298	388	516
ENSMUSG00000026384	chr1	Ptpn4	1.2E+08	1.2E+08	11321	-1.66988112	5.080351816	1.178E-11	2.52156E-10	0.06723	-1	808	578	1026	897	539	266	577	224	266	348
ENSMUSG00000001119	chr10	Col6a1	7.7E+07	7.7E+07	4380	1.522100154	7.462230869	1.18E-11	2.52387E-10	0.05735	1	1052	1035	1359	1453	2020	7427	3990	4146	6285	5313
ENSMUSG00000031778	chr8	Cx3cl1	9.5E+07	9.5E+07	3708	2.453509972	3.469813477	1.189E-11	2.53767E-10	0.13387	1	22	11	111	76	53	433	277	305	408	478
ENSMUSG00000000693	chr6	Loxl3	8.3E+07	8.3E+07	4196	1.469795519	3.366672037	1.192E-11	2.54152E-10	0.04663	1	66	72	79	73	115	437	314	207	314	293
ENSMUSG00000059479	chr7	B3gnt8	2.6E+07	2.6E+07	1475	2.004383583	1.668086873	1.303E-11	2.77314E-10	0.0723	1	19	12	18	17	25	141	72	65	121	106
ENSMUSG00000000555	chr15	Itga5	1E+08	1E+08	4379	1.486113583	4.914575506	1.341E-11	2.8494E-10	0.05355	1	151	114	312	327	333	1002	735	773	1038	993
ENSMUSG00000025225	chr19	Nfkb2	4.6E+07	4.6E+07	3289	1.257491486	4.910556166	1.355E-11	2.87077E-10	0.03831	1	216	136	425	290	315	962	801	668	977	957

ENSMUSG00000051650	chr11	B3gnt2	2.3E+07	2.3E+07	3350	1.529139592	3.466154333	1.357E-11	2.87077E-10	0.05227	1	81	47	85	78	142	431	299	245	294	417
ENSMUSG00000100679	chr1	Gm28778	5.3E+07	5.3E+07	785	-1.96126989	3.332550108	1.353E-11	2.87077E-10	0.0871	-1	267	209	274	251	177	82	162	56	58	71
ENSMUSG00000029361	chr5	Nos1	1.2E+08	1.2E+08	11151	-2.15617913	6.02458876	1.372E-11	2.89797E-10	0.11085	-1	982	1159	2471	2724	669	619	567	327	476	510
ENSMUSG00000053347	chr17	Zfp943	2.2E+07	2.2E+07	5277	-1.66614787	3.715661531	1.396E-11	2.94401E-10	0.06419	-1	305	275	361	316	209	158	185	106	98	104
ENSMUSG00000095079	chr12	Igha	1.1E+08	1.1E+08	2668	4.339213449	2.72978547	1.434E-11	3.02002E-10	0.34964	1	0	4	13	6	26	55	311	89	497	324
ENSMUSG00000041669	chr12	Prima1	1E+08	1E+08	1253	-2.95932313	1.004978362	1.447E-11	3.04387E-10	0.15847	-1	36	42	72	88	23	12	10	3	13	9
ENSMUSG00000028480	chr4	Glipr2	4.4E+07	4.4E+07	2320	1.646105267	3.463142017	1.466E-11	3.0791E-10	0.06051	1	59	75	62	74	123	479	281	263	354	335
ENSMUSG00000043719	chr9	Col6a6	1.1E+08	1.1E+08	9166	1.50157068	4.025483918	1.474E-11	3.09017E-10	0.05259	1	124	77	153	78	223	557	541	379	573	418
ENSMUSG00000031662	chr8	Snx20	8.9E+07	8.9E+07	1434	2.842124842	1.233077055	1.565E-11	3.2766E-10	0.14299	1	7	3	5	7	19	111	38	55	86	109
ENSMUSG00000031258	chrX	Xkrx	1.3E+08	1.3E+08	3024	2.929717755	0.025088364	1.6E-11	3.34413E-10	0.09499	1	3	1	4	3	4	32	27	34	36	27
ENSMUSG00000071793	chr8	2610005L07Rik	2E+07	2E+07	4163	-2.63810779	1.153201884	1.652E-11	3.44711E-10	0.12876	-1	62	72	67	29	44	13	16	8	12	14
ENSMUSG00000024397	chr17	Aif1	3.5E+07	3.5E+07	1532	3.002199838	2.310584106	1.697E-11	3.53607E-10	0.18136	1	13	14	6	8	39	352	83	133	162	164
ENSMUSG00000025930	chr1	Msc	1.5E+07	1.5E+07	2546	2.457647199	1.394942261	1.735E-11	3.60981E-10	0.11012	1	13	5	7	10	23	93	56	80	88	109
ENSMUSG00000063506	chr14	Arhgap22	3.3E+07	3.3E+07	3876	1.949140203	2.039065419	1.74E-11	3.61532E-10	0.07435	1	13	17	28	24	43	158	113	94	117	170
ENSMUSG00000039745	chr7	Htatip2	5E+07	5E+07	1465	1.534893297	4.284774862	1.768E-11	3.66747E-10	0.05593	1	164	108	141	98	244	808	424	476	648	622
ENSMUSG00000048779	chr7	P2ry6	1E+08	1E+08	1938	2.466037809	2.997064573	1.806E-11	3.74173E-10	0.13331	1	17	27	19	28	94	430	269	156	264	282
ENSMUSG00000022371	chr15	Col14a1	5.5E+07	5.5E+07	7013	1.886877059	6.296906726	1.86E-11	3.848E-10	0.0875	1	475	390	396	369	907	4455	1570	1928	2807	2195
ENSMUSG00000020422	chr11	Tns3	8431652	8434638	11182	1.043250493	4.676440271	1.903E-11	3.93163E-10	0.02588	1	212	191	328	245	287	834	772	507	711	740
ENSMUSG00000034801	chr12	Sos2	7E+07	7E+07	8514	-1.54475452	5.776853524	1.922E-11	3.9644E-10	0.05963	-1	1132	940	1696	1345	1038	517	977	388	527	505
ENSMUSG00000024883	chr19	Rin1	5050808	5050941	4176	2.710207665	1.891365043	1.978E-11	4.07292E-10	0.14908	1	7	4	41	15	8	144	153	112	89	134
ENSMUSG00000049687	chr15	Fam109b	8.2E+07	8.2E+07	3311	2.395297786	1.306653688	1.992E-11	4.09684E-10	0.10334	1	6	4	11	15	21	121	56	59	91	78
ENSMUSG00000042286	chr14	Stab1	3.1E+07	3.1E+07	10288	1.693713807	5.876329782	2.06E-11	4.22972E-10	0.0713	1	268	362	341	357	773	2848	1538	1334	2005	1652
ENSMUSG00000048126	chr1	Col6a3	9.1E+07	9.1E+07	11963	1.539564779	7.241587653	2.078E-11	4.26018E-10	0.05997	1	984	1116	1114	1081	1435	6729	3809	3695	5350	3798
ENSMUSG00000032383	chr9	Ppib	6.6E+07	6.6E+07	960	1.557243908	5.919652901	2.142E-11	4.38568E-10	0.06086	1	383	289	497	376	838	2738	1329	1501	2046	1747
ENSMUSG00000031506	chr1	Ptpn7	1.4E+08	1.4E+08	6102	2.465874928	1.381665566	2.263E-11	4.62661E-10	0.11038	1	8	8	6	8	27	111	65	70	90	91
ENSMUSG00000050761	chr16	Gp1bb	1.9E+07	1.9E+07	1881	2.261911534	2.152913566	2.34E-11	4.77666E-10	0.10628	1	11	13	25	22	44	224	88	138	157	122
ENSMUSG00000033420	chr6	Antxr1	8.7E+07	8.7E+07	5263	1.46620513	5.194402135	2.343E-11	4.7768E-10	0.05349	1	286	241	242	250	434	1869	887	694	1102	1117
ENSMUSG00000048534	chr9	Amica1	4.5E+07	4.5E+07	2457	2.463257257	1.562214534	2.365E-11	4.81406E-10	0.11267	1	9	16	7	7	24	148	82	71	85	106
ENSMUSG00000068373	chr2	D430041D05Rik	1E+08	1E+08	15851	-1.96062311	2.616562047	2.375E-11	4.82871E-10	0.08532	-1	131	82	237	197	97	65	73	32	46	45
ENSMUSG00000019122	chr11	Ccl9	8.4E+07	8.4E+07	3045	2.54305475	4.438545905	2.414E-11	4.90064E-10	0.14976	1	60	99	46	45	224	1173	544	785	574	682
ENSMUSG00000040715	chr4	Rsc1a1	1.4E+08	1.4E+08	1749	-1.4451764	4.603561937	2.438E-11	4.94099E-10	0.05161	-1	638	500	477	511	456	298	349	226	230	242
ENSMUSG00000023025	chr15	Larp4	1E+08	1E+08	6731	-1.38227392	5.019496388	2.502E-11	5.06475E-10	0.04781	-1	682	433	1086	769	624	403	555	297	302	303
ENSMUSG00000073421	chr17	H2-Ab1	3.4E+07	3.4E+07	1637	2.976730028	6.526411299	2.522E-11	5.09713E-10	0.20316	1	277	237	153	138	794	5996	1282	2072	2798	5169
ENSMUSG00000040699	chr11	Limd2	1.1E+08	1.1E+08	3707	2.002112589	2.918370787	2.661E-11	5.37057E-10	0.08923	1	32	42	38	35	75	373	139	206	253	254
ENSMUSG00000024521	chr18	Pmaip1	6.6E+07	6.6E+07	2646	3.072513409	-0.12121781	2.722E-11	5.4852E-10	0.09758	1	3	1	1	1	6	40	29	17	28	30
ENSMUSG00000018042	chr15	Cyb5r3	8.3E+07	8.3E+07	4298	1.474987396	6.663715019	2.757E-11	5.54751E-10	0.0558	1	677	459	877	712	1463	3818	2700	2202	3367	3417
ENSMUSG00000013707	chr3	Tnfaip8l2	9.5E+07	9.5E+07	1122	3.001830987	1.954662018	2.843E-11	5.71202E-10	0.18003	1	9	10	1	9	33	159	95	112	173	137
ENSMUSG00000071324	chr10	Armc2	4.2E+07	4.2E+07	7188	2.613248599	0.72233998	2.858E-11	5.73515E-10	0.10445	1	3	5	5	12	6	63	41	40	47	74
ENSMUSG00000091754	chr14	Gm3636	6735685	6736817	1746	2.348658697	1.646931219	2.944E-11	5.89809E-10	0.10429	1	8	15	10	27	11	121	89	88	107	104
ENSMUSG00000004530	chr5	Coro1c	1.1E+08	1.1E+08	9664	1.442584811	5.023881237	2.956E-11	5.90627E-10	0.05245	1	173	152	306	222	520	1172	918	704	1071	1060
ENSMUSG00000052812	chr12	Atad2b	4917404	4917921	4688	-2.9721765	2.190616948	2.952E-11	5.90627E-10	0.18604	-1	120	131	153	127	55	17	54	12	12	13
ENSMUSG00000090122	chrX	Kcne1l	1.4E+08	1.4E+08	1543	3.802398324	0.589728831	2.964E-11	5.91459E-10	0.21247	1	2	2	0	5	4	60	13	60	58	61
ENSMUSG00000026656	chr1	Fcgr2b	1.7E+08	1.7E+08	5790	2.356390975	4.448546889	2.988E-11	5.95366E-10	0.13129	1	82	117	36	73	212	1213	595	637	642	681
ENSMUSG00000031700	chr8	Gpt2	8.5E+07	8.5E+07	5643	-1.54684884	7.243392346	3.062E-11	6.09217E-10	0.06167	-1	3079	2829	4006	2956	4137	1433	2667	1081	1426	1440
ENSMUSG00000015947	chr3	Fcgr1	9.6E+07	9.6E+07	2589	2.761937967	1.930672275	3.074E-11	6.10666E-10	0.15236	1	13	16	10	6	24	253	89	127	117	71
ENSMUSG00000025937	chr1	Lactb2	1.4E+07	1.4E+07	4566	-1.11562307	4.6931267	3.097E-11	6.145E-10	0.03089	-1	497	391	717	528	549	445	419	236	307	299
ENSMUSG00000050199	chr2	Lgr4	1.1E+08	1.1E+08	5884	-1.28282697	4.594915312	3.138E-11	6.21563E-10	0.04108	-1	494	429	635	520	477	320	436	199	243	269
ENSMUSG00000021470	chr13	Ercc6l2	6.4E+07	6.4E+07	7681	-1.32496337	4.720850265	3.223E-11	6.37587E-10	0.04414	-1	587	501	575	603	505	354	451	207	278	281
ENSMUSG00000059326	chr19	Csf2ra	6.1E+07	6.1E+07	1849	2.826701517	3.326292851	3.568E-11	7.04763E-10	0.17906	1	26	31	10	17	102	360	357	210	386	490
ENSMUSG00000030592	chr7	Ryr1	2.9E+07	2.9E+07	15371	-1.58983967	11.30288261	3.682E-11	7.26326E-10	0.06587	-1	52336	39982	81365	69627	43753	23987	36931	18206	27723	23960
ENSMUSG00000074994	chr2	Qser1	1E+08	1E+08	8973	-1.59307964	6.294098992	3.826E-11	7.53738E-10	0.06557	-1	1969	1483	1994	1894	1354	774	1301	546	771	679
ENSMUSG00000022408	chr15	Fam83f	8.1E+07	8.1E+07	2988	3.026420485	0.3728023	3.906E-11	7.6843E-10	0.14039	1	2	0	7	5	5	33	33	25	50	69
ENSMUSG00000027827	chr3	Kcnab1	6.5E+07	6.5E+07	8593	-2.40053441	2.875519901	4.072E-11	7.99957E-10	0.1324	-1	212	229	135	156	138	48	96	27	34	41
ENSMUSG00000061111	chr11	Fam195b	1.2E+08	1.2E+08	1282	1.257545453	5.547297241	4.306E-11	8.44646E-10	0.04098	1	389	276	450	370	624	1556	1107	1016	1514	1615
ENSMUSG00000028063	chr3	Lmna	8.8E+07	8.8E+07	4252	1.443027196	7.071080675	4.317E-11	8.45691E-10	0.05472	1	822	559	1664	1218	1415	5297	3380	3182	4414	4096
ENSMUSG00000004951	chr5	Hspb1	1.4E+08	1.4E+08	1031	1.807271281	7.53494386	4.384E-11	8.57639E-10	0.08433	1	803	591	2368	1381	1420	8515	3682	4716	6710	6298
ENSMUSG00000039747	chr5	Orai2	1.4E+08	1.4E+08	3846	1.971840644	1.775098869	4.423E-11	8.63969E-10	0.07738	1	13	13	21	18	37	116	88	102	102	123
ENSMUSG00000033965	chrX	Slc16a2	1E+08	1E+08	4244	1.300001134	3.625140841	4.584E-11	8.94277E-10	0.0397	1	108	64	130	106	131	495	298	282	366	360
ENSMUSG00000078532	chr4	Nkain1	1.3E+08	1.3E+08	1426	-1.58300154	3.98431234	4.597E-11	8.95556E-10	0.06204	-1	419	298	350	365	312	172	242	108	196	106
ENSMUSG00000039981	chr10	Zc3h12d	7832470	7832562	4093	2.855032069	-0.03048065	4.74E-11	9.22185E-10	0.09251	1	3	1	2	2	7	30	30	21	32	38
ENSMUSG00000053205	chr14	Styx	4.5E+07	4.5E+07	672	-3.71880009	2.523404346	4.883E-11	9.48607E-10	0.2877	-1	227	178	143	142	68	16	51	9	6	4
ENSMUSG00000001542	chr13	Ell2	7.6E+07	7.6E+07	3647	-1.3634485	4.236624123	4.973E-11	9.64715E-10	0.04677	-1	394	311	461	429	442	168	337	161	219	201
ENSMUSG00000043832	chr6	Clec4a3	1.2E+08	1.2E+08	1327	2.500717069	2.645398881	5.024E-11	9.7324E-10	0.13785	1	22	37	12	18	42	423	174	148	160	189
ENSMUSG00000084796	chr11	Mir142hg	8.8E+07	8.8E+07	269	3.775658657	0.148178197	5.032E-11	9.73485E-10	0.17599	1	2	3	0	2	2	51	13	23	38	59
ENSMUSG00000026126	chr1	Ptpn18	3.4E+07	3.4E+07	6492	2.369234309	2.627828934	5.162E-11	9.97219E-10	0.12792	1	15	17	25	23	73	349	122	150	236	198
ENSMUSG00000022090	chr14	Pdlim2	7E+07	7E+07	4486	1.819986099	3.329609248	5.19E-11	1.00125E-09	0.07891	1	61	48	63	39	124	503	216	241	319	331
ENSMUSG00000034898	chr9	Filip1	8E+07	8E+07	4888	-1.68908747	5.192980743	5.317E-11	1.0243E-09	0.07368	-1	809	694	1104	1038	490	316	601	226	325	339

ENSMUSG00000035697	chr10	Hmha1	8E+07	8E+07	4478	2.070758142	3.510333351	5.412E-11	1.04131E-09	0.10277	1	54	55	35	42	141	526	291	243	373	469
ENSMUSG00000093327	chr18	Mir5107	6.1E+07	6.1E+07	88	3.000648762	5.693517635	5.588E-11	1.07375E-09	0.21287	1	141	131	77	79	457	3369	736	1116	1392	3132
ENSMUSG00000040433	chr9	Zbtb38	9.7E+07	9.7E+07	11733	-1.30407349	5.393957902	5.712E-11	1.09604E-09	0.04465	-1	958	712	1167	855	787	522	707	346	408	541
ENSMUSG00000037225	chr3	Fgf2	3.7E+07	3.7E+07	1801	-3.19183693	0.497668928	6.238E-11	1.19518E-09	0.18062	-1	30	44	36	55	14	5	9	3	7	4
ENSMUSG00000049988	chr8	Lrrc25	7.1E+07	7.1E+07	1273	2.739236	2.008045408	6.293E-11	1.20414E-09	0.16052	1	5	11	6	15	40	229	112	112	109	136
ENSMUSG00000050556	chr2	Kcnb1	1.7E+08	1.7E+08	4060	-1.54928602	4.132206988	6.362E-11	1.21577E-09	0.06065	-1	381	325	468	471	289	156	286	130	195	156
ENSMUSG00000049001	chr6	Ndnf	6.6E+07	6.6E+07	4718	2.617148936	0.838510506	6.405E-11	1.22235E-09	0.11555	1	8	4	10	9	3	100	37	49	47	58
ENSMUSG00000037106	chr15	Fer1l6	5.9E+07	5.9E+07	8053	-1.67220491	2.908037895	6.456E-11	1.23026E-09	0.06605	-1	218	145	162	169	140	99	68	51	81	73
ENSMUSG00000031609	chr8	Sap30	5.7E+07	5.7E+07	1178	1.726610839	2.889951838	6.671E-11	1.26957E-09	0.06758	1	45	56	50	48	47	237	191	222	230	251
ENSMUSG00000102049	chr1	Zbed6	1.3E+08	1.3E+08	5007	-3.84007	4.054848267	6.746E-11	1.28207E-09	0.32017	-1	572	536	475	444	172	43	149	8	18	19
ENSMUSG00000026043	chr1	Col3a1	4.5E+07	4.5E+07	9816	1.585882686	9.482203889	7.336E-11	1.39057E-09	0.06757	1	4121	4054	6237	4392	8683	32122	28015	15683	22365	14457
ENSMUSG00000030276	chr6	Ttll3	1.1E+08	1.1E+08	5059	1.537691378	4.768859141	7.337E-11	1.39057E-09	0.06147	1	163	153	188	192	367	1062	509	663	1096	834
ENSMUSG00000063406	chr5	Tmed5	1.1E+08	1.1E+08	7688	-1.3355474	4.42802417	7.489E-11	1.4172E-09	0.04613	-1	433	313	688	471	448	220	378	174	206	288
ENSMUSG00000068758	chr14	Il3ra	1.4E+07	1.4E+07	1394	2.093201479	3.38816613	7.497E-11	1.4172E-09	0.10651	1	43	39	54	30	140	421	260	198	462	409
ENSMUSG00000059422	chr9	Gm8116	7.9E+07	7.9E+07	1201	-1.64731856	4.502609706	7.657E-11	1.44536E-09	0.0704	-1	532	403	660	563	406	206	402	181	203	139
ENSMUSG00000020440	chr6	Arf5	2.8E+07	2.8E+07	1116	1.325309949	6.179167331	7.727E-11	1.45479E-09	0.04725	1	525	373	792	633	874	2481	1618	1671	2558	2347
ENSMUSG00000029862	chr6	Clcn1	4.2E+07	4.2E+07	5428	-1.45846222	6.91835994	7.727E-11	1.45479E-09	0.05734	-1	2893	2158	3007	2563	2592	1213	2060	896	1361	1186
ENSMUSG00000030223	chr6	Ptpro	1.4E+08	1.4E+08	6744	2.216677108	2.521588164	7.953E-11	1.49534E-09	0.11124	1	35	27	14	18	52	327	184	112	191	158
ENSMUSG00000053113	chr11	Socs3	1.2E+08	1.2E+08	2891	1.787716123	3.26214645	8.033E-11	1.50824E-09	0.07776	1	42	44	69	55	118	248	295	265	439	241
ENSMUSG00000074280	chr9	Gm6166	5.7E+07	5.7E+07	669	2.173810973	3.352012143	8.193E-11	1.53627E-09	0.11473	1	78	31	37	24	109	280	322	251	455	381
ENSMUSG00000048450	chr5	Msx1	3.8E+07	3.8E+07	3097	1.789018996	2.628597129	8.35E-11	1.56358E-09	0.07302	1	29	33	40	27	78	210	171	149	233	201
ENSMUSG00000023191	chr6	Leprel2	1.2E+08	1.2E+08	3930	1.37278195	3.969959969	8.389E-11	1.56892E-09	0.04706	1	121	107	128	108	188	720	377	304	472	483
ENSMUSG00000098112	chr15	Bin2	1E+08	1E+08	2530	2.473522861	0.552501885	8.62E-11	1.60992E-09	0.09271	1	4	4	6	7	9	56	41	24	44	68
ENSMUSG00000099329	chr17	Gm28052	3E+07	3E+07	380	-2.33284067	1.510281655	8.764E-11	1.63465E-09	0.11574	-1	73	53	100	77	50	32	33	8	10	16
ENSMUSG00000030657	chr7	Xylt1	1.2E+08	1.2E+08	3822	-3.04235276	0.684232138	8.833E-11	1.64526E-09	0.17399	-1	55	45	40	42	21	9	13	1	9	4
ENSMUSG00000021779	chr14	Thrb	1.8E+07	1.8E+07	6555	-1.5877183	4.356295026	9.084E-11	1.68979E-09	0.06543	-1	447	354	634	468	411	185	398	116	175	199
ENSMUSG00000026771	chr2	Spopl	2.4E+07	2.4E+07	10280	-1.49880135	4.054659514	9.181E-11	1.7056E-09	0.0576	-1	429	321	409	353	291	161	268	141	149	175
ENSMUSG00000032661	chr5	Oas3	1.2E+08	1.2E+08	5227	3.354664843	0.314797713	9.262E-11	1.71844E-09	0.16191	1	2	2	2	4	4	53	61	10	57	29
ENSMUSG00000007682	chr12	Dio2	9.1E+07	9.1E+07	5813	1.952142132	3.491456905	9.301E-11	1.72334E-09	0.09503	1	42	24	81	102	110	253	351	271	470	460
ENSMUSG00000008475	chr1	Arpc5	1.5E+08	1.5E+08	2276	1.668597675	5.300419613	9.522E-11	1.76187E-09	0.07388	1	247	183	236	188	606	1726	970	1036	1127	1324
ENSMUSG00000004730	chr17	Emr1	5.7E+07	5.7E+07	3245	2.153746257	4.031770683	9.608E-11	1.77545E-09	0.11619	1	56	85	45	73	187	1033	566	295	486	452
ENSMUSG00000031004	chr7	Mki67	1.4E+08	1.4E+08	10075	2.432690857	1.189130058	9.686E-11	1.78761E-09	0.10956	1	10	10	7	7	15	124	45	65	71	65
ENSMUSG00000030536	chr7	Iqgap1	8.1E+07	8.1E+07	7359	1.235878769	5.879938782	9.767E-11	1.80009E-09	0.04138	1	398	398	548	523	805	2228	1684	1158	1713	1849
ENSMUSG00000031548	chr8	Sfrp1	2.3E+07	2.3E+07	4372	2.370506174	4.392611238	9.784E-11	1.80094E-09	0.14015	1	78	120	50	40	209	1190	558	583	698	612
ENSMUSG00000009013	chr5	Dynll1	1.2E+08	1.2E+08	2926	1.150286132	5.388961519	9.84E-11	1.80879E-09	0.03542	1	325	297	439	400	507	1428	1041	1051	1261	1131
ENSMUSG00000013483	chr11	Card14	1.2E+08	1.2E+08	4605	3.146124426	1.617794119	1.003E-10	1.84148E-09	0.20429	1	4	5	15	8	14	162	84	171	54	44
ENSMUSG00000060591	chr7	Ifitm2	1.4E+08	1.4E+08	627	1.672847638	6.158666469	1.015E-10	1.8602E-09	0.07516	1	377	331	453	442	1045	3078	1561	1746	2567	2313
ENSMUSG00000052142	chr17	Rasal3	3.2E+07	3.2E+07	4897	3.113557103	0.394993049	1.036E-10	1.89733E-09	0.15364	1	2	2	2	2	10	52	27	27	35	75
ENSMUSG00000070354	chr11	Gm21975	8E+07	8E+07	3944	1.788979573	2.751373824	1.069E-10	1.95536E-09	0.07521	1	28	36	41	39	81	343	190	143	187	210
ENSMUSG00000021815	chr14	Mss51	2E+07	2E+07	1829	-2.63252031	9.07661147	1.071E-10	1.95581E-09	0.17536	-1	15886	15135	8851	9436	17764	3214	7487	1550	1290	2453
ENSMUSG00000054640	chr17	Slc8a1	8.1E+07	8.1E+07	2934	-3.52768622	2.947167385	1.11E-10	2.02488E-09	0.27751	-1	239	227	226	238	88	18	78	13	16	5
ENSMUSG00000062585	chr4	Cnr2	1.4E+08	1.4E+08	3982	2.461021618	0.563045773	1.146E-10	2.08677E-09	0.09659	1	3	3	7	7	11	37	41	40	52	59
ENSMUSG00000027215	chr2	Cd82	9.3E+07	9.3E+07	3005	1.538162622	4.571061048	1.157E-10	2.10473E-09	0.06263	1	183	120	176	102	355	806	616	597	775	822
ENSMUSG00000024885	chr19	Aldh3b1	3913493	3914084	1875	1.934570795	2.72952287	1.192E-10	2.16598E-09	0.08956	1	24	27	44	29	85	255	178	118	287	238
ENSMUSG00000039899	chr5	Fgl2	2.1E+07	2.1E+07	3788	1.410133114	5.260068051	1.226E-10	2.22499E-09	0.05369	1	233	254	474	259	378	1897	1159	993	797	934
ENSMUSG00000032766	chr6	Gng11	4003943	4004411	880	1.31645945	4.971380681	1.241E-10	2.24922E-09	0.04669	1	207	148	379	275	391	1212	616	778	1038	952
ENSMUSG00000070691	chr4	Runx3	1.4E+08	1.4E+08	5003	2.986656434	-0.09441565	1.283E-10	2.32221E-09	0.10723	1	1	2	1	2	7	30	26	19	30	40
ENSMUSG00000029254	chr5	Stap1	8.6E+07	8.6E+07	4083	3.048599317	0.13282867	1.286E-10	2.32388E-09	0.12428	1	2	2	2	3	6	29	59	21	24	42
ENSMUSG00000021939	chr14	Ctsb	6.3E+07	6.3E+07	4739	1.353604769	9.827955843	1.295E-10	2.33734E-09	0.05122	1	6786	4724	8802	7217	12068	31176	26479	18589	31416	28407
ENSMUSG00000033943	chr2	Mga	1.2E+08	1.2E+08	15340	-1.24936836	5.099591815	1.316E-10	2.37052E-09	0.04235	-1	714	593	879	801	603	506	567	325	318	392
ENSMUSG00000071379	chr12	Hpcal1	1.8E+07	1.8E+07	1561	1.525423077	3.447957112	1.317E-10	2.37052E-09	0.0583	1	61	54	102	63	152	386	274	233	359	408
ENSMUSG00000040167	chr7	Ikzf5	1.3E+08	1.3E+08	4885	-1.31875103	3.888760017	1.361E-10	2.4476E-09	0.04472	-1	320	230	361	383	286	170	243	121	158	186
ENSMUSG00000024726	chr19	2410127L17Rik	1.9E+07	1.9E+07	2090	-1.66295237	5.418109565	1.394E-10	2.50394E-09	0.07499	-1	924	766	1340	1058	790	348	795	314	377	290
ENSMUSG00000044499	chr10	Hs3st5	3.7E+07	3.7E+07	4340	-1.77974285	2.538430957	1.401E-10	2.5124E-09	0.07579	-1	150	109	148	156	98	52	79	35	42	63
ENSMUSG00000010830	chr15	Kdelr3	8E+07	8E+07	1414	1.883172579	2.922968227	1.431E-10	2.56416E-09	0.08622	1	34	36	31	45	95	365	188	167	255	248
ENSMUSG00000053024	chr1	Cntn2	1.3E+08	1.3E+08	9304	5.125386873	0.225962021	1.442E-10	2.57946E-09	0.38234	1	0	0	1	0	3	4	33	56	36	64
ENSMUSG00000031010	chrX	Usp9x	1.3E+07	1.3E+07	15051	-2.34342905	6.094226271	1.449E-10	2.58804E-09	0.14373	-1	1755	1548	2164	1998	899	560	1039	272	281	235
ENSMUSG00000049565	chr3	Aknad1	1.1E+08	1.1E+08	7459	2.964128538	0.238421254	1.45E-10	2.58804E-09	0.1224	1	3	5	2	0	7	40	27	29	42	49
ENSMUSG00000063142	chr14	Kcnma1	2.3E+07	2.3E+07	6513	-2.00532712	4.399593589	1.461E-10	2.60466E-09	0.10544	-1	470	376	850	631	215	176	292	93	126	200
ENSMUSG00000020919	chr11	Stat5b	1E+08	1E+08	5539	-1.45679553	7.755028134	1.475E-10	2.62574E-09	0.05918	-1	5165	4555	4400	4729	4201	2371	2956	1661	2465	2533
ENSMUSG00000030745	chr7	Il21r	1.3E+08	1.3E+08	2607	3.132465171	0.331865793	1.576E-10	2.80106E-09	0.15521	1	3	1	8	2	3	78	19	27	35	49
ENSMUSG00000028053	chr3	Ash1l	8.9E+07	8.9E+07	13076	-1.50208835	5.564817228	1.605E-10	2.84928E-09	0.06213	-1	1000	820	1397	1239	775	523	839	353	393	468
ENSMUSG00000026069	chr1	Il1rl1	4E+07	4E+07	6894	2.684141533	2.397735045	1.652E-10	2.92888E-09	0.16596	1	12	23	12	21	33	322	82	216	103	174
ENSMUSG00000047686	chrX	Zcchc5	1.1E+08	1.1E+08	2948	2.146763514	2.091022715	1.654E-10	2.92993E-09	0.10337	1	27	19	18	18	30	270	101	96	144	94
ENSMUSG00000055341	chr13	Zfp457	6.7E+07	6.7E+07	2836	-2.6900564	-0.07932023	1.721E-10	3.04396E-09	0.10335	-1	24	20	32	24	15	5	7	5	3	4
ENSMUSG00000052276	chr16	Ostn	2.7E+07	2.7E+07	1423	-3.24971804	4.967500191	1.726E-10	3.04936E-09	0.25561	-1	726	1036	583	1264	335	46	306	70	149	49
ENSMUSG00000052384	chr16	Nrros	3.2E+07	3.2E+07	4177	1.985396346	3.697773498	1.742E-10	3.07376E-09	0.10132	1	71	62	52	42	167	633	279	352	427	429

ENSMUSG00000001998	chr2	Ap4e1	1.3E+08	1.3E+08	9810	-2.02231135	3.271517981	1.758E-10	3.09422E-09	0.10437	-1	238	209	258	247	187	84	168	46	56	47
ENSMUSG00000078122	chrX	F630028O10Rik	9.6E+07	9.6E+07	3295	2.836187211	1.010564608	1.757E-10	3.09422E-09	0.15309	1	8	5	3	4	14	93	27	62	70	81
ENSMUSG00000030091	chr6	Nup210	9.1E+07	9.1E+07	8163	-1.10494185	4.901490044	1.785E-10	3.13477E-09	0.03333	-1	549	441	796	687	616	453	488	225	419	406
ENSMUSG00000033066	chr11	Gas7	6.7E+07	6.7E+07	11342	1.444724318	4.91796431	1.786E-10	3.13477E-09	0.05705	1	202	158	240	173	484	1311	789	635	842	1034
ENSMUSG00000049313	chr9	Sorl1	4.2E+07	4.2E+07	11321	-1.36771937	5.679483983	1.821E-10	3.1928E-09	0.05209	-1	1089	747	1445	1442	841	563	783	440	576	598
ENSMUSG00000027224	chr2	Duoxa1	1.2E+08	1.2E+08	3977	1.972180172	2.505933019	1.825E-10	3.19568E-09	0.09168	1	25	30	22	33	58	198	122	165	166	247
ENSMUSG00000004891	chr3	Nes	8.8E+07	8.8E+07	6416	1.465832326	6.525730876	1.84E-10	3.21771E-09	0.06019	1	596	321	1311	791	864	2963	2602	2341	3099	2870
ENSMUSG00000063564	chr11	Col23a1	5.1E+07	5.1E+07	5736	1.83759197	2.77826769	1.849E-10	3.22938E-09	0.08182	1	39	32	59	54	37	187	144	224	207	292
ENSMUSG00000054659	chr4	Pm20d2	3.3E+07	3.3E+07	1834	-3.55488562	3.080631414	1.862E-10	3.24761E-09	0.2909	-1	180	150	428	356	73	20	86	10	13	12
ENSMUSG00000027248	chr2	Pdia3	1.2E+08	1.2E+08	3139	1.601077918	7.286677202	1.877E-10	3.27105E-09	0.0716	1	1069	820	1122	1003	1903	8596	3351	3817	4319	4520
ENSMUSG00000034610	chr4	Zcchc11	1.1E+08	1.1E+08	8684	-1.66775552	4.202624921	1.943E-10	3.38035E-09	0.07454	-1	394	389	424	567	262	208	282	105	162	170
ENSMUSG00000032812	chr7	Arap1	1E+08	1E+08	7564	1.118307874	5.650846239	1.952E-10	3.39024E-09	0.03491	1	403	315	660	477	577	1841	1254	1053	1539	1451
ENSMUSG00000071361	chr14	Mcpt9	5.6E+07	5.6E+07	2000	3.239838991	2.777787483	1.953E-10	3.39024E-09	0.2393	1	16	27	3	21	22	426	65	206	337	217
ENSMUSG00000049173	chr18	Myoz3	6.1E+07	6.1E+07	870	-2.2915383	5.345398454	1.96E-10	3.39818E-09	0.13948	-1	1094	939	1130	1062	711	211	716	146	235	148
ENSMUSG00000052160	chr12	Pld4	1.1E+08	1.1E+08	1978	2.2458631	4.134809871	2.023E-10	3.50269E-09	0.13088	1	67	82	56	41	216	1043	394	396	614	586
ENSMUSG00000068606	chr18	Gm4841	6E+07	6E+07	2838	2.398838677	4.812589429	2.097E-10	3.62644E-09	0.14952	1	156	167	72	64	174	1839	457	959	814	785
ENSMUSG00000026580	chr1	Selp	1.6E+08	1.6E+08	4413	1.994052116	1.506956158	2.107E-10	3.63884E-09	0.08195	1	13	10	21	10	29	112	100	52	114	72
ENSMUSG00000015501	chr10	Hivep2	1.4E+07	1.4E+07	13720	-1.23481426	5.652132923	2.156E-10	3.71995E-09	0.04288	-1	1090	763	1467	1059	958	584	840	476	561	635
ENSMUSG00000087107	chr11	AI662270	8.3E+07	8.3E+07	1489	2.56062252	1.661627349	2.162E-10	3.72516E-09	0.14281	1	15	11	6	5	28	190	78	79	88	102
ENSMUSG00000064493	chr12	Snora28	1.1E+08	1.1E+08	127	-3.22416853	0.038274609	2.168E-10	3.7306E-09	0.16466	-1	42	26	27	22	12	3	6	4	4	2
ENSMUSG00000073489	chr1	Ifi204	1.7E+08	1.7E+08	3561	1.783928497	3.232149498	2.192E-10	3.76808E-09	0.08121	1	55	43	58	48	115	545	309	198	265	200
ENSMUSG00000033799	chr13	Fam208b	3566036	3566667	8337	-1.5879214	3.406169023	2.231E-10	3.8302E-09	0.06552	-1	242	196	263	300	170	127	157	71	85	112
ENSMUSG00000015094	chr2	Npdc1	2.5E+07	2.5E+07	3906	1.70561088	5.223132018	2.263E-10	3.87954E-09	0.08027	1	205	186	237	158	571	1414	825	889	1472	1292
ENSMUSG00000087038	chr9	2900079G21Rik	1.1E+08	1.1E+08	6718	3.714961592	1.270922572	2.265E-10	3.87955E-09	0.28687	1	1	0	19	2	4	59	44	82	121	114
ENSMUSG00000019768	chr10	Esr1	4611593	4612155	13661	-1.17143836	4.768255843	2.273E-10	3.88734E-09	0.03768	-1	601	437	656	609	510	366	379	318	357	290
ENSMUSG00000038607	chr4	Gng10	5.9E+07	5.9E+07	1314	1.239667298	3.85992297	2.288E-10	3.90809E-09	0.03979	1	136	86	135	103	193	452	403	313	429	493
ENSMUSG00000099023	chr11	Gm27456	1E+08	1E+08	63	-2.96939655	0.906247377	2.337E-10	3.98847E-09	0.17966	-1	59	35	85	45	22	8	20	5	3	7
ENSMUSG00000046318	chr18	Ccbe1	6.6E+07	6.6E+07	9511	1.580837924	2.306251353	2.341E-10	3.9896E-09	0.0565	1	24	25	53	33	50	190	162	117	118	159
ENSMUSG00000027533	chr3	Fabp5	1E+07	1E+07	3567	2.236022403	5.112950774	2.372E-10	4.0374E-09	0.13414	1	231	82	134	63	441	1124	1087	802	1418	1455
ENSMUSG00000032431	chr9	Crtap	1.1E+08	1.1E+08	1772	1.710867465	4.83877945	2.609E-10	4.43572E-09	0.08076	1	164	147	153	134	428	1257	595	737	1031	892
ENSMUSG00000101152	chr9	Gm28305	1E+08	1E+08	365	-2.56878595	2.542097239	2.62E-10	4.44834E-09	0.1632	-1	150	97	225	193	86	32	85	12	29	20
ENSMUSG00000027459	chr2	Fam110a	1.5E+08	1.5E+08	2207	1.78543452	2.692168532	2.644E-10	4.48502E-09	0.07829	1	40	31	42	33	70	179	134	174	232	277
ENSMUSG00000048960	chr1	Prex2	1.1E+07	1.1E+07	16609	-1.90878838	3.092695701	2.695E-10	4.56493E-09	0.09448	-1	192	153	254	192	225	92	148	51	44	40
ENSMUSG00000075122	chr16	Cd80	3.8E+07	3.8E+07	1701	2.996809411	-0.10762692	2.703E-10	4.57286E-09	0.12133	1	1	1	3	2	6	42	22	32	22	24
ENSMUSG00000000340	chr3	Dbt	1.2E+08	1.2E+08	3296	-1.33589985	4.909161826	2.708E-10	4.57604E-09	0.04992	-1	776	465	700	708	553	444	435	306	224	351
ENSMUSG00000026697	chr1	Myoc	1.6E+08	1.6E+08	2074	1.858698091	7.047242128	2.724E-10	4.59846E-09	0.0966	1	956	765	551	725	1210	7355	2331	3413	3944	4604
ENSMUSG00000021624	chr13	Cd180	1E+08	1E+08	4509	2.264817505	0.943315448	2.787E-10	4.69766E-09	0.09557	1	8	4	6	12	16	95	65	32	62	55
ENSMUSG00000087150	chr6	BC064078	1.3E+08	1.3E+08	2489	2.440485859	1.438386612	2.809E-10	4.72944E-09	0.12482	1	7	13	13	8	18	176	54	56	70	99
ENSMUSG00000026950	chr2	Neb	5.2E+07	5.2E+07	26369	-1.89320618	11.81156863	2.816E-10	4.73532E-09	0.10069	-1	79068	59717	118634	116834	51386	25964	57049	18872	28178	29603
ENSMUSG00000025647	chr9	Shisa5	1.1E+08	1.1E+08	1955	1.672876173	5.476416932	2.931E-10	4.92206E-09	0.07871	1	213	170	320	249	731	1703	1214	893	1594	1663
ENSMUSG00000037206	chr9	Islr	5.8E+07	5.8E+07	2354	1.374287074	6.182680129	2.934E-10	4.92206E-09	0.05401	1	584	490	513	597	837	2900	1599	1564	2552	2282
ENSMUSG00000050105	chr4	Grrp1	1.3E+08	1.3E+08	1275	2.072460049	2.44315285	2.99E-10	5.01026E-09	0.10625	1	18	12	53	31	47	218	90	161	221	182
ENSMUSG00000071253	chr10	Slc25a16	6.3E+07	6.3E+07	4799	-1.24538982	4.679021602	2.996E-10	5.01514E-09	0.04326	-1	550	409	626	498	632	337	495	246	249	246
ENSMUSG00000096146	chr7	Kcnj11	4.6E+07	4.6E+07	1173	-1.4793784	5.57607679	3.005E-10	5.02443E-09	0.06224	-1	1047	865	1073	1370	818	500	804	295	510	534
ENSMUSG00000057191	chr9	AB124611	2.2E+07	2.2E+07	1447	2.370231573	1.560923448	3.014E-10	5.0323E-09	0.1248	1	10	7	9	9	35	149	69	72	99	98
ENSMUSG00000035992	chr11	Fnip1	5.4E+07	5.4E+07	7119	-1.47114781	5.41611536	3.028E-10	5.0493E-09	0.0614	-1	1157	682	1332	898	631	489	677	355	356	470
ENSMUSG00000035840	chr13	Lysmd3	8.2E+07	8.2E+07	3124	-2.1218474	1.928596236	3.08E-10	5.13105E-09	0.10722	-1	92	74	131	96	67	33	58	16	23	18
ENSMUSG00000090157	chr2	Gm16534	3.2E+07	3.2E+07	1711	-2.38971182	1.856877797	3.133E-10	5.21213E-09	0.13598	-1	130	93	70	81	59	17	42	14	25	22
ENSMUSG00000001027	chr11	Scn4a	1.1E+08	1.1E+08	7041	-1.51674407	8.613715817	3.185E-10	5.2922E-09	0.0665	-1	8220	6373	11737	10483	6902	4036	6434	2697	4448	3573
ENSMUSG00000038127	chr16	Ccdc50	2.7E+07	2.7E+07	8639	-1.45487817	6.378684713	3.221E-10	5.34715E-09	0.06093	-1	1966	1848	1745	1599	1708	1072	1332	597	820	843
ENSMUSG00000053475	chr2	Tnfaip6	5.2E+07	5.2E+07	1710	1.984627549	1.536443998	3.282E-10	5.44121E-09	0.07902	1	19	20	17	9	16	104	88	72	90	97
ENSMUSG00000040446	chr18	Rprd1a	2.4E+07	2.4E+07	4297	-1.68762383	3.997734794	3.291E-10	5.45013E-09	0.07781	-1	445	328	362	345	300	168	273	116	92	138
ENSMUSG00000028152	chr3	Tspan5	1.4E+08	1.4E+08	3917	1.82737198	3.106464821	3.32E-10	5.49105E-09	0.08653	1	38	37	51	35	129	327	249	197	299	298
ENSMUSG00000039763	chr16	Dnajc28	9.2E+07	9.2E+07	3562	-1.36383933	4.973011627	3.42E-10	5.65046E-09	0.05277	-1	680	388	1160	761	492	394	491	256	322	365
ENSMUSG00000104217	chr1	RP24-426M1.3	4807892	4807982	825	-2.67445151	4.522710704	3.472E-10	5.72887E-09	0.1878	-1	675	553	733	635	303	111	360	54	79	61
ENSMUSG00000024907	chr19	Gal	3409919	3410165	712	3.378260527	-0.22131323	3.477E-10	5.7309E-09	0.14746	1	1	2	2	0	4	50	20	26	19	19
ENSMUSG00000020091	chr10	Eif4ebp2	6.1E+07	6.1E+07	1786	-1.72311664	5.482165201	3.485E-10	5.73476E-09	0.08413	-1	1027	794	1350	1034	956	415	900	216	373	296
ENSMUSG00000022453	chr15	Naga	8.2E+07	8.2E+07	1913	1.437845322	3.960118647	3.488E-10	5.73476E-09	0.05611	1	102	82	117	99	243	587	393	339	485	538
ENSMUSG00000026628	chr1	Atf3	1.9E+08	1.9E+08	2154	1.670487298	4.366605337	3.521E-10	5.78333E-09	0.07675	1	84	115	106	216	215	566	518	490	795	830
ENSMUSG00000040524	chr9	Zfp609	6.6E+07	6.6E+07	8268	-1.23425854	4.447185678	3.525E-10	5.78333E-09	0.04254	-1	430	349	532	580	393	291	367	173	263	263
ENSMUSG00000040061	chr2	Plcb2	1.2E+08	1.2E+08	6597	2.315267748	0.369900631	3.557E-10	5.82763E-09	0.0805	1	6	2	7	4	10	53	42	25	38	41
ENSMUSG00000026443	chr1	Lrrn2	1.3E+08	1.3E+08	3595	2.195726901	1.525113771	3.644E-10	5.96415E-09	0.10763	1	12	7	22	9	26	127	50	87	86	108
ENSMUSG00000002831	chr17	Plin4	5.6E+07	5.6E+07	5777	-1.36991353	7.91723211	3.654E-10	5.97314E-09	0.05496	-1	4176	3309	5502	4909	9155	3506	2968	2096	2413	3055
ENSMUSG00000072572	chr14	Slc39a2	5.2E+07	5.2E+07	3447	3.058854984	0.209184814	3.664E-10	5.98276E-09	0.15009	1	7	0	4	1	4	32	27	23	44	59
ENSMUSG00000035783	chr19	Acta2	3.4E+07	3.4E+07	1781	1.474902001	6.628322345	3.705E-10	6.04274E-09	0.06293	1	527	810	830	752	951	4514	2217	2400	2938	3049
ENSMUSG00000024298	chr17	Zfp871	3.3E+07	3.3E+07	5376	-2.79770491	2.18564402	3.749E-10	6.10727E-09	0.19112	-1	144	125	132	121	49	31	54	10	11	16
ENSMUSG00000070436	chr7	Serpinh1	9.9E+07	9.9E+07	2435	1.738070196	7.392339505	3.837E-10	6.24307E-09	0.08674	1	933	717	1033	1031	2310	8704	3597	4266	6051	4314

ENSMUSG00000019823	chr10	Mical1	4.1E+07	4.1E+07	6047	1.300292228	3.744194916	3.863E-10	6.27089E-09	0.04477	1	95	93	110	107	174	505	346	253	402	467
ENSMUSG00000031129	chr9	Slc9a9	9.5E+07	9.5E+07	5679	2.011644116	2.652501378	3.861E-10	6.27089E-09	0.10129	1	26	31	24	25	79	335	191	146	188	170
ENSMUSG00000031748	chr8	Gnao1	9.4E+07	9.4E+07	6785	-1.56320367	2.810634673	4.19E-10	6.79417E-09	0.06292	-1	167	104	156	168	193	93	114	46	58	59
ENSMUSG00000027589	chr2	Pcmtd2	1.8E+08	1.8E+08	4183	-1.42883518	5.585984909	4.338E-10	7.02531E-09	0.05923	-1	1138	775	1430	1056	869	512	900	331	433	548
ENSMUSG00000022587	chr15	Ly6e	7.5E+07	7.5E+07	3784	1.717944515	7.311376378	4.403E-10	7.12375E-09	0.08541	1	780	739	1085	840	2341	7362	3776	3269	6283	4876
ENSMUSG00000060216	chr11	Arrb2	7E+07	7E+07	2845	1.662127634	3.72611629	4.43E-10	7.15825E-09	0.07524	1	83	63	80	65	194	629	304	306	422	415
ENSMUSG00000035284	chr9	Vps13c	6.8E+07	6.8E+07	11523	-1.67651934	4.678478563	4.541E-10	7.32913E-09	0.08001	-1	545	395	906	764	339	312	425	148	182	221
ENSMUSG00000035373	chr11	Ccl7	8.2E+07	8.2E+07	801	3.348357139	2.206053939	4.549E-10	7.33419E-09	0.2598	1	4	9	5	12	31	302	78	244	107	76
ENSMUSG00000037254	chr2	Itih2	1E+07	1E+07	3315	2.883260217	0.498912355	4.615E-10	7.43178E-09	0.14583	1	5	3	2	6	6	82	19	37	42	50
ENSMUSG00000014547	chr14	Wdfy2	6.3E+07	6.3E+07	2011	-2.37127133	0.743761028	4.632E-10	7.44124E-09	0.11345	-1	35	36	67	43	24	19	10	6	12	8
ENSMUSG00000033624	chr8	Pdpr	1.1E+08	1.1E+08	5028	-3.90497891	6.201855273	4.629E-10	7.44124E-09	0.36584	-1	2065	1392	3613	2765	583	124	681	50	72	70
ENSMUSG00000022742	chr16	Cpox	5.9E+07	5.9E+07	3186	-1.33027629	4.462858647	4.659E-10	7.47749E-09	0.0503	-1	444	309	708	520	427	259	419	168	211	252
ENSMUSG00000100335	chr8	2310008N11Rik	2.7E+07	2.7E+07	568	2.879930964	0.7663423	4.734E-10	7.58856E-09	0.16081	1	6	1	8	9	4	53	24	60	54	83
ENSMUSG00000005339	chr1	Fcer1a	1.7E+08	1.7E+08	998	4.434792878	0.392679459	4.789E-10	7.6678E-09	0.31571	1	3	1	1	0	2	144	16	23	28	26
ENSMUSG00000078453	chr10	Abracl	1.8E+07	1.8E+07	807	2.024634839	2.263998374	4.797E-10	7.6718E-09	0.10103	1	14	21	31	18	58	219	120	149	122	155
ENSMUSG00000027293	chr2	Ehd4	1.2E+08	1.2E+08	4007	1.229860139	5.929471198	4.968E-10	7.93588E-09	0.04448	1	399	387	859	624	519	2200	1813	1336	1860	1649
ENSMUSG00000030074	chr6	Gxylt2	1E+08	1E+08	2678	3.003850372	0.382614857	4.974E-10	7.93731E-09	0.14058	1	7	6	2	0	3	66	36	30	47	33
ENSMUSG00000050232	chrX	Cxcr3	1E+08	1E+08	1731	3.271451825	0.02083561	5.047E-10	8.04477E-09	0.16478	1	1	1	2	1	7	33	28	12	31	60
ENSMUSG00000096764	chr2	Gm21985	1.1E+08	1.1E+08	4532	-2.80187183	3.464298761	5.167E-10	8.22643E-09	0.20484	-1	338	264	357	296	157	58	160	18	39	23
ENSMUSG00000002006	chrX	Pdzd4	7.4E+07	7.4E+07	3970	1.804415275	1.501026091	5.182E-10	8.23494E-09	0.06747	1	14	10	18	21	28	121	80	69	84	78
ENSMUSG00000023411	chr14	Nfatc4	5.6E+07	5.6E+07	4019	1.428621321	3.421292741	5.184E-10	8.23494E-09	0.05465	1	78	46	104	94	120	452	225	214	338	384
ENSMUSG00000034947	chr11	Tmem106a	1E+08	1E+08	3138	2.274326969	3.995142625	5.196E-10	8.24434E-09	0.14035	1	56	63	40	42	217	790	370	376	615	583
ENSMUSG00000030659	chr7	Nucb2	1.2E+08	1.2E+08	2301	1.790779516	3.296082542	5.274E-10	8.35853E-09	0.08577	1	45	59	65	38	123	535	242	214	296	292
ENSMUSG00000063550	chr7	Nup98	1E+08	1E+08	4051	-1.89535775	3.144647292	5.338E-10	8.45081E-09	0.09657	-1	187	170	318	229	139	77	142	63	53	51
ENSMUSG00000029161	chr5	Cgref1	3.1E+07	3.1E+07	1328	1.75147551	1.894676054	5.387E-10	8.51842E-09	0.06883	1	18	24	38	17	26	166	108	77	106	118
ENSMUSG00000097081	chr12	Gm10425	1.1E+08	1.1E+08	3364	3.371215772	-0.15806414	5.465E-10	8.6218E-09	0.18261	1	0	0	4	0	6	20	39	22	41	18
ENSMUSG00000103779	chr17	RP24-490B17.7	5.2E+07	5.2E+07	4801	-2.03364399	2.43232698	5.46E-10	8.6218E-09	0.10679	-1	161	115	150	120	88	42	83	21	43	33
ENSMUSG00000029616	chr5	Erp29	1.2E+08	1.2E+08	9060	1.175358828	5.742465835	5.556E-10	8.75579E-09	0.04076	1	437	337	624	437	685	2069	1204	1243	1595	1556
ENSMUSG00000039621	chr2	Prex1	1.7E+08	1.7E+08	10266	1.055187622	4.039094273	5.632E-10	8.86543E-09	0.03014	1	131	119	207	163	186	510	495	322	469	492
ENSMUSG00000020736	chr11	Nt5c	1.2E+08	1.2E+08	1140	1.764813708	3.198940971	5.691E-10	8.94792E-09	0.08276	1	60	58	48	35	106	389	200	234	327	291
ENSMUSG00000057230	chr6	Aak1	8.7E+07	8.7E+07	8272	-2.05215436	2.374793845	5.775E-10	9.0698E-09	0.10831	-1	110	100	208	142	65	47	70	24	38	31
ENSMUSG00000042817	chr5	Flt3	1.5E+08	1.5E+08	7760	3.104947208	-0.16135723	5.786E-10	9.0781E-09	0.10862	1	3	3	0	3	2	42	21	18	25	33
ENSMUSG00000020623	chr11	Map2k6	1.1E+08	1.1E+08	3444	-1.29706143	4.287227038	5.796E-10	9.08247E-09	0.04787	-1	483	289	564	391	364	220	310	195	258	174
ENSMUSG00000043903	chr8	Gm22	1.2E+08	1.2E+08	3082	2.520700218	0.812942249	5.864E-10	9.16913E-09	0.12049	1	11	4	4	8	8	76	35	33	85	55
ENSMUSG00000057396	chr13	Zfp759	6.7E+07	6.7E+07	3482	-1.78793452	2.261262085	5.863E-10	9.16913E-09	0.08042	-1	135	70	137	125	88	44	70	22	41	47
ENSMUSG00000030403	chr7	Vasp	1.9E+07	1.9E+07	2438	1.417499701	5.167645518	5.921E-10	9.24757E-09	0.05878	1	215	176	346	235	559	1296	735	867	1295	1179
ENSMUSG00000091649	chr14	Phf11b	5.9E+07	5.9E+07	1184	2.358838009	0.636068821	6.216E-10	9.69884E-09	0.09856	1	3	5	7	12	7	76	50	26	43	52
ENSMUSG00000028367	chr4	Txn1	5.8E+07	5.8E+07	1051	1.376048076	6.539369539	6.276E-10	9.78114E-09	0.05652	1	772	541	782	624	1231	3373	1953	2202	3095	3227
ENSMUSG00000074093	chr7	Svip	5.2E+07	5.2E+07	3059	-1.41743304	4.766186621	6.395E-10	9.95443E-09	0.05859	-1	639	469	777	599	471	284	531	212	260	254
ENSMUSG00000032698	chr2	Lmo2	1E+08	1E+08	2166	1.218534582	3.967251911	6.403E-10	9.95643E-09	0.04074	1	115	111	170	137	173	703	375	316	406	475
ENSMUSG00000033813	chr1	Tcea1	4857814	4857976	3017	-1.53089856	3.792888564	6.418E-10	9.96921E-09	0.06583	-1	339	256	375	289	270	170	258	91	123	105
ENSMUSG00000071203	chr13	Naip5	1E+08	1E+08	5204	3.241775769	0.738028412	6.569E-10	1.01915E-08	0.20996	1	4	1	1	2	14	98	27	43	43	73
ENSMUSG00000098906	chr11	Mir7652	5.6E+07	5.6E+07	56	-2.66230471	0.364037906	6.854E-10	1.06222E-08	0.13944	-1	48	19	35	35	23	6	15	2	6	6
ENSMUSG00000020427	chr11	Igfbp3	7206086	7207506	3130	1.310162892	4.873790384	7.011E-10	1.08535E-08	0.05004	1	235	214	269	237	300	1224	530	798	755	966
ENSMUSG00000087543	chr15	Gm16576	8E+07	8E+07	5404	-2.02943179	2.930867681	7.2E-10	1.11339E-08	0.1111	-1	185	160	227	213	116	56	129	35	48	46
ENSMUSG00000054008	chr18	Ndst1	6.1E+07	6.1E+07	6070	-1.58472104	5.55456996	7.217E-10	1.11479E-08	0.07433	-1	916	697	1781	1247	755	478	853	314	394	419
ENSMUSG00000026827	chr2	Gpd2	5.7E+07	5.7E+07	6549	-1.64257438	7.35638645	7.422E-10	1.14527E-08	0.08058	-1	4301	3888	2309	3457	3838	1597	2091	1235	1812	1485
ENSMUSG00000023067	chr17	Cdkn1a	2.9E+07	2.9E+07	2223	1.993266086	6.837299175	7.505E-10	1.15681E-08	0.1158	1	471	486	471	1286	690	3224	2322	3536	4149	5240
ENSMUSG00000024675	chr19	Ms4a4c	1.1E+07	1.1E+07	1751	3.381074099	-0.01517064	7.54E-10	1.16088E-08	0.18769	1	0	0	6	2	3	62	35	16	35	14
ENSMUSG00000040528	chr11	Milr1	1.1E+08	1.1E+08	2474	2.713240337	0.66528532	7.728E-10	1.18593E-08	0.13941	1	8	3	1	5	11	83	32	35	43	66
ENSMUSG00000045382	chr1	Cxcr4	1.3E+08	1.3E+08	1808	1.78667056	2.937735013	7.715E-10	1.18593E-08	0.0855	1	64	31	52	23	89	227	278	161	230	312
ENSMUSG00000074109	chr7	Mrgprx2	4.8E+07	4.8E+07	4735	3.343645592	-0.22679822	7.726E-10	1.18593E-08	0.14348	1	3	1	1	2	2	52	14	16	24	29
ENSMUSG00000044308	chr2	Ubr3	7E+07	7E+07	9719	-1.56731205	8.208131044	7.753E-10	1.18839E-08	0.074	-1	7052	5240	8072	7500	5015	2899	5242	2019	2658	2773
ENSMUSG00000039395	chr1	Mreg	7.2E+07	7.2E+07	2284	-1.47700821	5.060694702	7.771E-10	1.18993E-08	0.06458	-1	609	422	1372	839	575	333	571	248	291	391
ENSMUSG00000038618	chr7	Rassf7	1.4E+08	1.4E+08	1803	3.146411314	1.736076526	7.853E-10	1.20117E-08	0.23556	1	13	0	5	3	30	126	111	82	116	153
ENSMUSG00000018585	chr11	Atox1	5.5E+07	5.5E+07	541	1.25292403	5.081271147	7.953E-10	1.21507E-08	0.04649	1	279	197	285	270	498	1069	756	719	1290	1077
ENSMUSG00000039542	chr9	Ncam1	5E+07	5E+07	7995	1.366652028	3.785214377	8.008E-10	1.22213E-08	0.05192	1	93	91	171	137	82	520	345	319	396	456
ENSMUSG00000029174	chr5	Tbc1d1	6.4E+07	6.4E+07	7140	-1.87504709	6.270479673	8.224E-10	1.25375E-08	0.10363	-1	1069	1486	2263	3217	959	736	684	649	663	640
ENSMUSG00000031561	chr8	Tenm3	4.8E+07	4.8E+07	11132	-1.46398107	3.732356382	8.587E-10	1.3077E-08	0.06063	-1	329	199	460	284	202	151	195	125	125	129
ENSMUSG00000026335	chr1	Pam	9.8E+07	9.8E+07	11892	1.144767148	6.305637966	8.699E-10	1.32328E-08	0.03993	1	683	540	909	688	925	3041	2059	1806	2019	2363
ENSMUSG00000027007	chr2	Ssfa2	8E+07	8E+07	5599	-1.06453649	4.535107084	8.786E-10	1.33515E-08	0.03297	-1	448	333	576	494	524	327	440	207	298	289
ENSMUSG00000031266	chrX	Gla	1.3E+08	1.3E+08	3265	1.530848544	2.951451	8.814E-10	1.33801E-08	0.06221	1	42	44	81	46	87	207	281	132	282	274
ENSMUSG00000030249	chr6	Abcc9	1.4E+08	1.4E+08	7538	-1.4962597	7.568925797	8.929E-10	1.35391E-08	0.06811	-1	4542	3421	5147	4716	2939	2218	3122	1438	1715	1878
ENSMUSG00000079343	chr6	C1s2	1.2E+08	1.2E+08	2662	1.999772509	4.074736015	9.007E-10	1.36422E-08	0.11314	1	92	97	66	43	203	851	352	451	531	588
ENSMUSG00000026458	chr1	Ppfia4	1.3E+08	1.3E+08	6572	2.015844072	2.317706794	9.05E-10	1.36926E-08	0.10352	1	42	21	21	15	44	247	103	123	155	177
ENSMUSG00000031342	chrX	Gpm6b	1.7E+08	1.7E+08	5600	1.410330616	3.438718646	9.203E-10	1.39094E-08	0.05446	1	89	70	90	75	116	507	239	264	283	323
ENSMUSG00000040488	chr7	Ltbp4	2.7E+07	2.7E+07	6463	1.297258821	7.822106112	9.35E-10	1.41169E-08	0.05184	1	1549	1184	2531	2291	2564	7978	5275	4794	7193	8173

ENSMUSG00000003031	chr6	Cdkn1b	1.3E+08	1.3E+08	4552	-1.06533517	5.038239492	9.386E-10	1.41556E-08	0.03385	-1	722	527	791	643	637	466	554	314	392	479
ENSMUSG00000001751	chr11	Naglu	1E+08	1E+08	2658	1.437252444	3.747713094	9.436E-10	1.42155E-08	0.05858	1	93	59	106	105	193	444	331	252	522	474
ENSMUSG00000020077	chr10	Srgn	6.2E+07	6.2E+07	2196	1.143267587	4.216071617	9.522E-10	1.43298E-08	0.03753	1	134	121	222	159	249	741	462	356	508	595
ENSMUSG00000046138	chr19	9930021J03Rik	3E+07	3E+07	8134	-1.33872764	4.263671274	9.736E-10	1.46359E-08	0.05268	-1	384	306	544	480	356	226	369	133	215	196
ENSMUSG00000021482	chr13	Aaed1	6.4E+07	6.4E+07	972	-1.50593139	3.895632796	1.031E-09	1.54611E-08	0.06545	-1	365	285	370	316	288	183	264	129	115	111
ENSMUSG00000030306	chr6	Tmtc1	1.5E+08	1.5E+08	8578	-1.45675261	6.702062138	1.03E-09	1.54611E-08	0.06494	-1	2965	1894	2373	2315	1631	1231	1549	780	1181	1057
ENSMUSG00000068740	chr3	Celsr2	1.1E+08	1.1E+08	11513	-1.22282856	3.400773219	1.034E-09	1.54953E-08	0.04079	-1	204	140	295	250	236	130	140	99	128	154
ENSMUSG00000028132	chr3	Tmem56	1.2E+08	1.2E+08	7650	-1.84347744	5.973439117	1.045E-09	1.56404E-08	0.10153	-1	1478	1827	791	1696	1053	608	719	381	557	592
ENSMUSG00000031833	chr8	Mast3	7.1E+07	7.1E+07	5334	1.358526148	2.967641075	1.05E-09	1.57011E-08	0.04826	1	50	53	77	57	90	285	200	155	245	266
ENSMUSG00000032511	chr9	Scn5a	1.2E+08	1.2E+08	8764	2.817087229	0.706366963	1.054E-09	1.57482E-08	0.15429	1	3	8	8	3	5	38	36	70	45	67
ENSMUSG00000074519	chr2	Etohi1	1.8E+08	1.8E+08	2145	-2.70517547	2.528753328	1.057E-09	1.57711E-08	0.19336	-1	151	132	213	176	65	49	64	21	7	21
ENSMUSG00000020647	chr12	Ncoa1	4247363	4249750	7328	-1.06705789	4.980709581	1.06E-09	1.58039E-08	0.03409	-1	598	474	855	679	624	425	582	306	394	407
ENSMUSG00000032353	chr9	Tmed3	9E+07	9E+07	2848	1.227970429	5.149260382	1.065E-09	1.58524E-08	0.04537	1	337	229	310	258	471	1521	755	765	1084	1045
ENSMUSG00000022756	chr16	Slc7a4	1.8E+07	1.8E+07	3978	3.236137258	-0.4759701	1.072E-09	1.59469E-08	0.13216	1	1	0	4	2	1	28	16	10	22	33
ENSMUSG00000025326	chr7	Ube3a	5.9E+07	5.9E+07	5097	-1.71158509	5.033839607	1.077E-09	1.59809E-08	0.08752	-1	806	564	1159	876	346	312	524	222	253	284
ENSMUSG00000043019	chr1	Edem3	1.5E+08	1.5E+08	6381	-1.23521061	5.028609596	1.078E-09	1.59809E-08	0.04604	-1	764	586	799	661	577	444	587	304	337	347
ENSMUSG00000086712	chr4	AI427809	5.3E+07	5.3E+07	2369	2.938089498	-0.19377741	1.078E-09	1.59809E-08	0.10676	1	4	3	1	1	3	40	31	13	26	25
ENSMUSG00000021952	chr14	Xpo4	5.8E+07	5.8E+07	7266	-2.41093578	2.46554968	1.087E-09	1.61032E-08	0.15556	-1	132	95	206	207	54	28	71	16	34	34
ENSMUSG00000041426	chr1	Hibch	5.3E+07	5.3E+07	6059	-1.07498482	5.573109675	1.107E-09	1.63715E-08	0.03528	-1	952	597	1334	942	1141	748	783	485	566	598
ENSMUSG00000000244	chr7	Tspan32	1.4E+08	1.4E+08	2848	2.768787856	1.161211471	1.11E-09	1.63988E-08	0.16995	1	4	7	4	4	21	144	48	42	69	80
ENSMUSG00000005447	chr7	Pafah1b3	2.5E+07	2.5E+07	2107	2.037659424	1.147792387	1.119E-09	1.65216E-08	0.08815	1	12	6	18	8	18	113	60	39	77	61
ENSMUSG00000036879	chr8	Phkb	8.6E+07	8.6E+07	7417	-1.59047348	8.575007034	1.133E-09	1.67066E-08	0.07766	-1	9105	7345	9205	8378	8399	3708	7202	2592	3442	2931
ENSMUSG00000103229	chr3	Dcun1d1	3.6E+07	3.6E+07	780	-2.43295239	3.1666703	1.142E-09	1.68193E-08	0.16344	-1	267	259	190	244	110	55	131	32	45	33
ENSMUSG00000000058	chr6	Cav2	1.7E+07	1.7E+07	3335	-1.44714423	4.791957166	1.153E-09	1.69728E-08	0.06302	-1	496	415	721	370	1157	412	414	230	229	266
ENSMUSG00000024610	chr18	Cd74	6.1E+07	6.1E+07	1410	2.952855437	8.10241013	1.156E-09	1.69899E-08	0.24095	1	715	625	379	467	2747	17512	3724	5787	8234	16464
ENSMUSG00000030180	chr6	Kdm5a	1.2E+08	1.2E+08	14185	-1.20809169	4.64971814	1.193E-09	1.75196E-08	0.04381	-1	540	390	738	544	424	345	455	198	267	321
ENSMUSG00000024063	chr17	Lbh	7.3E+07	7.3E+07	3207	1.367971829	4.725637197	1.201E-09	1.76196E-08	0.05636	1	151	117	248	218	423	1013	617	653	703	934
ENSMUSG00000037946	chr13	Fgd3	4.9E+07	4.9E+07	6012	2.2854943	2.163688538	1.205E-09	1.76656E-08	0.13748	1	5	8	48	20	38	148	186	109	116	183
ENSMUSG00000036594	chr17	H2-Aa	3.4E+07	3.4E+07	1874	2.78407904	6.693501902	1.211E-09	1.77341E-08	0.2176	1	339	288	166	184	1051	6747	1497	2362	2716	5817
ENSMUSG00000035735	chr19	Dagla	1E+07	1E+07	5747	-1.22971823	3.842881736	1.237E-09	1.80855E-08	0.04351	-1	262	238	340	289	388	176	250	107	208	152
ENSMUSG00000002699	chr11	Lcp2	3.4E+07	3.4E+07	4459	2.011694888	1.871782271	1.246E-09	1.82043E-08	0.09939	1	15	17	19	13	42	184	85	73	106	142
ENSMUSG00000085457	chr13	1110046J04Rik	3.4E+07	3.4E+07	3487	1.83881065	1.335696437	1.25E-09	1.82508E-08	0.07358	1	13	9	22	9	27	104	73	53	77	80
ENSMUSG00000021945	chr14	Zmym2	5.7E+07	5.7E+07	6876	-1.13559297	5.152293868	1.263E-09	1.84138E-08	0.03934	-1	738	681	779	714	682	527	590	329	400	468
ENSMUSG00000048416	chr3	Mlf1	6.7E+07	6.7E+07	1719	-1.39102197	7.191611262	1.267E-09	1.84549E-08	0.06017	-1	3458	2697	3154	3349	2949	1647	2065	1508	1795	1232
ENSMUSG00000046157	chr12	Tmem229b	7.9E+07	7.9E+07	4732	1.403232066	3.284933199	1.335E-09	1.94189E-08	0.05471	1	61	51	97	84	112	409	196	220	281	343
ENSMUSG00000025903	chr1	Lypla1	4807788	4807982	7145	-1.68968784	5.908074318	1.357E-09	1.97168E-08	0.08721	-1	1363	1042	1993	1452	1054	451	1167	320	487	560
ENSMUSG00000095362	chr2	Gm14325	1.8E+08	1.8E+08	1616	-2.21180963	3.026053206	1.359E-09	1.97272E-08	0.13685	-1	238	188	269	195	87	74	113	41	32	43
ENSMUSG00000092345	chr4	Gm20503	5.9E+07	5.9E+07	1294	1.135846257	3.90437438	1.363E-09	1.97636E-08	0.03656	1	147	94	155	114	198	456	408	315	438	493
ENSMUSG00000022181	chr15	C6	4727175	4727317	4036	3.816782946	0.273221441	1.367E-09	1.98132E-08	0.26102	1	0	2	0	1	7	101	22	17	28	42
ENSMUSG00000022853	chr16	Ehhadh	2.2E+07	2.2E+07	3018	-1.53099314	3.074611903	1.379E-09	1.99675E-08	0.0657	-1	217	103	191	165	281	88	139	55	76	92
ENSMUSG00000031529	chr8	Tnks	3.5E+07	3.5E+07	6444	-1.76438619	3.363971743	1.388E-09	2.00633E-08	0.08954	-1	258	184	315	269	156	104	176	69	59	79
ENSMUSG00000032436	chr9	Cmtm7	1.1E+08	1.1E+08	1136	1.362801214	3.527910212	1.391E-09	2.00871E-08	0.05214	1	77	84	96	73	152	429	276	270	377	343
ENSMUSG00000051506	chr14	Wdfy4	3.3E+07	3.3E+07	10512	2.140681889	2.17109242	1.395E-09	2.01229E-08	0.11664	1	7	26	20	31	35	207	116	81	145	196
ENSMUSG00000022947	chr16	Cbr3	9.4E+07	9.4E+07	1170	1.774599477	2.239689991	1.432E-09	2.06479E-08	0.08025	1	26	26	32	19	54	190	99	115	149	178
ENSMUSG00000060586	chr17	H2-Eb1	3.4E+07	3.4E+07	1184	2.840439843	6.267527348	1.441E-09	2.07568E-08	0.22721	1	247	223	112	125	740	5022	1071	1601	2088	4581
ENSMUSG00000039840	chr18	Epg5	7.8E+07	7.8E+07	9672	-1.15859544	5.199582058	1.495E-09	2.15135E-08	0.04137	-1	774	616	946	833	607	484	616	353	464	435
ENSMUSG00000014602	chr1	Kif1a	9.3E+07	9.3E+07	9330	1.830285892	1.652096797	1.515E-09	2.17749E-08	0.07749	1	20	11	22	27	19	77	114	61	108	123
ENSMUSG00000037379	chr5	Spon2	3.3E+07	3.3E+07	2237	2.073123028	4.091309514	1.556E-09	2.23388E-08	0.12426	1	92	119	36	106	104	951	333	466	594	494
ENSMUSG00000047945	chr4	Marcksl1	1.3E+08	1.3E+08	1605	2.048416779	2.922638814	1.58E-09	2.26562E-08	0.11666	1	28	35	26	26	107	318	200	187	270	264
ENSMUSG00000042182	chr1	Bend6	3.4E+07	3.4E+07	3421	3.153797762	-0.53858531	1.586E-09	2.2723E-08	0.10775	1	1	1	4	0	2	24	28	15	15	20
ENSMUSG00000020169	chr10	Best3	1.2E+08	1.2E+08	2719	-2.35636734	3.411072626	1.598E-09	2.28696E-08	0.15799	-1	215	209	332	455	101	62	151	39	59	54
ENSMUSG00000047141	chr16	Zfp654	6.5E+07	6.5E+07	4741	-1.7291502	3.815320808	1.601E-09	2.28958E-08	0.08823	-1	347	288	373	345	235	142	258	93	79	109
ENSMUSG00000027272	chr2	Ubr1	1.2E+08	1.2E+08	9889	-1.22483359	5.325150754	1.613E-09	2.30157E-08	0.04661	-1	857	697	941	952	711	578	711	363	415	434
ENSMUSG00000042599	chr6	Kdm7a	3.9E+07	3.9E+07	10057	-1.26759069	5.421948513	1.612E-09	2.30157E-08	0.04999	-1	839	748	1289	945	718	517	766	369	445	517
ENSMUSG00000023942	chr17	Slc29a1	4.6E+07	4.6E+07	4008	1.147202396	5.931682844	1.616E-09	2.30324E-08	0.04128	1	457	341	762	654	716	2057	1542	1202	2011	1926
ENSMUSG00000023274	chr6	Cd4	1.2E+08	1.2E+08	4032	2.820896284	0.837200097	1.621E-09	2.30798E-08	0.16894	1	2	6	2	6	14	64	29	41	68	92
ENSMUSG00000036473	chr17	Tbc1d24	2.4E+07	2.4E+07	8053	-1.53879381	3.20883497	1.642E-09	2.33634E-08	0.06803	-1	180	143	297	265	152	115	137	48	91	107
ENSMUSG00000020101	chr10	4632428N05Rik	6E+07	6E+07	5014	1.642919107	5.480637859	1.663E-09	2.36371E-08	0.08305	1	273	235	245	191	725	1709	1333	923	1427	1656
ENSMUSG00000000753	chr11	Serpinf1	7.5E+07	7.5E+07	2359	1.704001155	7.73363295	1.769E-09	2.51177E-08	0.09046	1	1387	1301	1127	1005	2707	10337	4253	5129	6998	7248
ENSMUSG00000060147	chr13	Serpinb6a	3.4E+07	3.4E+07	5409	1.57061904	8.36470262	1.771E-09	2.51231E-08	0.07762	1	1671	1438	3865	1568	4727	12451	11864	8068	9217	9543
ENSMUSG00000029246	chr5	Ppat	7.7E+07	7.7E+07	4421	-1.15819972	4.526911992	1.792E-09	2.53821E-08	0.04084	-1	489	430	493	498	429	339	363	245	241	282
ENSMUSG00000039891	chr10	Txlnb	1.8E+07	1.8E+07	5504	-1.68975892	8.717907991	1.793E-09	2.53821E-08	0.08929	-1	10276	6926	13795	11145	6140	3869	7355	2595	3477	3577
ENSMUSG00000053746	chr2	Ptrh1	3.3E+07	3.3E+07	1135	1.847995446	1.719843081	1.803E-09	2.54961E-08	0.08106	1	20	17	19	13	34	121	70	85	111	118
ENSMUSG00000015133	chr7	Lrrk1	6.6E+07	6.6E+07	9487	1.26499091	3.174091956	1.809E-09	2.55576E-08	0.04377	1	66	56	103	73	101	344	214	214	262	263
ENSMUSG00000024276	chr18	Zfp397	2.4E+07	2.4E+07	5487	-1.19547353	4.095783419	1.842E-09	2.59867E-08	0.04292	-1	340	317	420	356	330	244	297	143	176	223
ENSMUSG00000006585	chr8	Cdt1	1.2E+08	1.2E+08	2189	1.86792934	1.269099299	1.865E-09	2.6271E-08	0.07786	1	14	7	21	10	23	83	57	60	90	75
ENSMUSG00000051910	chr7	Sox6	1.2E+08	1.2E+08	8852	-1.4119616	6.512540689	1.866E-09	2.6271E-08	0.06303	-1	2210	1488	2742	1933	1599	899	1643	686	985	977

ENSMUSG00000103405	chr1	Unspecified	3.4E+07	3.4E+07	7920	-3.03085668	3.24433809	1.896E-09	2.6673E-08	0.25027	-1	207	171	472	393	32	42	85	24	26	40
ENSMUSG00000036391	chr11	Sec24a	5.2E+07	5.2E+07	10683	-1.34740682	4.076960107	1.918E-09	2.69567E-08	0.05478	-1	392	335	412	339	301	217	296	109	187	191
ENSMUSG00000090799	chr14	Klhl33	5.1E+07	5.1E+07	1602	-1.49744355	5.32290367	1.924E-09	2.70153E-08	0.06991	-1	1226	553	1477	608	640	446	518	356	336	500
ENSMUSG00000042390	chr3	Gatad2b	9E+07	9E+07	1906	-2.19805004	2.66818283	1.93E-09	2.70727E-08	0.13533	-1	158	153	183	184	79	34	98	24	37	45
ENSMUSG00000045038	chr17	Prkce	8.6E+07	8.6E+07	7261	-1.10823641	3.910114564	1.955E-09	2.73894E-08	0.03584	-1	313	256	336	270	357	194	234	153	202	196
ENSMUSG00000034640	chr3	Tiparp	6.6E+07	6.6E+07	4358	-1.44798004	4.645820635	1.959E-09	2.74212E-08	0.06469	-1	414	613	447	666	494	302	360	242	256	219
ENSMUSG00000038658	chr19	Ric1	3E+07	3E+07	10727	-1.08522237	4.829710517	1.976E-09	2.76267E-08	0.03641	-1	554	475	713	603	542	373	503	234	397	392
ENSMUSG00000029202	chr5	Pds5a	6.6E+07	6.6E+07	4146	-1.71952417	4.188033908	2.003E-09	2.79788E-08	0.08943	-1	393	328	590	482	301	215	341	110	122	106
ENSMUSG00000045767	chr13	B230219D22Rik	5.6E+07	5.6E+07	4651	-1.35886021	5.373408272	2.01E-09	2.80563E-08	0.05804	-1	951	765	1039	958	689	464	775	299	470	423
ENSMUSG00000028822	chr4	Tmem50a	1.3E+08	1.3E+08	1270	1.342897605	5.852281939	2.017E-09	2.81204E-08	0.05695	1	478	340	481	331	877	2062	1386	1346	1799	1956
ENSMUSG00000028434	chr4	Epb4.1l4b	5.7E+07	5.7E+07	8858	-1.36134404	3.126109918	2.019E-09	2.8121E-08	0.05252	-1	163	149	229	174	232	160	111	80	73	84
ENSMUSG00000084899	chr10	Gm15344	8.7E+07	8.7E+07	421	1.585501757	5.61728794	2.034E-09	2.83075E-08	0.07857	1	353	214	456	304	575	2889	925	1342	1033	1478
ENSMUSG00000057181	chr11	5730455P16Rik	8E+07	8E+07	4842	-1.33095578	5.875764896	2.076E-09	2.88566E-08	0.05617	-1	1387	1075	1574	1212	975	702	1033	511	648	571
ENSMUSG00000050919	chr13	Zfp366	9.9E+07	9.9E+07	2763	-3.30166492	0.111486008	2.087E-09	2.89764E-08	0.21943	-1	30	20	50	35	6	2	8	3	2	4
ENSMUSG00000041362	chr19	4930506M07Rik	5.9E+07	5.9E+07	4081	1.932934014	2.296341015	2.132E-09	2.95773E-08	0.09989	1	32	19	21	16	63	185	189	83	153	183
ENSMUSG00000029622	chr5	Arpc1b	1.5E+08	1.5E+08	5103	1.482336389	5.758557963	2.156E-09	2.98763E-08	0.06927	1	328	311	413	278	877	2371	1489	1219	1729	1496
ENSMUSG00000055204	chr5	Ankrd17	9E+07	9E+07	10053	-1.18384072	5.614258371	2.166E-09	2.99668E-08	0.04449	-1	881	728	1525	1162	875	726	814	456	533	586
ENSMUSG00000027784	chr3	Ppm1l	6.9E+07	6.9E+07	10496	-1.46118748	7.60563786	2.175E-09	3.00797E-08	0.06823	-1	4622	3772	4850	4481	3301	1954	3274	1529	2230	1779
ENSMUSG00000060036	chr15	Rpl3	8E+07	8E+07	3119	1.464803902	6.422261301	2.179E-09	3.00797E-08	0.06813	1	553	481	649	515	1323	3673	1964	2130	2527	2739
ENSMUSG00000103319	chrX	AC055766.1	6.9E+07	6.9E+07	1019	-3.24127433	0.355618965	2.177E-09	3.00797E-08	0.22832	-1	41	35	40	33	15	7	14	1	1	2
ENSMUSG00000026278	chr1	Bok	9.4E+07	9.4E+07	1775	1.655514627	2.474050563	2.185E-09	3.01397E-08	0.07425	1	29	23	45	35	70	218	130	169	177	143
ENSMUSG00000005968	chr3	Tuft1	9.5E+07	9.5E+07	2564	2.292703624	1.090051422	2.201E-09	3.0329E-08	0.11934	1	15	4	12	5	15	79	37	51	77	94
ENSMUSG00000044066	chr11	Cep68	2E+07	2E+07	5865	-1.43122363	5.032064718	2.209E-09	3.03992E-08	0.06425	-1	609	501	1130	897	485	420	589	238	291	317
ENSMUSG00000023048	chr15	Prr13	1E+08	1E+08	1562	1.145036317	5.426998597	2.219E-09	3.05118E-08	0.04131	1	344	326	375	361	612	1451	1123	841	1321	1417
ENSMUSG00000023272	chr15	Creld2	8.9E+07	8.9E+07	1364	1.431491472	3.8159928	2.227E-09	3.06002E-08	0.06098	1	93	79	113	108	184	709	274	309	419	421
ENSMUSG00000055296	chr4	Tmem245	5.7E+07	5.7E+07	17090	-0.99237113	5.037686907	2.258E-09	3.09837E-08	0.03069	-1	636	429	925	654	699	530	570	332	390	462
ENSMUSG00000042460	chr6	C1galt1	7844842	7845394	2452	-2.13160047	2.496575965	2.308E-09	3.16409E-08	0.12695	-1	125	147	157	147	89	33	89	33	26	35
ENSMUSG00000020464	chr11	Pnpt1	2.9E+07	2.9E+07	3516	-1.32611013	4.000879304	2.339E-09	3.20036E-08	0.05328	-1	359	276	426	360	281	224	274	139	123	189
ENSMUSG00000022359	chr15	Wdyhv1	5.8E+07	5.8E+07	1322	1.30845434	3.06840719	2.337E-09	3.20036E-08	0.04764	1	53	45	108	75	85	307	213	167	255	283
ENSMUSG00000047415	chr12	Gpr68	1E+08	1E+08	3505	3.954758202	-0.09022704	2.39E-09	3.26681E-08	0.28125	1	0	0	1	0	6	13	43	9	46	43
ENSMUSG00000025898	chr9	Cwf19l2	3404085	3404190	3953	-1.48495953	4.182246021	2.414E-09	3.293E-08	0.06752	-1	426	286	535	472	284	194	332	145	137	183
ENSMUSG00000044177	chr11	Wfikkn2	9.4E+07	9.4E+07	3827	-1.23195716	3.795975319	2.413E-09	3.293E-08	0.04529	-1	293	185	427	287	297	195	234	88	170	185
ENSMUSG00000044786	chr7	Zfp36	2.8E+07	2.8E+07	1792	1.372793144	4.472014282	2.44E-09	3.32641E-08	0.05838	1	144	122	181	203	292	635	415	566	836	793
ENSMUSG00000057551	chr9	Zfp317	2E+07	2E+07	1824	-2.15447646	2.86599448	2.485E-09	3.38368E-08	0.13356	-1	174	182	209	193	106	50	120	27	32	53
ENSMUSG00000049606	chr5	Zfp644	1.1E+08	1.1E+08	8803	-1.43925999	3.929082721	2.488E-09	3.38489E-08	0.06301	-1	328	289	435	358	237	193	269	113	122	160
ENSMUSG00000097415	chr7	AU020206	7.6E+07	7.6E+07	656	1.762594643	2.177470502	2.492E-09	3.38677E-08	0.08137	1	33	18	23	27	50	184	119	87	117	200
ENSMUSG00000038112	chr9	AW551984	4E+07	4E+07	6082	2.071129383	2.001392393	2.495E-09	3.38704E-08	0.10939	1	15	28	18	24	22	195	79	124	99	140
ENSMUSG00000025262	chrX	Fam120c	1.5E+08	1.5E+08	5823	-2.38643724	2.699537912	2.511E-09	3.40599E-08	0.16156	-1	181	115	222	212	81	29	101	28	35	23
ENSMUSG00000064246	chr1	Chil1	1.3E+08	1.3E+08	2804	2.890008955	0.562792177	2.545E-09	3.44949E-08	0.16858	1	6	3	5	4	5	115	26	21	48	39
ENSMUSG00000024621	chr18	Csf1r	6.1E+07	6.1E+07	4885	1.771808076	6.144030289	2.56E-09	3.45882E-08	0.09875	1	333	406	287	345	1068	3158	2094	1539	2420	2229
ENSMUSG00000037872	chr1	Ackr1	1.7E+08	1.7E+08	1405	1.860812286	2.630498257	2.556E-09	3.45882E-08	0.09711	1	31	26	23	39	80	240	128	156	219	233
ENSMUSG00000057762	chr13	Gm6169	9.7E+07	9.7E+07	1060	1.770053306	1.812381177	2.559E-09	3.45882E-08	0.07743	1	27	17	22	14	35	117	85	92	134	104
ENSMUSG00000025932	chr1	Eya1	1.4E+07	1.4E+07	7808	-1.22508486	4.397698307	2.567E-09	3.46517E-08	0.04662	-1	462	371	505	439	414	272	408	180	209	245
ENSMUSG00000047557	chr3	Lxn	6.7E+07	6.7E+07	1508	1.848254923	1.48670646	2.599E-09	3.50576E-08	0.08013	1	19	10	22	12	25	117	61	58	112	84
ENSMUSG00000022307	chr15	Oxr1	4.1E+07	4.1E+07	5165	-1.23835559	5.644872357	2.616E-09	3.52505E-08	0.04924	-1	1151	828	1191	1028	1049	661	973	369	554	571
ENSMUSG00000041959	chr3	S100a10	9.4E+07	9.4E+07	1212	1.639140845	5.802341837	2.63E-09	3.54081E-08	0.08512	1	345	252	341	281	893	2805	1299	1322	1749	1641
ENSMUSG00000023905	chr17	Tnfrsf12a	2.4E+07	2.4E+07	963	2.004514062	5.866453363	2.634E-09	3.54213E-08	0.12466	1	142	192	371	647	440	2245	918	1876	2314	2105
ENSMUSG00000061755	chr5	Bod1l	4.2E+07	4.2E+07	10389	-1.08786817	4.657455985	2.681E-09	3.60134E-08	0.03699	-1	511	401	645	568	440	395	445	224	308	313
ENSMUSG00000072214	chr16	Sept5	1.9E+07	1.9E+07	2127	1.521630837	3.303394392	2.695E-09	3.61692E-08	0.06751	1	47	60	71	69	137	455	241	227	307	274
ENSMUSG00000028634	chr4	Hivep3	1.2E+08	1.2E+08	17427	1.833806067	2.317333787	2.777E-09	3.72351E-08	0.09352	1	29	11	64	17	48	181	157	127	132	182
ENSMUSG00000050310	chr15	Rictor	6708381	6708451	9311	-1.4352345	3.880183067	2.829E-09	3.78919E-08	0.0631	-1	402	316	305	288	241	196	218	104	159	154
ENSMUSG00000027499	chr3	Pkia	7366669	7366752	3721	-1.52639728	8.753442512	2.834E-09	3.79258E-08	0.07544	-1	11623	7753	11506	9906	6528	4559	7046	3520	3999	3922
ENSMUSG00000039883	chr5	Lrrc17	2.2E+07	2.2E+07	2186	2.03610906	2.998949548	2.851E-09	3.81232E-08	0.11961	1	46	38	25	30	92	479	181	198	271	192
ENSMUSG00000021245	chr12	Mlh3	8.5E+07	8.5E+07	5446	-1.30226177	3.91630516	2.863E-09	3.82447E-08	0.05183	-1	349	305	345	280	296	226	253	102	167	168
ENSMUSG00000021738	chr14	Atxn7	1.4E+07	1.4E+07	6847	-1.17395008	4.216018308	2.882E-09	3.84614E-08	0.04266	-1	338	326	513	424	320	257	305	153	214	260
ENSMUSG00000044224	chr15	Dnajc21	1E+07	1E+07	4777	-1.26426914	5.813260914	2.894E-09	3.85891E-08	0.0517	-1	1131	849	1577	1260	1205	731	1125	432	547	631
ENSMUSG00000052144	chr6	Ppp4r2	1E+08	1E+08	3641	-1.23126918	5.210213979	2.903E-09	3.86696E-08	0.04854	-1	845	703	826	769	669	517	659	352	368	398
ENSMUSG00000001687	chr5	Ubl3	1.5E+08	1.5E+08	2668	-1.40655581	6.568851383	2.922E-09	3.88828E-08	0.06415	-1	2200	2098	1974	1948	1775	1111	1576	789	953	973
ENSMUSG00000022285	chr15	Ywhaz	3.7E+07	3.7E+07	3999	1.21835605	6.28578904	2.933E-09	3.8989E-08	0.04828	1	538	507	819	600	1147	2758	1976	1874	2169	2466
ENSMUSG00000049164	chr19	Zfp518a	4.1E+07	4.1E+07	6840	-1.73824144	2.859236575	2.951E-09	3.91995E-08	0.0881	-1	159	125	243	178	134	70	129	45	41	63
ENSMUSG00000027994	chr3	Ccdc109b	1.3E+08	1.3E+08	1318	2.096749273	1.555627087	2.955E-09	3.92161E-08	0.01116	1	8	9	14	12	39	135	80	61	105	91
ENSMUSG00000027514	chr2	Zbp1	1.7E+08	1.7E+08	3529	3.015158946	1.334906922	2.984E-09	3.95483E-08	0.22186	1	1	7	6	7	18	214	59	33	64	84
ENSMUSG00000031887	chr8	Tradd	1.1E+08	1.1E+08	1866	1.548244448	2.615626674	2.986E-09	3.95483E-08	0.06637	1	32	31	53	40	79	244	135	137	221	188
ENSMUSG00000026977	chr2	March7	6E+07	6E+07	10391	-1.11776731	4.454531137	3.056E-09	4.04419E-08	0.03903	-1	465	351	591	436	407	331	388	214	229	273
ENSMUSG00000064280	chr5	Ccdc146	2.1E+07	2.1E+07	4366	-1.89440065	2.420684126	3.08E-09	4.07131E-08	0.10127	-1	131	112	111	138	125	48	81	45	33	24
ENSMUSG00000030427	chr7	Lilra6	3908280	3908822	2896	2.450033981	1.664993099	3.113E-09	4.11181E-08	0.15397	1	10	11	3	12	34	167	87	64	92	125
ENSMUSG00000015214	chrX	Mtmr1	7.1E+07	7.1E+07	5859	-1.12910828	4.86971	3.174E-09	4.18796E-08	0.04059	-1	625	400	837	656	523	410	536	262	320	382

ENSMUSG00000037270	chr3	4932438A13Rik	3.7E+07	3.7E+07	26985	-1.33992769	5.363516626	3.178E-09	4.18796E-08	0.05793	-1	881	713	1183	1027	587	632	684	308	389	440
ENSMUSG00000041702	chr12	Btbd7	1E+08	1E+08	4298	-2.20188095	3.114724141	3.18E-09	4.18796E-08	0.14323	-1	239	180	274	238	116	55	151	35	41	43
ENSMUSG00000017754	chr2	Pltp	1.6E+08	1.6E+08	2562	1.895799289	6.312885712	3.184E-09	4.18922E-08	0.1138	1	321	296	419	306	1334	3142	2165	1767	3014	2949
ENSMUSG00000026832	chr2	Cytip	5.8E+07	5.8E+07	6744	2.433283038	0.397168569	3.213E-09	4.22348E-08	0.10863	1	5	6	5	2	9	62	31	37	29	44
ENSMUSG00000037306	chr4	Man1c1	1.3E+08	1.3E+08	5722	1.198146732	3.834362127	3.236E-09	4.2493E-08	0.04274	1	104	113	126	115	187	584	409	286	386	394
ENSMUSG00000040616	chr4	Tmem51	1.4E+08	1.4E+08	1875	1.86292412	1.515109009	3.242E-09	4.25414E-08	0.08418	1	14	9	17	16	34	113	71	84	75	92
ENSMUSG00000036459	chr7	Wtip	3.4E+07	3.4E+07	2233	1.476357622	3.114066038	3.247E-09	4.25566E-08	0.06353	1	58	44	83	44	120	349	200	198	276	277
ENSMUSG00000039477	chr5	Tnrc18	1.4E+08	1.4E+08	6880	-1.81559209	3.457309499	3.262E-09	4.2721E-08	0.10004	-1	254	259	278	249	206	122	200	51	80	62
ENSMUSG00000051212	chr14	Gpr183	1.2E+08	1.2E+08	2942	2.202082829	1.308093336	3.294E-09	4.31026E-08	0.11301	1	14	16	8	6	16	123	82	65	69	56
ENSMUSG00000059791	chr17	Nrm	3.6E+07	3.6E+07	1466	2.071129853	1.473539702	3.309E-09	4.32587E-08	0.1079	1	8	7	14	18	31	122	59	60	113	87
ENSMUSG00000038844	chr2	Kif16b	1.4E+08	1.4E+08	6635	-1.64278165	5.129853444	3.341E-09	4.36352E-08	0.08618	-1	767	482	1317	865	648	296	713	188	335	254
ENSMUSG00000005611	chr7	Mrvi1	1.1E+08	1.1E+08	6827	1.22201376	3.587399331	3.35E-09	4.37111E-08	0.04401	1	91	84	148	95	124	330	426	276	398	280
ENSMUSG00000016262	chr1	Sertad4	1.9E+08	1.9E+08	3850	1.374547708	3.24203914	3.401E-09	4.4337E-08	0.0541	1	75	80	69	73	83	334	269	250	252	273
ENSMUSG00000030830	chr7	Itgal	1.3E+08	1.3E+08	6380	2.38366996	1.286333447	3.417E-09	4.45037E-08	0.14312	1	9	1	13	9	26	92	83	41	67	119
ENSMUSG00000040314	chr14	Ctsg	5.6E+07	5.6E+07	1002	2.959786444	0.067393432	3.445E-09	4.48228E-08	0.14963	1	1	3	2	4	5	53	14	34	34	28
ENSMUSG00000041650	chr14	Pcca	1.2E+08	1.2E+08	5210	-1.05037711	5.528740677	3.507E-09	4.55919E-08	0.03588	-1	865	535	1270	944	1209	688	777	440	625	596
ENSMUSG00000029373	chr5	Pf4	9.1E+07	9.1E+07	586	2.078828352	4.38875668	3.517E-09	4.56766E-08	0.13237	1	97	122	54	64	256	1148	483	572	762	533
ENSMUSG00000020593	chr12	Lpin1	1.7E+07	1.7E+07	5725	-1.45389007	7.898375362	3.57E-09	4.6315E-08	0.06951	-1	3570	4105	7192	6978	4554	2417	4027	1747	2389	2719
ENSMUSG00000036334	chr3	Igsf10	5.9E+07	5.9E+07	10150	1.44280294	3.793256099	3.616E-09	4.68689E-08	0.06315	1	113	98	77	94	166	680	408	295	357	368
ENSMUSG00000020914	chr11	Top2a	9.9E+07	9.9E+07	9013	2.56779374	1.175702675	3.648E-09	4.72482E-08	0.16527	1	4	2	9	8	25	120	51	71	77	51
ENSMUSG00000046718	chr8	Bst2	7.2E+07	7.2E+07	764	1.96065718	4.236470437	3.689E-09	4.77262E-08	0.1189	1	111	76	104	60	241	1330	373	344	653	492
ENSMUSG00000063160	chr7	Numbl	2.7E+07	2.7E+07	8673	1.368335475	3.190687257	3.729E-09	4.81627E-08	0.05433	1	63	67	81	53	115	339	230	189	310	279
ENSMUSG00000079547	chr17	H2-DMb1	3.4E+07	3.4E+07	1485	2.52590577	2.932805965	3.727E-09	4.81627E-08	0.18285	1	31	26	18	16	77	556	128	170	159	341
ENSMUSG00000013089	chr16	Etv5	2.2E+07	2.2E+07	4103	0.983719087	4.30307849	3.746E-09	4.83362E-08	0.02968	1	174	131	284	208	212	617	568	408	573	533
ENSMUSG00000010358	chr11	Ifi35	1E+08	1E+08	1727	1.094890221	4.570849357	3.782E-09	4.87525E-08	0.0379	1	182	154	272	178	381	879	674	472	641	697
ENSMUSG00000035569	chr8	Ankrd11	1.2E+08	1.2E+08	11637	-1.30375756	6.07619116	3.831E-09	4.93483E-08	0.05595	-1	1412	992	2136	1624	1119	843	1174	533	693	820
ENSMUSG00000040204	chr9	2810417H13Rik	6.6E+07	6.6E+07	4813	3.300267382	-0.43459998	3.867E-09	4.97646E-08	0.16088	1	2	0	3	0	3	42	20	17	24	10
ENSMUSG00000078970	chr11	Wdr92	1.7E+07	1.7E+07	2497	-1.37223513	5.130536133	4.005E-09	5.14849E-08	0.06127	-1	826	638	906	699	685	469	707	272	322	275
ENSMUSG00000041235	chr4	Chd7	8690406	8690775	13786	-1.26948292	4.954143064	4.024E-09	5.16824E-08	0.05232	-1	505	539	814	880	530	389	562	233	350	367
ENSMUSG00000018927	chr11	Ccl6	8.4E+07	8.4E+07	1795	2.477868322	5.215859911	4.042E-09	5.18719E-08	0.18766	1	135	138	55	74	463	2205	884	1156	1120	1146
ENSMUSG00000036155	chr1	Mgat5	1.3E+08	1.3E+08	10291	1.443293312	2.551718591	4.352E-09	5.57809E-08	0.05736	1	34	34	45	47	74	223	176	111	157	208
ENSMUSG00000039496	chr2	Cdnf	3513030	3513096	3111	-1.49236869	5.504274878	4.355E-09	5.57809E-08	0.07296	-1	1127	750	1373	1130	615	481	820	290	421	486
ENSMUSG00000046785	chr9	Epm2aip1	1.1E+08	1.1E+08	7169	-1.25426404	5.708292371	4.361E-09	5.58038E-08	0.05199	-1	1184	911	1373	1123	882	705	915	496	550	535
ENSMUSG00000044629	chr11	Cnrip1	1.7E+07	1.7E+07	4003	1.477424788	2.312093365	4.37E-09	5.58746E-08	0.05811	1	33	28	37	31	65	195	145	104	145	150
ENSMUSG00000010461	chr10	Eya4	2.3E+07	2.3E+07	4192	-1.88293947	3.780118615	4.448E-09	5.68173E-08	0.11029	-1	399	337	367	253	204	131	238	80	80	85
ENSMUSG00000021775	chr14	Nr1d2	1.8E+07	1.8E+07	5001	-1.30524084	6.228534381	4.506E-09	5.75099E-08	0.05665	-1	1910	982	2214	1630	1376	977	1219	728	648	894
ENSMUSG00000052397	chr17	Ezr	6738041	6739467	3290	1.635387571	3.025948887	4.535E-09	5.78293E-08	0.08097	1	43	23	98	41	107	323	251	185	202	299
ENSMUSG00000027962	chr3	Vcam1	1.2E+08	1.2E+08	3398	1.563022888	3.443293315	4.69E-09	5.97432E-08	0.07419	1	82	68	63	73	119	559	206	242	302	371
ENSMUSG00000039153	chr17	Runx2	4.4E+07	4.4E+07	8837	2.06697742	1.250330243	4.7E-09	5.98215E-08	0.10034	1	18	10	18	7	11	94	51	47	75	107
ENSMUSG00000026355	chr1	Mcm6	1.3E+08	1.3E+08	4666	2.036368089	1.23042076	4.717E-09	5.9985E-08	0.09878	1	12	9	16	10	18	142	66	42	72	52
ENSMUSG00000055172	chr6	C1ra	1.2E+08	1.2E+08	2751	1.594027513	5.445549849	4.803E-09	6.10187E-08	0.08297	1	292	283	212	228	611	2168	973	968	1383	1352
ENSMUSG00000071748	chrX	Gm14698	6.9E+07	6.9E+07	4226	-2.30368336	1.208882414	4.841E-09	6.14448E-08	0.13592	-1	73	63	53	40	45	22	27	12	8	11
ENSMUSG00000033671	chr1	Cep350	1.6E+08	1.6E+08	16487	-1.08220914	5.00407281	4.91E-09	6.22672E-08	0.03836	-1	648	520	811	739	530	456	542	298	441	401
ENSMUSG00000059897	chr8	Zfp930	6.9E+07	6.9E+07	1323	-2.90087395	0.853655589	4.979E-09	6.30909E-08	0.20917	-1	46	43	72	52	19	9	23	3	5	4
ENSMUSG00000034295	chr18	Fhod3	2.5E+07	2.5E+07	5408	-1.4607964	5.811329827	5.004E-09	6.33394E-08	0.07073	-1	1116	824	1932	1626	749	705	883	471	549	500
ENSMUSG00000060012	chr14	Kif13b	6.5E+07	6.5E+07	5603	-1.69261433	2.427213723	5.043E-09	6.37819E-08	0.08351	-1	132	120	135	102	111	69	86	27	40	45
ENSMUSG00000041075	chr1	Fzd7	5.9E+07	5.9E+07	4532	-1.28921867	5.546268175	5.08E-09	6.41905E-08	0.05527	-1	1262	871	990	838	903	568	813	379	553	513
ENSMUSG00000020899	chr11	Pfas	6.9E+07	6.9E+07	7933	-1.14539638	3.749989276	5.211E-09	6.57423E-08	0.04049	-1	281	227	311	249	316	203	217	130	129	188
ENSMUSG00000030068	chr6	Gm20696	9.9E+07	9.9E+07	3994	-1.50314558	2.818263811	5.217E-09	6.57423E-08	0.0672	-1	177	108	167	153	176	91	126	49	56	61
ENSMUSG00000031168	chrX	Ebp	8185329	8185833	2310	1.431807126	3.826447109	5.213E-09	6.57423E-08	0.06435	1	102	76	90	95	220	582	332	318	492	406
ENSMUSG00000052155	chr2	Acvr2a	4.9E+07	4.9E+07	5686	-1.2524886	4.968177028	5.278E-09	6.63945E-08	0.05174	-1	797	557	694	584	623	385	616	260	321	346
ENSMUSG00000099703	chr18	Gm28285	3.6E+07	3.6E+07	1264	-1.61602085	3.921167847	5.276E-09	6.63945E-08	0.08325	-1	344	294	509	312	245	189	287	84	114	114
ENSMUSG00000039168	chr15	Dap	3.1E+07	3.1E+07	1925	1.88070182	4.705414338	5.303E-09	6.66436E-08	0.11384	1	110	99	98	122	443	1131	611	648	935	908
ENSMUSG00000055022	chr15	Cntn1	9.2E+07	9.2E+07	9433	-3.30847206	-0.22576176	5.349E-09	6.71723E-08	0.21149	-1	17	35	14	26	12	5	0	3	4	3
ENSMUSG00000029311	chr5	Hsd17b11	1E+08	1E+08	3265	1.395954639	4.399117202	5.388E-09	6.75904E-08	0.06312	1	129	120	148	136	360	737	615	389	655	784
ENSMUSG00000070462	chr7	Mesdc1	8.4E+07	8.4E+07	4433	1.462726895	3.564504293	5.42E-09	6.78697E-08	0.06663	1	75	51	83	90	185	364	325	257	472	354
ENSMUSG00000090150	chr9	Acad11	1E+08	1E+08	9351	-1.27114547	6.364672251	5.415E-09	6.78697E-08	0.05444	-1	1671	1010	2670	2030	1590	1046	1443	693	860	989
ENSMUSG00000004360	chr10	9330159F19Rik	2.9E+07	2.9E+07	5644	-1.29463425	5.03629938	5.574E-09	6.9738E-08	0.05551	-1	858	530	825	713	534	371	625	280	345	351
ENSMUSG00000041488	chr19	Stx3	1.2E+07	1.2E+07	4979	1.47639144	2.158273502	5.633E-09	7.0417E-08	0.05814	1	25	24	50	32	44	150	132	86	119	175
ENSMUSG00000021180	chr12	Rps6ka5	1E+08	1E+08	4406	-1.90033416	2.869473433	5.718E-09	7.14225E-08	0.10957	-1	146	113	310	157	162	54	130	39	33	65
ENSMUSG00000023892	chr17	Zfp51	2.1E+07	2.1E+07	2600	-1.68459937	2.899770421	5.822E-09	7.26519E-08	0.08653	-1	198	152	187	180	113	85	121	42	60	63
ENSMUSG00000031540	chr8	Kat6a	2.3E+07	2.3E+07	9180	-1.13793789	4.928533422	5.847E-09	7.28966E-08	0.04285	-1	684	514	765	646	497	421	545	275	382	355
ENSMUSG00000035711	chr13	Dok3	5.6E+07	5.6E+07	1546	2.242833371	1.54193688	6.042E-09	7.52618E-08	0.13587	1	9	5	15	9	38	131	62	63	113	105
ENSMUSG00000005413	chr8	Hmox1	7.5E+07	7.5E+07	2161	1.617137276	4.189786701	6.098E-09	7.5824E-08	0.08423	1	89	98	134	72	302	625	504	528	562	567
ENSMUSG00000028525	chr4	Pde4b	1E+08	1E+08	10560	-1.43111731	5.879100729	6.093E-09	7.5824E-08	0.0688	-1	1310	1110	1351	1268	1328	657	1209	477	473	500
ENSMUSG00000027109	chr2	Sp3	7.3E+07	7.3E+07	4933	-1.18082274	4.419933379	6.148E-09	7.63767E-08	0.04554	-1	502	303	527	457	448	288	430	184	225	238
ENSMUSG00000028278	chr4	Rragd	3.3E+07	3.3E+07	5173	-1.33125968	7.972865882	6.155E-09	7.63997E-08	0.06049	-1	5897	4844	5400	5408	4842	3211	4314	1976	2609	2832

ENSMUSG00000024597	chr18	Slc12a2	5.8E+07	5.8E+07	6520	-1.27953242	6.21091317	6.179E-09	7.66266E-08	0.05549	-1	1446	1242	2012	1839	1315	785	1314	649	815	911
ENSMUSG00000047419	chr13	Cmya5	9.3E+07	9.3E+07	11850	-1.56358176	11.16950118	6.206E-09	7.68704E-08	0.08265	-1	50488	37822	66369	68070	34578	22301	39828	15260	22614	21762
ENSMUSG00000069892	chr11	9930111J21Rik2	4.9E+07	4.9E+07	7017	-2.49364411	0.103157251	6.209E-09	7.68704E-08	0.12871	-1	23	27	35	30	13	9	9	2	6	6
ENSMUSG00000068614	chr2	Actc1	1.1E+08	1.1E+08	1618	1.863815488	7.046976293	6.216E-09	7.68831E-08	0.11459	1	1217	860	657	758	558	4927	2954	4306	5877	2928
ENSMUSG00000024654	chr19	Asrgl1	9109868	9113208	4297	-1.15992549	5.849406285	6.238E-09	7.70914E-08	0.04557	-1	1197	1012	1378	1323	987	753	878	515	844	709
ENSMUSG00000070047	chr8	Fat1	4.5E+07	4.5E+07	15586	1.270995519	4.084425619	6.248E-09	7.71371E-08	0.05161	1	112	114	150	120	259	674	383	399	495	513
ENSMUSG00000056201	chr19	Cfl1	5490485	5490602	1148	1.605400237	7.008333169	6.262E-09	7.72006E-08	0.08653	1	675	586	917	701	2131	5238	2997	3296	4458	4012
ENSMUSG00000091712	chr16	Sec14l5	5147109	5147129	2337	-2.22374154	2.813679736	6.264E-09	7.72006E-08	0.14992	-1	201	173	172	176	114	42	124	26	36	33
ENSMUSG00000007039	chr17	Ddah2	3.5E+07	3.5E+07	1593	1.474963432	4.332321175	6.281E-09	7.73419E-08	0.07103	1	117	105	149	123	329	801	409	453	769	621
ENSMUSG00000023904	chr17	Hcfc1r1	2.4E+07	2.4E+07	958	1.208314341	7.229740381	6.311E-09	7.76517E-08	0.05	1	1284	839	1695	1389	1765	4906	3235	3639	4890	4837
ENSMUSG00000048852	chr11	Gm12185	4.9E+07	4.9E+07	5587	2.485700017	2.496940598	6.326E-09	7.77644E-08	0.17811	1	44	16	26	17	20	302	51	215	159	216
ENSMUSG00000099697	chr7	Gm4790	4E+07	4E+07	4345	-2.36955402	0.092809135	6.44E-09	7.9097E-08	0.11018	-1	26	26	29	26	18	8	11	2	8	5
ENSMUSG00000022525	chr16	Hrasls	2.9E+07	2.9E+07	3286	-1.14856953	5.634468805	6.468E-09	7.9301E-08	0.04461	-1	1107	732	1252	1024	1048	642	967	459	555	585
ENSMUSG00000084516	chr2	Mir1902	1E+08	1E+08	80	-2.0135987	3.464919747	6.466E-09	7.9301E-08	0.12726	-1	278	217	300	272	248	74	227	43	63	56
ENSMUSG00000058297	chr10	Spock2	6E+07	6E+07	5533	1.253548948	3.785440179	6.569E-09	8.04646E-08	0.04895	1	114	100	110	118	162	634	364	230	414	394
ENSMUSG00000028518	chr4	Prkaa2	1.1E+08	1.1E+08	7969	-1.40884214	7.739973668	6.613E-09	8.09268E-08	0.06773	-1	4966	3671	5873	4923	3738	2186	3954	1593	2317	2145
ENSMUSG00000040351	chr5	Ankib1	3690000	3693496	6610	-1.22297963	3.938011064	6.618E-09	8.09268E-08	0.04787	-1	319	279	376	325	290	202	286	124	184	161
ENSMUSG00000098470	chr6	C1rb	1.2E+08	1.2E+08	2429	1.981620603	2.541926356	6.668E-09	8.1473E-08	0.11541	1	29	27	19	23	76	288	129	157	160	203
ENSMUSG00000028656	chr4	Cap1	1.2E+08	1.2E+08	3494	1.199291808	5.996794297	6.705E-09	8.18521E-08	0.04886	1	499	449	563	472	964	2462	1672	1362	1773	1983
ENSMUSG00000025019	chr19	Lcor	4.1E+07	4.1E+07	7620	-2.32775871	1.927181338	6.747E-09	8.22138E-08	0.15603	-1	108	88	133	98	35	21	51	15	19	25
ENSMUSG00000055024	chr15	Ep300	8.2E+07	8.2E+07	13886	-1.33086799	5.27597954	6.742E-09	8.22138E-08	0.05958	-1	797	653	990	1015	675	376	761	291	408	459
ENSMUSG00000006728	chr10	Cdk4	1.3E+08	1.3E+08	3249	1.002148442	5.386579807	6.761E-09	8.2299E-08	0.03366	1	390	292	489	395	553	1350	997	974	1252	1150
ENSMUSG00000038028	chr6	9630033F20Rik	1.3E+08	1.3E+08	3651	-1.24111067	6.823825696	6.765E-09	8.2299E-08	0.05283	-1	2158	1803	3486	2117	2577	1572	2092	841	1389	1186
ENSMUSG00000046006	chr13	Gapt	1.1E+08	1.1E+08	2055	3.012044238	-0.48695051	6.821E-09	8.29073E-08	0.11077	1	2	2	1	1	3	34	17	14	16	25
ENSMUSG00000022383	chr15	Ppara	8.6E+07	8.6E+07	3836	-3.4186598	2.413427073	6.93E-09	8.41504E-08	0.32494	-1	144	29	309	183	112	13	59	2	12	11
ENSMUSG00000006575	chr11	Rundc3a	1E+08	1E+08	2941	3.023772665	-0.37616592	6.995E-09	8.48746E-08	0.1257	1	0	2	4	3	1	30	18	25	25	16
ENSMUSG00000022800	chr16	Fyttd1	3.3E+07	3.3E+07	6076	-1.23269093	6.23641155	7.028E-09	8.51965E-08	0.05198	-1	1557	1294	2102	1606	1356	1002	1334	723	775	830
ENSMUSG00000023845	chr17	Lnpep	1.8E+07	1.8E+07	5181	-1.90151265	3.821079569	7.267E-09	8.80224E-08	0.11586	-1	380	247	517	354	170	137	246	80	69	94
ENSMUSG00000058925	chr18	1700011I03Rik	5.8E+07	5.8E+07	1352	2.808020784	-0.33410896	7.332E-09	8.87325E-08	0.10973	1	4	1	6	0	1	24	23	20	24	26
ENSMUSG00000014303	chr16	Glis2	4594713	4594935	4373	1.271475738	3.480984555	7.38E-09	8.92383E-08	0.05017	1	81	66	106	86	157	462	254	256	328	319
ENSMUSG00000037646	chr15	Vps13b	3.5E+07	3.5E+07	13370	-1.22206022	3.875406829	7.406E-09	8.94712E-08	0.048	-1	288	253	346	369	267	231	243	112	143	194
ENSMUSG00000030031	chr6	Kbtbd8	9.5E+07	9.5E+07	5021	-1.95003341	1.44631464	7.511E-09	9.06664E-08	0.10122	-1	80	54	81	62	38	21	35	16	22	20
ENSMUSG00000025875	chr13	Tspan17	5.5E+07	5.5E+07	1657	1.351598171	4.46326656	7.533E-09	9.08464E-08	0.06047	1	155	130	176	125	368	858	562	456	795	613
ENSMUSG00000015127	chr17	Unkl	2.5E+07	2.5E+07	5673	-2.5234369	0.709045664	7.65E-09	9.21847E-08	0.16094	-1	38	41	56	39	27	10	22	1	10	7
ENSMUSG00000018821	chr19	Avpi1	4.2E+07	4.2E+07	1236	1.067191831	3.755357497	7.695E-09	9.24797E-08	0.03504	1	116	101	165	124	148	447	346	266	443	378
ENSMUSG00000025935	chr1	Tram1	1.4E+07	1.4E+07	3162	1.065624483	4.797971606	7.684E-09	9.24797E-08	0.0378	1	253	160	305	249	416	972	616	638	796	847
ENSMUSG00000029772	chr6	Ahcyl2	3E+07	3E+07	11896	-0.95761683	4.682182503	7.694E-09	9.24797E-08	0.03019	-1	486	322	606	487	698	468	440	253	338	322
ENSMUSG00000036256	chr5	Igfbp7	7.7E+07	7.7E+07	1213	1.283135219	6.702365145	7.849E-09	9.42518E-08	0.05675	1	743	663	1106	734	1419	4268	2274	2683	3352	2623
ENSMUSG00000046410	chr7	Kcnk6	2.9E+07	2.9E+07	4089	1.577008703	2.312429732	7.884E-09	9.45904E-08	0.07067	1	26	24	31	39	65	195	117	117	158	160
ENSMUSG00000092569	chr18	Gm20544	7.5E+07	7.5E+07	690	-2.04548315	0.881809171	7.983E-09	9.57047E-08	0.10248	-1	43	34	41	56	41	15	28	7	11	12
ENSMUSG00000027806	chr3	Tsc22d2	5.8E+07	5.8E+07	8829	-1.04391349	4.628050225	8.017E-09	9.60292E-08	0.03619	-1	487	396	563	541	499	345	478	231	299	325
ENSMUSG00000038506	chr8	Dcun1d2	1.3E+07	1.3E+07	3034	-1.35281143	6.577685485	8.061E-09	9.63825E-08	0.06303	-1	2147	1710	2494	2203	1631	1075	1782	752	1039	954
ENSMUSG00000081723	chr7	Gm15931	4274189	4274222	1852	2.541621753	0.356609674	8.058E-09	9.63825E-08	0.12129	1	6	6	5	2	5	59	51	14	44	36
ENSMUSG00000028986	chr5	Klhl7	2.4E+07	2.4E+07	3419	-1.30605991	5.243283481	8.24E-09	9.84447E-08	0.05806	-1	811	545	1107	983	627	412	750	287	406	421
ENSMUSG00000075602	chr15	Ly6a	7.5E+07	7.5E+07	1205	1.484831307	6.764140329	8.255E-09	9.85358E-08	0.07558	1	640	644	878	718	1515	6080	2385	2415	3105	2884
ENSMUSG00000057101	chr7	Zfp180	2.4E+07	2.4E+07	3886	-1.09073372	4.75391446	8.335E-09	9.94146E-08	0.03994	-1	524	493	648	531	527	401	510	247	339	298
ENSMUSG00000019139	chr8	Isyna1	7.1E+07	7.1E+07	1836	1.568354138	2.990114184	8.388E-09	9.9954E-08	0.07621	1	52	30	54	47	124	298	202	183	274	251
ENSMUSG00000005973	chr2	Rcn1	1.1E+08	1.1E+08	3196	1.276162847	4.41645527	8.762E-09	1.04328E-07	0.05405	1	214	139	188	137	258	1025	437	467	626	588
ENSMUSG00000074909	chr19	Ranbp6	3E+07	3E+07	4867	-1.13465396	3.947684636	8.783E-09	1.04482E-07	0.0416	-1	266	237	426	357	316	229	286	139	173	177
ENSMUSG00000062753	chr17	AI413582	2.8E+07	2.8E+07	1398	1.544599939	2.594671913	8.878E-09	1.05531E-07	0.06961	1	35	45	43	38	63	246	140	109	225	199
ENSMUSG00000055737	chr15	Ghr	3317760	3320722	9053	-1.26755701	7.182678717	8.913E-09	1.05858E-07	0.05604	-1	3413	2608	2767	2598	3865	1985	2414	1324	1583	1555
ENSMUSG00000033538	chr9	Casp4	5308828	5308914	3710	1.831540977	1.670883395	8.926E-09	1.0592E-07	0.09	1	18	12	21	15	36	173	89	72	69	94
ENSMUSG00000031897	chr8	Psmb10	1.1E+08	1.1E+08	1270	1.241586887	4.702950526	8.97E-09	1.06347E-07	0.05197	1	203	132	309	213	342	1218	496	467	767	899
ENSMUSG00000037685	chr5	Atp8a1	6.8E+07	6.8E+07	10962	-1.3433269	5.660174058	9.052E-09	1.07179E-07	0.0621	-1	1423	969	966	931	1002	715	836	405	593	440
ENSMUSG00000048747	chr4	E130114P18Rik	9.8E+07	9.8E+07	2046	2.142164321	0.321152841	9.055E-09	1.07179E-07	0.08599	1	4	3	7	5	12	53	31	28	36	39
ENSMUSG00000058056	chr8	Palld	6.2E+07	6.2E+07	8479	-1.44340187	4.782036217	9.167E-09	1.08418E-07	0.07064	-1	622	514	652	667	514	273	588	180	269	240
ENSMUSG00000076138	chr9	Gm26377	7.8E+07	7.8E+07	108	1.772529152	6.585277366	9.267E-09	1.09501E-07	0.10665	1	553	452	478	386	1502	4039	1996	2447	3065	3810
ENSMUSG00000026077	chr1	Npas2	3.9E+07	3.9E+07	4791	1.597485894	2.467136823	9.281E-09	1.09575E-07	0.0743	1	26	38	33	39	64	227	173	88	179	186
ENSMUSG00000026042	chr1	Col5a2	4.5E+07	4.5E+07	9591	1.28448034	6.577650524	9.293E-09	1.09628E-07	0.05737	1	693	631	922	687	1317	4515	3191	1962	2444	2145
ENSMUSG00000026222	chr1	Sp100	8.6E+07	8.6E+07	7556	1.234669475	4.332172463	9.453E-09	1.11418E-07	0.05059	1	138	155	213	125	277	873	490	347	599	655
ENSMUSG00000036655	chr12	Colec11	2.9E+07	2.9E+07	1383	2.05775254	0.466146582	9.507E-09	1.11964E-07	0.07963	1	6	5	9	6	10	60	37	26	49	36
ENSMUSG00000051235	chr12	Gen1	1.1E+07	1.1E+07	3283	-2.82417778	0.331895978	9.549E-09	1.12366E-07	0.18649	-1	45	25	27	48	10	9	6	4	8	4
ENSMUSG00000022788	chr16	Fgd4	1.6E+07	1.6E+07	17517	-1.29710032	3.859773117	9.582E-09	1.12658E-07	0.05507	-1	350	262	415	251	256	189	257	123	135	168
ENSMUSG00000049130	chr7	C5ar1	1.6E+07	1.6E+07	2570	2.171877993	2.601461399	9.749E-09	1.1451E-07	0.14186	1	25	36	15	21	61	321	106	193	188	185
ENSMUSG00000078870	chr2	Gm14410	1.8E+08	1.8E+08	2398	-2.15565982	0.823234362	9.756E-09	1.1451E-07	0.11608	-1	38	33	53	58	28	19	22	7	11	7
ENSMUSG00000067924	chrX	Cxx1b	5.4E+07	5.4E+07	1232	1.147717645	4.920000054	9.862E-09	1.1566E-07	0.04483	1	281	172	291	238	463	845	698	686	995	1042
ENSMUSG00000020865	chr11	Abcc3	9.4E+07	9.4E+07	5698	2.137369361	1.065915622	9.924E-09	1.16288E-07	0.10842	1	11	12	5	5	20	70	58	51	71	75

ENSMUSG00000020386	chr11	Sar1b	5.2E+07	5.2E+07	1255	-1.47876129	8.135824654	9.953E-09	1.16331E-07	0.0762	-1	7019	5891	6179	5635	5506	2701	5150	1943	2776	2948
ENSMUSG00000028641	chr4	Lepre1	1.2E+08	1.2E+08	3846	1.079094745	3.963216279	9.952E-09	1.16331E-07	0.03725	1	142	104	171	139	201	564	351	342	501	415
ENSMUSG00000030168	chr6	Adipor2	1.2E+08	1.2E+08	5979	-1.12518581	7.516421147	9.95E-09	1.16331E-07	0.04476	-1	3698	2528	4181	3504	5288	2706	2888	1662	2411	2329
ENSMUSG00000030761	chr7	Myo7a	9.8E+07	9.8E+07	8524	1.557440623	2.065998259	9.998E-09	1.16768E-07	0.06757	1	18	21	34	34	50	182	120	82	128	120
ENSMUSG00000021339	chr13	Mrs2	2.5E+07	2.5E+07	2035	-1.64374468	3.513595586	1.01E-08	1.17894E-07	0.08788	-1	236	178	436	321	138	136	178	73	90	102
ENSMUSG00000045608	chr15	Dbx2	9.6E+07	9.6E+07	3460	3.800855758	-0.78536338	1.02E-08	1.1891E-07	0.18038	1	1	0	0	1	2	30	5	15	20	15
ENSMUSG00000000958	chr14	Slc7a7	5.4E+07	5.4E+07	2142	2.096573493	2.225609275	1.027E-08	1.19661E-07	0.13092	1	15	12	16	27	64	224	103	138	147	142
ENSMUSG00000051502	chr5	Ufsp1	1.4E+08	1.4E+08	1037	1.236771547	4.36381527	1.045E-08	1.21615E-07	0.05139	1	196	108	232	148	256	547	552	464	893	490
ENSMUSG00000015342	chrX	Xk	9272756	9273234	5076	-1.67055635	2.85988822	1.051E-08	1.2219E-07	0.08805	-1	173	161	160	184	122	94	114	34	58	67
ENSMUSG00000063130	chr13	Calml3	3802893	3804318	1426	3.752901126	-0.4289678	1.051E-08	1.2219E-07	0.25323	1	0	0	1	0	5	42	9	21	32	11
ENSMUSG00000041058	chr4	Wwp1	2E+07	2E+07	6453	-1.4906395	7.7299704	1.057E-08	1.22777E-07	0.0776	-1	4655	3272	6749	5474	3529	2155	4047	1512	1994	1935
ENSMUSG00000051984	chr19	Sec31b	4.5E+07	4.5E+07	3950	-1.48035283	5.601433395	1.064E-08	1.23426E-07	0.07576	-1	986	743	1596	1317	771	448	920	287	577	456
ENSMUSG00000024399	chr17	Ltb	3.5E+07	3.5E+07	1516	2.496882361	0.63232952	1.083E-08	1.25567E-07	0.14401	1	5	3	6	5	13	57	23	32	49	85
ENSMUSG00000025610	chr16	Map3k7cl	8.8E+07	8.8E+07	1652	1.652811465	4.785347416	1.089E-08	1.26107E-07	0.0923	1	357	150	182	137	138	825	879	713	1178	666
ENSMUSG00000074862	chr10	BC025920	8.2E+07	8.2E+07	3306	-1.45701163	2.734590097	1.097E-08	1.26952E-07	0.06544	-1	143	108	186	174	116	69	110	48	65	75
ENSMUSG00000032085	chr9	Tagln	4.6E+07	4.6E+07	1586	1.230438542	5.761710191	1.099E-08	1.27102E-07	0.05263	1	409	494	515	427	540	1931	1126	1266	1865	1641
ENSMUSG00000018451	chr11	6330403K07Rik	7.1E+07	7.1E+07	1494	1.257610381	3.554222689	1.108E-08	1.2797E-07	0.05011	1	106	86	94	93	132	468	250	238	379	371
ENSMUSG00000032253	chr9	Phip	8.3E+07	8.3E+07	33312	-1.19756558	4.167479672	1.109E-08	1.28023E-07	0.0481	-1	394	297	481	409	280	256	298	168	176	233
ENSMUSG00000074676	chr2	Foxs1	1.5E+08	1.5E+08	1311	1.661752095	2.145300677	1.11E-08	1.28051E-07	0.07901	1	26	19	26	37	48	184	86	99	160	145
ENSMUSG00000024228	chr17	Nudt12	5.9E+07	5.9E+07	4401	-1.45791266	2.592790961	1.122E-08	1.29317E-07	0.06451	-1	150	103	169	104	134	61	100	53	59	56
ENSMUSG00000078920	chr11	Ifi47	4.9E+07	4.9E+07	2317	2.22651404	2.589940252	1.125E-08	1.2959E-07	0.15206	1	35	18	37	20	48	522	131	74	158	172
ENSMUSG00000020521	chr11	Rnft1	8.6E+07	8.6E+07	4719	-1.18114264	5.085988712	1.146E-08	1.31857E-07	0.04835	-1	726	545	840	821	580	505	667	272	364	373
ENSMUSG00000026491	chr1	Ahctf1	1.8E+08	1.8E+08	15116	-1.09847023	5.000779516	1.157E-08	1.33011E-07	0.04163	-1	651	542	731	655	673	508	606	336	330	333
ENSMUSG00000096727	chr17	Psmb9	3.4E+07	3.4E+07	3659	2.056405849	3.782677188	1.16E-08	1.33205E-07	0.13797	1	66	42	62	66	176	1001	206	250	390	509
ENSMUSG00000035933	chr12	Cog5	3.2E+07	3.2E+07	2997	-1.58709971	2.692347281	1.183E-08	1.3581E-07	0.07875	-1	155	103	204	167	95	83	102	43	53	55
ENSMUSG00000033186	chr14	Mzt1	9.9E+07	9.9E+07	2256	-1.1664856	4.425015172	1.187E-08	1.35997E-07	0.04626	-1	510	331	501	437	442	255	428	183	269	240
ENSMUSG00000052270	chr17	Fpr2	1.8E+07	1.8E+07	1296	3.264613343	-0.42855752	1.186E-08	1.35997E-07	0.1636	1	0	2	3	2	1	48	14	14	23	15
ENSMUSG00000058099	chr15	Nfam1	8.3E+07	8.3E+07	3222	2.090858198	2.411060213	1.188E-08	1.36032E-07	0.13321	1	18	19	14	23	78	247	144	134	165	178
ENSMUSG00000004591	chr3	Pkn2	1.4E+08	1.4E+08	7420	-1.15051267	5.226119477	1.191E-08	1.36224E-07	0.04612	-1	774	615	899	867	690	548	738	295	436	423
ENSMUSG00000047454	chr12	Gphn	7.8E+07	7.8E+07	3397	-1.18391122	5.109722238	1.192E-08	1.36231E-07	0.04874	-1	773	582	821	774	606	489	677	252	390	412
ENSMUSG00000020847	chr11	Rph3al	7.6E+07	7.6E+07	3814	-1.33378817	3.381805099	1.212E-08	1.38467E-07	0.05752	-1	222	141	316	243	213	131	197	67	114	111
ENSMUSG00000020100	chr10	Slc29a3	6.1E+07	6.1E+07	5834	1.342179419	3.137469436	1.226E-08	1.39731E-07	0.05616	1	64	48	58	80	123	310	256	181	294	250
ENSMUSG00000038775	chr9	Vill	1.2E+08	1.2E+08	4409	2.137958026	1.400599127	1.226E-08	1.39731E-07	0.12061	1	17	13	9	6	23	123	60	43	98	102
ENSMUSG00000049091	chr7	Sephs2	1.3E+08	1.3E+08	1359	-1.05100864	4.674868348	1.225E-08	1.39731E-07	0.03778	-1	469	383	652	445	676	369	511	211	355	293
ENSMUSG00000001865	chr3	Cpa3	2E+07	2E+07	1517	2.421570408	3.940933067	1.234E-08	1.40439E-07	0.18646	1	50	112	37	64	66	1206	196	409	468	430
ENSMUSG00000022629	chr15	Kif21a	9.1E+07	9.1E+07	6475	-1.3256768	4.503423487	1.24E-08	1.41021E-07	0.06028	-1	390	285	830	586	416	261	434	177	239	236
ENSMUSG00000021374	chr13	Nup153	4.7E+07	4.7E+07	6914	-1.25778462	5.050533851	1.252E-08	1.42027E-07	0.05506	-1	706	554	895	783	547	424	670	274	304	368
ENSMUSG00000029925	chr6	Tbxas1	3.9E+07	3.9E+07	9094	2.45383882	2.313398728	1.251E-08	1.42027E-07	0.17915	1	9	27	6	18	49	263	123	115	138	212
ENSMUSG00000033502	chr3	Cdc14a	1.2E+08	1.2E+08	11335	-1.25158811	3.607217884	1.25E-08	1.42027E-07	0.05128	-1	288	156	380	237	249	172	211	89	120	162
ENSMUSG00000019843	chr10	Fyn	3.9E+07	3.9E+07	4363	1.119957157	4.210161861	1.263E-08	1.43252E-07	0.04193	1	142	127	193	152	273	735	434	345	528	597
ENSMUSG00000034342	chr9	Cbl	4.4E+07	4.4E+07	5083	-2.35324808	1.491190138	1.297E-08	1.46987E-07	0.15973	-1	66	77	91	63	43	19	44	9	13	11
ENSMUSG00000033200	chr17	Tpsg1	2.5E+07	2.5E+07	1389	3.311571485	-0.38557238	1.299E-08	1.47105E-07	0.1747	1	0	2	1	2	3	47	12	10	29	21
ENSMUSG00000037613	chr7	Tnfrsf23	1.4E+08	1.4E+08	3353	1.381918022	4.281311503	1.314E-08	1.48576E-07	0.06441	1	175	161	106	158	176	517	477	506	692	647
ENSMUSG00000037989	chr13	Wnk2	4.9E+07	4.9E+07	8481	-1.41254655	5.739327622	1.332E-08	1.50582E-07	0.07018	-1	924	860	1953	1224	977	477	990	355	695	527
ENSMUSG00000024695	chr19	Zfp91	1.3E+07	1.3E+07	10046	-1.26525106	7.95533628	1.351E-08	1.52611E-07	0.05741	-1	5000	3859	7071	5890	4646	3033	4574	1999	2733	2891
ENSMUSG00000026096	chr1	Osgepl1	5.3E+07	5.3E+07	6147	-1.15586316	4.815731814	1.357E-08	1.53144E-07	0.04643	-1	617	429	740	619	512	367	577	228	323	328
ENSMUSG00000102869	chr2	RP24-114E18.7	1.6E+08	1.6E+08	1149	-2.17138825	4.173046026	1.368E-08	1.54278E-07	0.15619	-1	477	407	617	414	260	115	348	76	87	65
ENSMUSG00000020516	chr11	Rps6kb1	8.6E+07	8.7E+07	8658	-1.12807761	4.887831213	1.371E-08	1.54419E-07	0.04433	-1	661	504	725	557	577	461	575	252	290	369
ENSMUSG00000039879	chr10	Heca	1.8E+07	1.8E+07	3667	-1.79689483	3.711943576	1.391E-08	1.5663E-07	0.10778	-1	287	270	385	307	261	133	259	78	53	92
ENSMUSG00000025777	chr1	Gdap1	1.7E+07	1.7E+07	7731	-2.27972451	3.415965405	1.394E-08	1.56843E-07	0.16883	-1	335	287	197	133	329	71	183	30	45	60
ENSMUSG00000078862	chr2	Gm14326	1.8E+08	1.8E+08	2863	-1.93144289	3.018516205	1.414E-08	1.58951E-07	0.12093	-1	229	158	240	222	92	100	113	54	41	43
ENSMUSG00000005362	chr6	Crbn	1.1E+08	1.1E+08	5179	-1.0675994	5.009695918	1.425E-08	1.6008E-07	0.03985	-1	718	494	754	681	611	475	620	288	352	437
ENSMUSG00000015659	chr17	Serac1	6042196	6044250	4576	-1.86776932	2.654821625	1.427E-08	1.60151E-07	0.1111	-1	151	134	189	144	110	45	119	29	50	40
ENSMUSG00000039087	chr13	Rreb1	3.8E+07	3.8E+07	13991	-1.14714366	4.665431346	1.438E-08	1.61209E-07	0.04563	-1	484	335	645	615	584	282	530	207	300	324
ENSMUSG00000045875	chr14	Adra1a	6.7E+07	6.7E+07	8144	-2.30071498	1.806654196	1.462E-08	1.638E-07	0.15756	-1	97	78	39	41	176	30	28	15	27	22
ENSMUSG00000049037	chr6	Clec4a1	1.2E+08	1.2E+08	1558	2.103151101	2.495088682	1.465E-08	1.63965E-07	0.13648	1	23	25	18	17	75	340	155	124	176	143
ENSMUSG00000057948	chr11	Unc13d	1.2E+08	1.2E+08	4679	2.406039215	0.755144847	1.478E-08	1.65301E-07	0.14091	1	10	3	5	4	15	78	28	51	43	65
ENSMUSG00000015647	chr2	Lama5	1.8E+08	1.8E+08	11388	-0.97855048	4.398786913	1.479E-08	1.65309E-07	0.03249	-1	326	325	572	386	524	399	300	198	312	274
ENSMUSG00000030681	chr7	Mvp	1.3E+08	1.3E+08	2902	1.260409806	6.11177966	1.489E-08	1.66289E-07	0.05676	1	424	275	1033	698	801	2320	2103	1560	1949	2156
ENSMUSG00000038970	chr5	Lmtk2	1.4E+08	1.4E+08	8114	-0.99514441	5.36956168	1.499E-08	1.67296E-07	0.03495	-1	848	576	1050	818	881	561	760	424	560	552
ENSMUSG00000021112	chr12	Mpp5	7.9E+07	7.9E+07	5512	-1.02962067	4.83194982	1.51E-08	1.68283E-07	0.03689	-1	524	459	868	508	533	459	491	280	318	400
ENSMUSG00000029821	chr6	Dfna5	5E+07	5E+07	7375	2.051194516	0.607550346	1.511E-08	1.68283E-07	0.09222	1	3	6	16	5	11	52	41	31	53	53
ENSMUSG00000024644	chr18	Cndp2	8.5E+07	8.5E+07	2119	1.144665524	5.285114477	1.513E-08	1.68412E-07	0.04621	1	284	266	399	277	641	1370	987	784	1274	1156
ENSMUSG00000039084	chr11	Chad	9.5E+07	9.5E+07	1680	1.678802704	4.819134393	1.515E-08	1.6855E-07	0.09745	1	177	135	308	213	190	1877	479	399	676	1201
ENSMUSG00000034981	chr5	Parm1	9.2E+07	9.2E+07	5068	-1.25921399	5.596211724	1.521E-08	1.69E-07	0.05637	-1	1083	989	800	859	1266	748	699	432	653	436
ENSMUSG00000036745	chr3	Ttll7	1.5E+08	1.5E+08	8105	-1.66295146	6.583322822	1.529E-08	1.69747E-07	0.09745	-1	2272	1862	2558	1522	2738	880	2025	510	662	788
ENSMUSG00000103888	chr1	AC123072.1	3.4E+07	3.4E+07	23154	-1.91019964	8.239421231	1.556E-08	1.72654E-07	0.12711	-1	6752	4237	12458	9208	3953	2408	5510	1438	1992	2063

ENSMUSG00000034910	chr9	Pygo1	7.3E+07	7.3E+07	7916	-1.23155458	4.689915092	1.568E-08	1.73801E-07	0.05303	-1	555	363	787	628	405	303	494	218	272	315
ENSMUSG00000050288	chr11	Fzd2	1E+08	1E+08	3663	1.309687288	2.83040528	1.577E-08	1.74685E-07	0.05235	1	45	43	75	75	66	237	174	181	222	204
ENSMUSG00000047888	chr15	Tnrc6b	8.1E+07	8.1E+07	17327	-1.32515374	5.408079974	1.6E-08	1.77158E-07	0.06241	-1	870	813	1063	1063	657	505	780	299	397	560
ENSMUSG00000069662	chr10	Marcks	3.7E+07	3.7E+07	4048	1.470132785	6.80630072	1.607E-08	1.7771E-07	0.07718	1	840	619	769	628	1706	5184	2427	2754	3412	3306
ENSMUSG00000042810	chr6	Krba1	4.8E+07	4.8E+07	9314	-0.95169271	5.085498494	1.613E-08	1.78324E-07	0.03182	-1	708	570	712	631	701	551	553	316	480	513
ENSMUSG00000040430	chr11	Pitpnc1	1.1E+08	1.1E+08	6612	-1.3282299	6.455464856	1.663E-08	1.83649E-07	0.06347	-1	2065	1199	2750	2088	1428	1030	1587	694	849	1056
ENSMUSG00000006134	chr16	Crkl	1.7E+07	1.7E+07	3863	-1.22083247	4.713301632	1.695E-08	1.87105E-07	0.05241	-1	522	431	736	592	473	346	546	226	278	245
ENSMUSG00000022358	chr15	Fbxo32	5.8E+07	5.8E+07	6936	-1.40619112	8.472046366	1.701E-08	1.87608E-07	0.07149	-1	8597	6176	8684	9157	5458	5174	5910	2600	3285	3516
ENSMUSG00000028906	chr4	Epb4.1	1.3E+08	1.3E+08	8809	-1.2284175	6.634995348	1.71E-08	1.88443E-07	0.05465	-1	2069	1737	2411	2369	1748	1200	1747	843	1271	1123
ENSMUSG00000025355	chr10	Mmp19	1.3E+08	1.3E+08	3410	2.5541912	4.389608602	1.771E-08	1.94949E-07	0.21395	1	73	59	28	27	289	876	769	455	771	851
ENSMUSG00000046491	chr11	C1qtnf2	4.3E+07	4.3E+07	1308	1.800856499	3.007658628	1.782E-08	1.96009E-07	0.10482	1	63	46	38	30	85	364	135	201	240	330
ENSMUSG00000046731	chr11	Kctd11	7E+07	7E+07	3146	1.440529326	2.953405139	1.804E-08	1.98288E-07	0.06617	1	45	44	68	50	108	287	171	184	290	214
ENSMUSG00000026822	chr2	Lcn2	3.2E+07	3.2E+07	2623	2.210432928	0.832120406	1.811E-08	1.98904E-07	0.11619	1	4	9	9	8	13	110	47	30	48	49
ENSMUSG00000044968	chr5	Napepld	2.2E+07	2.2E+07	3956	-1.11567442	4.161875433	1.853E-08	2.03357E-07	0.04295	-1	326	283	439	439	347	249	340	148	210	232
ENSMUSG00000078779	chr7	Zfp59	2.8E+07	2.8E+07	1962	-2.25433711	0.461924968	1.864E-08	2.04385E-07	0.11969	-1	38	25	41	33	27	7	21	7	6	6
ENSMUSG00000025423	chr18	Pias2	7.7E+07	7.7E+07	5433	-1.00637919	5.399563968	1.882E-08	2.06173E-07	0.03633	-1	826	687	999	838	867	637	778	418	549	533
ENSMUSG00000090290	chr8	Gm17296	1.3E+08	1.3E+08	5060	-2.34283257	2.258109296	1.884E-08	2.06256E-07	0.17326	-1	132	91	148	166	50	24	72	14	35	20
ENSMUSG00000022197	chr15	Pdzd2	1.2E+07	1.2E+07	21645	-0.96249062	5.058123844	1.9E-08	2.07921E-07	0.03286	-1	637	443	762	623	898	570	583	309	368	534
ENSMUSG00000034390	chr8	Cmip	1.2E+08	1.2E+08	4732	1.21838201	4.266394616	1.939E-08	2.11801E-07	0.05177	1	117	105	199	151	327	617	484	433	572	654
ENSMUSG00000074203	chr8	G430095P16Rik	8.5E+07	8.5E+07	721	2.135991765	0.780584666	1.938E-08	2.11801E-07	0.10101	1	11	11	7	6	7	73	40	35	67	50
ENSMUSG00000014329	chr10	Bicc1	7.1E+07	7.1E+07	7441	1.267927169	4.757437444	1.978E-08	2.15851E-07	0.05667	1	223	219	189	187	357	1270	604	559	728	831
ENSMUSG00000028381	chr4	Ugcg	5.9E+07	5.9E+07	5212	1.186862864	4.15630977	2.006E-08	2.1881E-07	0.04879	1	151	104	177	125	277	561	428	473	458	591
ENSMUSG00000021871	chr14	Pnp	5.1E+07	5.1E+07	3085	1.168395477	4.265301309	2.021E-08	2.20244E-07	0.04757	1	138	107	207	159	304	808	459	452	482	544
ENSMUSG00000021760	chr13	Gpx8	1.1E+08	1.1E+08	1016	1.448668267	3.936054673	2.055E-08	2.23815E-07	0.07199	1	149	84	106	79	199	734	313	383	459	416
ENSMUSG00000035161	chr14	Ints6	6.3E+07	6.3E+07	4993	-1.46987162	2.6277635	2.06E-08	2.24173E-07	0.06842	-1	139	102	184	135	119	81	100	58	50	47
ENSMUSG00000027177	chr2	Hipk3	1E+08	1E+08	7987	-1.26127491	8.168385947	2.116E-08	2.30082E-07	0.05867	-1	6334	4773	7647	6285	5345	3385	5351	2477	3134	3267
ENSMUSG00000034664	chr11	Itga2b	1E+08	1E+08	5454	1.893034521	1.457879739	2.118E-08	2.30082E-07	0.09883	1	10	13	22	13	26	143	49	59	87	90
ENSMUSG00000033207	chr19	Mamdc2	2.3E+07	2.3E+07	3338	1.614141336	2.936655879	2.13E-08	2.31262E-07	0.08416	1	26	51	48	64	89	278	264	115	256	281
ENSMUSG00000038859	chr5	Baiap2l1	1.4E+08	1.4E+08	3366	2.926605526	0.811744532	2.15E-08	2.33181E-07	0.23232	1	2	0	22	4	2	67	56	50	50	67
ENSMUSG00000042851	chr2	Zc3h6	1.3E+08	1.3E+08	5668	-1.85547826	2.714030734	2.154E-08	2.3343E-07	0.11389	-1	172	102	217	161	122	56	123	20	45	57
ENSMUSG00000092907	chrX	Mir5132	7.4E+07	7.4E+07	71	-2.67882681	-0.10239445	2.157E-08	2.33633E-07	0.15584	-1	22	22	34	19	16	3	13	3	4	1
ENSMUSG00000026728	chr2	Vim	1.4E+07	1.4E+07	4743	1.668785378	8.377774247	2.161E-08	2.33826E-07	0.10058	1	1633	1570	1976	1577	5750	14091	9447	7179	11670	10541
ENSMUSG00000020182	chr11	Ddc	1.2E+07	1.2E+07	4461	2.479256951	0.244925514	2.182E-08	2.35549E-07	0.11867	1	3	7	4	3	6	44	20	36	38	41
ENSMUSG00000020700	chr11	Map3k3	1.1E+08	1.1E+08	4023	-1.09369861	4.638096719	2.181E-08	2.35549E-07	0.0425	-1	438	421	652	540	490	347	507	215	315	273
ENSMUSG00000039478	chr8	Micu3	4E+07	4E+07	6153	-1.17227368	4.136215929	2.179E-08	2.35549E-07	0.04806	-1	411	340	344	349	333	233	296	152	212	229
ENSMUSG00000037111	chr3	Setd7	5.2E+07	5.2E+07	10813	-1.47026415	8.256396922	2.185E-08	2.35743E-07	0.07905	-1	8347	6452	6587	6059	5128	3282	5282	2323	3076	2932
ENSMUSG00000055228	chr13	Zfp935	6.2E+07	6.2E+07	1062	-2.30010631	0.212577498	2.201E-08	2.37259E-07	0.12501	-1	39	20	27	31	19	11	12	2	5	9
ENSMUSG00000036792	chr2	Mbd5	4.9E+07	4.9E+07	14221	-1.32380045	3.619498157	2.214E-08	2.38278E-07	0.05999	-1	277	240	295	291	180	166	196	91	137	142
ENSMUSG00000079465	chr1	Col4a3	8.3E+07	8.3E+07	9967	-2.44468887	0.32381552	2.214E-08	2.38278E-07	0.14432	-1	28	28	41	25	30	3	20	5	5	5
ENSMUSG00000034653	chr18	Ythdc2	4.5E+07	4.5E+07	6299	-1.99273461	2.300543122	2.222E-08	2.39009E-07	0.12754	-1	120	107	155	133	61	37	78	16	43	34
ENSMUSG00000028643	chr4	Ccdc23	1.2E+08	1.2E+08	1065	1.117813905	3.5620596	2.255E-08	2.4235E-07	0.04139	1	89	73	165	99	143	395	274	257	370	357
ENSMUSG00000025323	chr12	Sp4	1.2E+08	1.2E+08	5770	-1.98828319	2.43428954	2.263E-08	2.43018E-07	0.12818	-1	146	92	183	147	75	42	90	15	37	46
ENSMUSG00000026737	chr2	Pip4k2a	1.9E+07	1.9E+07	3477	1.295363608	3.677191743	2.275E-08	2.44187E-07	0.05669	1	112	85	87	86	183	545	331	268	356	379
ENSMUSG00000069184	chr13	Zfp72	7.4E+07	7.4E+07	1629	-2.45678535	0.424941327	2.277E-08	2.44192E-07	0.15217	-1	40	27	45	38	12	9	14	6	5	7
ENSMUSG00000005698	chr8	Ctcf	1.1E+08	1.1E+08	4860	-1.02206352	5.172229593	2.303E-08	2.46758E-07	0.03775	-1	758	545	855	784	674	524	690	347	467	445
ENSMUSG00000073155	chr6	1810058I24Rik	3.5E+07	3.5E+07	2784	1.049334007	6.288927938	2.31E-08	2.47361E-07	0.04058	1	717	517	974	874	783	2730	1957	1662	2245	2331
ENSMUSG00000019838	chr10	Slc16a10	4E+07	4E+07	5394	-1.04793692	5.118533675	2.321E-08	2.48218E-07	0.03972	-1	725	564	841	525	877	463	635	277	484	509
ENSMUSG00000095538	chr7	Gm21983	2.7E+07	2.7E+07	1690	1.539820557	3.431150441	2.322E-08	2.48218E-07	0.08054	1	55	57	83	59	169	439	219	240	391	356
ENSMUSG00000018672	chr11	Copz2	9.7E+07	9.7E+07	2208	1.00217557	5.03541696	2.328E-08	2.48693E-07	0.0359	1	306	242	345	328	425	1117	668	766	990	943
ENSMUSG00000017418	chr2	Arl5b	1.5E+07	1.5E+07	10428	-1.25205131	3.918904131	2.362E-08	2.52158E-07	0.05438	-1	321	253	395	363	252	204	285	135	148	156
ENSMUSG00000022033	chr14	Pbk	6.6E+07	6.6E+07	1791	5.34582639	-0.86964106	2.396E-08	2.55564E-07	0.37954	1	0	0	0	0	1	32	3	22	21	3
ENSMUSG00000043017	chr7	Ptgir	1.7E+07	1.7E+07	3334	1.347052472	2.530064971	2.401E-08	2.55869E-07	0.05477	1	47	34	43	48	68	210	143	143	178	158
ENSMUSG00000066735	chr5	Vkorc1l1	1.3E+08	1.3E+08	2972	-0.98344859	4.358868905	2.412E-08	2.56906E-07	0.03381	-1	377	330	482	397	459	333	380	212	263	241
ENSMUSG00000020256	chr10	Aldh1l2	8.3E+07	8.3E+07	7503	-1.9777087	3.016093156	2.419E-08	2.57436E-07	0.13039	-1	340	186	156	106	132	73	74	70	65	50
ENSMUSG00000038342	chr5	Mlxip	1.2E+08	1.2E+08	8206	-1.13973829	6.841028571	2.433E-08	2.58679E-07	0.04829	-1	2365	1866	2902	2629	2015	1517	1798	1072	1583	1451
ENSMUSG00000076444	chr4	Mir761	1.1E+08	1.1E+08	76	-2.70967848	-0.15047877	2.452E-08	2.60493E-07	0.15676	-1	35	12	29	20	14	6	10	1	4	2
ENSMUSG00000031229	chrX	Atrx	1.1E+08	1.1E+08	15190	-1.22573484	5.296661294	2.505E-08	2.65782E-07	0.0549	-1	886	720	923	886	635	473	757	319	434	472
ENSMUSG00000036565	chr5	Ttyh3	1.4E+08	1.4E+08	4650	1.173642862	3.977597004	2.504E-08	2.65782E-07	0.04732	1	125	114	156	101	236	599	386	317	510	444
ENSMUSG00000059493	chrX	Nhs	1.6E+08	1.6E+08	8805	-1.96486854	2.124876891	2.508E-08	2.65908E-07	0.12199	-1	114	134	61	62	120	36	44	27	39	37
ENSMUSG00000036676	chr10	Tmtc3	1E+08	1E+08	8939	-1.41557216	3.152705184	2.549E-08	2.70002E-07	0.06738	-1	232	166	228	175	150	118	145	75	71	93
ENSMUSG00000024073	chr17	Birc6	7.5E+07	7.5E+07	28830	-1.23235463	5.360876494	2.576E-08	2.72515E-07	0.05565	-1	687	611	1268	1076	741	541	808	311	409	505
ENSMUSG00000039704	chr15	Lmbrd2	9140621	9140740	3863	-3.53445994	2.205582934	2.576E-08	2.72515E-07	0.37014	-1	155	139	136	145	30	10	50	9	4	4
ENSMUSG00000028214	chr4	Gem	1.2E+07	1.2E+07	2104	1.417064716	2.253614445	2.603E-08	2.75153E-07	0.0598	1	32	29	56	24	52	156	162	102	118	160
ENSMUSG00000041328	chr7	Pcf11	9.3E+07	9.3E+07	6412	-1.17202192	3.806755985	2.611E-08	2.75815E-07	0.04753	-1	289	225	382	308	246	211	243	118	132	193
ENSMUSG00000044795	chr11	Cyb5d1	6.9E+07	6.9E+07	1605	-1.76408478	3.187008476	2.628E-08	2.77385E-07	0.10652	-1	237	186	241	229	136	112	162	53	56	53
ENSMUSG00000027562	chr3	Car2	1.5E+07	1.5E+07	2422	-1.49996522	3.262404105	2.651E-08	2.79577E-07	0.07705	-1	156	109	400	242	202	117	150	49	111	100
ENSMUSG00000021036	chr12	Sptlc2	8.7E+07	8.7E+07	8115	1.136509767	4.019275423	2.672E-08	2.81537E-07	0.04482	1	126	102	154	130	262	615	399	335	461	493

ENSMUSG00000023966	chr17	Rsph9	4.6E+07	4.6E+07	1602	2.113895949	0.38906036	2.677E-08	2.81694E-07	0.09387	1	5	4	9	6	9	58	23	30	44	41
ENSMUSG00000047213	chr3	Ythdf3	1.6E+07	1.6E+07	5363	-1.15224931	5.214763402	2.677E-08	2.81694E-07	0.04863	-1	743	614	1082	772	634	461	726	325	386	500
ENSMUSG00000025993	chr1	Slc40a1	4.6E+07	4.6E+07	9000	-1.66052892	5.049258461	2.707E-08	2.84618E-07	0.09957	-1	547	395	1669	813	552	316	614	212	278	243
ENSMUSG00000032011	chr9	Thy1	4.4E+07	4.4E+07	1735	1.460363547	5.200989156	2.725E-08	2.86282E-07	0.07759	1	266	198	202	249	583	1686	708	793	1245	1190
ENSMUSG00000021061	chr12	Sptb	7.7E+07	7.7E+07	12147	-1.35740115	7.769513438	2.771E-08	2.90912E-07	0.06873	-1	4521	3429	6372	5939	3305	2217	3690	1682	2610	2541
ENSMUSG00000019806	chr10	Aig1	1.4E+07	1.4E+07	9196	1.36400221	3.676756779	2.819E-08	2.95547E-07	0.06487	1	79	51	207	81	146	519	303	290	374	408
ENSMUSG00000081208	chr11	Gm11400	3149742	3150955	1214	2.184721076	1.74514525	2.819E-08	2.95547E-07	0.14444	1	22	8	13	12	33	141	57	59	101	191
ENSMUSG00000028030	chr3	Tbck	1.3E+08	1.3E+08	4108	-2.3331498	1.901322806	2.826E-08	2.95905E-07	0.17107	-1	99	67	134	114	49	21	60	19	12	15
ENSMUSG00000059423	chr4	Zfp933	1.5E+08	1.5E+08	4270	-1.57767939	2.400630381	2.827E-08	2.95905E-07	0.08057	-1	127	86	162	119	97	56	97	29	47	47
ENSMUSG00000018415	chr11	Gid4	6E+07	6E+07	4864	-1.28731742	6.830254253	2.85E-08	2.98059E-07	0.0619	-1	2845	2229	2088	2231	2391	1443	1934	955	1391	1164
ENSMUSG00000023009	chr15	Nckap5l	9.9E+07	9.9E+07	5002	1.511447349	2.378387201	2.852E-08	2.98059E-07	0.06987	1	34	37	42	33	50	146	115	114	185	209
ENSMUSG00000028539	chr4	Artn	1.2E+08	1.2E+08	2405	2.762108765	-0.44611038	2.857E-08	2.98148E-07	0.09865	1	1	3	3	2	2	23	19	13	27	25
ENSMUSG00000064109	chr7	Hcst	3E+07	3E+07	437	3.122710611	-0.11570531	2.856E-08	2.98148E-07	0.19867	1	1	1	1	0	9	21	23	20	27	52
ENSMUSG00000056234	chr14	Ncoa4	3.2E+07	3.2E+07	4452	-1.57708545	4.46307037	2.895E-08	3.01923E-07	0.08978	-1	495	387	628	504	463	237	499	130	156	146
ENSMUSG00000051236	chr10	Msrb3	1.2E+08	1.2E+08	4048	-1.23456726	7.453364914	2.904E-08	3.02422E-07	0.05728	-1	3992	3083	4121	3465	3625	2018	3250	1579	2010	1981
ENSMUSG00000054206	chr10	Gzmm	8E+07	8E+07	1472	-1.53416872	2.606515192	2.904E-08	3.02422E-07	0.07727	-1	137	108	166	132	131	67	117	42	55	43
ENSMUSG00000034205	chr14	Loxl2	7E+07	7E+07	5405	1.197875439	4.712244309	2.938E-08	3.05701E-07	0.05204	1	190	167	233	196	434	1125	591	610	775	673
ENSMUSG00000099364	chr1	5730419F03Rik	7.9E+07	7.9E+07	2092	2.384752536	1.004033101	2.953E-08	3.07045E-07	0.15946	1	3	2	25	11	6	92	46	43	63	80
ENSMUSG00000020476	chr11	Dbnl	5788488	5788642	2346	1.072534878	4.689353066	2.983E-08	3.09887E-07	0.0417	1	227	125	299	238	404	915	582	539	787	791
ENSMUSG00000006423	chrX	C330007P06Rik	3.7E+07	3.7E+07	7424	-1.11783899	3.901181182	3.039E-08	3.15488E-07	0.04364	-1	327	245	371	240	352	252	260	149	158	159
ENSMUSG00000070547	chr7	Mrgprb1	4.8E+07	4.8E+07	4185	2.447609403	0.890635467	3.083E-08	3.1985E-07	0.15263	1	5	11	9	7	6	129	37	47	45	43
ENSMUSG00000034641	chr11	Cd300ld	1.1E+08	1.1E+08	2645	2.126201403	2.172842888	3.115E-08	3.22909E-07	0.14238	1	19	23	12	11	57	249	141	89	126	143
ENSMUSG00000040044	chr4	Orc3	3.5E+07	3.5E+07	6088	-1.03598475	4.776524935	3.19E-08	3.30445E-07	0.0392	-1	611	472	628	521	493	465	481	253	322	356
ENSMUSG00000023004	chr15	Tuba1b	9.9E+07	9.9E+07	1875	1.773960499	6.086337872	3.206E-08	3.31822E-07	0.11504	1	306	265	350	308	1206	2868	1594	1960	2259	2097
ENSMUSG00000048677	chr7	Tpcn2	1.5E+08	1.5E+08	2909	2.398805077	2.113876099	3.214E-08	3.32394E-07	0.18457	1	15	6	15	7	64	162	117	108	159	177
ENSMUSG00000032014	chr9	Oaf	4.3E+07	4.3E+07	2388	1.369059678	4.073532209	3.216E-08	3.32437E-07	0.06678	1	118	92	143	93	278	709	362	419	502	498
ENSMUSG00000029238	chr5	Clock	7.6E+07	7.6E+07	7478	-1.24847774	5.078735964	3.238E-08	3.34433E-07	0.05769	-1	666	694	681	901	505	486	571	267	388	384
ENSMUSG00000049526	chr9	Tmem202	6E+07	6E+07	1255	2.330196661	0.174023972	3.251E-08	3.35487E-07	0.11714	1	2	3	13	1	6	47	30	22	34	38
ENSMUSG00000023921	chr17	Mut	4.1E+07	4.1E+07	3675	-1.08525143	6.332196063	3.302E-08	3.40517E-07	0.04449	-1	1739	1156	2020	1794	1541	1240	1354	823	911	1028
ENSMUSG00000029082	chr5	Bst1	4.4E+07	4.4E+07	2419	2.964634112	-0.53256146	3.345E-08	3.4475E-07	0.13524	1	1	1	2	2	3	38	22	10	11	22
ENSMUSG00000008976	chr16	Gabpa	8.5E+07	8.5E+07	5687	-1.0568229	4.86570095	3.351E-08	3.45053E-07	0.04104	-1	523	398	881	633	575	430	585	261	326	374
ENSMUSG00000037860	chr1	Aim2	1.7E+08	1.7E+08	3501	2.184449772	1.047426199	3.359E-08	3.45646E-07	0.12951	1	3	10	7	9	23	93	46	43	66	79
ENSMUSG00000090622	chr10	A930033H14Rik	6.9E+07	6.9E+07	2969	-1.97374389	1.455465636	3.361E-08	3.45646E-07	0.11602	-1	92	60	51	69	39	29	22	20	23	19
ENSMUSG00000020326	chr11	Ccng1	4.1E+07	4.1E+07	3512	-1.3487381	9.524646838	3.382E-08	3.47484E-07	0.06892	-1	16670	13046	19018	17296	12449	7673	13213	5631	9026	7721
ENSMUSG00000090213	chr2	Tmem189	1.7E+08	1.7E+08	3265	0.938450691	5.10845504	3.406E-08	3.49758E-07	0.03232	1	316	247	431	300	516	957	929	683	1016	1090
ENSMUSG00000034595	chr17	Ppp1r18	3.6E+07	3.6E+07	4317	1.398071015	4.182563606	3.486E-08	3.57729E-07	0.07051	1	103	95	139	112	326	676	434	426	594	572
ENSMUSG00000074916	chr2	Chst14	1.2E+08	1.2E+08	2090	1.480967177	2.866495678	3.503E-08	3.59144E-07	0.07329	1	53	32	45	54	106	271	164	172	247	233
ENSMUSG00000000982	chr11	Ccl3	8.4E+07	8.4E+07	766	2.277672522	0.599859125	3.511E-08	3.5968E-07	0.13191	1	7	1	11	6	11	56	34	19	62	67
ENSMUSG00000081788	chr7	Gm5898	6.4E+07	6.4E+07	2071	-1.63481649	2.099469262	3.534E-08	3.61807E-07	0.08551	-1	90	68	120	129	75	45	57	19	59	37
ENSMUSG00000060180	chr11	Myh13	6.7E+07	6.7E+07	6180	-2.45407791	4.069906828	3.557E-08	3.63867E-07	0.20755	-1	81	385	626	782	252	226	114	56	67	96
ENSMUSG00000020116	chr11	Pno1	1.7E+07	1.7E+07	1717	-1.03054224	5.110756167	3.593E-08	3.67339E-07	0.03943	-1	670	543	931	690	657	496	678	361	424	391
ENSMUSG00000004846	chr5	Plod3	1.4E+08	1.4E+08	4519	1.035847097	5.329870078	3.609E-08	3.68727E-07	0.04002	1	324	254	423	373	657	1363	1004	851	1254	1115
ENSMUSG00000018377	chr11	Vezf1	8.8E+07	8.8E+07	4601	-1.24672059	6.645331707	3.615E-08	3.69044E-07	0.05898	-1	2198	1838	2406	2150	1820	1235	1915	767	1128	1170
ENSMUSG00000061544	chr17	Zfp229	2.2E+07	2.2E+07	5139	-1.50259727	2.112605364	3.619E-08	3.69114E-07	0.07118	-1	101	71	118	87	100	57	75	24	34	45
ENSMUSG00000099088	chr10	Gm27920	1.2E+08	1.2E+08	96	-2.98647826	0.077467241	3.631E-08	3.70118E-07	0.2228	-1	26	25	50	21	12	5	13	3	1	1
ENSMUSG00000045205	chr4	Dpy19l4	1.1E+07	1.1E+07	8101	-1.18066466	4.485677068	3.663E-08	3.73068E-07	0.05117	-1	528	408	521	468	358	316	415	191	248	260
ENSMUSG00000022912	chr16	Pros1	6.3E+07	6.3E+07	4088	1.291047437	4.810259528	3.691E-08	3.75628E-07	0.0615	1	199	195	221	171	451	1310	664	666	770	720
ENSMUSG00000041189	chr11	Chrnb1	7E+07	7E+07	2531	1.000360024	5.820180417	3.696E-08	3.75628E-07	0.03764	1	540	474	623	556	614	1693	1455	1186	1577	1860
ENSMUSG00000061577	chr8	Gpr114	9.5E+07	9.5E+07	3147	2.789329178	-0.18224928	3.695E-08	3.75628E-07	0.15611	1	1	2	3	0	8	30	21	25	16	40
ENSMUSG00000029762	chr6	Akr1b8	3.4E+07	3.4E+07	1499	1.926109855	3.313839472	3.723E-08	3.78118E-07	0.12951	1	46	29	43	33	174	392	282	262	316	347
ENSMUSG00000025006	chr19	Sorbs1	4E+07	4E+07	3075	-2.1079065	4.882672625	3.74E-08	3.79621E-07	0.15954	-1	550	271	1456	800	760	219	584	113	110	154
ENSMUSG00000082536	chr2	Gm13456	4.1E+07	4.1E+07	1365	1.573617662	3.636678393	3.752E-08	3.80491E-07	0.08755	1	81	64	61	62	208	451	502	260	359	349
ENSMUSG00000042686	chr1	Jph1	1.7E+07	1.7E+07	4998	-1.27412522	8.055842034	3.772E-08	3.82279E-07	0.06204	-1	6015	5088	5678	5509	5414	2822	4749	2182	3019	3411
ENSMUSG00000020793	chr11	Galr2	1.2E+08	1.2E+08	2456	2.641792313	-0.46124576	3.778E-08	3.82585E-07	0.1074	1	4	0	5	1	2	29	22	16	17	21
ENSMUSG00000048271	chr5	Rbm33	2.8E+07	2.8E+07	10592	-1.01989811	5.115944759	3.8E-08	3.84257E-07	0.03879	-1	653	603	828	773	584	511	574	343	413	535
ENSMUSG00000061136	chr2	Prpf40a	5.3E+07	5.3E+07	10273	-0.99625864	4.834132331	3.797E-08	3.84257E-07	0.03661	-1	550	461	705	572	556	419	565	285	339	369
ENSMUSG00000008384	chr7	Sertad1	2.7E+07	2.7E+07	1344	1.226010862	3.985276135	3.805E-08	3.84395E-07	0.05378	1	94	90	171	159	213	518	326	453	427	511
ENSMUSG00000029802	chr6	Abcg2	5.9E+07	5.9E+07	4987	0.928302574	5.155823844	3.807E-08	3.84395E-07	0.03185	1	364	242	449	412	392	1257	878	795	998	888
ENSMUSG00000094870	chr13	Zfp131	1.2E+08	1.2E+08	3067	-1.11401919	3.282399988	3.817E-08	3.85189E-07	0.04186	-1	188	163	230	205	205	136	162	93	113	130
ENSMUSG00000055214	chr1	Pld5	1.8E+08	1.8E+08	10094	-3.40034597	1.928696165	3.847E-08	3.8786E-07	0.34775	-1	148	169	33	44	78	4	32	14	10	7
ENSMUSG00000098265	chr11	Gm27517	3645286	3645521	236	-2.45171782	0.802189825	3.851E-08	3.87998E-07	0.17362	-1	32	52	51	47	28	19	22	5	5	5
ENSMUSG00000101678	chr5	Gm29609	3.1E+07	3.1E+07	3550	-1.04513463	4.636440003	3.868E-08	3.89458E-07	0.04026	-1	502	442	615	463	466	416	470	208	317	292
ENSMUSG00000064367	chrMT	mt-Nd5	11742	13565	1824	-2.05404236	11.80243453	3.885E-08	3.90903E-07	0.1541	-1	84096	48218	144799	108486	57478	20118	69339	11287	23500	23375
ENSMUSG00000030421	chr7	Uri1	3.8E+07	3.8E+07	3431	-0.88810135	5.113105999	3.89E-08	3.91138E-07	0.02921	-1	640	509	891	641	719	554	623	354	476	516
ENSMUSG00000055632	chr2	Hmcn2	3.1E+07	3.1E+07	16073	1.115683677	6.946874036	3.912E-08	3.93061E-07	0.04773	1	825	755	1413	1430	1572	4105	3415	2496	3493	4041
ENSMUSG00000072704	chr6	2700089E24Rik	1.3E+08	1.3E+08	2738	-1.11421606	7.546925449	3.951E-08	3.96732E-07	0.04782	-1	3867	2835	4903	3814	3910	2440	3345	1814	2281	2370
ENSMUSG00000045312	chr13	Lhfpl2	9.4E+07	9.4E+07	8276	1.918727714	4.434620348	3.982E-08	3.99516E-07	0.13247	1	139	112	77	42	314	732	759	470	702	870

ENSMUSG00000058291	chr5	Zfp68	1.4E+08	1.4E+08	3834	-1.11343229	4.495011276	4.013E-08	4.02292E-07	0.04561	-1	470	386	592	458	389	361	402	237	214	262
ENSMUSG00000085295	chr4	4930430E12Rik	6352105	6352529	1135	2.753697092	-0.57245588	4.016E-08	4.02305E-07	0.10915	1	3	0	2	3	2	22	27	10	17	21
ENSMUSG00000038352	chr11	Arl5c	9.8E+07	9.8E+07	2073	1.753655078	1.261343323	4.108E-08	4.11301E-07	0.08341	1	15	13	19	6	25	91	65	58	79	65
ENSMUSG00000025007	chr19	Aldh18a1	4.1E+07	4.1E+07	4072	1.457808845	2.653825795	4.127E-08	4.12889E-07	0.07087	1	27	32	82	39	77	258	163	148	202	164
ENSMUSG00000035954	chr12	Dock4	4E+07	4E+07	8063	-1.30508488	3.177094523	4.142E-08	4.14079E-07	0.0587	-1	158	137	316	201	168	115	149	88	83	100
ENSMUSG00000000787	chrX	Ddx3x	1.3E+07	1.3E+07	5277	-1.40259074	7.756548625	4.158E-08	4.15145E-07	0.07513	-1	5330	4623	3999	5408	3182	2759	3114	1791	2391	2290
ENSMUSG00000062646	chr2	Ganc	1.2E+08	1.2E+08	9096	-1.00528617	5.067302042	4.159E-08	4.15145E-07	0.03787	-1	741	534	705	669	679	492	652	287	447	453
ENSMUSG00000085604	chr11	Dhx58os	1E+08	1E+08	1594	3.175170415	-0.3320554	4.177E-08	4.16642E-07	0.17716	1	3	3	1	0	2	49	12	12	28	22
ENSMUSG00000085322	chr2	Gm14261	1.7E+08	1.7E+08	1429	-1.75361038	2.195880322	4.192E-08	4.17928E-07	0.1013	-1	81	65	177	117	101	34	84	25	42	31
ENSMUSG00000078853	chr11	Igtp	5.8E+07	5.8E+07	2022	1.848561353	4.871293227	4.251E-08	4.2346E-07	0.12531	1	224	110	222	144	274	2364	442	761	563	721
ENSMUSG00000031337	chrX	Mtm1	7.1E+07	7.1E+07	13935	-1.52757553	3.664935976	4.283E-08	4.26326E-07	0.08402	-1	262	228	421	300	199	146	247	96	83	108
ENSMUSG00000006010	chr1	BC003331	1.5E+08	1.5E+08	4100	-0.997877	4.769764196	4.293E-08	4.27002E-07	0.03699	-1	587	446	589	547	529	478	486	269	306	359
ENSMUSG00000090084	chrX	Srpx	1E+07	1E+07	2652	1.750527112	3.87527556	4.32E-08	4.29446E-07	0.10957	1	96	98	52	57	191	770	396	345	506	328
ENSMUSG00000073599	chr18	Ecscr	3.6E+07	3.6E+07	1680	1.230324516	3.37936355	4.37E-08	4.34108E-07	0.05224	1	71	68	114	88	128	417	206	264	291	305
ENSMUSG00000001418	chr3	Glmp	8.8E+07	8.8E+07	6291	1.079682105	5.223056318	4.375E-08	4.34316E-07	0.04399	1	297	223	415	302	623	1278	882	723	1219	1162
ENSMUSG00000021898	chr14	Asb14	2.7E+07	2.7E+07	2549	-1.27153441	6.409601373	4.415E-08	4.379E-07	0.06198	-1	2105	1498	2031	1764	1485	999	1598	780	899	882
ENSMUSG00000040147	chrX	Maob	1.7E+07	1.7E+07	2789	-0.9469517	5.291936463	4.467E-08	4.42775E-07	0.03384	-1	776	566	923	670	980	562	719	398	581	513
ENSMUSG00000036611	chr9	Eepd1	2.5E+07	2.5E+07	2935	-1.14723748	7.103251739	4.493E-08	4.45038E-07	0.05095	-1	3622	1835	3163	2346	3392	1744	2126	1293	1841	1853
ENSMUSG00000023074	chrX	Mospd1	5.3E+07	5.3E+07	2085	-1.24227629	5.986704786	4.526E-08	4.48034E-07	0.0591	-1	1577	1254	1282	1139	1260	839	1138	579	722	635
ENSMUSG00000035278	chr10	Plekhj1	8.1E+07	8.1E+07	1259	1.086930594	4.438348986	4.568E-08	4.51869E-07	0.04332	1	173	168	230	179	296	702	437	453	773	664
ENSMUSG00000031618	chr8	Nr3c2	7.7E+07	7.7E+07	6474	-1.47405732	3.415184689	4.62E-08	4.56693E-07	0.07761	-1	229	162	336	298	153	115	194	70	102	108
ENSMUSG00000027360	chr2	Hdc	1.3E+08	1.3E+08	6389	2.499475895	0.306505688	4.755E-08	4.69707E-07	0.13935	1	6	3	2	6	7	61	17	23	46	46
ENSMUSG00000095115	chr7	Itpripl2	1.2E+08	1.2E+08	6862	0.948388762	4.404202512	4.781E-08	4.71949E-07	0.03258	1	220	156	228	182	305	714	564	459	567	565
ENSMUSG00000041180	chr19	Hectd2	3.7E+07	3.7E+07	9066	-1.58690694	2.622900539	4.797E-08	4.73188E-07	0.08577	-1	148	124	146	152	104	53	103	56	51	50
ENSMUSG00000034617	chr13	Mtrr	6.9E+07	6.9E+07	3692	-1.05899173	4.483316342	4.83E-08	4.76036E-07	0.04167	-1	458	383	562	445	399	323	428	213	280	262
ENSMUSG00000044948	chr19	Cfap43	4.8E+07	4.8E+07	9955	1.803932317	1.434294619	4.892E-08	4.81897E-07	0.09641	1	8	6	24	21	30	123	82	48	82	83
ENSMUSG00000041134	chr16	Cyyr1	8.5E+07	8.5E+07	8894	-1.50689466	3.053297908	4.924E-08	4.84652E-07	0.08015	-1	144	126	299	185	187	94	166	44	74	76
ENSMUSG00000007659	chr2	Bcl2l1	1.5E+08	1.5E+08	4586	1.254549272	4.508624806	4.93E-08	4.84867E-07	0.05919	1	152	84	324	157	356	738	596	526	717	713
ENSMUSG00000021950	chr14	Anxa8	3.4E+07	3.4E+07	1880	2.241682391	2.83484097	4.943E-08	4.85554E-07	0.17368	1	11	15	33	32	106	203	228	248	175	306
ENSMUSG00000022102	chr14	Dok2	7.1E+07	7.1E+07	2902	2.028812192	2.973344835	4.946E-08	4.85554E-07	0.14261	1	22	42	26	30	111	422	171	202	253	240
ENSMUSG00000043614	chr5	Vps37d	1.4E+08	1.4E+08	1544	2.284412973	0.125326509	4.95E-08	4.85554E-07	0.10526	1	4	3	6	6	5	49	21	23	45	25
ENSMUSG00000060002	chr10	Chpt1	8.8E+07	8.8E+07	8324	-1.25789793	6.991495623	4.95E-08	4.85554E-07	0.06134	-1	2642	1351	4260	2014	3908	1598	2154	1183	1360	1479
ENSMUSG00000022876	chr16	Samsn1	7.6E+07	7.6E+07	4534	2.784594466	-0.42239153	5.028E-08	4.9281E-07	0.11288	1	2	3	1	1	4	27	18	11	24	30
ENSMUSG00000016559	chr11	H3f3b	1.2E+08	1.2E+08	2976	1.090211046	6.803796733	5.094E-08	4.97921E-07	0.04634	1	904	752	1288	944	1599	4035	2669	2574	2994	3436
ENSMUSG00000022020	chr14	Naa16	7.9E+07	7.9E+07	6145	-1.1422285	3.881800685	5.089E-08	4.97921E-07	0.04728	-1	289	301	262	288	342	213	216	159	162	194
ENSMUSG00000035164	chr9	Zc3h12c	5.2E+07	5.2E+07	6133	-1.6249226	2.400135984	5.094E-08	4.97921E-07	0.08954	-1	113	112	143	139	74	65	83	33	47	41
ENSMUSG00000036257	chr12	Pnpla8	4.4E+07	4.4E+07	3947	-1.33290045	6.88732223	5.089E-08	4.97921E-07	0.06878	-1	2278	1701	3844	2680	2491	1535	2468	871	1047	1155
ENSMUSG00000060032	chr6	H2afj	1.4E+08	1.4E+08	1827	1.208680739	3.870436873	5.115E-08	4.99585E-07	0.05278	1	105	91	128	130	216	489	288	333	505	469
ENSMUSG00000081665	chr7	Gm15922	3733021	3733157	2043	2.240864423	0.402997067	5.136E-08	5.01348E-07	0.10905	1	5	8	3	3	11	51	50	25	30	46
ENSMUSG00000038943	chr7	Prc1	8E+07	8E+07	8225	2.157392259	0.347014333	5.152E-08	5.0256E-07	0.10231	1	6	3	6	7	9	64	23	31	36	37
ENSMUSG00000044676	chr8	Zfp612	1.1E+08	1.1E+08	2301	-2.37237496	1.008148115	5.174E-08	5.0433E-07	0.16912	-1	61	39	57	54	34	10	32	5	5	15
ENSMUSG00000046167	chr9	Gldn	5.4E+07	5.4E+07	4658	2.201296204	1.457928047	5.217E-08	5.08105E-07	0.14872	1	22	5	17	7	20	155	50	83	54	98
ENSMUSG00000038650	chr7	Rnh1	1.4E+08	1.4E+08	1911	1.010378082	6.239162027	5.244E-08	5.10242E-07	0.03968	1	679	489	852	761	1058	2705	2003	1471	2181	2162
ENSMUSG00000050312	chr16	Nsun3	6.3E+07	6.3E+07	4816	-1.36813456	3.026168052	5.246E-08	5.10242E-07	0.06586	-1	192	104	240	190	165	111	147	47	77	96
ENSMUSG00000029490	chr5	Mfsd7a	1.1E+08	1.1E+08	2508	1.540600647	2.337219871	5.25E-08	5.10269E-07	0.07646	1	22	37	43	32	55	127	133	126	164	195
ENSMUSG00000033991	chr13	Ttc37	7.6E+07	7.6E+07	5381	-1.45108278	3.907463183	5.257E-08	5.10626E-07	0.07757	-1	320	342	337	357	231	187	273	123	137	115
ENSMUSG00000035493	chr13	Tgfbi	5.7E+07	5.7E+07	2678	1.486751886	6.105004454	5.287E-08	5.13165E-07	0.08465	1	500	433	354	389	1064	3007	1585	1779	2002	2106
ENSMUSG00000020407	chr11	Upp1	9118103	9118284	1961	2.164347407	0.711776397	5.304E-08	5.14115E-07	0.12139	1	6	6	9	7	13	86	31	47	57	30
ENSMUSG00000046432	chrX	Ngfrap1	1.4E+08	1.4E+08	973	1.6052798	2.106887129	5.302E-08	5.14115E-07	0.08226	1	32	17	24	31	53	191	92	107	139	119
ENSMUSG00000018363	chr11	Smurf2	1.1E+08	1.1E+08	6162	-0.99507556	5.0605317	5.31E-08	5.14357E-07	0.03766	-1	654	530	785	743	602	488	646	329	445	407
ENSMUSG00000033382	chr18	Trappc8	2.1E+07	2.1E+07	5482	-1.16269168	5.130394451	5.35E-08	5.17911E-07	0.05174	-1	779	546	868	776	652	520	728	320	338	351
ENSMUSG00000087370	chr13	Tmem170b	4.2E+07	4.2E+07	7160	-1.11483429	5.021877688	5.367E-08	5.192E-07	0.04743	-1	800	583	611	621	643	428	605	315	392	385
ENSMUSG00000021822	chr14	Plau	2.1E+07	2.1E+07	2343	1.28365895	5.757929192	5.405E-08	5.22466E-07	0.06353	1	327	339	467	344	966	1813	1497	1224	1641	1742
ENSMUSG00000038914	chr2	Dido1	1.8E+08	1.8E+08	13307	-1.07225167	4.314790725	5.444E-08	5.25902E-07	0.0428	-1	378	283	556	451	374	265	394	168	233	277
ENSMUSG00000042476	chr5	Abcb4	8893721	8893907	4074	-1.24177101	6.979701927	5.478E-08	5.28833E-07	0.06024	-1	2722	1873	3286	3178	2280	1433	2382	1017	1602	1383
ENSMUSG00000031207	chrX	Msn	9.6E+07	9.6E+07	6327	1.274295291	6.615037461	5.522E-08	5.3268E-07	0.06326	1	562	476	1175	756	1573	3911	2589	2344	2506	3017
ENSMUSG00000007872	chr4	Id3	1.4E+08	1.4E+08	1791	1.382099401	5.211985293	5.567E-08	5.36691E-07	0.07308	1	229	195	260	247	666	1395	787	921	1076	1326
ENSMUSG00000033436	chrX	Armcx2	1.3E+08	1.3E+08	4532	1.213503362	2.983775308	5.575E-08	5.3702E-07	0.04913	1	64	61	75	63	88	300	213	182	243	185
ENSMUSG00000055805	chr11	Fmnl1	1E+08	1E+08	4868	1.164547236	3.663671182	5.599E-08	5.3896E-07	0.04889	1	87	59	143	129	186	452	326	261	333	433
ENSMUSG00000024511	chr18	Rab27b	7E+07	7E+07	10679	1.998189542	0.962776343	5.609E-08	5.39214E-07	0.10951	1	6	7	11	10	21	109	61	44	45	43
ENSMUSG00000053291	chr7	Rab4b	2.7E+07	2.7E+07	1970	1.501403925	3.430672492	5.606E-08	5.39214E-07	0.08105	1	55	59	85	61	171	439	215	237	391	352
ENSMUSG00000038344	chrX	Txlng	1.6E+08	1.6E+08	7541	-1.27649683	2.816254282	5.696E-08	5.46898E-07	0.0554	-1	130	125	173	128	191	119	111	61	70	66
ENSMUSG00000052316	chr16	Lrrc15	3E+07	3E+07	5310	2.117868597	0.799178526	5.697E-08	5.46898E-07	0.12007	1	7	4	7	12	15	74	43	22	51	83
ENSMUSG00000020205	chr10	Phlda1	1.1E+08	1.1E+08	2205	1.526046924	3.049304488	5.765E-08	5.53045E-07	0.08237	1	45	35	76	39	136	280	229	218	220	292
ENSMUSG00000037709	chr6	Fam13a	5.9E+07	5.9E+07	6328	-1.20562916	4.040713535	5.769E-08	5.53122E-07	0.05378	-1	354	140	502	382	416	226	260	128	173	252
ENSMUSG00000034041	chr8	Lyl1	8.5E+07	8.5E+07	1800	1.83588409	2.936324496	5.781E-08	5.53507E-07	0.11839	1	29	36	38	31	121	341	159	175	255	290
ENSMUSG00000037486	chr12	Asxl2	3426857	3427212	14574	-1.16662404	3.947259684	5.778E-08	5.53507E-07	0.04999	-1	317	249	455	317	264	235	281	135	141	199

ENSMUSG00000024477	chr18	Pggt1b	4.6E+07	4.6E+07	2736	-1.90699706	2.646415939	5.792E-08	5.54139E-07	0.12776	-1	159	112	224	176	63	59	99	24	44	52
ENSMUSG00000057003	chr11	Myh4	6.7E+07	6.7E+07	6016	-1.34280696	14.94955432	5.827E-08	5.57128E-07	0.07085	-1	720281	521185	640757	809095	681295	304823	508948	294592	453990	275093
ENSMUSG00000032705	chr12	Exd2	8E+07	8E+07	3323	-1.07267863	5.009765233	5.852E-08	5.59087E-07	0.04412	-1	662	573	739	669	585	543	599	327	346	345
ENSMUSG00000040407	chr5	Akap9	3928054	3928342	15848	-1.26000769	5.85512947	5.898E-08	5.63156E-07	0.06177	-1	1269	842	1902	1317	860	748	1073	460	564	722
ENSMUSG00000039835	chr10	Nhsl1	1.8E+07	1.8E+07	11056	-1.23598914	3.169086217	5.926E-08	5.65403E-07	0.05364	-1	220	171	200	142	196	138	132	77	99	110
ENSMUSG00000022770	chr16	Dlg1	3.2E+07	3.2E+07	8963	-1.04966264	5.869036583	5.987E-08	5.70462E-07	0.04306	-1	1156	961	1386	1168	1228	877	1129	562	739	657
ENSMUSG00000078671	chr7	Chd2	7.3E+07	7.3E+07	9656	-1.101783	5.722467688	5.984E-08	5.70462E-07	0.04733	-1	1067	817	1437	1155	941	751	1024	454	608	672
ENSMUSG00000042515	chrX	Mum1l1	1.4E+08	1.4E+08	4859	-2.13096352	1.964418829	6.077E-08	5.78653E-07	0.15198	-1	89	106	76	124	56	23	60	23	23	20
ENSMUSG00000009207	chr2	Lnp	7.5E+07	7.5E+07	9154	-1.25608556	4.838711009	6.09E-08	5.7954E-07	0.0605	-1	686	427	735	720	441	290	559	251	284	363
ENSMUSG00000052087	chr13	Rgs14	5.5E+07	5.5E+07	2490	2.164434285	0.444654288	6.161E-08	5.85826E-07	0.10743	1	8	4	2	6	13	59	31	30	42	44
ENSMUSG00000012640	chr7	Zfp715	4.3E+07	4.3E+07	5119	-1.61687662	3.102338625	6.186E-08	5.87884E-07	0.09472	-1	198	178	271	192	114	98	132	36	71	110
ENSMUSG00000035448	chr9	Ccr3	1.2E+08	1.2E+08	3273	3.514106096	-0.30149972	6.202E-08	5.88965E-07	0.27821	1	0	0	2	0	6	32	10	16	15	54
ENSMUSG00000096944	chr4	Gm26722	1.3E+08	1.3E+08	1048	0.905183904	4.355651681	6.215E-08	5.89756E-07	0.02988	1	213	151	228	225	253	726	567	412	525	531
ENSMUSG00000033458	chr7	Fan1	6.4E+07	6.4E+07	5289	-1.37833123	2.580734276	6.22E-08	5.89858E-07	0.06444	-1	129	88	155	155	119	63	107	50	60	61
ENSMUSG00000028630	chr10	Dyrk2	1.2E+08	1.2E+08	2137	-1.51512834	4.361344399	6.244E-08	5.91751E-07	0.08713	-1	450	536	380	466	329	225	381	139	196	174
ENSMUSG00000026466	chr1	Tor1aip1	1.6E+08	1.6E+08	5406	-1.11844631	6.754336481	6.294E-08	5.95257E-07	0.04946	-1	2195	1726	2730	2411	2010	1538	1988	938	1349	1301
ENSMUSG00000026825	chr2	Dnm1	3.2E+07	3.2E+07	5240	1.30965736	4.227300157	6.294E-08	5.95257E-07	0.06429	1	157	136	131	107	274	739	483	295	689	590
ENSMUSG00000040548	chr11	Tex2	1.1E+08	1.1E+08	5576	-1.1832626	6.410675202	6.286E-08	5.95257E-07	0.05511	-1	1601	1134	2624	2101	1575	1114	1569	634	1032	1111
ENSMUSG00000032238	chr9	Rora	6.9E+07	6.9E+07	13071	-1.14430967	5.995586831	6.347E-08	5.99905E-07	0.05142	-1	1517	1150	1377	1139	1304	948	1176	554	700	779
ENSMUSG00000072640	chr11	Lyrm9	7.9E+07	7.9E+07	8146	-1.15717934	4.03765815	6.363E-08	6.01017E-07	0.04971	-1	368	267	453	368	229	215	244	152	228	211
ENSMUSG00000042323	chr14	Pbrm1	3.1E+07	3.1E+07	8846	-1.07006491	5.364864375	6.391E-08	6.03267E-07	0.04449	-1	858	699	1082	824	694	555	730	460	471	518
ENSMUSG00000028557	chr4	Rnf11	1.1E+08	1.1E+08	4263	-1.15327431	7.209408872	6.456E-08	6.08963E-07	0.05275	-1	3138	2211	3804	2811	3527	1773	2857	1402	1817	1661
ENSMUSG00000045362	chr7	Tnfrsf26	1.4E+08	1.4E+08	2977	2.45606572	0.347773457	6.56E-08	6.18325E-07	0.13924	1	5	7	2	4	7	30	54	30	23	58
ENSMUSG00000024424	chr18	Ttc39c	1.3E+07	1.3E+07	5197	1.504761291	1.864505973	6.566E-08	6.18529E-07	0.06982	1	20	14	37	29	41	163	93	66	100	122
ENSMUSG00000028796	chr4	Phc2	1.3E+08	1.3E+08	7064	0.986176716	5.187306829	6.574E-08	6.18828E-07	0.03762	1	266	233	525	321	557	1283	908	723	1022	1092
ENSMUSG00000004319	chr8	Clcn3	6.1E+07	6.1E+07	17071	-1.0984646	5.521910349	6.589E-08	6.19426E-07	0.04717	-1	1004	725	1160	932	869	581	922	437	540	554
ENSMUSG00000042249	chr5	Adrbk2	1.1E+08	1.1E+08	6537	-1.4757142	3.353722304	6.589E-08	6.19426E-07	0.07948	-1	254	178	164	138	395	116	124	87	93	136
ENSMUSG00000035352	chr11	Ccl12	8.2E+07	8.2E+07	537	2.855373511	0.607848724	6.635E-08	6.2331E-07	0.21999	1	4	2	4	5	10	129	19	34	45	28
ENSMUSG00000048583	chr7	Igf2	1.4E+08	1.4E+08	5723	1.169884573	5.538448349	6.667E-08	6.25884E-07	0.05328	1	394	344	521	558	302	1923	1184	1013	1293	1277
ENSMUSG00000044951	chr13	Mylk4	3.3E+07	3.3E+07	6128	-1.95765566	9.156210718	6.675E-08	6.26247E-07	0.14595	-1	15868	6070	19567	7468	23055	3634	11068	2951	3412	3423
ENSMUSG00000044678	chr15	Ly6k	7.5E+07	7.5E+07	829	2.50785918	0.035555683	6.685E-08	6.26806E-07	0.13953	1	5	1	5	0	9	42	27	23	43	20
ENSMUSG00000027763	chr3	Mbnl1	6E+07	6E+07	18717	-1.17059718	7.986767179	6.704E-08	6.28138E-07	0.05462	-1	5379	4301	5762	5693	4982	3212	4585	2070	3025	3415
ENSMUSG00000029007	chr4	Agtrap	1.5E+08	1.5E+08	4236	1.106377915	4.009569277	6.712E-08	6.28465E-07	0.04542	1	134	74	237	161	186	514	373	324	482	571
ENSMUSG00000024186	chr17	Rgs11	2.6E+07	2.6E+07	4206	2.301244266	0.528120151	6.73E-08	6.29744E-07	0.12707	1	6	8	10	3	5	66	25	28	41	64
ENSMUSG00000022339	chr15	Ebag9	4.5E+07	4.5E+07	1561	-1.12398771	3.750214912	6.738E-08	6.30069E-07	0.0463	-1	294	217	341	272	252	207	250	115	167	143
ENSMUSG00000079104	chr12	Prps1l3	5.7E+07	5.7E+07	1720	-1.4864409	3.59884258	6.788E-08	6.34338E-07	0.08192	-1	329	246	301	239	187	127	230	73	113	125
ENSMUSG00000013033	chr8	Lphn1	8.4E+07	8.4E+07	8587	-1.07801065	5.26373028	6.805E-08	6.35468E-07	0.04526	-1	632	546	1159	895	748	476	733	376	543	425
ENSMUSG00000037321	chr17	Tap1	3.4E+07	3.4E+07	5476	1.826361568	3.680628452	6.822E-08	6.36185E-07	0.12291	1	56	50	116	70	145	992	249	174	312	428
ENSMUSG00000055809	chr7	Dnaaf3	4522933	4523859	2224	2.344636923	0.273509395	6.82E-08	6.36185E-07	0.12656	1	3	5	5	3	10	58	21	20	37	50
ENSMUSG00000021311	chr13	Mtr	1.2E+07	1.2E+07	4482	-1.29374943	3.438383602	6.847E-08	6.38137E-07	0.06095	-1	233	168	336	256	162	115	180	96	121	134
ENSMUSG00000021948	chr14	Prkcd	3.1E+07	3.1E+07	4983	1.373928434	4.273888798	6.952E-08	6.4702E-07	0.07198	1	104	105	221	85	331	704	536	420	577	644
ENSMUSG00000091955	chr7	Gm9844	2.5E+07	2.5E+07	485	2.360556875	0.542021151	6.947E-08	6.4702E-07	0.14248	1	2	3	6	13	8	62	23	30	56	56
ENSMUSG00000022263	chr15	Trio	2.8E+07	2.8E+07	11494	-1.23354172	5.055903376	6.966E-08	6.47938E-07	0.05926	-1	636	589	985	795	472	479	643	233	374	363
ENSMUSG00000004849	chr5	Ap1s1	1.4E+08	1.4E+08	2198	1.099652148	5.098724696	7.065E-08	6.56243E-07	0.0469	1	294	237	294	256	581	1177	835	690	1134	1003
ENSMUSG00000076498	chr6	Trbc2	4.2E+07	4.2E+07	692	3.03568354	-0.39168007	7.063E-08	6.56243E-07	0.18768	1	0	1	3	1	5	23	19	17	10	45
ENSMUSG00000006095	chr7	Tbcb	3E+07	3E+07	1442	0.911549926	4.565663444	7.096E-08	6.58659E-07	0.03123	1	222	156	327	241	312	775	526	474	703	713
ENSMUSG00000030451	chr7	Herc2	5.6E+07	5.6E+07	15440	-1.37107058	6.518170091	7.165E-08	6.64563E-07	0.07417	-1	1922	1728	2156	2633	1241	1129	1554	761	989	885
ENSMUSG00000063065	chr7	Mapk3	1.3E+08	1.3E+08	2163	1.2452805	5.885585757	7.169E-08	6.64563E-07	0.06111	1	450	318	544	405	1015	1894	1414	1157	2081	2082
ENSMUSG00000032231	chr9	Anxa2	6.9E+07	6.9E+07	3731	1.905499222	7.66470257	7.248E-08	6.71445E-07	0.13937	1	843	769	885	715	3584	9768	5055	4990	7203	6377
ENSMUSG00000036894	chr3	Rap2b	6.1E+07	6.1E+07	6793	1.398628368	3.31308599	7.254E-08	6.71628E-07	0.07035	1	54	66	60	77	152	383	262	248	302	270
ENSMUSG00000034412	chr11	Tbc1d10a	4186789	4187099	2733	1.268307553	2.929915277	7.301E-08	6.75487E-07	0.05578	1	52	46	74	51	115	269	198	170	239	218
ENSMUSG00000024338	chr17	Psmb8	3.4E+07	3.4E+07	2736	1.64814938	4.485633101	7.339E-08	6.78514E-07	0.10366	1	128	110	143	118	335	1461	398	403	622	730
ENSMUSG00000063382	chr9	Bcl9l	4.4E+07	4.4E+07	5304	-1.02348161	4.768934414	7.389E-08	6.82742E-07	0.04044	-1	417	369	806	557	669	366	523	215	421	355
ENSMUSG00000039182	chr13	AW209491	1.5E+07	1.5E+07	2023	-1.14207546	3.671103209	7.456E-08	6.88421E-07	0.04783	-1	238	211	320	296	243	198	235	114	152	127
ENSMUSG00000021413	chr13	Prpf4b	3.5E+07	3.5E+07	4465	-1.11368078	4.561194877	7.472E-08	6.89002E-07	0.04783	-1	462	392	606	541	406	371	469	198	232	294
ENSMUSG00000022089	chr14	Bin3	7E+07	7E+07	1712	1.220859377	3.226358921	7.469E-08	6.89002E-07	0.0532	1	77	46	97	74	135	349	204	206	285	294
ENSMUSG00000025429	chr18	Pstpip2	7.8E+07	7.8E+07	1395	-1.54194241	4.219485771	7.672E-08	7.06986E-07	0.09076	-1	436	340	590	438	258	206	378	117	178	121
ENSMUSG00000032601	chr9	Prkar2a	1.1E+08	1.1E+08	6378	-1.28752477	7.558929215	7.701E-08	7.09199E-07	0.06626	-1	3670	2830	5338	4928	3459	2030	3717	1439	2098	2162
ENSMUSG00000031799	chr8	Tpm4	7.2E+07	7.2E+07	2203	1.055090547	5.634970743	7.862E-08	7.23588E-07	0.04411	1	370	301	678	416	752	1936	1324	1141	1275	1268
ENSMUSG00000023826	chr17	Park2	1.1E+07	1.1E+07	10101	-1.10738211	4.739473828	7.894E-08	7.26017E-07	0.04763	-1	593	439	680	594	400	383	479	284	309	292
ENSMUSG00000020130	chr10	Tbc1d15	1.2E+08	1.2E+08	3773	-1.07424587	4.621063456	7.916E-08	7.27545E-07	0.04464	-1	545	373	679	479	431	342	501	225	278	303
ENSMUSG00000078878	chr2	Gm14305	1.8E+08	1.8E+08	2500	-1.71480718	1.851196004	7.997E-08	7.34549E-07	0.09856	-1	102	78	84	71	65	47	56	18	25	30
ENSMUSG00000090118	chr8	Gm16163	1.2E+08	1.2E+08	1119	-2.23366166	3.195992464	8.044E-08	7.38419E-07	0.18131	-1	176	147	452	242	150	37	177	31	49	43
ENSMUSG00000032507	chr9	Fbxl2	1.1E+08	1.1E+08	4444	1.571596294	1.621527297	8.058E-08	7.39177E-07	0.07432	1	10	17	38	24	24	115	93	62	84	103
ENSMUSG00000019944	chr10	Rhobtb1	6.9E+07	6.9E+07	6075	-1.40210867	4.955103545	8.096E-08	7.42157E-07	0.0769	-1	805	706	568	745	375	408	334	276	425	315
ENSMUSG00000038170	chr3	Pde4dip	9.8E+07	9.8E+07	16508	-1.43145471	11.87547363	8.236E-08	7.54511E-07	0.08197	-1	77148	63067	103260	112995	51320	37967	62046	26515	40012	45676
ENSMUSG00000054418	chr11	2900041M22Rik	1.2E+08	1.2E+08	1784	2.224878485	0.248442555	8.306E-08	7.60437E-07	0.11648	1	4	2	8	5	9	61	19	27	32	40

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ENSMUSG00000021456	chr13	Fbp2	6.3E+07	6.3E+07	1325	-1.26665798	6.692070186	8.349E-08	7.63843E-07	0.06431	-1	1798	2314	1904	2285	2328	1278	1256	849	1135	1796
ENSMUSG00000008226	chr2	Scrn3	7.3E+07	7.3E+07	4815	-1.2876892	6.007189542	8.358E-08	7.6425E-07	0.06607	-1	1531	1217	1548	1375	1029	695	1239	569	668	701
ENSMUSG00000046245	chr5	Pilra	1.4E+08	1.4E+08	3077	2.418913751	0.458371408	8.397E-08	7.67241E-07	0.1405	1	3	8	1	5	11	65	28	35	41	44
ENSMUSG00000026739	chr2	Bmi1	1.9E+07	1.9E+07	3974	-1.24843028	5.223975043	8.435E-08	7.69705E-07	0.06162	-1	766	586	1030	920	647	427	816	297	353	419
ENSMUSG00000034765	chr19	Dusp5	5.4E+07	5.4E+07	2473	2.05451415	1.58021203	8.433E-08	7.69705E-07	0.13089	1	22	18	10	10	20	123	62	113	68	94
ENSMUSG00000020687	chr11	Cdc27	1E+08	1E+08	6248	-0.9477972	4.741423885	8.603E-08	7.84251E-07	0.03484	-1	594	410	594	533	491	449	476	272	327	375
ENSMUSG00000044501	chr17	Zfp758	2.2E+07	2.2E+07	2974	-1.63911101	2.156950821	8.605E-08	7.84251E-07	0.09159	-1	132	69	133	89	79	65	62	37	26	33
ENSMUSG00000024856	chr19	Cdk2ap2	4097182	4097507	1636	1.182242218	4.705716451	8.64E-08	7.86957E-07	0.05459	1	206	135	208	243	438	930	543	561	861	841
ENSMUSG00000021384	chr13	Susd3	4.9E+07	4.9E+07	2837	2.378073217	0.74084733	8.666E-08	7.88736E-07	0.16473	1	1	2	11	13	11	86	27	43	60	48
ENSMUSG00000020605	chr12	Hs1bp3	8313433	8313497	2958	1.055160082	4.088319272	8.703E-08	7.91582E-07	0.04181	1	145	124	159	161	242	443	489	308	557	568
ENSMUSG00000100826	chr7	D7Ertd715e	5.9E+07	5.9E+07	26093	-1.48466371	2.444839064	8.771E-08	7.9732E-07	0.07691	-1	101	73	173	161	99	50	84	33	63	66
ENSMUSG00000003348	chr10	Mob3a	8.1E+07	8.1E+07	2644	1.210768157	3.61322829	8.819E-08	8.01115E-07	0.05381	1	89	87	89	111	175	434	289	244	426	364
ENSMUSG00000081194	chrX	Gm8424	1.5E+08	1.5E+08	988	-3.54503672	3.195009995	8.844E-08	8.02912E-07	0.41421	-1	250	199	326	386	82	16	109	9	3	18
ENSMUSG00000000594	chr11	Gm2a	5.5E+07	5.5E+07	4127	1.406872459	5.230631994	8.856E-08	8.03417E-07	0.07804	1	281	216	225	196	661	1405	877	823	1306	1231
ENSMUSG00000042761	chr9	Mrap2	8.7E+07	8.7E+07	2257	1.956963208	1.452434259	8.934E-08	8.10003E-07	0.11795	1	16	11	19	14	20	110	45	69	55	145
ENSMUSG00000026082	chr1	Rev1	3.8E+07	3.8E+07	6168	-1.05076496	4.213772278	8.972E-08	8.12948E-07	0.04234	-1	355	295	478	364	390	311	371	166	216	199
ENSMUSG00000031885	chr8	Cbfb	1.1E+08	1.1E+08	3480	-1.50590998	6.562525734	9.017E-08	8.1651E-07	0.09029	-1	2949	2193	1420	1607	1774	1103	1311	862	817	980
ENSMUSG00000015575	chr17	Atp6v0e	2.7E+07	2.7E+07	3261	1.276715036	4.999059955	9.127E-08	8.25926E-07	0.06433	1	253	192	239	173	582	1221	854	698	967	949
ENSMUSG00000023224	chr2	Serping1	8.5E+07	8.5E+07	2325	1.389541963	7.51686	9.144E-08	8.26941E-07	0.07764	1	1045	1191	1295	1201	3041	8171	5073	3848	5407	5298
ENSMUSG00000028478	chr4	Clta	4.4E+07	4.4E+07	1800	1.038507297	5.993795371	9.343E-08	8.44375E-07	0.04346	1	573	396	693	572	978	2288	1552	1478	1759	1762
ENSMUSG00000002257	chr17	Def6	2.8E+07	2.8E+07	2524	1.556893171	2.090042334	9.421E-08	8.50841E-07	0.0806	1	26	15	32	29	60	162	99	82	159	138
ENSMUSG00000064225	chr9	Paqr9	9.6E+07	9.6E+07	8367	-1.80329648	3.16818609	9.444E-08	8.52351E-07	0.12073	-1	149	65	303	133	488	97	103	48	83	86
ENSMUSG00000021969	chr14	Zdhhc20	5.8E+07	5.8E+07	5173	1.229256641	4.623492738	9.551E-08	8.61468E-07	0.05913	1	205	178	213	145	373	929	490	639	620	853
ENSMUSG00000030516	chr7	Tjp1	6.5E+07	6.5E+07	7360	-0.99768612	4.724068937	9.637E-08	8.6867E-07	0.03894	-1	452	301	731	619	615	357	523	264	323	360
ENSMUSG00000069729	chr17	Arid1b	4994332	4994399	12600	-1.00915221	5.455782198	9.672E-08	8.71254E-07	0.04083	-1	853	665	1141	926	830	635	843	377	556	636
ENSMUSG00000008036	chr7	Ap2s1	1.7E+07	1.7E+07	1333	1.098722701	5.718145721	9.742E-08	8.77025E-07	0.04857	1	492	306	574	455	751	1755	1059	1198	1865	1499
ENSMUSG00000038663	chr7	Fsd2	8.2E+07	8.2E+07	3985	-1.29183617	8.331256228	9.947E-08	8.94952E-07	0.06798	-1	6546	4975	10677	7081	5462	3312	5986	2607	4003	3505
ENSMUSG00000022401	chr15	Xpnpep3	8.1E+07	8.1E+07	6117	-1.25356517	2.918593208	1.001E-07	9.00036E-07	0.05616	-1	173	106	186	169	166	121	129	67	76	70
ENSMUSG00000062232	chr3	Rapgef2	7.9E+07	7.9E+07	14051	-1.00696255	3.814645658	1.004E-07	9.02551E-07	0.03773	-1	260	223	373	278	277	220	246	152	176	170
ENSMUSG00000055865	chr3	Fam19a3	1E+08	1E+08	4484	-1.22019299	3.4448161	1.016E-07	9.1192E-07	0.05562	-1	273	185	247	228	189	145	188	101	126	115
ENSMUSG00000026837	chr2	Col5a1	2.8E+07	2.8E+07	8490	1.205471222	6.514718422	1.018E-07	9.13121E-07	0.05903	1	590	600	915	707	1458	3778	2538	1934	2990	2067
ENSMUSG00000079508	chrX	Apoo	9.4E+07	9.4E+07	1255	-1.08623969	6.197725851	1.034E-07	9.26978E-07	0.04804	-1	1467	1167	1974	1584	1297	1013	1342	702	960	864
ENSMUSG00000024339	chr17	Tap2	3.4E+07	3.4E+07	3781	1.334992279	4.721353974	1.043E-07	9.34734E-07	0.07067	1	150	134	254	182	452	1280	544	472	814	867
ENSMUSG00000021816	chr14	Ppp3cb	2E+07	2.1E+07	6018	-1.16680758	7.813313531	1.045E-07	9.35527E-07	0.0559	-1	5082	3802	5057	4643	4552	2752	4219	1949	2898	2612
ENSMUSG00000091498	chr12	Mpc1-ps	1.1E+08	1.1E+08	330	-1.31920198	5.339496172	1.045E-07	9.35527E-07	0.06985	-1	757	576	1563	871	686	507	840	309	366	405
ENSMUSG00000050347	chr7	Gm9844	2.5E+07	2.5E+07	135	2.268789843	0.429619168	1.048E-07	9.37514E-07	0.13333	1	2	3	6	12	8	56	22	28	53	47
ENSMUSG00000066571	chr7	4931406P16Rik	3.4E+07	3.4E+07	6437	-0.87660359	5.141244082	1.058E-07	9.45904E-07	0.03049	-1	642	505	889	746	666	545	609	385	507	528
ENSMUSG00000022905	chr16	Kpna1	3.6E+07	3.6E+07	8486	-1.11273636	7.400358316	1.066E-07	9.52013E-07	0.05093	-1	3481	2870	3870	3735	3213	2373	2951	1512	2244	2057
ENSMUSG00000032041	chr9	Tirap	3.5E+07	3.5E+07	4929	-1.07588756	4.315938297	1.072E-07	9.57067E-07	0.04522	-1	409	308	562	328	439	262	419	174	234	245
ENSMUSG00000017009	chr2	Sdc4	1.6E+08	1.6E+08	2547	0.992603691	5.423350477	1.075E-07	9.591E-07	0.03956	1	378	314	540	462	478	1470	857	1011	1200	1322
ENSMUSG00000026223	chr1	Itm2c	8.6E+07	8.6E+07	2491	1.240657674	6.197857437	1.077E-07	9.59424E-07	0.06252	1	598	472	623	457	1199	2655	1688	1580	2533	2232
ENSMUSG00000079110	chr2	Capn3	1.2E+08	1.2E+08	5023	-1.20220525	7.017931781	1.077E-07	9.59424E-07	0.05918	-1	2603	1903	3687	3246	2207	1568	2415	1178	1534	1453
ENSMUSG00000029233	chr5	Srd5a3	7.6E+07	7.6E+07	4648	1.420988771	3.145261099	1.078E-07	9.60087E-07	0.0738	1	49	68	66	49	125	350	198	201	266	299
ENSMUSG00000038594	chr10	Cep85l	5.3E+07	5.3E+07	2691	-3.56405092	1.778953638	1.081E-07	9.62076E-07	0.40736	-1	81	74	190	101	32	9	40	2	1	5
ENSMUSG00000098701	chr10	Mir6914	1.3E+08	1.3E+08	69	-2.40161948	-0.08002417	1.096E-07	9.75152E-07	0.14051	-1	17	20	29	32	13	4	12	2	6	5
ENSMUSG00000026980	chr2	Ly75	6E+07	6E+07	6905	2.919416336	-0.39395102	1.103E-07	9.80782E-07	0.14444	1	2	4	1	3	0	27	21	9	22	35
ENSMUSG00000043991	chr18	Pura	3.6E+07	3.6E+07	14943	-0.97044908	5.416559459	1.105E-07	9.81341E-07	0.03804	-1	855	718	964	860	803	701	763	421	536	586
ENSMUSG00000099398	chr19	Ms4a14	1.1E+07	1.1E+07	4065	2.953100624	-0.27742147	1.114E-07	9.88862E-07	0.16568	1	1	5	0	0	5	32	28	22	13	29
ENSMUSG00000027288	chr2	Zfp106	1.2E+08	1.2E+08	10429	-1.38613933	10.1401153	1.124E-07	9.96821E-07	0.07866	-1	23855	16620	35369	31789	15558	13153	19571	8765	11279	12416
ENSMUSG00000045752	chr7	Tssc4	1.4E+08	1.4E+08	1760	1.070087963	3.959911382	1.129E-07	1.00132E-06	0.04365	1	146	90	170	133	228	562	322	345	456	478
ENSMUSG00000035199	chr6	Arl6ip5	9.7E+07	9.7E+07	1442	1.090868972	7.749160855	1.13E-07	1.00166E-06	0.04923	1	1944	1380	2975	2197	2002	6758	5165	5432	6218	6382
ENSMUSG00000021767	chr14	Kat6b	2.1E+07	2.1E+07	16826	-1.03308413	3.949450494	1.136E-07	1.00609E-06	0.04076	-1	294	250	373	360	267	238	262	135	205	216
ENSMUSG00000038179	chr1	Slamf7	1.7E+08	1.7E+08	4577	2.15935687	0.306660215	1.144E-07	1.01277E-06	0.11205	1	3	3	8	10	6	31	46	17	41	51
ENSMUSG00000020954	chr12	Strn3	5.2E+07	5.2E+07	4164	-1.27262849	7.370410767	1.152E-07	1.01913E-06	0.06654	-1	3717	2662	4351	3935	2824	1957	3258	1370	1609	1910
ENSMUSG00000018076	chr5	Med13l	1.2E+08	1.2E+08	9293	-0.9556094	4.586351179	1.16E-07	1.02495E-06	0.03594	-1	428	397	524	550	456	356	439	256	306	332
ENSMUSG00000041642	chr1	Kif21b	1.4E+08	1.4E+08	12184	1.765082323	1.75347706	1.164E-07	1.02766E-06	0.09889	1	13	25	15	20	35	116	102	62	90	149
ENSMUSG00000000305	chr2	Cdh4	1.8E+08	1.8E+08	7257	-1.9693725	3.270313691	1.175E-07	1.03676E-06	0.14611	-1	201	324	145	214	185	47	140	61	100	55
ENSMUSG00000054178	chr19	Gm9938	2.4E+07	2.4E+07	1756	-3.34590689	-0.20138421	1.18E-07	1.04103E-06	0.29782	-1	19	22	34	23	13	1	13	0	0	1
ENSMUSG00000017760	chr2	Ctsa	1.6E+08	1.6E+08	4715	1.02853731	7.115068043	1.192E-07	1.05098E-06	0.04384	1	1204	1025	1663	1369	1659	4341	3585	2519	4608	4333
ENSMUSG00000022139	chr14	Mbnl2	1.2E+08	1.2E+08	4552	-1.31522688	6.91344596	1.196E-07	1.05348E-06	0.07099	-1	2337	1798	3841	3220	1827	1463	2276	951	1182	1351
ENSMUSG00000022978	chr16	Mis18a	9.1E+07	9.1E+07	2863	1.746849152	1.173303631	1.203E-07	1.0593E-06	0.08966	1	14	7	14	14	25	104	45	47	74	69
ENSMUSG00000032218	chr9	Ccnb2	7E+07	7E+07	1541	2.727618882	-0.4696091	1.204E-07	1.05931E-06	0.12557	1	3	1	1	4	2	34	13	15	26	17
ENSMUSG00000025195	chr19	Dnmbp	4.4E+07	4.4E+07	4882	-1.27490174	3.752288939	1.209E-07	1.06347E-06	0.06281	-1	275	237	405	284	223	179	269	91	152	136
ENSMUSG00000020150	chr10	Gamt	8E+07	8E+07	1444	1.551515123	4.994460883	1.216E-07	1.06896E-06	0.096	1	269	216	132	153	430	1023	732	861	1405	806
ENSMUSG00000046532	chrX	Ar	9.8E+07	9.8E+07	9096	-0.90191253	5.040601748	1.219E-07	1.07036E-06	0.03257	-1	525	513	872	653	679	485	609	345	426	512
ENSMUSG00000030263	chr6	Lrmp	1.5E+08	1.5E+08	4070	2.04298774	1.806117737	1.227E-07	1.07725E-06	0.13874	1	13	22	11	9	42	170	85	66	114	130
ENSMUSG00000029560	chr5	Snx8	1.4E+08	1.4E+08	2615	0.899290846	4.495723751	1.235E-07	1.08291E-06	0.03142	1	201	156	286	257	298	738	526	431	701	641

ENSMUSG00000021796	chr14	Bmpr1a	3.4E+07	3.4E+07	6351	-1.15307795	6.127349453	1.237E-07	1.08471E-06	0.05472	-1	1509	1138	1904	1345	1347	1011	1390	591	665	887
ENSMUSG00000026315	chr1	Serpinb8	1.1E+08	1.1E+08	4795	1.371629526	2.376790649	1.252E-07	1.09716E-06	0.06476	1	32	28	61	31	66	216	168	112	111	154
ENSMUSG00000024677	chr19	Ms4a6b	1.2E+07	1.2E+07	4485	1.837012063	1.776758921	1.257E-07	1.10011E-06	0.1107	1	15	21	16	16	39	196	107	60	104	76
ENSMUSG00000035620	chr10	Ric8b	8.5E+07	8.5E+07	3068	-1.13524521	5.301366	1.258E-07	1.10034E-06	0.05246	-1	787	427	1284	915	787	471	788	341	488	478
ENSMUSG00000022667	chr16	Cd200r1	4.5E+07	4.5E+07	2034	2.17156074	0.688970369	1.259E-07	1.10121E-06	0.13512	1	6	4	6	3	22	46	64	33	44	61
ENSMUSG00000039968	chr5	Rsbn1l	2.1E+07	2.1E+07	5550	-1.27850763	3.589542026	1.265E-07	1.10509E-06	0.06303	-1	237	253	306	229	227	138	226	95	108	163
ENSMUSG00000048490	chr16	Nrip1	7.6E+07	7.6E+07	11457	-1.06514418	4.04351068	1.266E-07	1.10598E-06	0.04412	-1	340	277	393	224	446	246	265	185	178	222
ENSMUSG00000021091	chr12	Serpina3n	1E+08	1E+08	2064	2.283229277	5.338735879	1.269E-07	1.10799E-06	0.2008	1	144	138	127	61	619	2635	1711	873	1069	851
ENSMUSG00000006342	chr10	Susd2	7.6E+07	7.6E+07	3255	1.394722558	2.706783666	1.277E-07	1.1138E-06	0.06979	1	35	45	73	32	85	246	155	135	221	205
ENSMUSG00000037621	chr6	Atoh8	7.2E+07	7.2E+07	2355	1.433451614	2.262952818	1.278E-07	1.1141E-06	0.07129	1	31	18	57	38	52	172	99	127	126	173
ENSMUSG00000000392	chr2	Fap	6.3E+07	6.3E+07	5662	1.377241134	4.490681629	1.292E-07	1.12545E-06	0.07527	1	230	173	152	150	203	1263	441	474	656	571
ENSMUSG00000030782	chr7	Tgfb1i1	1.3E+08	1.3E+08	3598	1.196140117	3.637781818	1.293E-07	1.12572E-06	0.05451	1	88	77	132	90	191	475	269	268	437	330
ENSMUSG00000032038	chr9	St3gal4	3.5E+07	3.5E+07	2029	1.378882206	3.285192541	1.298E-07	1.1296E-06	0.0714	1	84	56	68	60	138	385	185	247	287	325
ENSMUSG00000015755	chr10	Tab2	7905653	7907577	6135	-1.160989	7.228376109	1.303E-07	1.1333E-06	0.05608	-1	3208	2575	3431	3340	2821	1911	2811	1294	1864	1779
ENSMUSG00000024371	chr17	C2	3.5E+07	3.5E+07	3872	1.833985938	3.657064281	1.305E-07	1.13423E-06	0.12856	1	57	82	32	55	182	599	328	307	422	371
ENSMUSG00000020697	chr11	Lig3	8.3E+07	8.3E+07	7284	-1.03866527	4.828307512	1.317E-07	1.14391E-06	0.04348	-1	584	439	681	687	453	484	489	306	317	332
ENSMUSG00000034792	chr10	Gna15	8.2E+07	8.2E+07	2135	2.051394563	0.569820598	1.321E-07	1.14659E-06	0.10215	1	8	10	6	3	11	58	44	25	41	57
ENSMUSG00000049791	chr7	Fzd4	8.9E+07	8.9E+07	3685	-1.28889544	4.737419946	1.323E-07	1.14751E-06	0.06712	-1	587	448	511	392	922	428	492	239	198	262
ENSMUSG00000023328	chr5	Ache	1.4E+08	1.4E+08	4623	1.261739917	5.457302544	1.325E-07	1.14802E-06	0.06494	1	438	287	342	271	613	1164	1463	919	1854	980
ENSMUSG00000030016	chr6	Zfml	8.4E+07	8.4E+07	6470	-1.04506991	5.100182236	1.325E-07	1.14802E-06	0.04443	-1	665	569	912	667	650	591	647	335	298	468
ENSMUSG00000092470	chr16	Gm20518	1.8E+07	1.8E+07	3811	-1.23968489	3.651079298	1.334E-07	1.15485E-06	0.05948	-1	247	214	293	329	224	148	247	101	148	132
ENSMUSG00000045201	chr14	Lrrc3b	1.5E+07	1.5E+07	1835	1.407307682	2.457354139	1.337E-07	1.15637E-06	0.07042	1	28	26	79	39	57	177	203	138	119	163
ENSMUSG00000067149	chr5	Igj	8.9E+07	8.9E+07	1814	2.427789586	0.490327514	1.337E-07	1.15637E-06	0.15841	1	4	6	1	4	14	34	62	21	57	46
ENSMUSG00000052981	chr13	Ube2ql1	7E+07	7E+07	2679	1.945301234	1.28325542	1.344E-07	1.16112E-06	0.12077	1	12	6	32	15	8	104	66	67	87	49
ENSMUSG00000029581	chr5	Fscn1	1.4E+08	1.4E+08	3012	1.369255529	4.642058665	1.345E-07	1.16149E-06	0.07572	1	141	91	261	195	419	818	484	680	927	740
ENSMUSG00000056708	chr1	Ier5	1.6E+08	1.6E+08	3276	1.152987707	3.940896217	1.346E-07	1.1615E-06	0.05181	1	90	85	215	116	238	513	386	311	494	478
ENSMUSG00000030753	chr7	Prkrir	9.9E+07	9.9E+07	4125	-1.18543918	7.237817015	1.351E-07	1.16531E-06	0.05856	-1	3219	2518	3905	3272	2747	1939	2918	1376	1732	1621
ENSMUSG00000074238	chr3	Ap1ar	1.3E+08	1.3E+08	2391	-1.00065785	4.677216573	1.352E-07	1.16533E-06	0.04018	-1	527	439	612	448	514	377	523	244	296	334
ENSMUSG00000097296	chr8	Gm26532	8.4E+07	8.4E+07	690	1.919356986	1.897838878	1.358E-07	1.17031E-06	0.12708	1	13	13	24	34	30	147	60	84	89	206
ENSMUSG00000028033	chr1	Kcnq5	2.1E+07	2.1E+07	7689	-1.32906153	4.762843279	1.365E-07	1.17548E-06	0.07159	-1	596	592	536	692	375	356	489	216	243	311
ENSMUSG00000034297	chr11	Med13	8.6E+07	8.6E+07	10840	-1.05262345	5.388283074	1.366E-07	1.17548E-06	0.04544	-1	809	690	1147	898	682	614	744	439	438	585
ENSMUSG00000067081	chr1	Asb18	9E+07	9E+07	3952	-1.21476485	4.781465687	1.373E-07	1.18084E-06	0.05985	-1	617	301	987	600	469	357	536	207	337	297
ENSMUSG00000034738	chr2	Nostrin	6.9E+07	6.9E+07	1888	1.858101689	0.983939116	1.374E-07	1.18111E-06	0.10258	1	7	5	22	9	19	76	47	58	43	70
ENSMUSG00000030557	chr7	Mef2a	6.7E+07	6.7E+07	6283	-1.08581946	6.787077425	1.376E-07	1.18144E-06	0.04923	-1	2292	1725	2919	2221	2141	1512	2094	1071	1315	1354
ENSMUSG00000022844	chr16	Pdia5	3.5E+07	3.5E+07	1808	1.4028784	2.459063638	1.386E-07	1.18965E-06	0.06857	1	36	32	42	39	75	254	136	112	171	141
ENSMUSG00000032307	chr9	Ube2q2	5.5E+07	5.5E+07	4305	-0.90388632	5.147705546	1.402E-07	1.20294E-06	0.03314	-1	667	563	862	649	726	610	594	445	439	452
ENSMUSG00000040605	chr16	Bace2	9.7E+07	9.7E+07	3736	1.38211508	2.349528371	1.411E-07	1.21008E-06	0.06627	1	40	23	50	40	58	229	104	112	163	138
ENSMUSG00000054648	chr8	Zfp869	7E+07	7E+07	1590	-1.26774414	3.355668257	1.416E-07	1.21308E-06	0.06128	-1	237	154	270	234	187	151	195	87	88	104
ENSMUSG00000037994	chr3	Slc9b2	1.4E+08	1.4E+08	2877	2.53514792	-0.22828031	1.419E-07	1.21508E-06	0.11495	1	6	3	1	2	3	36	30	12	28	21
ENSMUSG00000032369	chr9	Plscr1	9.2E+07	9.2E+07	2462	1.473931711	1.383275816	1.437E-07	1.22945E-06	0.06125	1	17	15	22	23	21	104	66	54	71	82
ENSMUSG00000031538	chr8	Plat	2.3E+07	2.3E+07	2531	1.248947959	3.671296474	1.441E-07	1.23251E-06	0.06015	1	80	77	97	109	211	536	360	276	364	315
ENSMUSG00000031099	chrX	Smarca1	4.8E+07	4.8E+07	6118	-1.37962009	3.460961498	1.444E-07	1.23425E-06	0.07374	-1	282	186	255	255	196	151	210	87	110	79
ENSMUSG00000018899	chr11	Irf1	5.4E+07	5.4E+07	3976	1.500235778	4.741050942	1.452E-07	1.24057E-06	0.09094	1	165	144	215	151	402	1614	464	510	630	969
ENSMUSG00000031149	chrX	Praf2	7728439	7728762	1339	1.326819385	3.004260511	1.478E-07	1.26151E-06	0.06545	1	62	43	73	53	115	385	186	162	233	218
ENSMUSG00000020230	chr10	Prmt2	7.6E+07	7.6E+07	3177	1.34632784	3.366909185	1.5E-07	1.2795E-06	0.06933	1	72	55	71	68	178	391	291	204	350	289
ENSMUSG00000036995	chr4	Asap3	1.4E+08	1.4E+08	4225	1.374738059	2.758328281	1.501E-07	1.27986E-06	0.06761	1	58	53	51	41	70	266	140	167	193	219
ENSMUSG00000026781	chr2	Acbd5	2.3E+07	2.3E+07	4154	-0.91143991	4.725136866	1.507E-07	1.28447E-06	0.03339	-1	516	331	694	537	557	410	533	259	351	358
ENSMUSG00000020546	chr11	Stxbp4	9E+07	9E+07	11834	-1.36868203	4.262741353	1.511E-07	1.28667E-06	0.0756	-1	419	478	402	321	369	210	378	142	186	202
ENSMUSG00000021221	chr12	Dpf3	8.3E+07	8.3E+07	4225	-1.16347247	3.127380929	1.515E-07	1.28883E-06	0.05021	-1	170	145	215	182	190	98	160	75	108	115
ENSMUSG00000095253	chr17	Zfp799	3.3E+07	3.3E+07	5833	-1.28796534	2.584933942	1.515E-07	1.28883E-06	0.05955	-1	125	97	172	128	114	74	99	50	52	84
ENSMUSG00000073664	chr1	Nbeal1	6E+07	6E+07	28441	-0.97107752	4.751806542	1.517E-07	1.28979E-06	0.03816	-1	477	392	766	592	473	435	490	273	295	399
ENSMUSG00000049686	chr5	Orai1	1.2E+08	1.2E+08	2289	0.996129459	5.496987697	1.528E-07	1.29802E-06	0.04102	1	363	280	559	505	613	1209	1108	903	1539	1436
ENSMUSG00000027187	chr2	Cat	1E+08	1E+08	2613	-1.09617302	7.009112648	1.53E-07	1.29859E-06	0.05061	-1	2698	1551	3837	2510	2956	2229	2074	1166	1251	1890
ENSMUSG00000049339	chr1	Fam134a	7.5E+07	7.5E+07	2999	1.14406971	4.848327065	1.538E-07	1.30469E-06	0.05346	1	239	158	250	226	515	982	637	612	899	962
ENSMUSG00000040022	chr19	Rab11fip2	6E+07	6E+07	6080	-1.14500752	3.322680179	1.541E-07	1.30646E-06	0.04979	-1	209	157	258	215	191	132	185	75	120	137
ENSMUSG00000024294	chr18	Mib1	1.1E+07	1.1E+07	10369	-1.25463583	5.880517775	1.55E-07	1.3135E-06	0.06546	-1	1564	792	1575	873	1538	728	1233	490	576	605
ENSMUSG00000034761	chr12	Map4k5	7E+07	7E+07	8614	-0.98186196	4.927455928	1.555E-07	1.31695E-06	0.03934	-1	616	422	809	667	536	438	601	313	394	373
ENSMUSG00000037234	chr8	Hook3	2.6E+07	2.6E+07	13132	-1.13746045	6.476817751	1.556E-07	1.31695E-06	0.0543	-1	1892	1345	2446	2031	1493	1175	1679	740	1082	1142
ENSMUSG00000042719	chr5	Naa25	1.2E+08	1.2E+08	8298	-1.03422512	5.381489583	1.597E-07	1.35099E-06	0.04435	-1	818	718	1059	894	669	657	724	443	529	479
ENSMUSG00000091474	chr7	2610021A01Rik	4.2E+07	4.2E+07	4004	-1.57507088	1.801208035	1.606E-07	1.35803E-06	0.08473	-1	99	57	84	78	65	43	56	21	24	37
ENSMUSG00000030361	chr6	Klrb1a	1.3E+08	1.3E+08	1274	2.329220071	-0.28884734	1.628E-07	1.37527E-06	0.10955	1	2	1	4	2	8	23	31	13	21	30
ENSMUSG00000050989	chr4	Sepn1	1.3E+08	1.3E+08	3619	1.052568799	4.416327333	1.636E-07	1.38159E-06	0.04436	1	189	167	197	160	333	786	490	449	646	603
ENSMUSG00000040282	chr2	BC052040	1.2E+08	1.2E+08	4349	-1.39095733	2.491472795	1.654E-07	1.39575E-06	0.07065	-1	130	120	98	123	117	66	72	41	78	63
ENSMUSG00000074813	chr2	Gm14005	1.3E+08	1.3E+08	2045	1.630985044	1.400923999	1.668E-07	1.40642E-06	0.08127	1	11	13	29	20	20	109	56	71	66	86
ENSMUSG00000079426	chr6	Arpc4	1.1E+08	1.1E+08	2323	1.112144716	5.911150388	1.67E-07	1.40732E-06	0.0518	1	498	388	562	548	915	2134	1228	1335	2098	1695
ENSMUSG00000029552	chr6	Tes	1.7E+07	1.7E+07	3199	1.737467027	2.075118937	1.675E-07	1.41103E-06	0.10753	1	21	16	28	14	68	144	112	99	146	144
ENSMUSG00000024308	chr17	Tapbp	3.4E+07	3.4E+07	3296	1.227620688	6.339581811	1.679E-07	1.41344E-06	0.06332	1	589	423	799	592	1391	3373	1927	1538	2618	2445

ENSMUSG00000061455	chr4	Stx17	4.8E+07	4.8E+07	5935	-0.94534292	4.913178758	1.693E-07	1.42446E-06	0.03661	-1	585	486	741	585	568	456	594	319	357	408
ENSMUSG00000066687	chr9	Zbtb16	4.9E+07	4.9E+07	5100	-1.73937847	4.941605111	1.702E-07	1.43158E-06	0.1231	-1	581	513	1308	835	365	289	636	155	209	209
ENSMUSG00000028780	chr5	Sema3c	1.8E+07	1.8E+07	7140	-1.20681297	5.487800691	1.731E-07	1.45483E-06	0.06089	-1	1087	932	647	878	977	761	666	357	504	565
ENSMUSG00000040563	chr9	Lppr2	2.2E+07	2.2E+07	2750	1.559544039	1.411286923	1.747E-07	1.46699E-06	0.07291	1	18	16	19	13	30	88	67	50	90	95
ENSMUSG00000021552	chr13	Gkap1	5.8E+07	5.8E+07	1518	-0.96206464	4.235615487	1.752E-07	1.47052E-06	0.03692	-1	372	258	507	382	367	329	351	195	224	229
ENSMUSG00000033033	chr19	Calhm2	4.7E+07	4.7E+07	4361	1.478956091	2.28066842	1.754E-07	1.47124E-06	0.07713	1	36	24	29	31	70	180	128	88	183	146
ENSMUSG00000038482	chr8	Tfdp1	1.3E+07	1.3E+07	1700	-1.19261622	5.045641797	1.755E-07	1.47124E-06	0.0591	-1	720	670	745	661	558	437	689	255	382	344
ENSMUSG00000045246	chr8	Kcng4	1.2E+08	1.2E+08	3806	-2.57021882	5.234706901	1.775E-07	1.48725E-06	0.25477	-1	600	617	2146	730	1025	99	719	77	166	95
ENSMUSG00000021690	chr13	Jmy	9.3E+07	9.3E+07	8780	-1.11402632	5.212792562	1.786E-07	1.49516E-06	0.05178	-1	808	639	941	793	576	515	749	316	430	439
ENSMUSG00000017830	chr11	Dhx58	1E+08	1E+08	3272	1.558701668	1.55260294	1.788E-07	1.49627E-06	0.07748	1	20	9	23	21	36	125	83	47	85	99
ENSMUSG00000005886	chr1	Ncoa2	1.3E+07	1.3E+07	15642	-1.1277633	4.5888703	1.816E-07	1.51778E-06	0.05225	-1	468	329	789	486	456	285	520	214	270	280
ENSMUSG00000044147	chr12	Arf6	6.9E+07	6.9E+07	3730	1.018964937	5.304757582	1.815E-07	1.51778E-06	0.04333	1	317	238	452	352	667	1318	903	913	1176	1126
ENSMUSG00000056629	chr19	Fkbp2	6977741	6977934	663	1.194064324	3.844788199	1.826E-07	1.52573E-06	0.05625	1	102	96	142	119	203	634	268	274	471	431
ENSMUSG00000020640	chr12	Itsn2	4593008	4593232	5987	-1.27333254	3.677745048	1.828E-07	1.52622E-06	0.06439	-1	277	242	324	307	177	184	216	112	116	150
ENSMUSG00000061462	chr11	Obscn	5.9E+07	5.9E+07	28892	-1.39050855	10.65558905	1.836E-07	1.53181E-06	0.08191	-1	29989	20359	57651	47525	24069	16925	26577	11586	19100	18808
ENSMUSG00000030122	chr6	Ptms	1.2E+08	1.2E+08	1554	1.496303828	7.252543893	1.837E-07	1.53197E-06	0.09392	1	1062	680	909	909	2681	5134	3574	3410	5959	5198
ENSMUSG00000058486	chr6	Wdr91	3.5E+07	3.5E+07	2990	1.091310938	3.202133454	1.851E-07	1.54222E-06	0.04421	1	71	55	108	81	132	273	278	167	267	301
ENSMUSG00000030474	chr7	Siglece	4.4E+07	4.4E+07	1849	2.033839863	0.602079993	1.866E-07	1.55409E-06	0.107	1	4	8	5	9	14	58	30	32	58	50
ENSMUSG00000100131	chr1	Gm28439	2.5E+07	2.5E+07	876	-1.61425126	2.698228474	1.868E-07	1.55457E-06	0.09904	-1	134	92	177	185	151	44	135	41	47	63
ENSMUSG00000003484	chr8	Cyp4f18	7.2E+07	7.2E+07	1855	3.43627902	-0.09392262	1.873E-07	1.55789E-06	0.29746	1	0	0	1	1	8	52	9	12	34	45
ENSMUSG00000019942	chr10	Cdk1	6.9E+07	6.9E+07	3445	2.385108709	0.506181295	1.889E-07	1.57052E-06	0.15494	1	5	7	3	4	11	78	22	45	40	34
ENSMUSG00000040325	chr9	Vprbp	1.1E+08	1.1E+08	7786	-0.99701356	4.440204257	1.897E-07	1.57636E-06	0.04045	-1	422	303	569	511	374	320	410	219	291	261
ENSMUSG00000035208	chr11	Slfn8	8.3E+07	8.3E+07	4091	1.906517129	1.466902457	1.91E-07	1.5858E-06	0.11623	1	22	19	7	12	19	138	79	64	68	81
ENSMUSG00000027490	chr2	E2f1	1.5E+08	1.5E+08	3154	2.023766282	1.895873302	1.912E-07	1.58664E-06	0.14453	1	12	18	10	15	52	165	80	80	151	120
ENSMUSG00000025372	chr11	Baiap2	1.2E+08	1.2E+08	4992	1.666905906	2.807185693	1.921E-07	1.59315E-06	0.10615	1	53	23	32	36	111	258	169	147	240	269
ENSMUSG00000042208	chr11	0610010F05Rik	2.4E+07	2.4E+07	5226	-1.06205294	4.323164942	1.926E-07	1.5968E-06	0.04596	-1	370	344	487	460	348	313	378	212	219	219
ENSMUSG00000030109	chr6	Slc6a12	1.2E+08	1.2E+08	3052	2.828258913	0.291599774	1.934E-07	1.6023E-06	0.22114	1	1	3	2	1	13	28	39	14	57	58
ENSMUSG00000031250	chrX	Tnmd	1.3E+08	1.3E+08	1353	1.337252252	4.758941764	1.94E-07	1.60602E-06	0.07384	1	268	184	303	164	228	1546	540	683	535	738
ENSMUSG00000044749	chr11	Abca6	1.1E+08	1.1E+08	5398	-1.62921863	2.711164774	1.947E-07	1.61097E-06	0.10228	-1	140	153	129	150	145	90	117	32	36	64
ENSMUSG00000040550	chr4	Otud6b	1.5E+07	1.5E+07	3387	-1.22005547	5.93529619	1.972E-07	1.63056E-06	0.06308	-1	1238	990	1786	1426	988	766	1258	546	622	632
ENSMUSG00000026238	chr1	Ptma	8.7E+07	8.7E+07	1462	1.052980268	6.358872394	1.983E-07	1.63888E-06	0.04732	1	706	556	896	636	1313	2800	2090	1702	2302	2596
ENSMUSG00000022969	chr16	Il10rb	9.1E+07	9.1E+07	3808	1.437854821	4.305764733	1.998E-07	1.6496E-06	0.08499	1	120	97	149	91	377	701	526	426	566	762
ENSMUSG00000029771	chr6	Irf5	3E+07	3E+07	2903	1.540539144	4.015082569	1.997E-07	1.6496E-06	0.09657	1	61	43	280	147	133	637	426	337	553	536
ENSMUSG00000007783	chr7	Cpt1c	4.5E+07	4.5E+07	2793	1.852996263	1.437479081	2.036E-07	1.67993E-06	0.11266	1	22	13	15	8	25	131	46	61	88	91
ENSMUSG00000042766	chr3	Trim46	8.9E+07	8.9E+07	3792	2.103751573	0.478524071	2.041E-07	1.68325E-06	0.12091	1	5	3	9	5	14	77	35	18	43	42
ENSMUSG00000070000	chr8	Fcho1	7.2E+07	7.2E+07	4467	2.52270046	-0.3758958	2.047E-07	1.68659E-06	0.13002	1	1	1	4	2	6	23	18	10	35	26
ENSMUSG00000045636	chr8	Mtus1	4.1E+07	4.1E+07	10078	-1.05023899	7.131537774	2.058E-07	1.69467E-06	0.04754	-1	2605	1764	4109	2760	3375	1878	2571	1382	1731	1910
ENSMUSG00000003762	chr7	Adck4	2.7E+07	2.7E+07	3175	1.319700882	3.358086696	2.067E-07	1.70117E-06	0.06823	1	69	54	89	65	173	425	266	206	356	257
ENSMUSG00000002076	chr17	Hsf2bp	3.2E+07	3.2E+07	2973	2.328697188	-0.15283562	2.077E-07	1.70784E-06	0.11848	1	3	2	10	3	1	27	20	26	29	27
ENSMUSG00000020614	chr11	Fam20a	1.1E+08	1.1E+08	3634	1.658847702	1.99420628	2.076E-07	1.70784E-06	0.09869	1	16	13	33	20	64	145	110	99	110	137
ENSMUSG00000042312	chr3	S100a13	9.1E+07	9.1E+07	715	1.457796609	4.940754397	2.1E-07	1.72518E-06	0.08862	1	214	164	220	139	533	1370	553	771	982	966
ENSMUSG00000022508	chr16	Bcl6	2.4E+07	2.4E+07	6700	-1.05374483	6.173468013	2.103E-07	1.72721E-06	0.04756	-1	1092	1362	1561	1499	1741	1020	1248	697	869	1041
ENSMUSG00000032754	chr5	Slc8b1	1.2E+08	1.2E+08	3463	1.05764938	4.473844451	2.131E-07	1.74908E-06	0.04596	1	191	156	238	153	364	833	547	415	578	752
ENSMUSG00000028573	chr4	Fggy	9.6E+07	9.6E+07	5844	3.16797595	1.54905853	2.14E-07	1.75509E-06	0.33882	1	7	3	1	1	32	68	70	120	116	119
ENSMUSG00000024431	chr18	Nr3c1	3.9E+07	3.9E+07	7425	-1.14990983	6.477057977	2.144E-07	1.75762E-06	0.05676	-1	1803	1763	1752	2098	1528	1279	1475	838	1115	1045
ENSMUSG00000052949	chr11	Rnf157	1.2E+08	1.2E+08	9537	-0.90123964	4.727961369	2.146E-07	1.75832E-06	0.03355	-1	474	372	692	531	551	382	488	223	443	394
ENSMUSG00000029167	chr5	Ppargc1a	5.1E+07	5.1E+07	6641	-1.42206024	4.62932333	2.148E-07	1.75838E-06	0.08432	-1	478	288	1098	552	405	255	498	154	228	277
ENSMUSG00000005534	chr8	Insr	3150922	3156023	9633	-1.06500265	6.097048733	2.149E-07	1.75862E-06	0.0486	-1	1332	959	1870	1658	1186	1001	1185	678	742	992
ENSMUSG00000050592	chr2	Fam78a	3.2E+07	3.2E+07	5973	-1.04311824	5.128204351	2.151E-07	1.75918E-06	0.04585	-1	758	566	638	660	888	409	656	332	556	409
ENSMUSG00000051285	chr1	Pcmtd1	7088920	7089216	6654	-1.09540924	6.285514256	2.152E-07	1.75918E-06	0.05151	-1	1723	1234	1925	1622	1439	1213	1476	733	787	984
ENSMUSG00000021188	chr12	Trip11	1E+08	1E+08	10150	-1.12449241	5.233589283	2.168E-07	1.77137E-06	0.05349	-1	719	533	1219	866	586	561	737	353	391	423
ENSMUSG00000096252	chr13	Tes3-ps	4.9E+07	4.9E+07	1205	-2.38392124	0.332358783	2.176E-07	1.77692E-06	0.17446	-1	44	32	28	27	16	8	17	2	8	6
ENSMUSG00000022639	chr16	5330426P16Rik	5.1E+07	5.1E+07	4679	1.373238055	2.660589786	2.194E-07	1.79002E-06	0.06984	1	46	39	50	34	94	249	155	160	184	171
ENSMUSG00000031626	chr8	Sorbs2	4.6E+07	4.6E+07	19432	-1.21998167	5.396832002	2.218E-07	1.80905E-06	0.06323	-1	1077	818	940	655	837	549	859	345	461	431
ENSMUSG00000069495	chr2	Epc2	4.9E+07	4.9E+07	4697	-1.04032714	4.006085908	2.223E-07	1.81188E-06	0.04378	-1	331	255	402	341	283	238	301	173	178	194
ENSMUSG00000030413	chr7	Pglyrp1	1.9E+07	1.9E+07	681	2.523896735	-0.04506906	2.231E-07	1.81717E-06	0.14691	1	3	2	3	5	5	45	13	16	25	48
ENSMUSG00000039232	chr10	Stx11	1.3E+07	1.3E+07	2396	2.067336528	0.623682075	2.233E-07	1.81808E-06	0.11522	1	9	10	10	7	3	36	52	41	38	62
ENSMUSG00000074457	chr3	S100a16	9.1E+07	9.1E+07	1617	1.081165007	6.2803931	2.243E-07	1.82461E-06	0.05027	1	648	519	796	659	1205	2611	1720	1810	2551	2161
ENSMUSG00000020590	chr12	Snx13	3.5E+07	3.5E+07	7387	-1.23942605	5.938194308	2.27E-07	1.84561E-06	0.06573	-1	1357	1043	1619	1481	888	774	1193	549	585	693
ENSMUSG00000043241	chr2	Upf2	5951469	5951553	5474	-1.04657792	5.232255043	2.275E-07	1.84844E-06	0.04652	-1	786	571	954	821	664	586	787	321	424	454
ENSMUSG00000046034	chr15	Otulin	2.8E+07	2.8E+07	1491	1.092913758	4.526077438	2.277E-07	1.84906E-06	0.04977	1	184	96	304	295	262	714	543	508	619	836
ENSMUSG00000022141	chr15	Nipbl	8291225	8291590	8815	-0.94071492	4.918312932	2.293E-07	1.86124E-06	0.03713	-1	616	489	715	593	548	529	571	301	350	410
ENSMUSG00000071042	chr17	Rasgrp3	7.5E+07	7.5E+07	4921	-1.00672221	5.036361459	2.317E-07	1.87975E-06	0.04283	-1	787	480	841	591	588	523	647	308	410	388
ENSMUSG00000023022	chr15	Lima1	1E+08	1E+08	7167	0.962325269	4.701635713	2.333E-07	1.89184E-06	0.03829	1	239	216	269	208	397	991	619	523	680	756
ENSMUSG00000024981	chr19	Acsl5	5.5E+07	5.5E+07	3150	1.22161841	4.352789411	2.36E-07	1.91227E-06	0.06205	1	204	101	151	140	345	830	505	458	519	644
ENSMUSG00000046688	chr3	Tifa	1.3E+08	1.3E+08	2527	1.612810793	2.049353806	2.391E-07	1.93657E-06	0.09058	1	30	31	21	18	45	165	112	91	96	161
ENSMUSG00000022462	chr15	Slc38a2	9.7E+07	9.7E+07	4626	-1.06128973	6.43987036	2.397E-07	1.94009E-06	0.04881	-1	1343	1182	2799	1868	1870	1171	1519	905	1007	1211

ENSMUSG00000018412	chr11	Kansl1	1E+08	1E+08	6874	-1.05329361	4.635430497	2.404E-07	1.94487E-06	0.04652	-1	455	422	643	546	435	341	525	233	290	291
ENSMUSG00000036564	chr8	Ndrg4	9.6E+07	9.6E+07	4887	1.60429567	2.960631597	2.42E-07	1.95635E-06	0.10151	1	28	23	60	91	94	293	190	181	198	329
ENSMUSG00000086298	chr11	Gm11716	1.1E+08	1.1E+08	470	-1.40007919	4.569545846	2.439E-07	1.97093E-06	0.08243	-1	597	294	691	756	247	320	286	178	231	347
ENSMUSG00000038387	chr7	Rras	4.5E+07	4.5E+07	1103	1.20701672	5.333103147	2.449E-07	1.97744E-06	0.0622	1	276	236	349	285	747	1384	902	902	1293	1316
ENSMUSG00000015476	chr17	Prrt1	3.5E+07	3.5E+07	2306	2.105073773	0.97074483	2.459E-07	1.98443E-06	0.13997	1	5	9	10	5	23	88	32	47	57	80
ENSMUSG00000032418	chr9	Me1	8.7E+07	8.7E+07	3848	-1.16611975	7.369551008	2.466E-07	1.98913E-06	0.05922	-1	3914	2876	2931	2682	4622	2164	2638	1588	2323	1837
ENSMUSG00000029119	chr5	Man2b2	3.7E+07	3.7E+07	3528	1.092739542	4.002080696	2.47E-07	1.99096E-06	0.04832	1	114	122	169	123	247	573	406	270	569	451
ENSMUSG00000060791	chr7	Gmfg	2.8E+07	2.8E+07	2817	2.079837674	2.089504244	2.48E-07	1.99836E-06	0.15893	1	14	21	13	15	56	250	73	106	123	141
ENSMUSG00000002222	chr6	Rmnd5a	7.1E+07	7.1E+07	6783	-1.19591947	7.743457146	2.483E-07	1.99922E-06	0.06233	-1	4914	3565	5536	4305	3955	2822	4335	1821	2243	2391
ENSMUSG00000004364	chr1	Cul3	8E+07	8E+07	4873	-1.16639948	7.743227135	2.494E-07	2.007E-06	0.05938	-1	4355	3497	5495	4562	4346	2636	4434	1937	2365	2369
ENSMUSG00000061838	chr6	Suclg2	9.5E+07	9.5E+07	2279	-1.0573722	6.054973664	2.499E-07	2.01014E-06	0.0484	-1	1339	884	1976	1546	1082	1028	1002	730	769	927
ENSMUSG00000031103	chrX	Elf4	4.8E+07	4.8E+07	6148	1.219040654	2.885803052	2.511E-07	2.01695E-06	0.0554	1	60	51	66	49	105	274	191	149	233	209
ENSMUSG00000031934	chr9	Panx1	1.5E+07	1.5E+07	2997	0.962988109	4.225192691	2.51E-07	2.01695E-06	0.03771	1	130	139	210	226	254	604	474	418	478	559
ENSMUSG00000044452	chr7	Zfp507	3.6E+07	3.6E+07	7121	-1.01731043	4.204642436	2.515E-07	2.01893E-06	0.04264	-1	398	297	420	417	293	310	284	202	227	236
ENSMUSG00000023972	chr17	Ptk7	4.7E+07	4.7E+07	4255	1.556477212	1.458565597	2.516E-07	2.01908E-06	0.07518	1	21	18	19	18	22	106	70	60	105	61
ENSMUSG00000026475	chr1	Rgs16	1.5E+08	1.5E+08	2339	2.3548116	0.877779906	2.531E-07	2.02962E-06	0.17459	1	2	6	7	10	17	51	26	47	99	64
ENSMUSG00000026915	chr2	Strbp	3.7E+07	3.7E+07	18487	-1.21136302	3.918898537	2.536E-07	2.0327E-06	0.06029	-1	357	327	270	272	299	181	264	141	181	174
ENSMUSG00000026153	chr1	Fam135a	2.4E+07	2.4E+07	7773	-1.2641789	4.208217285	2.545E-07	2.03759E-06	0.0669	-1	378	292	549	434	309	211	373	124	156	276
ENSMUSG00000031376	chrX	Atp2b3	7.4E+07	7.4E+07	4820	-1.37682627	3.520469847	2.545E-07	2.03759E-06	0.07661	-1	240	180	375	312	133	127	160	114	140	110
ENSMUSG00000021785	chr14	Ngly1	1.6E+07	1.6E+07	5274	-0.9562176	5.455750056	2.559E-07	2.04715E-06	0.03927	-1	898	688	1042	784	936	721	864	429	536	565
ENSMUSG00000027843	chr3	Ptpn22	1E+08	1E+08	3064	2.295179162	0.697239074	2.582E-07	2.06497E-06	0.15902	1	7	4	8	4	15	79	29	39	25	82
ENSMUSG00000028369	chr4	Svep1	5.8E+07	5.8E+07	16117	1.28100285	5.24935461	2.59E-07	2.06977E-06	0.07007	1	269	260	281	204	684	1438	1041	925	1203	941
ENSMUSG00000039988	chr3	Ankrd13c	1.6E+08	1.6E+08	2668	-1.06370387	3.666286575	2.607E-07	2.08221E-06	0.04536	-1	252	197	321	259	259	163	252	124	140	169
ENSMUSG00000002985	chr7	Apoe	2E+07	2E+07	1980	2.388064054	9.153696255	2.653E-07	2.11811E-06	0.23091	1	2075	1987	774	1055	8391	25414	14413	14575	22979	21993
ENSMUSG00000045319	chr2	Proser2	6097607	6101360	9563	1.613531969	1.424957567	2.655E-07	2.11834E-06	0.0847	1	17	10	23	17	29	79	85	40	119	77
ENSMUSG00000030538	chr7	Cib1	8E+07	8E+07	2052	1.350932532	3.505155533	2.667E-07	2.12684E-06	0.07395	1	79	50	93	75	198	473	251	238	372	347
ENSMUSG00000053175	chr7	Bcl3	2E+07	2E+07	2485	2.021923344	2.354925778	2.676E-07	2.13224E-06	0.15502	1	19	21	16	16	80	152	115	131	214	202
ENSMUSG00000043262	chr7	Uevld	4.7E+07	4.7E+07	7226	-1.16664556	3.438082799	2.694E-07	2.14236E-06	0.05456	-1	235	171	294	227	194	163	206	99	116	109
ENSMUSG00000050855	chr7	Zfp940	3E+07	3E+07	6090	-1.62854994	0.74271155	2.692E-07	2.14236E-06	0.07445	-1	31	32	44	30	47	23	22	10	13	14
ENSMUSG00000051146	chr16	Camk2n2	2.1E+07	2.1E+07	1291	1.891985023	1.018516744	2.694E-07	2.14236E-06	0.1129	1	10	5	15	8	24	64	35	51	78	75
ENSMUSG00000075415	chr2	Fnbp1	3.1E+07	3.1E+07	10030	0.926008441	4.705524956	2.693E-07	2.14236E-06	0.03591	1	210	190	348	232	401	871	590	535	670	864
ENSMUSG00000039967	chr4	Zfp292	3.5E+07	3.5E+07	9986	-1.1791497	3.7518945	2.705E-07	2.14935E-06	0.05671	-1	279	255	335	314	186	187	212	127	148	179
ENSMUSG00000071083	chr8	Gm10311	6.9E+07	6.9E+07	387	-2.85526984	-0.60526723	2.709E-07	2.15127E-06	0.17073	-1	14	12	27	20	5	2	4	4	1	3
ENSMUSG00000024236	chr18	Svil	4920540	4920874	10640	-1.27358223	7.937973706	2.716E-07	2.1559E-06	0.07093	-1	5162	3591	7667	6259	3542	3040	4499	1964	2498	2998
ENSMUSG00000050299	chr16	Gm9843	7.6E+07	7.6E+07	504	1.05124137	4.374744582	2.759E-07	2.18899E-06	0.04597	1	177	159	219	168	296	643	431	374	747	698
ENSMUSG00000055407	chr7	Map6	9.9E+07	9.9E+07	6958	1.471481085	3.144459749	2.776E-07	2.20108E-06	0.08737	1	54	22	89	58	147	317	237	197	269	306
ENSMUSG00000020137	chr10	Thap2	1.2E+08	1.2E+08	3408	-1.48597305	2.532165312	2.802E-07	2.22033E-06	0.08478	-1	142	124	125	134	90	59	93	52	48	59
ENSMUSG00000040229	chrX	Gpr34	1.4E+07	1.4E+07	2090	1.674504642	1.716389527	2.808E-07	2.22395E-06	0.09547	1	21	22	16	16	36	162	120	58	73	92
ENSMUSG00000021579	chr13	Lrrc14b	7.4E+07	7.4E+07	2755	-1.16948638	6.976107796	2.816E-07	2.22515E-06	0.06003	-1	2649	1756	3879	2920	2030	1652	2365	1101	1490	1469
ENSMUSG00000027353	chr2	Mcm8	1.3E+08	1.3E+08	3718	-1.57086873	1.269705048	2.818E-07	2.22515E-06	0.08012	-1	59	45	65	53	40	24	35	16	21	27
ENSMUSG00000039851	chr16	4932438H23Rik	9.1E+07	9.1E+07	2865	2.603948567	-0.56725042	2.816E-07	2.22515E-06	0.11025	1	3	2	1	0	5	23	24	11	17	21
ENSMUSG00000040867	chr12	Begain	1.1E+08	1.1E+08	3751	2.511534993	0.334462611	2.814E-07	2.22515E-06	0.18815	1	2	0	6	5	13	60	19	30	55	32
ENSMUSG00000045498	chr18	Pcdhb3	3.7E+07	3.7E+07	3787	2.371619511	-0.28272769	2.811E-07	2.22515E-06	0.10186	1	2	5	2	3	4	30	18	22	25	22
ENSMUSG00000002325	chr14	Irf9	5.6E+07	5.6E+07	5386	1.19358791	3.592774339	2.827E-07	2.23116E-06	0.0573	1	86	86	128	82	173	542	264	213	370	361
ENSMUSG00000035042	chr11	Ccl5	8.4E+07	8.4E+07	960	2.388227731	0.886789751	2.849E-07	2.24745E-06	0.19185	1	2	1	14	12	14	65	35	39	44	112
ENSMUSG00000031903	chr8	Pla2g15	1.1E+08	1.1E+08	2704	1.374265433	4.550446324	2.853E-07	2.24929E-06	0.08009	1	168	125	125	150	435	964	573	496	745	731
ENSMUSG00000036667	chr6	Fam115a	4.3E+07	4.3E+07	9622	1.170146734	3.549126785	2.858E-07	2.25243E-06	0.05465	1	98	85	103	80	174	435	250	281	347	338
ENSMUSG00000028514	chr4	Usp24	1.1E+08	1.1E+08	12350	-1.13115102	7.162973061	2.864E-07	2.2552E-06	0.05636	-1	2654	2023	4134	3612	2513	2028	2644	1306	1759	1626
ENSMUSG00000027104	chr2	Atf2	7.4E+07	7.4E+07	8187	-0.96043681	4.164537619	2.88E-07	2.26707E-06	0.03811	-1	358	270	406	319	431	282	361	177	211	234
ENSMUSG00000098900	chr7	Gm18190	7265498	7266077	832	-1.79609668	1.042998376	2.886E-07	2.27032E-06	0.10726	-1	50	34	55	60	34	24	31	6	16	18
ENSMUSG00000033685	chr7	Ucp2	1E+08	1E+08	6989	1.702019515	6.151543083	2.901E-07	2.27915E-06	0.12367	1	372	253	367	299	1376	2641	1922	1526	2342	2880
ENSMUSG00000093674	chr10	Rpl41	1.3E+08	1.3E+08	1168	1.164834855	7.897549341	2.9E-07	2.27915E-06	0.05987	1	1970	1611	1950	2107	3545	7866	5134	5166	8182	7744
ENSMUSG00000042734	chr12	Ttc9	8.2E+07	8.2E+07	2042	1.999302971	3.773863792	2.911E-07	2.28577E-06	0.16329	1	42	23	215	122	35	559	482	324	417	470
ENSMUSG00000022255	chr15	Mtdh	3.4E+07	3.4E+07	12096	-1.19074113	6.469977493	2.933E-07	2.30169E-06	0.0622	-1	1995	1551	2235	1847	1515	1233	1801	738	945	939
ENSMUSG00000036322	chr17	H2-Ea-ps	3.4E+07	3.4E+07	686	2.277884843	5.388786889	2.95E-07	2.3145E-06	0.21216	1	188	178	85	92	547	2914	630	974	916	1919
ENSMUSG00000074622	chr2	Mafb	1.6E+08	1.6E+08	3363	1.096085438	5.281335128	2.954E-07	2.31565E-06	0.05213	1	251	182	630	346	560	1141	1351	810	958	1219
ENSMUSG00000032925	chr14	Itgbl1	1.2E+08	1.2E+08	4229	1.198793774	4.212508195	2.959E-07	2.31874E-06	0.06026	1	148	130	249	120	208	950	637	331	367	444
ENSMUSG00000033276	chr1	Stk36	7.5E+07	7.5E+07	6437	1.981476888	1.209087368	2.968E-07	2.32344E-06	0.12493	1	14	15	4	13	17	71	59	49	108	68
ENSMUSG00000063895	chr14	Nupl1	6E+07	6E+07	2787	-1.34441112	3.664230903	2.967E-07	2.32344E-06	0.07462	-1	244	243	350	302	206	162	261	102	116	105
ENSMUSG00000046753	chr14	Ccdc66	2.7E+07	2.7E+07	2940	-1.31470575	3.075855998	2.975E-07	2.32695E-06	0.06902	-1	178	126	272	202	127	119	150	63	79	93
ENSMUSG00000019461	chr11	Plscr3	7E+07	7E+07	3148	1.09438959	4.82049252	2.985E-07	2.33362E-06	0.05135	1	217	158	308	234	484	940	556	618	962	880
ENSMUSG00000028041	chr3	Adam15	8.9E+07	8.9E+07	6145	1.220305134	5.765536524	3.033E-07	2.36964E-06	0.06497	1	316	318	543	400	978	2070	1235	1136	1806	1661
ENSMUSG00000022748	chr16	Cmss1	5.7E+07	5.7E+07	930	-0.91282417	4.268915002	3.065E-07	2.3936E-06	0.03445	-1	399	248	457	417	380	288	321	226	294	244
ENSMUSG00000043140	chr16	Tmem186	8633884	8636392	2736	-0.90312758	4.444495866	3.067E-07	2.3936E-06	0.03409	-1	374	309	541	461	463	326	431	232	272	309
ENSMUSG00000014956	chr5	Ppp1cb	3.2E+07	3.2E+07	7004	-1.32309076	8.427882928	3.095E-07	2.41413E-06	0.07717	-1	7982	5065	9961	8185	5943	3828	7268	2572	3350	3581
ENSMUSG00000029759	chr6	Pon3	5220852	5221722	3385	-0.85709343	4.922888974	3.099E-07	2.41592E-06	0.03121	-1	591	373	743	565	717	455	574	352	450	393
ENSMUSG00000034460	chr12	Six4	7.3E+07	7.3E+07	10855	-1.04724225	4.306518473	3.103E-07	2.41784E-06	0.04626	-1	430	274	475	502	312	261	349	193	248	283

ENSMUSG00000027366	chr2	Sppl2a	1.3E+08	1.3E+08	8665	-1.10488422	6.594487964	3.109E-07	2.42094E-06	0.05397	-1	2064	1550	2511	2164	1555	1403	1776	892	1134	1189
ENSMUSG00000038205	chr3	Prkab2	9.8E+07	9.8E+07	5096	-1.36222949	8.501459055	3.115E-07	2.42299E-06	0.08168	-1	9537	7471	7767	6755	6415	4075	6961	3100	3563	3384
ENSMUSG00000100685	chr1	Gm28610	1.5E+08	1.5E+08	406	-3.32828104	-0.07013171	3.114E-07	2.42299E-06	0.31329	-1	20	33	14	45	5	7	4	3	3	0
ENSMUSG00000039824	chr10	Myl6b	1.3E+08	1.3E+08	1026	1.341594814	3.695688574	3.126E-07	2.43055E-06	0.07445	1	71	63	162	141	125	378	324	194	399	634
ENSMUSG00000051242	chr18	Pcdhb9	3.7E+07	3.7E+07	3055	2.419337959	-0.25201511	3.152E-07	2.44904E-06	0.12162	1	5	3	2	2	4	42	24	21	21	14
ENSMUSG00000035561	chr4	Aldh1b1	4.6E+07	4.6E+07	2298	2.508598983	-0.30068215	3.157E-07	2.45193E-06	0.14502	1	1	0	3	7	4	34	13	19	28	24
ENSMUSG00000002897	chr6	Il17ra	1.2E+08	1.2E+08	3970	1.528761751	2.836378595	3.188E-07	2.47315E-06	0.09299	1	21	39	70	49	102	268	156	200	212	227
ENSMUSG00000015852	chr3	Fcrls	8.7E+07	8.7E+07	2334	1.872921159	4.201230755	3.186E-07	2.47315E-06	0.14501	1	90	142	48	59	232	966	419	492	623	479
ENSMUSG00000034161	chr15	Scx	7.6E+07	7.6E+07	1136	1.384062593	3.189757169	3.193E-07	2.47562E-06	0.07682	1	49	49	80	96	107	328	152	258	252	334
ENSMUSG00000028469	chr4	Npr2	4.4E+07	4.4E+07	4667	-1.07382176	5.737613779	3.218E-07	2.49381E-06	0.05069	-1	837	725	1707	1357	913	824	826	432	689	833
ENSMUSG00000001128	chrX	Cfp	2.1E+07	2.1E+07	1736	1.94278935	4.154933516	3.224E-07	2.49665E-06	0.15578	1	70	120	36	76	237	952	366	440	667	502
ENSMUSG00000021589	chr13	Rhobtb3	7.6E+07	7.6E+07	5684	-1.043926	5.407367343	3.257E-07	2.52078E-06	0.04767	-1	849	743	966	965	694	608	789	446	506	518
ENSMUSG00000038776	chr1	Ephx1	1.8E+08	1.8E+08	1950	1.201925375	4.956463404	3.263E-07	2.52459E-06	0.06245	1	243	213	238	191	551	971	770	590	996	1158
ENSMUSG00000002871	chr6	Tpra1	8.9E+07	8.9E+07	3026	1.003435042	4.823105632	3.268E-07	2.52695E-06	0.04338	1	214	145	414	329	365	844	639	573	981	852
ENSMUSG00000051980	chr16	Casr	3.6E+07	3.6E+07	4718	-2.00035088	2.020533646	3.314E-07	2.56121E-06	0.15328	-1	145	103	74	71	67	37	56	20	41	15
ENSMUSG00000032202	chr9	Rab27a	7.3E+07	7.3E+07	3879	1.67149524	1.296684268	3.349E-07	2.58674E-06	0.08996	1	15	16	31	10	11	80	65	64	72	79
ENSMUSG00000030208	chr6	Emp1	1.4E+08	1.4E+08	3046	1.338480028	6.655478162	3.375E-07	2.60556E-06	0.07898	1	569	608	816	660	1788	4098	2576	2792	2598	2765
ENSMUSG00000094441	chr17	Zfp955a	3.3E+07	3.3E+07	1638	-2.49987389	1.081701413	3.402E-07	2.62433E-06	0.22018	-1	53	36	95	58	26	17	33	5	7	4
ENSMUSG00000033107	chr18	Rnf125	2.1E+07	2.1E+07	1334	-2.49285193	-0.01566361	3.418E-07	2.63526E-06	0.17977	-1	33	25	27	9	23	7	13	4	2	3
ENSMUSG00000028059	chr3	Arhgef2	8.9E+07	8.9E+07	9496	0.979258262	5.010260313	3.513E-07	2.70751E-06	0.04168	1	226	201	364	328	562	1015	848	660	846	1049
ENSMUSG00000032046	chr2	Abhd12	1.5E+08	1.5E+08	2823	0.923455813	5.453126779	3.529E-07	2.71792E-06	0.03744	1	360	283	582	421	698	1358	1139	862	1245	1336
ENSMUSG00000021646	chr13	Mccc2	1E+08	1E+08	2123	-0.81705098	5.075055472	3.533E-07	2.72009E-06	0.02873	-1	671	434	719	587	861	601	483	402	503	531
ENSMUSG00000032312	chr9	Csk	5.8E+07	5.8E+07	2748	1.111689266	4.180090394	3.537E-07	2.72168E-06	0.05244	1	154	103	155	146	323	689	449	367	528	533
ENSMUSG00000004665	chr10	Cnn2	8E+07	8E+07	2460	1.111871972	4.136009358	3.571E-07	2.7458E-06	0.05261	1	97	95	242	161	275	666	420	372	485	540
ENSMUSG00000024878	chr19	Cbwd1	2.5E+07	2.5E+07	1944	-1.07482455	3.675244487	3.592E-07	2.76095E-06	0.04757	-1	276	210	302	257	242	188	249	108	145	167
ENSMUSG00000019853	chr10	Hebp2	1.9E+07	1.9E+07	1910	1.914029133	1.38012851	3.604E-07	2.76799E-06	0.12395	1	13	19	10	11	22	116	41	71	92	78
ENSMUSG00000010663	chr19	Fads1	1E+07	1E+07	3456	1.246245827	4.896971224	3.62E-07	2.77904E-06	0.06762	1	241	182	188	190	552	1094	754	657	912	913
ENSMUSG00000022723	chr16	Crybg3	5.9E+07	5.9E+07	7488	-0.95917	4.290577969	3.63E-07	2.78216E-06	0.03878	-1	325	210	602	425	446	264	316	220	263	302
ENSMUSG00000033792	chrX	Atp7a	1.1E+08	1.1E+08	8734	-3.06392577	1.776018206	3.626E-07	2.78216E-06	0.34233	-1	103	113	94	88	35	18	47	1	6	8
ENSMUSG00000051747	chr2	Ttn	7.7E+07	7.7E+07	116825	-1.18357009	12.51065955	3.63E-07	2.78216E-06	0.06306	-1	109683	77716	177580	159376	92762	72829	88433	52210	79102	77633
ENSMUSG00000027236	chr2	Eif3j1	1.2E+08	1.2E+08	5830	-1.08508684	5.655303483	3.663E-07	2.80614E-06	0.0522	-1	1235	829	1180	950	884	853	923	504	499	587
ENSMUSG00000026492	chr1	Tfb2m	1.8E+08	1.8E+08	2804	-0.900209	5.159339498	3.67E-07	2.80823E-06	0.03537	-1	696	531	878	735	653	605	635	421	405	510
ENSMUSG00000042505	chr6	Acn9	6956004	6956200	5095	-1.15350038	3.628417491	3.669E-07	2.80823E-06	0.05522	-1	276	193	283	285	231	138	247	113	153	140
ENSMUSG00000024588	chr18	Fech	6.4E+07	6.4E+07	2901	-1.17248995	7.025168383	3.681E-07	2.81522E-06	0.06156	-1	2851	2154	3819	2672	2012	1742	2438	1196	1504	1447
ENSMUSG00000023284	chr5	Zfp605	1.1E+08	1.1E+08	3497	-1.73699166	1.303474286	3.687E-07	2.81788E-06	0.10558	-1	64	54	65	54	36	30	34	18	13	21
ENSMUSG00000025241	chr9	Fyco1	1.2E+08	1.2E+08	8653	-1.46668087	8.083631937	3.702E-07	2.82784E-06	0.09529	-1	5636	3932	9993	7619	3097	2908	4684	2162	2456	2772
ENSMUSG00000022759	chr16	Lrrc74b	1.8E+07	1.8E+07	3941	-2.06183288	0.415795556	3.708E-07	2.82804E-06	0.13168	-1	50	18	39	24	24	18	10	3	8	13
ENSMUSG00000062627	chr4	Mysm1	9.5E+07	9.5E+07	8946	-1.32203556	2.755471961	3.707E-07	2.82804E-06	0.06985	-1	170	129	156	137	112	110	98	42	71	84
ENSMUSG00000072955	chrX	Tmsb15l	1.4E+08	1.4E+08	816	2.981481033	-0.52964023	3.708E-07	2.82804E-06	0.16983	1	1	2	0	1	5	10	16	21	28	24
ENSMUSG00000040829	chr11	Zmynd15	7E+07	7E+07	4409	2.088898046	0.75752489	3.728E-07	2.8415E-06	0.13371	1	5	7	5	9	18	87	29	31	51	64
ENSMUSG00000024087	chr17	Cyp1b1	8E+07	8E+07	5128	2.035621254	2.758256269	3.741E-07	2.85038E-06	0.16546	1	37	25	20	15	104	360	210	182	141	214
ENSMUSG00000067851	chr1	Arfgef1	1E+07	1E+07	11318	-1.15726855	6.78038053	3.767E-07	2.86845E-06	0.06004	-1	2282	1686	2993	2489	1973	1339	2270	924	1351	1217
ENSMUSG00000023809	chr17	Rps6ka2	7170115	7170443	5404	-1.30713885	7.077265852	3.785E-07	2.88083E-06	0.07626	-1	2711	1829	4546	3536	2062	1423	2614	1012	1513	1555
ENSMUSG00000013878	chr8	Rnf170	2.6E+07	2.6E+07	5032	-1.05684122	4.574455531	3.797E-07	2.88814E-06	0.04845	-1	549	440	489	474	399	335	444	219	334	275
ENSMUSG00000026064	chr1	Ptp4a1	3.1E+07	3.1E+07	5763	-0.97659449	4.918942941	3.825E-07	2.90767E-06	0.04158	-1	547	366	895	494	816	425	612	318	341	414
ENSMUSG00000025138	chr11	Sirt7	1.2E+08	1.2E+08	5148	1.18370319	3.619700726	3.832E-07	2.9116E-06	0.05822	1	83	67	126	93	211	462	286	239	362	414
ENSMUSG00000032942	chr7	Ucp3	1E+08	1E+08	3135	-1.40008909	6.770944152	3.837E-07	2.91405E-06	0.08706	-1	2952	954	4050	2047	2446	1124	1620	1007	786	1642
ENSMUSG00000039294	chr11	BC017643	1.2E+08	1.2E+08	4213	1.128206627	3.687893601	3.846E-07	2.91933E-06	0.05242	1	105	94	114	93	203	522	329	286	314	369
ENSMUSG00000038781	chr17	Stap2	5.6E+07	5.6E+07	1491	1.380018051	3.199360763	3.852E-07	2.92193E-06	0.07792	1	50	58	83	44	154	309	255	224	316	240
ENSMUSG00000031858	chr8	Mau2	7E+07	7E+07	5390	-0.96571497	4.750664035	3.856E-07	2.9237E-06	0.04053	-1	516	343	780	549	536	463	554	244	302	348
ENSMUSG00000072294	chr14	Klf12	1E+08	1E+08	1856	-2.91150872	0.010140082	3.882E-07	2.94177E-06	0.25688	-1	32	17	57	18	4	8	7	2	3	3
ENSMUSG00000096145	chr7	Vkorc1	1.3E+08	1.3E+08	767	1.467343181	4.107922271	3.915E-07	2.96509E-06	0.09198	1	116	92	92	99	302	724	330	395	602	557
ENSMUSG00000027424	chr2	Mgme1	1.4E+08	1.4E+08	3348	-1.04221231	3.779386895	3.921E-07	2.96793E-06	0.04516	-1	296	244	260	282	275	219	236	131	183	162
ENSMUSG00000027180	chr2	Fbxo3	1E+08	1E+08	7237	-1.09161078	6.228124241	3.93E-07	2.973E-06	0.05345	-1	1464	1007	2432	1462	1475	1023	1485	711	791	971
ENSMUSG00000036446	chr10	Lum	9.8E+07	9.8E+07	2075	1.222624282	6.3522815	3.943E-07	2.97814E-06	0.06666	1	868	757	597	652	648	3371	2111	1760	2531	2141
ENSMUSG00000050538	chr11	B230217C12Rik	9.8E+07	9.8E+07	2245	2.272957004	-0.34086024	3.942E-07	2.97814E-06	0.11099	1	1	1	6	3	6	24	20	25	18	23
ENSMUSG00000071267	chr17	Zfp942	2.2E+07	2.2E+07	5259	-1.23175365	2.756778164	3.942E-07	2.97814E-06	0.05946	-1	134	100	192	159	127	105	118	58	75	62
ENSMUSG00000099906	chr1	Gm28653	2.1E+07	2.1E+07	5276	3.063784938	1.922356271	3.966E-07	2.99384E-06	0.3474	1	3	0	30	27	2	139	127	113	94	190
ENSMUSG00000042350	chr12	Arel1	8.5E+07	8.5E+07	6044	-0.96122759	5.28719634	3.986E-07	3.00722E-06	0.04089	-1	845	607	906	810	672	634	738	394	474	518
ENSMUSG00000028860	chr4	Sytl1	1.3E+08	1.3E+08	2518	2.58101041	-0.4365737	4.01E-07	3.02359E-06	0.15156	1	0	1	3	0	9	27	19	13	23	25
ENSMUSG00000039701	chr3	Usp53	1.2E+08	1.2E+08	4014	-2.08716419	1.957594283	4.063E-07	3.06195E-06	0.16804	-1	84	62	145	124	57	29	69	23	11	20
ENSMUSG00000042744	chr5	Gm15800	1.2E+08	1.2E+08	16416	-0.91953699	4.513547914	4.086E-07	3.07815E-06	0.03645	-1	394	376	556	516	382	396	369	223	309	348
ENSMUSG00000023982	chr17	Guca1a	4.7E+07	4.7E+07	871	2.641468087	-0.35036935	4.096E-07	3.08344E-06	0.16275	1	3	0	3	5	2	45	13	11	20	28
ENSMUSG00000031497	chr8	Tnfsf13b	1E+07	1E+07	930	1.992004249	0.153663867	4.14E-07	3.11521E-06	0.089	1	5	6	5	3	10	39	26	25	31	39
ENSMUSG00000019467	chr10	Arhgef25	1.3E+08	1.3E+08	2387	0.910779972	4.276667368	4.219E-07	3.17109E-06	0.03492	1	185	152	222	185	270	743	457	342	523	573
ENSMUSG00000033964	chr1	Zbtb41	1.4E+08	1.4E+08	8362	-1.04182549	3.918328028	4.219E-07	3.17109E-06	0.04571	-1	291	226	391	346	273	206	292	150	157	217
ENSMUSG00000038039	chr10	Gcc2	5.8E+07	5.8E+07	9630	-0.92278267	4.66518775	4.275E-07	3.21149E-06	0.03706	-1	461	395	678	506	457	422	503	257	337	304

ENSMUSG00000076387	chr5	Mir671	2.5E+07	2.5E+07	98	1.797354047	2.236332402	4.337E-07	3.25675E-06	0.12602	1	28	21	27	16	65	167	69	133	172	181
ENSMUSG00000032562	chr9	Gnai2	1.1E+08	1.1E+08	3779	1.061157042	6.962093411	4.366E-07	3.27618E-06	0.05123	1	898	774	1430	1165	2008	4088	3199	2536	4084	3578
ENSMUSG00000050530	chr2	Fam171a1	3114224	3114265	4442	1.137843225	3.631013769	4.369E-07	3.27695E-06	0.05412	1	81	73	143	90	211	437	302	261	383	366
ENSMUSG00000023953	chr17	Polh	4.6E+07	4.6E+07	2569	-1.09550119	3.561950075	4.416E-07	3.31057E-06	0.04975	-1	231	186	334	255	199	147	207	133	143	139
ENSMUSG00000053560	chr8	Ier2	8.5E+07	8.5E+07	1522	1.274151895	3.958129184	4.44E-07	3.32683E-06	0.0694	1	88	104	119	170	201	397	305	431	541	529
ENSMUSG00000074766	chr2	Ism1	1.4E+08	1.4E+08	2965	2.301736364	2.084588377	4.452E-07	3.33365E-06	0.19971	1	15	33	9	9	31	257	64	128	139	114
ENSMUSG00000024789	chr19	Jak2	2.9E+07	2.9E+07	5030	-0.97201842	5.0332983	4.485E-07	3.35696E-06	0.04195	-1	687	447	918	589	659	538	699	292	396	393
ENSMUSG00000040722	chr9	Scamp5	5.7E+07	5.7E+07	3190	1.509438498	3.216493645	4.489E-07	3.35799E-06	0.0948	1	45	51	60	46	168	385	241	199	309	278
ENSMUSG00000051469	chr18	Zfp191	2.4E+07	2.4E+07	6271	-0.97629869	5.376285312	4.504E-07	3.36735E-06	0.04268	-1	785	693	1072	845	715	629	804	418	552	505
ENSMUSG00000040945	chr4	Rcc2	1.4E+08	1.4E+08	4155	1.044031358	4.616470465	4.512E-07	3.37196E-06	0.04773	1	216	164	240	212	389	799	484	666	734	660
ENSMUSG00000031666	chr8	Rbl2	9.1E+07	9.1E+07	6963	-1.11491633	5.619109336	4.555E-07	3.40017E-06	0.056	-1	1276	930	936	970	762	729	737	456	657	649
ENSMUSG00000065516	chr1	Mir214	1.6E+08	1.6E+08	110	2.970906528	-0.63575292	4.554E-07	3.40017E-06	0.15821	1	1	2	0	3	2	26	8	10	28	21
ENSMUSG00000097705	chr10	Gm26740	2.2E+07	2.2E+07	1724	-1.40628054	3.034549008	4.578E-07	3.41554E-06	0.08205	-1	236	180	151	135	153	119	125	59	75	91
ENSMUSG00000037664	chr7	Cdkn1c	1.4E+08	1.4E+08	1931	1.151380794	4.340619553	4.582E-07	3.41628E-06	0.05811	1	132	106	297	133	323	551	598	356	663	724
ENSMUSG00000026469	chr1	Xpr1	1.6E+08	1.6E+08	17880	-1.11849717	6.343887223	4.584E-07	3.4166E-06	0.05681	-1	1962	1496	1614	1337	1782	1056	1520	781	973	982
ENSMUSG00000016757	chr15	Ttll12	8.4E+07	8.4E+07	4010	1.064593279	4.06546094	4.592E-07	3.42062E-06	0.04839	1	139	116	147	189	221	586	333	349	585	475
ENSMUSG00000069792	chr11	Wfdc17	8.4E+07	8.4E+07	533	2.55487471	3.054249581	4.605E-07	3.42678E-06	0.25932	1	27	37	6	17	89	607	168	231	301	155
ENSMUSG00000072623	chr6	Zfp9	1.2E+08	1.2E+08	3968	-1.01378583	3.593181182	4.604E-07	3.42678E-06	0.04263	-1	258	191	300	229	226	228	197	111	148	150
ENSMUSG00000027715	chr3	Ccna2	3.7E+07	3.7E+07	3510	1.904739833	0.522952061	4.624E-07	3.43917E-06	0.10025	1	3	7	7	10	14	53	30	39	45	42
ENSMUSG00000063884	chr6	Ptcd3	7.2E+07	7.2E+07	2585	-1.01717648	5.495846674	4.633E-07	3.44349E-06	0.04656	-1	941	608	1256	1026	738	668	863	435	584	555
ENSMUSG00000025132	chr11	Arhgdia	1.2E+08	1.2E+08	2258	1.088723574	7.496606575	4.659E-07	3.46125E-06	0.0543	1	1344	1081	1995	1707	2840	5844	4379	3525	6144	5639
ENSMUSG00000078619	chr11	Smarcd2	1.1E+08	1.1E+08	3589	1.114551244	4.47897532	4.696E-07	3.48648E-06	0.05439	1	177	158	192	172	371	900	450	507	659	629
ENSMUSG00000079278	chr5	Tmem233	1.2E+08	1.2E+08	2477	-1.30809107	7.418444578	4.704E-07	3.49061E-06	0.07772	-1	4310	3510	2664	2757	4557	1989	2854	1378	2378	1641
ENSMUSG00000069920	chr8	B3gnt9	1.1E+08	1.1E+08	2516	1.261996547	2.450426168	4.707E-07	3.49163E-06	0.05951	1	44	35	45	50	62	248	160	110	143	127
ENSMUSG00000057346	chr15	Apol9a	7.7E+07	7.7E+07	1573	3.802188324	-0.7208479	4.711E-07	3.49258E-06	0.26307	1	1	2	0	0	1	32	9	2	28	21
ENSMUSG00000051067	chr10	Lingo3	8.1E+07	8.1E+07	3433	-1.1420296	3.781715207	4.739E-07	3.51132E-06	0.05583	-1	301	234	248	222	408	174	228	95	211	188
ENSMUSG00000041073	chr11	Nacad	6597823	6597909	4892	1.457754327	1.375094032	4.76E-07	3.52514E-06	0.06873	1	18	9	24	25	24	95	75	42	76	89
ENSMUSG00000021254	chr12	Gpatch2l	8.6E+07	8.6E+07	3953	-1.10596817	3.86685378	4.769E-07	3.53014E-06	0.05227	-1	240	231	485	304	251	213	275	133	187	153
ENSMUSG00000029204	chr5	Rhoh	6.6E+07	6.6E+07	4960	2.233166401	0.198560142	4.814E-07	3.56143E-06	0.12943	1	7	3	2	6	8	56	21	30	23	41
ENSMUSG00000019990	chr10	Pde7b	2E+07	2E+07	7232	-1.19999606	4.885745875	4.817E-07	3.56163E-06	0.06428	-1	599	393	974	765	400	401	575	260	281	351
ENSMUSG00000030282	chr6	Cmas	1.4E+08	1.4E+08	2783	0.816859089	5.270812515	4.84E-07	3.57676E-06	0.02962	1	391	284	556	373	535	1152	998	768	1017	1152
ENSMUSG00000044328	chr11	Trp53i13	7.8E+07	7.8E+07	2157	1.294546186	2.988150295	4.849E-07	3.58131E-06	0.0687	1	62	35	76	55	124	309	174	160	282	229
ENSMUSG00000039599	chr14	Fam149b	2E+07	2E+07	3146	-0.9950512	4.002400044	4.853E-07	3.58262E-06	0.04252	-1	299	235	411	363	297	259	317	141	212	189
ENSMUSG00000001983	chr11	Taco1	1.1E+08	1.1E+08	1383	-1.15275181	5.405439483	4.885E-07	3.60401E-06	0.05995	-1	790	576	1437	919	766	563	918	363	484	418
ENSMUSG00000026775	chr2	Yme1l1	2.3E+07	2.3E+07	8009	-1.02450576	5.824893753	4.908E-07	3.61947E-06	0.04772	-1	1188	849	1526	1136	1025	890	1142	543	622	703
ENSMUSG00000030587	chr7	2200002D01Rik	2.9E+07	2.9E+07	1530	2.038651592	0.701372294	4.913E-07	3.62102E-06	0.13478	1	4	5	12	4	20	60	28	35	61	62
ENSMUSG00000035273	chr5	Hpse	1E+08	1E+08	3516	1.985222634	2.536460579	4.918E-07	3.62311E-06	0.15933	1	31	24	15	15	90	299	171	108	211	163
ENSMUSG00000038664	chr9	Herc1	6.6E+07	6.6E+07	27464	-1.10014026	6.185860198	5.004E-07	3.68458E-06	0.05528	-1	1435	1136	1955	1808	1092	1043	1309	688	855	923
ENSMUSG00000041685	chr13	Fcho2	9.9E+07	9.9E+07	5229	-1.06222501	4.322187229	5.007E-07	3.68486E-06	0.04955	-1	420	291	615	406	311	312	375	188	199	275
ENSMUSG00000078680	chr4	Mup10	6.1E+07	6.1E+07	1391	5.606796559	0.569108956	5.016E-07	3.68905E-06	0.74486	1	0	3	0	0	0	168	0	19	51	41
ENSMUSG00000020859	chr11	Spag9	9.4E+07	9.4E+07	11209	-1.26474386	7.673156076	5.028E-07	3.69628E-06	0.07323	-1	3930	3026	6655	5039	3251	2594	4095	1671	1894	2293
ENSMUSG00000034463	chr14	Scara3	6.6E+07	6.6E+07	3405	1.234456931	4.503072223	5.149E-07	3.78304E-06	0.0674	1	192	157	139	146	386	905	518	515	676	669
ENSMUSG00000055480	chr13	Zfp458	6.7E+07	6.7E+07	3488	-2.49879726	-0.624545	5.199E-07	3.81816E-06	0.15273	-1	19	12	16	19	7	6	6	0	3	3
ENSMUSG00000085614	chr4	1700123M08Rik	1.2E+07	1.2E+07	1260	-1.30455697	2.593899951	5.233E-07	3.84105E-06	0.06804	-1	142	115	153	122	97	81	96	56	69	55
ENSMUSG00000037573	chr11	Tob1	9.4E+07	9.4E+07	2288	-1.16898927	7.034680621	5.271E-07	3.86634E-06	0.0629	-1	2502	1862	3055	3177	3174	1391	2813	1074	1457	1680
ENSMUSG00000037490	chr10	Slc2a12	2.3E+07	2.3E+07	4237	-1.4123112	3.163749989	5.286E-07	3.87566E-06	0.08433	-1	176	125	278	276	126	117	162	56	92	86
ENSMUSG00000003178	chr6	Mical3	1.2E+08	1.2E+08	2893	-1.47149208	2.943383767	5.324E-07	3.90129E-06	0.09056	-1	151	122	283	208	86	102	113	64	71	71
ENSMUSG00000046541	chr7	Zfp526	2.5E+07	2.5E+07	3354	-2.03336744	1.782586817	5.327E-07	3.90129E-06	0.16222	-1	73	57	127	103	54	39	58	12	24	9
ENSMUSG00000097317	chr2	Gm17281	9.1E+07	9.1E+07	3589	-1.12994741	4.120705303	5.331E-07	3.90267E-06	0.0562	-1	349	287	514	362	276	200	312	126	212	289
ENSMUSG00000003355	chr15	Fkbp11	9.9E+07	9.9E+07	731	1.970513638	1.284188201	5.339E-07	3.90612E-06	0.14082	1	11	7	33	7	15	121	42	73	79	59
ENSMUSG00000037706	chr7	Cd81	1.4E+08	1.4E+08	2270	1.016882403	7.320587973	5.344E-07	3.90829E-06	0.04793	1	1419	1081	1766	1415	2439	5747	3916	3376	4771	4401
ENSMUSG00000079487	chrX	Med12	1E+08	1E+08	7704	-0.94031786	4.219673755	5.362E-07	3.91915E-06	0.03853	-1	343	300	422	408	351	289	334	160	240	310
ENSMUSG00000022772	chr16	Senp5	3.2E+07	3.2E+07	4426	-1.4769599	2.520811997	5.372E-07	3.92459E-06	0.0891	-1	119	113	155	124	112	63	121	36	45	51
ENSMUSG00000074785	chr10	Plxnc1	9.5E+07	9.5E+07	7836	1.776371512	1.697194619	5.398E-07	3.94102E-06	0.11184	1	25	27	9	18	20	136	94	59	105	107
ENSMUSG00000028048	chr3	Gba	8.9E+07	8.9E+07	1950	0.835427833	4.474901047	5.438E-07	3.96824E-06	0.03002	1	229	175	245	240	312	741	573	437	618	576
ENSMUSG00000024042	chr17	Sik1	3.2E+07	3.2E+07	4511	1.328618651	4.280520256	5.449E-07	3.97208E-06	0.07821	1	86	103	231	254	172	488	448	514	516	840
ENSMUSG00000033355	chr16	Rtp4	2.4E+07	2.4E+07	1573	1.405388072	2.54977971	5.448E-07	3.97208E-06	0.07908	1	38	24	58	49	74	279	147	97	225	129
ENSMUSG00000020986	chr12	Sec23a	5.9E+07	5.9E+07	4840	-1.19338968	6.648970918	5.465E-07	3.98218E-06	0.06556	-1	2543	1854	2078	2120	1594	1476	1828	873	1133	1073
ENSMUSG00000023959	chr17	Clic5	4.4E+07	4.4E+07	5870	-1.10278099	7.1166145	5.513E-07	4.01329E-06	0.05632	-1	2639	1883	4054	3271	2591	2017	2687	1379	1519	1561
ENSMUSG00000050578	chr9	Mmp13	7272514	7272677	2675	2.099297226	-0.03292807	5.514E-07	4.01329E-06	0.10535	1	3	1	6	7	7	42	33	23	17	26
ENSMUSG00000022651	chr16	Retnlg	4.9E+07	4.9E+07	608	2.965332058	-0.50974202	5.518E-07	4.01445E-06	0.17899	1	3	1	0	3	2	42	10	15	12	25
ENSMUSG00000082694	chr6	Gm16187	1.3E+08	1.3E+08	199	2.744384909	-0.15749368	5.619E-07	4.08561E-06	0.18345	1	2	4	2	1	5	57	14	15	16	36
ENSMUSG00000056498	chr3	Tmem154	8.5E+07	8.5E+07	4738	1.675098952	1.315121081	5.631E-07	4.09255E-06	0.09943	1	18	6	22	10	31	109	62	47	63	93
ENSMUSG00000026259	chr1	Ngef	8.7E+07	8.7E+07	3905	2.256992765	0.101603807	5.69E-07	4.13108E-06	0.13224	1	5	4	3	1	11	49	19	26	30	35
ENSMUSG00000053799	chr19	Exoc6	3.8E+07	3.8E+07	2729	-1.08908193	5.771966457	5.688E-07	4.13108E-06	0.05447	-1	1146	809	1570	1174	908	729	1131	507	602	668
ENSMUSG00000024887	chr19	Asah2	3.2E+07	3.2E+07	4682	-1.0224093	3.344801344	5.728E-07	4.15622E-06	0.04311	-1	224	152	229	205	205	164	176	104	125	123
ENSMUSG00000033453	chr9	Adamts15	3.1E+07	3.1E+07	5928	1.250833114	3.096554392	5.781E-07	4.19244E-06	0.06404	1	51	79	82	75	81	323	205	236	241	206

ENSMUSG00000028760	chr4	Eif4g3	1.4E+08	1.4E+08	11063	-1.08169014	7.031473131	5.799E-07	4.20381E-06	0.05442	-1	2775	2154	3323	2816	2167	1852	2408	1189	1526	1782
ENSMUSG00000035898	chr5	Uba6	8.6E+07	8.6E+07	6726	-1.54741847	2.263268201	5.821E-07	4.21736E-06	0.09608	-1	118	66	138	130	83	59	89	35	28	42
ENSMUSG00000026502	chr1	Desi2	1.8E+08	1.8E+08	9156	-0.97330636	5.817538507	5.853E-07	4.23857E-06	0.04365	-1	1065	900	1429	1193	1008	839	1086	579	700	747
ENSMUSG00000048351	chr4	Coa7	1.1E+08	1.1E+08	3851	-0.93783891	4.622490982	5.872E-07	4.24953E-06	0.03931	-1	474	366	580	586	411	416	464	222	343	322
ENSMUSG00000031604	chr8	Msmo1	6.5E+07	6.5E+07	6144	1.312895349	3.541601229	5.928E-07	4.28811E-06	0.07445	1	60	69	101	72	213	460	380	253	284	334
ENSMUSG00000028337	chr4	Coro2a	4.7E+07	4.7E+07	6459	2.135265736	1.178029322	5.98E-07	4.32351E-06	0.16904	1	9	3	9	6	35	101	52	53	61	90
ENSMUSG00000020097	chr10	Sgpl1	6.1E+07	6.1E+07	6143	1.280015354	5.181263472	6.017E-07	4.34829E-06	0.07464	1	307	188	260	194	696	1245	1086	654	1202	1177
ENSMUSG00000089075	chr3	Gm23820	1E+08	1E+08	300	-2.45665936	-0.19273244	6.048E-07	4.36808E-06	0.16996	-1	24	25	13	20	18	3	10	2	2	9
ENSMUSG00000011884	chr5	Gltp	1.1E+08	1.1E+08	1757	1.264285788	4.760684744	6.063E-07	4.37659E-06	0.07237	1	183	144	210	166	541	919	719	514	897	926
ENSMUSG00000031111	chrX	Igsf1	5E+07	5E+07	5768	1.522214211	1.908692237	6.096E-07	4.39803E-06	0.08744	1	18	18	37	40	29	77	101	104	132	127
ENSMUSG00000032525	chr9	Nktr	1.2E+08	1.2E+08	17457	-0.95458927	5.678210721	6.12E-07	4.41351E-06	0.04207	-1	1040	874	1168	1006	918	884	853	479	609	822
ENSMUSG00000025656	chrX	Arhgef9	9.5E+07	9.5E+07	8714	-1.03861726	4.101433959	6.142E-07	4.42722E-06	0.04766	-1	375	258	431	397	258	259	306	155	239	210
ENSMUSG00000039512	chr17	Uhrf1bp1	2.8E+07	2.8E+07	8708	-1.06038035	5.373210458	6.22E-07	4.48056E-06	0.05168	-1	707	577	1269	1021	691	616	799	387	566	430
ENSMUSG00000037977	chr9	6430571L13Rik	1.1E+08	1.1E+08	2912	-0.8593463	5.121781544	6.231E-07	4.48616E-06	0.03345	-1	672	435	840	627	862	475	588	367	637	487
ENSMUSG00000100934	chr2	FMN1	1.1E+08	1.1E+08	3615	2.189795119	-0.15058227	6.321E-07	4.54881E-06	0.10488	1	6	4	5	2	3	40	29	18	16	27
ENSMUSG00000022098	chr14	Bmp1	7E+07	7E+07	3757	1.185980813	5.199302871	6.388E-07	4.59378E-06	0.06437	1	273	267	276	228	666	1540	966	728	984	1117
ENSMUSG00000027751	chr3	Supt20	5.5E+07	5.5E+07	1968	-1.52054959	2.221836581	6.39E-07	4.59378E-06	0.09416	-1	114	78	120	109	91	61	93	23	42	34
ENSMUSG00000032508	chr9	Myd88	1.2E+08	1.2E+08	2576	1.42022241	3.581460551	6.414E-07	4.60877E-06	0.08795	1	57	73	97	65	208	472	244	322	354	376
ENSMUSG00000060470	chr8	Gpr97	9.5E+07	9.5E+07	2436	2.162000276	-0.0086822	6.457E-07	4.63743E-06	0.11233	1	3	4	6	6	4	28	25	14	29	49
ENSMUSG00000020128	chr11	Vps54	2.1E+07	2.1E+07	7515	-0.88182647	4.693707732	6.47E-07	4.64455E-06	0.03494	-1	485	439	587	493	487	439	501	260	336	360
ENSMUSG00000061244	chr14	Exoc5	4.9E+07	4.9E+07	9932	-0.89871582	4.826706692	6.507E-07	4.66861E-06	0.03652	-1	529	423	689	613	517	436	577	290	364	391
ENSMUSG00000050212	chr4	Eva1b	1.3E+08	1.3E+08	1942	1.478589787	2.961603029	6.556E-07	4.70079E-06	0.09294	1	39	37	64	42	135	306	162	179	283	235
ENSMUSG00000061232	chr17	H2-K1	3.4E+07	3.4E+07	2608	1.64465919	7.598580684	6.57E-07	4.70855E-06	0.12372	1	1171	933	1094	820	3315	9841	3493	3808	6058	7802
ENSMUSG00000039158	chr4	Akna	6.3E+07	6.3E+07	5765	1.25109983	2.745725024	6.578E-07	4.71196E-06	0.06356	1	51	36	56	52	104	242	171	139	165	245
ENSMUSG00000020024	chr10	Cep83	9.5E+07	9.5E+07	2986	-1.03867045	3.621615229	6.609E-07	4.7321E-06	0.04627	-1	253	195	338	216	241	176	239	125	139	153
ENSMUSG00000015846	chr2	Rxra	2.8E+07	2.8E+07	5462	-1.02397194	7.405546766	6.669E-07	4.77266E-06	0.04948	-1	2906	2489	4385	3672	3836	2278	3264	1529	2454	2126
ENSMUSG00000054477	chr18	Kcnn2	4.5E+07	4.5E+07	7321	-2.34673038	0.628797738	6.678E-07	4.77651E-06	0.19681	-1	31	12	81	41	32	8	19	1	15	8
ENSMUSG00000005893	chr6	Nr2c2	9.2E+07	9.2E+07	9152	-0.91961946	5.061055924	6.901E-07	4.93354E-06	0.03882	-1	630	578	868	612	562	575	631	325	408	472
ENSMUSG00000004317	chrX	Clcn5	7153810	7159819	11452	1.184534163	2.425322814	6.943E-07	4.96094E-06	0.05329	1	39	43	55	38	66	179	145	129	150	144
ENSMUSG00000030126	chr6	Tmcc1	1.2E+08	1.2E+08	7250	-1.01396053	5.846747378	6.998E-07	4.99755E-06	0.0481	-1	1164	1030	1206	1171	1108	830	1133	530	792	689
ENSMUSG00000073409	chr17	H2-Q6	3.5E+07	3.5E+07	2085	1.518551839	4.841570879	7.019E-07	5.01001E-06	0.10499	1	218	139	166	159	458	1632	503	510	683	1180
ENSMUSG00000064147	chr17	Rab44	2.9E+07	2.9E+07	4109	2.773081164	0.117900335	7.024E-07	5.01127E-06	0.21181	1	0	6	5	3	3	71	18	11	39	35
ENSMUSG00000018796	chr8	Acsl1	4.6E+07	4.6E+07	9449	-1.42617906	8.646383819	7.044E-07	5.01267E-06	0.09492	-1	6208	2985	18043	9530	10570	5193	6015	2905	3587	5096
ENSMUSG00000021786	chr14	Oxsm	1.6E+07	1.6E+07	4082	-0.94476596	3.811949381	7.044E-07	5.01267E-06	0.03852	-1	272	202	386	258	280	245	253	151	180	165
ENSMUSG00000025789	chr7	St8sia2	7.4E+07	7.4E+07	5384	1.897693525	1.180768218	7.032E-07	5.01267E-06	0.12878	1	20	5	18	15	10	49	45	69	89	84
ENSMUSG00000040113	chr1	Mettl11b	1.6E+08	1.6E+08	1848	-3.44826198	2.645436306	7.038E-07	5.01267E-06	0.45462	-1	52	69	372	328	84	4	74	13	8	9
ENSMUSG00000096910	chr17	Zfp955b	3.3E+07	3.3E+07	1638	-2.49530693	1.383919285	7.033E-07	5.01267E-06	0.24329	-1	88	47	92	74	24	25	38	3	9	9
ENSMUSG00000025094	chr19	Slc18a2	5.9E+07	5.9E+07	3803	2.843076396	0.728977302	7.064E-07	5.02413E-06	0.25804	1	3	11	1	4	6	134	23	32	42	49
ENSMUSG00000034744	chr6	Nagk	8.4E+07	8.4E+07	3293	1.069834078	3.782468577	7.102E-07	5.04877E-06	0.04989	1	126	85	124	113	227	494	331	250	445	410
ENSMUSG00000006398	chr4	Cdc20	1.2E+08	1.2E+08	1868	1.962637862	0.152665736	7.123E-07	5.06099E-06	0.09916	1	4	3	7	7	9	48	20	30	33	28
ENSMUSG00000035673	chr10	Sbno2	8E+07	8E+07	4227	1.083290776	4.114902369	7.163E-07	5.08679E-06	0.05253	1	135	104	202	146	268	654	352	483	434	463
ENSMUSG00000040761	chr4	Spen	1.4E+08	1.4E+08	14089	-1.07532406	4.34565845	7.198E-07	5.10953E-06	0.05246	-1	360	291	601	457	387	317	448	158	230	223
ENSMUSG00000054263	chr15	Lifr	7129559	7129826	10330	-0.88095356	5.293693445	7.22E-07	5.12208E-06	0.03586	-1	734	491	1125	689	873	669	766	406	503	532
ENSMUSG00000067925	chrX	Cxx1a	5.4E+07	5.4E+07	1195	0.912669658	4.376045815	7.313E-07	5.18594E-06	0.03719	1	183	133	245	223	319	562	495	424	674	624
ENSMUSG00000026131	chr1	Dst	3.4E+07	3.4E+07	38847	-1.41065497	8.51697679	7.332E-07	5.19636E-06	0.09323	-1	7382	4585	13758	10118	5145	3880	7105	2647	3559	3757
ENSMUSG00000030301	chr6	Ccdc91	1.5E+08	1.5E+08	2827	-1.01141394	6.501842488	7.34E-07	5.19971E-06	0.04838	-1	1847	1390	2143	1726	2018	1331	1809	814	1312	1013
ENSMUSG00000005410	chr8	Mcm5	7.5E+07	7.5E+07	3422	1.637164178	1.461057551	7.354E-07	5.20699E-06	0.09813	1	23	7	27	15	26	138	67	55	96	58
ENSMUSG00000052760	chr1	A630001G21Rik	8.6E+07	8.6E+07	2709	2.318819602	0.584092513	7.389E-07	5.22903E-06	0.17448	1	2	7	5	2	18	80	30	32	40	53
ENSMUSG00000078684	chr3	5830417I10Rik	8.9E+07	8.9E+07	6190	-1.93797773	0.253238522	7.403E-07	5.23591E-06	0.11131	-1	22	15	45	28	28	10	20	6	6	6
ENSMUSG00000038543	chr3	BC028528	9.6E+07	9.6E+07	1402	1.638751828	1.777720322	7.411E-07	5.23906E-06	0.10574	1	22	7	29	18	50	154	78	69	100	119
ENSMUSG00000030655	chr7	Smg1	1.2E+08	1.2E+08	21225	-1.01065082	5.708717668	7.43E-07	5.24988E-06	0.04789	-1	919	840	1491	1197	798	915	811	540	600	744
ENSMUSG00000040359	chr4	Ufl1	2.5E+07	2.5E+07	5706	-0.95667522	4.725120502	7.46E-07	5.26869E-06	0.04191	-1	555	385	647	583	442	453	531	244	330	324
ENSMUSG00000037638	chr12	Zbtb42	1.1E+08	1.1E+08	3490	1.453380368	1.566115522	7.519E-07	5.30782E-06	0.07502	1	18	16	30	13	39	78	99	62	92	95
ENSMUSG00000027287	chr2	Snap23	1.2E+08	1.2E+08	4293	-1.15085949	5.199380973	7.62E-07	5.37625E-06	0.0617	-1	881	666	875	779	512	640	641	376	364	353
ENSMUSG00000032690	chr5	Oas2	1.2E+08	1.2E+08	4451	1.839265786	1.644612074	7.631E-07	5.38121E-06	0.1296	1	17	15	21	9	37	185	78	40	112	83
ENSMUSG00000026117	chr1	Zap70	3.7E+07	3.7E+07	2992	2.489751284	-0.19690178	7.642E-07	5.38637E-06	0.15189	1	7	1	2	4	2	28	19	13	23	46
ENSMUSG00000022235	chr15	Cmbl	3.2E+07	3.2E+07	1228	-1.24332098	5.580652565	7.71E-07	5.42891E-06	0.07235	-1	1210	1035	586	778	1245	726	628	425	618	561
ENSMUSG00000084843	chr2	B230312C02Rik	1.8E+08	1.8E+08	1703	2.495406303	3.673111056	7.71E-07	5.42891E-06	0.26268	1	61	56	30	93	28	204	154	452	1015	288
ENSMUSG00000097715	chr13	Gpr137b-ps	1.3E+07	1.3E+07	2997	1.500945775	1.451718145	7.722E-07	5.43473E-06	0.07937	1	15	12	24	19	34	76	99	40	88	98
ENSMUSG00000070348	chr7	Ccnd1	1.4E+08	1.4E+08	3835	1.384203539	4.11434234	7.753E-07	5.45333E-06	0.08703	1	78	70	222	118	276	759	352	492	526	421
ENSMUSG00000098598	chr15	Pou6f1	1E+08	1E+08	906	-1.92683467	1.454416823	7.78E-07	5.4698E-06	0.1437	-1	61	49	89	72	50	14	53	15	22	12
ENSMUSG00000034636	chr4	Zyg11b	1.1E+08	1.1E+08	9046	-1.13535403	6.483515823	7.802E-07	5.48232E-06	0.06105	-1	1799	1263	2920	2055	1309	1301	1631	845	1003	1047
ENSMUSG00000045348	chr5	Nyap1	1.4E+08	1.4E+08	4260	2.372817733	-0.46621013	7.851E-07	5.51394E-06	0.11373	1	1	3	4	1	5	21	17	11	28	25
ENSMUSG00000027650	chr2	Tti1	1.6E+08	1.6E+08	4129	-0.85683342	4.660608269	7.916E-07	5.55724E-06	0.03333	-1	474	312	637	556	500	396	498	257	381	337
ENSMUSG00000020635	chr12	Fkbp1b	4833175	4833795	979	2.012614874	0.934147814	7.94E-07	5.57094E-06	0.13512	1	14	12	11	3	11	88	35	32	63	78
ENSMUSG00000076033	chr13	Mir692-3	7.4E+07	7.4E+07	109	2.093505905	0.69876627	7.944E-07	5.57094E-06	0.14868	1	5	3	8	5	23	60	37	56	51	38
ENSMUSG00000023973	chr17	Cnpy3	4.7E+07	4.7E+07	2659	1.036072093	4.309314808	8.017E-07	5.61931E-06	0.04859	1	150	141	189	169	342	762	460	362	625	565

ENSMUSG00000032382	chr9	Snx1	6.6E+07	6.6E+07	4339	0.841671357	4.579821621	8.079E-07	5.66007E-06	0.03191	1	206	175	299	241	390	786	586	471	653	677
ENSMUSG00000000901	chr10	Mmp11	7.6E+07	7.6E+07	2572	1.244747767	2.864828147	8.121E-07	5.68644E-06	0.06467	1	58	44	70	43	111	298	201	123	198	239
ENSMUSG00000035963	chr10	Odf3l2	8E+07	8E+07	1248	-4.20668916	1.924656033	8.21E-07	5.74591E-06	0.62288	-1	16	16	129	23	428	2	25	4	3	5
ENSMUSG00000034266	chr12	Batf	8.6E+07	8.6E+07	955	2.592409501	0.123083002	8.229E-07	5.7565E-06	0.20477	1	6	1	0	2	11	45	18	16	42	48
ENSMUSG00000055884	chr12	Fancm	6.5E+07	6.5E+07	7775	-1.57245468	1.062176277	8.312E-07	5.81167E-06	0.08617	-1	60	34	45	52	34	27	25	15	19	20
ENSMUSG00000036599	chr5	Chst12	1.4E+08	1.4E+08	2362	1.373860738	3.898554659	8.513E-07	5.9496E-06	0.08494	1	121	98	90	67	250	543	339	316	539	476
ENSMUSG00000038312	chr2	Edem2	1.6E+08	1.6E+08	3463	1.159051581	3.744652197	8.572E-07	5.98781E-06	0.05993	1	124	72	125	89	226	479	340	221	416	470
ENSMUSG00000011382	chr7	Dhdh	4.5E+07	4.5E+07	3678	-1.14382506	5.491972795	8.604E-07	6.00685E-06	0.06184	-1	1117	871	640	677	1230	707	692	419	510	593
ENSMUSG00000037151	chr10	Lrrc20	6.1E+07	6.1E+07	2619	-1.14843906	7.6112026	8.612E-07	6.00949E-06	0.06328	-1	4141	2978	5704	3887	3683	2433	4161	1647	2303	2156
ENSMUSG00000021486	chr13	Prelid1	5.5E+07	5.5E+07	1088	1.261517305	4.982751804	8.661E-07	6.04052E-06	0.0744	1	189	200	245	190	618	1176	730	738	1043	907
ENSMUSG00000103268	chr9	AC161246.1	1.1E+08	1.1E+08	3165	-2.04518334	7.214574306	8.712E-07	6.07348E-06	0.19021	-1	3576	2490	5486	4437	2049	1170	3248	568	636	566
ENSMUSG00000006169	chr11	Clint1	4.6E+07	4.6E+07	6946	-0.9548139	5.304391988	8.775E-07	6.11385E-06	0.04297	-1	667	602	1047	866	753	577	840	374	484	529
ENSMUSG00000006191	chr13	Cdkal1	2.9E+07	2.9E+07	12799	-0.98162051	3.998459378	8.789E-07	6.1209E-06	0.04333	-1	303	260	388	347	281	241	312	167	187	204
ENSMUSG00000033400	chr3	Agl	1.2E+08	1.2E+08	12803	-1.18837329	9.646156236	8.838E-07	6.15196E-06	0.06799	-1	14911	12708	21853	19661	14727	8318	16172	7024	9334	9872
ENSMUSG00000047747	chr8	Rnf150	8.3E+07	8.3E+07	9685	-1.02685384	5.7403804	8.911E-07	6.1994E-06	0.05022	-1	1241	920	1249	902	1004	785	1060	473	649	713
ENSMUSG00000054277	chr15	Arfgap3	8.3E+07	8.3E+07	2618	1.081497489	3.551607315	8.921E-07	6.20329E-06	0.05109	1	105	79	104	85	196	431	319	252	316	317
ENSMUSG00000042404	chr3	Dennd4b	9E+07	9E+07	6031	-1.04809401	6.980896623	8.953E-07	6.22267E-06	0.05291	-1	2370	1731	3510	2870	2486	1624	2443	1074	1880	1574
ENSMUSG00000050122	chr1	Vwa3b	3.7E+07	3.7E+07	5386	-1.73536665	2.108303692	9.04E-07	6.28043E-06	0.12548	-1	94	54	95	185	63	43	63	24	45	31
ENSMUSG00000020681	chr11	Ace	1.1E+08	1.1E+08	5287	1.094732156	6.236820095	9.123E-07	6.33431E-06	0.05742	1	484	439	896	636	1319	2631	2522	1377	2308	1913
ENSMUSG00000012819	chr10	Cdh23	6E+07	6E+07	16939	-1.41833118	1.763973959	9.134E-07	6.33922E-06	0.07704	-1	65	50	102	62	94	28	59	32	27	40
ENSMUSG00000040387	chr4	Klhl32	2.5E+07	2.5E+07	7826	2.597355099	-0.24919122	9.199E-07	6.38115E-06	0.15779	1	4	4	1	4	1	12	35	16	27	33
ENSMUSG00000043496	chr6	Tril	5.4E+07	5.4E+07	5365	1.147959038	3.411754076	9.24E-07	6.40667E-06	0.05708	1	92	79	76	84	161	415	275	217	321	281
ENSMUSG00000056211	chr1	R3hdm1	1.3E+08	1.3E+08	31486	-1.01034447	5.84084791	9.281E-07	6.43143E-06	0.04882	-1	1001	781	1676	1340	1041	778	1154	522	743	766
ENSMUSG00000020532	chr11	Acaca	8.4E+07	8.4E+07	15155	-1.92740176	4.227474309	9.291E-07	6.43525E-06	0.16779	-1	663	283	167	202	928	187	119	155	220	111
ENSMUSG00000019726	chr13	Lyst	1.4E+07	1.4E+07	11806	-1.36489457	2.123121137	9.329E-07	6.45223E-06	0.07574	-1	85	81	124	92	82	66	79	30	40	38
ENSMUSG00000024164	chr17	C3	5.7E+07	5.7E+07	5143	1.470290783	8.210448705	9.329E-07	6.45223E-06	0.10279	1	1883	2157	1357	1725	4674	13179	7089	5652	9819	10089
ENSMUSG00000026548	chr1	Slamf9	1.7E+08	1.7E+08	1313	1.800155756	2.09498466	9.328E-07	6.45223E-06	0.1317	1	19	24	17	19	60	233	90	72	122	162
ENSMUSG00000036291	chr14	Ap5m1	4.9E+07	4.9E+07	3165	-1.22664067	3.099687031	9.471E-07	6.54741E-06	0.06547	-1	183	144	238	185	143	110	164	86	81	86
ENSMUSG00000023861	chr17	Mpc1	8282904	8283017	2082	-1.24864189	6.964483355	9.533E-07	6.58683E-06	0.07492	-1	2404	1442	4681	2933	2216	1644	2525	1010	1299	1268
ENSMUSG00000041992	chr12	Rapgef5	1.2E+08	1.2E+08	3987	-1.99758453	1.10024539	9.635E-07	6.65355E-06	0.15221	-1	41	21	86	64	49	23	35	8	6	16
ENSMUSG00000024725	chr19	Ostf1	1.9E+07	1.9E+07	4784	1.11770677	5.390466569	9.651E-07	6.66176E-06	0.05938	1	337	286	360	276	774	1449	1012	882	1351	1246
ENSMUSG00000048874	chr1	Phf3	3.1E+07	3.1E+07	14190	-0.84394382	5.097881771	9.714E-07	6.7021E-06	0.03346	-1	648	513	794	688	654	536	686	368	438	514
ENSMUSG00000009731	chrX	Kcnd1	7822289	7824963	5287	2.206044149	0.133125147	9.735E-07	6.70982E-06	0.13299	1	4	6	3	2	10	39	21	21	51	30
ENSMUSG00000023984	chr17	Gm20517	4.8E+07	4.8E+07	6495	-1.17383245	3.029378233	9.735E-07	6.70982E-06	0.05992	-1	161	141	210	176	152	117	162	64	91	88
ENSMUSG00000021820	chr14	Camk2g	2.1E+07	2.1E+07	3703	-1.06206016	7.501631614	9.778E-07	6.73626E-06	0.05483	-1	3661	3060	3811	4158	3469	2540	3336	1703	2575	2058
ENSMUSG00000023019	chr15	Gpd1	1E+08	1E+08	2961	-1.29154449	9.332456163	9.808E-07	6.7498E-06	0.08054	-1	13969	9641	10632	11784	23613	6308	9422	5389	10913	6583
ENSMUSG00000028584	chr4	Lrrc38	1.4E+08	1.4E+08	2324	-1.01835336	5.264841604	9.803E-07	6.7498E-06	0.04934	-1	796	642	743	647	1020	449	744	352	637	451
ENSMUSG00000025862	chrX	Stag2	4.2E+07	4.2E+07	8273	-1.03436164	5.794011508	9.823E-07	6.751E-06	0.05139	-1	1258	1002	1245	1019	963	810	1080	514	680	712
ENSMUSG00000054400	chr8	Cklf	1E+08	1E+08	2098	2.260454931	0.330839872	9.824E-07	6.751E-06	0.15135	1	3	9	4	1	11	51	23	28	42	46
ENSMUSG00000079297	chrX	Gm2223	3.4E+07	3.4E+07	1350	-1.85823293	1.935967745	9.821E-07	6.751E-06	0.14412	-1	105	84	76	114	50	34	66	23	30	18
ENSMUSG00000056268	chr1	Dennd1b	1.4E+08	1.4E+08	8314	-0.957842	4.188499235	9.846E-07	6.76277E-06	0.04199	-1	366	291	486	339	319	287	355	187	215	241
ENSMUSG00000022439	chr15	Parvg	8.4E+07	8.4E+07	3090	2.087235933	1.136238197	9.859E-07	6.76832E-06	0.15913	1	10	8	4	8	29	81	57	35	63	111
ENSMUSG00000039202	chr7	Abhd2	7.9E+07	7.9E+07	10571	1.108849874	3.480074311	9.906E-07	6.79765E-06	0.05469	1	79	63	161	76	169	395	305	253	256	351
ENSMUSG00000020598	chr12	Nrcam	4.4E+07	4.4E+07	7581	1.765886192	1.358007337	9.935E-07	6.81382E-06	0.11688	1	11	12	16	15	30	85	54	99	53	82
ENSMUSG00000025314	chr2	Ptprj	9E+07	9E+07	8352	1.252669203	3.423157079	9.945E-07	6.81739E-06	0.06912	1	69	92	71	78	157	467	292	210	286	310
ENSMUSG00000038244	chr7	Mical2	1.1E+08	1.1E+08	11510	-1.56293969	6.863165569	9.983E-07	6.84022E-06	0.1159	-1	2270	2759	2561	3452	1435	720	1871	791	1540	1162
ENSMUSG00000056608	chr8	Chd9	9.1E+07	9.1E+07	11565	-0.92893488	4.350594111	1.003E-06	6.87225E-06	0.03973	-1	370	323	569	423	319	357	339	223	260	276
ENSMUSG00000037098	chr17	Rab11fip3	2.6E+07	2.6E+07	6789	-1.11339176	6.795656029	1.007E-06	6.89449E-06	0.06009	-1	1999	1663	3108	2917	1762	1325	2002	985	1385	1602
ENSMUSG00000038023	chr5	Atp6v0a2	1.2E+08	1.2E+08	3019	-1.12032474	4.243546182	1.016E-06	6.95068E-06	0.05844	-1	346	251	603	458	322	266	406	157	224	194
ENSMUSG00000048047	chrX	Zbtb33	3.8E+07	3.8E+07	5122	-1.2482729	2.899369934	1.028E-06	7.02963E-06	0.0677	-1	153	135	180	171	135	94	146	56	90	73
ENSMUSG00000039987	chr5	Phtf2	2.1E+07	2.1E+07	6929	-1.13206889	7.295563042	1.031E-06	7.04915E-06	0.06235	-1	3509	2460	3850	3707	2545	2030	3082	1438	1763	1931
ENSMUSG00000014599	chr3	Csf1	1.1E+08	1.1E+08	5262	1.121434413	4.929860844	1.033E-06	7.05282E-06	0.05945	1	229	239	220	229	532	1183	739	751	823	795
ENSMUSG00000063904	chr19	Dpp3	4907229	4907797	2683	0.819668078	4.979954145	1.033E-06	7.05282E-06	0.03151	1	279	202	523	346	418	995	812	618	921	821
ENSMUSG00000020571	chr12	Pdia6	1.7E+07	1.7E+07	3745	1.100627009	6.684570837	1.037E-06	7.07866E-06	0.05878	1	911	681	965	903	1533	4558	2135	2453	2814	2593
ENSMUSG00000006344	chr10	Ggt5	7.6E+07	7.6E+07	4736	1.456860165	3.375827324	1.052E-06	7.16992E-06	0.09474	1	80	77	49	69	129	430	164	267	368	315
ENSMUSG00000033781	chr13	Asb13	3634032	3634175	3347	-0.93184743	4.093895282	1.052E-06	7.16992E-06	0.03969	-1	344	291	396	328	299	296	301	175	231	216
ENSMUSG00000040428	chr7	Plekha4	4.6E+07	4.6E+07	4187	1.343437166	2.200287232	1.051E-06	7.16992E-06	0.07069	1	36	35	42	35	39	163	105	70	160	172
ENSMUSG00000024379	chr18	Tslp	3.3E+07	3.3E+07	1133	2.235740232	1.275884178	1.056E-06	7.19621E-06	0.18903	1	9	14	5	6	24	165	44	38	71	81
ENSMUSG00000005881	chr2	Ergic3	1.6E+08	1.6E+08	2121	0.994628724	6.006601423	1.058E-06	7.20046E-06	0.04785	1	616	428	649	603	986	2178	1375	1255	2142	1936
ENSMUSG00000031601	chr8	Cnot7	4E+07	4E+07	5821	-0.8845341	5.249191654	1.058E-06	7.20228E-06	0.0373	-1	741	589	913	708	749	605	781	401	466	524
ENSMUSG00000021669	chr13	Col4a3bp	9.7E+07	9.7E+07	5390	-0.888337	5.637968418	1.061E-06	7.21577E-06	0.03795	-1	781	731	1349	974	1092	757	957	560	678	659
ENSMUSG00000036932	chrX	Aifm1	4.8E+07	4.8E+07	4006	-1.02466724	5.592276345	1.067E-06	7.25422E-06	0.0506	-1	902	546	1587	1070	903	787	941	439	557	605
ENSMUSG00000046111	chr9	Cep295	1.5E+07	1.5E+07	11641	-1.30665643	2.857904205	1.081E-06	7.34702E-06	0.07442	-1	163	118	220	172	94	114	107	63	82	66
ENSMUSG00000029190	chr5	D5Ertd579e	3.7E+07	3.7E+07	8215	-1.06675172	6.964967991	1.094E-06	7.43191E-06	0.05567	-1	2607	1737	3333	2897	2205	1696	2491	1136	1597	1496
ENSMUSG00000025616	chr16	Usp16	8.7E+07	8.7E+07	9454	-0.87060753	5.454778197	1.101E-06	7.4715E-06	0.03641	-1	790	617	1084	927	870	665	859	463	611	619
ENSMUSG00000063659	chr1	Zbtb18	1.8E+08	1.8E+08	6138	-1.14173546	6.659806106	1.115E-06	7.56807E-06	0.06361	-1	2059	1480	2929	2039	2075	1194	2292	842	1100	1161
ENSMUSG00000002732	chr2	Fkbp7	7.7E+07	7.7E+07	1485	1.197349432	3.241496481	1.121E-06	7.6064E-06	0.06283	1	98	64	80	70	113	461	205	190	251	257

ENSMUSG00000061825	chr8	Ces2c	1E+08	1E+08	1970	2.708837052	-0.01980021	1.124E-06	7.61941E-06	0.24502	1	0	0	12	2	4	24	24	44	23	30
ENSMUSG00000091462	chr13	Gm17084	3.4E+07	3.4E+07	4085	1.338741549	2.584889231	1.126E-06	7.62947E-06	0.07561	1	38	35	39	45	97	240	143	127	171	193
ENSMUSG00000025261	chrX	Huwe1	1.5E+08	1.5E+08	23507	-1.09309595	7.464893641	1.13E-06	7.6516E-06	0.05869	-1	3375	2731	4860	4421	2654	2482	3059	1667	2141	2380
ENSMUSG00000026812	chr2	Tsc1	2.9E+07	2.9E+07	11833	-1.10339306	5.422382166	1.131E-06	7.65318E-06	0.05882	-1	864	641	1197	1070	618	559	872	344	514	562
ENSMUSG00000018501	chr11	Ncor1	6.2E+07	6.2E+07	12811	-1.07019462	6.580697102	1.133E-06	7.66622E-06	0.05604	-1	1761	1392	2732	2371	1543	1368	1805	924	1085	1242
ENSMUSG00000022744	chr16	Cldn25	5.9E+07	5.9E+07	2563	-0.95457893	4.911641966	1.147E-06	7.75961E-06	0.0435	-1	602	469	639	591	670	405	675	261	421	377
ENSMUSG00000038121	chr18	Fam210a	6.8E+07	6.8E+07	9813	-1.47286781	7.05948917	1.148E-06	7.76277E-06	0.10469	-1	2456	1578	5697	3792	1730	1481	2488	1012	1094	1300
ENSMUSG00000025784	chr9	Clec3b	1.2E+08	1.2E+08	990	1.475030262	7.03344751	1.151E-06	7.77923E-06	0.10493	1	922	812	681	682	2191	5352	2459	3114	4897	4119
ENSMUSG00000001376	chr6	Ccdc132	3498382	3498555	9936	-0.93710341	4.947403558	1.156E-06	7.80811E-06	0.0419	-1	626	506	708	625	544	439	632	341	364	410
ENSMUSG00000093133	chr11	Gm25994	1.1E+08	1.1E+08	101	-1.13676382	3.550625028	1.161E-06	7.83549E-06	0.05877	-1	227	253	232	222	236	241	134	114	131	143
ENSMUSG00000036968	chr5	Cnpy4	1.4E+08	1.4E+08	2399	1.2731546	3.196091581	1.162E-06	7.83798E-06	0.0718	1	87	50	65	59	143	395	204	200	283	248
ENSMUSG00000100975	chr12	Gm28875	1E+08	1E+08	642	1.628290316	1.572859459	1.163E-06	7.84297E-06	0.10523	1	15	8	24	22	39	122	51	68	85	117
ENSMUSG00000071076	chr8	Jund	7.1E+07	7.1E+07	2878	1.410100527	6.085003221	1.181E-06	7.95735E-06	0.0961	1	279	297	586	605	1172	1849	1494	1546	2700	2522
ENSMUSG00000083307	chrX	AA414768	1.3E+07	1.3E+07	1257	2.089020589	0.366250547	1.186E-06	7.9898E-06	0.12996	1	8	8	7	2	7	40	22	42	46	37
ENSMUSG00000034055	chrX	Phka1	1E+08	1E+08	6259	-1.23723162	9.471889039	1.187E-06	7.99277E-06	0.07528	-1	15162	12932	15653	15076	15067	7675	15186	5079	9273	7140
ENSMUSG00000034377	chr17	Tulp4	6106437	6106582	18054	-1.14229062	6.437076583	1.188E-06	7.99277E-06	0.0639	-1	1772	1470	2304	1998	1327	1041	1763	778	1014	1021
ENSMUSG00000029580	chr5	Actb	1.4E+08	1.4E+08	2679	1.264745467	8.674882909	1.188E-06	7.9946E-06	0.07849	1	2509	2546	3331	2894	7368	14065	9293	9416	13487	13339
ENSMUSG00000082361	chr5	Btc	9.1E+07	9.1E+07	2876	-1.70630099	0.511471836	1.19E-06	7.99977E-06	0.09205	-1	35	16	30	27	52	18	17	9	9	13
ENSMUSG00000026080	chr1	Chst10	3.9E+07	3.9E+07	11964	1.880026438	0.378649481	1.194E-06	8.02772E-06	0.09414	1	7	9	3	8	9	46	36	32	31	42
ENSMUSG00000025240	chr9	Sacm1l	1.2E+08	1.2E+08	3433	-0.84346617	4.902367484	1.196E-06	8.03571E-06	0.03376	-1	557	440	707	605	576	566	550	352	355	396
ENSMUSG00000078515	chr4	Ddi2	1.4E+08	1.4E+08	9553	-1.02999393	6.405640952	1.197E-06	8.03571E-06	0.05212	-1	2051	1458	1708	1660	1483	1219	1392	909	1077	1160
ENSMUSG00000022634	chr15	Yaf2	9.3E+07	9.3E+07	1873	-0.92376596	4.011180225	1.201E-06	8.06264E-06	0.03922	-1	297	231	401	299	372	236	339	139	229	218
ENSMUSG00000040018	chr19	Cox15	4.4E+07	4.4E+07	4909	-0.83324896	4.912193222	1.205E-06	8.08249E-06	0.03291	-1	542	403	789	617	577	455	590	346	431	412
ENSMUSG00000066232	chr7	Ipo7	1.1E+08	1.1E+08	3117	-1.32620849	6.41705674	1.21E-06	8.11354E-06	0.08567	-1	1883	1420	2630	1929	1299	1119	1870	653	659	820
ENSMUSG00000052698	chr9	Tln2	6.7E+07	6.7E+07	12193	-1.0814411	6.424357161	1.213E-06	8.12864E-06	0.05746	-1	1495	1150	2697	2073	1514	1061	1643	756	1239	1036
ENSMUSG00000000489	chr15	Pdgfb	8E+07	8E+07	2918	0.949766447	5.021851679	1.222E-06	8.18551E-06	0.04343	1	255	180	428	301	572	939	791	751	963	932
ENSMUSG00000091971	chr17	Hspa1a	3.5E+07	3.5E+07	2967	1.53169991	2.317657662	1.242E-06	8.31282E-06	0.09988	1	22	18	50	60	42	180	84	118	160	199
ENSMUSG00000020534	chr11	Shmt1	6.1E+07	6.1E+07	3883	-1.27103095	2.915135916	1.244E-06	8.32284E-06	0.07134	-1	171	147	137	171	149	86	73	76	124	90
ENSMUSG00000040540	chr10	Gm9770	1.3E+08	1.3E+08	810	-1.46535578	2.565990408	1.247E-06	8.34199E-06	0.09454	-1	134	93	183	149	90	77	117	31	48	58
ENSMUSG00000037851	chr13	Iars	5E+07	5E+07	5272	-1.06344439	6.322004377	1.257E-06	8.40683E-06	0.05571	-1	1512	1236	2216	1904	1260	1085	1534	799	933	1018
ENSMUSG00000029004	chr5	Kmt2e	2.3E+07	2.3E+07	7607	-0.91340392	4.669941749	1.259E-06	8.41164E-06	0.03974	-1	474	381	580	504	564	372	538	217	291	430
ENSMUSG00000090691	chr14	Gm3667	6868502	6869647	2053	2.20647084	0.027109072	1.259E-06	8.41164E-06	0.1175	1	5	8	1	6	2	34	30	23	31	30
ENSMUSG00000021880	chr14	Rnase6	5.1E+07	5.1E+07	1072	2.839832042	0.389012492	1.266E-06	8.45338E-06	0.28137	1	3	1	2	1	15	90	15	35	28	44
ENSMUSG00000035948	chr10	Acss3	1.1E+08	1.1E+08	4549	-2.59918784	0.789794257	1.268E-06	8.46096E-06	0.25849	-1	65	44	18	18	67	16	19	8	4	3
ENSMUSG00000102351		Cd47	5E+07	5E+07	1815	1.498137143	4.584055316	1.269E-06	8.46096E-06	0.10697	1	153	121	130	102	469	1071	539	565	654	838
ENSMUSG00000020794	chr11	Ube2g1	7.3E+07	7.3E+07	4579	-0.94911264	6.476281321	1.274E-06	8.49029E-06	0.04458	-1	1812	1362	2224	1727	1685	1408	1678	878	1138	1232
ENSMUSG00000028245	chr4	Nsmaf	6396207	6396817	8368	-0.87521594	5.249718044	1.274E-06	8.49029E-06	0.03712	-1	708	615	927	750	676	674	729	363	532	511
ENSMUSG00000035247	chr12	Hectd1	5.2E+07	5.2E+07	9048	-1.14745924	7.242017436	1.289E-06	8.58729E-06	0.06519	-1	3015	2108	4781	3618	2336	2267	2880	1319	1580	1814
ENSMUSG00000000134	chrX	Tfe3	7762560	7762630	9261	0.938637487	4.447606309	1.307E-06	8.69996E-06	0.04141	1	194	178	228	179	351	728	478	461	655	627
ENSMUSG00000037348	chr4	Paqr7	1.3E+08	1.3E+08	4259	1.56434836	2.891868859	1.308E-06	8.69996E-06	0.11031	1	42	28	49	32	140	284	204	152	276	217
ENSMUSG00000031328	chrX	Flna	7.4E+07	7.4E+07	9400	0.99418489	6.98588361	1.315E-06	8.74369E-06	0.04912	1	880	1111	1401	1288	1701	4475	3163	2577	3603	3729
ENSMUSG00000023243	chr14	Kcnk5	2E+07	2E+07	3364	1.518469986	1.457967149	1.316E-06	8.74513E-06	0.08422	1	16	14	15	30	26	77	78	75	66	97
ENSMUSG00000049556	chr9	Lingo1	5.7E+07	5.7E+07	3925	2.30795096	-0.10719698	1.319E-06	8.76221E-06	0.13012	1	3	6	2	3	5	39	26	17	39	15
ENSMUSG00000040596	chr1	Pogk	1.7E+08	1.7E+08	9586	-0.82455057	4.338681144	1.324E-06	8.7926E-06	0.03164	-1	360	339	425	367	433	338	336	209	324	307
ENSMUSG00000021366	chr13	Hivep1	4.2E+07	4.2E+07	8753	-1.11015234	4.208751885	1.328E-06	8.81575E-06	0.05864	-1	343	250	588	432	313	250	403	143	214	216
ENSMUSG00000032323	chr9	Cyp11a1	5.8E+07	5.8E+07	4804	3.286304045	1.167177744	1.331E-06	8.83346E-06	0.38714	1	3	10	1	7	5	256	19	34	41	62
ENSMUSG00000022601	chr16	Zbtb11	5.6E+07	5.6E+07	7440	-1.08820219	3.339631787	1.332E-06	8.83384E-06	0.05343	-1	194	179	267	208	173	139	191	87	114	141
ENSMUSG00000041420	chr7	Meis3	1.6E+07	1.6E+07	3173	1.774728985	1.35409506	1.336E-06	8.85893E-06	0.1189	1	15	15	14	7	31	98	47	59	74	107
ENSMUSG00000027652	chr2	Ralgapb	1.6E+08	1.6E+08	12992	-0.96472504	5.619392414	1.341E-06	8.88204E-06	0.04575	-1	960	747	1269	1062	839	750	1002	450	642	637
ENSMUSG00000022305	chr15	Lrp12	4E+07	4E+07	4574	1.09510841	2.868907338	1.346E-06	8.91444E-06	0.05044	1	59	55	65	65	101	209	223	146	195	238
ENSMUSG00000008496	chr7	Pou2f2	2.5E+07	2.5E+07	8231	1.967960347	1.111590296	1.354E-06	8.96137E-06	0.14253	1	11	12	6	6	26	101	38	48	69	77
ENSMUSG00000027961	chr3	Lrrc39	1.2E+08	1.2E+08	5230	-1.13578434	6.354217441	1.354E-06	8.96137E-06	0.06384	-1	1549	1155	2715	1912	1236	1083	1577	732	844	1097
ENSMUSG00000084349	chrX	Rpl3-ps1	1.3E+07	1.3E+07	1210	1.007541959	3.939718058	1.357E-06	8.97259E-06	0.04673	1	131	118	143	128	248	620	374	302	423	406
ENSMUSG00000059248	chr11	Sept9	1.2E+08	1.2E+08	7565	1.066930449	4.893668853	1.358E-06	8.97832E-06	0.05538	1	190	144	468	216	514	1010	889	599	832	843
ENSMUSG00000020392	chr11	Cdkn2aipnl	5.2E+07	5.2E+07	1958	-0.97349244	4.715131595	1.359E-06	8.98134E-06	0.0457	-1	434	542	468	563	525	402	449	244	404	345
ENSMUSG00000024548	chr18	Setbp1	7.9E+07	7.9E+07	9953	-1.26040914	2.713311718	1.36E-06	8.98257E-06	0.06971	-1	134	110	208	125	116	100	117	57	50	76
ENSMUSG00000000823	chr2	Znf512b	1.8E+08	1.8E+08	6810	-0.81516017	4.469915057	1.371E-06	9.04256E-06	0.03115	-1	353	361	528	434	439	383	357	255	308	356
ENSMUSG00000090659	chr13	Zfp493	6.8E+07	6.8E+07	4693	-1.63589452	1.332257816	1.37E-06	9.04256E-06	0.10592	-1	54	60	45	65	47	32	31	10	32	22
ENSMUSG00000024986	chr19	Hhex	3.7E+07	3.7E+07	1918	1.341834635	1.675222048	1.376E-06	9.07326E-06	0.06781	1	18	20	33	21	40	112	76	83	80	98
ENSMUSG00000089762	chr2	Ier5l	3E+07	3E+07	2683	1.619666431	2.613222512	1.384E-06	9.12414E-06	0.11718	1	39	22	51	26	93	205	103	172	275	161
ENSMUSG00000063439	chr7	B9d2	2.6E+07	2.6E+07	1021	1.135437066	3.180391591	1.389E-06	9.15181E-06	0.0581	1	63	38	153	91	95	293	274	184	273	251
ENSMUSG00000028991	chr4	Mtor	1.5E+08	1.5E+08	10109	-1.10816839	5.613699728	1.42E-06	9.34855E-06	0.06058	-1	807	527	1693	1359	804	734	838	443	551	671
ENSMUSG00000048410	chr18	Zfp407	8.4E+07	8.4E+07	15167	-1.16234359	2.858579476	1.422E-06	9.35984E-06	0.05963	-1	145	118	226	136	127	98	131	58	93	84
ENSMUSG00000024180	chr17	Tmem8	2.6E+07	2.6E+07	3464	1.893077078	2.370585355	1.429E-06	9.39733E-06	0.15705	1	17	27	28	20	72	261	88	200	137	112
ENSMUSG00000029405	chr5	G3bp2	9.2E+07	9.2E+07	4677	-0.93866672	6.690529563	1.429E-06	9.39733E-06	0.04411	-1	2071	1587	2297	2098	2113	1628	1933	1086	1317	1394
ENSMUSG00000031441	chr8	Atp11a	1.3E+07	1.3E+07	11150	-1.04027906	5.401690709	1.431E-06	9.40622E-06	0.05332	-1	738	677	1150	1001	701	643	901	364	502	489
ENSMUSG00000045404	chr12	Kcnk13	1E+08	1E+08	3112	1.972461581	0.57801132	1.44E-06	9.45806E-06	0.12608	1	4	7	4	8	18	72	37	27	53	36

ENSMUSG00000026730	chr2	Pter	1.3E+07	1.3E+07	4682	-0.84829271	4.223097798	1.443E-06	9.47551E-06	0.03359	-1	334	277	481	379	334	322	315	201	294	249
ENSMUSG00000035606	chr9	Ky	1E+08	1E+08	5879	-1.17629855	7.998033665	1.445E-06	9.48728E-06	0.06922	-1	6601	4633	4885	4922	4915	2823	4292	2418	3995	2650
ENSMUSG00000037060	chr7	Prkcdbp	1.1E+08	1.1E+08	1035	1.368250602	4.955947766	1.45E-06	9.51394E-06	0.0909	1	218	225	182	158	525	1213	555	797	1107	908
ENSMUSG00000030717	chr7	Nupr1	1.3E+08	1.3E+08	2514	1.633298502	4.271451596	1.455E-06	9.54303E-06	0.12658	1	121	103	71	71	355	701	472	466	556	801
ENSMUSG00000017390	chr11	Aldoc	7.8E+07	7.8E+07	3263	2.033582797	-0.11865182	1.456E-06	9.54502E-06	0.09702	1	1	5	7	3	7	23	26	21	28	31
ENSMUSG00000082519	chr2	Vamp7-ps	1.7E+08	1.7E+08	655	-2.28546315	1.657278021	1.457E-06	9.54749E-06	0.22032	-1	107	105	52	68	28	25	41	19	13	13
ENSMUSG00000030701	chr7	Plekhb1	1E+08	1E+08	3554	-1.13832311	5.228230596	1.46E-06	9.55928E-06	0.06378	-1	969	745	517	569	946	540	573	290	514	536
ENSMUSG00000029516	chr5	Cit	1.2E+08	1.2E+08	15387	1.928762009	0.21391134	1.474E-06	9.64823E-06	0.10762	1	5	5	9	2	11	39	31	15	38	46
ENSMUSG00000036550	chr8	Cnot1	9.6E+07	9.6E+07	8390	-0.94580164	6.024785139	1.479E-06	9.67482E-06	0.04459	-1	1216	992	1694	1412	1126	994	1225	657	853	898
ENSMUSG00000022811	chr16	Zfp148	3.3E+07	3.3E+07	9545	-0.90586331	4.538585605	1.48E-06	9.67903E-06	0.03932	-1	423	340	623	460	444	396	481	253	259	290
ENSMUSG00000051048	chr7	P4ha3	1E+08	1E+08	3043	2.039771338	0.74003542	1.483E-06	9.69431E-06	0.14576	1	6	5	9	13	12	102	29	49	30	44
ENSMUSG00000049658	chr13	Bdp1	1E+08	1E+08	11005	-1.16560771	3.873426479	1.497E-06	9.7828E-06	0.0644	-1	312	258	368	365	187	229	266	123	162	164
ENSMUSG00000066324	chr4	Impad1	4762484	4767972	6543	-0.98001432	6.789405849	1.512E-06	9.87178E-06	0.04831	-1	2345	1666	2524	2247	2222	1615	2190	1095	1378	1466
ENSMUSG00000026207	chr1	Speg	7.5E+07	7.5E+07	12741	-1.17837745	8.078141651	1.517E-06	9.90346E-06	0.06976	-1	4872	3923	8171	6877	4634	2978	5243	1949	3854	3325
ENSMUSG00000023046	chr15	Igfbp6	1E+08	1E+08	1112	1.30261958	6.608597834	1.527E-06	9.96464E-06	0.08433	1	618	632	594	796	1660	3472	1965	2031	3528	3412
ENSMUSG00000042066	chr1	Tmcc2	1.3E+08	1.3E+08	5692	-0.95052811	5.833864352	1.532E-06	9.98759E-06	0.04504	-1	1207	814	1384	1104	1160	729	1140	553	896	716
ENSMUSG00000026404	chr1	Ddx59	1.4E+08	1.4E+08	2953	-0.85274223	4.028831244	1.544E-06	1.00654E-05	0.0337	-1	288	225	415	287	384	279	316	176	207	228
ENSMUSG00000021175	chr12	Cdca7l	1.2E+08	1.2E+08	3258	2.284307031	0.778849204	1.552E-06	1.01098E-05	0.19113	1	12	4	0	4	20	57	45	37	66	63
ENSMUSG00000020664	chr12	Dld	3.1E+07	3.1E+07	2241	-1.21688819	8.034422909	1.559E-06	1.01515E-05	0.07441	-1	5074	3006	9517	6262	4619	3366	5269	2213	2708	2922
ENSMUSG00000068566	chr7	Myadm	3289038	3289325	3238	1.088571128	6.313176828	1.563E-06	1.01718E-05	0.0594	1	534	457	855	667	1475	2708	2107	1643	2528	2234
ENSMUSG00000027782	chr3	Kpna4	6.9E+07	6.9E+07	8940	-1.0522491	7.175153221	1.565E-06	1.01783E-05	0.05588	-1	2894	2206	3544	3188	2820	2004	3043	1310	1689	1774
ENSMUSG00000001247	chr7	Lsr	3.1E+07	3.1E+07	2167	1.800592102	0.270646671	1.573E-06	1.02304E-05	0.09186	1	10	3	7	4	12	43	29	28	30	41
ENSMUSG00000059811	chr17	Atl2	8E+07	8E+07	3616	-1.09671955	7.733390997	1.583E-06	1.02912E-05	0.06079	-1	4884	3893	4246	3980	4330	2708	4156	2005	2492	2727
ENSMUSG00000019877	chr10	Serinc1	5.8E+07	5.8E+07	5150	-1.17189606	7.232023451	1.587E-06	1.0312E-05	0.06911	-1	3232	2369	3935	3301	2787	1891	3368	1210	1549	1669
ENSMUSG00000040481	chr11	Bptf	1.1E+08	1.1E+08	13907	-0.88231137	4.969522119	1.588E-06	1.0312E-05	0.03812	-1	586	544	705	641	524	477	590	317	443	461
ENSMUSG00000010142	chr11	Tnfrsf13b	6.1E+07	6.1E+07	2836	1.993714436	1.411198443	1.592E-06	1.03308E-05	0.15608	1	12	15	4	15	28	150	60	69	81	57
ENSMUSG00000065228	chr1	Gm25789	1.6E+08	1.6E+08	76	2.382820417	-0.23960744	1.594E-06	1.03406E-05	0.15444	1	1	3	4	3	6	40	17	30	12	22
ENSMUSG00000029563	chr6	Foxp2	1.5E+07	1.5E+07	13457	-1.82144005	0.597276599	1.596E-06	1.03511E-05	0.11497	-1	48	28	26	33	32	8	15	8	15	20
ENSMUSG00000026785	chr2	Pkn3	3E+07	3E+07	4255	1.408011847	3.023232453	1.615E-06	1.04665E-05	0.09077	1	27	48	119	63	84	318	154	170	256	309
ENSMUSG00000090553	chr1	Snrpe	1.3E+08	1.3E+08	1372	0.798449483	4.509554847	1.616E-06	1.04696E-05	0.03011	1	248	174	314	228	295	743	527	509	588	597
ENSMUSG00000029922	chr6	Mkrn1	3.9E+07	3.9E+07	4439	0.82395806	4.605732559	1.617E-06	1.04709E-05	0.03249	1	241	175	397	203	336	727	655	460	623	753
ENSMUSG00000029634	chr5	Rnf6	1.5E+08	1.5E+08	4022	-0.95945119	5.664120255	1.652E-06	1.06943E-05	0.04608	-1	1056	806	1198	1086	833	851	954	525	639	615
ENSMUSG00000031557	chr8	Plekha2	2.5E+07	2.5E+07	5397	0.921905173	5.095724939	1.662E-06	1.07459E-05	0.04188	1	379	239	475	214	507	1159	1029	620	1006	851
ENSMUSG00000035024	chr9	Ncapd3	2.7E+07	2.7E+07	5499	-1.16286999	3.0876586	1.661E-06	1.07459E-05	0.06153	-1	219	121	250	143	150	121	147	73	85	118
ENSMUSG00000022201	chr15	Zfr	1.2E+07	1.2E+07	5911	-0.91873337	5.67021725	1.665E-06	1.07629E-05	0.04224	-1	881	746	1379	1080	957	741	1017	537	629	729
ENSMUSG00000028164	chr3	Manba	1.4E+08	1.4E+08	6971	1.008700313	3.174229503	1.673E-06	1.08064E-05	0.0448	1	64	66	103	101	115	309	217	174	271	265
ENSMUSG00000017466	chr11	Timp2	1.2E+08	1.2E+08	3896	1.311828279	8.008080463	1.675E-06	1.08139E-05	0.08656	1	1788	1728	1528	1625	4640	9841	6758	5525	7869	8229
ENSMUSG00000020821	chr11	Kif1c	7.1E+07	7.1E+07	7276	-1.08877985	10.10509254	1.676E-06	1.08146E-05	0.06043	-1	20609	15361	32107	24462	21807	13724	22152	8697	14956	14273
ENSMUSG00000040565	chr19	Btaf1	3.7E+07	3.7E+07	7204	-1.09505429	3.486341216	1.676E-06	1.08146E-05	0.05591	-1	229	214	239	217	221	186	206	114	106	128
ENSMUSG00000030029	chr6	Lrig1	9.5E+07	9.5E+07	5585	-0.99619271	6.058665656	1.681E-06	1.08425E-05	0.05001	-1	1427	921	1794	1249	1350	994	1385	670	852	728
ENSMUSG00000042473	chrX	Tbc1d8b	1.4E+08	1.4E+08	5211	-1.50446154	2.469090381	1.694E-06	1.09211E-05	0.10198	-1	142	125	123	112	87	84	95	41	39	42
ENSMUSG00000006476	chr2	Nsmf	2.5E+07	2.5E+07	4896	0.913115521	4.044294704	1.7E-06	1.09556E-05	0.03906	1	146	135	190	143	249	565	364	323	464	507
ENSMUSG00000042284	chr13	Itga1	1.1E+08	1.1E+08	5984	-1.1110465	3.221257946	1.706E-06	1.09896E-05	0.05649	-1	187	134	267	175	203	197	137	98	81	100
ENSMUSG00000025823	chr6	Pdia4	4.8E+07	4.8E+07	2480	1.184265705	4.922440568	1.718E-06	1.10582E-05	0.06937	1	233	187	239	218	548	1468	637	709	800	762
ENSMUSG00000030486	chr7	Zfp108	2.4E+07	2.4E+07	1929	-1.63076799	0.44769405	1.724E-06	1.10902E-05	0.08205	-1	31	25	36	27	28	9	19	9	13	15
ENSMUSG00000028977	chr4	Casz1	1.5E+08	1.5E+08	12224	-1.09837923	5.025165527	1.731E-06	1.11323E-05	0.06002	-1	569	483	927	901	457	424	650	247	416	436
ENSMUSG00000041638	chr5	Gcn1l1	1.2E+08	1.2E+08	15903	-0.97155814	5.583532931	1.734E-06	1.11445E-05	0.04737	-1	746	648	1411	1233	801	759	836	459	679	642
ENSMUSG00000059901	chr10	Adamts14	6.1E+07	6.1E+07	5197	1.526294962	1.014587695	1.741E-06	1.1187E-05	0.07867	1	9	11	17	19	17	80	42	47	65	54
ENSMUSG00000041774	chr16	Ydjc	1.7E+07	1.7E+07	5556	2.572004777	-0.16767282	1.749E-06	1.12336E-05	0.2102	1	1	0	10	2	4	32	12	35	20	30
ENSMUSG00000003541	chr17	Ier3	3.6E+07	3.6E+07	1131	1.239945578	3.104419231	1.753E-06	1.12554E-05	0.07156	1	49	33	129	65	126	251	231	213	257	266
ENSMUSG00000038521	chr6	C1s1	1.2E+08	1.2E+08	3129	1.438530562	6.669845984	1.757E-06	1.12704E-05	0.10338	1	783	734	524	467	1615	5048	2338	2273	2794	3134
ENSMUSG00000036810	chr8	Cnep1r1	8.8E+07	8.8E+07	3563	-0.90977723	5.01926294	1.765E-06	1.132E-05	0.04106	-1	647	550	724	618	598	485	687	301	424	454
ENSMUSG00000084817	chr1	Gm5526	4.6E+07	4.6E+07	423	1.947269947	1.479962138	1.769E-06	1.13424E-05	0.15598	1	11	10	5	16	41	91	77	49	120	99
ENSMUSG00000052459	chr16	Atp6v1a	4.4E+07	4.4E+07	6044	0.868509874	5.400315422	1.772E-06	1.13513E-05	0.03756	1	432	320	462	369	692	1232	1251	802	1125	1245
ENSMUSG00000009569	chr16	Mkl2	1.3E+07	1.3E+07	8990	-0.85142657	4.889531457	1.782E-06	1.14124E-05	0.03565	-1	534	491	665	640	496	496	514	334	436	406
ENSMUSG00000039523	chr4	Cep104	1.5E+08	1.5E+08	5279	-1.03267552	5.573465791	1.783E-06	1.14129E-05	0.05365	-1	896	686	1310	1110	832	595	1040	434	581	604
ENSMUSG00000031312	chrX	Itgb1bp2	1E+08	1E+08	1799	1.062261612	7.675209211	1.791E-06	1.14618E-05	0.05768	1	1958	1115	3215	2170	1771	6550	4647	4701	6469	6075
ENSMUSG00000041997	chr2	Tlk1	7.1E+07	7.1E+07	6474	-0.94577765	5.717104025	1.804E-06	1.15359E-05	0.04516	-1	1040	752	1375	1063	1005	822	1110	487	636	706
ENSMUSG00000015882	chr5	Lcorl	4.6E+07	4.6E+07	10945	-1.49389716	1.824083667	1.809E-06	1.15611E-05	0.09451	-1	93	64	75	88	59	48	57	30	22	33
ENSMUSG00000042529	chr11	Kcnj12	6.1E+07	6.1E+07	2750	-0.98489157	5.217598544	1.809E-06	1.15611E-05	0.0486	-1	702	587	899	778	741	585	789	277	590	392
ENSMUSG00000027900	chr3	Dram2	1.1E+08	1.1E+08	3863	-1.00800565	5.70619112	1.836E-06	1.17224E-05	0.05137	-1	1240	939	1067	977	881	837	939	538	613	676
ENSMUSG00000045665	chr15	Mfsd5	1E+08	1E+08	1742	0.921263505	4.941433661	1.836E-06	1.17224E-05	0.04214	1	231	176	395	322	533	957	756	594	1004	848
ENSMUSG00000039242	chr13	B3galnt2	1.4E+07	1.4E+07	3681	-1.10423482	6.711148237	1.838E-06	1.17295E-05	0.06212	-1	2191	2110	2156	2182	1770	1389	1957	1073	1259	1201
ENSMUSG00000021929	chr14	Kpna3	6.1E+07	6.1E+07	4167	-1.06933017	7.14942734	1.845E-06	1.17685E-05	0.05847	-1	2953	2109	4126	2843	2518	1962	2938	1293	1665	1705
ENSMUSG00000017831	chr17	Rab5a	5.3E+07	5.3E+07	2357	-1.13875086	4.873753624	1.859E-06	1.18434E-05	0.06467	-1	634	467	796	575	555	464	658	288	240	259
ENSMUSG00000027996	chr3	Sfrp2	8.4E+07	8.4E+07	2153	2.294632318	3.567763683	1.858E-06	1.18434E-05	0.24145	1	38	78	12	26	133	795	289	255	467	257
ENSMUSG00000018554	chr11	Ybx2	7E+07	7E+07	1885	-1.52504798	3.524590443	1.866E-06	1.18863E-05	0.11161	-1	185	80	569	291	249	118	188	63	115	137

ENSMUSG00000022361	chr15	Zhx1	5.8E+07	5.8E+07	6031	-0.86783762	5.446334491	1.87E-06	1.19028E-05	0.03788	-1	852	687	912	847	904	790	838	446	568	581
ENSMUSG00000003119	chr11	Cdk12	9.8E+07	9.8E+07	11730	-1.0996147	3.288565615	1.881E-06	1.19668E-05	0.05615	-1	203	178	213	208	176	137	190	91	114	111
ENSMUSG00000026361	chr1	Cdc73	1.4E+08	1.4E+08	17538	-0.84981483	5.086594447	1.881E-06	1.19668E-05	0.03588	-1	622	492	844	685	652	488	714	384	457	461
ENSMUSG00000024579	chr18	Pcyox1l	6.2E+07	6.2E+07	2645	1.394236173	1.187283228	1.894E-06	1.2045E-05	0.06538	1	14	13	18	19	25	83	54	51	60	72
ENSMUSG00000055639	chr14	Dach1	9.8E+07	9.8E+07	7317	-1.48008791	2.039645476	1.914E-06	1.21648E-05	0.09575	-1	85	28	145	103	111	48	56	22	53	45
ENSMUSG00000028402	chr4	Mpdz	8.1E+07	8.1E+07	12437	-1.14784384	6.384637405	1.921E-06	1.22021E-05	0.06714	-1	1571	1206	2562	2174	1196	1126	1653	733	954	956
ENSMUSG00000013921	chr7	Clip3	3E+07	3E+07	3991	1.216635924	2.609163987	1.952E-06	1.23937E-05	0.06448	1	41	42	56	54	79	244	114	139	179	187
ENSMUSG00000081519	chr2	Gm13331	2.4E+07	2.4E+07	448	-1.68265907	1.196753865	1.955E-06	1.24095E-05	0.11135	-1	46	44	61	69	33	23	38	17	16	16
ENSMUSG00000016494	chr1	Cd34	1.9E+08	1.9E+08	7290	1.046392454	7.011251143	1.968E-06	1.24822E-05	0.05626	1	932	910	1382	1101	2164	4802	3003	2531	3656	4147
ENSMUSG00000031558	chr5	Slit2	4.8E+07	4.8E+07	15079	2.096012629	0.147256515	1.971E-06	1.2495E-05	0.13083	1	2	6	4	8	7	46	30	38	25	20
ENSMUSG00000074577	chr2	Fam65c	1.7E+08	1.7E+08	4244	2.454041723	0.243491803	1.978E-06	1.25366E-05	0.20515	1	11	1	4	0	8	45	17	26	44	49
ENSMUSG00000000902	chr10	Smarcb1	7.6E+07	7.6E+07	7930	0.868067917	4.67925854	1.992E-06	1.26187E-05	0.03713	1	226	171	336	225	444	840	612	585	663	694
ENSMUSG00000001082	chr5	Mfsd10	3.5E+07	3.5E+07	2752	1.582243775	2.732922234	1.997E-06	1.26457E-05	0.11543	1	32	31	38	34	119	283	130	140	226	237
ENSMUSG00000021193	chr13	Pitrm1	6548157	6548229	3524	-0.8681881	5.406854618	2.007E-06	1.27023E-05	0.03809	-1	834	595	1096	858	753	715	823	437	567	586
ENSMUSG00000033004	chr14	Mycbp2	1E+08	1E+08	19248	-0.92313868	5.81792903	2.018E-06	1.27659E-05	0.04348	-1	896	776	1494	1390	1054	912	1043	583	701	813
ENSMUSG00000050910	chr11	Cdr2l	1.2E+08	1.2E+08	3700	1.448285413	2.251311145	2.024E-06	1.27978E-05	0.09089	1	17	33	34	36	68	208	119	93	124	164
ENSMUSG00000036819	chr11	Jmjd4	5.9E+07	5.9E+07	7115	-1.20141381	3.668310339	2.026E-06	1.28053E-05	0.06947	-1	241	183	422	324	169	161	234	126	137	135
ENSMUSG00000043008	chr16	Klhl6	2E+07	2E+07	2606	1.238974997	1.720365339	2.028E-06	1.28133E-05	0.0575	1	26	20	33	30	33	132	82	59	100	91
ENSMUSG00000047721	chr7	Bola2	1.3E+08	1.3E+08	1658	0.956639369	3.943322871	2.03E-06	1.28193E-05	0.04348	1	154	127	161	127	212	514	321	346	487	405
ENSMUSG00000026426	chr1	Arl8a	1.4E+08	1.4E+08	2299	0.795163396	4.675777035	2.032E-06	1.28267E-05	0.0309	1	229	181	346	266	414	697	664	516	756	698
ENSMUSG00000063558	chr1	Aox1	5.8E+07	5.8E+07	8690	-0.87341812	4.598442937	2.036E-06	1.28454E-05	0.03767	-1	394	356	603	361	686	436	429	200	336	398
ENSMUSG00000047843	chr5	Bri3	1.4E+08	1.4E+08	1648	0.850295432	4.73837879	2.037E-06	1.28493E-05	0.03577	1	238	158	378	277	428	790	626	517	761	850
ENSMUSG00000045826	chr19	Ptprcap	4154606	4154703	927	2.298065143	-0.24676857	2.04E-06	1.28549E-05	0.15318	1	4	0	3	3	8	22	16	14	28	41
ENSMUSG00000047996	chrX	Prrg1	7.8E+07	7.8E+07	11614	-1.77085888	1.977744274	2.04E-06	1.28549E-05	0.13996	-1	112	111	64	93	44	44	47	19	35	42
ENSMUSG00000031357	chrX	Syap1	1.6E+08	1.6E+08	2351	-0.8439242	5.057713591	2.044E-06	1.28736E-05	0.03563	-1	679	446	692	564	865	571	682	350	411	468
ENSMUSG00000020897	chr11	Aurkb	6.9E+07	6.9E+07	2946	2.648446204	-0.64016362	2.062E-06	1.29789E-05	0.14859	1	0	2	1	4	3	27	13	14	26	10
ENSMUSG00000035064	chr7	Eef2k	1.2E+08	1.2E+08	7166	-0.91479846	5.92974016	2.068E-06	1.30143E-05	0.04286	-1	1078	988	1502	1096	1333	938	1226	643	849	730
ENSMUSG00000000708	chr17	Kat2b	5.4E+07	5.4E+07	4867	-0.94862224	6.274991148	2.074E-06	1.3046E-05	0.04631	-1	1662	1125	1992	1513	1384	1303	1421	811	899	1068
ENSMUSG00000040249	chr10	Lrp1	1.3E+08	1.3E+08	17717	1.072055537	7.82551828	2.077E-06	1.30608E-05	0.05947	1	1719	1766	1845	2118	3618	7809	5504	4638	7062	6929
ENSMUSG00000029723	chr5	Tsc22d4	1.4E+08	1.4E+08	7509	0.94711637	6.303921063	2.09E-06	1.31365E-05	0.04618	1	735	493	1239	759	953	2014	2457	1403	2610	2315
ENSMUSG00000031657	chr8	Heatr3	8.8E+07	8.8E+07	4497	-0.90825468	5.585015447	2.092E-06	1.31418E-05	0.04205	-1	825	835	1104	1030	850	778	872	527	665	615
ENSMUSG00000041658	chrX	Rragb	1.5E+08	1.5E+08	2258	-1.73103045	0.943318449	2.101E-06	1.31918E-05	0.11705	-1	40	23	69	54	34	28	24	8	8	23
ENSMUSG00000020124	chr10	Usp15	1.2E+08	1.2E+08	3227	-1.12668337	6.672421043	2.11E-06	1.32398E-05	0.06537	-1	1908	1481	3280	2343	1630	1433	2118	907	1077	1161
ENSMUSG00000025978	chr1	Rftn2	5.5E+07	5.5E+07	5871	1.08846133	2.630237395	2.115E-06	1.32663E-05	0.05016	1	45	54	76	51	65	221	175	135	153	169
ENSMUSG00000018217	chr11	Pmp22	6.3E+07	6.3E+07	2354	1.003781744	6.06491287	2.128E-06	1.33424E-05	0.05178	1	578	398	664	647	1159	2528	1602	1449	1805	1882
ENSMUSG00000025289	chrX	Prdx4	1.6E+08	1.6E+08	2106	1.26937839	3.617032316	2.137E-06	1.33929E-05	0.07783	1	98	72	102	70	207	600	256	275	350	312
ENSMUSG00000027742	chr3	Cog6	5.3E+07	5.3E+07	4957	-1.0278844	6.423932755	2.141E-06	1.34101E-05	0.05452	-1	2141	1293	1949	1651	1547	1290	1605	949	1014	982
ENSMUSG00000026858	chr2	Fam73b	3E+07	3E+07	6249	-0.87309609	5.029186438	2.152E-06	1.34732E-05	0.03835	-1	518	389	867	670	821	599	655	319	479	361
ENSMUSG00000043943	chr9	Naalad2	1.8E+07	1.8E+07	4749	0.963138365	3.3896925	2.159E-06	1.35102E-05	0.04243	1	91	74	122	111	136	351	261	262	237	292
ENSMUSG00000098503	chr11	Gm27937	3646942	3647029	88	-2.26747107	-0.20600454	2.177E-06	1.36203E-05	0.15877	-1	20	19	28	19	13	2	14	4	6	2
ENSMUSG00000039100	chr15	March6	3.1E+07	3.1E+07	6236	-0.97232422	7.533965737	2.181E-06	1.36391E-05	0.04927	-1	3592	2774	4785	3970	3365	2831	3460	1918	2276	2518
ENSMUSG00000023150	chr1	Ivns1abp	1.5E+08	1.5E+08	5435	-1.03208954	7.419769358	2.197E-06	1.37334E-05	0.05542	-1	3819	2290	4909	3315	3161	2853	3102	1788	1715	2248
ENSMUSG00000021282	chr12	Eif5	1.1E+08	1.1E+08	4061	-1.02899016	7.505648049	2.224E-06	1.38899E-05	0.05517	-1	3830	3131	4386	3416	3370	3008	3331	1959	2103	2010
ENSMUSG00000040462	chr10	Os9	1.3E+08	1.3E+08	4049	0.922691044	5.452874748	2.224E-06	1.38899E-05	0.04341	1	377	305	428	479	720	1532	994	903	1263	1245
ENSMUSG00000008090	chr5	Fgfrl1	1.1E+08	1.1E+08	2656	1.192842277	6.208904001	2.238E-06	1.39693E-05	0.07334	1	505	245	1036	664	1171	1969	2188	1770	2129	2477
ENSMUSG00000038535	chr9	Zfp280d	7.2E+07	7.2E+07	19017	-1.08643841	3.549686119	2.26E-06	1.41032E-05	0.05701	-1	275	208	247	243	192	195	198	90	126	177
ENSMUSG00000041258	chr18	Zfp236	8.3E+07	8.3E+07	10471	-0.89999879	3.923569036	2.265E-06	1.41281E-05	0.03896	-1	255	207	367	370	291	235	284	162	202	211
ENSMUSG00000021918	chr14	Nek4	3.1E+07	3.1E+07	2754	-1.47460528	1.821766864	2.271E-06	1.41555E-05	0.09321	-1	74	71	87	81	66	42	69	27	27	27
ENSMUSG00000026535	chr1	Ifi202b	1.7E+08	1.7E+08	1697	1.541232722	4.21350981	2.276E-06	1.41844E-05	0.1168	1	126	155	71	80	259	1013	522	429	513	403
ENSMUSG00000067942	chr17	Zfp160	2.1E+07	2.1E+07	3791	-1.10655773	2.283880738	2.312E-06	1.44E-05	0.05193	-1	98	69	114	89	130	91	73	40	53	63
ENSMUSG00000016018	chr13	Skiv2l2	1.1E+08	1.1E+08	3309	-0.89445169	5.054468289	2.316E-06	1.4421E-05	0.04061	-1	659	536	722	699	589	505	683	363	452	403
ENSMUSG00000050410	chr17	Tcf19	3.6E+07	3.6E+07	1782	1.737793487	0.927684249	2.325E-06	1.44669E-05	0.11278	1	7	6	15	9	26	83	37	34	71	58
ENSMUSG00000004798	chr11	Ulk2	6.2E+07	6.2E+07	5977	-1.02738091	7.107471771	2.336E-06	1.45324E-05	0.05514	-1	2930	2236	3243	2845	2531	1926	2805	1302	1775	1648
ENSMUSG00000050379	chrX	Sept6	3.7E+07	3.7E+07	9882	1.291456797	2.469391574	2.338E-06	1.45388E-05	0.07244	1	50	50	45	36	48	249	131	110	149	163
ENSMUSG00000030697	chr7	Ppp4c	1.3E+08	1.3E+08	1293	0.826758702	4.945272246	2.362E-06	1.46782E-05	0.03427	1	268	250	373	329	465	934	661	606	957	904
ENSMUSG00000031245	chrX	Hmgn5	1.1E+08	1.1E+08	1934	-1.11917893	3.522813701	2.363E-06	1.46782E-05	0.06047	-1	323	175	211	243	203	171	192	115	123	147
ENSMUSG00000052299	chr16	Ltn1	8.7E+07	8.7E+07	7737	-0.88655338	5.088077525	2.376E-06	1.47509E-05	0.04002	-1	633	509	827	735	606	529	730	341	405	482
ENSMUSG00000022867	chr16	Usp25	7.7E+07	7.7E+07	4412	-1.13289886	6.692616155	2.384E-06	1.47955E-05	0.0668	-1	2138	1859	2455	2222	1838	1389	2272	837	1014	1288
ENSMUSG00000001313	chr11	Rnd2	1E+08	1E+08	1990	1.226218302	2.26992605	2.394E-06	1.4848E-05	0.06397	1	27	33	65	43	46	167	109	88	149	171
ENSMUSG00000037475	chrX	Thoc2	4.2E+07	4.2E+07	12666	-1.09204559	3.965003209	2.415E-06	1.49739E-05	0.0591	-1	352	262	429	306	229	270	283	122	147	227
ENSMUSG00000025754	chr7	Agbl1	7.6E+07	7.6E+07	4594	-2.40080431	0.964842323	2.44E-06	1.51208E-05	0.24123	-1	71	11	73	68	23	16	25	4	5	14
ENSMUSG00000049470	chr11	Aff4	5.3E+07	5.3E+07	13450	-0.93671664	6.037080468	2.444E-06	1.5139E-05	0.04569	-1	1266	998	1595	1386	1228	1021	1338	632	836	877
ENSMUSG00000025759	chr3	Mfsd8	4.1E+07	4.1E+07	3184	-0.94352316	4.206597424	2.446E-06	1.51497E-05	0.04417	-1	388	340	332	355	360	311	306	205	262	220
ENSMUSG00000026640	chr1	Plxna2	1.9E+08	1.9E+08	17174	-0.9619359	3.715125357	2.466E-06	1.52607E-05	0.04425	-1	246	209	348	271	222	212	182	166	150	200
ENSMUSG00000063450	chr12	Syne2	7.6E+07	7.6E+07	26726	-0.7815963	4.616550361	2.467E-06	1.52607E-05	0.03037	-1	455	367	503	444	558	441	473	237	373	361
ENSMUSG00000020186	chr10	Csrp2	1.1E+08	1.1E+08	973	1.705773624	2.896811309	2.469E-06	1.52672E-05	0.13795	1	38	41	37	27	120	405	124	156	236	254
ENSMUSG00000040097	chr17	Flywch1	2.4E+07	2.4E+07	2977	-1.00741666	4.871805358	2.47E-06	1.52672E-05	0.05179	-1	465	395	905	683	546	418	645	259	398	311

ENSMUSG00000074749	chr2	Kiz	1.5E+08	1.5E+08	2278	-0.98660248	4.651535516	2.487E-06	1.5368E-05	0.04935	-1	655	291	637	526	413	384	488	241	288	354
ENSMUSG00000040415	chr10	Dtx3	1.3E+08	1.3E+08	2572	0.947589786	5.477969975	2.49E-06	1.53805E-05	0.0463	1	367	332	561	391	682	1475	970	758	1258	1668
ENSMUSG00000095930	chr13	Nim1k	1.2E+08	1.2E+08	8466	-1.1282854	2.703837171	2.493E-06	1.53875E-05	0.05749	-1	127	119	162	142	107	96	96	67	67	93
ENSMUSG00000026623	chr1	Lpgat1	1.9E+08	1.9E+08	7610	-0.84801967	5.611750047	2.494E-06	1.53878E-05	0.03715	-1	750	649	1298	936	1203	824	911	534	590	770
ENSMUSG00000038095	chr5	Sbno1	1.2E+08	1.2E+08	10197	-0.79355144	5.006222632	2.495E-06	1.5391E-05	0.03187	-1	569	466	814	633	591	518	621	350	436	514
ENSMUSG00000031902	chr8	Nfatc3	1.1E+08	1.1E+08	6014	-0.86874029	5.455864156	2.502E-06	1.54262E-05	0.03893	-1	848	700	888	944	828	678	812	481	623	621
ENSMUSG00000006395	chr4	Hyi	1.2E+08	1.2E+08	2209	1.097461982	3.46085917	2.51E-06	1.5467E-05	0.05753	1	105	71	96	98	156	417	200	259	328	325
ENSMUSG00000030862	chr7	Cpxm2	1.3E+08	1.3E+08	4450	1.326398756	5.570716498	2.514E-06	1.54875E-05	0.09039	1	340	354	284	262	805	2327	992	1102	1329	1332
ENSMUSG00000036412	chr18	Arsi	6.1E+07	6.1E+07	2975	1.340893941	2.754025514	2.517E-06	1.54982E-05	0.08223	1	46	52	36	54	90	276	154	179	201	163
ENSMUSG00000050425	chr7	Mrgprb2	4.9E+07	4.9E+07	2077	2.818293216	-0.62220209	2.519E-06	1.55025E-05	0.19762	1	0	1	1	5	2	37	12	5	22	19
ENSMUSG00000052917	chr16	Senp7	5.6E+07	5.6E+07	5287	-1.47064817	2.838527881	2.522E-06	1.55132E-05	0.10332	-1	181	131	203	140	122	78	154	58	53	49
ENSMUSG00000046470	chr2	Sox18	1.8E+08	1.8E+08	1620	1.273992254	4.362760135	2.524E-06	1.55206E-05	0.08254	1	110	71	296	132	363	639	531	450	761	605
ENSMUSG00000053768	chr6	Chchd3	3.3E+07	3.3E+07	2905	-1.12739574	7.926121054	2.527E-06	1.55346E-05	0.0668	-1	4546	3031	8176	5664	4312	3441	4997	1975	2703	2923
ENSMUSG00000064057	chr11	Scgb3a1	5E+07	5E+07	598	2.768347047	-0.50878074	2.532E-06	1.55565E-05	0.2244	1	2	0	4	2	3	21	10	33	8	26
ENSMUSG00000018334	chr11	Ksr1	7.9E+07	7.9E+07	6621	-1.02619252	7.315643294	2.554E-06	1.56836E-05	0.0555	-1	3150	3135	2959	3046	3346	2085	2543	1534	2433	2277
ENSMUSG00000024242	chr17	Map4k3	8.1E+07	8.1E+07	4231	-0.86449198	4.029642364	2.569E-06	1.57657E-05	0.03646	-1	346	217	413	287	332	282	313	166	203	240
ENSMUSG00000035212	chr4	Leprot	1E+08	1E+08	1898	0.852074279	4.658026581	2.57E-06	1.57657E-05	0.0363	1	241	210	298	208	407	950	671	503	651	598
ENSMUSG00000046873	chrX	Mbtps2	1.6E+08	1.6E+08	10105	-1.02032313	4.129322022	2.571E-06	1.57681E-05	0.05216	-1	359	285	406	411	273	258	356	146	210	238
ENSMUSG00000059408	chr17	Mrgprh	1.3E+07	1.3E+07	1809	-1.52691158	1.816727922	2.577E-06	1.57971E-05	0.10241	-1	87	63	102	83	48	26	55	23	49	32
ENSMUSG00000029270	chr5	Fam69a	1.1E+08	1.1E+08	2892	-1.02841733	4.886290041	2.58E-06	1.58102E-05	0.05421	-1	615	591	465	445	793	397	526	326	391	361
ENSMUSG00000028710	chr4	Atpaf1	1.2E+08	1.2E+08	3609	-0.99032551	5.251623736	2.598E-06	1.59114E-05	0.0507	-1	631	498	1266	838	664	560	804	333	482	490
ENSMUSG00000098364	chr4	Gm27646	1.4E+08	1.4E+08	110	-1.41712146	4.466626841	2.601E-06	1.5926E-05	0.10191	-1	444	260	937	608	236	228	382	200	258	170
ENSMUSG00000097216	chr5	4932441J04Rik	5.8E+07	5.8E+07	4716	2.263071696	-0.40117936	2.604E-06	1.59341E-05	0.12408	1	1	1	1	4	9	26	25	12	23	21
ENSMUSG00000029510	chr5	Gpc2	1.4E+08	1.4E+08	8309	1.895001841	0.138313122	2.623E-06	1.60422E-05	0.09943	1	7	4	2	9	8	41	24	21	34	37
ENSMUSG00000045776	chr14	Lrtm1	2.9E+07	2.9E+07	7318	-1.70200564	5.318725915	2.631E-06	1.60881E-05	0.14669	-1	797	1083	774	1300	327	293	257	421	496	405
ENSMUSG00000034621	chr11	Gpatch8	1E+08	1E+08	8178	-0.83554454	5.176590739	2.638E-06	1.61238E-05	0.03589	-1	712	542	851	684	686	550	743	348	504	563
ENSMUSG00000034613	chr10	Ppm1h	1.2E+08	1.2E+08	10226	1.430113507	1.963796872	2.673E-06	1.63312E-05	0.09061	1	26	10	38	24	63	154	105	85	113	113
ENSMUSG00000039145	chr2	Camk1d	5293457	5299101	7427	1.200904433	2.592620696	2.679E-06	1.63567E-05	0.06407	1	50	47	41	52	76	262	163	113	160	164
ENSMUSG00000025743	chr4	Sdc3	1.3E+08	1.3E+08	5989	1.050832477	5.420679618	2.68E-06	1.6357E-05	0.05749	1	283	217	613	354	746	1561	1059	780	1454	1177
ENSMUSG00000044573	chr12	Acp1	3.1E+07	3.1E+07	3221	-1.1688174	3.731516956	2.684E-06	1.63738E-05	0.0677	-1	284	213	405	255	224	193	289	116	136	118
ENSMUSG00000049288	chr3	Lix1l	9.7E+07	9.7E+07	2509	1.017172874	3.953319167	2.687E-06	1.63876E-05	0.05088	1	128	109	140	136	264	625	347	311	439	425
ENSMUSG00000020170	chr10	Frs2	1.2E+08	1.2E+08	5682	-1.0546039	3.71750553	2.738E-06	1.66903E-05	0.05495	-1	260	214	330	278	242	161	283	100	165	183
ENSMUSG00000038582	chr5	Pptc7	1.2E+08	1.2E+08	4719	-1.52975021	7.146291555	2.746E-06	1.67313E-05	0.12116	-1	2155	1527	6783	4040	2142	1221	2688	790	1346	1622
ENSMUSG00000051329	chr2	Nup160	9.1E+07	9.1E+07	8761	-1.11939857	2.699952941	2.751E-06	1.67545E-05	0.05717	-1	133	105	165	143	114	105	115	61	65	77
ENSMUSG00000038116	chr2	Phf20	1.6E+08	1.6E+08	9988	-0.85385905	4.792699149	2.757E-06	1.67852E-05	0.03722	-1	490	476	630	556	493	500	535	279	383	363
ENSMUSG00000013662	chr19	Atad1	3.3E+07	3.3E+07	2813	-1.14547304	6.210484597	2.761E-06	1.67922E-05	0.06891	-1	1488	1060	2350	1683	1164	989	1589	685	700	840
ENSMUSG00000038174	chr1	Fam126b	5.9E+07	5.9E+07	12041	-1.1417988	3.190042612	2.761E-06	1.67922E-05	0.06238	-1	170	112	197	167	320	97	149	97	95	142
ENSMUSG00000020668	chr12	Kif3c	3365132	3367531	6849	-1.0230251	5.759638107	2.788E-06	1.69521E-05	0.05491	-1	884	790	1573	1066	1249	666	1242	439	714	679
ENSMUSG00000028212	chr4	Ccne2	1.1E+07	1.1E+07	3495	-1.34776323	2.122346077	2.801E-06	1.70119E-05	0.08106	-1	82	62	135	103	89	49	88	38	34	42
ENSMUSG00000034868	chr17	Myl12b	7.1E+07	7.1E+07	1711	1.052277916	6.16409194	2.801E-06	1.70119E-05	0.05838	1	517	328	1039	728	1083	2548	1584	1568	1946	2365
ENSMUSG00000031696	chr8	Vps35	8.5E+07	8.5E+07	3180	-1.07386493	6.041724276	2.813E-06	1.70789E-05	0.0607	-1	1371	1069	1658	1450	1111	1070	1389	615	704	663
ENSMUSG00000067818	chr2	Myl9	1.6E+08	1.6E+08	1162	0.960150907	5.593209145	2.829E-06	1.71668E-05	0.04813	1	351	427	586	439	673	1683	937	1075	1497	1374
ENSMUSG00000031227	chrX	Magee1	1.1E+08	1.1E+08	3550	1.286733725	1.886043186	2.867E-06	1.73871E-05	0.06851	1	27	23	27	26	54	142	90	81	103	107
ENSMUSG00000040663	chr19	Clcf1	4214238	4214500	3713	1.937122085	0.745526613	2.867E-06	1.73871E-05	0.13663	1	17	7	7	2	14	51	39	36	54	70
ENSMUSG00000002028	chr9	Kmt2a	4.5E+07	4.5E+07	16670	-0.82431375	4.730037901	2.87E-06	1.73934E-05	0.03459	-1	505	375	642	580	442	447	464	273	350	458
ENSMUSG00000024486	chr18	Hbegf	3.7E+07	3.7E+07	2373	1.221925839	3.914203676	2.873E-06	1.74073E-05	0.07522	1	112	73	196	124	197	456	275	555	416	371
ENSMUSG00000043602	chr11	Zfp3	7.1E+07	7.1E+07	2061	-0.82137664	4.258670908	2.875E-06	1.7413E-05	0.03343	-1	366	284	434	382	362	317	329	230	304	243
ENSMUSG00000090112	chr10	Shprh	1.1E+07	1.1E+07	14066	-1.1340848	3.542188387	2.877E-06	1.74167E-05	0.06353	-1	265	187	280	242	215	204	214	124	86	127
ENSMUSG00000030315	chr6	Vgll4	1.1E+08	1.1E+08	4133	-0.90383276	4.31099079	2.886E-06	1.7463E-05	0.04121	-1	335	347	369	424	438	316	364	202	320	231
ENSMUSG00000025353	chr10	Ormdl2	1.3E+08	1.3E+08	2055	1.271612868	2.651615235	2.913E-06	1.76169E-05	0.07526	1	38	37	57	38	109	232	154	126	177	216
ENSMUSG00000002983	chr7	Relb	2E+07	2E+07	3885	0.988992302	3.937942797	2.942E-06	1.77784E-05	0.04864	1	82	99	212	174	225	498	386	324	441	443
ENSMUSG00000006651	chr7	Aplp1	3E+07	3E+07	2391	1.580449505	0.887895332	2.942E-06	1.77784E-05	0.08838	1	13	7	13	13	19	77	34	42	66	46
ENSMUSG00000027134	chr2	Lpcat4	1.1E+08	1.1E+08	2823	1.585327414	1.579363899	2.956E-06	1.78533E-05	0.10968	1	10	9	30	16	48	104	75	66	106	90
ENSMUSG00000021200	chr12	Asb2	1E+08	1E+08	3542	-1.00318715	9.330498893	2.959E-06	1.78664E-05	0.05403	-1	13123	8800	15911	14473	12698	8740	11721	5783	10408	8017
ENSMUSG00000049421	chr7	Zfp260	3E+07	3E+07	5790	-0.95203971	5.375939871	2.964E-06	1.78886E-05	0.04756	-1	848	681	942	864	728	752	854	368	487	516
ENSMUSG00000027368	chr2	Dusp2	1.3E+08	1.3E+08	2003	2.053938326	0.659205439	2.971E-06	1.79215E-05	0.1547	1	6	7	10	14	4	82	24	49	32	50
ENSMUSG00000031433	chrX	Rbm41	1.4E+08	1.4E+08	6638	-1.98594072	1.074328514	2.988E-06	1.801E-05	0.16959	-1	53	49	57	51	31	18	42	7	11	10
ENSMUSG00000041954	chr4	Tnfrsf18	1.6E+08	1.6E+08	1524	2.616222641	-0.69205464	2.988E-06	1.801E-05	0.17615	1	3	0	4	1	2	23	5	12	20	26
ENSMUSG00000029860	chr6	Zyx	4.2E+07	4.2E+07	3739	1.008433861	5.349728196	2.994E-06	1.80396E-05	0.05329	1	267	272	417	361	784	1333	1052	785	1231	1253
ENSMUSG00000014850	chr13	Msh3	9.2E+07	9.2E+07	11254	-0.90361035	4.022561917	3E-06	1.80678E-05	0.04065	-1	313	245	432	335	261	260	300	173	218	220
ENSMUSG00000037731	chr4	Themis2	1.3E+08	1.3E+08	3079	1.681459723	2.406012859	3.055E-06	1.83913E-05	0.13331	1	26	23	22	26	93	278	120	107	141	181
ENSMUSG00000030609	chr7	Aen	7.9E+07	7.9E+07	5687	-0.84185361	5.08970417	3.058E-06	1.84003E-05	0.0368	-1	612	451	890	770	587	541	681	352	499	462
ENSMUSG00000021556	chr13	Golm1	6E+07	6E+07	3693	1.268809303	1.796072757	3.093E-06	1.8601E-05	0.0673	1	22	16	39	24	51	135	91	71	95	99
ENSMUSG00000017548	chr11	Suz12	8E+07	8E+07	4945	-0.86687901	4.388505123	3.094E-06	1.86039E-05	0.03805	-1	383	326	515	410	392	302	428	237	271	291
ENSMUSG00000024622	chr18	Hmgxb3	6.1E+07	6.1E+07	5101	-0.84620989	4.528983828	3.126E-06	1.87764E-05	0.03643	-1	371	328	645	478	430	350	451	254	356	294
ENSMUSG00000027447	chr2	Cst3	1.5E+08	1.5E+08	1266	1.061328571	9.302999152	3.126E-06	1.87764E-05	0.0606	1	6649	4694	5965	4177	9534	21305	15839	14035	18241	18908
ENSMUSG00000039419	chr6	Cntnap2	4.5E+07	4.5E+07	7183	-2.51826506	2.825554102	3.173E-06	1.9054E-05	0.29723	-1	263	221	41	130	185	15	23	57	79	31

ENSMUSG00000019579	chr17	D17Wsu104e	5.6E+07	5.6E+07	2222	0.810810975	4.680871964	3.181E-06	1.90903E-05	0.0335	1	245	191	324	253	409	864	565	548	752	632
ENSMUSG00000064351	chrMT	mt-Co1	5328	6872	1545	-1.4621778	14.7462915	3.209E-06	1.92499E-05	0.11303	-1	572822	293069	1104982	718824	461159	304837	601505	160855	212737	270509
ENSMUSG00000026496	chr1	Parp1	1.8E+08	1.8E+08	5293	-0.85538688	5.93216261	3.227E-06	1.93496E-05	0.03893	-1	1091	884	1490	1272	1198	895	1121	703	912	852
ENSMUSG00000040423	chr1	Rc3h1	1.6E+08	1.6E+08	11308	-0.97874198	5.359687286	3.228E-06	1.93496E-05	0.05056	-1	769	753	747	1028	675	629	609	500	511	586
ENSMUSG00000100862	chr1	Gm10925	2.5E+07	2.5E+07	678	-1.21499662	4.168878944	3.232E-06	1.9362E-05	0.07601	-1	411	177	565	476	304	200	385	153	211	174
ENSMUSG00000036890	chr2	Gtdc1	4.5E+07	4.5E+07	7928	-0.99883541	3.802587678	3.257E-06	1.95044E-05	0.05002	-1	285	196	378	287	257	244	281	121	135	194
ENSMUSG00000096472	chr9	Cdkn2d	2.1E+07	2.1E+07	1271	0.850162863	4.084420214	3.268E-06	1.95635E-05	0.03608	1	168	103	276	159	228	571	449	359	438	428
ENSMUSG00000039197	chr14	Adk	2.1E+07	2.1E+07	1781	-1.06891598	5.954097773	3.277E-06	1.96069E-05	0.06087	-1	1126	694	2111	1604	948	846	1092	625	758	822
ENSMUSG00000031519	chr8	Asb5	5.5E+07	5.5E+07	1579	-1.00576752	6.656638382	3.288E-06	1.96564E-05	0.05432	-1	2205	1593	2472	1856	1959	1504	1974	1188	1073	1173
ENSMUSG00000090272	chr1	Mndal	1.7E+08	1.7E+08	3443	1.637408436	1.162115079	3.287E-06	1.96564E-05	0.10844	1	11	9	20	8	31	87	95	41	64	45
ENSMUSG00000030087	chr6	Klf15	9E+07	9E+07	2527	-1.14596835	4.89954552	3.294E-06	1.96828E-05	0.06897	-1	818	537	578	697	338	420	440	270	405	394
ENSMUSG00000092787	chrX	Mir5116	5.7E+07	5.7E+07	63	-1.94296584	1.111981183	3.295E-06	1.96828E-05	0.16347	-1	53	53	42	54	42	17	42	13	8	11
ENSMUSG00000030750	chr7	Nsmce1	1.3E+08	1.3E+08	1329	0.906427108	3.930513669	3.337E-06	1.99276E-05	0.04074	1	160	114	225	122	182	522	322	308	472	421
ENSMUSG00000003623	chr5	Crot	8966033	8966972	5456	-0.96701308	5.080323062	3.356E-06	2.00281E-05	0.04932	-1	747	619	696	541	693	557	725	316	384	414
ENSMUSG00000060923	chr11	Acyp2	3.1E+07	3.1E+07	863	-0.93845366	6.362512665	3.368E-06	2.00941E-05	0.04735	-1	1851	1234	1972	1607	1414	1281	1523	829	1112	1126
ENSMUSG00000093402	chr3	Gm18588	6.9E+07	6.9E+07	492	-2.02829589	0.688882466	3.392E-06	2.02265E-05	0.16995	-1	33	35	46	50	21	13	30	4	9	9
ENSMUSG00000059883	chr15	Irak4	9.5E+07	9.5E+07	5021	1.299075869	1.779435389	3.396E-06	2.02452E-05	0.07036	1	21	21	33	20	51	132	106	60	98	95
ENSMUSG00000029299	chr5	Abcg3	1E+08	1E+08	3550	2.579795833	-0.34568956	3.404E-06	2.02848E-05	0.16899	1	2	5	2	3	1	43	17	19	10	26
ENSMUSG00000070802	chr7	Pnmal2	1.7E+07	1.7E+07	4147	1.593083557	1.428511278	3.428E-06	2.04188E-05	0.10774	1	11	8	41	25	14	100	64	64	74	93
ENSMUSG00000020220	chr4	Vps13d	1.4E+08	1.4E+08	24771	-1.02528645	5.974882725	3.462E-06	2.06123E-05	0.05632	-1	1040	655	2116	1579	1183	858	1129	675	779	836
ENSMUSG00000055489	chr7	Ano5	5.2E+07	5.2E+07	7785	-1.24252785	7.243948266	3.47E-06	2.06478E-05	0.08285	-1	3373	3305	2982	3665	1951	2054	2508	1478	1754	1527
ENSMUSG00000001794	chr7	Capns1	3E+07	3E+07	2397	0.953375364	7.73067839	3.514E-06	2.09047E-05	0.04945	1	1699	1305	2748	2312	3170	6181	5303	4298	6706	6479
ENSMUSG00000027188	chr2	Pamr1	1E+08	1E+08	6046	1.188622046	3.282270287	3.538E-06	2.10351E-05	0.06962	1	62	63	76	81	167	429	227	199	252	289
ENSMUSG00000030059	chr6	Tmf1	9.7E+07	9.7E+07	3465	-1.17111505	4.190602949	3.545E-06	2.10613E-05	0.07146	-1	378	333	432	429	288	293	405	131	183	174
ENSMUSG00000034006	chr18	Pqlc1	8E+07	8E+07	6100	1.092256976	4.918533575	3.545E-06	2.10613E-05	0.06296	1	195	160	442	437	251	847	683	636	903	1160
ENSMUSG00000040118	chr5	Cacna2d1	1.6E+07	1.6E+07	7514	-1.13043882	8.304860439	3.552E-06	2.10924E-05	0.06925	-1	7703	5563	7671	6311	4730	4278	6099	3064	3636	3517
ENSMUSG00000056481	chr19	Cd248	5068078	5070637	2560	1.233471596	5.507785666	3.566E-06	2.11668E-05	0.08096	1	232	267	327	394	892	1642	1066	1070	1498	1297
ENSMUSG00000017716	chr11	Birc5	1.2E+08	1.2E+08	3402	2.628548412	0.220455415	3.573E-06	2.11969E-05	0.24833	1	1	5	1	1	13	67	16	28	43	28
ENSMUSG00000019590	chr11	Cyb561	1.1E+08	1.1E+08	3653	1.167535289	2.939581488	3.582E-06	2.12452E-05	0.06546	1	42	50	96	52	121	291	201	182	199	205
ENSMUSG00000039699	chr19	Batf2	6140983	6141087	2522	2.448797694	0.368150251	3.62E-06	2.1457E-05	0.22922	1	7	1	4	1	14	80	29	15	25	57
ENSMUSG00000093575	chr16	Gm20695	3884648	3884806	1088	-1.15198468	3.166993713	3.631E-06	2.15153E-05	0.06543	-1	165	153	232	198	175	132	194	76	95	83
ENSMUSG00000051735	chr7	Rinl	2.9E+07	2.9E+07	2871	1.444537844	1.863404592	3.633E-06	2.15168E-05	0.09207	1	24	22	24	18	55	128	99	82	76	144
ENSMUSG00000050493	chr4	Fam167b	1.3E+08	1.3E+08	959	2.632119151	-0.19220661	3.635E-06	2.15195E-05	0.22026	1	3	3	0	0	9	37	17	26	36	13
ENSMUSG00000032491	chr9	Nradd	1.1E+08	1.1E+08	1162	1.799769684	1.307926122	3.643E-06	2.15418E-05	0.13532	1	8	18	8	11	32	106	53	52	88	77
ENSMUSG00000036990	chr8	Otud4	8E+07	8E+07	8096	-0.93322861	5.883925249	3.645E-06	2.15418E-05	0.04688	-1	1208	913	1506	1220	945	833	1124	642	748	849
ENSMUSG00000037016	chr3	Frem2	5.4E+07	5.4E+07	12347	-1.33506296	2.639556857	3.641E-06	2.15418E-05	0.08534	-1	168	78	123	185	106	79	59	70	88	61
ENSMUSG00000041117	chr7	Ccdc8	1.7E+07	1.7E+07	4809	1.148283338	2.145573293	3.643E-06	2.15418E-05	0.05601	1	35	27	44	47	49	162	106	98	138	107
ENSMUSG00000033313	chr8	Fbxl8	1.1E+08	1.1E+08	2103	1.392247889	1.508702819	3.652E-06	2.15744E-05	0.07984	1	17	11	30	20	38	84	60	66	102	90
ENSMUSG00000020086	chr10	H2afy2	6.2E+07	6.2E+07	2175	1.377560221	1.108981616	3.67E-06	2.16767E-05	0.06873	1	14	13	23	14	21	85	54	47	68	48
ENSMUSG00000041607	chr18	Mbp	8.2E+07	8.2E+07	8403	0.894640998	4.687625561	3.68E-06	2.17222E-05	0.04172	1	262	168	294	243	413	888	577	396	796	852
ENSMUSG00000045690	chr12	Wdr89	7.6E+07	7.6E+07	3192	0.975973563	4.592388008	3.701E-06	2.18386E-05	0.04987	1	182	163	324	216	369	705	425	525	825	790
ENSMUSG00000021223	chr12	Papln	8.4E+07	8.4E+07	5635	-1.95820355	1.320636879	3.751E-06	2.21226E-05	0.17008	-1	24	37	133	56	57	11	39	15	21	16
ENSMUSG00000036769	chrX	Wdr44	2.4E+07	2.4E+07	8353	-1.12135775	4.25440023	3.793E-06	2.2362E-05	0.0659	-1	482	351	394	399	275	296	378	168	183	231
ENSMUSG00000073684	chr4	2610002J02Rik	1.6E+08	1.6E+08	1743	1.924994979	2.683509378	3.804E-06	2.24186E-05	0.18266	1	29	18	33	12	118	270	125	155	249	228
ENSMUSG00000027009	chr2	Itga4	7.9E+07	7.9E+07	13978	-1.55319775	4.081147901	3.82E-06	2.25039E-05	0.12516	-1	449	537	219	320	196	214	195	122	171	196
ENSMUSG00000027470	chr2	Mylk2	1.5E+08	1.5E+08	2951	-1.07703093	9.8447475	3.827E-06	2.25339E-05	0.06354	-1	23526	13993	16784	16695	21988	13472	17894	7653	11813	11222
ENSMUSG00000023800	chr17	Tiam2	3326573	3326726	6281	1.290879579	3.744631646	3.861E-06	2.2723E-05	0.08575	1	94	49	220	153	88	343	467	408	343	339
ENSMUSG00000064345	chrMT	mt-Nd2	3914	4951	1038	-1.45633448	12.89810456	3.876E-06	2.28017E-05	0.11406	-1	155567	79760	278654	208105	151338	65220	175238	42089	67037	81027
ENSMUSG00000025804	chr9	Ccr1	1.2E+08	1.2E+08	2831	2.077822098	1.634509625	3.885E-06	2.28491E-05	0.19029	1	7	26	9	11	28	201	74	87	64	72
ENSMUSG00000062694	chr6	Cav3	1.1E+08	1.1E+08	1160	0.865080249	6.111121878	3.893E-06	2.28829E-05	0.04059	1	607	513	1065	731	840	2169	1827	1634	1844	1675
ENSMUSG00000022037	chr14	Clu	6.6E+07	6.6E+07	3438	1.136365475	6.229322148	3.908E-06	2.29639E-05	0.06999	1	564	366	1105	681	976	3653	1479	1414	2600	1718
ENSMUSG00000037369	chrX	Kdm6a	1.8E+07	1.8E+07	8158	-1.20277958	4.10189755	3.911E-06	2.29705E-05	0.07572	-1	384	376	303	429	214	267	214	177	177	238
ENSMUSG00000063856	chr9	Gpx1	1.1E+08	1.1E+08	1441	1.36938762	7.178514159	3.925E-06	2.30425E-05	0.10106	1	960	897	876	740	2777	5249	3415	3161	5031	4809
ENSMUSG00000029571	chr6	Tmem106b	1.3E+07	1.3E+07	6931	-0.95240405	5.807863315	3.94E-06	2.31197E-05	0.04914	-1	1147	763	1555	1209	913	898	1133	528	681	751
ENSMUSG00000029313	chr5	Aff1	1E+08	1E+08	9458	-0.80318625	5.473660822	3.952E-06	2.31744E-05	0.03459	-1	817	661	1155	818	806	791	760	515	629	659
ENSMUSG00000046080	chr6	Clec9a	1.3E+08	1.3E+08	3294	2.779292027	-0.32343807	3.951E-06	2.31744E-05	0.23101	1	2	2	0	2	6	40	9	8	21	43
ENSMUSG00000026928	chr2	Card9	2.6E+07	2.6E+07	2293	1.60845775	1.085580515	3.955E-06	2.31809E-05	0.1049	1	19	6	16	9	25	93	42	38	75	64
ENSMUSG00000031749	chr8	St3gal2	1.1E+08	1.1E+08	5041	-1.03662922	6.031337957	3.963E-06	2.32214E-05	0.05836	-1	1312	987	1971	1452	895	924	1229	594	828	895
ENSMUSG00000068284	chr16	Gm608	4.4E+07	4.4E+07	13050	-1.02314857	6.200771141	3.998E-06	2.34133E-05	0.05701	-1	1384	1103	1979	1705	1252	968	1568	638	869	1027
ENSMUSG00000067150	chr17	Xpo5	4.6E+07	4.6E+07	3709	-0.97314606	3.606190114	4.029E-06	2.35854E-05	0.04762	-1	199	205	273	272	252	173	248	105	158	171
ENSMUSG00000023484	chr15	Prph	9.9E+07	9.9E+07	1865	1.767883896	0.575488209	4.045E-06	2.36715E-05	0.11204	1	15	3	9	9	10	64	29	30	36	58
ENSMUSG00000020948	chr12	Klhl28	6.5E+07	6.5E+07	2854	-2.03077143	1.603326538	4.06E-06	2.37476E-05	0.19129	-1	82	59	101	83	32	32	56	13	12	12
ENSMUSG00000027200	chr2	Sema6d	1.2E+08	1.2E+08	10559	-0.8449079	4.509935105	4.064E-06	2.3758E-05	0.03729	-1	412	376	471	492	415	410	428	251	299	303
ENSMUSG00000038384	chr5	Setd1b	1.2E+08	1.2E+08	10874	-1.12278389	3.362651941	4.074E-06	2.37974E-05	0.0636	-1	176	122	307	276	197	152	209	77	127	112
ENSMUSG00000071266	chr17	Zfp946	2.2E+07	2.2E+07	3504	-1.31748094	2.14317801	4.073E-06	2.37974E-05	0.08114	-1	103	71	108	86	100	61	93	32	37	39
ENSMUSG00000032118	chr9	Fez1	3.7E+07	3.7E+07	4029	1.033508027	3.222901038	4.093E-06	2.38988E-05	0.05256	1	73	51	148	80	120	358	208	206	252	259
ENSMUSG00000019947	chr10	Arid5b	6.8E+07	6.8E+07	4494	-1.7542403	2.774260007	4.096E-06	2.39074E-05	0.15389	-1	190	128	181	173	102	78	147	37	26	42

ENSMUSG00000029465	chr5	Arpc3	1.2E+08	1.2E+08	2581	0.880886912	5.970321119	4.109E-06	2.39755E-05	0.04222	1	657	435	868	568	856	2362	1390	1392	1674	1586
ENSMUSG00000047139	chr10	Cd24a	4.4E+07	4.4E+07	1813	-1.0370446	8.21313339	4.132E-06	2.4095E-05	0.0593	-1	6338	4717	6676	5351	6874	6014	5546	2639	3311	3039
ENSMUSG00000038773	chr18	Kdm3b	3.5E+07	3.5E+07	7112	-0.83500632	5.035840953	4.14E-06	2.41366E-05	0.0372	-1	633	471	903	637	525	576	623	321	457	485
ENSMUSG00000044098	chr3	Rsbn1	1E+08	1E+08	6861	-1.10174583	3.093599779	4.144E-06	2.41406E-05	0.06005	-1	158	137	246	167	167	103	177	71	89	122
ENSMUSG00000055991	chr5	Zkscan5	1.5E+08	1.5E+08	4114	-0.86701266	3.726982044	4.143E-06	2.41406E-05	0.03727	-1	223	200	335	256	274	179	234	145	211	194
ENSMUSG00000042010	chr5	Acacb	1.1E+08	1.1E+08	9632	-1.20855104	7.989706261	4.159E-06	2.42176E-05	0.07994	-1	3680	2481	10143	6995	4744	3055	4075	2195	3195	3431
ENSMUSG00000047181	chr11	Samd14	9.5E+07	9.5E+07	3379	1.325501224	1.803493709	4.187E-06	2.4368E-05	0.07543	1	22	19	24	34	46	150	94	56	94	111
ENSMUSG00000022636	chr16	Alcam	5.2E+07	5.2E+07	7121	1.726540423	2.148471043	4.196E-06	2.4411E-05	0.14035	1	35	23	14	12	66	155	168	79	124	163
ENSMUSG00000054939	chr16	Zfp174	3847268	3848274	5897	-1.22195728	1.800360917	4.203E-06	2.44384E-05	0.06487	-1	75	51	93	80	62	51	59	28	40	36
ENSMUSG00000035299	chrX	Mid1	1.7E+08	1.7E+08	6720	-1.63649406	1.261181248	4.22E-06	2.45287E-05	0.11632	-1	64	61	51	44	36	25	35	16	16	27
ENSMUSG00000093456	chr9	Gm20662	1.1E+08	1.1E+08	1853	-1.30312422	2.401208222	4.234E-06	2.45998E-05	0.08213	-1	98	101	154	99	106	84	104	31	42	59
ENSMUSG00000003352	chr15	Cacnb3	9.9E+07	9.9E+07	3120	1.396071352	1.612855376	4.255E-06	2.47152E-05	0.08202	1	28	17	34	14	29	130	62	65	77	106
ENSMUSG00000048521	chr9	Cxcr6	1.2E+08	1.2E+08	1893	2.850404365	-0.53398347	4.28E-06	2.48483E-05	0.23185	1	2	1	1	0	6	21	12	25	7	33
ENSMUSG00000010277	chr11	2610507B11Rik	7.8E+07	7.8E+07	8798	-1.04591618	8.799494268	4.3E-06	2.49439E-05	0.06057	-1	7875	6053	13823	10654	7442	6239	8489	3992	5854	5787
ENSMUSG00000052934	chr8	Fbxo31	1.2E+08	1.2E+08	5482	-1.07016863	7.319509794	4.3E-06	2.49439E-05	0.06313	-1	2852	2476	3841	4565	2393	2194	2666	1368	2228	2304
ENSMUSG00000001366	chr9	Fbxo9	7.8E+07	7.8E+07	3103	-0.78360003	5.542411325	4.313E-06	2.50091E-05	0.03321	-1	839	675	1074	923	927	863	814	550	657	666
ENSMUSG00000041298	chr5	Katnal1	1.5E+08	1.5E+08	11881	-0.9809285	3.344002981	4.344E-06	2.51757E-05	0.04762	-1	183	121	324	197	212	168	184	93	117	148
ENSMUSG00000044350	chr14	Lacc1	7.7E+07	7.7E+07	3644	1.381930006	1.947208049	4.38E-06	2.53732E-05	0.08578	1	18	25	37	22	56	165	116	58	100	129
ENSMUSG00000029196	chr5	Tada2b	3.6E+07	3.6E+07	3791	-0.85290141	4.35396959	4.383E-06	2.53818E-05	0.03798	-1	338	275	546	381	473	315	435	196	319	252
ENSMUSG00000037553	chr4	Zdhhc18	1.3E+08	1.3E+08	5382	0.835191887	5.595535372	4.4E-06	2.5472E-05	0.03785	1	428	376	643	501	704	1258	1292	844	1497	1533
ENSMUSG00000060438	chr3	Rps10-ps1	9.6E+07	9.6E+07	498	1.258394725	2.096011079	4.432E-06	2.56334E-05	0.07159	1	27	26	56	34	44	134	78	98	150	139
ENSMUSG00000076068	chr10	Mir678	7.6E+07	7.6E+07	84	1.796120114	1.271938224	4.431E-06	2.56334E-05	0.14196	1	10	7	20	6	37	106	55	39	95	75
ENSMUSG00000026618	chr1	Iars2	1.9E+08	1.9E+08	8885	-0.85185937	6.289270645	4.437E-06	2.56443E-05	0.03997	-1	1425	1001	2034	1601	1626	1277	1466	822	1112	1124
ENSMUSG00000102627	chr7	Snurf	6E+07	6E+07	216	-0.91293311	4.702597379	4.437E-06	2.56443E-05	0.04447	-1	535	339	725	536	444	364	567	247	366	335
ENSMUSG00000092416	chr7	Zfp141	4.2E+07	4.2E+07	4665	-1.12653935	2.348391259	4.466E-06	2.57982E-05	0.05881	-1	114	85	126	99	91	77	88	46	59	59
ENSMUSG00000038080	chr13	Kdm1b	4.7E+07	4.7E+07	4829	-1.12240764	3.553858403	4.483E-06	2.58884E-05	0.06475	-1	249	181	330	239	208	149	258	121	114	119
ENSMUSG00000042109	chr15	Csdc2	8.2E+07	8.2E+07	4623	1.463486531	1.440917095	4.499E-06	2.59697E-05	0.09319	1	12	8	39	27	21	110	68	64	79	70
ENSMUSG00000024074	chr17	Crim1	7.8E+07	7.8E+07	5995	-0.99323146	5.01292504	4.516E-06	2.60571E-05	0.05339	-1	675	417	913	591	691	433	790	261	374	407
ENSMUSG00000000804	chr11	Usp32	8.5E+07	8.5E+07	7680	-1.02881911	4.120322459	4.54E-06	2.61839E-05	0.05588	-1	361	289	471	320	301	235	390	156	184	226
ENSMUSG00000028654	chr4	Mycl	1.2E+08	1.2E+08	4038	2.169969198	0.575224817	4.567E-06	2.63296E-05	0.19211	1	6	3	3	3	23	49	27	46	44	57
ENSMUSG00000046798	chr5	Cldn12	5505015	5508454	4169	-0.90485766	3.890082587	4.608E-06	2.65509E-05	0.04203	-1	319	226	301	245	354	228	297	157	200	185
ENSMUSG00000045896	chr6	Paip2b	8.4E+07	8.4E+07	6157	-1.02521904	7.001608868	4.615E-06	2.65834E-05	0.05831	-1	2912	1879	3509	2596	2013	1957	2454	1247	1394	1751
ENSMUSG00000003226	chr10	Ranbp2	5.8E+07	5.8E+07	9477	-1.01719907	6.217872637	4.621E-06	2.66043E-05	0.05711	-1	1520	1219	1821	1560	1304	1215	1540	754	729	896
ENSMUSG00000022946	chr16	Dopey2	9.4E+07	9.4E+07	7313	-1.02714979	4.992952817	4.645E-06	2.67357E-05	0.05728	-1	698	668	482	627	595	433	533	302	518	386
ENSMUSG00000078578	chr3	Ube2d3	1.4E+08	1.4E+08	2675	-0.95233002	7.646735701	4.648E-06	2.67405E-05	0.0506	-1	3900	2980	5268	4007	3794	2926	4009	2031	2495	2740
ENSMUSG00000020366	chr11	Mapk9	5E+07	5E+07	6784	-0.86944641	5.683797401	4.651E-06	2.67463E-05	0.04148	-1	1009	880	1046	969	1010	851	976	538	738	679
ENSMUSG00000022961	chr16	Son	9.2E+07	9.2E+07	14354	-0.91338116	7.252817599	4.676E-06	2.68792E-05	0.04654	-1	2650	2435	3762	3195	2911	2471	2780	1498	1987	2306
ENSMUSG00000055612	chr2	Cdca7	7.2E+07	7.2E+07	3202	2.009904904	0.360855329	4.72E-06	2.71188E-05	0.14183	1	6	6	8	5	9	65	22	46	30	23
ENSMUSG00000025860	chrX	Xiap	4.2E+07	4.2E+07	9262	-0.85786737	4.89261254	4.793E-06	2.75302E-05	0.03972	-1	574	465	682	559	582	546	637	286	342	403
ENSMUSG00000070577	chr4	Gm572	1.5E+08	1.5E+08	1385	-1.76317073	1.901895478	4.837E-06	2.77698E-05	0.15064	-1	92	61	135	87	56	37	79	22	21	17
ENSMUSG00000002668	chr17	Dennd1c	5.7E+07	5.7E+07	2520	2.230104366	1.45103277	4.843E-06	2.77938E-05	0.22722	1	13	10	4	4	38	129	49	60	72	133
ENSMUSG00000042155	chr2	Klhl23	7E+07	7E+07	4925	-1.07596862	4.686504009	4.864E-06	2.7902E-05	0.06251	-1	592	259	824	342	723	300	508	288	319	282
ENSMUSG00000022816	chr16	Fstl1	3.8E+07	3.8E+07	4914	1.133520169	7.298389	4.867E-06	2.79067E-05	0.0714	1	1220	1112	1278	1201	2729	6932	3927	3718	4184	3718
ENSMUSG00000028150	chr3	Rorc	9.4E+07	9.4E+07	2098	-0.99041034	5.976834162	4.919E-06	2.81944E-05	0.05436	-1	1032	818	1955	1393	1251	903	1340	480	862	854
ENSMUSG00000040813	chr9	Tex264	1.1E+08	1.1E+08	2874	0.852273769	5.351679598	4.979E-06	2.85261E-05	0.03975	1	413	242	488	457	644	1202	936	764	1223	1315
ENSMUSG00000049881	chr1	2810025M15Rik	1.6E+08	1.6E+08	1410	1.167459383	3.211969192	5.02E-06	2.87512E-05	0.06956	1	59	45	92	85	159	349	185	201	298	277
ENSMUSG00000068205	chr2	Macrod2	1.4E+08	1.4E+08	10308	-1.1069335	3.503592039	5.038E-06	2.88403E-05	0.06352	-1	263	244	213	208	185	183	151	111	167	131
ENSMUSG00000026748	chr2	Plxdc2	1.6E+07	1.6E+07	6947	0.866003413	5.167350209	5.052E-06	2.89009E-05	0.04076	1	382	291	404	306	540	1476	806	674	862	1036
ENSMUSG00000050002	chr13	Idnk	5.8E+07	5.8E+07	1511	1.192908241	2.987639263	5.05E-06	2.89009E-05	0.07156	1	70	39	95	53	112	313	136	167	255	256
ENSMUSG00000049323	chr11	Smcr8	6.1E+07	6.1E+07	8078	-0.87670528	4.940361787	5.078E-06	2.9037E-05	0.04177	-1	578	497	738	657	483	463	609	332	376	462
ENSMUSG00000030203	chr6	Dusp16	1.3E+08	1.3E+08	7650	-0.84435304	4.393577847	5.106E-06	2.91713E-05	0.03769	-1	363	254	582	438	432	321	418	252	251	306
ENSMUSG00000089862	chr6	Gm16039	8259288	8259493	10430	-0.90760686	3.99834714	5.104E-06	2.91713E-05	0.04323	-1	312	235	353	273	400	250	352	144	197	217
ENSMUSG00000028226	chr4	Mmp16	1.8E+07	1.8E+07	8667	1.993111424	-0.31757807	5.125E-06	2.92704E-05	0.09913	1	5	1	4	5	5	33	19	20	17	21
ENSMUSG00000018924	chr11	Alox15	7E+07	7E+07	2454	2.622123274	1.852526329	5.136E-06	2.93194E-05	0.32353	1	10	9	6	4	46	227	38	49	93	227
ENSMUSG00000001665	chr10	Gstt3	7.6E+07	7.6E+07	2627	1.32928231	2.696793717	5.14E-06	2.93301E-05	0.08811	1	43	31	53	45	109	240	111	159	223	200
ENSMUSG00000038886	chr7	Man2a2	8E+07	8E+07	6553	-0.98929953	7.617413171	5.146E-06	2.93542E-05	0.05505	-1	4025	3435	4504	3743	3650	2792	3739	2030	2858	2216
ENSMUSG00000006463	chr19	Zdhhc24	4878668	4878736	2916	1.396334325	2.948255363	5.234E-06	2.98419E-05	0.09769	1	68	71	36	34	94	272	198	170	247	249
ENSMUSG00000051851	chrX	Cxx1c	5.4E+07	5.4E+07	401	1.280484668	2.151040794	5.27E-06	3.00358E-05	0.07548	1	33	31	40	27	59	170	82	90	148	143
ENSMUSG00000020577	chr12	Tspan13	3.6E+07	3.6E+07	2474	0.958929878	5.557279685	5.279E-06	3.00684E-05	0.051	1	350	279	605	410	865	1351	1167	977	1346	1566
ENSMUSG00000025907	chr1	Rb1cc1	6206197	6206270	14690	-0.99635725	6.140162995	5.28E-06	3.00684E-05	0.05546	-1	1523	1079	1866	1431	1137	1016	1467	653	820	961
ENSMUSG00000019338	chr3	Zfp687	9.5E+07	9.5E+07	5952	-0.83038101	4.055484272	5.29E-06	3.01155E-05	0.03603	-1	260	265	369	321	383	269	313	150	255	261
ENSMUSG00000032293	chr9	Ireb2	5.5E+07	5.5E+07	5808	-0.81505983	5.0876102	5.36E-06	3.04981E-05	0.03629	-1	637	543	784	667	597	665	604	419	418	445
ENSMUSG00000018654	chr11	Ikzf1	1.2E+07	1.2E+07	5777	1.685975781	1.667522455	5.397E-06	3.06968E-05	0.12809	1	19	25	9	14	38	141	82	81	69	105
ENSMUSG00000041084	chr3	Ostc	1.3E+08	1.3E+08	1058	0.792218113	4.829176569	5.399E-06	3.06968E-05	0.03371	1	297	226	388	318	341	1052	621	644	711	680
ENSMUSG00000034071	chr7	Zfp551	1.2E+07	1.2E+07	2636	-1.9486569	-0.29476097	5.412E-06	3.07599E-05	0.11766	-1	18	15	24	16	16	10	12	1	6	3
ENSMUSG00000001288	chr15	Rarg	1E+08	1E+08	4109	0.919605142	4.428717283	5.444E-06	3.09075E-05	0.04542	1	212	139	244	199	346	794	451	428	486	761
ENSMUSG00000029126	chr5	Nsg1	3.8E+07	3.8E+07	2140	1.371350585	2.488710895	5.441E-06	3.09075E-05	0.09159	1	31	43	42	35	79	242	107	161	147	151

ENSMUSG00000045838	chr2	A430105I19Rik	1.2E+08	1.2E+08	4779	-0.99585349	4.832630161	5.445E-06	3.09075E-05	0.05435	-1	405	306	942	636	688	377	621	237	348	407
ENSMUSG00000020463	chr11	Smek2	2.9E+07	2.9E+07	5694	-0.87017306	4.491413184	5.486E-06	3.11288E-05	0.04077	-1	441	364	478	460	412	385	454	255	272	281
ENSMUSG00000034165	chr17	Ccnd3	4.8E+07	4.8E+07	8775	1.203473259	5.047007413	5.494E-06	3.11597E-05	0.07979	1	208	192	255	224	682	1175	667	749	1119	1034
ENSMUSG00000042759	chr7	Apobr	1.3E+08	1.3E+08	3779	1.713188244	2.62319695	5.572E-06	3.15909E-05	0.14913	1	37	22	25	19	118	257	191	110	188	223
ENSMUSG00000024043	chr17	Arhgap28	6.8E+07	6.8E+07	5377	1.145630956	2.107697161	5.6E-06	3.1731E-05	0.05739	1	32	35	34	40	53	137	117	96	118	124
ENSMUSG00000038181	chr5	Chpf2	2.5E+07	2.5E+07	5371	0.866258457	4.93179463	5.601E-06	3.1731E-05	0.04095	1	275	243	340	253	538	908	724	571	946	927
ENSMUSG00000009555	chr2	Cdk9	3.3E+07	3.3E+07	4611	0.886639915	5.026696546	5.653E-06	3.20096E-05	0.04316	1	302	234	334	296	585	1050	716	614	1023	980
ENSMUSG00000028673	chr4	Fuca1	1.4E+08	1.4E+08	3276	0.874823227	5.146864833	5.66E-06	3.20346E-05	0.04214	1	341	263	403	282	627	1140	855	631	1129	1012
ENSMUSG00000003402	chr9	Prkcsh	2.2E+07	2.2E+07	2013	0.885095104	5.365623891	5.664E-06	3.2049E-05	0.04343	1	346	280	455	462	680	1242	941	736	1389	1243
ENSMUSG00000003200	chr17	Sh3gl1	5.6E+07	5.6E+07	2072	0.935041846	4.064455082	5.69E-06	3.218E-05	0.04612	1	158	139	162	141	261	560	350	346	533	467
ENSMUSG00000046345	chr16	Smco1	3.2E+07	3.2E+07	1408	-0.92714292	5.68110579	5.692E-06	3.21815E-05	0.04809	-1	1115	834	1065	977	995	642	1039	515	763	702
ENSMUSG00000034968	chr6	Lbx2	8.3E+07	8.3E+07	934	2.296898696	-0.49253995	5.711E-06	3.22757E-05	0.12052	1	2	5	3	2	2	24	14	22	17	20
ENSMUSG00000052920	chr19	Prkg1	3.1E+07	3.1E+07	7799	-2.54488945	3.38137587	5.718E-06	3.22974E-05	0.3248	-1	214	68	740	345	67	75	155	37	33	21
ENSMUSG00000058230	chr7	Arhgap35	1.6E+07	1.6E+07	9147	-0.80582387	5.502853879	5.734E-06	3.23758E-05	0.03607	-1	745	576	1162	997	924	739	869	517	640	652
ENSMUSG00000059555	chr2	Tor4a	2.5E+07	2.5E+07	3301	1.25914256	2.740338906	5.744E-06	3.24184E-05	0.08003	1	42	31	67	39	125	240	180	146	198	193
ENSMUSG00000002718	chr2	Cse1l	1.7E+08	1.7E+08	5273	-0.95606312	6.077035686	5.806E-06	3.27583E-05	0.05151	-1	1279	1128	1618	1500	1088	1011	1326	686	905	844
ENSMUSG00000060550	chr17	H2-Q7	3.5E+07	3.5E+07	4265	1.57925174	3.06564112	5.847E-06	3.29749E-05	0.12939	1	54	47	51	55	105	523	128	110	200	368
ENSMUSG00000030610	chr7	Det1	7.9E+07	7.9E+07	2877	-0.87298599	3.956813366	5.88E-06	3.31488E-05	0.04024	-1	269	226	421	312	289	236	311	140	237	218
ENSMUSG00000024598	chr18	Fbn2	5.8E+07	5.8E+07	10480	2.820255654	-0.48663717	5.981E-06	3.37067E-05	0.22053	1	2	4	1	2	1	28	6	29	24	14
ENSMUSG00000104344	chr9	RP23-444I6.3	1.1E+08	1.1E+08	3245	-1.92789816	0.852014877	5.995E-06	3.3769E-05	0.16124	-1	52	58	27	33	26	12	17	14	19	13
ENSMUSG00000042447	chr6	Mios	8209222	8209411	6552	-0.8850433	4.089277695	5.998E-06	3.37754E-05	0.0417	-1	318	228	483	341	306	264	340	192	202	236
ENSMUSG00000026854	chr2	Usp20	3.1E+07	3.1E+07	9017	0.764446684	4.664526606	6.041E-06	3.39984E-05	0.03143	1	272	172	393	315	280	791	737	414	684	704
ENSMUSG00000045679	chr12	Pqlc3	1.7E+07	1.7E+07	5408	1.419751139	2.608366032	6.049E-06	3.40335E-05	0.10065	1	46	42	29	28	99	222	196	107	168	216
ENSMUSG00000021298	chr12	Gpr132	1.1E+08	1.1E+08	2439	2.544104517	0.477404108	6.086E-06	3.42282E-05	0.27304	1	1	4	2	2	19	38	22	29	47	82
ENSMUSG00000024750	chr19	Zfand5	2.1E+07	2.1E+07	6193	-0.99777152	7.629886215	6.14E-06	3.45196E-05	0.05691	-1	4556	2738	5203	3608	3876	2707	4141	1983	2305	2599
ENSMUSG00000058290	chr15	Espl1	1E+08	1E+08	6630	2.261209817	-0.09001075	6.193E-06	3.48005E-05	0.18288	1	2	0	2	6	11	46	19	13	36	25
ENSMUSG00000101655	chr6	2310040G24Rik	8.6E+07	8.6E+07	775	-0.9195796	5.988373793	6.227E-06	3.49806E-05	0.04794	-1	1320	1156	1129	1256	1214	1015	910	640	1042	952
ENSMUSG00000040410	chr4	Fbxl4	2.2E+07	2.2E+07	3798	-1.04461483	4.556282614	6.232E-06	3.49914E-05	0.06032	-1	512	440	457	321	617	411	490	223	239	244
ENSMUSG00000004677	chr8	Myo9b	7.1E+07	7.1E+07	7297	0.800001123	4.362476432	6.255E-06	3.51071E-05	0.03405	1	174	180	251	199	331	639	555	383	515	611
ENSMUSG00000001323	chr11	Srr	7.5E+07	7.5E+07	4560	-0.77837753	3.989554067	6.27E-06	3.51792E-05	0.03152	-1	290	221	354	326	316	284	259	195	234	232
ENSMUSG00000020248	chr10	Nfyb	8.3E+07	8.3E+07	5068	-0.8160946	5.145088308	6.273E-06	3.51812E-05	0.03699	-1	747	500	898	583	677	540	719	405	493	492
ENSMUSG00000031333	chrX	Abcb7	1E+08	1E+08	5905	-0.99183777	5.968430274	6.319E-06	3.54261E-05	0.05577	-1	1177	850	1781	1556	941	803	1203	650	821	853
ENSMUSG00000048332	chr3	Lhfp	5.3E+07	5.3E+07	2108	0.897534661	4.352585893	6.344E-06	3.55521E-05	0.0436	1	187	159	256	159	326	815	555	450	429	500
ENSMUSG00000060743	chr1	H3f3a	1.8E+08	1.8E+08	3504	-0.88623999	6.378775307	6.35E-06	3.55664E-05	0.0448	-1	1743	1256	1928	1592	1564	1286	1618	852	1120	1203
ENSMUSG00000026495	chr1	Efcab2	1.8E+08	1.8E+08	4151	-0.87779163	4.174215042	6.352E-06	3.55684E-05	0.04146	-1	330	220	476	394	363	241	366	172	240	301
ENSMUSG00000026581	chr1	Sell	1.6E+08	1.6E+08	5911	2.187237963	0.201976964	6.362E-06	3.56061E-05	0.18567	1	5	1	4	4	14	58	18	34	18	42
ENSMUSG00000049872	chr10	Fam26e	3.4E+07	3.4E+07	1786	1.310163186	1.876892555	6.408E-06	3.58492E-05	0.07773	1	22	26	30	29	46	182	88	69	92	99
ENSMUSG00000027230	chr2	Creb3l1	9.2E+07	9.2E+07	2603	1.330932484	3.194038729	6.424E-06	3.59284E-05	0.09284	1	66	59	64	40	165	363	227	235	274	229
ENSMUSG00000003233	chr16	Dvl3	2.1E+07	2.1E+07	4899	-1.20881249	3.660058822	6.459E-06	3.61082E-05	0.07893	-1	206	207	398	311	207	151	282	76	160	134
ENSMUSG00000042042	chr6	Csgalnact2	1.2E+08	1.2E+08	5438	-0.88668972	5.142461675	6.464E-06	3.61207E-05	0.04404	-1	699	568	785	721	633	592	766	353	391	487
ENSMUSG00000058883	chr13	Zfp708	6.7E+07	6.7E+07	2450	-1.7303744	1.030798256	6.467E-06	3.61244E-05	0.13156	-1	48	43	61	46	28	15	30	22	9	17
ENSMUSG00000090100	chr2	Ttbk2	1.2E+08	1.2E+08	11406	-1.06719864	3.652637993	6.513E-06	3.63648E-05	0.06086	-1	236	204	354	305	168	189	236	103	158	162
ENSMUSG00000015335	chr2	Zdhhc12	3E+07	3E+07	1785	1.095445736	2.006492812	6.533E-06	3.64607E-05	0.0514	1	31	30	42	35	49	122	118	81	124	102
ENSMUSG00000079003	chr8	Samd1	8.4E+07	8.4E+07	2071	0.941913016	4.145201495	6.552E-06	3.65536E-05	0.04773	1	111	144	208	235	211	632	399	317	511	557
ENSMUSG00000021745	chr14	Ptprg	1.2E+07	1.2E+07	10917	-0.80789607	4.358304312	6.556E-06	3.65651E-05	0.03512	-1	351	277	532	394	431	323	411	257	281	260
ENSMUSG00000020432	chr11	Tcn2	3917192	3917709	2178	0.86134761	5.300752411	6.581E-06	3.6673E-05	0.04172	1	368	231	577	383	622	1319	836	754	1263	1100
ENSMUSG00000038515	chr8	Grtp1	1.3E+07	1.3E+07	1310	-1.09627733	2.173656424	6.581E-06	3.6673E-05	0.05523	-1	91	47	124	98	108	76	69	39	54	58
ENSMUSG00000051457	chr7	Spn	1.3E+08	1.3E+08	4607	2.066158962	0.784479632	6.599E-06	3.67452E-05	0.18251	1	6	5	7	4	25	83	42	39	24	77
ENSMUSG00000101257	chr1	2310015K22Rik	8E+07	8E+07	1461	-1.72453828	0.454593493	6.597E-06	3.67452E-05	0.11542	-1	20	38	27	30	32	12	19	8	15	9
ENSMUSG00000090841	chr10	Myl6	1.3E+08	1.3E+08	665	1.092599375	7.641687897	6.634E-06	3.69251E-05	0.06849	1	1535	1311	1759	1592	3653	7629	4315	4476	5942	5818
ENSMUSG00000060019	chr8	Gm10073	1.1E+08	1.1E+08	496	1.396595348	3.250666916	6.661E-06	3.70604E-05	0.10285	1	71	50	59	87	125	256	168	147	463	381
ENSMUSG00000042302	chr11	Ehbp1	2.2E+07	2.2E+07	5825	-1.02187932	3.745713612	6.675E-06	3.7125E-05	0.05608	-1	273	232	317	258	252	222	293	104	163	148
ENSMUSG00000041912	chr3	Tdrkh	9.4E+07	9.4E+07	3806	-1.2748833	2.490398866	6.741E-06	3.74608E-05	0.08212	-1	146	107	76	98	151	84	55	55	74	68
ENSMUSG00000087555	chr2	Gm13997	1.2E+08	1.2E+08	336	-2.26596761	0.643769073	6.74E-06	3.74608E-05	0.22569	-1	37	39	44	40	24	6	30	7	9	2
ENSMUSG00000022228	chr13	Zscan26	2.1E+07	2.1E+07	4371	-0.88584945	4.20552755	6.786E-06	3.76944E-05	0.04286	-1	365	304	392	318	404	386	343	152	219	268
ENSMUSG00000029651	chr5	Mtus2	1.5E+08	1.5E+08	9905	2.394006783	0.212763991	6.831E-06	3.79296E-05	0.20347	1	2	8	8	5	0	52	56	23	15	32
ENSMUSG00000036206	chr1	Sh3bp4	8.9E+07	8.9E+07	5112	0.972488471	3.352645702	6.834E-06	3.79337E-05	0.04873	1	102	68	111	78	163	346	250	214	248	327
ENSMUSG00000022221	chr14	Ripk3	5.6E+07	5.6E+07	1964	1.58642102	1.22511041	6.851E-06	3.80113E-05	0.11081	1	10	12	27	7	29	107	50	50	77	59
ENSMUSG00000028832	chr4	Stmn1	1.3E+08	1.3E+08	1922	1.384271824	1.396522689	6.858E-06	3.80345E-05	0.08102	1	21	14	21	15	34	108	51	60	81	73
ENSMUSG00000030850	chr7	Ate1	1.3E+08	1.3E+08	4875	-0.88218906	5.7178795	6.879E-06	3.81341E-05	0.04437	-1	1029	856	1224	1051	915	867	1047	511	764	677
ENSMUSG00000022807	chr16	Osbpl11	3.3E+07	3.3E+07	4520	-0.84639937	4.421612391	6.906E-06	3.82717E-05	0.03915	-1	337	259	572	381	584	352	451	225	265	299
ENSMUSG00000030082	chr6	Sec61a1	8.9E+07	8.9E+07	6407	0.888182321	5.306567689	6.934E-06	3.84009E-05	0.04448	1	363	302	390	366	693	1511	930	803	1092	1003
ENSMUSG00000050965	chr11	Prkca	1.1E+08	1.1E+08	8992	-0.95007046	6.292155264	6.935E-06	3.84009E-05	0.05186	-1	1656	1205	1760	1855	1182	1205	1364	762	1111	1124
ENSMUSG00000043940	chr5	Wdfy3	1E+08	1E+08	15351	-0.8848646	5.083160501	6.962E-06	3.85373E-05	0.0441	-1	597	497	914	764	538	609	702	328	443	411
ENSMUSG00000024210	chr17	Ip6k3	2.7E+07	2.7E+07	2307	1.152414321	5.641901216	6.969E-06	3.85615E-05	0.07563	1	337	171	874	584	503	1357	1364	1384	1526	1334
ENSMUSG00000025762	chr3	Larp1b	4.1E+07	4.1E+07	7216	-0.8690174	5.583067538	7.134E-06	3.94565E-05	0.04308	-1	951	814	978	954	876	736	944	491	664	691
ENSMUSG00000025266	chrX	Gnl3l	1.5E+08	1.5E+08	5570	-0.82892205	5.085108715	7.146E-06	3.95055E-05	0.03867	-1	675	535	800	663	558	517	696	352	490	484

ENSMUSG00000038949	chr1	Cnst	1.8E+08	1.8E+08	8859	-0.86403102	5.707364155	7.186E-06	3.97125E-05	0.04269	-1	894	797	1394	1006	1005	789	1100	529	674	765
ENSMUSG00000101111	chr1	Gm28437	2.5E+07	2.5E+07	783	-0.97517098	4.222451905	7.193E-06	3.97353E-05	0.05248	-1	352	213	560	431	343	270	415	164	223	242
ENSMUSG00000015653	chr5	Steap2	5664831	5673696	12142	1.429281759	0.83757425	7.209E-06	3.98083E-05	0.07218	1	11	11	13	13	19	73	57	30	47	45
ENSMUSG00000003814	chr8	Calr	8.5E+07	8.5E+07	2880	0.944044073	8.139794761	7.221E-06	3.98585E-05	0.05189	1	2499	1957	3242	3042	4025	11621	6114	5803	7888	7330
ENSMUSG00000041408	chr14	Wapal	3.5E+07	3.5E+07	6623	-0.84980464	5.401717305	7.232E-06	3.99059E-05	0.04106	-1	806	614	1075	838	762	685	897	440	540	579
ENSMUSG00000001123	chr11	Lgals9	7.9E+07	7.9E+07	2137	0.963810937	4.28403337	7.235E-06	3.99073E-05	0.05124	1	148	131	221	159	360	787	505	359	586	449
ENSMUSG00000025498	chr7	Irf7	1.4E+08	1.4E+08	3020	1.555838386	2.680656004	7.259E-06	4.00192E-05	0.12682	1	42	20	49	40	99	339	184	73	276	132
ENSMUSG00000039275	chr11	Foxk2	1.2E+08	1.2E+08	5258	-0.84344256	5.573452023	7.279E-06	4.0116E-05	0.04061	-1	844	722	1121	991	912	765	993	505	661	619
ENSMUSG00000022389	chr15	Tef	8.2E+07	8.2E+07	7865	-0.92926108	7.723527533	7.327E-06	4.03639E-05	0.05032	-1	4403	3263	5276	3359	4608	3062	3965	2391	2998	2608
ENSMUSG00000021792	chr14	Fam213a	4.1E+07	4.1E+07	2948	-1.32087244	5.431152547	7.34E-06	4.042E-05	0.09899	-1	987	582	638	474	2095	706	444	373	514	534
ENSMUSG00000006304	chr1	Arpc2	7.4E+07	7.4E+07	2033	0.84198259	6.728654019	7.365E-06	4.05406E-05	0.04113	1	1009	743	1360	1177	1536	3386	2544	2200	2805	3147
ENSMUSG00000032300	chr9	1700017B05Rik	5.7E+07	5.7E+07	4934	1.107764017	3.412653178	7.37E-06	4.0554E-05	0.06509	1	89	69	84	80	189	302	255	225	360	338
ENSMUSG00000054717	chr8	Hmgb2	5.8E+07	5.8E+07	2692	1.085110175	2.495078818	7.39E-06	4.06486E-05	0.05586	1	51	43	65	43	64	231	124	122	151	149
ENSMUSG00000033152	chr6	Podxl2	8.9E+07	8.9E+07	3948	-0.84513832	5.649511463	7.435E-06	4.08791E-05	0.04092	-1	928	669	1202	1047	1046	706	932	475	942	678
ENSMUSG00000058402	chr7	Zfp420	3E+07	3E+07	4238	-1.31312937	1.156705783	7.455E-06	4.09712E-05	0.07237	-1	53	29	52	54	45	36	33	15	23	23
ENSMUSG00000016206	chr17	H2-M3	3.7E+07	3.7E+07	1438	1.380035723	2.762313792	7.539E-06	4.14201E-05	0.09829	1	51	46	35	49	95	339	128	117	194	237
ENSMUSG00000031710	chr8	Ucp1	8.3E+07	8.3E+07	1644	-6.7290088	5.572255731	7.545E-06	4.14374E-05	1.54532	-1	2235	21	2	0	5552	39	11	15	8	20
ENSMUSG00000020048	chr10	Hsp90b1	8.7E+07	8.7E+07	4032	1.008862394	7.904768568	7.596E-06	4.16817E-05	0.05938	1	2149	1624	2932	2304	3186	11375	5170	5457	5257	6192
ENSMUSG00000038248	chr10	Sobp	4.3E+07	4.3E+07	5529	-0.87906464	4.831310288	7.595E-06	4.16817E-05	0.04354	-1	448	384	788	564	643	388	633	248	469	355
ENSMUSG00000040006	chr10	Ginm1	7767947	7768585	2996	-0.78544799	5.832085302	7.601E-06	4.16948E-05	0.03545	-1	1026	683	1507	1010	1329	1011	1022	639	765	910
ENSMUSG00000029659	chr5	Medag	1.5E+08	1.5E+08	3956	0.873748758	4.448990251	7.642E-06	4.19028E-05	0.04199	1	201	202	231	190	328	789	566	522	500	518
ENSMUSG00000027770	chr3	Dhx36	6.2E+07	6.2E+07	10217	-0.78854647	4.987882231	7.734E-06	4.23881E-05	0.03507	-1	614	458	717	629	595	587	652	325	388	480
ENSMUSG00000030554	chr7	Synm	6.8E+07	6.8E+07	7866	-1.03755015	9.579730717	7.754E-06	4.24653E-05	0.06304	-1	17127	10799	18576	13571	17992	10676	16652	6635	10494	8032
ENSMUSG00000040310	chr2	Alx4	9.4E+07	9.4E+07	7060	1.463243248	1.286662549	7.751E-06	4.24653E-05	0.08952	1	21	15	16	16	23	124	69	53	49	58
ENSMUSG00000071302	chr8	2610044O15Rik8	1.3E+08	1.3E+08	3858	-0.96548743	4.429979066	7.779E-06	4.25885E-05	0.05221	-1	438	270	673	443	352	373	450	214	231	255
ENSMUSG00000067288	chr17	Rps28	3.4E+07	3.4E+07	1464	0.946857044	6.985050301	7.783E-06	4.25941E-05	0.0523	1	1112	918	1446	1383	1730	4300	2344	2767	3886	3916
ENSMUSG00000014418	chr7	Hps5	4.7E+07	4.7E+07	6482	-0.86662174	4.42460634	7.789E-06	4.26099E-05	0.04173	-1	430	400	388	396	411	356	347	258	322	281
ENSMUSG00000037337	chr7	Map4k1	2.9E+07	2.9E+07	2699	1.588136256	1.219622046	7.797E-06	4.26336E-05	0.11163	1	9	12	18	11	34	93	47	52	54	94
ENSMUSG00000056342	chr11	Usp34	2.3E+07	2.3E+07	18453	-0.87049131	6.101079551	7.814E-06	4.27101E-05	0.04396	-1	1270	1053	1699	1415	1218	1120	1320	707	880	1029
ENSMUSG00000098926	chr1	Mir6904	1.8E+08	1.8E+08	67	-1.9266941	1.049179957	7.817E-06	4.27128E-05	0.17347	-1	53	34	75	50	29	18	39	13	12	5
ENSMUSG00000060419	chr5	Rps16-ps2	1.3E+08	1.3E+08	441	0.967735832	4.16323879	7.845E-06	4.28459E-05	0.05137	1	166	155	146	170	262	571	359	375	506	621
ENSMUSG00000039219	chr13	Arid4b	1.4E+07	1.4E+07	13702	-0.967096	3.748585847	7.863E-06	4.29271E-05	0.0508	-1	268	220	333	289	208	196	254	120	160	216
ENSMUSG00000023143	chr16	Nagpa	5195289	5196058	2370	0.872765711	3.570676636	7.888E-06	4.30492E-05	0.03962	1	95	87	157	115	185	347	341	207	335	355
ENSMUSG00000031673	chr8	Cdh11	1E+08	1E+08	4216	1.316454709	2.082900967	7.898E-06	4.30855E-05	0.082	1	38	36	36	30	32	164	167	96	82	98
ENSMUSG00000022203	chr14	Efs	5.5E+07	5.5E+07	3571	1.355029834	2.800862537	7.92E-06	4.31917E-05	0.09567	1	57	40	37	39	120	292	156	147	216	212
ENSMUSG00000033278	chr17	Ptprm	6.7E+07	6.7E+07	5569	-0.88823615	5.148263862	7.94E-06	4.32828E-05	0.04503	-1	556	449	1079	825	622	540	727	369	433	515
ENSMUSG00000039372	chr1	March4	7.2E+07	7.2E+07	4553	-1.70275505	0.755032788	7.95E-06	4.33178E-05	0.12439	-1	49	40	20	36	35	19	18	14	16	12
ENSMUSG00000037419	chr9	Endod1	1.4E+07	1.4E+07	4470	0.897271026	3.389921756	7.998E-06	4.35659E-05	0.04148	1	95	77	128	92	162	372	253	204	284	290
ENSMUSG00000089847	chr7	Timm10b	1.1E+08	1.1E+08	4087	0.746577929	4.727360661	8.01E-06	4.36149E-05	0.03083	1	284	205	338	290	382	823	556	548	773	711
ENSMUSG00000028696	chr4	Ipp	1.2E+08	1.2E+08	2126	-1.02036988	3.421321787	8.022E-06	4.36597E-05	0.0556	-1	213	151	310	227	181	165	220	101	128	120
ENSMUSG00000092544	chr8	Gm20422	7E+07	7E+07	1358	-1.54627276	0.888082537	8.027E-06	4.3673E-05	0.10377	-1	53	36	34	37	36	28	28	11	12	17
ENSMUSG00000027602	chr2	Map1lc3a	1.6E+08	1.6E+08	1181	0.955994626	7.931248982	8.052E-06	4.37924E-05	0.05372	1	1978	1656	3053	2429	3708	6342	5730	4846	8282	8030
ENSMUSG00000022299	chr15	Slc25a32	3.9E+07	3.9E+07	2945	-1.07010313	2.573803152	8.058E-06	4.38052E-05	0.0568	-1	126	100	135	116	118	83	106	68	65	69
ENSMUSG00000036249	chr2	Rbm43	5.2E+07	5.2E+07	2633	1.27703033	2.088530961	8.065E-06	4.38298E-05	0.07849	1	33	25	28	30	67	169	104	99	101	130
ENSMUSG00000024515	chr18	Smad4	7.4E+07	7.4E+07	3712	-0.7919401	5.179245141	8.122E-06	4.41168E-05	0.03573	-1	687	544	845	705	657	548	741	403	551	502
ENSMUSG00000091337	chr2	Eid1	1.3E+08	1.3E+08	1691	0.765622095	5.394629759	8.124E-06	4.41168E-05	0.03341	1	433	326	590	539	466	1155	1118	859	1125	1193
ENSMUSG00000037001	chr11	Zfp39	5.9E+07	5.9E+07	3890	-1.05273596	2.055345058	8.139E-06	4.41798E-05	0.05079	-1	75	57	103	90	95	68	60	38	46	65
ENSMUSG00000032423	chr9	Syncrip	8.8E+07	8.8E+07	9575	-0.86183083	6.168389089	8.165E-06	4.43049E-05	0.04331	-1	1243	1178	1673	1480	1353	1213	1342	776	913	1065
ENSMUSG00000026094	chr1	Stk17b	5.4E+07	5.4E+07	5185	0.890629606	3.710873658	8.195E-06	4.44508E-05	0.04167	1	122	119	133	115	193	402	398	270	303	371
ENSMUSG00000102040	chr6	Clec7a	1.3E+08	1.3E+08	735	2.173869538	0.050483028	8.21E-06	4.45103E-05	0.16639	1	7	2	4	5	6	24	67	14	19	29
ENSMUSG00000027708	chr3	Dcun1d1	3.6E+07	3.6E+07	4563	-0.96439183	5.300118026	8.249E-06	4.4708E-05	0.05361	-1	941	736	708	753	639	605	721	432	491	512
ENSMUSG00000043639	chr19	Rbm20	5.4E+07	5.4E+07	6790	-1.08175015	5.872697568	8.256E-06	4.47263E-05	0.06792	-1	988	1016	1470	1655	752	689	1036	550	756	862
ENSMUSG00000036368	chr17	Rmdn2	8E+07	8E+07	1802	-0.9861453	2.988008387	8.288E-06	4.48806E-05	0.04989	-1	168	109	217	159	139	117	141	76	102	113
ENSMUSG00000017929	chr2	B4galt5	1.7E+08	1.7E+08	4308	0.838346385	4.126248282	8.308E-06	4.49726E-05	0.03788	1	173	169	186	191	203	479	534	359	500	421
ENSMUSG00000033228	chr15	Scaf11	9.6E+07	9.6E+07	7724	-0.82347406	5.578368025	8.335E-06	4.51015E-05	0.0392	-1	837	639	1241	994	931	728	978	482	653	751
ENSMUSG00000079018	chr15	Ly6c1	7.5E+07	7.5E+07	1677	1.026273212	6.389838675	8.376E-06	4.53083E-05	0.06153	1	624	560	964	720	1410	3827	1814	1893	2045	2143
ENSMUSG00000040483	chr11	Xaf1	7.2E+07	7.2E+07	4689	1.068435994	3.722407498	8.413E-06	4.54882E-05	0.06255	1	111	72	138	116	218	637	384	195	364	309
ENSMUSG00000025964	chr1	Adam23	6.3E+07	6.3E+07	17907	1.327185501	2.254530037	8.477E-06	4.58201E-05	0.08642	1	39	39	35	19	65	201	132	92	139	129
ENSMUSG00000028457	chr4	Atp8b5	4.3E+07	4.3E+07	6473	2.716004748	0.183656491	8.557E-06	4.62343E-05	0.28002	1	3	7	0	4	4	82	15	39	24	17
ENSMUSG00000073411	chr17	H2-D1	3.5E+07	3.5E+07	2579	1.610077822	8.651212282	8.565E-06	4.62565E-05	0.14844	1	2370	1733	2102	1527	7995	18910	7591	8004	12634	16606
ENSMUSG00000056383	chr7	AI987944	4.1E+07	4.1E+07	2671	-1.19219582	2.486626574	8.583E-06	4.63357E-05	0.07223	-1	144	83	151	113	87	78	101	54	55	62
ENSMUSG00000032410	chr9	Xrn1	9.6E+07	9.6E+07	18585	-0.84800831	4.109464615	8.6E-06	4.64095E-05	0.03973	-1	315	286	403	314	335	301	355	169	233	227
ENSMUSG00000000056	chr11	Narf	1.2E+08	1.2E+08	4806	-1.07405037	6.954342689	8.617E-06	4.64854E-05	0.06776	-1	2500	2161	2751	3231	1703	1795	2346	1133	1539	1521
ENSMUSG00000051790	chr11	Nlgn2	7E+07	7E+07	5785	1.086340324	3.616878628	8.646E-06	4.66216E-05	0.06416	1	100	101	105	88	192	491	237	227	379	393
ENSMUSG00000036561	chr15	Ppp6r2	8.9E+07	8.9E+07	2887	-0.90387448	5.58154026	8.729E-06	4.70547E-05	0.04756	-1	851	676	1281	1051	866	713	1051	429	683	614
ENSMUSG00000013367	chr7	Iglon5	4.3E+07	4.3E+07	2619	1.608671763	0.551552096	8.767E-06	4.72425E-05	0.09465	1	8	9	12	7	13	65	32	22	36	55
ENSMUSG00000028383	chr4	Hsdl2	6E+07	6E+07	2795	-1.39816012	6.150112791	8.777E-06	4.72776E-05	0.11302	-1	1169	562	3598	1650	1330	797	1374	512	584	824

ENSMUSG00000104453	chr7	WI1-1616M8.3	8.2E+07	8.2E+07	2213	-1.07819787	6.475569352	8.88E-06	4.78141E-05	0.06829	-1	1752	1190	2722	1901	1671	988	2083	719	1096	1093
ENSMUSG00000020309	chr11	Chac2	3.1E+07	3.1E+07	1315	-1.26000759	3.377465917	8.898E-06	4.78899E-05	0.08711	-1	197	174	348	229	153	110	224	92	79	127
ENSMUSG00000032024	chr9	Clmp	4.1E+07	4.1E+07	4591	0.914068398	3.795752891	8.927E-06	4.80297E-05	0.04476	1	129	139	140	108	194	464	420	255	359	378
ENSMUSG00000044033	chr2	Ccdc141	7.7E+07	7.7E+07	11717	1.435224477	2.46284785	8.972E-06	4.82496E-05	0.10484	1	39	44	50	57	21	173	120	178	147	171
ENSMUSG00000045658	chr1	Pid1	8.4E+07	8.4E+07	8172	1.304847155	3.728031788	9.016E-06	4.84727E-05	0.09516	1	115	62	105	60	250	615	396	314	278	345
ENSMUSG00000028108	chr3	Ecm1	9.6E+07	9.6E+07	2521	1.583859101	5.933865506	9.053E-06	4.86477E-05	0.14398	1	254	189	391	279	1380	2429	1754	1193	2244	1970
ENSMUSG00000025425	chr18	St8sia5	7.7E+07	7.7E+07	2097	-0.77777549	4.674954929	9.095E-06	4.88559E-05	0.03413	-1	443	344	573	579	492	402	524	297	347	374
ENSMUSG00000030545	chr7	Pex11a	8E+07	8E+07	2368	-0.84947709	4.70843424	9.098E-06	4.88559E-05	0.0411	-1	438	290	846	482	562	417	545	246	352	389
ENSMUSG00000041762	chr2	Gpr155	7.3E+07	7.3E+07	6679	-1.06193405	4.101351655	9.142E-06	4.90737E-05	0.06388	-1	475	333	291	294	277	286	267	172	215	213
ENSMUSG00000048371	chr8	Pdp2	1E+08	1E+08	3485	-1.19364018	2.131932075	9.177E-06	4.92393E-05	0.06984	-1	90	38	141	95	106	70	67	41	45	50
ENSMUSG00000049532	chr14	Sall2	5.2E+07	5.2E+07	5433	1.428361141	1.619633201	9.27E-06	4.97229E-05	0.09541	1	18	17	25	16	46	132	63	79	69	98
ENSMUSG00000071456	chr12	1110002L01Rik	3403878	3406711	4131	-1.15414222	3.060106617	9.349E-06	5.01066E-05	0.07171	-1	170	138	217	189	140	108	180	80	85	80
ENSMUSG00000091736	chrX	Yy2	1.6E+08	1.6E+08	2867	-1.72561597	1.467557161	9.347E-06	5.01066E-05	0.14938	-1	55	49	67	92	47	31	57	11	13	22
ENSMUSG00000020671	chr12	Rab10	3247430	3249870	3511	-0.98442665	8.082746674	9.47E-06	5.07368E-05	0.05785	-1	4870	4211	7150	5588	5375	3914	5915	2732	3108	3279
ENSMUSG00000020872	chr11	Tac4	9.5E+07	9.5E+07	1251	2.404479381	-0.62582045	9.485E-06	5.07985E-05	0.16611	1	1	2	3	1	5	36	9	14	10	21
ENSMUSG00000037742	chr9	Eef1a1	7.8E+07	7.8E+07	2493	1.19659127	9.698188917	9.511E-06	5.09166E-05	0.08488	1	6789	5651	5783	5027	15476	31963	21161	17760	22999	26650
ENSMUSG00000026383	chr1	Epb4.1l5	1.2E+08	1.2E+08	14758	-1.12632528	1.99924972	9.587E-06	5.13044E-05	0.06046	-1	77	64	73	90	100	48	64	38	56	49
ENSMUSG00000063019	chr2	Manbal	1.6E+08	1.6E+08	1107	0.827603711	4.770837088	9.632E-06	5.15256E-05	0.03888	1	289	255	270	264	382	829	604	546	879	735
ENSMUSG00000027254	chr2	Map1a	1.2E+08	1.2E+08	12166	1.202085531	5.530397205	9.673E-06	5.17241E-05	0.0846	1	384	194	765	518	322	1681	2097	686	1414	943
ENSMUSG00000017002	chr2	Slpi	1.6E+08	1.6E+08	1180	1.923571087	0.045000034	9.72E-06	5.19537E-05	0.12628	1	2	5	4	3	14	35	32	13	35	33
ENSMUSG00000013698	chr1	Pea15a	1.7E+08	1.7E+08	3861	0.974944504	6.347484197	9.734E-06	5.20121E-05	0.05638	1	613	566	829	737	1496	3017	1918	1583	2282	2457
ENSMUSG00000051627	chr13	Hist1h1e	2.4E+07	2.4E+07	748	-1.86059061	1.117531791	9.747E-06	5.20611E-05	0.16572	-1	76	29	48	66	27	21	26	12	29	7
ENSMUSG00000021843	chr14	Ktn1	4.8E+07	4.8E+07	9582	-1.00511439	7.650509628	9.843E-06	5.25544E-05	0.06042	-1	4090	3019	5261	4637	3087	2999	4013	1862	2308	2786
ENSMUSG00000003680	chr19	Taf6l	8772522	8772834	5884	0.920569225	3.739676662	9.879E-06	5.27251E-05	0.04615	1	113	98	147	137	203	451	267	274	444	356
ENSMUSG00000029992	chr6	Gfpt1	8.7E+07	8.7E+07	7419	-0.95033717	5.435002332	9.9E-06	5.28168E-05	0.05315	-1	1029	737	824	850	736	699	859	429	601	486
ENSMUSG00000019988	chr10	Nedd1	9.3E+07	9.3E+07	3534	-0.98981818	3.337144397	9.915E-06	5.2875E-05	0.0529	-1	212	159	274	193	164	169	181	113	107	127
ENSMUSG00000083405	chr16	Gm15725	3.8E+07	3.8E+07	1090	-2.39810606	1.609141762	9.947E-06	5.3029E-05	0.29063	-1	73	64	108	58	80	18	67	6	6	6
ENSMUSG00000006740	chr18	Kif5b	6201002	6203707	7395	-1.06045245	6.671176152	9.969E-06	5.31243E-05	0.06694	-1	2110	1660	2624	2324	1533	1371	2204	892	1070	1371
ENSMUSG00000035173	chr19	Ccdc186	5.7E+07	5.7E+07	6899	-0.85526227	4.559343094	1.001E-05	5.33008E-05	0.042	-1	468	435	526	399	403	389	455	222	352	333
ENSMUSG00000042747	chr3	Krtcap2	8.9E+07	8.9E+07	1522	0.836455173	5.073368963	1.009E-05	5.36983E-05	0.04066	1	314	233	391	356	559	1001	666	713	1112	936
ENSMUSG00000062115	chr11	Rai1	6E+07	6E+07	9591	-0.87542915	4.380171774	1.009E-05	5.36983E-05	0.04366	-1	294	250	649	471	419	345	395	193	332	268
ENSMUSG00000001034	chr11	Mapk7	6.1E+07	6.1E+07	4394	1.125479876	3.143266829	1.009E-05	5.37055E-05	0.06815	1	52	64	64	87	149	325	231	175	264	248
ENSMUSG00000022620	chr15	Arsa	8.9E+07	8.9E+07	3680	1.108609129	4.330352153	1.018E-05	5.41619E-05	0.07074	1	151	133	174	119	406	762	461	397	591	639
ENSMUSG00000010751	chr7	Tnfrsf22	1.4E+08	1.4E+08	4289	1.317885485	3.089533126	1.024E-05	5.44316E-05	0.09352	1	59	83	40	67	98	207	229	191	339	257
ENSMUSG00000022018	chr14	Rgcc	7.9E+07	7.9E+07	918	1.062820661	5.89990862	1.029E-05	5.46878E-05	0.0671	1	442	247	672	554	1161	2255	1522	1245	1710	1664
ENSMUSG00000015968	chr14	Cacna1d	3E+07	3E+07	9242	1.637116277	0.258223632	1.034E-05	5.49538E-05	0.08835	1	9	5	12	3	10	34	31	21	38	42
ENSMUSG00000083563	chr2	Gm13340	2.3E+07	2.3E+07	1545	-1.36080733	3.611473335	1.048E-05	5.56316E-05	0.10509	-1	208	116	500	324	234	114	252	58	146	151
ENSMUSG00000025437	chr3	Usp33	1.5E+08	1.5E+08	5950	-0.80354966	4.450635961	1.05E-05	5.57419E-05	0.03678	-1	396	286	580	437	413	371	464	215	291	321
ENSMUSG00000030760	chr7	Acer3	9.8E+07	9.8E+07	4319	0.955304151	2.68969306	1.053E-05	5.58871E-05	0.04509	1	50	49	89	61	79	217	190	137	152	168
ENSMUSG00000038418	chr18	Egr1	3.5E+07	3.5E+07	4484	1.513013054	4.667139258	1.056E-05	5.60132E-05	0.13208	1	179	123	113	357	201	470	449	900	771	1107
ENSMUSG00000030465	chr8	Psd3	6.8E+07	6.8E+07	15304	-0.86345995	5.04890349	1.059E-05	5.61441E-05	0.04375	-1	651	496	784	636	638	551	756	279	491	392
ENSMUSG00000070427	chr7	Il18bp	1E+08	1E+08	1400	1.710117779	1.80696767	1.064E-05	5.64192E-05	0.14865	1	18	16	27	19	40	269	63	60	83	77
ENSMUSG00000050144	chr3	Slc25a44	8.8E+07	8.8E+07	3578	-0.71745614	5.092818136	1.067E-05	5.65341E-05	0.02983	-1	629	456	643	594	893	591	605	385	548	547
ENSMUSG00000034855	chr5	Cxcl10	9.2E+07	9.2E+07	1520	1.981497197	0.170194066	1.069E-05	5.6635E-05	0.15365	1	2	1	10	6	12	57	22	20	22	44
ENSMUSG00000034382	chr17	AI661453	4.7E+07	4.7E+07	5056	1.760939127	0.26505738	1.078E-05	5.7062E-05	0.11076	1	4	5	4	13	10	43	30	23	47	27
ENSMUSG00000032648	chr19	Pygm	6384399	6384721	3218	-0.92813699	12.57681063	1.082E-05	5.72459E-05	0.0524	-1	115121	91393	127901	135525	131073	79721	101941	63260	105326	84776
ENSMUSG00000098557	chr14	Kctd12	1E+08	1E+08	6057	0.839186545	4.683953673	1.083E-05	5.73156E-05	0.04065	1	253	183	266	233	475	885	755	508	671	599
ENSMUSG00000008822	chr12	Acyp1	8.5E+07	8.5E+07	1380	-0.94746398	3.882279076	1.084E-05	5.73162E-05	0.0506	-1	337	274	249	228	332	233	219	139	204	250
ENSMUSG00000038168	chr16	Leprel1	2.6E+07	2.6E+07	3721	1.19767951	2.887430494	1.086E-05	5.7431E-05	0.07749	1	44	33	80	103	80	286	181	157	157	272
ENSMUSG00000045165	chr7	AI467606	1.3E+08	1.3E+08	1918	1.729672327	1.946027632	1.09E-05	5.76017E-05	0.15337	1	16	27	14	11	61	174	90	82	112	136
ENSMUSG00000073139	chrX	BC023829	7E+07	7E+07	2513	-0.85000621	4.952007379	1.105E-05	5.83782E-05	0.04239	-1	677	545	569	517	614	483	607	334	457	407
ENSMUSG00000074800	chr13	Gm4149	7.6E+07	7.6E+07	362	0.905259399	4.526158367	1.108E-05	5.85167E-05	0.04722	1	283	164	216	226	312	689	440	458	778	722
ENSMUSG00000024892	chr19	Pcx	4510472	4510581	4272	-2.13399332	8.146881874	1.116E-05	5.89095E-05	0.25739	-1	3965	9924	1491	11668	4182	2109	1133	1723	3425	2379
ENSMUSG00000032396	chr9	Dis3l	6.4E+07	6.4E+07	5458	-0.75924313	5.223464121	1.125E-05	5.93464E-05	0.03391	-1	666	493	957	779	664	661	725	396	535	574
ENSMUSG00000067736	chr1	Gm10222	2.5E+07	2.5E+07	294	-1.72456562	1.647331141	1.129E-05	5.95314E-05	0.15192	-1	71	46	98	84	60	12	67	14	30	26
ENSMUSG00000037029	chr7	Zfp146	3E+07	3E+07	2071	-0.89331667	4.160260681	1.132E-05	5.96773E-05	0.04565	-1	391	291	383	337	315	326	331	214	200	221
ENSMUSG00000034684	chr9	Sema3f	1.1E+08	1.1E+08	5197	1.038540582	3.593394091	1.136E-05	5.98361E-05	0.06073	1	84	48	191	153	140	389	291	272	343	361
ENSMUSG00000038774	chr10	Ascc3	5.1E+07	5.1E+07	7477	-0.92174092	4.208530298	1.136E-05	5.98361E-05	0.04898	-1	358	268	435	433	315	332	395	170	219	222
ENSMUSG00000030804	chr7	Gm21974	1.3E+08	1.3E+08	2037	1.190663645	4.127601412	1.136E-05	5.98435E-05	0.08201	1	146	111	107	122	323	707	329	370	579	525
ENSMUSG00000015981	chr7	Stk32c	1.4E+08	1.4E+08	2302	2.001382946	0.108049407	1.141E-05	6.0075E-05	0.15034	1	6	5	5	1	11	51	15	27	25	37
ENSMUSG00000002799	chr12	Jag2	1.1E+08	1.1E+08	4054	-0.83552184	4.712013202	1.145E-05	6.02837E-05	0.0407	-1	429	339	701	620	464	367	528	246	419	398
ENSMUSG00000097295	chr10	Hmgb1-ps8	2.2E+07	2.2E+07	626	-2.97903494	0.353040119	1.146E-05	6.03143E-05	0.40005	-1	52	43	13	24	23	2	19	0	2	7
ENSMUSG00000030067	chr6	Foxp1	9.9E+07	9.9E+07	14266	0.840502509	3.783295609	1.151E-05	6.05421E-05	0.03852	1	150	102	160	150	178	507	336	246	314	431
ENSMUSG00000019961	chr10	Tmpo	9.1E+07	9.1E+07	6478	-0.73017987	5.035058502	1.153E-05	6.06355E-05	0.0312	-1	605	467	786	531	707	617	660	319	481	507
ENSMUSG00000026393	chr1	Nek7	1.4E+08	1.4E+08	7376	-0.92885606	7.040381998	1.16E-05	6.09322E-05	0.05242	-1	2552	1952	3369	2742	2380	2073	2747	1301	1571	1773
ENSMUSG00000069769	chr11	Msi2	8.8E+07	8.8E+07	10405	-1.04328278	6.689275012	1.16E-05	6.09322E-05	0.06579	-1	1942	1311	3409	2452	1529	1375	2063	984	1196	1394
ENSMUSG00000041415	chr12	Dicer1	1E+08	1E+08	9851	-0.80208134	5.779285573	1.171E-05	6.1507E-05	0.03865	-1	1040	882	1138	1056	1075	925	958	523	857	921

ENSMUSG00000022351	chr15	Sqle	5.9E+07	5.9E+07	5546	1.176526438	2.83529103	1.177E-05	6.17605E-05	0.0748	1	54	39	54	60	124	293	217	164	153	182
ENSMUSG00000051786	chr15	Tubgcp6	8.9E+07	8.9E+07	7965	-0.85127292	3.970215214	1.182E-05	6.20152E-05	0.041	-1	302	238	363	319	282	227	323	162	223	221
ENSMUSG00000036943	chr9	Rab8b	6.7E+07	6.7E+07	4743	0.902402035	4.154708353	1.187E-05	6.22549E-05	0.04624	1	149	177	184	140	273	649	514	366	415	454
ENSMUSG00000103653	chr1	Wi1-1003N17.1	1.9E+08	1.9E+08	631	0.873032117	4.76209702	1.188E-05	6.22947E-05	0.04455	1	288	209	281	269	396	626	634	511	1009	820
ENSMUSG00000038453	chr11	Srcin1	9.8E+07	9.8E+07	8386	-1.45771067	1.453865764	1.194E-05	6.25616E-05	0.10457	-1	48	54	86	39	71	31	49	11	37	23
ENSMUSG00000013160	chr8	Atp6v0d1	1.1E+08	1.1E+08	1793	0.841335169	5.699987894	1.195E-05	6.26163E-05	0.04244	1	487	412	531	513	887	1581	1264	1055	1463	1526
ENSMUSG00000022752	chr16	Tomm70a	5.7E+07	5.7E+07	3778	-0.87701952	6.196244649	1.197E-05	6.26605E-05	0.04657	-1	1379	976	2007	1447	1427	1187	1495	834	884	958
ENSMUSG00000048279	chr14	Sacs	6.1E+07	6.1E+07	20414	-1.36381875	4.503691763	1.197E-05	6.26605E-05	0.1095	-1	430	218	931	678	290	309	447	125	178	289
ENSMUSG00000027709	chr3	Mccc1	3.6E+07	3.6E+07	2977	-0.76681134	5.613873719	1.199E-05	6.27495E-05	0.03517	-1	933	600	1006	866	1310	944	790	579	708	740
ENSMUSG00000051316	chr18	Taf7	3.8E+07	3.8E+07	3302	-0.9718351	3.330251439	1.2E-05	6.28031E-05	0.05181	-1	228	145	266	184	174	156	186	115	128	112
ENSMUSG00000064340	chrMT	mt-Tl1	2676	2750	75	-1.68372147	6.368524754	1.21E-05	6.32635E-05	0.16659	-1	1457	884	3969	2194	1478	616	1995	267	628	694
ENSMUSG00000029415	chr5	Sdad1	9.2E+07	9.2E+07	5020	-0.77222982	4.159974547	1.21E-05	6.32723E-05	0.03375	-1	330	286	406	331	324	339	298	207	257	265
ENSMUSG00000039774	chr4	Galnt12	4.7E+07	4.7E+07	2288	2.082350185	-0.35178691	1.212E-05	6.33184E-05	0.11878	1	3	5	1	2	7	28	28	18	19	15
ENSMUSG00000020572	chr12	Nampt	3.3E+07	3.3E+07	4547	-1.13153723	6.850800596	1.214E-05	6.34421E-05	0.07758	-1	2009	1493	4167	2599	1984	1601	2605	991	1154	1228
ENSMUSG00000033014	chr3	Trim33	1E+08	1E+08	8868	-0.92316681	3.747286705	1.225E-05	6.39814E-05	0.04803	-1	230	215	326	279	265	221	287	144	153	155
ENSMUSG00000079323	chr9	Gm20661	1.1E+08	1.1E+08	2160	1.591864692	1.168337951	1.228E-05	6.41266E-05	0.11763	1	8	11	18	11	33	104	46	54	47	77
ENSMUSG00000030861	chr7	Acadsb	1.3E+08	1.3E+08	4474	-0.90967546	6.781462725	1.241E-05	6.47582E-05	0.05056	-1	2415	1782	2229	2318	1847	1685	1803	1249	1462	1694
ENSMUSG00000027796	chr3	Smad9	5.5E+07	5.5E+07	5368	1.846609222	-0.29189889	1.244E-05	6.48958E-05	0.08827	1	5	3	5	5	4	19	23	15	24	29
ENSMUSG00000000439	chr6	Mkrn2	1.2E+08	1.2E+08	2240	-0.78584583	5.831452541	1.263E-05	6.57896E-05	0.03736	-1	981	789	1352	1170	1165	961	1149	601	849	794
ENSMUSG00000035941	chr9	Ibtk	8.6E+07	8.6E+07	8628	-0.94348773	6.839121012	1.263E-05	6.57896E-05	0.05447	-1	2415	1747	2677	2612	1753	1792	2141	1186	1543	1480
ENSMUSG00000043962	chr4	Thrap3	1.3E+08	1.3E+08	9234	-0.78875352	6.028467026	1.262E-05	6.57896E-05	0.03776	-1	1145	888	1643	1333	1263	1144	1165	731	896	1036
ENSMUSG00000059146	chr7	Ntrk3	7.8E+07	7.8E+07	5358	-3.56045931	0.265932434	1.263E-05	6.57896E-05	0.55998	-1	24	14	2	4	125	6	5	2	2	3
ENSMUSG00000042331	chr11	Specc1	6.2E+07	6.2E+07	13276	0.993327899	2.575831792	1.275E-05	6.63968E-05	0.04898	1	54	49	79	55	56	170	161	132	178	156
ENSMUSG00000103866	chr18	Setbp1	7.9E+07	7.9E+07	4749	-3.25490377	0.689903231	1.277E-05	6.64555E-05	0.49689	-1	47	38	68	46	13	3	26	0	1	2
ENSMUSG00000031393	chrX	Mecp2	7.4E+07	7.4E+07	10592	-0.72077633	5.18138799	1.284E-05	6.67748E-05	0.03085	-1	640	541	828	720	652	635	664	402	551	594
ENSMUSG00000075593	chr5	Gal3st4	1.4E+08	1.4E+08	3252	2.010721358	-0.22436279	1.284E-05	6.67986E-05	0.12227	1	1	4	2	8	6	27	17	16	28	31
ENSMUSG00000032050	chr9	Rdx	5.2E+07	5.2E+07	4841	-0.97670829	7.117213376	1.285E-05	6.68183E-05	0.05851	-1	2777	2220	3217	3078	2416	1768	2922	1386	1887	1739
ENSMUSG00000079507	chr17	H2-Q1	3.5E+07	3.5E+07	2860	1.668069779	1.964580688	1.289E-05	6.70104E-05	0.14549	1	17	24	17	14	65	181	89	93	84	147
ENSMUSG00000036002	chr4	Fam214b	4.3E+07	4.3E+07	4129	0.762385197	5.744389551	1.291E-05	6.70166E-05	0.03507	1	488	400	769	696	681	1643	1421	1037	1458	1428
ENSMUSG00000041695	chr11	Kcnj2	1.1E+08	1.1E+08	5444	-0.94675292	6.090653081	1.29E-05	6.70166E-05	0.05464	-1	1342	988	1818	1530	1070	1010	1412	585	889	985
ENSMUSG00000044468	chr3	Fam46c	1E+08	1E+08	6097	1.348721329	1.84724364	1.293E-05	6.71444E-05	0.08849	1	23	34	25	17	45	121	127	84	89	91
ENSMUSG00000024507	chr18	Hsd17b4	5E+07	5E+07	3404	-0.88156562	6.290751865	1.298E-05	6.73577E-05	0.04749	-1	1311	921	2578	1487	1594	1353	1444	819	1042	1082
ENSMUSG00000090935	chr12	Synj2bp	8.1E+07	8.2E+07	5866	-0.86450405	5.892203793	1.3E-05	6.74253E-05	0.04547	-1	1103	874	1560	1261	968	974	1180	628	730	870
ENSMUSG00000029915	chr6	Clec5a	4.1E+07	4.1E+07	3840	1.758678525	0.802959669	1.301E-05	6.74511E-05	0.14164	1	5	4	8	11	29	77	59	37	36	49
ENSMUSG00000049804	chrX	Armcx4	1.3E+08	1.3E+08	7996	-1.15011773	4.762551393	1.304E-05	6.75892E-05	0.0791	-1	506	336	710	922	342	372	544	229	334	281
ENSMUSG00000024908	chr19	Ppp6r3	3454933	3457051	4952	-0.85879451	6.468745262	1.305E-05	6.7614E-05	0.04521	-1	1634	1325	2258	1822	1547	1421	1712	908	1241	1275
ENSMUSG00000048138	chr19	Dmrt2	2.6E+07	2.6E+07	2347	-1.6051524	2.835838023	1.307E-05	6.76907E-05	0.14441	-1	170	165	84	70	301	96	53	70	57	84
ENSMUSG00000053436	chr17	Mapk14	2.9E+07	2.9E+07	4361	-0.93298796	7.222912644	1.308E-05	6.77201E-05	0.05358	-1	2340	2194	4350	3068	3015	2244	3050	1405	2215	1810
ENSMUSG00000020608	chr12	Smc6	1.1E+07	1.1E+07	5603	-0.79436069	5.111477324	1.314E-05	6.8E-05	0.03771	-1	644	530	883	653	575	622	681	393	426	504
ENSMUSG00000040482	chr17	Dxo	3.5E+07	3.5E+07	1961	0.922826116	3.245394832	1.314E-05	6.80031E-05	0.0461	1	89	61	105	102	137	284	207	192	302	280
ENSMUSG00000019124	chr6	Scrn1	5.5E+07	5.5E+07	8371	1.224698678	2.089984139	1.319E-05	6.82123E-05	0.07474	1	29	31	38	30	59	164	97	116	92	122
ENSMUSG00000029685	chr6	Asb15	2.5E+07	2.5E+07	4497	-1.25232282	4.14479351	1.319E-05	6.82123E-05	0.09254	-1	455	178	616	401	267	172	399	157	177	175
ENSMUSG00000029464	chr5	Gpn3	1.2E+08	1.2E+08	2508	-0.85984844	3.793691695	1.324E-05	6.84377E-05	0.04181	-1	310	226	295	207	288	256	210	161	198	191
ENSMUSG00000028339	chr4	Col15a1	4.7E+07	4.7E+07	6349	0.84840958	6.129032654	1.327E-05	6.85416E-05	0.04392	1	662	580	867	700	975	2303	1424	1564	2076	1886
ENSMUSG00000044674	chr5	Fzd1	4753873	4758035	4163	1.235719335	3.007564082	1.338E-05	6.90845E-05	0.08567	1	55	41	85	40	150	344	218	179	219	196
ENSMUSG00000026579	chr1	F5	1.6E+08	1.6E+08	7430	2.633102989	0.4719826	1.345E-05	6.93795E-05	0.30803	1	0	5	2	2	17	66	18	27	34	77
ENSMUSG00000030341	chr6	Tnfrsf1a	1.3E+08	1.3E+08	2591	1.140736178	5.617310925	1.345E-05	6.93795E-05	0.07903	1	309	251	570	310	998	1811	1071	1270	1357	1407
ENSMUSG00000040661	chr9	Rad54l2	1.1E+08	1.1E+08	11828	-0.81005338	3.715115877	1.344E-05	6.93795E-05	0.03653	-1	241	195	280	277	254	232	229	147	200	177
ENSMUSG00000044550	chrX	Tceal3	1.4E+08	1.4E+08	3546	1.830901908	0.283015935	1.348E-05	6.95346E-05	0.13303	1	11	2	14	4	5	59	25	27	26	38
ENSMUSG00000041548	chr5	Hspb8	1.2E+08	1.2E+08	1950	0.87983994	9.076115775	1.355E-05	6.98208E-05	0.04814	1	5755	4334	7184	4889	6628	17999	12422	12297	14796	14558
ENSMUSG00000080811	chrX	Gm14513	1.2E+07	1.2E+07	123	0.934385439	3.824225248	1.372E-05	7.06983E-05	0.04978	1	95	106	175	151	213	442	275	303	465	414
ENSMUSG00000019659	chr9	Ccdc12	1.1E+08	1.1E+08	818	0.760035624	5.222187048	1.377E-05	7.08838E-05	0.03467	1	368	256	530	401	580	1215	786	769	1058	1013
ENSMUSG00000052675	chr7	Zfp112	2.4E+07	2.4E+07	4095	-1.02032306	2.621732278	1.376E-05	7.08838E-05	0.0548	-1	127	100	161	113	111	87	112	58	71	90
ENSMUSG00000022682	chr16	Rrn3	1.4E+07	1.4E+07	3597	-0.7724276	5.695950732	1.378E-05	7.09234E-05	0.0363	-1	932	776	1233	984	989	854	974	595	815	725
ENSMUSG00000031157	chrX	Pqbp1	7894519	7894867	1636	0.759112458	4.552334105	1.383E-05	7.11364E-05	0.03354	1	221	182	306	269	346	673	495	447	738	683
ENSMUSG00000040511	chr7	Pvr	2E+07	2E+07	5408	1.026289128	3.255624734	1.383E-05	7.11364E-05	0.05905	1	94	43	96	103	144	288	234	259	241	263
ENSMUSG00000048330	chr7	Ric3	1.1E+08	1.1E+08	8561	-1.34523909	1.479904734	1.391E-05	7.1496E-05	0.08665	-1	46	55	58	42	94	33	39	32	26	27
ENSMUSG00000063273	chr3	Naa15	5.1E+07	5.1E+07	15427	-0.86293672	5.906389292	1.4E-05	7.19358E-05	0.04566	-1	1152	1029	1350	1112	1094	883	1199	678	818	820
ENSMUSG00000035764	chr16	Fbxo45	3.2E+07	3.2E+07	4179	-0.74575364	5.034678165	1.402E-05	7.20484E-05	0.03319	-1	574	470	778	656	612	529	664	395	503	436
ENSMUSG00000038736	chr15	Nudcd1	4.4E+07	4.4E+07	3447	-1.04952396	2.878753195	1.41E-05	7.24381E-05	0.06044	-1	161	132	157	156	118	116	123	62	103	93
ENSMUSG00000000530	chr15	Acvrl1	1E+08	1E+08	4265	0.865887809	4.479853319	1.416E-05	7.26739E-05	0.04454	1	160	130	343	224	382	736	533	482	630	581
ENSMUSG00000028497	chr4	Ptplad2	8.8E+07	8.8E+07	6756	1.046769628	2.587568914	1.42E-05	7.28547E-05	0.05609	1	58	49	52	53	74	236	181	119	131	160
ENSMUSG00000028249	chr4	Sdcbp	6365650	6365759	6904	0.798696529	6.201302033	1.421E-05	7.2876E-05	0.03928	1	646	538	1160	749	1058	2245	2198	1396	1886	1984
ENSMUSG00000006611	chr13	Hfe	2.4E+07	2.4E+07	3572	0.87140498	4.220853989	1.423E-05	7.30002E-05	0.04393	1	172	179	169	176	280	624	420	382	546	508
ENSMUSG00000101304	chr9	Plet1os	5E+07	5E+07	1245	-1.27371709	2.873203431	1.428E-05	7.31902E-05	0.09118	-1	211	147	154	127	108	96	60	78	90	112
ENSMUSG00000038145	chr9	Snrk	1.2E+08	1.2E+08	5763	-0.82416737	5.200747787	1.432E-05	7.34009E-05	0.04109	-1	515	417	1153	667	932	601	715	351	550	556
ENSMUSG00000033020	chr15	Polr2f	7.9E+07	7.9E+07	543	0.746768006	4.733870126	1.435E-05	7.3513E-05	0.03282	1	262	217	365	285	378	751	538	575	770	774

ENSMUSG00000033307	chr10	Mif	7.6E+07	7.6E+07	554	0.935140497	5.47652302	1.443E-05	7.38735E-05	0.05348	1	343	246	679	542	572	1149	926	911	1610	1402
ENSMUSG00000055200	chr7	Sertad3	2.7E+07	2.7E+07	1324	1.243573426	2.918868069	1.443E-05	7.38735E-05	0.08555	1	40	66	62	48	116	278	148	183	236	229
ENSMUSG00000100235	chr13	Gm28557	6.7E+07	6.7E+07	5037	-1.30039592	1.856499422	1.446E-05	7.39937E-05	0.08609	-1	84	72	97	68	53	51	56	35	27	44
ENSMUSG00000074656	chr2	Eif2s2	1.5E+08	1.5E+08	6755	-0.93530635	7.359516296	1.448E-05	7.40542E-05	0.05444	-1	3539	3078	3218	2924	3016	2602	2807	1748	2308	2236
ENSMUSG00000022040	chr14	Ephx2	6.6E+07	6.6E+07	2035	-1.29573356	5.881217082	1.457E-05	7.44584E-05	0.10238	-1	1046	332	2365	1093	2010	926	836	455	476	893
ENSMUSG00000098457	chr15	Mir8097	3.6E+07	3.6E+07	119	1.400629251	0.954923477	1.456E-05	7.44584E-05	0.08126	1	11	10	15	17	22	67	36	51	56	57
ENSMUSG00000024270	chr18	Slc39a6	2.5E+07	2.5E+07	4073	1.201845325	2.868868143	1.461E-05	7.4639E-05	0.07953	1	42	55	51	57	125	263	186	184	178	216
ENSMUSG00000030682	chr7	Cdipt	1.3E+08	1.3E+08	1876	0.870723129	5.51404399	1.463E-05	7.47244E-05	0.04644	1	333	270	665	489	777	1372	1121	863	1390	1375
ENSMUSG00000045975	chr16	C2cd2	9.8E+07	9.8E+07	6555	-0.90951581	7.196713294	1.468E-05	7.49437E-05	0.05155	-1	2999	2321	3337	2929	2686	2139	2907	1367	2187	2040
ENSMUSG00000053830	chr10	Gm9923	7.2E+07	7.2E+07	2624	-1.79371307	-0.08623695	1.47E-05	7.50498E-05	0.11807	-1	23	19	21	23	14	8	15	7	5	5
ENSMUSG00000040785	chr16	Ttc3	9.4E+07	9.4E+07	15134	-0.92290108	6.086932909	1.472E-05	7.51099E-05	0.05264	-1	1386	1033	1822	1385	1043	1096	1370	632	941	873
ENSMUSG00000027712	chr3	Anxa5	3.6E+07	3.6E+07	1721	1.457397049	7.148628532	1.473E-05	7.51346E-05	0.12926	1	765	685	776	681	3094	5487	3347	3182	4497	5092
ENSMUSG00000099689	chr7	Unspecified	3E+07	3E+07	3208	-1.09529506	2.453330768	1.474E-05	7.5148E-05	0.06354	-1	126	82	130	101	116	73	112	50	55	69
ENSMUSG00000021994	chr14	Wnt5a	2.9E+07	2.9E+07	7822	-0.91097306	3.373658512	1.495E-05	7.61977E-05	0.0464	-1	159	172	225	210	245	205	149	125	110	152
ENSMUSG00000022812	chr16	Gsk3b	3.8E+07	3.8E+07	9831	-0.78544899	5.908013081	1.502E-05	7.65035E-05	0.03805	-1	1068	779	1435	1265	1227	952	1121	599	883	1041
ENSMUSG00000078190	chr1	Dnm3os	1.6E+08	1.6E+08	7928	1.557739435	1.413892195	1.502E-05	7.65035E-05	0.1154	1	9	22	19	22	22	121	48	46	74	106
ENSMUSG00000079014	chr12	Serpina3i	1E+08	1E+08	2224	2.343703423	-0.34204093	1.506E-05	7.66537E-05	0.18688	1	1	2	7	3	3	49	9	16	14	26
ENSMUSG00000096493	chr1	Csnk2a3	1.6E+08	1.6E+08	2568	-1.2434824	1.922473824	1.508E-05	7.67678E-05	0.07991	-1	64	76	99	87	63	53	71	28	41	39
ENSMUSG00000101523	chr1	Csnk2a1	1.6E+08	1.6E+08	2653	-1.24348549	1.922473824	1.512E-05	7.69429E-05	0.07993	-1	64	76	99	87	63	53	71	28	41	39
ENSMUSG00000042439	chr18	Zfp532	6.6E+07	6.6E+07	11192	-0.75360218	4.328388521	1.531E-05	7.78433E-05	0.03321	-1	356	306	444	393	385	328	400	216	317	289
ENSMUSG00000028224	chr4	Nbn	1.6E+07	1.6E+07	2533	-0.76291046	4.394640684	1.532E-05	7.78839E-05	0.03408	-1	372	276	518	442	394	352	400	270	277	304
ENSMUSG00000026407	chr1	Cacna1s	1.4E+08	1.4E+08	6550	-1.01287974	9.403858834	1.542E-05	7.83156E-05	0.06435	-1	12618	10063	17634	17415	10215	8381	11558	6290	10840	9515
ENSMUSG00000097353	chr10	A430046D13Rik	1.3E+08	1.3E+08	1997	-0.75660846	4.700231362	1.541E-05	7.83156E-05	0.0341	-1	536	375	600	495	432	448	472	318	352	404
ENSMUSG00000009563	chr2	Tor2a	3.3E+07	3.3E+07	3050	0.934984508	3.288256636	1.563E-05	7.93951E-05	0.04848	1	87	76	110	71	162	310	267	193	291	252
ENSMUSG00000021281	chr12	Tnfaip2	1.1E+08	1.1E+08	4984	0.926396349	6.734204414	1.567E-05	7.9572E-05	0.05364	1	1115	705	1503	770	1588	2592	3363	2594	2835	2832
ENSMUSG00000003731	chr4	Kpna6	1.3E+08	1.3E+08	6729	-0.89410633	6.78119908	1.575E-05	7.99187E-05	0.05006	-1	1960	1668	2865	2325	1950	1685	2260	1082	1553	1445
ENSMUSG00000027206	chr2	Cops2	1.3E+08	1.3E+08	3549	-0.93568273	6.286543117	1.577E-05	7.99794E-05	0.05458	-1	1555	1260	1842	1642	1330	1136	1688	800	950	998
ENSMUSG00000041203	chr8	2310036O22Rik	8.5E+07	8.5E+07	891	0.791288059	5.540908194	1.588E-05	8.05413E-05	0.03854	1	385	349	702	473	723	1330	1087	980	1383	1283
ENSMUSG00000055305	chr7	Zfp93	2.4E+07	2.4E+07	2666	-1.07178567	2.763035968	1.589E-05	8.05471E-05	0.06357	-1	153	115	148	116	148	101	141	54	76	83
ENSMUSG00000030882	chr7	Dnhd1	1.1E+08	1.1E+08	15578	0.734510146	4.584917673	1.597E-05	8.0927E-05	0.03179	1	247	195	317	257	348	731	497	489	720	642
ENSMUSG00000027978	chr3	Prss12	1.2E+08	1.2E+08	2607	1.482923888	1.175919798	1.598E-05	8.09559E-05	0.10012	1	15	12	16	25	15	94	42	41	57	92
ENSMUSG00000014198	chr11	Zfp385c	1E+08	1E+08	3101	2.159923553	0.000617163	1.606E-05	8.13005E-05	0.17139	1	1	5	4	10	3	31	16	33	21	41
ENSMUSG00000046031	chr10	Fam26f	3.4E+07	3.4E+07	1080	2.500574956	-0.21554907	1.61E-05	8.14836E-05	0.23324	1	2	2	0	1	11	50	19	8	29	24
ENSMUSG00000100153	chr7	Gm5601	1.2E+08	1.2E+08	972	-1.18233056	2.40378789	1.613E-05	8.16048E-05	0.07647	-1	90	94	129	142	85	80	96	33	66	63
ENSMUSG00000046480	chr9	Scn4b	4.5E+07	4.5E+07	4940	-0.95247298	8.944546973	1.614E-05	8.16347E-05	0.05728	-1	9649	6112	14023	10747	9188	6385	9921	4923	7049	6551
ENSMUSG00000035929	chr17	H2-Q4	3.5E+07	3.5E+07	2596	1.309770716	6.21209465	1.621E-05	8.19703E-05	0.10589	1	520	390	580	398	1456	3838	1424	1420	1903	2580
ENSMUSG00000064145	chr9	Arih2	1.1E+08	1.1E+08	7672	-0.8678388	6.280158367	1.63E-05	8.23725E-05	0.04714	-1	1496	1226	1837	1453	1506	1138	1619	766	1182	1024
ENSMUSG00000030731	chr7	Syt3	4.4E+07	4.4E+07	3118	-1.39029533	1.744238071	1.633E-05	8.25136E-05	0.10104	-1	66	63	47	100	74	32	50	26	50	30
ENSMUSG00000021614	chr13	Vcan	9E+07	9E+07	14462	0.970006603	3.995698737	1.637E-05	8.267E-05	0.05548	1	130	134	167	140	238	687	485	360	365	286
ENSMUSG00000018846	chr11	Pank3	3.6E+07	3.6E+07	7376	-0.88057335	5.100068645	1.64E-05	8.2775E-05	0.04759	-1	609	499	581	498	1203	585	548	379	514	474
ENSMUSG00000022124	chr14	Fbxl3	1E+08	1E+08	5103	-0.81481995	5.715869396	1.64E-05	8.2775E-05	0.04122	-1	1058	782	1223	969	991	911	1029	594	621	802
ENSMUSG00000056130	chr18	Ticam2	4.7E+07	4.7E+07	3928	1.682946892	0.367215402	1.641E-05	8.2775E-05	0.10661	1	3	7	6	10	15	53	39	24	41	26
ENSMUSG00000020017	chr10	Hal	9.3E+07	9.3E+07	5549	1.686880461	1.573374191	1.642E-05	8.28377E-05	0.14672	1	11	17	10	15	49	146	81	72	86	64
ENSMUSG00000044339	chr5	Alkbh2	1.1E+08	1.1E+08	1115	1.238223272	2.032094947	1.658E-05	8.35906E-05	0.08	1	28	19	47	31	58	165	73	101	125	108
ENSMUSG00000053510	chr4	Nrd1	1.1E+08	1.1E+08	7140	-0.89202084	7.916480019	1.659E-05	8.35931E-05	0.05037	-1	4701	3417	6364	5058	4174	3719	4620	2344	3309	3667
ENSMUSG00000062031	chr7	Athl1	1.4E+08	1.4E+08	3346	1.250841676	3.383136615	1.661E-05	8.36842E-05	0.09138	1	82	64	65	57	201	381	225	234	315	345
ENSMUSG00000028180	chr3	Zranb2	1.6E+08	1.6E+08	4301	-0.80442125	5.679941511	1.67E-05	8.41017E-05	0.04023	-1	1010	801	1173	951	928	886	967	551	642	840
ENSMUSG00000035621	chr10	Midn	8E+07	8E+07	4307	1.02154386	5.512754688	1.69E-05	8.50791E-05	0.065	1	301	207	873	472	548	1441	970	1123	1338	1376
ENSMUSG00000056973	chr8	Ces1d	9.3E+07	9.3E+07	2369	-2.18013061	6.45130649	1.701E-05	8.56242E-05	0.2787	-1	2192	1609	289	1085	5772	1058	303	579	601	733
ENSMUSG00000027347	chr2	Rasgrp1	1.2E+08	1.2E+08	5600	1.922258309	-0.09633269	1.707E-05	8.58561E-05	0.12461	1	5	3	3	3	11	39	18	20	18	36
ENSMUSG00000032411	chr9	Tfdp2	9.6E+07	9.6E+07	14029	-0.88833322	4.958500239	1.707E-05	8.58561E-05	0.04855	-1	575	435	876	689	473	433	671	284	399	488
ENSMUSG00000019971	chr10	Cep290	1E+08	1E+08	8006	-1.35326096	1.889792905	1.72E-05	8.64476E-05	0.09769	-1	72	76	101	81	58	53	73	29	27	33
ENSMUSG00000078861	chr2	Zfp931	1.8E+08	1.8E+08	2299	-1.29861186	2.050679874	1.722E-05	8.65459E-05	0.09019	-1	102	61	127	85	63	63	73	40	29	40
ENSMUSG00000035397	chr10	Klf16	8.1E+07	8.1E+07	2674	1.225589229	2.793940097	1.735E-05	8.71457E-05	0.08474	1	40	36	48	80	109	218	149	160	255	196
ENSMUSG00000039789	chr16	Zfp597	3858321	3858581	6660	-0.89272975	2.933739788	1.736E-05	8.72006E-05	0.04298	-1	155	103	161	152	173	116	128	84	114	106
ENSMUSG00000066880	chr8	Zfp617	7.2E+07	7.2E+07	3024	-1.14066325	3.144918076	1.775E-05	8.91105E-05	0.07569	-1	203	134	250	191	129	139	175	79	69	112
ENSMUSG00000044763	chr16	Trmt10c	5.6E+07	5.6E+07	3002	-0.80701648	4.088431138	1.776E-05	8.91231E-05	0.03838	-1	312	226	454	340	307	280	330	209	216	238
ENSMUSG00000030589	chr7	Rasgrp4	2.9E+07	2.9E+07	6359	2.021877003	1.929351749	1.778E-05	8.91714E-05	0.22049	1	23	22	9	4	49	231	86	62	100	146
ENSMUSG00000029267	chr5	Mtf2	1.1E+08	1.1E+08	5263	-0.98341962	3.259368213	1.78E-05	8.92384E-05	0.05557	-1	216	133	218	199	184	140	194	79	103	154
ENSMUSG00000042444	chr9	Fam63b	7.1E+07	7.1E+07	8081	-0.7798354	5.090900162	1.783E-05	8.93546E-05	0.03749	-1	597	464	903	720	575	580	703	334	451	554
ENSMUSG00000068220	chr15	Lgals1	7.9E+07	7.9E+07	800	1.173107118	8.41482571	1.791E-05	8.97337E-05	0.08691	1	2723	2189	2925	1877	6570	14109	8249	8149	10026	8481
ENSMUSG00000024095	chr17	Hnrnpll	8E+07	8E+07	11677	-0.87834474	4.052568544	1.798E-05	9.00838E-05	0.04602	-1	369	243	417	295	283	227	340	186	222	228
ENSMUSG00000044646	chr18	Zbtb7c	7.6E+07	7.6E+07	4729	1.237354143	1.489091705	1.799E-05	9.00838E-05	0.07033	1	21	20	18	24	36	102	76	58	64	89
ENSMUSG00000049225	chr4	Pdp1	1.2E+07	1.2E+07	4507	-1.10519668	6.191734719	1.808E-05	9.05232E-05	0.07688	-1	1458	934	2761	1365	1203	1013	1661	594	782	821
ENSMUSG00000034457	chrX	Eda2r	9.7E+07	9.7E+07	5891	0.946647751	4.541237196	1.811E-05	9.06387E-05	0.05432	1	324	208	248	198	179	757	629	573	550	618
ENSMUSG00000017631	chr11	Abr	7.6E+07	7.6E+07	9730	0.759049433	4.413442299	1.813E-05	9.06705E-05	0.03435	1	245	136	338	254	235	698	636	382	535	533
ENSMUSG00000101153	chr7	4933404I11Rik	4E+07	4E+07	1202	1.704075302	0.385102758	1.826E-05	9.13239E-05	0.11233	1	7	6	15	10	3	53	44	25	41	23

ENSMUSG00000024068	chr17	Spast	7.4E+07	7.4E+07	4696	-0.7629098	5.570195477	1.828E-05	9.1397E-05	0.03639	-1	849	732	1054	943	889	816	914	525	714	691
ENSMUSG00000089669	chr11	Tnfsf13	7E+07	7E+07	1637	1.200381582	1.632896144	1.833E-05	9.15857E-05	0.06774	1	18	23	30	25	40	130	81	56	77	89
ENSMUSG00000008305	chr4	Tle1	7.2E+07	7.2E+07	8711	-0.82062114	4.297827961	1.837E-05	9.17647E-05	0.04041	-1	283	279	471	490	370	277	321	226	341	295
ENSMUSG00000040782	chr1	Rfwd2	1.6E+08	1.6E+08	17516	-0.84903874	6.137040667	1.841E-05	9.19334E-05	0.04563	-1	1352	1090	1689	1383	1257	1171	1432	734	963	935
ENSMUSG00000098302	chr5	Gm28039	1.1E+08	1.1E+08	254	-1.63575015	0.698732162	1.842E-05	9.19593E-05	0.12697	-1	34	42	33	34	29	21	26	5	11	18
ENSMUSG00000035093	chr2	Secisbp2l	1.3E+08	1.3E+08	8222	-0.71916433	4.687089912	1.843E-05	9.19691E-05	0.03125	-1	446	364	560	413	648	469	513	287	342	413
ENSMUSG00000039985	chr6	Fam60a	1.5E+08	1.5E+08	3851	1.635150863	0.142026926	1.846E-05	9.20959E-05	0.08634	1	5	8	8	5	9	35	22	26	33	34
ENSMUSG00000078877	chr2	Gm14295	1.8E+08	1.8E+08	3527	-1.74070299	2.335289167	1.853E-05	9.23972E-05	0.17233	-1	149	130	109	116	43	70	76	41	29	25
ENSMUSG00000037876	chr10	Jmjd1c	6.7E+07	6.7E+07	14397	-0.86667784	4.633736039	1.859E-05	9.26579E-05	0.04616	-1	493	386	602	521	383	471	491	256	254	365
ENSMUSG00000022443	chr15	Myh9	7.8E+07	7.8E+07	12928	0.981636329	6.74686656	1.865E-05	9.29131E-05	0.06131	1	711	536	1634	1044	1825	3306	2747	2156	3287	3275
ENSMUSG00000005125	chr15	Ndrg1	6.7E+07	6.7E+07	6593	0.876911199	5.504683506	1.878E-05	9.35263E-05	0.04826	1	341	306	483	522	817	1621	1075	848	1217	1366
ENSMUSG00000046447	chr4	Camk2n1	1.4E+08	1.4E+08	4444	1.017048023	3.391552453	1.884E-05	9.37875E-05	0.06051	1	79	67	122	77	188	356	229	224	271	356
ENSMUSG00000064341	chrMT	mt-Nd1	2751	3707	957	-1.09006627	13.58530344	1.888E-05	9.39932E-05	0.07592	-1	229997	130627	401424	295548	243635	158105	272162	97323	139873	157593
ENSMUSG00000000562	chr3	Adora3	1.1E+08	1.1E+08	2524	2.67527791	-0.32475767	1.897E-05	9.43626E-05	0.23094	1	1	8	0	1	2	36	12	25	20	23
ENSMUSG00000021302	chr13	Ggps1	1.4E+07	1.4E+07	2367	-1.03985802	2.973465777	1.897E-05	9.43626E-05	0.0614	-1	170	143	158	151	151	120	145	88	76	98
ENSMUSG00000044172	chr17	Ptx4	2.5E+07	2.5E+07	1582	1.356316056	0.807658227	1.901E-05	9.44932E-05	0.07188	1	13	11	12	12	20	63	41	41	44	50
ENSMUSG00000057133	chr2	Chd6	1.6E+08	1.6E+08	19093	-0.95800548	4.200113698	1.901E-05	9.44932E-05	0.056	-1	269	253	648	388	307	306	368	158	211	266
ENSMUSG00000060510	chr9	Zfp266	2E+07	2.1E+07	6283	-0.81390812	3.792236061	1.902E-05	9.45236E-05	0.03855	-1	274	196	308	275	269	283	233	155	160	212
ENSMUSG00000029471	chr5	Camkk2	1.2E+08	1.2E+08	4843	1.213489118	3.271289685	1.909E-05	9.47924E-05	0.08696	1	92	47	78	48	182	374	239	235	275	250
ENSMUSG00000021549	chr13	Rasa1	8.5E+07	8.5E+07	7296	-1.02866232	4.161109721	1.924E-05	9.55033E-05	0.06501	-1	394	332	389	352	289	278	404	127	197	236
ENSMUSG00000029401	chr5	Rilpl2	1.2E+08	1.2E+08	1391	1.052963963	3.156516749	1.933E-05	9.58858E-05	0.06295	1	74	81	79	59	135	272	257	143	278	290
ENSMUSG00000097882	chr8	0610038B21Rik	7.8E+07	7.8E+07	3071	-1.4427069	0.429108905	1.933E-05	9.58858E-05	0.07869	-1	21	19	42	27	34	14	18	13	9	16
ENSMUSG00000037940	chr8	Inpp4b	8.1E+07	8.1E+07	10176	-2.31395652	1.838597384	1.934E-05	9.59259E-05	0.29557	-1	57	37	179	170	13	19	46	14	16	28
ENSMUSG00000040021	chr10	Lats1	7681209	7681450	7300	-0.7468294	4.366835563	1.937E-05	9.60248E-05	0.03358	-1	384	306	451	356	444	359	417	195	294	345
ENSMUSG00000090389	chr14	Gm7236	4.3E+07	4.3E+07	330	-1.8489238	0.03194978	1.945E-05	9.63756E-05	0.1412	-1	21	15	28	36	12	8	17	4	7	7
ENSMUSG00000029169	chr5	Dhx15	5.2E+07	5.2E+07	3009	-0.82373325	5.270028824	1.947E-05	9.6455E-05	0.04248	-1	715	535	980	748	756	615	868	453	478	468
ENSMUSG00000030522	chr7	Mtmr10	6.4E+07	6.4E+07	7474	-0.82415525	4.322439167	1.957E-05	9.69267E-05	0.04113	-1	365	248	537	446	346	325	409	233	269	255
ENSMUSG00000101904	chr1	Gm29427	1.3E+08	1.3E+08	1909	-1.5353495	1.670146034	1.958E-05	9.69541E-05	0.12854	-1	71	42	127	77	39	33	63	18	26	28
ENSMUSG00000033350	chr9	Chst2	9.5E+07	9.5E+07	7328	1.250060374	1.2146476	1.965E-05	9.7227E-05	0.07082	1	15	10	26	17	32	87	55	50	59	68
ENSMUSG00000026004	chr1	Kansl1l	6.7E+07	6.7E+07	6664	-0.97676817	3.953290077	1.967E-05	9.73164E-05	0.0579	-1	294	280	331	369	228	232	309	168	187	181
ENSMUSG00000092486	chr5	2610524H06Rik	1.1E+08	1.1E+08	947	1.682684599	0.501816717	1.972E-05	9.7532E-05	0.12036	1	6	7	6	5	22	56	37	26	33	51
ENSMUSG00000030061	chr6	Uba3	9.7E+07	9.7E+07	2589	-0.88291903	5.160967697	1.98E-05	9.78778E-05	0.04894	-1	704	548	925	713	583	575	817	374	415	438
ENSMUSG00000051985	chr1	Igfn1	1.4E+08	1.4E+08	8996	1.563852533	6.893131903	1.981E-05	9.7904E-05	0.15241	1	564	244	1411	1774	751	2677	5539	2540	2645	4978
ENSMUSG00000036672	chr8	Cenpt	1.1E+08	1.1E+08	1767	1.315844474	1.700825582	1.983E-05	9.79525E-05	0.08774	1	18	23	30	17	48	130	67	78	99	84
ENSMUSG00000027863	chr3	Cd2	1E+08	1E+08	1741	1.905258062	0.114054776	1.99E-05	9.83009E-05	0.14435	1	9	1	4	6	10	32	21	20	26	55
ENSMUSG00000048387	chr12	Osr1	9574442	9574742	2010	1.174963039	2.304904912	2.004E-05	9.89236E-05	0.07398	1	29	41	37	39	76	164	130	123	120	146
ENSMUSG00000021025	chr12	Nfkbia	5.5E+07	5.5E+07	1577	0.69302035	4.742168601	2.006E-05	9.89849E-05	0.02916	1	242	211	425	309	378	778	628	559	680	749
ENSMUSG00000030772	chr7	Dkk3	1.1E+08	1.1E+08	3357	-2.12848242	4.698235258	2.01E-05	9.91624E-05	0.26928	-1	1485	529	144	134	700	277	182	137	179	238
ENSMUSG00000027300	chr2	Ubox5	1.3E+08	1.3E+08	5585	-0.80573398	3.871926879	2.012E-05	9.92351E-05	0.03835	-1	267	214	349	313	249	240	275	166	214	204
ENSMUSG00000069763	chr11	Tmem100	9E+07	9E+07	1767	-1.18961059	3.457551957	2.014E-05	9.92714E-05	0.08494	-1	132	158	299	147	461	151	189	84	113	161
ENSMUSG00000024122	chr17	Pdpk1	2.4E+07	2.4E+07	10935	-0.80919624	5.194615629	2.023E-05	9.96937E-05	0.04113	-1	650	561	852	788	632	547	797	355	520	555
ENSMUSG00000034557	chr4	Zfyve9	1.1E+08	1.1E+08	6459	-0.87781769	5.598532412	2.024E-05	9.97155E-05	0.04889	-1	1009	637	1267	1008	824	705	1072	470	671	641
ENSMUSG00000033581	chr16	Igf2bp2	2.2E+07	2.2E+07	7131	1.284709495	2.136674929	2.026E-05	9.97612E-05	0.0865	1	35	40	20	39	46	158	112	102	140	110
ENSMUSG00000031028	chr7	Tub	1.1E+08	1.1E+08	6919	1.479103185	0.523518334	2.029E-05	9.98917E-05	0.07994	1	8	9	11	14	9	51	38	29	48	32
ENSMUSG00000091705	chr17	H2-Q2	3.5E+07	3.5E+07	2181	1.859641508	2.490069545	2.031E-05	9.9952E-05	0.20031	1	20	22	31	9	106	264	107	108	201	219
ENSMUSG00000039262	chr2	Prrc2b	3.2E+07	3.2E+07	11262	-0.94558469	7.461902621	2.046E-05	0.000100662	0.05767	-1	3241	2724	4504	4166	2728	2419	3320	1713	2688	2384
ENSMUSG00000046722	chr3	Cdc42se1	9.5E+07	9.5E+07	3258	0.82957444	5.152719397	2.047E-05	0.000100671	0.04309	1	312	293	381	335	627	1194	735	764	1027	967
ENSMUSG00000037712	chr14	Fermt2	4.5E+07	4.5E+07	3746	-0.90944014	7.561396006	2.048E-05	0.000100693	0.05343	-1	3923	2791	4841	3545	3460	3069	3902	2010	2258	2423
ENSMUSG00000021908	chr12	Gm6768	1.2E+08	1.2E+08	3339	-1.50637384	1.166427198	2.053E-05	0.000100895	0.11482	-1	41	43	43	54	60	20	48	16	20	14
ENSMUSG00000008658	chr16	Rbfox1	6809222	6809248	4151	-0.93335619	7.204267012	2.057E-05	0.000101042	0.05618	-1	3351	2500	3050	2746	2620	2037	2826	1555	2074	2003
ENSMUSG00000034435	chr12	Tmem30b	7.4E+07	7.4E+07	3282	1.470217888	0.691126769	2.057E-05	0.000101042	0.09441	1	8	4	24	12	13	52	58	34	34	47
ENSMUSG00000078945	chr13	Naip2	1E+08	1E+08	4846	1.86322654	0.863755807	2.06E-05	0.000101151	0.16476	1	9	14	9	1	20	84	70	29	45	49
ENSMUSG00000023118	chr7	Sympk	1.9E+07	1.9E+07	7777	-0.89560599	6.991708407	2.068E-05	0.000101503	0.05175	-1	2231	1769	3332	2928	2277	1942	2562	1163	1927	1715
ENSMUSG00000019791	chr10	Hint3	3.1E+07	3.1E+07	990	-0.77060818	4.494746932	2.072E-05	0.000101633	0.03621	-1	438	346	467	466	390	380	358	308	324	333
ENSMUSG00000006782	chr11	Cnp	1E+08	1E+08	3639	0.829268776	4.109164918	2.078E-05	0.000101887	0.04118	1	164	145	197	151	281	576	395	304	545	468
ENSMUSG00000002602	chr7	Axl	2.6E+07	2.6E+07	5033	0.872135286	6.337564578	2.09E-05	0.000102443	0.0488	1	676	645	778	900	1336	2878	2130	1461	2198	2272
ENSMUSG00000027130	chr2	Slc12a6	1.1E+08	1.1E+08	10165	-0.80538947	5.066792858	2.09E-05	0.000102443	0.04078	-1	684	567	714	644	528	572	653	330	453	539
ENSMUSG00000038025	chr13	Phf2	4.9E+07	4.9E+07	5260	-0.80644612	5.734121865	2.091E-05	0.000102462	0.04143	-1	860	746	1326	1082	1133	784	1130	546	843	722
ENSMUSG00000001229	chr17	Dpp9	5.6E+07	5.6E+07	3509	-0.87426027	5.76172554	2.096E-05	0.000102628	0.0488	-1	930	745	1566	1154	949	830	1146	512	844	667
ENSMUSG00000028933	chr5	Xrcc2	2.6E+07	2.6E+07	5216	-1.01618839	2.35325049	2.101E-05	0.000102855	0.05523	-1	87	98	113	87	118	79	76	50	78	63
ENSMUSG00000043099	chr11	Hic1	7.5E+07	7.5E+07	3750	0.954526399	3.777054975	2.107E-05	0.000103134	0.05503	1	108	69	180	133	237	523	283	286	389	382
ENSMUSG00000086219	chr5	Srrm4os	1.2E+08	1.2E+08	3655	2.445309591	2.666756519	2.138E-05	0.000104616	0.3338	1	62	33	3	23	8	266	90	219	271	213
ENSMUSG00000029472	chr5	Anapc5	1.2E+08	1.2E+08	2750	-0.96583625	9.266914571	2.142E-05	0.000104725	0.06065	-1	13000	11179	10284	12259	12991	8987	10847	5715	9927	8021
ENSMUSG00000081344	chr2	Gm14303	1.7E+08	1.7E+08	171	0.815995267	5.528632111	2.142E-05	0.000104725	0.04223	1	444	380	531	495	677	1371	920	886	1499	1404
ENSMUSG00000049092	chr14	Gpr137c	4.5E+07	4.5E+07	3679	-2.02495603	-0.3887128	2.146E-05	0.000104858	0.14788	-1	26	12	24	14	7	8	8	4	4	4
ENSMUSG00000103316	chr11	Coil	8.9E+07	8.9E+07	1722	-1.19701321	1.246095659	2.162E-05	0.000105628	0.06545	-1	42	43	65	45	46	31	38	20	29	27
ENSMUSG00000096696	chr17	Zfp960	1.7E+07	1.7E+07	2667	-1.4688085	1.298396473	2.163E-05	0.000105642	0.11063	-1	54	46	80	48	36	27	49	16	23	18

ENSMUSG00000025588	chr8	Nat1	6.7E+07	6.7E+07	1347	-1.61606052	0.039838092	2.173E-05	0.000106076	0.09395	-1	18	17	35	24	15	9	14	8	9	8
ENSMUSG00000009585	chr15	Apobec3	8E+07	8E+07	6083	1.444559011	1.796349358	2.174E-05	0.000106095	0.1117	1	18	25	24	13	56	150	81	76	85	115
ENSMUSG00000087153	chr8	Gm6483	2E+07	2E+07	6290	-1.59347806	0.426983851	2.175E-05	0.000106113	0.11193	-1	43	21	30	24	25	23	15	11	9	8
ENSMUSG00000001521	chr6	Tulp3	1.3E+08	1.3E+08	6704	0.829731105	3.535828019	2.182E-05	0.000106435	0.03965	1	106	84	153	104	189	375	296	243	315	290
ENSMUSG00000063236	chr15	1110038F14Rik	7.7E+07	7.7E+07	1010	0.867955534	4.253761847	2.187E-05	0.00010661	0.04629	1	181	126	232	174	324	557	362	434	563	594
ENSMUSG00000029070	chr4	Mxra8	1.6E+08	1.6E+08	2918	1.002880989	6.137234218	2.204E-05	0.000107396	0.06458	1	704	632	477	601	1051	2556	1599	1360	2255	2009
ENSMUSG00000063894	chr13	Zkscan8	2.2E+07	2.2E+07	8901	-0.94677086	3.013517557	2.207E-05	0.000107506	0.05111	-1	184	119	151	147	189	136	141	81	91	121
ENSMUSG00000042903	chrX	Foxo4	1E+08	1E+08	3485	-0.88986723	7.467416949	2.208E-05	0.000107554	0.05157	-1	3660	2519	4138	3687	3267	2481	3450	1682	2836	2474
ENSMUSG00000005338	chr1	Cadm3	1.7E+08	1.7E+08	7248	1.044903844	4.805463669	2.239E-05	0.000108999	0.06898	1	206	192	200	228	575	1066	664	576	892	706
ENSMUSG00000027312	chr2	Atrn	1.3E+08	1.3E+08	13208	-0.72372778	4.621508943	2.245E-05	0.000109259	0.03223	-1	445	310	583	526	456	434	493	293	353	348
ENSMUSG00000038084	chr16	Opa1	3E+07	3E+07	7875	-0.9495318	6.878569439	2.271E-05	0.000110502	0.05862	-1	2087	1333	3694	2757	2107	1594	2385	1125	1589	1663
ENSMUSG00000073590	chr18	3222401L13Rik	3.8E+07	3.8E+07	6292	-1.57068654	1.349479177	2.279E-05	0.000110821	0.13284	-1	74	42	57	62	41	30	47	15	10	30
ENSMUSG00000022676	chr16	Snai2	1.5E+07	1.5E+07	2031	1.182985711	1.345504245	2.303E-05	0.000111905	0.06358	1	22	13	25	22	30	84	68	66	59	65
ENSMUSG00000048895	chr11	Cdk5r1	8E+07	8E+07	4162	1.752634858	0.207098368	2.302E-05	0.000111905	0.1168	1	5	10	8	4	7	49	25	31	21	35
ENSMUSG00000020974	chr12	Pole2	6.9E+07	6.9E+07	1695	2.062594253	0.503091433	2.309E-05	0.000112198	0.19223	1	6	5	1	13	11	88	35	33	38	21
ENSMUSG00000015843	chr1	Rxrg	1.7E+08	1.7E+08	2297	-0.89058915	5.512622055	2.316E-05	0.000112491	0.05106	-1	809	792	939	832	1043	622	976	355	775	629
ENSMUSG00000002083	chr7	Bbc3	1.6E+07	1.6E+07	2008	1.321855234	2.225865298	2.323E-05	0.000112796	0.09739	1	30	31	30	25	82	150	101	100	153	165
ENSMUSG00000007035	chr17	Msh5	3.5E+07	3.5E+07	5526	1.985627078	0.511798491	2.327E-05	0.000112946	0.18381	1	6	6	4	3	20	73	21	23	55	43
ENSMUSG00000025701	chr6	Alox5	1.2E+08	1.2E+08	4106	1.762498278	1.644781654	2.34E-05	0.00011352	0.16942	1	7	17	11	16	53	160	77	74	70	99
ENSMUSG00000054978	chr9	Kbtbd13	6.5E+07	6.5E+07	2969	-0.86638185	4.859328702	2.344E-05	0.000113673	0.0475	-1	522	306	884	655	529	399	624	311	388	405
ENSMUSG00000061689	chr2	Dlgap4	1.6E+08	1.6E+08	8451	0.82149962	6.122310568	2.345E-05	0.000113673	0.04379	1	603	465	925	751	1157	1872	1778	1466	2025	2003
ENSMUSG00000030147	chr6	Clec4b1	1.2E+08	1.2E+08	784	2.21835985	0.140208666	2.36E-05	0.000114398	0.22251	1	3	2	3	4	14	64	9	27	37	27
ENSMUSG00000020817	chr11	Rabep1	7.1E+07	7.1E+07	6868	-0.77742895	5.810843165	2.363E-05	0.000114469	0.03905	-1	1070	821	1344	1091	995	959	1095	615	790	842
ENSMUSG00000093989	chr11	Rnasek	7E+07	7E+07	885	0.814089718	5.946346839	2.375E-05	0.00011504	0.04293	1	620	420	776	668	949	1669	1380	1198	1998	1860
ENSMUSG00000022265	chr15	Ank	2.7E+07	2.7E+07	3608	-1.0249948	7.280007281	2.376E-05	0.00011505	0.06861	-1	2631	1857	5247	3432	3010	2060	3509	1328	1791	2038
ENSMUSG00000058603	chr1	Rpl28-ps1	1.3E+08	1.3E+08	414	1.120542768	2.917587331	2.38E-05	0.000115195	0.07387	1	57	34	72	88	111	199	177	132	265	282
ENSMUSG00000020627	chr12	Klhl29	5077472	5081334	7041	-0.96435386	2.707461017	2.402E-05	0.000116206	0.05199	-1	119	87	195	117	138	101	127	67	80	80
ENSMUSG00000020778	chr11	Ten1	1.2E+08	1.2E+08	2728	0.786608787	3.961040919	2.404E-05	0.000116277	0.03695	1	190	121	178	164	201	468	365	337	465	377
ENSMUSG00000020766	chr11	Galk1	1.2E+08	1.2E+08	1406	1.289416266	2.574723128	2.414E-05	0.000116696	0.09643	1	38	38	34	42	106	226	119	136	203	169
ENSMUSG00000052681	chr10	Rap1b	1.2E+08	1.2E+08	2024	0.860800876	5.496167049	2.42E-05	0.000116975	0.04781	1	400	300	541	389	859	1614	1138	993	1075	1195
ENSMUSG00000045954	chr1	Sdpr	5.1E+07	5.1E+07	3055	-0.95018976	5.728450499	2.423E-05	0.000117081	0.05847	-1	857	534	1395	764	2000	902	851	561	693	749
ENSMUSG00000033940	chr6	Brk1	1.1E+08	1.1E+08	1092	0.819342605	6.028117459	2.427E-05	0.000117198	0.04364	1	624	467	826	635	1081	2140	1422	1437	1790	1788
ENSMUSG00000032889	chr11	Gm6685	2.8E+07	2.8E+07	764	-2.75924823	-0.23622676	2.428E-05	0.000117246	0.3461	-1	33	24	24	12	7	8	12	0	1	1
ENSMUSG00000026842	chr2	Abl1	3.2E+07	3.2E+07	11596	-0.7013123	5.366339579	2.443E-05	0.000117875	0.03142	-1	641	598	948	757	925	730	791	453	674	619
ENSMUSG00000034800	chr2	Zfp661	1.3E+08	1.3E+08	5165	-1.1198204	1.840938997	2.443E-05	0.000117875	0.06533	-1	70	66	95	67	61	62	44	39	42	42
ENSMUSG00000001785	chr10	Pwp1	8.6E+07	8.6E+07	2730	-0.74331212	4.620123806	2.462E-05	0.000118743	0.03454	-1	483	375	578	447	412	444	466	275	392	331
ENSMUSG00000038555	chr18	Reep2	3.5E+07	3.5E+07	1926	2.019358191	-0.03557908	2.471E-05	0.000119132	0.16738	1	6	3	3	2	11	31	10	30	32	33
ENSMUSG00000074227	chr7	Spint2	2.9E+07	2.9E+07	1459	1.160720353	2.784386938	2.492E-05	0.000120094	0.07932	1	53	34	87	40	114	204	158	120	251	238
ENSMUSG00000097145	chr5	9230114K14Rik	5.2E+07	5.2E+07	2118	-1.95690165	0.017339101	2.502E-05	0.000120534	0.16886	-1	20	24	32	27	8	14	10	8	4	4
ENSMUSG00000067194	chrX	Eif1ax	1.6E+08	1.6E+08	5266	-0.88804473	6.739035329	2.504E-05	0.000120601	0.05184	-1	2343	1791	2204	2060	1821	1731	1922	1242	1508	1342
ENSMUSG00000055320	chr7	Tead1	1.1E+08	1.1E+08	11237	-1.03161789	7.63585619	2.516E-05	0.000121125	0.06998	-1	3528	2161	6585	4848	3620	2432	4134	2008	2162	2797
ENSMUSG00000005981	chr16	Trap1	4039971	4040224	2573	-0.80703068	7.479339207	2.523E-05	0.000121435	0.0431	-1	3433	2656	3934	3372	3655	2924	3111	1975	2808	2647
ENSMUSG00000032177	chr9	Pde4a	2.1E+07	2.1E+07	7655	-1.08627045	6.131233736	2.524E-05	0.000121468	0.07695	-1	1071	718	2673	1702	1336	818	1417	504	976	994
ENSMUSG00000005103	chr5	Wdr1	3.9E+07	3.9E+07	2948	0.851299051	6.49335765	2.533E-05	0.000121819	0.04762	1	696	563	1396	1191	1137	2707	2289	1833	2431	2725
ENSMUSG00000024776	chr19	Stambpl1	3.4E+07	3.4E+07	5557	1.478573285	1.290689676	2.539E-05	0.000122073	0.1084	1	21	15	13	11	31	110	47	46	63	89
ENSMUSG00000007812	chr5	Zfp655	1.5E+08	1.5E+08	4514	-0.76321919	3.723992728	2.543E-05	0.000122244	0.03436	-1	267	163	295	234	301	258	224	149	186	198
ENSMUSG00000079165	chr5	Sap25	1.4E+08	1.4E+08	1569	1.456835941	2.322405882	2.554E-05	0.000122743	0.12275	1	25	33	32	25	83	180	114	69	148	240
ENSMUSG00000035798	chr10	Zdhhc17	1.1E+08	1.1E+08	4948	-0.77165109	4.062224338	2.575E-05	0.000123689	0.03646	-1	289	268	434	284	303	295	311	182	245	246
ENSMUSG00000026205	chr1	Slc23a3	7.5E+07	7.5E+07	2167	2.145138524	-0.21948513	2.586E-05	0.000124168	0.16004	1	6	5	4	4	0	28	17	22	38	15
ENSMUSG00000022792	chr16	Yars2	1.6E+07	1.6E+07	3149	-0.7902275	3.922965071	2.595E-05	0.000124581	0.0379	-1	263	205	415	300	273	269	278	187	218	192
ENSMUSG00000026958	chr2	Dpp7	2.5E+07	2.5E+07	3337	0.686314295	4.685329679	2.597E-05	0.000124603	0.02914	1	288	218	312	284	383	780	635	444	750	683
ENSMUSG00000024617	chr18	Camk2a	6.1E+07	6.1E+07	7465	-0.99009258	8.3676962	2.605E-05	0.000124952	0.06493	-1	7457	5435	6527	5428	7906	4059	6799	2845	5399	3974
ENSMUSG00000007867	chr12	Ift43	8.6E+07	8.6E+07	775	0.851084121	3.155988585	2.607E-05	0.000124999	0.04123	1	93	61	132	84	110	258	238	200	218	248
ENSMUSG00000018995	chr7	Nars2	9.7E+07	9.7E+07	4213	-0.90369266	3.308896089	2.616E-05	0.00012541	0.04806	-1	185	119	281	211	187	174	170	125	117	121
ENSMUSG00000025962	chr1	Fastkd2	6.4E+07	6.4E+07	5873	-0.86743397	4.340232528	2.62E-05	0.000125559	0.04744	-1	364	279	604	442	290	315	396	206	301	270
ENSMUSG00000041471	chr14	Fam35a	3.4E+07	3.4E+07	3446	-1.05236752	2.805553604	2.621E-05	0.000125565	0.0652	-1	194	99	145	128	131	121	109	62	72	108
ENSMUSG00000041763	chr1	Tpp2	4.4E+07	4.4E+07	10078	-0.89708004	5.278379576	2.623E-05	0.000125627	0.05225	-1	655	536	1141	884	619	653	852	380	425	526
ENSMUSG00000026773	chr2	Pfkfb3	1.1E+07	1.1E+07	7561	-1.37663707	7.32401396	2.627E-05	0.000125733	0.12312	-1	4903	3344	1607	1974	4929	1699	2623	1078	2029	1899
ENSMUSG00000028690	chr4	Mmachc	1.2E+08	1.2E+08	2224	-0.83790615	5.127956258	2.632E-05	0.000125931	0.04531	-1	583	415	1024	836	576	552	718	362	518	458
ENSMUSG00000040560	chr18	Wdr7	6.4E+07	6.4E+07	7109	-0.73422817	5.249782011	2.643E-05	0.00012643	0.03472	-1	671	550	858	805	677	633	762	429	552	587
ENSMUSG00000040466	chr7	Blvrb	2.7E+07	2.7E+07	1414	1.411876576	3.910217926	2.676E-05	0.000127986	0.12539	1	113	85	76	60	295	747	294	286	500	456
ENSMUSG00000075700	chr3	Selt	5.9E+07	5.9E+07	3436	-0.89131871	7.38380152	2.688E-05	0.000128504	0.05282	-1	3392	2539	3847	3339	3123	2513	3539	1706	2143	2282
ENSMUSG00000057469	chr12	E2f6	1.7E+07	1.7E+07	2421	-0.93863612	7.216858616	2.691E-05	0.000128607	0.05847	-1	2767	1810	4505	3430	2473	2237	2948	1312	2008	2182
ENSMUSG00000035914	chr9	Cd276	5.9E+07	5.9E+07	3297	1.106394938	3.44060406	2.712E-05	0.000129567	0.07641	1	72	41	207	74	155	342	341	225	315	296
ENSMUSG00000000567	chr11	Sox9	1.1E+08	1.1E+08	4135	1.641146273	1.330800726	2.714E-05	0.000129625	0.14095	1	10	16	33	17	11	111	38	79	54	84
ENSMUSG00000014444	chr8	Piezo1	1.2E+08	1.2E+08	9933	0.971005387	5.358605158	2.719E-05	0.000129799	0.06135	1	298	394	404	256	739	1414	1104	889	1181	1023
ENSMUSG00000046229	chr2	Scand1	1.6E+08	1.6E+08	759	0.969105027	4.405990817	2.724E-05	0.000129991	0.06006	1	162	115	307	240	289	606	349	467	821	617

ENSMUSG00000093710	chr5	Mir5625	3.1E+07	3.1E+07	80	-1.55234494	0.141056301	2.727E-05	0.000130091	0.09653	-1	21	16	33	23	24	9	20	6	13	6
ENSMUSG00000039414	chr17	Heatr5b	7.9E+07	7.9E+07	6437	-0.82911047	3.319842689	2.729E-05	0.000130151	0.04016	-1	164	126	254	188	244	165	186	92	159	145
ENSMUSG00000055053	chr10	Nfic	8.1E+07	8.1E+07	6534	-0.91508781	8.195611241	2.73E-05	0.000130165	0.05588	-1	5560	4190	7415	6254	5527	3675	6021	2743	4698	4000
ENSMUSG00000028413	chr4	B4galt1	4.1E+07	4.1E+07	4234	0.77862499	6.033733458	2.766E-05	0.000131812	0.03997	1	642	453	956	663	1015	2160	1509	1345	1725	1824
ENSMUSG00000025894	chr9	Aasdhppt	4294793	4296839	2870	-0.81233068	4.219270353	2.771E-05	0.000132012	0.04118	-1	346	252	482	384	327	297	346	259	220	257
ENSMUSG00000027259	chr2	Adal	1.2E+08	1.2E+08	5317	-0.86000373	4.127449121	2.778E-05	0.000132295	0.04634	-1	360	298	368	312	324	303	289	244	239	191
ENSMUSG00000051166	chr12	Eml5	9.9E+07	9.9E+07	10136	-1.25652579	1.898655853	2.784E-05	0.000132544	0.089	-1	84	75	83	58	83	45	55	20	38	70
ENSMUSG00000017485	chr14	Top2b	1.6E+07	1.6E+07	6355	-0.80861989	5.505744156	2.786E-05	0.000132593	0.04282	-1	868	735	1027	819	861	863	901	520	502	651
ENSMUSG00000006736	chr10	Tspan31	1.3E+08	1.3E+08	1516	0.702983366	5.323638775	2.787E-05	0.000132611	0.03191	1	407	311	530	439	641	1265	930	768	1098	1075
ENSMUSG00000035934	chr9	Pknox2	3.7E+07	3.7E+07	6942	-1.151922	5.421172094	2.789E-05	0.000132635	0.08676	-1	839	804	761	1384	472	557	688	439	585	471
ENSMUSG00000026712	chr2	Mrc1	1.4E+07	1.4E+07	6371	1.392527297	5.507044077	2.804E-05	0.000133298	0.12548	1	295	409	176	263	694	2548	1249	1122	1027	946
ENSMUSG00000039218	chr17	Srrm2	2.4E+07	2.4E+07	10982	-0.86077679	7.567965849	2.815E-05	0.000133819	0.04959	-1	3267	3303	4569	3627	3447	3012	3501	1830	2777	2955
ENSMUSG00000075284	chr2	Wipf1	7.3E+07	7.3E+07	5896	0.763337316	4.050965993	2.818E-05	0.000133892	0.03568	1	180	125	210	149	270	513	466	316	376	482
ENSMUSG00000036533	chr17	Cdc42ep3	7.9E+07	7.9E+07	1967	-0.75689892	4.796494817	2.821E-05	0.000133986	0.03662	-1	472	388	754	519	516	483	561	344	326	420
ENSMUSG00000086866	chr8	4930512H18Rik	6.2E+07	6.2E+07	1493	1.930179415	-0.39021577	2.822E-05	0.000133986	0.11074	1	4	4	3	6	2	19	17	16	30	20
ENSMUSG00000026103	chr1	Gls	5.2E+07	5.2E+07	15057	-0.89327054	5.915702314	2.841E-05	0.000134834	0.05278	-1	1098	895	1628	1358	919	984	1272	596	756	805
ENSMUSG00000039206	chr5	Daglb	1.4E+08	1.4E+08	5677	0.705113762	4.78113032	2.843E-05	0.000134891	0.03152	1	271	193	365	375	390	708	741	509	789	766
ENSMUSG00000067629	chr17	Syngap1	2.7E+07	2.7E+07	6267	1.259943339	1.904879681	2.845E-05	0.000134966	0.08432	1	28	34	31	23	41	151	74	65	135	107
ENSMUSG00000040321	chr2	Zfp770	1.1E+08	1.1E+08	6793	-0.94053962	4.854295288	2.85E-05	0.000135116	0.05745	-1	529	345	897	749	379	432	514	291	331	489
ENSMUSG00000020650	chr12	Bcap29	3.2E+07	3.2E+07	2008	-0.78186298	4.867436522	2.852E-05	0.000135146	0.03935	-1	675	432	577	535	514	466	535	373	417	413
ENSMUSG00000034768	chr11	Asb16	1E+08	1E+08	2843	-0.87102963	6.298064201	2.852E-05	0.000135146	0.05041	-1	1534	1093	1884	1786	1352	1068	1544	767	1305	1096
ENSMUSG00000002015	chrX	Bcap31	7.4E+07	7.4E+07	1219	1.024398742	6.384284064	2.862E-05	0.000135594	0.06956	1	764	559	701	693	1504	2973	1505	1973	2540	2524
ENSMUSG00000046982	chr18	Tshz1	8.4E+07	8.4E+07	5656	-0.90861431	3.782435462	2.866E-05	0.000135718	0.05139	-1	241	209	337	311	245	205	309	123	162	198
ENSMUSG00000021678	chr13	F2rl1	9.6E+07	9.6E+07	2754	1.786247306	0.005441751	2.867E-05	0.000135723	0.10914	1	5	9	4	5	5	38	39	17	25	21
ENSMUSG00000026987	chr2	Baz2b	6E+07	6E+07	17604	-0.79955279	3.920980543	2.871E-05	0.000135854	0.03955	-1	269	230	344	309	285	300	278	161	168	244
ENSMUSG00000035437	chr2	Rabgap1	3.7E+07	3.7E+07	7607	-0.76537217	5.300490747	2.88E-05	0.000136231	0.03825	-1	779	540	921	812	674	716	803	423	517	585
ENSMUSG00000017493	chr11	Igfbp4	9.9E+07	9.9E+07	4416	1.445796518	7.07023653	2.885E-05	0.00013645	0.13652	1	829	796	600	611	2758	5613	2724	3224	4811	3986
ENSMUSG00000021027	chr12	Ralgapa1	5.6E+07	5.6E+07	7874	-0.82651931	5.525425275	2.917E-05	0.000137892	0.04499	-1	861	680	1235	947	701	778	902	526	595	642
ENSMUSG00000006262	chr5	Mob1b	8.9E+07	8.9E+07	10927	-0.79683399	5.15602937	2.933E-05	0.000138598	0.04144	-1	709	507	886	734	555	578	744	402	469	507
ENSMUSG00000021140	chr12	Pcnx	8.2E+07	8.2E+07	12139	-0.98599345	6.328596178	2.96E-05	0.000139754	0.06475	-1	1332	943	2900	1780	1344	1136	1677	763	996	1048
ENSMUSG00000027852	chr3	Nras	1E+08	1E+08	4514	0.777628637	5.666673592	2.96E-05	0.000139754	0.03981	1	499	437	564	484	850	1514	1307	1018	1274	1515
ENSMUSG00000057858	chr19	Fam204a	6E+07	6E+07	2035	-0.77372072	3.858309951	2.96E-05	0.000139754	0.03671	-1	292	198	378	254	257	245	262	156	209	236
ENSMUSG00000050029	chrX	Rap2c	5.1E+07	5.1E+07	3545	-0.76875765	5.078305172	2.983E-05	0.000140759	0.0385	-1	666	501	832	599	595	581	739	377	434	466
ENSMUSG00000047407	chr17	Tgif1	7.1E+07	7.1E+07	5625	0.993042342	3.172565447	2.991E-05	0.000141133	0.05888	1	90	69	74	80	134	261	200	224	224	298
ENSMUSG00000046185	chr7	Zfp84	3E+07	3E+07	4113	-1.13690716	2.657543271	3.012E-05	0.00014203	0.07724	-1	150	101	176	108	110	102	133	53	62	60
ENSMUSG00000046994	chr1	Mars2	5.5E+07	5.5E+07	11294	-1.000582	3.371102768	3.013E-05	0.00014203	0.06163	-1	172	137	324	240	177	132	220	105	117	136
ENSMUSG00000061983	chr10	Rps12	2.4E+07	2.4E+07	476	0.865528019	7.944304405	3.014E-05	0.00014203	0.05055	1	2455	1901	3251	2480	3195	8952	4723	5447	6952	6806
ENSMUSG00000022200	chr15	Golph3	1.2E+07	1.2E+07	2606	-0.84682904	5.916903953	3.023E-05	0.00014245	0.04775	-1	1096	791	1602	1108	1348	955	1410	557	795	809
ENSMUSG00000020003	chr10	Pex7	2E+07	2E+07	2351	-0.74916551	4.501867689	3.046E-05	0.000143442	0.03575	-1	493	301	493	430	411	425	427	262	346	292
ENSMUSG00000008730	chr3	Hipk1	1E+08	1E+08	8591	-0.75656428	5.748291475	3.049E-05	0.000143564	0.03796	-1	954	803	1286	962	1083	861	1087	601	736	862
ENSMUSG00000030796	chr7	Tead2	4.5E+07	4.5E+07	4668	1.09133073	1.605644947	3.061E-05	0.000144055	0.05762	1	22	17	34	32	37	83	83	70	88	82
ENSMUSG00000014498	chr10	Ankrd52	1.3E+08	1.3E+08	8401	-1.00055484	5.849539894	3.071E-05	0.000144507	0.06669	-1	1034	743	1570	1614	860	873	1252	473	793	647
ENSMUSG00000039377	chr1	Hlx	1.8E+08	1.8E+08	2278	0.962502214	3.211404232	3.085E-05	0.000145121	0.05622	1	74	48	115	91	156	260	215	179	295	300
ENSMUSG00000026536	chr1	Mnda	1.7E+08	1.7E+08	1785	1.294809134	1.811913141	3.09E-05	0.000145269	0.09249	1	20	23	28	17	62	126	119	73	90	90
ENSMUSG00000059866	chr5	Tnip2	3.4E+07	3.4E+07	2879	1.060651231	2.997200162	3.091E-05	0.000145269	0.0673	1	65	61	98	44	122	300	187	202	193	209
ENSMUSG00000028757	chr4	Ddost	1.4E+08	1.4E+08	2120	0.783377483	6.243460369	3.097E-05	0.000145526	0.04105	1	716	599	961	844	1121	2625	1771	1422	2262	1898
ENSMUSG00000025150	chr11	Cbr2	1.2E+08	1.2E+08	1327	1.721961387	5.644191747	3.102E-05	0.000145724	0.1911	1	191	256	186	119	1084	2018	1730	1207	1820	1175
ENSMUSG00000022100	chr14	Xpo7	7.1E+07	7.1E+07	15121	-0.8047713	5.842786183	3.115E-05	0.000146275	0.04322	-1	1007	902	1331	1160	1058	968	1223	561	812	807
ENSMUSG00000064289	chr2	Tank	6.2E+07	6.2E+07	6096	-0.91610763	3.696042418	3.126E-05	0.000146723	0.05246	-1	258	200	335	244	230	221	284	128	161	140
ENSMUSG00000001281	chr15	Itgb7	1E+08	1E+08	2743	1.795359255	2.410153432	3.176E-05	0.000149057	0.19575	1	20	19	17	19	108	235	101	114	155	231
ENSMUSG00000040734	chr7	Ppp1r13l	1.9E+07	1.9E+07	3604	1.010801025	2.347001708	3.178E-05	0.000149097	0.05684	1	44	29	66	48	66	131	157	84	176	141
ENSMUSG00000000374	chr10	Trappc10	7.8E+07	7.8E+07	5048	-0.95261929	5.675768447	3.188E-05	0.00014951	0.06059	-1	822	663	1577	1166	948	677	1226	460	665	609
ENSMUSG00000030680	chr7	Pagr1a	1.3E+08	1.3E+08	4405	0.708867921	4.858595951	3.207E-05	0.000150335	0.03237	1	273	236	398	331	438	921	636	484	840	866
ENSMUSG00000026357	chr1	Rgs18	1.4E+08	1.4E+08	2031	1.556889136	0.809188602	3.219E-05	0.000150873	0.11118	1	8	12	7	10	24	81	46	33	39	53
ENSMUSG00000027010	chr2	Slc25a12	7.1E+07	7.1E+07	7342	-1.03077983	8.749967996	3.223E-05	0.000150918	0.07194	-1	7671	5766	12564	11797	6020	5349	7980	3943	6367	5770
ENSMUSG00000038524	chr18	Fchsd1	3.8E+07	3.8E+07	5473	1.251292117	1.548853369	3.222E-05	0.000150918	0.08095	1	19	15	23	21	49	101	67	56	93	91
ENSMUSG00000056569	chr1	Mpz	1.7E+08	1.7E+08	2111	0.805247479	5.319668751	3.226E-05	0.000151043	0.04287	1	457	250	577	499	435	1409	952	583	1173	1231
ENSMUSG00000003161	chr5	Sri	8046078	8046215	3734	1.026921377	4.45457728	3.239E-05	0.000151607	0.06872	1	183	171	189	125	432	870	545	469	565	596
ENSMUSG00000037236	chr18	Matr3	3.6E+07	3.6E+07	9869	-0.86061185	6.066153375	3.252E-05	0.00015213	0.04982	-1	1342	957	1700	1268	1253	1185	1419	674	712	992
ENSMUSG00000062519	chr6	Zfp398	4.8E+07	4.8E+07	6478	-1.34688465	1.227839097	3.257E-05	0.000152284	0.09422	-1	57	37	66	51	34	38	40	16	22	19
ENSMUSG00000096740	chr19	Lbhd1	8883732	8884079	3289	0.794073952	3.794623536	3.257E-05	0.000152284	0.0386	1	137	109	183	127	213	469	295	276	374	396
ENSMUSG00000027639	chr2	Samhd1	1.6E+08	1.6E+08	9150	0.886612712	5.249636037	3.264E-05	0.000152572	0.05211	1	334	290	466	297	665	1678	890	622	877	1151
ENSMUSG00000064043	chr17	Trerf1	4.7E+07	4.7E+07	9070	1.402566273	1.844232901	3.288E-05	0.000153609	0.1097	1	19	27	21	17	59	130	77	74	107	131
ENSMUSG00000062190	chr6	Lancl2	5.8E+07	5.8E+07	2958	-0.9123689	3.471935738	3.297E-05	0.000154008	0.05151	-1	221	175	269	212	202	176	242	108	140	133
ENSMUSG00000029838	chr6	Ptn	3.7E+07	3.7E+07	2021	1.320272292	0.927839996	3.311E-05	0.000154571	0.07712	1	16	11	22	15	12	64	45	53	49	46
ENSMUSG00000031253	chrX	Srpx2	1.3E+08	1.3E+08	2922	1.166178912	3.534901564	3.315E-05	0.000154737	0.08561	1	90	102	81	69	186	579	253	231	285	321
ENSMUSG00000031647	chr8	Mfap3l	6.1E+07	6.1E+07	6837	-1.02287617	3.306406544	3.323E-05	0.000155017	0.06514	-1	212	135	251	203	197	148	233	92	91	114

ENSMUSG00000075012	chr2	Fjx1	1E+08	1E+08	3134	1.55105579	0.791130625	3.323E-05	0.000155017	0.12108	1	6	5	17	15	20	67	28	51	38	58
ENSMUSG00000031156	chrX	Slc35a2	7884041	7884433	3081	0.77151331	3.770982625	3.329E-05	0.000155232	0.03608	1	130	112	159	157	199	455	326	258	392	343
ENSMUSG00000062078	chr17	Qk	1E+07	1E+07	9879	-1.11585982	7.442485534	3.333E-05	0.000155361	0.0841	-1	2828	1957	5892	5017	2715	2134	3614	1585	1798	2300
ENSMUSG00000034998	chr17	Foxn2	8.8E+07	8.8E+07	7357	-0.86459848	3.798280782	3.343E-05	0.000155773	0.04679	-1	282	161	408	281	238	205	266	158	171	215
ENSMUSG00000047242	chrX	Taf9b	1.1E+08	1.1E+08	3158	-0.97596022	3.436201422	3.346E-05	0.000155886	0.05965	-1	250	213	215	160	206	206	179	103	140	132
ENSMUSG00000078485	chr4	Plekhn1	1.6E+08	1.6E+08	2210	2.093104922	0.601252238	3.358E-05	0.000156367	0.21139	1	3	13	6	6	9	21	50	20	50	89
ENSMUSG00000028167	chr3	Bdh2	1.4E+08	1.4E+08	1202	1.448895103	1.070193144	3.376E-05	0.000157163	0.10013	1	20	15	10	13	19	77	40	38	79	64
ENSMUSG00000022674	chr16	Ube2v2	1.6E+07	1.6E+07	4275	-1.0154262	3.625882704	3.414E-05	0.000158874	0.06567	-1	279	224	259	241	204	171	279	110	137	153
ENSMUSG00000031730	chr8	Dhodh	1.1E+08	1.1E+08	6326	-0.74913104	3.82049131	3.423E-05	0.000159239	0.03476	-1	237	200	306	286	303	236	270	144	237	206
ENSMUSG00000075707	chr12	Dio3	1.1E+08	1.1E+08	2030	1.953440245	-0.08071916	3.428E-05	0.000159441	0.15024	1	5	2	4	8	6	26	18	38	30	16
ENSMUSG00000048497	chr11	Mmgt2	6.3E+07	6.3E+07	4898	1.063380855	2.632685239	3.43E-05	0.000159453	0.06471	1	64	54	42	57	72	217	140	131	174	187
ENSMUSG00000025255	chr3	Zfhx4	5218526	5218927	15737	-1.04170368	3.869152226	3.432E-05	0.000159514	0.07023	-1	397	266	256	224	289	341	200	117	159	195
ENSMUSG00000032456	chr9	Nmnat3	9.8E+07	9.8E+07	5004	-0.83328358	3.846414767	3.45E-05	0.000160295	0.0435	-1	295	184	392	280	242	230	270	181	193	186
ENSMUSG00000020844	chr11	Nxn	7.6E+07	7.6E+07	3239	0.821568312	6.036324078	3.462E-05	0.000160782	0.04571	1	558	400	1202	726	824	1831	1870	1364	1787	1786
ENSMUSG00000024816	chr19	Frmd8	5849702	5852742	5082	1.003873115	3.254833294	3.479E-05	0.000161523	0.06236	1	75	60	98	68	186	303	258	180	286	280
ENSMUSG00000038633	chr1	Degs1	1.8E+08	1.8E+08	2591	0.795400376	5.460552386	3.489E-05	0.000161951	0.04238	1	369	323	552	444	796	1467	1001	920	1117	1266
ENSMUSG00000034959	chr14	5031414D18Rik	7.5E+07	7.5E+07	2651	2.285398142	-0.41894247	3.502E-05	0.000162494	0.1865	1	2	5	1	0	7	33	10	16	18	28
ENSMUSG00000046058	chr7	Eid2	2.8E+07	2.8E+07	1392	1.028261177	2.502891762	3.515E-05	0.000163027	0.06209	1	42	25	80	53	86	163	154	130	172	144
ENSMUSG00000061410	chr8	Zcchc14	1.2E+08	1.2E+08	7780	-0.6943478	4.801900031	3.517E-05	0.000163069	0.03138	-1	432	382	713	567	520	520	540	332	390	427
ENSMUSG00000027601	chr3	Mtfr1	1.9E+07	1.9E+07	4372	-0.81998204	5.118149839	3.518E-05	0.000163073	0.04478	-1	566	373	1076	773	648	528	734	342	485	528
ENSMUSG00000015013	chr8	Trappc2l	1.2E+08	1.2E+08	607	0.683835563	4.948357798	3.53E-05	0.000163549	0.03051	1	350	245	442	315	450	916	656	636	869	832
ENSMUSG00000020029	chr10	Nudt4	9.6E+07	9.6E+07	3231	-1.00130363	8.574940362	3.532E-05	0.000163601	0.06864	-1	8624	7143	6701	8678	5657	5612	6501	3864	5198	5197
ENSMUSG00000040451	chr19	Sgms1	3.2E+07	3.2E+07	10299	-0.76363386	5.335437401	3.534E-05	0.000163632	0.03899	-1	710	596	1089	728	715	699	852	438	545	582
ENSMUSG00000049672	chr17	Zbtb14	6.9E+07	6.9E+07	4231	-0.91184394	3.310387091	3.538E-05	0.00016376	0.05155	-1	186	172	189	200	207	169	202	87	122	138
ENSMUSG00000026577	chr1	Blzf1	1.6E+08	1.6E+08	5336	-0.72353929	4.242042174	3.549E-05	0.000164208	0.03327	-1	370	246	495	331	343	341	354	217	287	279
ENSMUSG00000102573	chr9	RP23-296I6.8	7.3E+07	7.3E+07	3502	-3.26090413	2.722283474	3.555E-05	0.000164467	0.59745	-1	191	140	279	189	95	17	111	3	2	3
ENSMUSG00000103627	chr6	IFFO1	1.3E+08	1.3E+08	1680	0.889539438	3.188632392	3.588E-05	0.000165942	0.04675	1	91	91	92	79	114	278	243	183	255	248
ENSMUSG00000089715	chr15	Cbx6	8E+07	8E+07	6290	0.792028846	5.342933421	3.592E-05	0.000166036	0.04194	1	408	324	457	405	662	1345	823	765	1321	1079
ENSMUSG00000028282	chr4	Casp8ap2	3.3E+07	3.3E+07	6826	-1.078875	2.579276434	3.621E-05	0.000167333	0.07017	-1	134	85	162	126	98	86	126	45	71	71
ENSMUSG00000070003	chr8	Ssbp4	7.1E+07	7.1E+07	1474	0.870912993	4.019862861	3.622E-05	0.000167348	0.049	1	103	104	280	163	244	559	423	279	501	418
ENSMUSG00000033386	chr3	Frrs1	1.2E+08	1.2E+08	2396	1.254728902	1.203739508	3.627E-05	0.000167523	0.07569	1	14	14	26	14	30	81	49	49	57	80
ENSMUSG00000038679	chr15	Trps1	5.1E+07	5.1E+07	13380	-0.84371683	3.198573524	3.637E-05	0.00016791	0.04299	-1	182	121	204	185	194	156	179	87	119	141
ENSMUSG00000022150	chr15	Dab2	6299788	6299899	7342	1.112281517	5.421652785	3.649E-05	0.00016842	0.08318	1	355	353	271	300	755	2156	1146	887	1014	958
ENSMUSG00000059355	chr8	Wdr83os	8.5E+07	8.5E+07	1031	0.76865678	5.25591402	3.663E-05	0.000169014	0.03948	1	367	292	443	419	634	1022	868	688	1260	1137
ENSMUSG00000022436	chr15	Sh3bp1	7.9E+07	7.9E+07	4649	1.091728153	3.014809609	3.683E-05	0.000169864	0.07418	1	58	42	93	56	150	277	169	159	262	257
ENSMUSG00000020744	chr11	Slc25a19	1.2E+08	1.2E+08	4026	-0.81966635	5.648907817	3.686E-05	0.000169948	0.0455	-1	805	587	1200	775	1631	792	888	494	853	752
ENSMUSG00000061273	chrX	Mmgt1	5.7E+07	5.7E+07	4234	-0.75443168	5.580620293	3.716E-05	0.000171269	0.03847	-1	884	709	1054	949	902	798	979	555	708	650
ENSMUSG00000059839	chr13	Zfp874b	6.7E+07	6.7E+07	3743	-0.83295408	3.831270482	3.749E-05	0.00017275	0.04398	-1	307	227	321	236	261	205	249	179	177	236
ENSMUSG00000024429	chr17	Gnl1	3.6E+07	3.6E+07	3077	0.707631017	5.544715274	3.756E-05	0.000173019	0.0337	1	451	363	654	523	723	1253	1194	898	1354	1272
ENSMUSG00000021596	chr13	Mctp1	7.6E+07	7.6E+07	8193	1.441870992	0.598813508	3.76E-05	0.000173145	0.08875	1	5	8	9	15	19	56	45	27	41	41
ENSMUSG00000099858	chr1	Gm6652	1.5E+08	1.5E+08	1070	-1.54541413	0.2217751	3.77E-05	0.000173537	0.1041	-1	25	18	33	27	20	11	23	6	10	8
ENSMUSG00000073418	chr17	C4b	3.5E+07	3.5E+07	5695	2.196452037	7.109139094	3.78E-05	0.000173958	0.30769	1	354	514	182	198	2705	7372	4703	2731	4450	4777
ENSMUSG00000067653	chr1	Ankrd23	3.7E+07	3.7E+07	2697	-1.04004163	11.52455771	3.804E-05	0.000175011	0.07468	-1	64328	37321	87961	71945	39029	41725	57491	25537	36622	40446
ENSMUSG00000032279	chr9	Idh3a	5.5E+07	5.5E+07	2403	-0.94528365	9.196982113	3.806E-05	0.000175041	0.06187	-1	10632	6876	18182	13027	10921	7616	12195	5716	8172	8007
ENSMUSG00000024811	chr19	Tnks2	3.7E+07	3.7E+07	10406	-0.8781036	7.459293979	3.809E-05	0.000175118	0.05331	-1	3191	2465	4613	3983	2970	2664	3548	1761	2375	2576
ENSMUSG00000006498	chr10	Ptbp1	8E+07	8E+07	4740	0.906955664	4.940485131	3.822E-05	0.00017563	0.05522	1	236	227	329	249	606	1147	613	636	905	844
ENSMUSG00000022885	chr16	St6gal1	2.3E+07	2.3E+07	4916	0.991452753	3.48965359	3.825E-05	0.000175739	0.06238	1	82	78	107	84	224	343	306	234	311	334
ENSMUSG00000040111	chr9	Gramd1b	4E+07	4E+07	9721	0.787061946	3.684472793	3.837E-05	0.000176199	0.03857	1	131	81	187	136	187	394	316	217	390	366
ENSMUSG00000008398	chr10	Elk3	9.3E+07	9.3E+07	4550	0.800374142	4.807038904	3.846E-05	0.000176584	0.04277	1	210	182	428	287	487	900	599	633	741	771
ENSMUSG00000033102	chr13	Cdc14b	6.4E+07	6.4E+07	6083	-1.05939189	2.810257856	3.847E-05	0.000176584	0.0694	-1	151	118	191	115	130	127	136	45	76	95
ENSMUSG00000025212	chr19	Sfxn3	4.5E+07	4.5E+07	2966	0.886715547	4.842040437	3.858E-05	0.000177009	0.05221	1	307	313	242	206	401	897	739	541	790	887
ENSMUSG00000033379	chr4	Atp6v0b	1.2E+08	1.2E+08	2051	0.811674279	6.514529827	3.864E-05	0.000177211	0.0453	1	932	797	1055	920	1289	2874	1941	1734	2760	2774
ENSMUSG00000042737	chr3	Dpm3	8.9E+07	8.9E+07	919	0.97393059	3.297857085	3.867E-05	0.000177294	0.05898	1	90	70	94	86	159	339	185	205	337	264
ENSMUSG00000026411	chr1	Tmem9	1.4E+08	1.4E+08	2726	0.74871131	4.005595085	3.871E-05	0.000177433	0.03531	1	165	133	185	167	252	490	367	321	469	419
ENSMUSG00000052825	chr8	Gm9892	5.2E+07	5.2E+07	992	-1.07210777	3.142522678	3.878E-05	0.000177715	0.07245	-1	181	189	161	157	177	138	172	92	102	83
ENSMUSG00000058927	chr19	Gm10053	2.5E+07	2.5E+07	949	-1.01485336	4.324566233	3.886E-05	0.000178015	0.06856	-1	347	217	733	465	319	329	442	170	218	233
ENSMUSG00000020561	chr12	Twistnb	3.3E+07	3.3E+07	2324	-0.91453718	3.301561485	3.898E-05	0.000178519	0.05239	-1	190	164	232	203	163	150	201	103	128	123
ENSMUSG00000027598	chr2	Itch	1.6E+08	1.6E+08	9709	-0.75026963	4.730502014	3.9E-05	0.000178549	0.03738	-1	504	420	573	477	504	497	566	273	320	413
ENSMUSG00000030468	chr7	Siglecg	4.3E+07	4.3E+07	4806	2.705988015	-0.24883564	3.904E-05	0.000178667	0.32459	1	0	2	0	1	11	52	9	22	17	26
ENSMUSG00000029538	chr5	Srsf9	1.2E+08	1.2E+08	1360	0.893075757	3.922307391	3.92E-05	0.000179327	0.05151	1	131	123	173	121	256	518	288	363	409	428
ENSMUSG00000020019	chr10	Ntn4	9.4E+07	9.4E+07	3741	0.860409973	4.66492754	3.931E-05	0.000179699	0.04968	1	201	116	459	284	366	833	735	545	537	724
ENSMUSG00000026341	chr1	Actr3	1.3E+08	1.3E+08	4631	0.74307613	5.957315675	3.932E-05	0.000179699	0.03776	1	575	491	854	635	1011	2030	1647	1249	1483	1653
ENSMUSG00000089832	chr7	Shkbp1	2.7E+07	2.7E+07	4230	1.156318255	2.837448448	3.93E-05	0.000179699	0.08381	1	41	35	82	47	139	234	182	158	240	185
ENSMUSG00000030986	chr7	Dhx32	1.3E+08	1.3E+08	4173	-0.84893452	5.325116879	3.937E-05	0.000179849	0.04895	-1	640	582	1126	846	716	606	938	412	513	510
ENSMUSG00000045691	chr14	Thtpa	5.5E+07	5.5E+07	5967	-0.70697476	4.776569505	3.958E-05	0.00018076	0.03303	-1	464	396	669	523	508	434	571	313	438	398
ENSMUSG00000079197	chr14	Psme2	5.6E+07	5.6E+07	1764	0.843356891	5.294653778	3.971E-05	0.000181323	0.04825	1	373	276	477	348	690	1592	766	818	986	1075
ENSMUSG00000001098	chr5	Kctd10	1.1E+08	1.1E+08	4046	0.755717404	5.180536991	3.981E-05	0.000181711	0.03847	1	296	273	448	389	672	1202	899	652	1016	971

ENSMUSG00000029434	chr5	Vps33a	1.2E+08	1.2E+08	4107	-0.76380073	5.80659019	3.988E-05	0.000181946	0.03995	-1	1053	822	1216	1154	1022	918	1122	608	864	799
ENSMUSG00000022456	chr15	Sept3	8.2E+07	8.2E+07	4971	1.844002097	0.341435006	4.025E-05	0.000183571	0.15951	1	13	2	6	4	12	65	25	23	22	50
ENSMUSG00000099913	chr1	Gm28551	5.3E+07	5.3E+07	3142	-0.82847942	6.427350025	4.113E-05	0.000187543	0.04759	-1	1650	1114	2266	1833	1494	1414	1743	832	1278	1217
ENSMUSG00000024835	chr19	Coro1b	4148619	4148722	2372	1.040965549	5.314655578	4.126E-05	0.000188029	0.07408	1	304	233	355	262	887	1414	980	785	1177	1209
ENSMUSG00000032254	chr9	Kif23	6.2E+07	6.2E+07	3423	1.744374302	-0.06036957	4.125E-05	0.000188029	0.11373	1	7	5	6	5	5	36	14	29	28	22
ENSMUSG00000028992	chr4	Nmnat1	1.5E+08	1.5E+08	3037	-0.89405484	4.495063524	4.149E-05	0.000188995	0.05351	-1	378	261	656	612	329	336	425	238	288	346
ENSMUSG00000037563	chr7	Rps16	2.8E+07	2.8E+07	807	0.871072603	7.129492022	4.152E-05	0.00018908	0.05283	1	1250	1217	1452	1504	2018	4252	2860	2867	4483	4227
ENSMUSG00000031592	chr8	Pcm1	4.1E+07	4.1E+07	8380	-0.92090712	6.048406006	4.163E-05	0.000189523	0.05864	-1	1274	1325	1372	1317	1001	1014	1280	685	847	928
ENSMUSG00000026709	chr1	Dars2	1.6E+08	1.6E+08	5195	-0.83474963	3.921772318	4.178E-05	0.000190126	0.0453	-1	298	170	438	304	277	275	313	145	212	192
ENSMUSG00000079019	chr8	Insl3	7.2E+07	7.2E+07	623	2.035784124	0.433805282	4.179E-05	0.000190126	0.21154	1	7	4	3	3	19	41	17	22	57	64
ENSMUSG00000059325	chr5	Hopx	7.7E+07	7.7E+07	1516	1.17564253	2.108070433	4.186E-05	0.000190362	0.08083	1	26	27	55	24	67	142	89	90	148	129
ENSMUSG00000048000	chr1	Gigyf2	8.7E+07	8.7E+07	14216	-0.71164173	5.107916422	4.217E-05	0.000191726	0.03421	-1	656	465	778	729	585	613	679	379	488	561
ENSMUSG00000027953	chr3	Slc50a1	8.9E+07	8.9E+07	1466	0.954765312	4.020920212	4.221E-05	0.000191862	0.06034	1	145	97	162	130	319	565	334	317	446	549
ENSMUSG00000047368	chr19	Abhd17b	2.2E+07	2.2E+07	2475	-0.7755551	3.858723709	4.242E-05	0.000192734	0.03846	-1	248	221	348	276	279	221	290	181	194	211
ENSMUSG00000103661	chr1	ANKRD23	3.7E+07	3.7E+07	2327	-1.03068859	11.49609416	4.249E-05	0.000192987	0.07429	-1	63069	36603	85720	70353	38238	41140	56403	25195	36081	39904
ENSMUSG00000027364	chr2	Usp50	1.3E+08	1.3E+08	3093	1.201214161	1.750984385	4.251E-05	0.000193002	0.08113	1	35	10	34	33	39	87	81	86	106	98
ENSMUSG00000027406	chr2	Idh3b	1.3E+08	1.3E+08	3422	-0.9523234	8.92405795	4.256E-05	0.000193186	0.06355	-1	9262	5947	14810	11178	7857	6758	9936	4730	6792	6237
ENSMUSG00000091661	chr9	Gm17021	1.2E+08	1.2E+08	462	-1.03913959	3.719223926	4.269E-05	0.00019372	0.07108	-1	262	170	431	285	201	183	304	116	128	167
ENSMUSG00000021127	chr12	Zfp36l1	8E+07	8E+07	2984	0.763542732	5.341673985	4.281E-05	0.000194177	0.03976	1	470	304	489	334	701	1325	1096	812	946	1107
ENSMUSG00000003660	chr2	Snrnp200	1.3E+08	1.3E+08	7819	-0.82370503	6.240139387	4.288E-05	0.000194446	0.04716	-1	1317	908	2036	1784	1334	1272	1447	794	1137	1033
ENSMUSG00000020133	chr10	2310011J03Rik	8E+07	8E+07	1649	0.75414075	4.224171971	4.289E-05	0.000194446	0.0371	1	201	128	236	192	306	638	394	380	509	496
ENSMUSG00000022180	chr14	Slc7a8	5.5E+07	5.5E+07	4033	0.822917148	3.616146879	4.353E-05	0.000197291	0.04305	1	124	74	163	126	191	409	277	266	362	287
ENSMUSG00000041707	chr14	1810011H11Rik	3.3E+07	3.3E+07	1473	1.987114178	-0.0630689	4.356E-05	0.000197353	0.16984	1	2	4	2	2	15	43	23	25	18	26
ENSMUSG00000029234	chr5	Tmem165	7.6E+07	7.6E+07	2588	0.726869232	4.265457725	4.367E-05	0.00019776	0.03435	1	180	155	235	207	323	610	458	413	490	487
ENSMUSG00000062093	chr14	Gm10110	9E+07	9E+07	2169	-0.83858153	3.808811346	4.374E-05	0.000198047	0.04534	-1	223	170	459	262	273	218	269	154	215	181
ENSMUSG00000049562	chr19	Ap5b1	5568074	5568607	3092	1.159718224	2.726311651	4.386E-05	0.00019852	0.08476	1	41	28	68	58	121	204	157	136	262	166
ENSMUSG00000038456	chr6	Dennd2a	3.9E+07	3.9E+07	5429	1.002014886	3.047027653	4.403E-05	0.000199225	0.06282	1	81	58	71	59	144	288	193	176	241	225
ENSMUSG00000021242	chr12	Npc2	8.5E+07	8.5E+07	3261	1.267665486	6.913162178	4.408E-05	0.000199372	0.11103	1	917	659	704	647	2601	4250	2844	2427	4225	3969
ENSMUSG00000028364	chr4	Tnc	6.4E+07	6.4E+07	7772	0.94078586	4.66393096	4.425E-05	0.000200098	0.05976	1	208	244	254	220	365	1218	512	585	546	599
ENSMUSG00000044258	chr13	Ctla2a	6.1E+07	6.1E+07	1373	1.05210432	3.599839869	4.441E-05	0.000200758	0.07332	1	78	49	222	106	171	502	294	283	300	300
ENSMUSG00000067424	chr17	Zfp563	3.3E+07	3.3E+07	2198	-1.57688399	0.615912504	4.446E-05	0.00020092	0.12982	-1	35	36	32	31	27	29	21	5	15	9
ENSMUSG00000029804	chr6	Herc3	5.9E+07	5.9E+07	7027	-0.87196612	5.700914697	4.465E-05	0.000201708	0.05272	-1	842	598	1655	1142	972	766	1138	549	654	710
ENSMUSG00000003184	chr7	Irf3	4.5E+07	4.5E+07	3187	0.797245545	4.517784683	4.467E-05	0.000201729	0.0426	1	220	153	277	217	423	718	495	408	693	699
ENSMUSG00000006014	chr1	Prg4	1.5E+08	1.5E+08	4280	1.880169142	5.627462794	4.469E-05	0.000201742	0.23501	1	183	72	797	262	446	4012	2073	889	506	978
ENSMUSG00000041297	chr13	Cdk13	1.8E+07	1.8E+07	7081	-0.76894467	4.195910177	4.476E-05	0.000201976	0.03891	-1	349	260	450	368	304	343	338	222	220	278
ENSMUSG00000079083	chr9	Jrkl	1.3E+07	1.3E+07	2952	-1.04147359	1.871311651	4.493E-05	0.000202716	0.06016	-1	70	61	98	57	79	56	65	31	42	51
ENSMUSG00000049550	chr5	Clip1	1.2E+08	1.2E+08	9801	-0.8698572	7.906377055	4.513E-05	0.000203532	0.05342	-1	4455	3389	6550	5100	3959	3833	4792	2487	3015	3556
ENSMUSG00000020280	chr11	Pus10	2.4E+07	2.4E+07	4325	-0.97605166	3.394737879	4.527E-05	0.000204092	0.06148	-1	191	148	315	219	182	153	227	120	111	117
ENSMUSG00000025812	chr8	Pard3	1.3E+08	1.3E+08	14506	-0.75156974	5.010373599	4.556E-05	0.000205357	0.0385	-1	594	427	907	618	523	507	671	339	484	495
ENSMUSG00000023021	chr15	Cers5	1E+08	1E+08	3542	1.00807402	3.766601539	4.59E-05	0.000206815	0.06727	1	101	85	137	98	278	538	314	287	351	385
ENSMUSG00000006301	chr1	Tmbim1	7.4E+07	7.4E+07	12659	0.772455168	6.550125292	4.634E-05	0.000208719	0.04194	1	1002	714	1113	945	1506	2878	2362	1992	2400	2559
ENSMUSG00000010095	chr19	Slc3a2	8706882	8708094	2958	0.769514764	5.876245066	4.638E-05	0.00020873	0.04123	1	548	476	754	619	914	1638	1272	1132	1892	1704
ENSMUSG00000059588	chr2	Calcrl	8.4E+07	8.4E+07	4882	-0.93472208	3.373649912	4.636E-05	0.00020873	0.05634	-1	216	134	270	209	199	136	220	81	127	178
ENSMUSG00000079509	chrX	Zfx	9.4E+07	9.4E+07	7755	-0.73912027	4.173709925	4.639E-05	0.00020873	0.03586	-1	330	263	380	383	326	327	312	223	230	302
ENSMUSG00000017144	chr2	Rnd3	5.1E+07	5.1E+07	4432	0.838903769	3.223698044	4.641E-05	0.000208761	0.04324	1	81	73	107	93	150	292	257	197	215	261
ENSMUSG00000079442	chr2	St6galnac4	3.3E+07	3.3E+07	6482	0.740620327	4.897963053	4.648E-05	0.000209034	0.03727	1	262	193	484	430	347	817	768	586	837	832
ENSMUSG00000042938	chr2	Gm14117	1.5E+08	1.5E+08	843	-1.60501398	1.206718964	4.654E-05	0.000209227	0.1468	-1	48	27	91	59	36	23	48	17	15	12
ENSMUSG00000022022	chr14	Mtrf1	7.9E+07	7.9E+07	1862	-0.81058753	3.484787081	4.666E-05	0.000209703	0.0417	-1	194	178	256	219	215	197	218	111	168	150
ENSMUSG00000000711	chr10	Rab5b	1.3E+08	1.3E+08	3166	-0.81180679	6.866840726	4.686E-05	0.000210518	0.04656	-1	2350	1666	2683	2276	2198	1913	2397	1198	1624	1706
ENSMUSG00000051367	chr12	Six1	7.3E+07	7.3E+07	4383	-0.80426736	6.339283763	4.718E-05	0.000211914	0.04551	-1	1304	1219	1899	1819	1492	1154	1449	919	1168	1398
ENSMUSG00000062980	chr6	Cped1	2.2E+07	2.2E+07	8279	-0.80481721	4.895054414	4.728E-05	0.000212273	0.04452	-1	588	513	585	471	645	649	579	266	348	447
ENSMUSG00000009418	chr1	Nav1	1.4E+08	1.4E+08	17303	0.861025188	4.440099761	4.74E-05	0.000212729	0.0499	1	156	195	200	224	385	752	511	453	527	644
ENSMUSG00000031403	chrX	Dkc1	7.5E+07	7.5E+07	4121	-0.74512464	4.61343793	4.746E-05	0.000212966	0.03748	-1	477	400	506	469	410	407	480	291	373	337
ENSMUSG00000026558	chr1	Uck2	1.7E+08	1.7E+08	5464	0.825848116	4.715245778	4.756E-05	0.000213315	0.04666	1	241	154	452	266	364	889	565	716	618	614
ENSMUSG00000049739	chr7	Zfp646	1.3E+08	1.3E+08	6727	-0.78912857	3.805398832	4.762E-05	0.000213488	0.04049	-1	233	194	359	298	252	222	273	128	219	225
ENSMUSG00000093661	chr6	Eif4e3	1E+08	1E+08	2515	-0.83056496	5.236623718	4.763E-05	0.000213488	0.04786	-1	826	501	723	624	975	694	847	311	532	482
ENSMUSG00000024516	chr18	Sec11c	6.6E+07	6.6E+07	3084	0.750026986	4.59061794	4.771E-05	0.000213809	0.03751	1	259	230	241	249	355	849	550	464	580	688
ENSMUSG00000059159	chr6	Gm8129	5.2E+07	5.2E+07	213	1.411073835	1.404020617	4.775E-05	0.000213912	0.1114	1	18	12	9	23	42	82	70	49	83	94
ENSMUSG00000049321	chr11	Zfp2	5.1E+07	5.1E+07	4019	-0.93867699	2.58790792	4.79E-05	0.000214489	0.05237	-1	126	80	145	117	124	91	120	62	76	74
ENSMUSG00000044461	chr14	Shisa2	6E+07	6E+07	3144	-0.89319559	6.425085334	4.792E-05	0.000214546	0.05625	-1	1800	1319	1879	1701	1634	1189	1968	921	1119	1038
ENSMUSG00000057219	chr11	Armc7	1.2E+08	1.2E+08	3069	1.162218418	1.879607909	4.81E-05	0.000215284	0.07613	1	30	22	27	34	53	119	72	83	98	132
ENSMUSG00000019936	chr10	Epyc	9.8E+07	9.8E+07	2561	3.199543109	-0.12520038	4.819E-05	0.000215599	0.49036	1	2	0	1	8	0	2	38	34	40	24
ENSMUSG00000032560	chr9	Dnajc13	1E+08	1E+08	11938	-0.72846574	5.247668971	4.828E-05	0.000215943	0.03662	-1	648	518	966	783	669	696	791	433	519	535
ENSMUSG00000032540	chr9	Abhd5	1.2E+08	1.2E+08	3618	-0.72467854	5.493867087	4.845E-05	0.000216608	0.03643	-1	759	470	1224	886	1018	806	861	495	691	683
ENSMUSG00000034075	chr2	Zdhhc5	8.5E+07	8.5E+07	5047	-0.89349849	6.550697843	4.864E-05	0.000217422	0.05643	-1	1500	1090	2897	2220	1707	1347	1947	937	1295	1300
ENSMUSG00000026986	chr2	Hnmt	2.4E+07	2.4E+07	1769	-1.00792926	2.464518473	4.885E-05	0.00021829	0.0615	-1	110	79	113	92	160	100	101	44	77	59
ENSMUSG00000021636	chr13	Marveld2	1E+08	1E+08	3382	1.637842255	0.026933626	4.892E-05	0.000218538	0.10574	1	5	3	5	14	5	31	26	25	29	26

ENSMUSG00000026743	chr2	Mllt10	1.8E+07	1.8E+07	5907	-0.77698395	3.778943979	4.926E-05	0.000219986	0.03901	-1	247	214	313	258	260	203	254	174	215	188
ENSMUSG00000037679	chr12	Inf2	1.1E+08	1.1E+08	4600	0.911210533	4.211002984	4.929E-05	0.000220034	0.05615	1	155	132	186	141	374	642	430	379	475	568
ENSMUSG00000069895	chr8	Atxn1l	1.1E+08	1.1E+08	7526	-0.73032575	4.537788863	4.935E-05	0.000220239	0.03604	-1	427	309	516	403	544	400	522	206	338	367
ENSMUSG00000061848	chr15	Gm5805	8.2E+07	8.2E+07	456	1.336863911	2.512248804	4.939E-05	0.000220343	0.11258	1	49	30	26	48	86	119	134	108	234	225
ENSMUSG00000006673	chr9	Qrich1	1.1E+08	1.1E+08	7728	-0.74138167	5.181787068	4.947E-05	0.000220627	0.03804	-1	612	496	901	744	686	667	815	366	476	521
ENSMUSG00000025940	chr1	Tmem70	1.7E+07	1.7E+07	1820	-0.75483233	5.694860118	4.952E-05	0.00022078	0.03988	-1	920	677	1408	1077	857	923	889	639	714	818
ENSMUSG00000042712	chrX	Wbp5	1.4E+08	1.4E+08	1037	0.698291124	4.626605711	4.98E-05	0.000221975	0.03256	1	313	201	274	274	349	842	574	473	612	664
ENSMUSG00000023951	chr17	Vegfa	4.6E+07	4.6E+07	4293	-1.02769993	6.98276142	4.987E-05	0.000222208	0.0748	-1	1831	1301	4603	3189	2409	1707	2553	1018	1547	1908
ENSMUSG00000025920	chr1	Stau2	1.6E+07	1.6E+07	6747	-0.85370716	6.038594601	4.998E-05	0.000222607	0.05147	-1	1317	824	1593	1607	1042	1139	1303	653	853	949
ENSMUSG00000039000	chr5	Ube3c	3E+07	3E+07	5033	-0.80820621	6.082129012	5.006E-05	0.000222921	0.04614	-1	1149	1051	1644	1477	1130	1055	1305	761	1041	937
ENSMUSG00000033009	chr8	Ogfod1	9.4E+07	9.4E+07	5846	-0.77709266	5.018198053	5.025E-05	0.000223677	0.04174	-1	606	474	775	711	489	499	675	369	456	471
ENSMUSG00000023094	chr2	Msrb2	1.9E+07	1.9E+07	1377	-0.76472973	4.432368381	5.036E-05	0.000224075	0.03946	-1	385	234	666	415	400	369	426	219	329	323
ENSMUSG00000029725	chr5	Ppp1r35	1.4E+08	1.4E+08	1085	1.098859953	2.612530644	5.038E-05	0.000224123	0.07476	1	38	44	57	64	86	187	116	110	235	198
ENSMUSG00000034059	chr2	Ypel4	8.5E+07	8.5E+07	2614	1.705211495	0.408825428	5.081E-05	0.000225946	0.13278	1	9	8	4	6	14	58	28	20	27	58
ENSMUSG00000005505	chr2	Kbtbd4	9.1E+07	9.1E+07	3139	-0.72994978	4.374472819	5.102E-05	0.000226813	0.03575	-1	370	273	518	419	377	336	425	224	352	280
ENSMUSG00000034707	chr10	Gns	1.2E+08	1.2E+08	3855	0.75108046	6.346260326	5.105E-05	0.00022688	0.04	1	874	607	995	873	1282	2553	2005	1520	2263	2263
ENSMUSG00000047281	chr4	Sfn	1.3E+08	1.3E+08	1613	1.761378726	0.450637066	5.108E-05	0.000226959	0.15745	1	6	4	12	6	15	27	82	17	40	32
ENSMUSG00000020649	chr12	Rrm2	2.5E+07	2.5E+07	2771	1.379386054	1.192280758	5.141E-05	0.000228311	0.10384	1	14	8	39	17	15	88	47	58	54	72
ENSMUSG00000018923	chr11	Med11	7E+07	7E+07	1046	1.016720716	2.391438829	5.144E-05	0.000228379	0.06135	1	51	34	54	42	77	188	111	115	168	125
ENSMUSG00000021902	chr14	Phf7	3.1E+07	3.1E+07	1984	-0.83791387	2.87177846	5.165E-05	0.000229261	0.04239	-1	126	104	164	131	182	137	115	73	104	114
ENSMUSG00000037278	chr11	Tmem97	7.9E+07	7.9E+07	1375	1.11428706	2.24645274	5.181E-05	0.000229893	0.07417	1	32	31	43	41	76	172	89	113	128	147
ENSMUSG00000068245	chr14	Phf11d	5.9E+07	5.9E+07	4498	1.108291555	1.91468652	5.2E-05	0.000230646	0.06878	1	30	28	35	29	52	167	101	61	102	93
ENSMUSG00000029221	chr5	Slc30a9	6.7E+07	6.7E+07	9861	-0.81466342	6.741938418	5.211E-05	0.000231069	0.04742	-1	2011	1497	2571	2349	1838	1655	2119	1121	1535	1640
ENSMUSG00000022485	chr15	Hoxc5	1E+08	1E+08	3089	-0.79262134	4.407805613	5.214E-05	0.000231124	0.04273	-1	384	279	574	293	539	356	469	210	278	308
ENSMUSG00000025432	chr10	Avil	1.3E+08	1.3E+08	3398	-1.23442432	1.589718299	5.235E-05	0.000232008	0.08807	-1	65	58	68	47	70	42	57	19	23	44
ENSMUSG00000020171	chr10	Yeats4	1.2E+08	1.2E+08	1407	0.738945107	4.045704241	5.242E-05	0.000232246	0.03597	1	165	115	217	194	252	519	354	328	490	431
ENSMUSG00000052852	chr6	Reep1	7.2E+07	7.2E+07	3924	-0.80920123	6.739882149	5.259E-05	0.000232927	0.04683	-1	2039	1762	2213	1868	2250	1507	2066	1203	1662	1586
ENSMUSG00000038485	chr11	Socs7	9.7E+07	9.7E+07	7265	-0.88352668	6.438735204	5.266E-05	0.000233031	0.05568	-1	1550	1431	2020	1925	1433	1224	1855	808	1303	1174
ENSMUSG00000042804	chr4	Gpr153	1.5E+08	1.5E+08	3909	0.945415128	3.378877929	5.267E-05	0.000233031	0.05883	1	72	59	138	97	185	393	258	233	286	231
ENSMUSG00000058355	chr8	Abce1	8E+07	8E+07	3813	-0.8206713	5.999103312	5.266E-05	0.000233031	0.04782	-1	1218	1052	1397	1329	1047	1147	1184	788	788	874
ENSMUSG00000024241	chr17	Sos1	8E+07	8E+07	8919	-0.7186825	4.605466252	5.289E-05	0.000233957	0.03511	-1	428	298	649	500	431	380	492	271	407	354
ENSMUSG00000038274	chr19	Fau	6057888	6058001	815	0.855115534	7.217479146	5.312E-05	0.000234906	0.05244	1	1452	1157	1526	1538	2373	4720	3152	2926	4663	4402
ENSMUSG00000006456	chr19	Rbm14	4800569	4801805	3910	0.837444104	3.607330141	5.341E-05	0.000236047	0.04565	1	106	86	129	142	199	393	262	254	363	326
ENSMUSG00000083325	chr2	Gm14121	1.5E+08	1.5E+08	1380	-1.6452771	0.622608212	5.342E-05	0.000236047	0.14737	-1	29	14	70	41	20	13	21	6	20	14
ENSMUSG00000071226	chr6	Cecr2	1.2E+08	1.2E+08	13306	-0.97816699	3.755472288	5.376E-05	0.000237499	0.06434	-1	239	162	403	318	248	142	291	143	141	216
ENSMUSG00000024059	chr17	Clip4	7.2E+07	7.2E+07	4055	-1.25474123	6.589481097	5.391E-05	0.000238084	0.1113	-1	1915	1030	3967	2420	1244	1112	2207	668	853	1149
ENSMUSG00000031631	chr8	Cfap97	4.6E+07	4.6E+07	5157	-0.81946269	3.979548331	5.404E-05	0.000238601	0.04518	-1	335	235	390	300	239	257	302	156	206	265
ENSMUSG00000032030	chr9	Cul5	5.4E+07	5.4E+07	8165	-0.83885447	6.447240167	5.412E-05	0.000238837	0.05036	-1	1824	1337	1996	1730	1445	1353	1752	1025	1147	1190
ENSMUSG00000037606	chr7	Osbpl5	1.4E+08	1.4E+08	4915	0.674715709	4.728560013	5.438E-05	0.000239937	0.03087	1	271	231	332	278	433	720	622	559	719	715
ENSMUSG00000085438	chr2	1700020I14Rik	1.2E+08	1.2E+08	8306	-0.95629633	9.316500435	5.459E-05	0.000240789	0.06596	-1	13221	8635	18564	14170	9075	8935	12707	6368	8107	8979
ENSMUSG00000051721	chr12	BC068281	4843303	4843451	3131	-1.05594433	1.69050473	5.462E-05	0.000240844	0.06169	-1	61	51	91	62	57	48	55	26	44	41
ENSMUSG00000037418	chr19	Best1	9985174	9985422	2152	1.606665994	0.035579332	5.499E-05	0.00024237	0.10125	1	4	6	7	5	11	37	22	20	19	41
ENSMUSG00000003573	chr8	Homer3	7E+07	7E+07	3440	0.969519051	3.144858456	5.507E-05	0.00024267	0.06028	1	85	71	78	62	150	271	234	162	288	244
ENSMUSG00000028273	chr3	Pdlim5	1.4E+08	1.4E+08	6448	-1.07652694	8.92214028	5.509E-05	0.00024267	0.08321	-1	7327	7100	14951	12796	7905	6295	10474	3813	4570	7650
ENSMUSG00000020444	chr11	Guk1	5.9E+07	5.9E+07	1835	0.716688666	5.521623035	5.532E-05	0.000243602	0.03616	1	392	386	638	511	728	1394	1065	878	1294	1278
ENSMUSG00000028645	chr4	Slc2a1	1.2E+08	1.2E+08	2853	0.776249206	3.503222706	5.582E-05	0.000245732	0.03821	1	124	81	141	146	134	322	337	208	280	324
ENSMUSG00000032327	chr9	Stra6	5.8E+07	5.8E+07	5829	1.968379216	0.589617785	5.6E-05	0.000246412	0.20984	1	9	0	11	19	3	46	41	26	45	67
ENSMUSG00000038354	chr3	Ankrd35	9.7E+07	9.7E+07	3688	1.510257805	0.427545392	5.601E-05	0.000246412	0.10011	1	16	4	6	8	13	50	32	29	34	40
ENSMUSG00000033880	chr11	Lgals3bp	1.2E+08	1.2E+08	2847	1.23475854	5.320066613	5.608E-05	0.000246654	0.10745	1	277	246	267	208	853	1613	902	684	1689	990
ENSMUSG00000029422	chr5	Rsrc2	1.2E+08	1.2E+08	8172	-0.74240136	5.315749721	5.624E-05	0.000247282	0.03883	-1	813	574	925	735	683	728	776	506	520	548
ENSMUSG00000038871	chr6	Bpgm	3.4E+07	3.4E+07	3588	-0.85029507	6.704552181	5.63E-05	0.000247485	0.0521	-1	2210	1844	1957	1855	1983	1498	1935	1135	1612	1520
ENSMUSG00000037905	chr5	Bri3bp	1.3E+08	1.3E+08	6975	0.865588653	3.035043501	5.634E-05	0.00024757	0.04676	1	86	54	108	89	99	232	175	184	240	237
ENSMUSG00000031907	chr8	Zfp90	1.1E+08	1.1E+08	2632	1.26520697	1.945312691	5.658E-05	0.000248521	0.09411	1	34	35	31	17	44	165	92	86	77	125
ENSMUSG00000025871	chr13	4833439L19Rik	5.5E+07	5.5E+07	3187	-0.82034783	7.83789715	5.666E-05	0.000248825	0.04884	-1	4256	3453	5480	4475	4279	3397	4615	2478	3485	3187
ENSMUSG00000022708	chr16	Zbtb20	4.3E+07	4.3E+07	30730	-0.82103395	6.531543154	5.678E-05	0.000249254	0.04857	-1	1875	1391	2105	1834	1616	1374	1566	919	1291	1809
ENSMUSG00000041859	chr1	Mcm3	2.1E+07	2.1E+07	3752	0.996987277	2.779639251	5.68E-05	0.000249275	0.06208	1	68	49	59	66	97	286	155	148	191	153
ENSMUSG00000045098	chr19	Suv420h1	3767421	3767730	14116	-0.69383407	4.414756513	5.691E-05	0.000249676	0.03258	-1	370	279	501	446	394	401	417	255	292	323
ENSMUSG00000037568	chr1	Vash2	1.9E+08	1.9E+08	4314	1.557677602	1.829849528	5.693E-05	0.000249696	0.1522	1	16	14	32	7	69	127	116	80	98	106
ENSMUSG00000024959	chr19	Bad	6941861	6942440	2007	0.737394893	3.932128927	5.724E-05	0.00025098	0.03584	1	154	114	198	161	243	484	334	286	451	411
ENSMUSG00000054814	chr5	Usp46	7.4E+07	7.4E+07	5533	-0.73711958	3.754849011	5.763E-05	0.000252599	0.03549	-1	236	192	267	285	281	238	231	168	211	192
ENSMUSG00000027247	chr2	Arhgap1	9.2E+07	9.2E+07	4275	0.865547064	4.138026711	5.776E-05	0.000253109	0.05131	1	135	124	199	155	349	628	431	302	497	509
ENSMUSG00000102543	chr18	PCDHGC5	3.8E+07	3.8E+07	7627	1.093000849	6.027889271	5.778E-05	0.000253109	0.08533	1	518	482	445	462	1271	2335	1211	1482	2093	2036
ENSMUSG00000024442	chr18	0610009O20Rik	3.8E+07	3.8E+07	2404	-0.89632209	6.67860241	5.781E-05	0.000253159	0.05799	-1	1906	1328	3150	2225	1559	1456	2079	1102	1423	1356
ENSMUSG00000038102	chr8	Trappc11	4.7E+07	4.7E+07	6482	-0.75434781	5.013801963	5.784E-05	0.000253182	0.03998	-1	530	566	678	664	552	586	640	371	479	419
ENSMUSG00000041845	chr19	Rhod	4425459	4426256	1714	1.630664061	0.904613996	5.785E-05	0.000253182	0.14687	1	13	5	11	6	31	58	33	55	67	52
ENSMUSG00000028670	chr4	Lypla2	1.4E+08	1.4E+08	2054	0.785115652	5.414067295	5.795E-05	0.000253507	0.04374	1	405	291	471	506	728	1205	935	818	1384	1224
ENSMUSG00000048154	chr15	Kmt2d	9.9E+07	9.9E+07	19887	-0.68494243	5.518522473	5.805E-05	0.000253883	0.0332	-1	786	614	1058	952	858	803	752	563	763	749

ENSMUSG00000032802	chr2	Srxn1	1.5E+08	1.5E+08	2820	0.750988374	5.556619626	5.83E-05	0.000254908	0.04019	1	471	301	782	479	696	1590	1231	1072	1087	1095
ENSMUSG00000023994	chr17	Nfya	4.8E+07	4.8E+07	7315	0.801132748	3.360013241	5.834E-05	0.000254977	0.04046	1	97	90	115	121	132	332	246	184	276	304
ENSMUSG00000026051	chr1	1500015O10Rik	4.4E+07	4.4E+07	902	1.929434821	2.145681342	5.84E-05	0.000255185	0.23654	1	30	20	11	16	56	395	67	72	111	90
ENSMUSG00000101746	chr1	2310043L19Rik	1.8E+08	1.8E+08	698	1.750028379	-0.24601475	5.882E-05	0.000256915	0.11894	1	2	2	13	4	4	21	25	16	20	31
ENSMUSG00000085772	chr11	D630024D03Rik	3.2E+07	3.2E+07	1567	1.867504352	1.233288639	5.911E-05	0.000258104	0.21506	1	9	1	40	16	11	64	42	61	76	109
ENSMUSG00000022425	chr15	Enpp2	5.5E+07	5.5E+07	3473	-1.12060281	4.614635106	5.916E-05	0.000258248	0.08847	-1	425	268	629	240	1111	462	386	236	256	272
ENSMUSG00000028737	chr4	Aldh4a1	1.4E+08	1.4E+08	4907	-0.72120175	5.805012556	5.92E-05	0.000258339	0.03723	-1	1082	758	1139	1165	1076	917	987	670	940	845
ENSMUSG00000033790	chr7	Tubgcp5	5.6E+07	5.6E+07	3681	-0.9057731	3.401713016	5.924E-05	0.00025844	0.05429	-1	183	171	260	198	219	180	240	100	121	125
ENSMUSG00000022536	chr16	Glyr1	5013906	5015602	3348	-0.730081	5.772705147	5.928E-05	0.000258523	0.03817	-1	927	758	1193	1097	1181	979	1157	607	768	772
ENSMUSG00000099083	chr15	Atf7	1E+08	1E+08	10988	-0.73140303	5.634915565	5.965E-05	0.00026006	0.03826	-1	890	733	1143	1012	866	910	974	525	691	800
ENSMUSG00000002781	chr7	Tmem143	4.6E+07	4.6E+07	5636	-0.81979331	5.972349712	5.984E-05	0.000260758	0.0484	-1	992	709	1778	1411	1307	866	1187	624	1151	885
ENSMUSG00000021096	chr12	Ppm1a	7.3E+07	7.3E+07	2789	-0.84104002	7.546131547	5.984E-05	0.000260758	0.05158	-1	3425	2662	4781	3879	3375	2988	3974	1774	2669	2615
ENSMUSG00000000739	chr8	Sult5a1	1.2E+08	1.2E+08	1764	1.46420604	2.824738597	5.988E-05	0.000260827	0.13982	1	47	74	20	37	85	269	148	150	235	256
ENSMUSG00000030788	chr7	Rnf141	1.1E+08	1.1E+08	5861	-0.70963705	4.893363386	6.002E-05	0.000261366	0.03519	-1	654	437	544	511	591	527	532	378	431	456
ENSMUSG00000045071	chr4	E130308A19Rik	6E+07	6E+07	12617	-1.04909208	2.626230199	6.004E-05	0.000261366	0.07023	-1	104	106	112	123	173	74	133	52	71	85
ENSMUSG00000064344	chrMT	mt-Tm	3845	3913	69	-2.07547855	5.425844073	6.011E-05	0.000261575	0.29165	-1	844	308	2699	1277	484	214	1041	136	158	208
ENSMUSG00000021258	chr12	Ccnk	1.1E+08	1.1E+08	2627	-0.81182593	5.925637084	6.021E-05	0.000261933	0.04751	-1	999	817	1292	1413	1342	883	1228	523	1094	890
ENSMUSG00000048440	chr17	Cyp4f16	3.3E+07	3.3E+07	3017	1.418225774	2.096549912	6.025E-05	0.000261963	0.12598	1	26	32	27	17	68	178	66	94	138	148
ENSMUSG00000103332	chr18	Pcdhga2	3.8E+07	3.8E+07	4689	1.07942565	6.029680394	6.025E-05	0.000261963	0.08368	1	522	482	461	467	1273	2323	1205	1484	2092	2034
ENSMUSG00000059142	chr17	Zfp945	2.3E+07	2.3E+07	10173	-1.04301374	2.568401639	6.033E-05	0.000262204	0.06891	-1	139	92	144	125	88	102	69	64	61	101
ENSMUSG00000104346	chr18	PCDHGB6	3.8E+07	3.8E+07	4720	1.085246262	6.028962975	6.037E-05	0.000262323	0.08459	1	520	477	451	469	1279	2325	1213	1484	2091	2033
ENSMUSG00000102440	chr18	PCDHGA9	3.8E+07	3.8E+07	5586	1.084232379	6.027715344	6.063E-05	0.000263382	0.08447	1	521	481	451	467	1272	2328	1205	1481	2089	2034
ENSMUSG00000024012	chr17	Mtch1	2.9E+07	2.9E+07	2878	0.827408397	6.831450101	6.086E-05	0.000264262	0.04985	1	968	683	1652	1241	1881	3396	2678	2217	3279	3517
ENSMUSG00000028328	chr4	Tmod1	4.6E+07	4.6E+07	3946	-0.86069548	7.869433615	6.088E-05	0.000264288	0.05416	-1	5155	4059	4447	4018	4504	3729	4161	2685	3556	3045
ENSMUSG00000071653	chr19	1810009A15Rik	8888853	8888964	1444	0.793232347	3.687124329	6.096E-05	0.00026454	0.0414	1	131	100	166	118	198	434	264	250	351	381
ENSMUSG00000026173	chr1	Plcd4	7.5E+07	7.5E+07	7045	-1.08847833	6.007486249	6.14E-05	0.000266364	0.08536	-1	1556	1449	872	1020	1353	739	1164	583	1054	723
ENSMUSG00000059263	chr7	Usp47	1.1E+08	1.1E+08	5540	-0.8636196	8.55088486	6.143E-05	0.000266415	0.05467	-1	6985	5103	9408	8483	6612	5685	7837	3695	5425	5114
ENSMUSG00000027460	chr2	Angpt4	1.5E+08	1.5E+08	2335	1.872716832	1.224741406	6.192E-05	0.000268473	0.20594	1	8	17	7	9	28	113	28	48	117	52
ENSMUSG00000032112	chr9	Trappc4	4.4E+07	4.4E+07	1166	0.772525843	4.917393876	6.23E-05	0.000270048	0.04213	1	304	219	334	296	556	974	626	680	850	775
ENSMUSG00000024983	chr19	Vti1a	5.5E+07	5.5E+07	3405	-0.70435321	4.448127337	6.245E-05	0.000270582	0.03421	-1	429	309	465	429	387	405	428	232	307	357
ENSMUSG00000035401	chr7	2210018M11Rik	9.9E+07	9.9E+07	4005	-0.83219817	3.488919212	6.257E-05	0.000271018	0.04594	-1	217	155	308	219	183	174	214	108	166	175
ENSMUSG00000028926	chr5	Cdk14	4803391	4806731	15344	1.167319082	3.254340083	6.301E-05	0.000272786	0.09134	1	99	74	61	48	152	450	272	194	223	229
ENSMUSG00000102742	chr18	PCDHGB6	3.8E+07	3.8E+07	4756	1.088481857	6.024926651	6.299E-05	0.000272786	0.08551	1	516	481	447	460	1276	2322	1207	1481	2086	2031
ENSMUSG00000037730	chr3	Mynn	3.1E+07	3.1E+07	6764	-0.90324903	3.515480596	6.312E-05	0.000273082	0.05513	-1	243	170	301	216	183	205	226	105	117	179
ENSMUSG00000102748	chr18	Pcdhgb2	3.8E+07	3.8E+07	4882	1.077213319	6.042881411	6.312E-05	0.000273082	0.08381	1	525	486	467	473	1288	2355	1221	1490	2107	2049
ENSMUSG00000027086	chr2	Fastkd1	7E+07	7E+07	5853	-0.83253605	4.064183502	6.316E-05	0.000273165	0.0477	-1	315	186	539	334	274	306	319	176	225	225
ENSMUSG00000103897	chr18	PCDHGB6	3.8E+07	3.8E+07	4730	1.084051426	6.026494384	6.331E-05	0.000273749	0.08488	1	519	480	451	464	1277	2322	1206	1481	2086	2033
ENSMUSG00000041779	chr1	Tram2	2.1E+07	2.1E+07	6661	0.88720643	3.534623055	6.34E-05	0.00027405	0.05197	1	119	102	99	97	186	397	270	241	301	332
ENSMUSG00000036555	chr5	Iqce	1.4E+08	1.4E+08	12037	1.018162969	2.217493074	6.349E-05	0.000274324	0.06105	1	30	34	45	43	76	138	130	99	121	136
ENSMUSG00000022261	chr15	Sdc2	3.3E+07	3.3E+07	3322	0.94928017	5.295869326	6.36E-05	0.000274737	0.06452	1	446	349	271	300	618	1522	807	841	1065	1126
ENSMUSG00000050812	chr4	AI314180	5.9E+07	5.9E+07	11447	-0.85768745	8.156302751	6.376E-05	0.000275317	0.05413	-1	5403	4617	6674	5997	4646	4424	5696	3048	3956	3962
ENSMUSG00000004455	chr5	Ppp1cc	1.2E+08	1.2E+08	3424	-0.81073748	6.027944013	6.378E-05	0.000275346	0.04774	-1	1044	1015	1518	1550	1078	1079	1175	789	999	847
ENSMUSG00000010721	chr5	Lmbr1	2.9E+07	2.9E+07	4940	-0.90465971	3.680844071	6.383E-05	0.00027548	0.05575	-1	284	247	239	210	234	187	239	149	176	165
ENSMUSG00000021981	chr14	Cab39l	5.9E+07	5.9E+07	3037	-0.68071147	4.92688097	6.404E-05	0.000276276	0.03262	-1	591	439	605	494	682	601	607	337	479	412
ENSMUSG00000025816	chr2	Sec61a2	5870987	5872021	4572	-0.73039936	5.239653937	6.416E-05	0.000276716	0.03813	-1	739	640	727	678	686	606	726	442	560	603
ENSMUSG00000022893	chr16	Adamts1	8.6E+07	8.6E+07	5302	-0.70296523	4.97354976	6.446E-05	0.00027775	0.03487	-1	422	454	627	671	769	552	597	402	435	479
ENSMUSG00000026024	chr1	Als2	5.9E+07	5.9E+07	9496	-0.76669035	4.669785145	6.444E-05	0.00027775	0.0414	-1	510	365	628	487	411	451	552	276	374	307
ENSMUSG00000034602	chr10	Mon2	1.2E+08	1.2E+08	9303	-0.71636765	5.204025	6.444E-05	0.00027775	0.03664	-1	723	596	698	682	685	716	704	423	535	523
ENSMUSG00000102428	chr18	PCDHGA12	3.8E+07	3.8E+07	6664	1.083770262	6.030412852	6.455E-05	0.000278046	0.08504	1	523	481	449	468	1278	2329	1208	1486	2090	2039
ENSMUSG00000040502	chr10	March9	1.3E+08	1.3E+08	3037	1.602993404	0.917715705	6.46E-05	0.000278176	0.14926	1	5	2	24	17	21	45	52	32	75	68
ENSMUSG00000023036	chr18	Pcdhgc4	3.8E+07	3.8E+07	5596	1.088184424	6.027367027	6.462E-05	0.000278191	0.08573	1	519	481	447	460	1279	2324	1207	1482	2096	2033
ENSMUSG00000035476	chrX	Tab3	8.6E+07	8.6E+07	6639	-0.81853065	3.176954159	6.47E-05	0.000278473	0.04309	-1	162	132	238	167	168	158	171	93	128	127
ENSMUSG00000024083	chr17	Pja2	6.4E+07	6.4E+07	4740	-0.87356228	7.25302531	6.486E-05	0.000279045	0.05606	-1	2658	2185	3995	3567	2476	2345	3175	1546	2000	2160
ENSMUSG00000023913	chr17	Pla2g7	4.4E+07	4.4E+07	2905	-1.24827209	6.327942118	6.499E-05	0.00027947	0.11255	-1	1402	2445	944	1486	1545	936	1273	585	1010	1176
ENSMUSG00000024991	chr19	Eif3a	6.1E+07	6.1E+07	5176	-0.8723768	7.085118688	6.5E-05	0.00027947	0.05588	-1	2525	1906	3830	2703	2365	2288	2871	1480	1483	1868
ENSMUSG00000102222	chr18	Pcdhga10	3.8E+07	3.8E+07	4732	1.074414551	6.032372991	6.507E-05	0.000279709	0.08368	1	527	479	459	474	1281	2328	1209	1484	2087	2038
ENSMUSG00000005672	chr5	Kit	7.6E+07	7.6E+07	5831	1.348864665	2.216321158	6.529E-05	0.000280561	0.11576	1	32	29	28	30	74	244	74	101	111	148
ENSMUSG00000005871	chr18	Apc	3.4E+07	3.4E+07	15753	-0.74642155	5.46012538	6.549E-05	0.000281316	0.04015	-1	756	576	1090	954	805	696	947	464	634	680
ENSMUSG00000026810	chr2	Dpm2	3.3E+07	3.3E+07	1971	0.854040501	3.857610164	6.555E-05	0.000281353	0.04952	1	150	109	159	119	245	464	277	309	434	424
ENSMUSG00000047284	chr11	Neurl4	7E+07	7E+07	5889	-0.72728525	5.090072994	6.552E-05	0.000281353	0.03766	-1	519	425	952	717	641	526	730	365	549	493
ENSMUSG00000103472	chr18	Pcdhga7	3.8E+07	3.8E+07	5217	1.079434631	6.030900594	6.555E-05	0.000281353	0.08452	1	523	482	453	470	1279	2328	1209	1486	2091	2032
ENSMUSG00000021464	chr13	Ror2	5.3E+07	5.3E+07	4242	1.436629784	0.655952556	6.571E-05	0.000281932	0.09957	1	9	7	9	21	12	58	34	38	48	38
ENSMUSG00000022463	chr15	Srebf2	8.2E+07	8.2E+07	4989	0.66658361	5.11087631	6.575E-05	0.000281955	0.03142	1	342	256	421	460	558	1004	879	680	912	897
ENSMUSG00000033054	chr9	Npat	5.4E+07	5.4E+07	6248	-1.1921632	2.418420805	6.575E-05	0.000281955	0.09223	-1	141	77	139	114	79	76	113	44	41	63
ENSMUSG00000024645	chr18	Timm21	8.5E+07	8.5E+07	1315	-0.79907764	4.247093413	6.61E-05	0.000283358	0.04436	-1	373	205	585	372	319	341	358	214	235	289
ENSMUSG00000005124	chr15	Wisp1	6.7E+07	6.7E+07	5518	1.551762529	0.969884307	6.628E-05	0.000284033	0.13358	1	23	4	23	8	13	100	45	44	43	51
ENSMUSG00000037463	chr7	Fbxo27	2.9E+07	2.9E+07	3062	1.685239002	0.046752474	6.633E-05	0.000284168	0.11802	1	4	6	5	3	14	30	35	23	17	36

ENSMUSG00000045210	chr1	Vcpip1	9718622	9725350	9749	-0.71398984	4.09577903	6.661E-05	0.000285271	0.03469	-1	292	230	381	344	356	309	357	194	225	258
ENSMUSG00000037286	chr9	Stag1	1E+08	1E+08	11781	-0.75407631	4.754738236	6.668E-05	0.000285486	0.04031	-1	511	389	608	524	509	544	596	294	331	335
ENSMUSG00000058905	chr5	Gm10051	1.3E+08	1.3E+08	414	1.702859598	0.916428895	6.67E-05	0.000285502	0.16254	1	10	7	6	15	24	38	39	28	81	90
ENSMUSG00000038578	chr4	Susd1	5.9E+07	5.9E+07	4766	1.694318812	1.290146509	6.677E-05	0.000285711	0.16867	1	18	18	6	9	28	132	41	53	55	87
ENSMUSG00000046985	chr5	Tapt1	4.4E+07	4.4E+07	3487	-0.74831567	5.968407135	6.694E-05	0.000286215	0.04085	-1	1150	965	1457	1186	1109	1025	1228	726	943	917
ENSMUSG00000075705	chr17	Msrb1	2.5E+07	2.5E+07	1258	0.862009231	6.758469719	6.694E-05	0.000286215	0.05469	1	840	593	1944	1165	1535	2912	3112	2074	3328	3030
ENSMUSG00000103749	chr18	Pcdhgb5	3.8E+07	3.8E+07	6733	1.084246278	6.029179266	6.695E-05	0.000286215	0.08548	1	518	485	446	466	1279	2325	1213	1482	2094	2032
ENSMUSG00000061393	chr9	Acvr2b	1.2E+08	1.2E+08	1753	-1.31894641	1.570749429	6.701E-05	0.000286363	0.1062	-1	67	50	62	82	46	28	56	21	44	24
ENSMUSG00000051518	chr15	Rps19bp1	8E+07	8E+07	830	0.834066069	3.279042095	6.704E-05	0.000286395	0.0452	1	91	65	117	102	154	292	227	176	319	261
ENSMUSG00000031015	chr7	Swap70	1.1E+08	1.1E+08	4032	0.777556596	3.930181159	6.744E-05	0.000288047	0.04085	1	157	131	166	142	247	545	340	305	379	416
ENSMUSG00000045948	chr7	Mrps12	2.9E+07	2.9E+07	1040	0.699804218	5.237611855	6.774E-05	0.00028923	0.03513	1	392	240	593	438	563	1198	823	707	1125	985
ENSMUSG00000103088	chr18	Pcdhgb6	3.8E+07	3.8E+07	4684	1.078650931	6.031706326	6.797E-05	0.000290106	0.08477	1	522	481	452	472	1284	2330	1211	1486	2089	2034
ENSMUSG00000020573	chr12	Pik3cg	3.2E+07	3.2E+07	6786	1.437350905	1.982806105	6.838E-05	0.000291704	0.12973	1	23	33	16	16	65	163	115	90	92	118
ENSMUSG00000059436	chr12	Max	7.7E+07	7.7E+07	2005	0.645158201	4.815281963	6.837E-05	0.000291704	0.02907	1	299	225	377	312	460	835	662	525	703	825
ENSMUSG00000103081	chr18	Pcdhgb8	3.8E+07	3.8E+07	4615	1.077240885	6.03036686	6.872E-05	0.000293059	0.08466	1	531	478	450	469	1282	2326	1212	1483	2087	2031
ENSMUSG00000068246	chr15	Apol9b	7.8E+07	7.8E+07	1545	2.350805455	-0.38766447	6.88E-05	0.000293319	0.2333	1	2	2	1	2	8	44	15	3	25	25
ENSMUSG00000045659	chr7	Plekha7	1.2E+08	1.2E+08	11618	1.173143022	1.278565337	6.902E-05	0.000294143	0.07262	1	13	13	25	24	33	94	58	53	66	58
ENSMUSG00000103793	chr18	Pcdhga6	3.8E+07	3.8E+07	4733	1.075239911	6.033310164	6.921E-05	0.000294889	0.08443	1	529	482	457	466	1286	2328	1216	1484	2091	2035
ENSMUSG00000038374	chr3	Rbm8a	9.7E+07	9.7E+07	2604	0.716016779	5.174370392	6.952E-05	0.000296093	0.03677	1	408	287	489	327	572	1042	746	788	933	1087
ENSMUSG00000055493	chr10	Epm2a	1.1E+07	1.1E+07	3287	-0.89498391	6.860200417	6.993E-05	0.000297765	0.05923	-1	2552	1692	2887	2306	1876	1717	2586	1186	1498	1472
ENSMUSG00000031242	chrX	2610002M06Rik	1.1E+08	1.1E+08	6337	-0.98722337	3.286362411	7.01E-05	0.000298399	0.06627	-1	236	196	175	162	165	175	119	102	152	127
ENSMUSG00000006517	chr8	Mvd	1.2E+08	1.2E+08	1761	0.959464957	3.01396658	7.014E-05	0.00029846	0.06107	1	48	47	129	88	110	229	202	144	247	269
ENSMUSG00000037815	chr18	Ctnna1	3.5E+07	3.5E+07	3698	0.736737958	6.527159607	7.018E-05	0.00029846	0.04007	1	930	705	1288	1032	1337	2912	2139	2009	2327	2484
ENSMUSG00000090093	chr2	Gm14399	1.8E+08	1.8E+08	2561	-1.37740829	0.520232085	7.016E-05	0.00029846	0.09606	-1	32	20	41	31	25	19	28	9	11	12
ENSMUSG00000047824	chr3	Pygo2	8.9E+07	8.9E+07	3631	0.735700751	4.666971639	7.029E-05	0.000298862	0.03809	1	203	235	293	303	400	758	540	519	747	695
ENSMUSG00000002020	chr12	Ltbp2	8.5E+07	8.5E+07	8184	2.265410861	3.231273588	7.038E-05	0.00029912	0.34309	1	34	10	19	8	194	483	255	237	255	364
ENSMUSG00000030839	chr7	Sergef	4.6E+07	4.6E+07	2368	0.957184895	2.260364439	7.04E-05	0.00029912	0.05561	1	44	24	68	43	67	151	124	110	131	117
ENSMUSG00000103585	chr18	Pcdhgb4	3.8E+07	3.8E+07	5812	1.065986472	6.033697623	7.101E-05	0.000301644	0.08326	1	529	487	461	477	1278	2326	1207	1483	2087	2034
ENSMUSG00000034459	chr19	Ifit1	3.5E+07	3.5E+07	2656	1.428828149	1.51301278	7.117E-05	0.000302235	0.12365	1	14	15	36	13	36	159	75	40	94	54
ENSMUSG00000004626	chr8	Stxbp2	3630955	3631204	4159	1.406129388	2.67422069	7.162E-05	0.000304025	0.13392	1	40	27	42	27	134	252	165	93	182	266
ENSMUSG00000011831	chr5	Evi5	1.1E+08	1.1E+08	8060	-0.7624892	3.848650592	7.178E-05	0.00030461	0.03993	-1	272	228	282	287	272	276	277	141	197	224
ENSMUSG00000042228	chr4	Lyn	3678115	3678364	4073	1.042916575	3.519100304	7.189E-05	0.000305007	0.07587	1	93	49	156	78	214	510	272	226	286	308
ENSMUSG00000064127	chrX	Med14	1.3E+07	1.3E+07	8763	-0.78171527	4.916699786	7.207E-05	0.000305672	0.04405	-1	577	430	737	633	485	470	686	324	370	458
ENSMUSG00000029512	chr5	Ulk1	1.1E+08	1.1E+08	5213	-0.80724934	6.27549805	7.223E-05	0.000306263	0.04818	-1	1497	877	2124	1605	1464	1113	1587	821	1085	1241
ENSMUSG00000103037	chr18	Pcdhgb1	3.8E+07	3.8E+07	5776	1.072944421	6.031083296	7.226E-05	0.000306272	0.08451	1	524	485	456	469	1283	2324	1208	1481	2090	2032
ENSMUSG00000073485	chr1	H3f3aos	1.8E+08	1.8E+08	3044	-1.31154826	0.756530459	7.233E-05	0.000306517	0.08541	-1	29	22	65	24	39	20	22	17	17	19
ENSMUSG00000103567	chr18	Pcdhga5	3.8E+07	3.8E+07	4664	1.07170028	6.033292641	7.242E-05	0.000306778	0.08434	1	532	486	454	469	1281	2330	1213	1483	2089	2032
ENSMUSG00000021987	chr14	Mtmr6	6E+07	6E+07	3836	-0.84918555	5.896708478	7.245E-05	0.000306803	0.05314	-1	1283	870	1328	1116	1138	1033	1374	629	754	649
ENSMUSG00000028807	chr4	Zbtb8a	1.3E+08	1.3E+08	2321	1.228895475	1.519176399	7.258E-05	0.000307211	0.08731	1	14	15	29	19	50	116	76	58	73	76
ENSMUSG00000039756	chr3	Dnttip2	1.2E+08	1.2E+08	2401	-0.71720217	4.697663131	7.259E-05	0.000307211	0.03657	-1	512	397	606	419	477	490	493	324	300	423
ENSMUSG00000026932	chr2	Nacc2	2.6E+07	2.6E+07	7815	-0.73161145	5.722574579	7.263E-05	0.000307319	0.03924	-1	937	734	1185	1098	1008	927	1060	614	837	679
ENSMUSG00000025997	chr1	Ikzf2	7E+07	7E+07	11613	-0.90984722	2.844268322	7.269E-05	0.000307448	0.05393	-1	147	124	166	109	147	105	134	69	98	108
ENSMUSG00000020993	chr12	Trappc6b	5.9E+07	5.9E+07	1254	-0.67873576	5.081352566	7.285E-05	0.000308042	0.03306	-1	646	454	700	568	782	615	711	431	443	491
ENSMUSG00000023000	chr15	Dhh	9.9E+07	9.9E+07	2363	1.335167201	0.533496773	7.298E-05	0.000308487	0.08208	1	9	5	19	14	10	49	32	28	40	46
ENSMUSG00000044250	chr15	Pced1b	9.7E+07	9.7E+07	2198	1.556925322	1.175282848	7.331E-05	0.000309821	0.14821	1	9	4	22	11	40	76	60	33	69	93
ENSMUSG00000018800	chr11	Abca5	1.1E+08	1.1E+08	11437	-0.93371376	3.798636082	7.348E-05	0.000310443	0.06086	-1	241	186	430	285	251	202	316	156	127	185
ENSMUSG00000034780	chr2	B3galt1	6.8E+07	6.8E+07	5753	-1.19369679	2.409706431	7.351E-05	0.000310463	0.09376	-1	108	79	166	142	54	79	84	53	53	62
ENSMUSG00000055435	chr8	Maf	1.2E+08	1.2E+08	8241	-0.92218034	7.142678308	7.365E-05	0.000310953	0.06333	-1	3213	2443	2133	2522	3278	1974	2807	1351	2091	1943
ENSMUSG00000103144	chr18	Pcdhga1	3.8E+07	3.8E+07	5366	1.067971304	6.042702777	7.408E-05	0.000312696	0.084	1	538	494	460	472	1282	2341	1220	1489	2101	2049
ENSMUSG00000073705	chr4	Apitd1	1.5E+08	1.5E+08	1909	1.66351822	0.327180602	7.417E-05	0.000312986	0.13038	1	4	5	5	16	10	37	26	28	53	30
ENSMUSG00000035629	chr16	1700021K19Rik	3.3E+07	3.3E+07	7478	-0.65617239	5.208528363	7.425E-05	0.000313201	0.03108	-1	653	512	827	695	721	702	720	419	638	507
ENSMUSG00000040701	chr14	Ap1g2	5.5E+07	5.5E+07	4177	0.890073846	3.428602393	7.466E-05	0.000314844	0.05384	1	74	74	148	105	178	408	230	194	303	312
ENSMUSG00000039753	chr5	Fbxl5	4.4E+07	4.4E+07	9788	-0.6808208	5.178044174	7.471E-05	0.000314962	0.0335	-1	745	452	858	636	685	603	748	424	532	574
ENSMUSG00000038260	chr7	Trpm4	4.5E+07	4.5E+07	4245	-0.79085119	4.811722341	7.498E-05	0.000315897	0.04519	-1	435	332	897	593	490	477	585	250	443	402
ENSMUSG00000058070	chr12	Eml1	1.1E+08	1.1E+08	7436	-0.80771421	6.831429058	7.497E-05	0.000315897	0.0487	-1	2212	1749	2577	2227	2060	1646	2176	1394	1807	1493
ENSMUSG00000051674	chr5	Dcun1d4	7.3E+07	7.3E+07	5803	-0.84341298	3.629937813	7.512E-05	0.000316417	0.04864	-1	267	200	233	229	242	193	239	158	163	153
ENSMUSG00000027398	chr2	Il1b	1.3E+08	1.3E+08	1907	1.666464534	0.002756481	7.537E-05	0.000317361	0.12401	1	1	2	8	10	11	22	25	22	33	33
ENSMUSG00000035215	chr10	Lsm7	8.1E+07	8.1E+07	468	0.900900721	3.055187594	7.569E-05	0.000318597	0.05378	1	83	48	123	87	99	291	169	202	234	198
ENSMUSG00000027422	chr2	Rrbp1	1.4E+08	1.4E+08	8786	0.837115559	6.195476442	7.582E-05	0.000319076	0.05208	1	696	462	870	748	1302	2959	1710	1463	1933	1744
ENSMUSG00000026571	chr1	Dcaf6	1.7E+08	1.7E+08	6424	-0.87534753	8.107312771	7.59E-05	0.000319308	0.05753	-1	5356	4267	6727	6091	4165	4152	5403	3083	3649	3863
ENSMUSG00000026005	chr1	Rpe	6.7E+07	6.7E+07	3113	-0.93365065	3.452960469	7.633E-05	0.000321026	0.06009	-1	227	166	166	172	346	197	195	104	150	137
ENSMUSG00000038495	chr3	Otud7b	9.6E+07	9.6E+07	8497	-0.78896731	6.204015026	7.653E-05	0.000321753	0.04634	-1	1379	1059	1829	1506	1249	1093	1498	766	1094	1167
ENSMUSG00000037857	chr11	Nufip2	7.8E+07	7.8E+07	5792	-0.77070794	4.481803288	7.66E-05	0.000321959	0.04243	-1	414	372	541	367	403	390	476	269	277	295
ENSMUSG00000025237	chr9	Parp6	6E+07	6E+07	2714	-0.63841567	4.992406274	7.673E-05	0.000322415	0.02922	-1	569	402	689	637	634	581	655	349	506	502
ENSMUSG00000032548	chr9	Slco2a1	1E+08	1E+08	13545	1.273741277	2.368766057	7.678E-05	0.000322517	0.10372	1	45	56	33	36	40	151	100	156	160	149
ENSMUSG00000034620	chr10	Tmem5	1.2E+08	1.2E+08	5614	-0.70478109	4.760221825	7.727E-05	0.000324442	0.03564	-1	504	430	535	500	522	514	539	345	366	365
ENSMUSG00000036052	chr4	Dnajb5	4.3E+07	4.3E+07	5936	-0.82332772	7.57759153	7.733E-05	0.000324442	0.051	-1	3916	3023	4395	3627	3192	2835	3557	2032	2968	2920

ENSMUSG00000049233	chr13	Apoo-ps	1.1E+08	1.1E+08	903	-0.9366504	2.719731217	7.732E-05	0.000324442	0.05689	-1	129	100	177	128	111	93	130	60	98	85
ENSMUSG00000054484	chr2	Tmem62	1.2E+08	1.2E+08	3348	0.784256234	3.162666209	7.733E-05	0.000324442	0.03954	1	81	66	134	99	117	297	247	162	213	247
ENSMUSG00000020038	chr10	Cry1	8.5E+07	8.5E+07	3014	-0.9583369	3.636010688	7.739E-05	0.000324583	0.06445	-1	234	227	262	262	219	176	295	103	166	142
ENSMUSG00000048572	chr19	Tmem252	2.5E+07	2.5E+07	2462	1.608897684	0.367358106	7.795E-05	0.000326849	0.12111	1	6	10	6	6	14	39	22	24	54	40
ENSMUSG00000092511	chr17	Gm20547	3.5E+07	3.5E+07	3902	1.679571776	5.456140125	7.802E-05	0.000327032	0.20244	1	168	241	116	131	978	1945	1252	1005	1578	1180
ENSMUSG00000104063	chr18	Pcdhgb7	3.8E+07	3.8E+07	4713	1.060255152	6.037555319	7.808E-05	0.000327211	0.08333	1	535	494	460	477	1280	2325	1214	1486	2092	2032
ENSMUSG00000090066	chr3	1110002E22Rik	1.4E+08	1.4E+08	9998	-0.91764394	8.054783268	7.834E-05	0.000328199	0.06336	-1	5688	4123	6070	6119	3751	3505	4370	3459	3664	3775
ENSMUSG00000026121	chr1	Sema4c	3.7E+07	3.7E+07	4593	0.855648679	3.832052057	7.865E-05	0.000329381	0.05146	1	120	80	190	137	261	443	293	303	402	435
ENSMUSG00000025040	chrX	Fundc1	1.8E+07	1.8E+07	2353	-0.6886671	4.638414233	7.896E-05	0.000330587	0.03392	-1	480	361	512	483	455	464	525	272	350	375
ENSMUSG00000025572	chr11	Tmc6	1.2E+08	1.2E+08	4091	1.078287756	2.66991343	7.933E-05	0.000332029	0.07765	1	42	41	81	33	116	197	173	120	176	213
ENSMUSG00000083992	chr11	Gm11478	8.7E+07	8.7E+07	599	0.986627648	3.003696887	7.937E-05	0.000332095	0.06534	1	60	57	80	87	119	218	153	155	271	285
ENSMUSG00000026424	chr1	Gpr37l1	1.4E+08	1.4E+08	2269	1.311571575	0.632370409	7.959E-05	0.000332935	0.07558	1	11	12	10	14	13	52	41	25	46	46
ENSMUSG00000001173	chrX	Ocrl	4.8E+07	4.8E+07	9486	-0.76427325	4.45291628	7.967E-05	0.000333055	0.042	-1	415	374	417	437	381	415	435	217	335	294
ENSMUSG00000017652	chr2	Cd40	1.7E+08	1.7E+08	3406	1.580677667	0.513325918	7.965E-05	0.000333055	0.13104	1	5	5	20	8	12	78	26	23	43	34
ENSMUSG00000025969	chr1	Nrp2	6.3E+07	6.3E+07	11842	0.790862051	4.624581129	7.989E-05	0.000333902	0.04531	1	206	155	287	247	511	780	668	501	604	673
ENSMUSG00000054519	chr11	Zfp867	5.9E+07	5.9E+07	3412	-1.0807931	2.593742305	7.994E-05	0.000334004	0.07753	-1	111	88	191	143	81	85	110	68	59	73
ENSMUSG00000087380	chr6	2210408F21Rik	3.1E+07	3.1E+07	1476	-0.66511296	4.966249533	7.996E-05	0.000334004	0.03205	-1	587	466	709	512	599	577	630	307	506	510
ENSMUSG00000043702	chr14	Pde12	2.7E+07	2.7E+07	7725	-0.92358123	3.248226337	8.013E-05	0.000334584	0.05789	-1	140	143	233	232	185	125	192	114	133	105
ENSMUSG00000048285	chr12	Frmd6	7.1E+07	7.1E+07	4660	0.666537871	4.975955715	8.015E-05	0.000334594	0.03205	1	347	253	486	294	480	1002	736	664	864	705
ENSMUSG00000044296	chr11	Zfp879	5.1E+07	5.1E+07	2414	-1.21588107	1.269834051	8.032E-05	0.000335172	0.08477	-1	53	38	53	61	39	30	46	18	28	25
ENSMUSG00000031617	chr8	Tmem184c	7.8E+07	7.8E+07	2723	-1.16835693	2.961683623	8.051E-05	0.000335867	0.0946	-1	174	171	125	147	157	119	168	72	70	69
ENSMUSG00000031750	chr8	Il34	1.1E+08	1.1E+08	1959	1.001874802	3.238052767	8.064E-05	0.000336332	0.06892	1	72	61	82	78	186	316	218	189	312	252
ENSMUSG00000003581	chr11	Rnf215	4135202	4135563	2232	0.888215465	3.076891861	8.076E-05	0.00033674	0.05245	1	80	55	93	85	134	325	174	162	227	238
ENSMUSG00000021585	chr13	Cast	7.5E+07	7.5E+07	2894	-0.83872236	6.256223341	8.109E-05	0.000337983	0.05277	-1	1477	986	2045	1661	1268	1344	1624	784	885	1096
ENSMUSG00000026471	chr1	Mr1	1.6E+08	1.6E+08	5981	-0.73366917	4.405917438	8.13E-05	0.000338773	0.03841	-1	365	244	574	395	459	383	471	210	271	330
ENSMUSG00000030689	chr7	Ino80e	1.3E+08	1.3E+08	4648	0.789297226	3.774924944	8.146E-05	0.00033933	0.04288	1	130	94	167	142	233	462	289	271	406	355
ENSMUSG00000068922	chr3	Msto1	8.9E+07	8.9E+07	5418	0.723960602	3.575777559	8.201E-05	0.000341538	0.03484	1	122	86	171	124	181	376	302	231	303	314
ENSMUSG00000038670	chr7	Mybpc2	4.5E+07	4.5E+07	3624	-0.93863371	11.74028176	8.205E-05	0.000341588	0.06682	-1	75371	55702	62767	72944	64857	45404	62168	34031	63542	37946
ENSMUSG00000025791	chr4	Pgm2	1E+08	1E+08	2921	-0.87417947	10.27326884	8.238E-05	0.000342875	0.05811	-1	22216	20787	22773	25637	27470	15797	22294	12933	22135	17144
ENSMUSG00000029536	chr5	Gatc	1.2E+08	1.2E+08	1794	-0.69954701	5.052663957	8.284E-05	0.000344685	0.03579	-1	622	482	668	703	582	539	689	393	505	489
ENSMUSG00000048118	chr12	Arid4a	7.1E+07	7.1E+07	5615	-0.87664005	3.371176732	8.291E-05	0.000344878	0.05307	-1	199	176	233	181	203	168	227	104	141	116
ENSMUSG00000021959	chr14	Lats2	5.8E+07	5.8E+07	7303	-0.70590871	4.364858818	8.297E-05	0.000345029	0.03537	-1	355	305	433	348	481	330	442	250	275	318
ENSMUSG00000081434	chr2	Gm14165	1.5E+08	1.5E+08	952	1.004715779	3.220354994	8.324E-05	0.000346054	0.06894	1	100	73	69	90	123	309	171	183	250	359
ENSMUSG00000020154	chr10	Ptprb	1.2E+08	1.2E+08	11912	-0.77946511	5.536050623	8.343E-05	0.000346561	0.0452	-1	767	491	1490	893	931	740	932	482	644	758
ENSMUSG00000034158	chr16	Lrrc58	3.8E+07	3.8E+07	8604	-0.86264358	5.237430484	8.342E-05	0.000346561	0.05517	-1	615	459	824	540	1355	666	767	435	429	480
ENSMUSG00000048264	chr13	Dip2c	9276528	9277066	8223	-0.87884123	4.394766558	8.344E-05	0.000346561	0.05615	-1	410	298	599	475	262	334	426	223	247	307
ENSMUSG00000051853	chr15	Arf3	9.9E+07	9.9E+07	3837	0.907649593	5.276860931	8.396E-05	0.000348635	0.06134	1	290	224	422	324	863	1262	1074	763	1145	998
ENSMUSG00000032407	chr9	U2surp	9.5E+07	9.5E+07	14642	-0.69714057	4.797120075	8.432E-05	0.000350012	0.03525	-1	530	378	634	551	489	502	573	346	360	412
ENSMUSG00000022897	chr16	Dyrk1a	9.5E+07	9.5E+07	8251	-0.76744844	6.455341908	8.466E-05	0.000351302	0.04449	-1	1480	1176	2269	1821	1659	1333	1800	982	1295	1321
ENSMUSG00000022940	chr16	Pigp	9.4E+07	9.4E+07	1888	-0.80316943	6.059336597	8.494E-05	0.000352386	0.04858	-1	1418	1153	1322	1173	1161	1217	1224	762	897	948
ENSMUSG00000040820	chr16	Hlcs	9.4E+07	9.4E+07	5060	-0.83556147	3.801350039	8.498E-05	0.00035245	0.04913	-1	271	148	398	241	323	239	313	126	186	183
ENSMUSG00000026672	chr2	Optn	5020642	5021228	3753	-0.95535415	5.952386309	8.506E-05	0.000352658	0.06855	-1	923	597	2434	1260	1271	920	1283	557	724	925
ENSMUSG00000026761	chr2	Orc4	4.9E+07	4.9E+07	7458	-0.74236254	3.95623886	8.523E-05	0.000353272	0.03864	-1	269	234	360	301	289	271	318	180	188	244
ENSMUSG00000031807	chr8	Pgls	7.2E+07	7.2E+07	3770	0.791159643	4.802931747	8.55E-05	0.000354286	0.04612	1	242	145	439	305	477	790	603	547	879	822
ENSMUSG00000005465	chr8	Il27ra	8.4E+07	8.4E+07	2657	1.442912355	0.418178445	8.575E-05	0.000355199	0.09249	1	14	7	9	7	11	42	34	20	34	53
ENSMUSG00000070520	chr7	Ndnl2	6.5E+07	6.5E+07	5946	0.802470844	3.727607946	8.582E-05	0.000355396	0.0449	1	125	88	194	142	189	428	263	335	334	343
ENSMUSG00000037174	chr3	Elf2	5.1E+07	5.1E+07	9563	-0.64006173	5.20431056	8.586E-05	0.000355468	0.03005	-1	609	533	856	656	732	682	744	430	553	585
ENSMUSG00000038206	chr8	Fbxo8	5.7E+07	5.7E+07	3740	-0.69015312	4.369984684	8.622E-05	0.00035684	0.03393	-1	370	281	471	340	473	397	435	234	260	320
ENSMUSG00000017721	chr2	Pigt	1.6E+08	1.6E+08	3856	0.767183392	5.897314143	8.629E-05	0.000357001	0.04425	1	563	393	787	702	962	1694	1310	1089	1923	1758
ENSMUSG00000035890	chr10	Rnf126	8E+07	8E+07	1639	-0.73159754	4.955111855	8.64E-05	0.000357295	0.03936	-1	379	500	675	635	727	473	546	320	580	499
ENSMUSG00000062210	chr18	Tnfaip8	5E+07	5E+07	10328	1.265834623	3.307112948	8.641E-05	0.000357295	0.11334	1	79	66	52	43	199	410	237	203	269	321
ENSMUSG00000020225	chr10	Tmbim4	1.2E+08	1.2E+08	2581	0.65595947	5.488780809	8.644E-05	0.000357331	0.03185	1	494	352	636	518	657	1371	1047	925	1129	1188
ENSMUSG00000020075	chr10	Ddx21	6.3E+07	6.3E+07	4742	-0.79175509	5.605453749	8.651E-05	0.000357529	0.04696	-1	837	806	1113	1015	810	913	926	633	594	613
ENSMUSG00000026657	chr2	Frmd4a	4017717	4018019	23350	0.835791911	2.913552381	8.696E-05	0.000359265	0.04497	1	64	60	112	86	82	231	202	151	181	218
ENSMUSG00000021147	chr13	Wdr37	8802968	8805946	8729	-0.78890461	4.883915714	8.715E-05	0.000359945	0.04592	-1	501	459	769	621	447	439	657	325	399	422
ENSMUSG00000019975	chr10	Ikbip	9.1E+07	9.1E+07	4894	0.838472857	3.756536304	8.739E-05	0.000360813	0.04875	1	176	113	150	108	172	539	316	268	324	346
ENSMUSG00000030060	chr6	Hmces	8.8E+07	8.8E+07	2308	0.938156627	2.739154892	8.765E-05	0.000361778	0.05804	1	54	40	75	66	112	207	147	130	218	189
ENSMUSG00000038368	chr4	Focad	8.8E+07	8.8E+07	11311	-0.81203671	3.591446453	8.77E-05	0.000361912	0.04552	-1	222	174	258	268	222	186	202	176	160	162
ENSMUSG00000027800	chr3	Tm4sf1	5.7E+07	5.7E+07	3355	0.687971684	4.828011328	8.791E-05	0.000362653	0.03447	1	258	223	430	311	447	994	594	606	681	737
ENSMUSG00000035900	chr15	Gramd4	8.6E+07	8.6E+07	5567	-0.67025662	4.48629816	8.795E-05	0.000362693	0.03219	-1	401	338	449	367	507	398	452	256	354	333
ENSMUSG00000037580	chr14	Gch1	4.7E+07	4.7E+07	2775	1.103142239	2.279065571	8.836E-05	0.000364288	0.07979	1	24	23	80	49	60	172	110	123	117	139
ENSMUSG00000026421	chr1	Csrp1	1.4E+08	1.4E+08	1956	1.039031687	6.088934848	8.842E-05	0.000364418	0.08143	1	409	441	677	493	1479	2479	1565	1288	2003	2219
ENSMUSG00000016541	chr15	Atxn10	8.5E+07	8.5E+07	2425	0.690200818	5.729766614	8.866E-05	0.000365302	0.0357	1	572	403	774	559	804	1631	1198	1097	1344	1484
ENSMUSG00000060467	chr9	Gm10080	4.4E+07	4.4E+07	613	1.924973189	-0.42779827	8.879E-05	0.000365754	0.15249	1	3	3	2	1	10	30	10	15	20	25
ENSMUSG00000054404	chr11	Slfn5	8.3E+07	8.3E+07	4427	-1.11730154	4.061483208	8.926E-05	0.000367577	0.09177	-1	300	284	497	318	321	290	439	99	148	149
ENSMUSG00000035891	chr15	Cerk	8.6E+07	8.6E+07	4812	0.748357698	3.812966944	8.929E-05	0.000367588	0.039	1	107	108	240	158	190	411	417	247	387	358
ENSMUSG00000010492	chr2	Uckl1os	1.8E+08	1.8E+08	2522	-0.8010047	5.803643612	8.992E-05	0.000369984	0.04846	-1	1206	649	1625	922	1046	913	1166	570	881	716

ENSMUSG00000025287	chrX	Acot9	1.6E+08	1.6E+08	2273	0.664366967	5.220179441	8.992E-05	0.000369984	0.03242	1	391	365	485	421	492	1279	925	758	886	880
ENSMUSG00000005610	chr7	Eif4g2	1.1E+08	1.1E+08	7348	-0.8398978	9.684355614	9.019E-05	0.000370987	0.05429	-1	14640	12046	19222	18128	15358	12690	17370	8785	11086	11419
ENSMUSG00000036545	chr11	Adamts2	5.1E+07	5.1E+07	9336	0.815761245	5.008787785	9.024E-05	0.000371072	0.04938	1	245	282	339	284	628	1197	831	622	859	763
ENSMUSG00000007207	chr5	Stx1a	1.4E+08	1.4E+08	2666	1.759058152	0.472097631	9.074E-05	0.000373032	0.17254	1	2	5	11	8	18	48	17	22	62	51
ENSMUSG00000103677	chr18	Pcdhga4	3.8E+07	3.8E+07	4727	1.057928974	6.037660024	9.085E-05	0.000373348	0.08454	1	533	492	456	478	1293	2325	1215	1483	2090	2033
ENSMUSG00000007827	chr6	Ankrd26	1.2E+08	1.2E+08	7253	-1.03267864	2.025153907	9.09E-05	0.000373438	0.06689	-1	80	68	107	76	72	74	65	47	37	49
ENSMUSG00000046828	chr1	Mettl21e	4.4E+07	4.4E+07	3961	-1.27320841	5.806411373	9.095E-05	0.000373563	0.12148	-1	1158	1393	1015	1432	575	530	1180	480	480	727
ENSMUSG00000041809	chr1	Efhc1	2.1E+07	2.1E+07	2208	1.58412897	-0.04882453	9.119E-05	0.00037441	0.09435	1	7	6	6	3	9	35	19	25	25	24
ENSMUSG00000034210	chr4	Efcab14	1.2E+08	1.2E+08	8201	-0.78277161	5.937420572	9.128E-05	0.000374674	0.04648	-1	1222	1050	1281	1125	1030	1036	1209	681	871	883
ENSMUSG00000033972	chr17	Zfp944	2.2E+07	2.2E+07	2784	-1.0290757	2.349855929	9.137E-05	0.000374962	0.06931	-1	108	94	104	109	81	73	92	55	57	65
ENSMUSG00000035150	chrX	Eif2s3x	9.4E+07	9.4E+07	3812	-0.95376675	5.708984889	9.181E-05	0.000376637	0.06883	-1	1265	910	971	1233	614	913	765	612	688	700
ENSMUSG00000058569	chr13	Tmed9	5.6E+07	5.6E+07	1420	0.731925539	6.580925458	9.284E-05	0.000380761	0.04095	1	972	731	1457	1079	1269	3174	2137	1853	2705	2536
ENSMUSG00000021322	chr13	Aoah	2.1E+07	2.1E+07	2915	1.778049452	0.359971325	9.289E-05	0.000380856	0.1605	1	7	6	1	9	15	64	25	17	39	42
ENSMUSG00000024193	chr17	Phf1	2.7E+07	2.7E+07	2429	0.666337613	4.623206786	9.318E-05	0.000381923	0.03216	1	256	178	374	277	377	834	527	432	616	736
ENSMUSG00000025735	chr17	Rhbdl1	2.6E+07	2.6E+07	1723	-0.74590156	4.842606672	9.364E-05	0.000383694	0.04123	-1	412	378	647	664	631	398	497	262	576	496
ENSMUSG00000021666	chr13	Gfm2	9.7E+07	9.7E+07	10685	-0.80674549	6.511746112	9.399E-05	0.000385026	0.04984	-1	1586	1151	2565	2007	1554	1384	1860	935	1352	1378
ENSMUSG00000048106	chr3	4632415L05Rik	2E+07	2E+07	1077	-1.40044478	0.762721753	9.409E-05	0.000385302	0.11353	-1	32	34	59	24	29	19	23	7	16	29
ENSMUSG00000031555	chr8	Adam9	2.5E+07	2.5E+07	4011	-0.87900976	6.051466988	9.412E-05	0.000385325	0.05893	-1	1477	1063	1441	1252	1128	1223	1471	662	769	774
ENSMUSG00000047022	chr12	Mipol1	5.7E+07	5.7E+07	9342	-1.214357	1.459840668	9.425E-05	0.000385721	0.08862	-1	73	52	47	38	67	41	29	31	32	33
ENSMUSG00000049349	chr3	Gm5105	1.4E+08	1.4E+08	1665	-1.28042148	0.845317009	9.427E-05	0.000385721	0.09105	-1	54	25	35	31	38	21	29	11	22	22
ENSMUSG00000090187	chr13	AK157302	2.1E+07	2.1E+07	390	-1.55170924	2.083826631	9.495E-05	0.00038837	0.16516	-1	93	69	148	100	62	23	105	21	45	29
ENSMUSG00000025239	chr9	Limd1	1.2E+08	1.2E+08	4849	-0.7355286	6.260283047	9.507E-05	0.000388775	0.04137	-1	1340	1117	1920	1450	1396	1369	1472	913	1075	1136
ENSMUSG00000018476	chr11	Kdm6b	6.9E+07	6.9E+07	6954	-0.67197888	5.335023092	9.513E-05	0.000388876	0.03377	-1	645	467	949	786	968	644	774	453	601	756
ENSMUSG00000021018	chr16	Polr2h	2.1E+07	2.1E+07	1448	0.840979282	3.443758835	9.529E-05	0.00038932	0.04901	1	106	81	129	100	173	375	221	260	296	265
ENSMUSG00000024846	chr19	Cst6	5344705	5348049	3951	0.731973133	4.490892372	9.529E-05	0.00038932	0.03903	1	222	177	329	236	323	552	474	432	773	643
ENSMUSG00000046201	chr17	Scaf8	3114972	3115418	4869	-0.67144676	4.526766709	9.552E-05	0.000390155	0.03258	-1	373	299	555	487	430	386	438	314	322	363
ENSMUSG00000035692	chr4	Isg15	1.6E+08	1.6E+08	756	1.426461669	1.619793382	9.558E-05	0.000390297	0.1276	1	23	21	16	14	45	144	71	41	123	74
ENSMUSG00000036948	chr5	BC037034	1.4E+08	1.4E+08	3860	1.124205767	2.861358964	9.631E-05	0.00039301	0.08772	1	44	55	58	57	128	320	136	138	209	222
ENSMUSG00000091964	chr5	BC037034	1.4E+08	1.4E+08	3581	1.124205787	2.861358964	9.628E-05	0.00039301	0.08772	1	44	55	58	57	128	320	136	138	209	222
ENSMUSG00000040123	chr14	Zmym5	5.7E+07	5.7E+07	5541	-0.65782805	4.415093558	9.687E-05	0.000395212	0.03122	-1	393	299	455	400	410	427	406	242	291	356
ENSMUSG00000021701	chr13	Plk2	1.1E+08	1.1E+08	2802	0.730056824	3.861037777	9.717E-05	0.000396289	0.03738	1	122	126	219	141	222	420	336	281	399	424
ENSMUSG00000060206	chr4	Zfp462	5.5E+07	5.5E+07	10702	-0.8237395	3.878948909	9.739E-05	0.000397074	0.04892	-1	306	186	415	277	240	218	290	145	179	270
ENSMUSG00000026879	chr2	Gsn	3.5E+07	3.5E+07	2977	1.082917649	11.24768365	9.747E-05	0.000397283	0.09023	1	20831	19833	15358	16970	44732	91907	52994	53971	66086	77904
ENSMUSG00000046818	chr3	Ddit4l	1.4E+08	1.4E+08	2916	-0.83506737	8.038772876	9.771E-05	0.000398152	0.05406	-1	5905	3634	6038	4220	5657	3768	5489	2547	4127	3767
ENSMUSG00000032495	chr9	Lrrc2	1.1E+08	1.1E+08	3657	-1.1638357	6.100923173	9.827E-05	0.000400312	0.10309	-1	1353	679	2917	1660	819	946	1365	635	574	893
ENSMUSG00000103970	chr9	RP23-250G8.14	1.1E+08	1.1E+08	1146	-1.14975169	1.37017443	9.887E-05	0.000402638	0.07694	-1	48	31	75	58	54	41	51	22	24	25
ENSMUSG00000019883	chr10	Echdc1	2.9E+07	2.9E+07	3317	-0.85035014	4.816076615	9.895E-05	0.000402864	0.05422	-1	695	312	457	406	898	520	393	339	403	419
ENSMUSG00000031309	chrX	Rps6ka3	1.6E+08	1.6E+08	8322	-0.77901766	6.037481489	9.913E-05	0.000403492	0.04657	-1	1232	1133	1256	1158	1355	1284	1231	763	949	804
ENSMUSG00000017776	chr11	Crk	7.6E+07	7.6E+07	4730	-0.78480769	5.985258944	9.989E-05	0.000406447	0.04725	-1	1131	892	1492	1168	1393	1138	1433	735	760	773
ENSMUSG00000037325	chr3	Bbs7	3.7E+07	3.7E+07	3957	-0.87019964	3.072171611	0.0001001	0.000407289	0.05173	-1	171	140	175	152	163	130	138	118	108	108
ENSMUSG00000037343	chr15	Taf2	5.5E+07	5.5E+07	5033	-0.72761559	3.862008761	0.0001003	0.000407844	0.03759	-1	250	193	338	310	275	270	301	159	195	212
ENSMUSG00000033268	chr2	Duox1	1.2E+08	1.2E+08	5267	1.223976795	2.55528535	0.0001007	0.000409336	0.10423	1	34	23	37	70	104	175	128	151	170	196
ENSMUSG00000018293	chr11	Pfn1	7.1E+07	7.1E+07	2405	0.804924984	7.91870593	0.0001012	0.000411139	0.05044	1	2162	2084	2711	2691	3676	7566	5252	5010	7555	6404
ENSMUSG00000014932	chr5	Yes1	3.3E+07	3.3E+07	4608	-1.077184	2.931344009	0.0001015	0.000411924	0.0822	-1	173	119	186	147	144	108	185	74	67	73
ENSMUSG00000026116	chr1	Tmem131	3.7E+07	3.7E+07	9413	-0.87124838	5.173258196	0.0001015	0.000411924	0.05765	-1	535	409	1118	969	559	549	762	381	453	503
ENSMUSG00000032372	chr9	Plscr2	9.2E+07	9.2E+07	3180	1.331221477	0.740615015	0.0001014	0.000411924	0.0913	1	8	13	24	8	13	65	41	31	40	52
ENSMUSG00000034252	chr9	Senp6	8E+07	8E+07	7016	-0.68636607	5.392647039	0.0001015	0.000411924	0.03571	-1	795	606	931	761	792	839	845	459	569	653
ENSMUSG00000063714	chr2	Sp3os	7.3E+07	7.3E+07	892	1.280686375	1.032268744	0.000102	0.000413961	0.09268	1	8	11	32	16	19	81	47	36	48	71
ENSMUSG00000023156	chr14	Rpp14	8080367	8080512	2401	-0.6214339	4.956573337	0.0001027	0.000416448	0.02859	-1	550	428	678	577	597	551	573	387	559	455
ENSMUSG00000036617	chr2	Etl4	2E+07	2E+07	16067	-1.06910632	6.162397786	0.0001027	0.000416448	0.08782	-1	1615	997	2215	1585	907	985	1730	617	684	831
ENSMUSG00000029056	chr4	Pank4	1.5E+08	1.5E+08	3487	-0.7762885	5.244496451	0.0001028	0.000416762	0.0458	-1	631	472	1092	851	607	624	824	375	578	517
ENSMUSG00000038884	chr9	A230050P20Rik	2.1E+07	2.1E+07	3417	1.263080146	2.341792415	0.0001029	0.000417088	0.10779	1	34	39	29	33	83	202	98	91	126	212
ENSMUSG00000067235	chr17	H2-Q10	3.5E+07	3.5E+07	4348	1.288830743	3.880306093	0.0001031	0.000417717	0.12301	1	107	83	111	55	308	756	279	296	376	475
ENSMUSG00000033088	chr15	Triobp	7.9E+07	7.9E+07	10681	-1.05925933	5.476257245	0.0001033	0.000418387	0.08587	-1	643	1134	587	991	910	634	658	377	816	524
ENSMUSG00000098098	chr18	Gm20748	6.2E+07	6.2E+07	699	1.245750543	1.611482072	0.0001034	0.000418969	0.09997	1	19	11	51	13	44	96	91	70	80	86
ENSMUSG00000018012	chr11	Rac3	1.2E+08	1.2E+08	1293	1.343763141	1.017984873	0.0001035	0.000418999	0.10106	1	16	11	14	10	30	94	47	33	64	47
ENSMUSG00000021893	chr14	Capn7	3.1E+07	3.1E+07	4733	-0.71353209	5.824402802	0.0001035	0.000418999	0.03907	-1	1052	755	1398	1078	1046	971	1186	663	823	810
ENSMUSG00000044469	chr17	Tnfaip8l1	5.6E+07	5.6E+07	2379	1.311909618	0.977331631	0.0001044	0.000422653	0.09794	1	12	6	19	15	30	50	41	42	72	63
ENSMUSG00000004069	chr16	Dnaja3	4639989	4640148	3912	-0.82695986	7.01389383	0.0001045	0.000422678	0.05324	-1	2022	1512	4105	2670	2519	2000	2627	1402	1812	1835
ENSMUSG00000041112	chr13	Elmo1	2E+07	2E+07	10113	0.965734304	2.89394735	0.0001045	0.000422678	0.06504	1	47	40	130	68	105	270	228	136	167	211
ENSMUSG00000053870	chr3	Fpgt	1.6E+08	1.6E+08	6282	-0.90506061	2.599897017	0.0001047	0.000423352	0.05437	-1	125	93	136	110	122	100	121	66	74	72
ENSMUSG00000021500	chr13	Ddx46	5.6E+07	5.6E+07	5747	-0.68155918	5.342442341	0.0001047	0.000423353	0.03521	-1	767	537	1023	728	728	712	764	531	541	663
ENSMUSG00000017291	chr11	Taok1	7.8E+07	7.8E+07	12421	-0.78150846	5.987483694	0.0001049	0.000424091	0.04713	-1	1182	804	1730	1238	1165	1055	1363	766	762	884
ENSMUSG00000086742	chr7	Gm16201	1.4E+08	1.4E+08	2917	1.781644305	-0.26003424	0.000105	0.000424161	0.12362	1	5	6	3	3	6	32	11	18	22	29
ENSMUSG00000049307	chr9	Fut4	1.5E+07	1.5E+07	3664	1.427537781	0.651812181	0.0001054	0.000425829	0.10627	1	12	9	13	5	20	59	45	44	38	28
ENSMUSG00000038552	chr5	Fndc4	3.1E+07	3.1E+07	2261	1.197045808	1.722259457	0.0001056	0.000426419	0.08929	1	21	20	27	33	45	157	65	80	76	79
ENSMUSG00000074165	chr7	Zfp788	4.2E+07	4.2E+07	4350	-0.90551861	3.114419993	0.0001058	0.000427135	0.05705	-1	167	118	236	150	184	143	189	97	90	102

ENSMUSG00000099998	chr19	Gm6501	1.1E+07	1.1E+07	916	-1.46396943	0.066772759	0.0001061	0.000428087	0.09906	-1	21	17	28	27	14	17	13	6	7	11
ENSMUSG00000030704	chr7	Rab6a	1E+08	1E+08	3728	-0.83459964	6.416306607	0.0001063	0.000428612	0.05414	-1	1824	1404	1830	1560	1475	1628	1748	926	1009	1101
ENSMUSG00000063428	chr10	Ddo	4.1E+07	4.1E+07	3000	-0.8255652	5.206937734	0.0001067	0.000430231	0.05201	-1	639	383	1128	815	695	492	841	425	514	475
ENSMUSG00000027162	chr2	Lin7c	1.1E+08	1.1E+08	4521	-0.67997118	4.816869926	0.0001068	0.000430718	0.03449	-1	476	355	643	567	596	412	613	336	387	487
ENSMUSG00000028197	chr3	Col24a1	1.5E+08	1.5E+08	7621	-1.73961014	2.955981709	0.0001071	0.00043171	0.21786	-1	301	255	78	97	71	68	90	60	88	62
ENSMUSG00000014905	chr12	Dnajb9	4.4E+07	4.4E+07	1865	-0.70197976	5.020003681	0.0001077	0.000433783	0.03728	-1	618	429	695	733	533	588	667	353	466	499
ENSMUSG00000062995	chr6	Ica1	8630527	8630797	3243	1.177044754	1.210626569	0.0001077	0.000433848	0.07826	1	11	15	31	15	31	62	59	49	63	78
ENSMUSG00000084790	chr16	Gm15879	4032839	4033052	1023	-1.31329165	0.668823361	0.0001078	0.000433954	0.0928	-1	47	26	36	26	26	25	20	11	18	17
ENSMUSG00000099292	chr10	Mir6916	1.3E+08	1.3E+08	63	1.610670804	-0.18447135	0.000108	0.000434859	0.10761	1	3	2	7	7	9	30	22	11	20	35
ENSMUSG00000031931	chr9	Ankrd49	1.5E+07	1.5E+07	1753	-1.06273816	2.607927176	0.0001081	0.000435123	0.07745	-1	99	96	163	147	110	106	117	71	62	48
ENSMUSG00000060261	chr5	Gtf2i	1.3E+08	1.3E+08	7120	-0.75706609	6.834576627	0.0001081	0.000435123	0.0448	-1	1990	1528	2756	2493	2083	1812	2180	1323	1782	1685
ENSMUSG00000019960	chr10	Dusp6	9.9E+07	9.9E+07	2796	0.778142868	4.442200847	0.0001085	0.00043631	0.04527	1	205	141	278	203	413	607	507	529	517	627
ENSMUSG00000001420	chr3	Tmem79	8.8E+07	8.8E+07	2912	-1.84127784	1.9785216	0.0001089	0.000437938	0.23442	-1	75	46	47	30	287	30	44	31	40	27
ENSMUSG00000034265	chr17	Zdhhc14	5492600	5493691	3115	0.850836818	2.671999772	0.0001091	0.000438777	0.04692	1	52	48	79	68	93	193	155	114	195	178
ENSMUSG00000029669	chr6	Tspan12	2.2E+07	2.2E+07	2626	-0.86955759	4.27699397	0.0001093	0.000439403	0.05643	-1	340	152	384	490	585	297	344	227	253	290
ENSMUSG00000021496	chr13	Pcbd2	5.6E+07	5.6E+07	546	0.828276765	2.89720988	0.0001097	0.000440726	0.04579	1	66	49	106	82	103	217	177	164	207	198
ENSMUSG00000026933	chr2	Camsap1	2.6E+07	2.6E+07	8368	-0.71756136	5.203306581	0.0001103	0.000442878	0.03934	-1	615	560	823	811	606	583	736	386	639	551
ENSMUSG00000028179	chr3	Cth	1.6E+08	1.6E+08	2263	-1.14300076	1.304632945	0.0001103	0.000442995	0.07475	-1	56	36	51	57	47	26	36	31	27	32
ENSMUSG00000049907	chr5	Rasl11b	7.4E+07	7.4E+07	1941	1.456958962	1.684372533	0.0001105	0.000443462	0.14131	1	12	8	23	54	29	137	75	68	83	106
ENSMUSG00000090516	chr9	Rps11-ps1	5.9E+07	5.9E+07	475	1.777428734	0.627987219	0.000111	0.000445569	0.1874	1	3	6	7	15	17	40	21	23	72	69
ENSMUSG00000030319	chr6	Cand2	1.2E+08	1.2E+08	4810	-0.86904613	6.77634198	0.0001112	0.000446148	0.05913	-1	1730	1329	3347	2648	1837	1548	2187	1159	1748	1395
ENSMUSG00000036499	chr10	Eea1	9.6E+07	9.6E+07	7836	-0.83658082	5.021748074	0.0001113	0.000446285	0.05363	-1	665	444	796	724	492	498	770	323	355	487
ENSMUSG00000024924	chr19	Vldlr	2.7E+07	2.7E+07	10068	-0.9356529	7.805492249	0.000112	0.000449241	0.06877	-1	3808	2358	7415	4029	5517	3383	5203	2140	2375	2972
ENSMUSG00000022584	chr15	Ly6c2	7.5E+07	7.5E+07	2740	2.0784878	0.813129779	0.0001126	0.000451458	0.26783	1	5	6	1	9	26	101	27	53	59	28
ENSMUSG00000037361	chr12	Sf3b6	4817608	4817819	1115	0.680838154	4.479482421	0.0001128	0.000452184	0.03422	1	257	171	286	231	357	722	486	489	537	582
ENSMUSG00000001151	chr10	Pcnt	7.6E+07	7.6E+07	9530	-0.99918567	6.173671891	0.0001129	0.000452223	0.07779	-1	1252	857	2458	1835	1001	906	1599	614	950	962
ENSMUSG00000000486	chr7	Sept1	1.3E+08	1.3E+08	2060	1.548565803	1.049716363	0.0001131	0.000453138	0.14763	1	10	12	14	8	31	74	41	43	35	105
ENSMUSG00000058748	chr8	Zfp958	4625840	4625966	1401	-1.07884492	1.838600121	0.0001133	0.00045371	0.07359	-1	88	50	84	80	54	62	52	37	35	48
ENSMUSG00000031148	chrX	Gpkow	7697131	7697395	3737	-0.72718579	4.131097649	0.0001136	0.000454634	0.03879	-1	303	250	438	357	292	309	347	216	227	262
ENSMUSG00000053332	chr1	Gas5	1.6E+08	1.6E+08	3760	0.745729176	5.04708509	0.0001136	0.000454634	0.04234	1	348	281	413	340	482	1217	600	768	717	952
ENSMUSG00000058388	chr3	Phtf1	1E+08	1E+08	7294	0.803162218	2.993777798	0.0001137	0.000454896	0.04338	1	67	61	98	89	121	255	229	156	189	206
ENSMUSG00000036698	chr15	Ago2	7.3E+07	7.3E+07	13705	-0.75982855	6.352945279	0.0001141	0.000456449	0.04524	-1	1401	1234	1877	1743	1438	1188	1542	935	1347	1257
ENSMUSG00000024943	chr19	Smc5	2.3E+07	2.3E+07	5730	-0.80845612	3.703174431	0.0001143	0.000456737	0.04762	-1	222	218	341	217	241	274	251	118	158	193
ENSMUSG00000032596	chr9	Uba7	1.1E+08	1.1E+08	6692	1.049415974	3.318779204	0.0001143	0.000456737	0.0795	1	78	86	89	68	163	478	218	156	231	328
ENSMUSG00000062101	chr17	Zfp119b	5.6E+07	5.6E+07	2166	-1.17209852	1.364060116	0.0001143	0.000456737	0.08146	-1	68	35	64	48	46	32	41	32	24	28
ENSMUSG00000034290	chr12	Nek9	8.5E+07	8.5E+07	5386	-0.82642826	7.658194622	0.0001144	0.000456859	0.05395	-1	3398	2764	5604	4142	3783	3189	4478	2004	2912	2637
ENSMUSG00000037608	chr10	Bclaf1	2E+07	2E+07	8426	-0.72140545	5.432619611	0.0001149	0.000458678	0.04017	-1	856	586	1047	840	714	838	800	536	521	685
ENSMUSG00000071540	chr14	3425401B19Rik	3.3E+07	3.3E+07	5547	-1.07547738	8.062955797	0.0001149	0.000458678	0.09068	-1	4634	2431	9804	6947	4695	2750	5610	2284	3246	4018
ENSMUSG00000076236	chr13	Mir682	7.6E+07	7.6E+07	96	0.973433888	3.630237689	0.0001149	0.000458678	0.06917	1	151	88	97	121	161	370	221	215	463	418
ENSMUSG00000043391	chr16	2510009E07Rik	2.2E+07	2.2E+07	5164	-0.67304697	5.288356991	0.0001151	0.00045947	0.03475	-1	600	585	913	790	720	768	744	459	625	535
ENSMUSG00000029575	chr5	Mmab	1.1E+08	1.1E+08	3530	-0.78192486	5.535888741	0.0001155	0.00046049	0.04749	-1	1001	718	870	912	832	744	1004	488	705	609
ENSMUSG00000036721	chr13	Zscan12	2.1E+07	2.1E+07	2228	-0.86131902	2.928420502	0.0001154	0.00046049	0.05105	-1	179	101	186	136	131	139	121	82	101	114
ENSMUSG00000032932	chr16	Hspa13	7.6E+07	7.6E+07	5894	-0.75625386	4.199081484	0.0001157	0.000461194	0.04254	-1	350	297	339	335	387	356	376	218	219	247
ENSMUSG00000030674	chr7	Qprt	1.3E+08	1.3E+08	2645	1.511725673	1.57182149	0.0001157	0.000461313	0.14791	1	13	26	12	24	32	118	38	65	121	91
ENSMUSG00000036246	chr8	Gmip	7E+07	7E+07	5552	1.104519993	3.125571081	0.0001161	0.000462538	0.08746	1	58	76	63	61	153	362	194	146	223	311
ENSMUSG00000005043	chr11	Sgsh	1.2E+08	1.2E+08	4414	0.74777811	3.54872621	0.0001164	0.000463536	0.03904	1	110	100	149	124	173	316	332	185	322	360
ENSMUSG00000021770	chr14	Samd8	2.2E+07	2.2E+07	7638	-0.8576885	6.21148721	0.0001165	0.000464038	0.05774	-1	1546	1422	1344	1450	1153	1221	1368	800	1061	1024
ENSMUSG00000086247	chr5	Gm15787	1.1E+08	1.1E+08	2992	-1.21025668	1.299913668	0.0001166	0.000464038	0.09075	-1	54	31	76	58	35	44	41	17	24	26
ENSMUSG00000025855	chr5	Prkar1b	1.4E+08	1.4E+08	3810	1.16243089	1.719089942	0.0001168	0.000465003	0.085	1	22	20	42	17	50	116	69	59	90	121
ENSMUSG00000031872	chr8	Bean1	1E+08	1E+08	3386	2.14745726	-0.77904929	0.0001171	0.000466068	0.16151	1	2	3	1	2	4	25	8	14	7	22
ENSMUSG00000013701	chr14	Timm23	3.2E+07	3.2E+07	1786	-0.79887686	6.804482515	0.0001174	0.000467038	0.05039	-1	1896	1541	3137	2227	2005	1635	2348	1185	1755	1549
ENSMUSG00000085208	chr11	Brip1os	8.6E+07	8.6E+07	6498	0.88531341	3.864110684	0.0001174	0.000467038	0.05809	1	133	102	172	101	278	560	313	267	442	378
ENSMUSG00000004446	chr6	Bid	1.2E+08	1.2E+08	3550	1.745629178	1.786402795	0.0001176	0.000467456	0.20681	1	10	23	14	6	63	166	85	83	82	113
ENSMUSG00000040883	chr9	Tmem205	2.2E+07	2.2E+07	862	1.076233326	4.41681704	0.0001178	0.000467999	0.08839	1	197	143	128	137	443	738	431	466	723	618
ENSMUSG00000029594	chr5	Rbm19	1.2E+08	1.2E+08	2963	-0.91700412	3.199825052	0.0001184	0.000470549	0.06009	-1	142	104	307	209	163	123	175	88	137	133
ENSMUSG00000020333	chr11	Acsl6	5.4E+07	5.4E+07	9914	-0.82205998	4.627838223	0.000119	0.000472614	0.05151	-1	400	347	758	533	357	308	501	304	354	361
ENSMUSG00000042724	chr12	Map3k9	8.2E+07	8.2E+07	10619	1.749515169	-0.0115656	0.0001191	0.000472867	0.16262	1	2	0	17	7	5	34	31	19	23	30
ENSMUSG00000037652	chr3	Phc3	3.1E+07	3.1E+07	17485	-0.69457487	4.230259542	0.0001193	0.00047378	0.03558	-1	350	267	473	327	327	346	286	238	254	352
ENSMUSG00000005501	chr1	Usp40	8.8E+07	8.8E+07	11871	-0.67735722	3.856842236	0.0001198	0.000475633	0.03278	-1	248	195	363	247	298	293	215	181	217	244
ENSMUSG00000035296	chr14	Sgcg	6.1E+07	6.1E+07	1878	-0.78726916	6.932978779	0.0001199	0.000475685	0.04912	-1	2422	1711	3107	2273	2164	1958	2546	1364	1576	1868
ENSMUSG00000006333	chr7	Rps9	3703993	3704064	2526	0.806004404	8.586961769	0.0001202	0.000476847	0.05179	1	3982	3100	5041	3631	5560	12813	7453	8065	10567	11705
ENSMUSG00000070544	chr2	Top1	1.6E+08	1.6E+08	10426	-0.68655563	5.02861981	0.000121	0.000480009	0.03609	-1	578	487	672	622	650	519	703	434	468	445
ENSMUSG00000052192	chr16	Gm5963	3.6E+07	3.6E+07	236	1.460687544	0.503118854	0.0001214	0.000481272	0.11222	1	9	4	13	15	11	39	22	29	57	46
ENSMUSG00000015357	chr9	Clpx	6.5E+07	6.5E+07	3494	-0.85165278	6.401079266	0.0001215	0.000481535	0.05729	-1	1481	963	2803	1803	1359	1489	1618	911	988	1274
ENSMUSG00000058006	chr4	Mdn1	3.3E+07	3.3E+07	21836	-0.79434058	3.530043598	0.0001221	0.000483678	0.04524	-1	205	183	261	252	183	185	183	148	163	184
ENSMUSG00000034673	chr17	Pbx2	3.5E+07	3.5E+07	3640	0.684930884	4.900032508	0.0001222	0.000484039	0.03577	1	302	222	382	307	546	988	659	545	826	803
ENSMUSG00000066440	chr12	Zfyve26	7.9E+07	7.9E+07	9368	-0.72106521	4.188636412	0.0001228	0.000486121	0.03881	-1	298	276	485	322	329	344	369	169	290	270

ENSMUSG00000020570	chr12	Sypl	3.3E+07	3.3E+07	7535	-0.79482495	7.202377747	0.0001231	0.000487151	0.0503	-1	2773	1980	3708	2857	2862	2273	3169	1745	1965	1987
ENSMUSG00000062203	chr16	Gspt1	1.1E+07	1.1E+07	4297	-0.74979691	5.792878152	0.0001232	0.000487591	0.04413	-1	1015	805	1360	1130	906	986	1039	745	767	715
ENSMUSG00000079575	chr6	Rbpsuh-rs3	4.7E+07	4.7E+07	1441	-1.50577503	1.214293688	0.0001232	0.000487591	0.14846	-1	59	45	56	48	39	35	51	13	15	11
ENSMUSG00000035165	chr7	Kcne3	1E+08	1E+08	1718	1.624549759	0.575028112	0.0001234	0.0004882	0.15099	1	10	8	5	3	24	62	32	38	37	41
ENSMUSG00000004285	chr6	Atp6v1f	2.9E+07	2.9E+07	1063	0.706149733	5.962077704	0.0001243	0.000491328	0.03915	1	692	553	762	655	904	1757	1406	1249	1835	1713
ENSMUSG00000026778	chr2	Prkcq	1.1E+07	1.1E+07	7081	-0.84887009	6.61383785	0.0001246	0.000492485	0.0572	-1	1979	1463	2433	2135	1382	1351	1833	1193	1265	1544
ENSMUSG00000051596	chr5	Otop1	3.8E+07	3.8E+07	3442	-3.36596646	2.176141677	0.0001247	0.000492942	0.72	-1	117	15	6	7	535	30	8	11	17	16
ENSMUSG00000043126	chr10	D830039M14Rik	6.1E+07	6.1E+07	1693	-0.89123733	3.200053107	0.0001248	0.000493012	0.05735	-1	146	121	242	211	185	127	206	74	137	126
ENSMUSG00000064120	chr17	Mocs1	4.9E+07	4.9E+07	3110	-0.67808578	4.073057514	0.0001249	0.000493392	0.03369	-1	305	213	316	358	366	337	278	200	273	252
ENSMUSG00000018068	chr11	Ints2	8.6E+07	8.6E+07	10609	-1.19371206	2.068543264	0.000125	0.000493436	0.09896	-1	76	83	121	81	67	70	91	26	37	43
ENSMUSG00000021458	chr13	2010111I01Rik	6.3E+07	6.3E+07	6349	0.752774039	5.036031529	0.000125	0.000493436	0.04389	1	297	218	629	415	328	882	823	717	786	1006
ENSMUSG00000060681	chrX	Slc9a6	5.7E+07	5.7E+07	4961	-0.67353939	5.367857497	0.000125	0.000493436	0.03526	-1	801	588	914	779	714	724	818	482	649	627
ENSMUSG00000023047	chr15	Amhr2	1E+08	1E+08	2002	1.505763974	3.013586751	0.0001258	0.000496466	0.16913	1	22	14	152	63	92	161	324	175	287	257
ENSMUSG00000022516	chr16	Nudt16l1	4939111	4939293	1269	0.787809439	4.287065248	0.0001266	0.000499355	0.04693	1	191	146	214	173	370	606	398	437	528	556
ENSMUSG00000024818	chr19	Slc25a45	5877808	5878095	2650	1.175841903	2.259772162	0.0001267	0.000499403	0.09312	1	33	46	34	27	72	203	101	93	133	144
ENSMUSG00000025362	chr10	Rps26	1.3E+08	1.3E+08	447	0.830487851	7.134554253	0.0001267	0.000499403	0.05502	1	1448	1132	1465	1549	2033	4349	2572	2999	4097	4508
ENSMUSG00000035439	chr8	Haus8	7.1E+07	7.1E+07	5278	0.986551606	1.915465203	0.0001274	0.000502205	0.06057	1	31	19	49	43	46	123	92	61	109	121
ENSMUSG00000006442	chr4	Srm	1.5E+08	1.5E+08	1599	0.980727513	3.383891296	0.0001277	0.000503196	0.07106	1	88	59	108	116	164	373	169	298	277	272
ENSMUSG00000103392	chr3	RP23-436F15.5	1E+07	1E+07	536	-0.922823	1.911693917	0.0001278	0.000503215	0.05233	-1	69	54	82	75	85	65	61	45	44	48
ENSMUSG00000040363	chrX	Bcor	1.2E+07	1.2E+07	7190	-0.74330766	4.585095241	0.000128	0.000504168	0.0421	-1	389	263	712	542	406	378	457	306	332	371
ENSMUSG00000031803	chr8	B3gnt3	7.2E+07	7.2E+07	2103	1.263158829	0.626082059	0.0001286	0.000506228	0.08296	1	7	6	22	14	15	60	38	27	42	41
ENSMUSG00000047746	chr16	Fbxo40	3.7E+07	3.7E+07	5517	-0.92017803	8.705562112	0.0001288	0.000506933	0.06787	-1	7179	5848	10886	10849	6419	5128	8543	3849	6271	6258
ENSMUSG00000066682	chr5	Pilrb2	1.4E+08	1.4E+08	1807	1.84646764	-0.19887399	0.000129	0.000507552	0.14573	1	5	6	0	4	8	42	20	12	26	21
ENSMUSG00000038740	chr2	Mvb12b	3.4E+07	3.4E+07	8741	-0.77392132	5.720493943	0.0001294	0.000509044	0.04734	-1	933	762	1204	1164	925	747	1105	528	946	718
ENSMUSG00000066442	chr9	Mthfs	8.9E+07	8.9E+07	7498	1.071731547	1.633519174	0.0001297	0.000510146	0.06887	1	22	22	29	29	43	115	63	65	75	99
ENSMUSG00000027706	chr3	Sec62	3.1E+07	3.1E+07	4343	-0.71203425	5.961998702	0.0001302	0.000511692	0.04019	-1	1363	849	1242	1083	1264	1119	1185	699	920	993
ENSMUSG00000015733	chr6	Capza2	1.8E+07	1.8E+07	5890	-0.82644062	8.093422025	0.0001304	0.000512422	0.05494	-1	5709	4481	5683	4793	5238	4362	5719	3050	3823	3494
ENSMUSG00000036902	chr8	Neto2	8.6E+07	8.6E+07	5610	-1.50956455	1.967969479	0.0001307	0.000513568	0.16233	-1	47	70	126	56	144	27	96	17	34	37
ENSMUSG00000031451	chr8	Gas6	1.3E+07	1.3E+07	2593	0.793893928	7.57825303	0.000131	0.000514378	0.05066	1	1403	1553	2870	2574	2264	6046	4802	3648	5450	5244
ENSMUSG00000065529	chr11	Mir22	7.5E+07	7.5E+07	95	-1.1338327	1.351682924	0.0001331	0.000522601	0.07902	-1	55	43	68	37	54	46	45	20	30	22
ENSMUSG00000029265	chr5	Dr1	1.1E+08	1.1E+08	3478	-0.73223219	4.243466871	0.0001333	0.000523434	0.04052	-1	336	262	464	356	367	296	442	212	240	284
ENSMUSG00000030055	chr6	Rab43	8.8E+07	8.8E+07	5526	0.708979987	3.814548377	0.0001336	0.000524199	0.0367	1	145	94	180	155	243	436	396	248	360	366
ENSMUSG00000031070	chr7	Mrgprf	1.5E+08	1.5E+08	2214	1.067163748	2.689952542	0.0001343	0.00052695	0.08056	1	48	52	40	58	109	220	147	165	186	157
ENSMUSG00000031600	chr8	Vps37a	4.1E+07	4.1E+07	6379	-0.81087149	6.158008712	0.0001346	0.000527962	0.05255	-1	1607	1297	1342	1077	1328	1257	1157	870	1015	1056
ENSMUSG00000055313	chr13	Pgbd1	2.1E+07	2.1E+07	3585	-1.29393217	0.900336724	0.0001346	0.000527962	0.09735	-1	44	29	58	37	24	23	33	15	16	21
ENSMUSG00000032405	chr9	Pias1	6.3E+07	6.3E+07	3855	-0.75436384	3.771255585	0.0001359	0.000532624	0.04199	-1	233	194	319	303	234	233	281	147	190	202
ENSMUSG00000025188	chr19	Hps1	4.3E+07	4.3E+07	5855	1.489711463	1.720984575	0.0001359	0.000532779	0.1491	1	19	26	10	14	54	143	74	58	104	109
ENSMUSG00000022951	chr16	Rcan1	9.2E+07	9.2E+07	2506	0.968118729	6.789653052	0.0001363	0.000533851	0.07517	1	779	545	2018	1432	1121	3335	2769	3173	2421	3112
ENSMUSG00000037370	chr10	Enpp1	2.5E+07	2.5E+07	10257	0.858625816	3.101209812	0.0001364	0.000534198	0.05164	1	84	74	95	104	91	279	220	217	185	213
ENSMUSG00000081214	chr1	Rpl35a-ps2	1.8E+08	1.8E+08	333	1.652726891	0.438929765	0.0001367	0.000535348	0.14524	1	9	7	3	13	11	36	23	22	49	61
ENSMUSG00000066148	chr4	Prpf4	6.2E+07	6.2E+07	5671	-0.6836856	5.077290408	0.0001369	0.000536003	0.03645	-1	548	461	799	768	554	520	662	399	551	542
ENSMUSG00000026853	chr2	Crat	3E+07	3E+07	5388	-0.91233836	9.413717098	0.0001372	0.000536981	0.06733	-1	10940	7933	22346	15652	12185	8837	14184	6197	9839	10325
ENSMUSG00000031986	chr8	Sprtn	1.2E+08	1.2E+08	2116	-1.22780299	1.784255982	0.0001375	0.000537863	0.10282	-1	72	51	106	67	64	58	78	23	27	28
ENSMUSG00000078622	chr11	Ccdc47	1.1E+08	1.1E+08	6414	-0.77380669	6.816090925	0.000138	0.000539579	0.04829	-1	2224	1728	2616	2112	1933	1912	2264	1317	1509	1623
ENSMUSG00000048200	chr7	Cracr2b	1.4E+08	1.4E+08	2764	0.994019872	3.462911975	0.0001382	0.000540299	0.07442	1	67	65	135	82	226	328	259	207	337	375
ENSMUSG00000096842	chr13	Gm10736	1.1E+08	1.1E+08	78	0.753812383	5.125337341	0.0001385	0.000541268	0.04463	1	369	271	527	306	517	1109	624	675	1216	898
ENSMUSG00000060212	chr8	Pcnxl2	1.3E+08	1.3E+08	9574	-1.75765193	0.00367438	0.0001385	0.000541421	0.16273	-1	19	9	43	29	11	4	14	6	8	11
ENSMUSG00000020580	chr12	Rock2	1.7E+07	1.7E+07	8012	-0.79603683	7.118547472	0.0001387	0.000541752	0.05122	-1	2266	2110	3449	3080	2334	2128	2775	1527	1962	2147
ENSMUSG00000052707	chr7	Tnrc6a	1.2E+08	1.2E+08	8471	-0.67176367	5.218081237	0.0001398	0.000546028	0.03549	-1	650	630	798	657	647	697	685	427	549	625
ENSMUSG00000039095	chr5	En2	2.8E+07	2.8E+07	3539	-1.79548625	-0.24629659	0.00014	0.000546483	0.15749	-1	21	19	9	24	14	7	7	8	10	3
ENSMUSG00000039787	chr2	Cercam	3E+07	3E+07	3383	1.230307437	2.954581782	0.0001422	0.000555234	0.11135	1	55	72	34	48	127	339	164	158	222	233
ENSMUSG00000030978	chr7	Rrm1	1E+08	1E+08	3997	-0.71514639	5.386615193	0.0001425	0.000555962	0.04055	-1	879	591	859	854	682	700	766	539	659	594
ENSMUSG00000030934	chr7	Oat	1.3E+08	1.3E+08	2155	-0.81625013	7.807775215	0.000143	0.00055808	0.05421	-1	4901	3646	4210	4511	3738	3811	3950	2637	3224	3181
ENSMUSG00000092534	chr7	Pagr1b	1.3E+08	1.3E+08	693	0.663255935	4.242410244	0.0001431	0.000558329	0.03303	1	169	137	291	250	275	573	468	325	505	534
ENSMUSG00000057375	chr4	Yipf1	1.1E+08	1.1E+08	6783	0.881707597	3.605685486	0.0001434	0.000559216	0.05838	1	90	76	131	117	247	414	313	206	351	352
ENSMUSG00000037395	chr1	Rcor3	1.9E+08	1.9E+08	13622	-0.65244133	4.509339518	0.0001437	0.000560236	0.03236	-1	350	252	621	431	497	417	447	280	331	357
ENSMUSG00000073609	chr1	D2hgdh	9.4E+07	9.4E+07	4281	-0.87581057	3.377019472	0.0001438	0.000560236	0.05674	-1	181	154	279	201	197	130	228	118	162	112
ENSMUSG00000030824	chr7	Nucb1	4.5E+07	4.5E+07	5796	0.754448562	6.384081944	0.000144	0.00056101	0.046	1	783	536	1185	892	1447	2618	1989	1501	2506	2299
ENSMUSG00000039841	chr6	Zfp800	2.8E+07	2.8E+07	4827	-1.16714202	1.39169924	0.0001441	0.000561158	0.08636	-1	57	46	72	49	40	35	52	22	24	31
ENSMUSG00000021610	chr13	Clptm1l	7.4E+07	7.4E+07	2378	0.672009392	5.660987062	0.0001446	0.000563198	0.03597	1	502	411	687	516	874	1566	1231	998	1321	1312
ENSMUSG00000007777	chr11	0610009B22Rik	5.2E+07	5.2E+07	998	-0.76078791	4.330522682	0.0001457	0.000566797	0.04477	-1	420	351	395	344	343	426	354	240	267	263
ENSMUSG00000038132	chr13	Rbm24	4.6E+07	4.6E+07	3215	-0.74950157	7.043092965	0.0001456	0.000566797	0.04572	-1	2489	2019	2990	2424	2450	2259	2644	1432	1885	2028
ENSMUSG00000059970	chr12	Hspa2	7.6E+07	7.6E+07	2520	1.110926111	2.933303946	0.0001457	0.000566797	0.09198	1	36	39	138	63	102	234	272	213	167	159
ENSMUSG00000033526	chr2	Ppip5k1	1.2E+08	1.2E+08	12486	-1.22431645	6.700128074	0.0001466	0.000569969	0.12005	-1	1689	881	4506	3142	1282	1452	2124	820	986	1165
ENSMUSG00000052146	chr17	Rps10	2.8E+07	2.8E+07	1937	0.787208459	7.219202252	0.0001466	0.000569969	0.05045	1	1584	1243	1855	1555	2023	5186	2793	3197	4155	4164
ENSMUSG00000076372	chr16	Mir568	4.4E+07	4.4E+07	83	-1.33118553	0.728077209	0.0001467	0.000570169	0.10569	-1	43	23	22	36	46	22	29	12	12	19
ENSMUSG00000045594	chr9	Glb1	1.1E+08	1.1E+08	2395	1.096414167	2.518616738	0.0001468	0.000570568	0.08626	1	46	37	53	28	112	204	142	120	153	172

ENSMUSG00000032528	chr9	Vipr1	1.2E+08	1.2E+08	5564	-1.15919134	1.266602304	0.0001471	0.000571666	0.0814	-1	34	38	84	33	60	31	40	23	27	28
ENSMUSG00000040904	chr11	Gm21988	7E+07	7E+07	1692	0.746422237	6.346210774	0.0001476	0.000573428	0.04512	1	839	567	1083	904	1282	2247	1782	1513	2596	2404
ENSMUSG00000020423	chr1	Btg2	1.3E+08	1.3E+08	2743	0.825413688	4.776321858	0.0001482	0.000575453	0.05387	1	211	166	337	365	449	660	535	651	784	918
ENSMUSG00000043342	chr2	Hoxd9	7.5E+07	7.5E+07	2136	1.014276767	3.164835467	0.0001487	0.000577192	0.07594	1	70	76	94	94	104	154	259	168	382	249
ENSMUSG00000103508	chr9	Map4	1.1E+08	1.1E+08	3378	-1.00111906	7.72541348	0.0001488	0.000577413	0.08145	-1	3992	2722	6099	5398	3245	3094	5191	1768	2474	2309
ENSMUSG00000090019	chr6	Gimap1	4.9E+07	4.9E+07	1872	1.060821789	1.956028265	0.000149	0.000578004	0.07545	1	37	12	58	38	45	122	90	86	102	122
ENSMUSG00000059474	chr11	Mbtd1	9.4E+07	9.4E+07	13896	-0.85757364	3.005058231	0.0001492	0.000578735	0.05276	-1	181	115	184	153	134	122	118	104	105	131
ENSMUSG00000022562	chr15	Oplah	7.6E+07	7.6E+07	5596	-0.87491953	5.999358698	0.0001496	0.000579966	0.06185	-1	938	501	2190	1479	1481	1051	949	663	1063	961
ENSMUSG00000028127	chr3	Abcd3	1.2E+08	1.2E+08	3399	-0.78092828	6.305639591	0.0001497	0.000580188	0.04946	-1	1294	868	2502	1583	1528	1223	1547	873	1102	1292
ENSMUSG00000002227	chr3	Mov10	1E+08	1E+08	4223	1.324526478	1.959151658	0.0001498	0.00058045	0.12333	1	21	23	19	27	74	154	76	70	126	134
ENSMUSG00000030172	chr6	Erc1	1.2E+08	1.2E+08	11598	-0.83621016	5.191893018	0.0001499	0.000580822	0.05589	-1	546	456	950	1052	547	531	758	381	510	543
ENSMUSG00000046330	chr1	Rpl37a	7.3E+07	7.3E+07	584	0.788337492	7.514343091	0.0001505	0.000583028	0.05084	1	2054	1487	2136	1983	2445	5832	3533	3695	5599	5288
ENSMUSG00000037826	chr6	Ppm1k	5.8E+07	5.8E+07	5560	-0.95739241	3.797767034	0.0001512	0.000585671	0.07061	-1	266	121	490	344	205	231	237	127	162	228
ENSMUSG00000021156	chr13	Zmynd11	9684836	9686984	7055	-0.73980462	6.406423538	0.0001514	0.000585933	0.04453	-1	1583	1242	1874	1766	1465	1401	1674	958	1218	1345
ENSMUSG00000031458	chr8	Coprs	1.4E+07	1.4E+07	802	0.810119617	3.165532449	0.0001514	0.000585933	0.04696	1	85	61	140	108	98	272	192	177	274	250
ENSMUSG00000008855	chr11	Hdac5	1E+08	1E+08	8780	-0.76803308	5.981026772	0.0001515	0.000585998	0.04777	-1	1099	776	1668	1392	1136	999	1377	626	1019	857
ENSMUSG00000042628	chr12	Zfyve1	8.4E+07	8.4E+07	3869	-0.67491745	4.73017874	0.0001516	0.000586384	0.03561	-1	439	390	690	458	487	444	587	266	402	434
ENSMUSG00000030102	chr6	Itpr1	1.1E+08	1.1E+08	9848	-0.69330551	4.316683762	0.0001522	0.000588386	0.03692	-1	395	269	385	291	522	387	386	222	280	309
ENSMUSG00000028923	chr4	Necap2	1.4E+08	1.4E+08	3095	0.682256696	4.986178938	0.0001525	0.000589572	0.03671	1	307	235	421	316	598	1033	733	580	921	785
ENSMUSG00000095098	chr19	Ccdc85b	5456789	5457397	609	0.861905122	4.396106432	0.000153	0.000591175	0.05869	1	174	101	325	206	374	589	423	461	741	556
ENSMUSG00000037075	chr15	Rnf139	5.9E+07	5.9E+07	4348	-0.68452978	5.617385733	0.0001532	0.000592015	0.03765	-1	901	665	1260	822	946	965	976	603	660	706
ENSMUSG00000026634	chr1	Angel2	1.9E+08	1.9E+08	5559	-0.58900584	4.999190709	0.0001537	0.000593832	0.02707	-1	524	451	734	560	629	589	616	373	533	540
ENSMUSG00000040170	chr1	Fmo2	1.6E+08	1.6E+08	5609	-0.93141735	3.389928082	0.0001546	0.000597037	0.06531	-1	187	123	242	188	318	183	211	118	78	155
ENSMUSG00000042961	chr15	Egflam	7206120	7207802	6121	-0.72441154	4.556996452	0.0001546	0.000597037	0.04102	-1	502	320	511	293	597	366	450	260	344	417
ENSMUSG00000032939	chr8	Nup93	9.4E+07	9.4E+07	2882	0.651870047	4.271605453	0.0001553	0.000599398	0.03224	1	192	151	301	206	299	636	428	384	472	513
ENSMUSG00000041057	chr17	Wdr43	7.2E+07	7.2E+07	3450	-0.68056793	4.843432118	0.0001553	0.000599398	0.0364	-1	513	421	668	565	476	527	550	398	369	422
ENSMUSG00000020385	chr11	Clk4	5.1E+07	5.1E+07	5797	-0.6289545	4.84171441	0.0001561	0.000602304	0.03091	-1	501	359	705	501	588	550	554	325	369	547
ENSMUSG00000067158	chr1	Col4a4	8.2E+07	8.2E+07	10612	-1.46523314	1.073991203	0.0001574	0.000607054	0.14186	-1	27	40	57	21	86	30	33	8	18	26
ENSMUSG00000035268	chr2	Pkig	1.6E+08	1.6E+08	3990	0.757883072	6.159109323	0.0001576	0.000607463	0.04688	1	685	432	1259	868	891	1811	1940	1458	2133	1890
ENSMUSG00000029263	chr5	Pigg	1.1E+08	1.1E+08	4573	-0.98074011	2.939333405	0.0001578	0.000608085	0.071	-1	161	89	242	161	121	112	167	70	90	95
ENSMUSG00000032412	chr9	Atp1b3	9.6E+07	9.6E+07	2389	0.855761548	5.689252996	0.0001582	0.000609607	0.05945	1	437	347	537	431	1106	1782	1249	1101	1304	1436
ENSMUSG00000020657	chr12	Dnajc27	4082574	4082873	4713	-0.89887899	6.323623723	0.0001585	0.000610603	0.06599	-1	1321	884	2944	1657	1334	1102	1701	820	1115	1066
ENSMUSG00000022504	chr16	Ciita	1E+07	1E+07	5254	1.819547164	0.80804997	0.0001589	0.000611805	0.21127	1	7	11	9	4	22	106	41	33	16	69
ENSMUSG00000064370	chrMT	mt-Cytb	14145	15288	1144	-0.9940441	13.81490209	0.0001589	0.000611805	0.08128	-1	271571	137854	485305	348630	254356	208452	323606	126158	157817	194811
ENSMUSG00000025384	chr11	2310003H01Rik	1.2E+08	1.2E+08	5212	-0.7381012	4.067560134	0.0001591	0.000612516	0.04184	-1	253	206	445	359	340	270	349	167	300	220
ENSMUSG00000026972	chr2	Arrdc1	2.5E+07	2.5E+07	2510	1.162380061	3.530271026	0.0001592	0.000612549	0.1039	1	84	101	63	62	220	394	249	229	348	420
ENSMUSG00000024889	chr19	Rce1	4622551	4623242	1446	0.911098378	2.920527831	0.0001594	0.000613158	0.06069	1	66	44	84	75	131	254	152	168	197	231
ENSMUSG00000095990	chr17	Zfp97	1.7E+07	1.7E+07	2684	-1.37107718	1.324323935	0.0001595	0.000613597	0.12818	-1	56	41	76	45	48	46	53	10	18	19
ENSMUSG00000020982	chr12	Nemf	6.9E+07	6.9E+07	3721	-0.78185958	4.476004405	0.0001597	0.000614146	0.04827	-1	387	376	522	439	360	382	509	239	259	314
ENSMUSG00000021996	chr14	Esd	7.5E+07	7.5E+07	3366	0.697432818	6.315875466	0.0001599	0.000614639	0.03976	1	845	629	1122	844	1206	2247	1884	1708	1970	2314
ENSMUSG00000063108	chr9	Zfp26	2E+07	2E+07	9631	-0.79367958	3.045013	0.0001605	0.000616796	0.04503	-1	121	125	198	154	190	139	157	81	110	138
ENSMUSG00000055447	chr16	Cd47	5E+07	5E+07	5277	0.839530286	5.642151028	0.0001608	0.000617899	0.05722	1	505	383	502	369	985	1905	1200	959	1222	1400
ENSMUSG00000032047	chr9	Acat1	5.4E+07	5.4E+07	3758	-0.88348471	8.066257331	0.0001618	0.000621455	0.06445	-1	4604	2880	9160	5794	4636	4127	5491	2814	3295	3879
ENSMUSG00000040675	chr10	Mthfd1l	3973118	3973478	4435	1.53280627	0.297544979	0.0001625	0.000623945	0.13054	1	10	3	8	8	14	43	19	41	37	24
ENSMUSG00000040618	chr14	Pck2	5.6E+07	5.6E+07	3400	1.015666801	3.020557115	0.0001628	0.000625002	0.07683	1	57	57	86	60	148	303	167	131	298	222
ENSMUSG00000021252	chr12	0610007P14Rik	8.6E+07	8.6E+07	4235	1.098410752	2.618302342	0.0001633	0.000626843	0.08759	1	50	46	40	47	106	256	118	144	166	163
ENSMUSG00000065979	chr16	Cpped1	1.2E+07	1.2E+07	5205	-0.63491978	5.526077543	0.0001642	0.00062984	0.0325	-1	777	588	1079	850	974	837	924	553	738	692
ENSMUSG00000019796	chr10	Lrp11	7589800	7590613	3418	0.826204718	2.977040838	0.0001642	0.000629904	0.04791	1	72	72	86	87	101	231	246	175	177	190
ENSMUSG00000022195	chr15	6030458C11Rik	1.3E+07	1.3E+07	3974	-0.69171683	5.378723626	0.0001646	0.000631251	0.03869	-1	806	668	836	778	708	745	813	466	625	659
ENSMUSG00000021375	chr13	Kif13a	4.7E+07	4.7E+07	6866	-0.80798847	7.000557851	0.0001648	0.000631759	0.05394	-1	2200	1741	3560	2832	2030	1921	2616	1359	1897	1879
ENSMUSG00000103480	chr3	Bdh2	1.4E+08	1.4E+08	768	1.297371924	0.895750877	0.0001656	0.000634609	0.09413	1	19	15	10	12	17	63	37	34	65	55
ENSMUSG00000039844	chr2	Rapgef1	3E+07	3E+07	7385	-0.88802372	7.569967716	0.0001661	0.000636309	0.06525	-1	2858	2279	5982	4744	3157	2660	3919	1780	2728	2824
ENSMUSG00000037855	chr10	Zfp365	6.8E+07	6.8E+07	5205	1.500425668	-0.02561824	0.0001665	0.00063768	0.09303	1	7	5	7	7	7	45	18	18	23	27
ENSMUSG00000057322	chr11	Rpl38	1.1E+08	1.1E+08	542	0.800292735	6.487190031	0.0001667	0.000638307	0.05278	1	879	648	1190	1050	1236	2942	1492	2046	2630	2583
ENSMUSG00000034973	chr9	Dopey1	8.6E+07	8.6E+07	20476	-0.74823543	3.717246144	0.0001671	0.000639507	0.04218	-1	237	176	354	259	218	233	234	174	165	200
ENSMUSG00000041028	chr14	Ghitm	3.7E+07	3.7E+07	3081	-0.83227881	8.83765271	0.0001671	0.000639507	0.05763	-1	9329	5420	13750	8033	8575	7356	9744	4907	6180	6073
ENSMUSG00000020227	chr10	Irak3	1.2E+08	1.2E+08	3676	0.900539669	2.684280474	0.0001676	0.000641366	0.05714	1	52	47	65	61	111	240	159	126	150	180
ENSMUSG00000072969	chrX	Armcx5	1.4E+08	1.4E+08	4247	-0.89610671	2.453939756	0.0001678	0.000641648	0.0555	-1	107	72	134	104	118	81	99	64	54	92
ENSMUSG00000044617	chr10	Zbtb39	1.3E+08	1.3E+08	5946	-0.79660245	3.023239254	0.0001683	0.000643509	0.04543	-1	154	114	207	141	159	124	137	102	136	106
ENSMUSG00000020738	chr11	Sumo2	1.2E+08	1.2E+08	1736	-0.65410849	4.626090502	0.0001694	0.000647463	0.03365	-1	458	375	570	404	450	462	496	303	396	328
ENSMUSG00000027805	chr3	Pfn2	5.8E+07	5.8E+07	3017	-0.75822457	7.340818935	0.0001695	0.000647463	0.0478	-1	3161	2322	3663	2946	3244	2442	3370	1854	2516	2290
ENSMUSG00000033871	chr18	Ppargc1b	6.1E+07	6.1E+07	3990	-1.1545728	3.122988258	0.0001694	0.000647463	0.10279	-1	155	67	322	272	118	109	137	70	129	113
ENSMUSG00000035239	chr7	Neu3	1E+08	1E+08	3341	-0.80844272	3.283158289	0.0001697	0.000648216	0.04854	-1	210	162	186	144	212	156	158	114	160	137
ENSMUSG00000049932	chr9	H2afx	4.4E+07	4.4E+07	1384	0.884562951	2.770633088	0.0001697	0.000648216	0.05557	1	52	51	84	64	110	242	161	133	211	156
ENSMUSG00000041961	chr11	Znrf3	5276324	5279761	7893	-1.00724371	1.996176249	0.00017	0.000648813	0.06781	-1	72	48	123	85	74	50	74	47	46	50
ENSMUSG00000032012	chr9	Pvrl1	4.4E+07	4.4E+07	5054	1.014788964	2.097309001	0.0001701	0.000649333	0.0702	1	44	26	48	38	53	149	95	121	114	85
ENSMUSG00000049734	chr9	Trex1	1.1E+08	1.1E+08	1314	0.654574649	4.616738578	0.0001702	0.000649502	0.03354	1	255	198	342	295	356	752	484	492	756	599

ENSMUSG00000027508	chr3	Pag1	9687479	9694129	9580	-1.25977813	2.447712035	0.0001704	0.000650011	0.11816	-1	121	147	61	110	97	72	60	55	84	57
ENSMUSG00000022148	chr15	Fyb	6579871	6581046	5186	0.787599662	3.403963651	0.0001711	0.000652377	0.046	1	91	78	186	119	116	384	253	198	264	284
ENSMUSG00000063838	chr7	Cdc42ep5	4151260	4151787	1288	1.420181548	1.710770869	0.0001717	0.000654461	0.14223	1	14	19	21	15	63	117	59	63	134	100
ENSMUSG00000026637	chr1	Traf5	1.9E+08	1.9E+08	4566	0.939261411	2.092171275	0.0001719	0.000655255	0.05689	1	41	35	46	37	54	154	94	75	115	129
ENSMUSG00000026594	chr1	Ralgps2	1.6E+08	1.6E+08	12085	1.107688058	1.460187976	0.0001723	0.000656402	0.07406	1	32	20	26	23	22	114	71	47	64	79
ENSMUSG00000037318	chr1	Traf3ip3	1.9E+08	1.9E+08	5756	1.386698712	0.547209701	0.0001736	0.000661348	0.10287	1	8	10	17	10	10	62	22	26	48	42
ENSMUSG00000031402	chrX	Mpp1	7.5E+07	7.5E+07	5343	0.853731286	5.10842331	0.0001741	0.000663086	0.05912	1	381	303	259	263	634	1270	840	654	974	885
ENSMUSG00000036856	chr4	Wnt4	1.4E+08	1.4E+08	4194	-1.1817369	4.104243758	0.0001744	0.000663861	0.11188	-1	425	401	156	365	333	191	162	170	304	249
ENSMUSG00000015023	chr8	Ddx19a	1.1E+08	1.1E+08	2957	-0.63094918	4.247149535	0.000175	0.00066625	0.03051	-1	356	259	422	324	374	353	335	258	297	287
ENSMUSG00000031392	chrX	Irak1	7.4E+07	7.4E+07	4716	-0.68528521	5.94276721	0.0001752	0.000666708	0.03871	-1	1040	929	1402	1202	1107	1212	1164	671	940	940
ENSMUSG00000047030	chr2	Spata2	1.7E+08	1.7E+08	4510	-0.64958135	4.553027514	0.0001753	0.000666708	0.0333	-1	387	376	477	445	444	409	463	245	414	370
ENSMUSG00000013736	chr6	Trnt1	1.1E+08	1.1E+08	3869	-0.68012131	3.99914642	0.0001755	0.000667286	0.03533	-1	260	219	388	324	293	305	290	212	210	247
ENSMUSG00000042650	chr11	Alkbh5	6.1E+07	6.1E+07	5987	-0.75163633	7.363477204	0.000176	0.00066918	0.04723	-1	2875	2370	3971	3160	3234	2625	3484	1706	2550	2430
ENSMUSG00000028541	chr4	B4galt2	1.2E+08	1.2E+08	5031	0.970361695	2.893025459	0.0001762	0.000669484	0.06884	1	56	76	83	59	93	291	156	134	253	176
ENSMUSG00000037674	chr9	Rfx7	7.3E+07	7.3E+07	15302	-0.77568021	4.473647333	0.0001761	0.000669484	0.04805	-1	408	304	564	498	332	320	499	239	323	315
ENSMUSG00000013846	chr15	St3gal1	6.7E+07	6.7E+07	4985	0.794054171	4.913816289	0.0001764	0.000670241	0.05099	1	337	242	338	191	575	886	755	628	828	833
ENSMUSG00000059552	chr11	Trp53	7E+07	7E+07	4045	0.727850153	4.504675176	0.0001768	0.000671331	0.04174	1	220	221	237	238	358	616	470	461	673	677
ENSMUSG00000028417	chr4	Tal2	5.4E+07	5.4E+07	2971	1.13842905	1.201291291	0.0001773	0.000673077	0.07679	1	20	9	22	28	24	85	78	39	58	52
ENSMUSG00000001467	chr5	Cyp51	4081145	4083303	4286	0.80766921	3.782851873	0.0001773	0.000673111	0.05071	1	102	83	175	147	270	468	371	273	342	352
ENSMUSG00000030386	chr7	Zfp606	1.2E+07	1.2E+07	7680	-0.94482712	3.014694543	0.0001779	0.00067523	0.06731	-1	154	109	238	177	123	149	165	82	86	91
ENSMUSG00000069972	chr7	Rps13-ps2	8.9E+07	8.9E+07	453	1.077066137	2.613298529	0.0001781	0.000675509	0.08508	1	55	46	34	57	96	168	143	105	216	211
ENSMUSG00000069874	chr11	Irgm2	5.8E+07	5.8E+07	3621	1.040682558	4.547099812	0.0001781	0.000675601	0.08759	1	264	132	277	242	244	1321	431	633	374	497
ENSMUSG00000037990	chr10	Sh3rf3	5.9E+07	5.9E+07	7242	1.294479736	0.655614135	0.0001784	0.000676616	0.0864	1	15	9	9	15	14	58	35	40	35	42
ENSMUSG00000035762	chr13	Tmem161b	8.4E+07	8.4E+07	2572	-0.82233477	3.402610418	0.000179	0.000678542	0.05098	-1	170	133	341	201	190	176	203	124	129	154
ENSMUSG00000020566	chr12	Atp6v1c2	1.7E+07	1.7E+07	2070	2.1840815	-0.15898906	0.0001791	0.000678788	0.27433	1	1	2	3	1	14	21	59	10	16	24
ENSMUSG00000028057	chr3	Rit1	8.9E+07	8.9E+07	3229	0.654294323	4.753769071	0.0001793	0.00067941	0.03407	1	318	203	400	234	454	868	625	512	699	710
ENSMUSG00000024793	chr4	Tnfrsf25	1.5E+08	1.5E+08	2277	1.536947215	0.591286686	0.0001805	0.000683616	0.13769	1	11	10	5	6	20	44	31	26	39	71
ENSMUSG00000045871	chr14	Slitrk6	1.1E+08	1.1E+08	4242	1.768028994	-0.53408055	0.0001807	0.000684097	0.11869	1	5	2	5	2	5	25	12	17	11	24
ENSMUSG00000078139	chr13	AK157302	2.1E+07	2.1E+07	1924	-1.38309506	2.198189418	0.0001811	0.000685562	0.14364	-1	96	72	151	104	73	26	115	24	54	44
ENSMUSG00000075706	chr10	Gpx4	8E+07	8E+07	1724	0.788864042	8.513251233	0.000182	0.000688731	0.05241	1	3628	2517	4561	3361	6713	10667	9470	7020	10491	10349
ENSMUSG00000002458	chr2	Rgs19	1.8E+08	1.8E+08	2230	1.188756967	2.216607343	0.0001822	0.000689192	0.10259	1	39	29	31	23	89	200	116	98	122	118
ENSMUSG00000020621	chr12	Rdh14	1E+07	1E+07	1472	-0.6667708	5.316300112	0.0001822	0.000689192	0.03625	-1	723	525	1009	754	689	695	829	492	600	569
ENSMUSG00000020904	chr11	Cfap52	6.8E+07	6.8E+07	2320	1.509978942	0.501648667	0.0001823	0.000689571	0.13031	1	18	5	10	6	11	40	26	48	35	41
ENSMUSG00000099764	chr16	Rps10-ps2	2.1E+07	2.1E+07	496	0.84535063	3.260234582	0.0001828	0.000691218	0.0528	1	97	87	106	107	106	336	176	205	285	252
ENSMUSG00000020166	chr10	Cnot2	1.2E+08	1.2E+08	3711	-0.62146326	4.647065763	0.0001832	0.000692445	0.03053	-1	433	341	580	451	487	435	542	300	401	365
ENSMUSG00000025779	chr1	Ly96	1.7E+07	1.7E+07	1021	1.458518756	0.434680543	0.0001846	0.000697335	0.11905	1	5	5	17	12	11	49	26	39	22	46
ENSMUSG00000035936	chr13	Aldh5a1	2.5E+07	2.5E+07	5647	-0.74470336	3.846317898	0.0001851	0.000699307	0.04275	-1	218	145	417	301	317	216	260	168	246	215
ENSMUSG00000021264	chr12	Yy1	1.1E+08	1.1E+08	2902	-0.64273132	4.512234707	0.0001857	0.000701294	0.03256	-1	419	305	546	401	429	396	464	305	314	353
ENSMUSG00000004633	chr6	Chn2	5.4E+07	5.4E+07	5745	1.204973337	1.104818807	0.0001867	0.000704882	0.0877	1	12	14	23	15	29	83	45	29	67	72
ENSMUSG00000015757	chr10	Ppil4	7792891	7793020	6450	-0.65430072	3.970268829	0.000187	0.000705986	0.03285	-1	272	233	348	292	286	289	292	181	245	253
ENSMUSG00000015461	chr17	Atf6b	3.5E+07	3.5E+07	2757	0.772807786	3.874263533	0.0001872	0.000706261	0.04624	1	143	132	163	127	248	543	327	281	419	342
ENSMUSG00000049090	chr18	Zadh2	8.4E+07	8.4E+07	3321	-0.67717288	5.800259162	0.0001872	0.000706261	0.03798	-1	1024	685	1330	995	1200	948	1195	659	770	876
ENSMUSG00000039001	chr2	Rps21	1.8E+08	1.8E+08	810	0.800005651	7.196367398	0.0001873	0.000706384	0.05381	1	1542	1215	1760	1532	2035	4954	2591	3088	4577	4031
ENSMUSG00000074846	chr2	Gm10774	1.3E+08	1.3E+08	204	1.110524234	1.499077978	0.0001875	0.000706787	0.08031	1	33	9	32	27	30	75	68	71	82	79
ENSMUSG00000083716	chr2	Gm13436	3.7E+07	3.7E+07	567	0.951317963	3.032820528	0.0001875	0.000706916	0.06869	1	57	47	97	89	137	193	175	167	268	287
ENSMUSG00000038500	chr17	Prr3	3.6E+07	3.6E+07	3783	1.317870538	1.765213282	0.0001878	0.000707521	0.12537	1	29	9	38	16	56	115	58	71	98	139
ENSMUSG00000029672	chr6	Fam3c	2.2E+07	2.2E+07	3713	0.644473333	3.895380955	0.0001889	0.000711475	0.03131	1	154	124	211	155	236	438	381	287	364	395
ENSMUSG00000080268	chr19	Brms1	5041404	5041490	1338	0.625424667	4.221053586	0.0001897	0.00071458	0.03014	1	197	149	255	217	296	485	521	331	488	508
ENSMUSG00000029778	chr6	Adcyap1r1	5.5E+07	5.5E+07	6601	1.019352952	2.809025867	0.0001898	0.000714709	0.07679	1	69	66	50	56	94	230	137	177	170	227
ENSMUSG00000020364	chr11	Zfp354a	5.1E+07	5.1E+07	4318	-0.89474875	2.039887718	0.0001901	0.000715536	0.05341	-1	86	56	96	82	76	64	71	42	58	58
ENSMUSG00000009291	chr10	Pttg1ip	7.8E+07	7.8E+07	3426	0.844229746	5.885592119	0.0001903	0.000716095	0.05944	1	518	426	652	466	1217	2140	1292	1129	1533	1817
ENSMUSG00000029475	chr5	Kdm2b	1.2E+08	1.2E+08	11818	-0.79226321	3.196049451	0.0001905	0.000716898	0.04673	-1	192	125	219	164	170	167	185	99	116	127
ENSMUSG00000022749	chr16	Tbc1d23	5.7E+07	5.7E+07	3648	-0.63642307	4.575455577	0.0001928	0.000725153	0.03233	-1	427	333	535	412	478	465	524	253	340	368
ENSMUSG00000066647	chr7	Gm5113	3E+07	3E+07	3002	-1.14292818	2.865244053	0.0001937	0.000728218	0.10088	-1	123	96	251	187	105	84	172	69	66	76
ENSMUSG00000024911	chr19	Fibp	5460607	5460778	1240	0.614375078	4.585133008	0.0001939	0.000729118	0.02985	1	251	189	332	289	384	679	527	455	672	656
ENSMUSG00000001768	chr2	Rin2	1.5E+08	1.5E+08	5399	0.836390423	4.853845837	0.0001949	0.000732118	0.05718	1	396	249	262	195	442	1162	746	534	645	790
ENSMUSG00000019872	chr10	Smpdl3a	5.8E+07	5.8E+07	2065	-0.76950999	6.385851516	0.0001948	0.000732118	0.04986	-1	1774	1344	1734	1416	1544	1355	1776	876	1149	1289
ENSMUSG00000002688	chr12	Prkd1	5E+07	5E+07	3778	-1.16556993	2.434899789	0.0001961	0.000736704	0.10274	-1	85	60	132	66	243	96	91	43	59	57
ENSMUSG00000020838	chr11	Slc6a4	7.7E+07	7.7E+07	4531	1.572619635	0.852738092	0.0001963	0.000737069	0.14862	1	9	22	8	7	13	82	35	39	54	49
ENSMUSG00000056174	chr4	Col8a2	1.3E+08	1.3E+08	4489	1.072086297	2.840954643	0.0001966	0.000738204	0.08697	1	26	66	79	79	91	303	194	121	171	216
ENSMUSG00000020273	chr11	Papolg	2.4E+07	2.4E+07	5491	-1.02902365	2.331247031	0.0001968	0.000738629	0.07766	-1	96	83	128	110	81	80	104	48	40	69
ENSMUSG00000009112	chr6	Bcl2l13	1.2E+08	1.2E+08	6933	-0.78886838	6.604257486	0.0001983	0.000743895	0.05259	-1	1722	1248	2840	2092	1489	1588	1931	978	1516	1431
ENSMUSG00000024251	chr17	Thada	8.4E+07	8.4E+07	7884	-0.77408008	3.486030199	0.0001984	0.00074418	0.046	-1	215	156	267	210	213	148	236	113	173	183
ENSMUSG00000037487	chr15	Ubr5	3.8E+07	3.8E+07	9790	-0.78866354	6.95576607	0.0001984	0.00074418	0.05269	-1	2040	1790	3303	2638	2119	1946	2648	1421	1580	1843
ENSMUSG00000034032	chr2	Rpap1	1.2E+08	1.2E+08	6636	-0.68876135	4.438865929	0.0001995	0.000747876	0.03814	-1	345	293	516	472	394	370	448	208	397	310
ENSMUSG00000035595	chr10	1600002K03Rik	8E+07	8E+07	678	0.984326985	2.577672441	0.0001995	0.000747876	0.06954	1	56	56	47	47	85	187	120	129	181	181
ENSMUSG00000041827	chr5	Oasl1	1.1E+08	1.1E+08	2608	1.533013289	0.260904035	0.0002021	0.000757328	0.13312	1	3	5	8	6	20	43	33	18	47	24

ENSMUSG00000063179	chr7	Pstk	1.3E+08	1.3E+08	2179	-0.64036024	4.555472433	0.0002022	0.000757622	0.03282	-1	395	319	591	452	406	421	480	297	353	346
ENSMUSG00000042043	chr13	Tbca	9.5E+07	9.5E+07	503	0.685876041	4.656964567	0.0002027	0.000759034	0.03818	1	290	163	344	277	413	891	490	526	656	645
ENSMUSG00000057895	chr9	Zfp105	1.2E+08	1.2E+08	2130	1.409094317	0.188082756	0.0002039	0.00076338	0.09636	1	13	6	9	5	8	37	24	31	30	27
ENSMUSG00000019979	chr10	Apaf1	9.1E+07	9.1E+07	9028	1.027085837	2.371938098	0.0002044	0.00076522	0.07702	1	33	42	76	26	79	170	125	114	139	150
ENSMUSG00000061080	chr16	Lsamp	4E+07	4E+07	17213	1.439635616	1.293214377	0.0002051	0.000767377	0.13571	1	19	24	11	18	17	88	37	78	70	68
ENSMUSG00000078193	chr1	Gm2000	1.6E+08	1.6E+08	445	0.798199712	3.727606727	0.0002057	0.000769754	0.04934	1	138	129	130	133	182	402	262	247	425	390
ENSMUSG00000041731	chr19	Pgm5	2.5E+07	2.5E+07	3611	0.816997259	4.948633658	0.0002066	0.000772563	0.05558	1	310	141	625	380	299	960	878	681	713	818
ENSMUSG00000045799	chr14	Gm9800	8799589	8800294	914	1.110140304	1.475550043	0.0002066	0.000772563	0.07822	1	20	25	22	20	38	112	69	61	67	66
ENSMUSG00000018160	chr11	Med1	9.8E+07	9.8E+07	8753	-0.62847555	5.098813509	0.0002068	0.000773005	0.03243	-1	577	464	833	690	573	679	641	448	485	530
ENSMUSG00000049112	chr6	Oxtr	1.1E+08	1.1E+08	4568	-3.58079547	2.193540787	0.0002068	0.000773005	0.85697	-1	57	351	1	13	106	17	3	15	30	8
ENSMUSG00000025041	chr19	Nt5c2	4.7E+07	4.7E+07	4475	0.729218922	3.712876484	0.0002076	0.000775504	0.04105	1	126	88	181	159	199	456	306	230	292	412
ENSMUSG00000036315	chr17	Znrd1	3.7E+07	3.7E+07	819	0.726883423	4.055064304	0.0002076	0.000775504	0.04184	1	184	129	220	161	255	539	301	356	463	461
ENSMUSG00000072235	chr15	Tuba1a	9.9E+07	9.9E+07	1647	1.124131995	6.195377646	0.0002078	0.000776043	0.10626	1	416	480	513	479	1718	2899	1789	1655	2177	1894
ENSMUSG00000024592	chr18	C330018D20Rik	5.7E+07	5.7E+07	3233	-0.76169512	3.614328239	0.0002087	0.000779142	0.04512	-1	214	143	310	242	268	271	246	127	149	157
ENSMUSG00000034543	chr11	Morc2a	3649494	3650146	6013	-0.63689163	4.5492693	0.0002091	0.00078021	0.03267	-1	422	346	507	434	417	421	478	285	319	393
ENSMUSG00000038872	chr8	Zfhx3	1.1E+08	1.1E+08	17569	-0.67562568	3.84221464	0.0002091	0.00078021	0.03546	-1	265	209	254	246	344	273	237	168	233	230
ENSMUSG00000053559	chr15	Smagp	1E+08	1E+08	1142	1.265386675	2.39268805	0.0002092	0.00078021	0.12389	1	31	17	55	31	107	240	101	115	170	126
ENSMUSG00000038143	chr8	Stox2	4.7E+07	4.7E+07	10839	-0.71670698	3.767904265	0.0002102	0.000784053	0.04012	-1	234	190	325	298	221	230	242	144	216	235
ENSMUSG00000066026	chr4	Dhrs3	1.4E+08	1.4E+08	2927	1.066319807	5.463188669	0.0002107	0.000785402	0.09557	1	305	231	444	263	1025	1411	921	946	1160	1719
ENSMUSG00000035849	chr11	Krt222	9.9E+07	9.9E+07	3292	-1.04098025	2.19693478	0.0002115	0.000788233	0.07787	-1	92	56	113	122	77	51	58	50	88	55
ENSMUSG00000005986	chr19	Ankrd13d	4270180	4270549	2460	1.540494566	0.405432831	0.0002118	0.000789157	0.13425	1	8	6	3	7	22	47	28	31	31	45
ENSMUSG00000036634	chr7	Mag	3.1E+07	3.1E+07	4072	1.273577393	0.607621466	0.0002121	0.000790268	0.0861	1	13	10	13	8	17	61	31	23	47	44
ENSMUSG00000071855	chr18	Ccdc112	4.6E+07	4.6E+07	2801	1.771921834	-0.40962104	0.0002122	0.000790441	0.14011	1	3	1	2	9	6	31	12	18	18	20
ENSMUSG00000071669	chr16	Snx29	1.1E+07	1.1E+07	6435	-1.56208121	1.22240258	0.0002124	0.000790726	0.17431	-1	49	49	60	67	24	33	49	14	13	13
ENSMUSG00000019916	chr10	P4ha1	5.9E+07	5.9E+07	4114	0.682917903	6.121086601	0.0002126	0.000791281	0.03943	1	788	624	885	861	838	2212	1804	1289	1960	1648
ENSMUSG00000022096	chr14	Hr	7.1E+07	7.1E+07	6919	-0.92492663	6.137658743	0.0002126	0.000791281	0.07255	-1	800	821	1990	1428	2226	792	1484	691	838	1228
ENSMUSG00000010609	chr1	Psen2	1.8E+08	1.8E+08	4332	0.782719771	3.904449838	0.0002131	0.000792982	0.04887	1	157	105	169	141	267	381	314	296	449	494
ENSMUSG00000030720	chr7	Cln3	1.3E+08	1.3E+08	5781	0.806506591	3.333730048	0.0002143	0.000797	0.04985	1	116	60	117	92	174	308	245	177	278	312
ENSMUSG00000038831	chr2	Ralgps1	3.3E+07	3.3E+07	7657	-1.09382518	1.68035798	0.0002147	0.00079839	0.08329	-1	54	37	94	82	61	50	66	20	36	39
ENSMUSG00000033083	chr14	Tbc1d4	1E+08	1E+08	7676	-0.94194225	5.693951519	0.0002151	0.000799644	0.07504	-1	974	475	1975	1221	677	791	955	536	654	743
ENSMUSG00000043483	chr12	Gm6863	9.7E+07	9.7E+07	642	0.791611356	3.694879964	0.0002154	0.000800572	0.04965	1	112	76	186	138	222	419	254	263	349	398
ENSMUSG00000050732	chr6	Vamp8	7.2E+07	7.2E+07	2311	0.687078467	5.172576941	0.0002158	0.000801702	0.03948	1	319	219	672	386	577	1089	878	670	947	1026
ENSMUSG00000027002	chr2	Nckap1	8.1E+07	8.1E+07	4964	-0.70135398	6.622507306	0.000216	0.000802198	0.04207	-1	1620	1323	2476	1973	1879	1784	1950	1169	1417	1472
ENSMUSG00000027351	chr2	Spred1	1.2E+08	1.2E+08	6784	0.699699409	4.157177129	0.0002169	0.000805322	0.0391	1	169	141	220	182	325	601	448	367	384	475
ENSMUSG00000034858	chr9	Fam214a	7.5E+07	7.5E+07	4521	-0.67168223	4.558762114	0.0002169	0.000805427	0.03676	-1	395	300	604	495	401	400	501	255	325	409
ENSMUSG00000001424	chr6	Snd1	2.8E+07	2.8E+07	9757	0.69278977	6.071720192	0.0002171	0.000805926	0.0407	1	698	580	850	879	858	2066	1474	1341	1920	1781
ENSMUSG00000021217	chr7	Tshz3	3.7E+07	3.7E+07	5456	0.971497247	1.670706291	0.0002175	0.000806995	0.06058	1	33	16	42	24	44	88	88	62	93	87
ENSMUSG00000090231	chr17	Cfb	3.5E+07	3.5E+07	2825	1.668028246	5.122107359	0.000218	0.000808512	0.22772	1	121	174	93	87	847	1503	1012	775	1289	929
ENSMUSG00000062949	chrX	Atp11c	6E+07	6E+07	7312	-0.95026292	2.132565693	0.0002187	0.000811152	0.0637	-1	74	70	97	77	112	85	83	46	45	48
ENSMUSG00000033475	chr17	Tomm6	4.8E+07	4.8E+07	1131	0.734561531	5.694003549	0.0002193	0.000813147	0.04565	1	493	419	631	564	855	1333	1045	1026	1657	1580
ENSMUSG00000033589	chr14	Reep4	7.1E+07	7.1E+07	1668	1.127675229	2.256964316	0.0002198	0.000814872	0.09502	1	36	30	39	28	92	177	90	102	135	156
ENSMUSG00000028600	chr4	Podn	1.1E+08	1.1E+08	4270	1.230946067	4.597000369	0.0002204	0.000816758	0.12626	1	139	149	166	92	589	936	569	484	794	740
ENSMUSG00000086584	chr11	Gm12002	1.2E+07	1.2E+07	2757	-1.10660457	0.77724746	0.000221	0.000818889	0.0668	-1	26	23	51	30	42	25	23	17	24	18
ENSMUSG00000090264	chr18	Eif4ebp3	3.7E+07	3.7E+07	744	0.995190384	2.933983565	0.0002214	0.000819868	0.07646	1	42	55	74	84	130	242	142	178	226	238
ENSMUSG00000037499	chr1	Nenf	1.9E+08	1.9E+08	742	0.688306593	5.939895023	0.0002215	0.000820089	0.04027	1	589	477	938	725	875	1809	1275	1168	1867	1711
ENSMUSG00000074671	chr2	Tspyl3	1.5E+08	1.5E+08	3072	1.446231869	0.995259042	0.0002217	0.000820585	0.13144	1	22	14	8	7	22	90	37	43	55	57
ENSMUSG00000022898	chr16	Dscr3	9.4E+07	9.4E+07	3670	0.620075271	4.454614825	0.0002221	0.000822046	0.03079	1	266	165	291	244	348	705	510	414	558	559
ENSMUSG00000030890	chr7	Ilk	1.1E+08	1.1E+08	2744	0.687523299	6.036185329	0.0002222	0.000822118	0.04024	1	658	538	893	720	1027	2162	1382	1346	1708	1769
ENSMUSG00000036430	chr17	Tbcc	4.7E+07	4.7E+07	1843	0.870004138	3.471684554	0.0002225	0.000822812	0.06049	1	79	55	177	128	173	333	238	225	375	293
ENSMUSG00000024660	chr19	Incenp	9872297	9872873	3217	1.107109861	1.78466942	0.0002232	0.000825527	0.08257	1	17	34	31	31	43	144	83	61	88	98
ENSMUSG00000002320	chr14	Tm9sf1	5.6E+07	5.6E+07	3880	0.622851339	4.878446868	0.000224	0.000828074	0.03194	1	295	217	470	317	489	947	653	527	803	772
ENSMUSG00000021273	chr14	Fdft1	6.3E+07	6.3E+07	2860	-0.77668119	6.160611687	0.0002248	0.000830448	0.05161	-1	1190	727	2429	1371	1356	1131	1283	822	1062	1157
ENSMUSG00000027022	chr2	Xirp2	6.7E+07	6.7E+07	11979	-0.88381677	10.99448577	0.0002247	0.000830448	0.06762	-1	42133	25613	55931	46702	30206	33479	44363	18957	25436	28299
ENSMUSG00000052738	chr6	Suclg1	7.3E+07	7.3E+07	4617	-0.7316676	8.197609832	0.0002252	0.000831735	0.04644	-1	5075	3235	8048	5604	6430	4870	5580	3403	4595	4434
ENSMUSG00000000183	chr6	Fgf6	1.3E+08	1.3E+08	1232	-1.69629031	0.040741407	0.0002261	0.000835049	0.16439	-1	26	19	36	15	14	5	21	8	7	5
ENSMUSG00000041836	chr7	Ptpre	1.4E+08	1.4E+08	5411	1.088475079	2.590987466	0.0002262	0.000835272	0.08978	1	48	47	46	31	115	204	156	112	159	204
ENSMUSG00000028789	chr4	Azin2	1.3E+08	1.3E+08	4024	1.043173112	1.804962217	0.0002267	0.000836894	0.07494	1	33	21	45	20	50	132	88	51	90	116
ENSMUSG00000028106	chr3	Rprd2	9.6E+07	9.6E+07	8419	-0.66470322	4.503524051	0.000227	0.000837603	0.03611	-1	378	310	547	488	368	362	414	244	393	405
ENSMUSG00000019851	chr10	Perp	1.9E+07	1.9E+07	1901	1.249489204	1.16965394	0.0002272	0.000838177	0.10136	1	15	16	36	14	14	50	68	49	50	88
ENSMUSG00000014856	chr8	Tmem208	1.1E+08	1.1E+08	1511	0.686459839	4.49255688	0.0002277	0.000839913	0.03838	1	248	187	262	247	357	733	435	451	679	559
ENSMUSG00000011427	chr7	Zfp790	3E+07	3E+07	4525	-0.7905503	3.228357269	0.0002279	0.000840145	0.04809	-1	187	102	235	198	180	165	189	92	121	146
ENSMUSG00000085218	chr2	BB218582	1.1E+08	1.1E+08	1311	-1.03696432	2.321839527	0.0002279	0.000840145	0.07943	-1	97	56	143	122	90	49	81	67	50	80
ENSMUSG00000091460	chr9	Gm7808	2E+07	2E+07	387	1.702944472	1.631772105	0.0002281	0.000840492	0.21238	1	17	18	5	20	43	64	69	39	161	137
ENSMUSG00000024799	chr19	Tm7sf2	6062821	6063073	3484	0.844867415	3.42429048	0.0002288	0.000842773	0.05586	1	114	76	106	121	158	318	199	213	377	299
ENSMUSG00000038122	chr10	Tbc1d32	5.6E+07	5.6E+07	7235	-0.98097343	1.77038417	0.0002288	0.000842773	0.06607	-1	74	52	86	44	80	54	59	27	48	47
ENSMUSG00000044583	chrX	Tlr7	1.7E+08	1.7E+08	4082	1.337528341	1.727849443	0.0002296	0.000845297	0.127	1	19	31	14	20	48	156	117	55	76	77
ENSMUSG00000032870	chr4	Smap2	1.2E+08	1.2E+08	3160	0.666956696	4.968753128	0.0002303	0.000847906	0.03709	1	275	223	534	452	374	814	793	571	889	898

ENSMUSG00000034667	chr10	Xpot	1.2E+08	1.2E+08	5992	-0.67644743	5.256301828	0.0002304	0.000848006	0.03852	-1	601	532	957	814	644	676	760	511	510	572
ENSMUSG00000056116	chr17	H2-T22	3.6E+07	3.6E+07	3414	0.867967486	4.961300269	0.0002307	0.000848898	0.06362	1	294	206	323	251	632	1306	628	524	714	1061
ENSMUSG00000071648	chr19	Rom1	8927382	8927887	1526	0.705146422	3.730941631	0.000231	0.000849742	0.03893	1	128	96	192	144	211	365	345	226	430	330
ENSMUSG00000031616	chr8	Ednra	7.8E+07	7.8E+07	5476	0.936989374	2.628774031	0.0002314	0.00085058	0.06524	1	42	49	77	66	82	226	110	145	148	190
ENSMUSG00000073700	chr4	Klhl21	1.5E+08	1.5E+08	3986	-0.71695636	7.468990916	0.0002313	0.00085058	0.04464	-1	3299	2035	4572	3375	3640	2973	3356	2106	2620	2829
ENSMUSG00000028484	chr4	Psip1	8.3E+07	8.3E+07	5082	-0.74848035	4.481649625	0.0002314	0.00085071	0.04648	-1	532	340	387	404	395	469	404	262	298	300
ENSMUSG00000052310	chr3	Slc39a1	9E+07	9E+07	2364	0.690178893	6.185689473	0.0002317	0.000851059	0.0409	1	717	564	951	810	1230	2256	1706	1418	2043	1880
ENSMUSG00000079317	chrX	Trappc2	1.7E+08	1.7E+08	3643	-0.68923043	3.741566663	0.0002316	0.000851059	0.03723	-1	255	197	259	251	265	260	241	168	196	190
ENSMUSG00000047330	chr1	Kcne4	7.9E+07	7.9E+07	2657	1.24711655	1.705473332	0.0002322	0.000852802	0.10946	1	18	29	33	19	40	88	84	88	51	136
ENSMUSG00000040850	chr11	Psme4	3.1E+07	3.1E+07	8382	-0.8038864	7.839897265	0.0002334	0.000857108	0.05619	-1	4358	3072	5849	4328	4537	3544	5476	2374	3064	2952
ENSMUSG00000078670	chr7	Fam174b	7.4E+07	7.4E+07	2678	1.163417306	1.364101828	0.0002342	0.000859769	0.08714	1	26	20	15	15	36	99	75	51	65	61
ENSMUSG00000044338	chr2	Aplnr	8.5E+07	8.5E+07	3699	0.958123153	4.601884482	0.0002351	0.00086294	0.0777	1	174	109	399	179	462	776	454	638	784	594
ENSMUSG00000034472	chr8	Rasd2	7.5E+07	7.5E+07	3176	-0.90632789	5.04340817	0.0002373	0.000870611	0.06991	-1	564	528	795	374	1026	528	652	274	653	298
ENSMUSG00000024769	chr19	Cdc42bpg	6306456	6306875	6099	-0.7651367	3.177927623	0.0002384	0.000874538	0.04495	-1	126	140	223	188	177	154	160	89	141	150
ENSMUSG00000015002	chr15	Efr3a	6.6E+07	6.6E+07	11091	-0.67373095	5.453057539	0.0002386	0.000874947	0.03867	-1	817	647	991	842	722	751	894	488	666	710
ENSMUSG00000046312	chr4	AI464131	4.1E+07	4.1E+07	4701	-0.78021705	7.553472768	0.0002388	0.000875482	0.05308	-1	3311	3142	3933	4103	3044	2783	3237	2135	3065	3067
ENSMUSG00000072940	chr6	Gm10443	8.6E+07	8.6E+07	210	1.225089954	1.477394402	0.0002398	0.000879006	0.10427	1	18	14	21	30	38	82	44	52	113	92
ENSMUSG00000046997	chr9	Spsb4	9.7E+07	9.7E+07	4484	1.343089195	0.982083574	0.0002404	0.000880977	0.11458	1	9	12	18	30	8	68	58	34	51	64
ENSMUSG00000063047	chr7	Zfp780b	2.8E+07	2.8E+07	3004	-1.79559813	0.533561836	0.0002406	0.00088116	0.21926	-1	28	39	24	37	28	14	32	10	3	6
ENSMUSG00000022945	chr16	Chaf1b	9.4E+07	9.4E+07	5001	1.548589676	-0.09169198	0.0002408	0.000881864	0.12814	1	4	2	10	2	14	32	17	20	23	32
ENSMUSG00000099081	chr11	Gm27624	3644776	3644952	177	-1.35831282	0.802902815	0.000241	0.000882205	0.12218	-1	31	39	44	36	28	40	13	10	23	14
ENSMUSG00000082319	chrX	Gm8822	8.2E+07	8.2E+07	2347	0.944527909	2.760680398	0.0002415	0.00088385	0.06927	1	51	39	83	52	131	252	163	142	164	188
ENSMUSG00000002580	chr11	Mien1	9.8E+07	9.8E+07	747	0.722214734	5.057221587	0.0002424	0.000886908	0.04404	1	400	266	348	322	563	1073	623	715	972	873
ENSMUSG00000072594	chr14	Gm16439	4.5E+07	4.5E+07	564	-1.27274513	1.905693013	0.0002426	0.000887653	0.12169	-1	55	43	150	84	76	41	90	30	34	29
ENSMUSG00000030614	chr7	Tmem126b	9E+07	9E+07	3984	-0.65113536	4.56015343	0.0002431	0.00088921	0.03511	-1	461	351	453	423	454	482	484	258	368	323
ENSMUSG00000080824	chr6	Gm9001	7.6E+07	7.6E+07	399	-1.44773241	0.032791002	0.0002433	0.00088968	0.11264	-1	25	17	29	18	15	13	18	5	12	5
ENSMUSG00000032060	chr9	Cryab	5.1E+07	5.1E+07	1185	1.165611187	9.976655739	0.0002436	0.000890324	0.11734	1	6408	3841	20326	12941	5896	43028	22106	21169	27254	32232
ENSMUSG00000098387	chr2	Pet117	1.4E+08	1.4E+08	693	-1.1570769	1.805293042	0.0002443	0.000892859	0.09783	-1	54	45	131	65	73	42	75	38	29	34
ENSMUSG00000052997	chr7	Uba2	3.4E+07	3.4E+07	4092	-0.62699925	5.342476792	0.0002447	0.000893862	0.03333	-1	625	614	829	735	896	687	803	521	627	650
ENSMUSG00000020788	chr11	Atp2a3	7.3E+07	7.3E+07	5281	0.743368645	4.139440629	0.000245	0.00089494	0.0452	1	121	144	268	222	250	544	419	281	451	600
ENSMUSG00000025508	chr7	Rplp2	1.4E+08	1.4E+08	2072	0.787524584	7.963890019	0.0002466	0.000900388	0.05438	1	2374	1763	3676	2477	3898	8011	4591	5364	7499	7117
ENSMUSG00000032878	chr11	Ccdc85a	2.8E+07	2.8E+07	6971	-1.38904148	1.227618965	0.0002474	0.000903128	0.1372	-1	42	25	102	46	43	27	53	12	20	20
ENSMUSG00000038047	chr4	Haus6	8.7E+07	8.7E+07	6459	-0.86782646	2.925109673	0.0002474	0.000903128	0.05823	-1	167	125	174	109	151	114	156	80	101	102
ENSMUSG00000040721	chr14	Zfhx2	5.5E+07	5.5E+07	18166	-0.92513379	2.841414761	0.0002483	0.00090605	0.06732	-1	107	109	192	159	138	110	135	46	133	93
ENSMUSG00000031782	chr8	Coq9	9.5E+07	9.5E+07	3055	-0.87195698	8.53715811	0.0002486	0.000906408	0.06665	-1	6082	4104	11933	8818	6288	5377	7975	3692	5267	5043
ENSMUSG00000054256	chr5	Msi1	1.2E+08	1.2E+08	5800	1.678957142	-0.21871495	0.0002486	0.000906408	0.14233	1	1	4	5	7	9	27	10	17	30	30
ENSMUSG00000097675	chr6	1700101I11Rik	1.3E+08	1.3E+08	884	2.289141084	0.462657492	0.0002485	0.000906408	0.36353	1	1	1	25	3	5	62	19	68	26	27
ENSMUSG00000060802	chr2	B2m	1.2E+08	1.2E+08	860	1.20437214	8.22321105	0.0002495	0.000909456	0.12528	1	2430	1835	1888	1519	6384	14106	5553	5610	7836	10880
ENSMUSG00000074738	chr4	B930041F14Rik	1.6E+08	1.6E+08	2140	0.924581851	2.39426194	0.00025	0.000911167	0.06121	1	60	46	58	33	68	146	133	110	141	161
ENSMUSG00000070737	chr4	Gm12942	1.3E+08	1.3E+08	1910	1.081721212	2.013658901	0.0002509	0.000914201	0.08579	1	40	19	34	26	75	133	100	74	110	135
ENSMUSG00000051306	chr5	Usp42	1.4E+08	1.4E+08	6238	-0.77718539	2.923478176	0.0002513	0.000915289	0.04521	-1	136	106	174	142	160	141	122	105	102	99
ENSMUSG00000026479	chr1	Lamc2	1.5E+08	1.5E+08	8039	1.21730761	2.136845618	0.0002514	0.00091544	0.11417	1	21	13	42	49	78	121	186	77	128	109
ENSMUSG00000073402	chr17	Gm8909	3.6E+07	3.6E+07	1544	1.764943355	2.514690598	0.0002519	0.000917033	0.24569	1	70	16	17	35	50	316	61	52	172	326
ENSMUSG00000035953	chr14	Tmem55b	5.1E+07	5.1E+07	4489	0.800548282	4.23798042	0.0002523	0.000917925	0.05321	1	179	162	192	144	366	624	426	332	504	601
ENSMUSG00000041264	chr5	Uspl1	1.5E+08	1.5E+08	6648	-0.61318763	5.310072818	0.0002522	0.000917925	0.03194	-1	618	533	886	805	786	726	801	488	581	654
ENSMUSG00000085795	chr8	Zfp703	2.7E+07	2.7E+07	3304	0.895220203	5.397670018	0.0002526	0.000918663	0.06937	1	309	163	826	400	684	1245	1093	852	1087	1385
ENSMUSG00000004460	chr16	Dnajb11	2.3E+07	2.3E+07	3236	0.650508562	5.879789452	0.0002532	0.000920646	0.03656	1	603	457	864	731	848	1887	1290	1254	1462	1516
ENSMUSG00000067189	chr17	Gm7335	3.8E+07	3.8E+07	373	-1.18244758	0.938868802	0.0002534	0.000921248	0.0894	-1	48	31	38	41	32	27	36	14	17	24
ENSMUSG00000031343	chrX	Gabra3	7.2E+07	7.2E+07	3924	1.456332028	0.253665602	0.0002536	0.000921756	0.11427	1	9	6	3	9	15	46	24	18	41	33
ENSMUSG00000042104	chr14	Uggt2	1.2E+08	1.2E+08	12796	-0.83190096	2.760088167	0.0002551	0.000926919	0.05254	-1	132	110	152	129	116	106	126	79	95	92
ENSMUSG00000004040	chr11	Stat3	1E+08	1E+08	9527	0.723964052	6.511966299	0.0002558	0.000929085	0.04582	1	779	781	1323	1067	1297	2662	2001	2216	2372	2335
ENSMUSG00000021000	chr12	Ctage5	5.9E+07	5.9E+07	9323	-0.64552332	5.997172046	0.0002558	0.000929111	0.03616	-1	1104	873	1417	1231	1255	1113	1215	744	996	1102
ENSMUSG00000025083	chr19	Afap1l2	5.7E+07	5.7E+07	5591	0.915195199	2.456816968	0.0002561	0.000929754	0.0629	1	49	31	72	44	93	176	117	121	140	168
ENSMUSG00000036687	chr5	Tmem184a	1.4E+08	1.4E+08	5277	-1.38531331	0.027139667	0.0002561	0.000929754	0.10073	-1	26	14	24	16	23	14	6	6	9	19
ENSMUSG00000038545	chr17	Cul7	4.7E+07	4.7E+07	7410	0.77128666	3.770283977	0.0002568	0.000931759	0.04838	1	113	93	171	144	254	474	285	264	352	399
ENSMUSG00000028603	chr4	Scp2	1.1E+08	1.1E+08	3478	-0.71686053	7.19756676	0.0002568	0.000931832	0.04522	-1	2681	1676	3371	2481	3881	2698	2785	1735	2075	2244
ENSMUSG00000000600	chr5	Krit1	3803165	3803483	6151	-0.80121046	3.927859245	0.0002579	0.000935593	0.05324	-1	280	239	381	280	264	289	357	148	160	208
ENSMUSG00000081087	chr2	Rps15a-ps7	1.5E+08	1.5E+08	392	0.676062051	4.878958385	0.0002581	0.000935753	0.03854	1	266	244	345	411	445	903	616	630	674	891
ENSMUSG00000039648	chr2	Ccbl1	3E+07	3E+07	2923	-0.72338586	4.183121892	0.0002585	0.000936959	0.04326	-1	287	190	528	398	344	290	355	178	279	324
ENSMUSG00000027951	chr3	Adar	9E+07	9E+07	6786	0.874407282	3.219997176	0.0002594	0.000940205	0.06096	1	53	71	131	89	159	328	237	149	285	250
ENSMUSG00000029673	chr5	Auts2	1.3E+08	1.3E+08	16200	-0.77029604	4.011545729	0.0002596	0.000940594	0.04901	-1	298	263	283	313	345	196	334	203	217	267
ENSMUSG00000048728	chr11	Zfp454	5.1E+07	5.1E+07	2423	-1.19156177	1.18013687	0.0002597	0.000940761	0.09599	-1	44	46	46	55	33	32	42	17	27	22
ENSMUSG00000042115	chr1	Klhdc8a	1.3E+08	1.3E+08	4269	1.68966516	0.558193792	0.0002598	0.000940766	0.20137	1	9	0	27	5	10	43	34	36	37	58
ENSMUSG00000082454	chr11	Gm12183	4.9E+07	4.9E+07	1848	-0.94179035	2.368239305	0.0002603	0.000942609	0.06701	-1	87	83	129	101	105	69	119	42	62	73
ENSMUSG00000019831	chr10	Wasf1	4.1E+07	4.1E+07	2854	1.494659569	-0.11803774	0.0002605	0.000943089	0.09804	1	9	2	4	7	9	36	20	18	22	25
ENSMUSG00000045624	chr2	Esf1	1.4E+08	1.4E+08	4471	-0.75705229	3.85520932	0.000261	0.000944649	0.04708	-1	267	253	330	235	258	270	305	163	175	203
ENSMUSG00000026930	chr2	Gpsm1	2.6E+07	2.6E+07	5383	0.916728115	2.428459351	0.0002615	0.000945762	0.06156	1	59	41	56	41	78	181	112	110	130	178

ENSMUSG00000044921	chr10	Rassf9	1E+08	1E+08	2118	-1.13702627	1.225689455	0.0002615	0.000945762	0.08693	-1	53	28	77	40	41	37	34	22	17	37
ENSMUSG00000029603	chr5	Dtx1	1.2E+08	1.2E+08	4663	1.895125208	-0.25485536	0.000262	0.000947294	0.18899	1	2	2	4	10	4	17	27	6	25	41
ENSMUSG00000030677	chr7	Kif22	1.3E+08	1.3E+08	2063	1.85613186	0.273991782	0.0002622	0.000947901	0.20528	1	1	10	9	6	8	61	12	35	40	24
ENSMUSG00000024231	chr18	Cul2	3382988	3383172	4138	-0.69422362	5.722061139	0.0002624	0.000948149	0.04184	-1	992	688	1229	1081	932	834	1133	635	801	765
ENSMUSG00000039682	chr5	Lap3	4.5E+07	4.5E+07	3072	-0.66169256	5.697437869	0.0002624	0.000948149	0.03795	-1	912	652	1341	959	985	1047	1059	597	753	737
ENSMUSG00000001829	chr7	Clpb	1E+08	1E+08	7855	-0.7900606	6.356564566	0.0002627	0.00094892	0.05473	-1	1299	915	2318	2043	1410	1173	1599	839	1309	1318
ENSMUSG00000021488	chr13	Nsd1	5.5E+07	5.5E+07	12784	-0.69190168	6.090186538	0.0002633	0.000950906	0.04184	-1	1170	986	1762	1226	1213	1192	1357	831	1002	1012
ENSMUSG00000039646	chr16	Vasn	4639941	4640148	3007	1.137109806	4.27038466	0.0002634	0.000950999	0.11019	1	114	111	146	103	475	691	412	429	621	572
ENSMUSG00000045934	chr3	Mtmr11	9.6E+07	9.6E+07	3780	0.966237219	2.772880114	0.0002635	0.000950999	0.07279	1	47	50	80	54	119	278	131	143	165	206
ENSMUSG00000022747	chr16	St3gal6	5.8E+07	5.8E+07	6080	-0.77695106	6.908541696	0.0002643	0.000953681	0.05322	-1	2691	1843	2209	2217	2262	1878	2405	1430	1848	1587
ENSMUSG00000059890	chr9	Ube4a	4.5E+07	4.5E+07	8635	-0.67486883	5.425860272	0.0002644	0.000953681	0.03936	-1	890	667	802	789	753	834	775	513	613	703
ENSMUSG00000092060	chr5	Bend4	6.7E+07	6.7E+07	7935	1.712821255	-0.25296163	0.0002651	0.000955952	0.14675	1	1	2	6	9	7	15	39	13	22	23
ENSMUSG00000007892	chr9	Rplp1	6.2E+07	6.2E+07	495	0.767514253	9.078398646	0.0002656	0.000957559	0.05233	1	5945	4532	6174	5780	7749	17576	10848	10370	16552	15381
ENSMUSG00000022174	chr14	Dad1	5.4E+07	5.4E+07	3916	0.658023758	5.692017811	0.0002656	0.000957559	0.03752	1	554	402	669	600	836	1457	1171	953	1578	1384
ENSMUSG00000031479	chr8	Vps36	2.2E+07	2.2E+07	3706	-0.65919174	5.423951443	0.0002687	0.000968344	0.03756	-1	811	602	980	823	723	755	870	526	687	606
ENSMUSG00000033159	chr1	Cnppd1	7.5E+07	7.5E+07	5635	0.639026539	4.973299216	0.0002696	0.000971403	0.03472	1	304	245	412	334	593	948	713	583	823	891
ENSMUSG00000092035	chr6	Peg10	4747306	4747578	6667	1.322223092	1.611183889	0.0002726	0.000982002	0.12496	1	28	30	15	18	29	134	51	85	81	76
ENSMUSG00000027331	chr2	Knstrn	1.2E+08	1.2E+08	5158	1.53142797	0.092431993	0.0002733	0.00098422	0.11476	1	9	8	5	5	8	49	20	26	26	22
ENSMUSG00000041852	chr15	Tcf20	8.3E+07	8.3E+07	7347	-0.67794133	4.127297671	0.0002747	0.000988875	0.03806	-1	301	277	337	268	425	356	271	189	252	331
ENSMUSG00000085894	chr1	Gm15832	4E+07	4E+07	1832	1.023982884	2.411919503	0.0002757	0.000992203	0.08141	1	30	35	90	41	71	117	135	100	162	203
ENSMUSG00000027377	chr2	Mall	1.3E+08	1.3E+08	2006	1.013008	1.796419322	0.0002759	0.000992596	0.07228	1	18	21	50	32	51	122	80	62	107	95
ENSMUSG00000010067	chr9	Rassf1	1.1E+08	1.1E+08	5845	0.717594728	4.37447939	0.0002766	0.000994902	0.04319	1	187	178	226	224	372	677	435	464	479	585
ENSMUSG00000095306	chr8	Gm21807	6.8E+07	6.8E+07	897	-1.75187402	0.634696007	0.0002768	0.00099558	0.21728	-1	39	35	45	40	9	12	28	6	19	7
ENSMUSG00000032849	chr14	Abcc4	1.2E+08	1.2E+08	5729	-0.67755646	3.701284283	0.0002771	0.0009962	0.03669	-1	204	182	342	244	237	234	239	158	201	199
ENSMUSG00000085408	chr4	C530005A16Rik	1.2E+08	1.2E+08	2436	-1.05445207	1.637378119	0.0002785	0.001000988	0.07939	-1	67	47	76	46	75	48	61	25	24	49
ENSMUSG00000046865	chr7	Fbl	2.8E+07	2.8E+07	1159	0.688091384	4.473722073	0.0002794	0.001004091	0.03981	1	214	185	314	272	302	716	410	540	556	565
ENSMUSG00000079444	chr17	Gm21981	4.8E+07	4.8E+07	2721	0.723333515	5.715643631	0.0002795	0.001004091	0.04583	1	500	430	645	574	872	1354	1066	1033	1672	1600
ENSMUSG00000003534	chr17	Ddr1	3.6E+07	3.6E+07	4774	0.600434648	5.036864617	0.000282	0.001013012	0.03074	1	390	253	486	377	483	783	776	673	883	929
ENSMUSG00000002332	chr14	Dhrs1	5.6E+07	5.6E+07	2760	0.631644538	5.3442126	0.0002828	0.00101551	0.0346	1	402	287	597	470	709	1192	977	719	1157	1077
ENSMUSG00000082286	chr11	Pisd-ps1	3125904	3126058	1757	0.868149979	4.927792154	0.0002836	0.001018119	0.06521	1	330	277	247	232	520	1265	702	457	682	1051
ENSMUSG00000022765	chr16	Snap29	1.7E+07	1.7E+07	3429	-0.65019548	4.627744451	0.0002839	0.001019034	0.03575	-1	374	299	699	402	560	440	537	279	406	337
ENSMUSG00000022602	chr15	Arc	7.5E+07	7.5E+07	3057	1.351967361	1.153562449	0.0002847	0.001021377	0.12894	1	20	10	14	13	33	66	53	81	61	38
ENSMUSG00000033632	chr18	AW554918	2.5E+07	2.5E+07	7014	-0.87425111	2.375056674	0.000285	0.001022421	0.05678	-1	116	59	126	85	121	77	98	45	80	77
ENSMUSG00000030142	chr6	Clec4e	1.2E+08	1.2E+08	4965	1.733222881	-0.09247531	0.0002869	0.001028857	0.18295	1	0	1	9	9	10	20	37	18	35	17
ENSMUSG00000041958	chr11	Pigs	7.8E+07	7.8E+07	2501	0.597391165	4.849758894	0.0002872	0.00102973	0.03012	1	280	263	384	325	488	805	763	482	801	752
ENSMUSG00000038457	chr8	Tmem255b	1.3E+07	1.3E+07	1224	1.019695453	1.626100759	0.0002883	0.001033514	0.07287	1	24	11	40	28	50	103	88	58	85	78
ENSMUSG00000040312	chr17	Cchcr1	3.6E+07	3.6E+07	5508	1.069684221	1.307688567	0.0002895	0.001037544	0.07639	1	20	12	33	18	34	100	52	52	55	71
ENSMUSG00000070420	chr5	Zscan25	1.5E+08	1.5E+08	1996	-0.8122981	2.791524492	0.0002905	0.001040745	0.05081	-1	116	103	184	124	135	98	131	72	119	95
ENSMUSG00000060657	chr16	Marf1	1.4E+07	1.4E+07	7765	-0.63774167	5.36178775	0.0002907	0.001041087	0.03548	-1	761	600	879	778	718	801	830	474	588	658
ENSMUSG00000030660	chr7	Pik3c2a	1.2E+08	1.2E+08	8042	-0.83843709	2.855940894	0.0002912	0.001042842	0.05509	-1	146	116	182	101	147	132	138	77	87	102
ENSMUSG00000033253	chr4	Szt2	1.2E+08	1.2E+08	11947	-0.71067846	3.695311619	0.0002913	0.00104296	0.04118	-1	238	198	249	271	233	246	246	132	204	194
ENSMUSG00000005882	chr2	Uqcc1	1.6E+08	1.6E+08	6044	-0.75831043	7.311851184	0.000292	0.001045194	0.05154	-1	2619	1962	4888	3167	2732	2544	3009	1818	2491	2370
ENSMUSG00000020612	chr11	Prkar1a	1.1E+08	1.1E+08	4321	0.685607051	7.908151487	0.0002923	0.001045786	0.04229	1	2595	1986	3437	2678	3318	6759	5750	4896	6722	6411
ENSMUSG00000032096	chr9	Arcn1	4.5E+07	4.5E+07	6084	-0.71063809	6.65264804	0.0002924	0.001045786	0.04512	-1	1924	1568	2148	1812	1848	1978	1960	1146	1492	1383
ENSMUSG00000000154	chr7	Slc22a18	1.4E+08	1.4E+08	1718	1.61995264	0.90121369	0.0002926	0.001046296	0.17937	1	8	14	6	6	29	85	29	31	71	57
ENSMUSG00000044340	chr1	Phlpp1	1.1E+08	1.1E+08	6752	-0.7409672	3.668365533	0.0002928	0.00104675	0.04489	-1	195	177	302	264	263	200	296	131	181	179
ENSMUSG00000079043	chr2	Fastkd5	1.3E+08	1.3E+08	3015	-0.74980542	3.292480794	0.0002928	0.00104675	0.04477	-1	157	156	207	216	173	168	168	123	148	141
ENSMUSG00000011257	chr4	Pabpc4	1.2E+08	1.2E+08	4027	-0.7657897	8.013919793	0.0002938	0.00104979	0.05275	-1	4339	3378	6691	5126	5343	3768	5749	2411	4121	3979
ENSMUSG00000017843	chr12	Ppp2r5c	1.1E+08	1.1E+08	4224	-0.82844176	6.56414076	0.000294	0.001050268	0.06126	-1	1605	1597	2077	2318	1323	1507	1904	1039	1405	1221
ENSMUSG00000022420	chr15	Dnal4	8E+07	8E+07	2340	0.734457944	3.476018357	0.0002943	0.001051211	0.04332	1	121	79	161	91	186	348	284	196	307	298
ENSMUSG00000028334	chr4	Nans	4.6E+07	4.6E+07	4581	0.721550269	4.039084238	0.0002984	0.001065563	0.04313	1	190	149	179	164	242	526	366	285	556	383
ENSMUSG00000045817	chr17	Zfp36l2	8.4E+07	8.4E+07	3530	0.915158092	4.419938103	0.0002985	0.001065563	0.07269	1	181	144	227	122	481	740	514	481	574	563
ENSMUSG00000025491	chr7	Ifitm1	1.4E+08	1.4E+08	1094	1.608888068	0.653308152	0.0003	0.001070566	0.16348	1	9	14	3	8	17	72	25	34	57	36
ENSMUSG00000036893	chr2	Ehmt1	2.5E+07	2.5E+07	7136	-0.62783166	4.360922078	0.0003005	0.001072107	0.03314	-1	335	300	500	383	355	376	406	232	305	357
ENSMUSG00000006586	chr4	Runx1t1	1.4E+07	1.4E+07	7959	1.02466308	1.370880205	0.0003006	0.001072372	0.06579	1	28	19	30	15	30	87	65	48	64	78
ENSMUSG00000029231	chr5	Pdgfra	7.5E+07	7.5E+07	6737	0.920088215	5.662976232	0.0003008	0.001072375	0.07471	1	476	614	345	466	604	2204	1288	922	1210	1350
ENSMUSG00000034612	chr10	Chst11	8.3E+07	8.3E+07	5527	1.057164843	2.472200988	0.0003007	0.001072375	0.08783	1	46	35	50	36	104	166	227	77	148	153
ENSMUSG00000043885	chr9	Slc36a4	1.6E+07	1.6E+07	5563	0.836925342	2.753588475	0.0003011	0.001073102	0.05344	1	58	54	80	63	107	250	194	105	154	191
ENSMUSG00000046794	chr8	Ppp1r3b	3.5E+07	3.5E+07	4206	-1.52783493	2.450259585	0.0003015	0.001074571	0.1914	-1	147	54	78	40	315	79	45	41	78	46
ENSMUSG00000015467	chr17	Egfl8	3.5E+07	3.5E+07	1761	1.183530809	1.232504592	0.000303	0.001079608	0.09625	1	15	10	29	20	31	90	36	41	70	84
ENSMUSG00000028136	chr3	Snx27	9.4E+07	9.5E+07	6241	-0.65661942	5.780921465	0.0003036	0.001081174	0.03825	-1	1027	822	1173	959	1048	949	1139	616	885	849
ENSMUSG00000042694	chr19	Obfc1	4.8E+07	4.8E+07	4045	0.848724514	3.029723616	0.0003039	0.001081961	0.05683	1	86	63	122	64	103	324	187	126	255	198
ENSMUSG00000033352	chr11	Map2k4	6.6E+07	6.6E+07	4664	-0.70076705	6.359924152	0.0003049	0.001085238	0.04399	-1	1410	1135	2010	1664	1462	1302	1684	922	1368	1215
ENSMUSG00000027997	chr3	Casp6	1.3E+08	1.3E+08	1676	0.978115914	2.103972873	0.0003063	0.001089688	0.07223	1	34	16	57	41	73	145	124	84	118	104
ENSMUSG00000062040	chr7	Zfp27	3E+07	3E+07	4224	-0.83946465	2.475372156	0.0003062	0.001089688	0.05261	-1	96	69	146	100	130	106	98	67	58	79
ENSMUSG00000001036	chr11	Epn2	6.2E+07	6.2E+07	5228	-0.60391156	5.244931193	0.0003071	0.001092478	0.03182	-1	627	538	756	613	923	691	772	449	633	578
ENSMUSG00000070031	chr1	Sp140	8.6E+07	8.6E+07	3328	1.389287967	2.00361844	0.0003078	0.001094586	0.15193	1	30	24	13	21	74	211	86	74	115	105

ENSMUSG00000027384	chr2	Ndufaf5	1.4E+08	1.4E+08	1789	-0.65186933	5.358007567	0.0003081	0.001095309	0.03742	-1	806	619	831	750	714	735	817	499	679	572
ENSMUSG00000092412	chr17	Gm20507	3.4E+07	3.4E+07	2860	0.937053119	2.719518962	0.0003084	0.001096223	0.06843	1	62	56	54	59	101	201	123	133	211	207
ENSMUSG00000053137	chr15	Mapk11	8.9E+07	8.9E+07	2440	1.066722917	1.938613187	0.0003087	0.001096931	0.0856	1	35	18	47	21	66	125	82	94	115	97
ENSMUSG00000018750	chr11	Zbtb4	7E+07	7E+07	8117	-0.72755828	5.739682712	0.0003092	0.001098387	0.04722	-1	985	852	1194	1013	908	1056	1178	535	704	754
ENSMUSG00000030337	chr6	Vamp1	1.3E+08	1.3E+08	8746	-0.65328537	4.776882115	0.0003094	0.001098745	0.03694	-1	443	403	639	513	522	448	644	287	434	406
ENSMUSG00000026880	chr2	Stom	3.5E+07	3.5E+07	2787	0.902571148	7.032274061	0.0003098	0.001100083	0.07335	1	1049	535	2588	1613	1494	4311	3266	2915	3809	3286
ENSMUSG00000060509	chr9	Xcr1	1.2E+08	1.2E+08	4453	2.420225439	-0.27420923	0.00031	0.001100359	0.30571	1	3	10	1	0	0	37	16	19	16	32
ENSMUSG00000044056	chr11	Efcab9	3.3E+07	3.3E+07	1043	-1.42373715	-0.1160286	0.0003105	0.00110182	0.1049	-1	20	19	28	11	14	10	12	8	9	8
ENSMUSG00000027165	chr2	B230118H07Rik	1E+08	1E+08	4289	-0.65646931	5.826445314	0.0003109	0.001102996	0.03839	-1	1133	846	1157	1029	996	1062	1025	691	919	868
ENSMUSG00000024420	chr18	Zfp521	1.4E+07	1.4E+07	6152	-0.79904554	3.83443962	0.0003113	0.001104144	0.05433	-1	282	236	289	304	218	341	245	140	182	186
ENSMUSG00000024939	chr19	Fam89b	5728087	5728878	1209	0.71059116	5.046492128	0.0003124	0.001107952	0.0443	1	326	245	386	311	663	1050	813	518	1037	869
ENSMUSG00000056153	chr18	Socs6	8.9E+07	8.9E+07	8225	-0.79922814	5.106383661	0.0003139	0.001112778	0.05657	-1	707	508	853	681	517	555	880	332	429	436
ENSMUSG00000079941	chr13	Gm11273	2.2E+07	2.2E+07	390	0.864113726	4.860682621	0.000316	0.001120265	0.06601	1	206	140	412	437	414	662	692	482	1063	974
ENSMUSG00000023977	chr17	Ubr2	4.7E+07	4.7E+07	7747	-0.7647193	6.382392858	0.0003167	0.001122125	0.05271	-1	1433	1064	2448	1802	1261	1458	1700	856	1191	1255
ENSMUSG00000090942	chr18	F830016B08Rik	6E+07	6E+07	3297	-1.64903346	4.05459604	0.0003169	0.001122712	0.23236	-1	445	527	288	392	60	212	275	138	112	99
ENSMUSG00000071035	chr17	Gm5499	8.7E+07	8.7E+07	885	-1.30911953	0.106117853	0.0003172	0.001123344	0.09509	-1	20	15	35	16	23	18	10	5	9	18
ENSMUSG00000031813	chr8	Mvb12a	7.2E+07	7.2E+07	1060	0.710890544	4.08921857	0.0003177	0.001124814	0.04294	1	137	108	273	230	249	448	405	312	518	489
ENSMUSG00000055660	chr17	Mettl4	9.5E+07	9.5E+07	2150	-1.20735922	1.876248254	0.0003187	0.001128371	0.1123	-1	89	75	81	85	35	50	48	45	36	44
ENSMUSG00000042680	chr18	Garem	2.1E+07	2.1E+07	4923	-1.32293833	2.616067603	0.0003205	0.001134233	0.14511	-1	120	83	235	182	39	76	102	58	69	53
ENSMUSG00000025591	chr8	Tma16	6.6E+07	6.6E+07	4752	-0.76383108	2.663985164	0.0003213	0.001136806	0.04414	-1	123	88	137	119	127	106	104	68	91	113
ENSMUSG00000040760	chr14	Appl1	2.7E+07	2.7E+07	8719	-0.61014781	5.064687908	0.0003219	0.001138613	0.03258	-1	563	488	813	596	579	751	603	395	450	566
ENSMUSG00000034839	chr9	Larp6	6.1E+07	6.1E+07	2440	1.081259026	1.763201044	0.000323	0.00114241	0.08645	1	14	24	50	33	40	116	87	71	64	121
ENSMUSG00000022671	chr16	Mzt2	1.6E+07	1.6E+07	1236	0.765281016	3.587704207	0.0003236	0.001144069	0.04836	1	115	84	148	129	202	421	223	235	351	326
ENSMUSG00000034201	chr11	Gas2l1	5054132	5056689	6100	0.965139688	3.674025657	0.0003237	0.001144069	0.07975	1	101	79	103	92	293	416	341	247	392	341
ENSMUSG00000041130	chr17	Zfp598	2.5E+07	2.5E+07	3286	-0.60809004	4.895422037	0.0003243	0.00114608	0.03212	-1	448	380	663	567	682	537	668	331	476	443
ENSMUSG00000030884	chr7	Uqcrc2	1.2E+08	1.2E+08	2506	-0.89244322	9.080527658	0.0003245	0.001146318	0.0725	-1	9835	5614	18479	12215	8569	8103	11517	5710	6696	7392
ENSMUSG00000028229	chr4	Rmdn1	2E+07	2E+07	1963	-0.81803328	4.73680381	0.0003253	0.00114883	0.05894	-1	474	252	949	551	432	456	557	313	295	377
ENSMUSG00000036054	chr8	Sugp2	7E+07	7E+07	14428	-0.70160205	5.846763525	0.0003254	0.001148857	0.04421	-1	947	711	1482	1328	950	932	1140	656	955	859
ENSMUSG00000037601	chr11	Nme1	9.4E+07	9.4E+07	3342	0.765878727	5.798266731	0.0003254	0.001148857	0.0528	1	486	315	1137	653	651	1740	1275	1207	1526	1461
ENSMUSG00000042632	chr15	Pla2g6	7.9E+07	7.9E+07	4980	-0.61466369	5.083875374	0.0003266	0.001152567	0.03306	-1	502	396	774	632	856	549	702	383	628	516
ENSMUSG00000103974	chr13	AL589742.1	2.2E+07	2.2E+07	475	0.86273894	4.861516465	0.000327	0.001153812	0.06613	1	206	140	412	438	415	662	693	482	1063	974
ENSMUSG00000038564	chr5	Ift172	3.1E+07	3.1E+07	5407	-0.66633704	4.640984562	0.0003312	0.001168332	0.03866	-1	396	339	577	601	382	426	445	274	432	423
ENSMUSG00000024212	chr17	Mllt1	5.7E+07	5.7E+07	3608	-0.6001314	5.076637842	0.0003316	0.001169328	0.03158	-1	539	445	825	655	618	597	731	390	549	519
ENSMUSG00000085711	chrX	Gm15163	1.6E+08	1.6E+08	1302	-1.52862966	1.022315683	0.0003323	0.001171519	0.17078	-1	53	22	73	53	22	13	41	19	12	18
ENSMUSG00000045107	chr14	Saysd1	2E+07	2E+07	2294	0.749913393	3.494307447	0.0003335	0.001175557	0.04612	1	119	81	151	126	158	340	209	232	362	297
ENSMUSG00000079492	chr17	Gm11127	3.6E+07	3.6E+07	1344	1.354488131	3.603998075	0.0003336	0.001175557	0.15824	1	78	73	68	44	263	621	210	181	356	474
ENSMUSG00000026754	chr2	Golga1	3.9E+07	3.9E+07	5392	-0.64759321	4.068332452	0.0003338	0.001176174	0.03534	-1	283	243	364	336	304	336	324	206	229	258
ENSMUSG00000007613	chr4	Tgfbr1	4.7E+07	4.7E+07	6534	-0.71492736	5.038003626	0.0003346	0.001178593	0.04547	-1	681	538	541	640	590	561	726	350	463	491
ENSMUSG00000026037	chr1	Orc2	5.8E+07	5.8E+07	3857	-0.71048767	3.952786389	0.0003352	0.00118009	0.0429	-1	275	225	378	307	253	284	334	174	194	233
ENSMUSG00000030811	chr7	Fbxl19	1.3E+08	1.3E+08	4293	1.020227127	2.156860622	0.0003351	0.00118009	0.07803	1	36	35	30	46	67	184	100	74	132	119
ENSMUSG00000030814	chr7	Bcl7c	1.3E+08	1.3E+08	5331	0.637839417	4.496327611	0.0003353	0.00118027	0.03471	1	253	209	298	269	290	646	465	443	703	562
ENSMUSG00000018322	chr2	Tomm34	1.6E+08	1.6E+08	3040	0.673242972	4.144531901	0.0003367	0.001184909	0.0383	1	204	144	212	192	275	525	359	310	520	530
ENSMUSG00000048406	chr4	B330016D10Rik	1.4E+08	1.4E+08	1701	-0.85212029	2.693204146	0.0003368	0.001184909	0.05765	-1	132	82	187	116	111	108	95	52	117	106
ENSMUSG00000073423	chr17	Zfp414	3.4E+07	3.4E+07	1966	0.83746261	3.42283434	0.0003375	0.00118683	0.05794	1	104	88	93	114	174	338	208	204	353	305
ENSMUSG00000039901	chr19	9130011E15Rik	4.6E+07	4.6E+07	2896	-0.64003971	4.240399317	0.0003379	0.001187964	0.03491	-1	332	235	450	384	341	364	374	200	338	263
ENSMUSG00000021451	chr13	Sema4d	5.2E+07	5.2E+07	6449	-0.78743692	5.722640792	0.0003383	0.001189193	0.05608	-1	883	966	1164	1004	910	734	1223	486	853	750
ENSMUSG00000020275	chr11	Rel	2.4E+07	2.4E+07	2799	-1.40240542	0.698601235	0.0003385	0.001189552	0.13598	-1	29	40	38	40	17	19	25	16	18	10
ENSMUSG00000026187	chr1	Xrcc5	7.2E+07	7.2E+07	2555	-0.68458516	4.696806378	0.0003391	0.001191273	0.04123	-1	546	443	477	430	443	493	501	293	417	363
ENSMUSG00000055413	chr17	H2-Q5	3.5E+07	3.5E+07	1591	1.105537425	3.492592772	0.0003391	0.001191273	0.10503	1	78	82	79	72	231	528	228	181	266	408
ENSMUSG00000020747	chr11	2310067B10Rik	1.2E+08	1.2E+08	5920	-0.76368237	6.406134073	0.0003398	0.001193211	0.05312	-1	1308	1045	2167	2192	1408	1296	1580	856	1416	1396
ENSMUSG00000032352	chr9	Lrrc1	7.7E+07	7.7E+07	8247	1.307463813	0.169829275	0.0003402	0.001194334	0.08195	1	6	7	14	9	7	38	25	19	36	29
ENSMUSG00000010406	chr14	Mrpl52	5.4E+07	5.4E+07	412	0.614683042	4.966189592	0.0003423	0.001201289	0.03304	1	376	277	430	335	442	978	619	674	836	769
ENSMUSG00000029664	chr6	Tfpi2	3962589	3963447	1637	1.521157591	-0.25339362	0.0003423	0.001201289	0.11343	1	3	2	7	6	10	22	28	18	28	12
ENSMUSG00000028999	chr5	Rint1	2.4E+07	2.4E+07	6972	-0.79617719	3.088690555	0.0003426	0.001201909	0.05132	-1	171	100	251	141	160	153	165	84	108	135
ENSMUSG00000024691	chr19	Fam111a	1.3E+07	1.3E+07	4125	0.975941964	2.808500412	0.0003436	0.001205189	0.07785	1	52	53	63	59	127	323	170	141	161	161
ENSMUSG00000024620	chr18	Pdgfrb	6.1E+07	6.1E+07	5478	0.699008882	5.932519592	0.0003463	0.001214054	0.04439	1	508	417	1031	671	1013	2020	1405	1220	1524	1661
ENSMUSG00000039713	chr4	Plekhg5	1.5E+08	1.5E+08	4945	0.771324863	3.764709251	0.0003463	0.001214054	0.05078	1	117	91	164	131	271	412	314	245	419	376
ENSMUSG00000029551	chr5	Psmg3	1.4E+08	1.4E+08	2893	0.699409609	3.345983754	0.000347	0.001216258	0.03939	1	104	69	149	119	148	296	235	214	252	284
ENSMUSG00000031453	chr8	Rasa3	1.4E+07	1.4E+07	5093	0.851901406	4.652341964	0.0003474	0.001217271	0.06459	1	218	178	218	192	579	808	659	543	633	685
ENSMUSG00000068329	chr6	Htra2	8.3E+07	8.3E+07	2764	0.645776236	4.639843858	0.0003476	0.001217773	0.03652	1	270	162	359	263	451	763	524	502	681	659
ENSMUSG00000031613	chr8	Hpgd	5.6E+07	5.6E+07	1719	1.189359291	3.157191403	0.000348	0.001218701	0.12014	1	61	75	56	34	181	228	315	205	233	273
ENSMUSG00000033585	chr7	Ndn	6.2E+07	6.2E+07	1652	0.800332973	3.715439912	0.0003481	0.00121895	0.05459	1	124	87	129	125	269	416	323	252	392	333
ENSMUSG00000031805	chr8	Jak3	7.2E+07	7.2E+07	5352	0.97165586	3.248714397	0.0003484	0.001219194	0.08027	1	70	59	110	60	198	296	191	202	270	322
ENSMUSG00000034525	chr13	Ice1	7.1E+07	7.1E+07	7675	-0.83474352	5.274934748	0.0003484	0.001219194	0.06292	-1	885	685	790	795	443	681	753	415	504	543
ENSMUSG00000029826	chr6	Zc3hav1	3.8E+07	3.8E+07	6518	0.688364817	3.985921879	0.000349	0.001220946	0.04025	1	158	122	221	139	290	543	430	304	368	377
ENSMUSG00000040078	chr6	Gm9769	8.6E+07	8.6E+07	480	-0.86440558	2.72628432	0.00035	0.001224183	0.06017	-1	157	92	151	116	118	121	134	67	84	79
ENSMUSG00000084957	chr19	Bbip1	5.4E+07	5.4E+07	2488	-0.63205081	4.810923192	0.0003503	0.001224971	0.03523	-1	523	457	533	509	492	600	509	332	418	432

ENSMUSG00000092218	chr9	Gm20529	1.1E+08	1.1E+08	203	1.360248776	0.618619394	0.0003518	0.001230068	0.11846	1	4	7	13	19	17	48	26	42	44	45
ENSMUSG00000009772	chr1	Nuak2	1.3E+08	1.3E+08	3920	1.311518956	0.756666969	0.0003521	0.001230645	0.11098	1	14	8	12	10	24	71	25	43	40	49
ENSMUSG00000028445	chr4	Enho	4.2E+07	4.2E+07	1269	0.747154833	3.964934858	0.0003526	0.001231995	0.04767	1	177	142	211	127	216	392	309	355	496	427
ENSMUSG00000034354	chr11	Mtmr3	4480868	4482939	7588	-0.67337824	6.403309397	0.0003529	0.001232685	0.04152	-1	1423	1137	2109	1601	1633	1481	1769	926	1339	1284
ENSMUSG00000024824	chr19	Rad9a	4195198	4196082	2046	0.823051731	2.841534834	0.0003536	0.00123483	0.05365	1	72	50	73	68	126	225	186	122	194	212
ENSMUSG00000097187	chr2	Gm19426	8.5E+07	8.5E+07	726	1.695138767	-0.5287539	0.0003545	0.001237702	0.13521	1	6	1	4	2	7	27	8	14	20	20
ENSMUSG00000099471	chr1	Gm8451	1.3E+08	1.3E+08	447	1.668652683	0.932645613	0.0003559	0.001242302	0.19968	1	11	11	2	16	22	37	42	28	81	90
ENSMUSG00000020787	chr11	P2rx1	7.3E+07	7.3E+07	2625	1.612717234	0.445627057	0.0003567	0.001244699	0.17032	1	5	11	7	2	20	51	21	27	44	48
ENSMUSG00000066568	chr7	Lsm14a	3.4E+07	3.4E+07	3104	-0.66563874	6.174845947	0.0003581	0.001249166	0.04054	-1	1321	909	1791	1258	1482	1341	1508	773	1041	1177
ENSMUSG00000100370	chr7	Gm4790	4E+07	4E+07	3611	-0.7876127	2.907492777	0.0003581	0.001249166	0.04939	-1	136	103	148	174	145	126	119	99	103	113
ENSMUSG00000055148	chr8	Klf2	7.2E+07	7.2E+07	1847	1.079244087	4.386199872	0.0003586	0.001250391	0.10394	1	109	129	120	230	447	553	480	464	564	836
ENSMUSG00000026627	chr1	Tmem206	1.9E+08	1.9E+08	2246	0.973372961	1.752782172	0.000359	0.00125177	0.06599	1	24	30	34	38	37	109	79	53	102	105
ENSMUSG00000055239	chr6	Kcmf1	7.3E+07	7.3E+07	3251	-0.71109714	7.496214456	0.0003623	0.001262759	0.04685	-1	3034	2342	4542	3231	4015	2856	3850	1927	2969	2653
ENSMUSG00000035623	chr7	Rsf1	9.8E+07	9.8E+07	12635	-0.62557898	4.18104516	0.0003626	0.001263418	0.03342	-1	336	256	386	312	359	369	347	236	263	258
ENSMUSG00000048782	chr7	Insc	1.1E+08	1.1E+08	3717	1.349087565	0.54548771	0.0003646	0.001270316	0.10553	1	12	10	14	13	6	71	32	24	39	34
ENSMUSG00000029715	chr5	Pop7	1.4E+08	1.4E+08	1081	0.765504879	3.225816536	0.0003653	0.001272278	0.04813	1	106	52	129	95	148	277	208	190	274	251
ENSMUSG00000019188	chr2	H13	1.5E+08	1.5E+08	8884	0.694480083	5.717792496	0.0003659	0.001273963	0.04395	1	488	401	643	613	940	1607	1090	1102	1505	1388
ENSMUSG00000038807	chr11	Rap1gap2	7.4E+07	7.4E+07	6632	1.005361285	4.492699122	0.0003662	0.001274969	0.09113	1	169	86	527	178	247	476	858	489	553	693
ENSMUSG00000034675	chr13	Dbn1	5.5E+07	5.5E+07	4514	1.032572544	3.662794576	0.0003664	0.001275375	0.09341	1	80	76	94	103	291	505	270	285	333	353
ENSMUSG00000024806	chr19	Mlana	3E+07	3E+07	623	2.117345945	0.148132557	0.0003668	0.001276264	0.28944	1	7	7	1	2	9	54	5	37	32	32
ENSMUSG00000033855	chr17	Ston1	8.9E+07	8.9E+07	4521	-1.56600361	1.17275929	0.0003671	0.001277017	0.1895	-1	38	62	65	38	37	31	41	18	22	4
ENSMUSG00000021573	chr13	Tppp	7.4E+07	7.4E+07	5118	-1.04119851	3.836906012	0.0003685	0.00128163	0.09579	-1	399	236	156	187	437	248	246	164	138	168
ENSMUSG00000029605	chr5	Oas1b	1.2E+08	1.2E+08	1992	1.45368788	0.37130613	0.0003688	0.001282306	0.12541	1	11	6	7	10	12	71	22	17	34	36
ENSMUSG00000027809	chr3	Etfdh	8E+07	8E+07	7505	-1.06411874	7.515835715	0.000369	0.001282778	0.10403	-1	2984	1435	8226	4096	3110	2618	3705	1675	1703	2674
ENSMUSG00000023960	chr17	Enpp5	4.4E+07	4.4E+07	4858	-0.70610591	4.574935834	0.0003695	0.001283932	0.0442	-1	446	343	402	342	697	379	483	285	387	334
ENSMUSG00000040354	chr10	Mars	1.3E+08	1.3E+08	3423	-0.6702121	6.322829836	0.0003695	0.00128394	0.04138	-1	1422	1190	1696	1583	1452	1350	1419	901	1427	1314
ENSMUSG00000024013	chr17	Fgd2	2.9E+07	2.9E+07	4134	1.654229693	1.490053411	0.00037	0.001285246	0.21899	1	11	11	7	13	58	162	57	43	75	93
ENSMUSG00000021377	chr13	Dek	4.7E+07	4.7E+07	3089	-0.66997176	4.822122104	0.0003718	0.001290701	0.0401	-1	531	414	640	496	520	628	596	343	348	361
ENSMUSG00000037211	chr3	Spry1	3.8E+07	3.8E+07	2906	0.65600076	4.475477818	0.0003718	0.001290701	0.03778	1	260	149	304	233	381	542	550	426	562	713
ENSMUSG00000073176	chrX	Zfp449	5.6E+07	5.6E+07	3738	-0.87409534	2.258513467	0.0003727	0.001293566	0.05884	-1	100	68	121	97	72	92	71	48	70	66
ENSMUSG00000049717	chr8	Lig4	9970020	9973807	4255	-0.79926729	3.059917553	0.0003733	0.001295307	0.05217	-1	141	112	182	157	208	145	178	104	100	97
ENSMUSG00000071074	chr17	Yipf3	4.6E+07	4.6E+07	2693	0.700923389	5.54217628	0.0003738	0.001296906	0.04483	1	435	294	621	643	749	1293	997	853	1427	1394
ENSMUSG00000023965	chr17	Fbxl17	6.3E+07	6.3E+07	5526	-0.66003147	5.625483023	0.0003743	0.001298053	0.03973	-1	902	651	1230	997	781	858	981	589	762	775
ENSMUSG00000025017	chr19	Pik3ap1	4.1E+07	4.1E+07	2615	1.483114959	0.679702631	0.0003752	0.001300893	0.14722	1	7	8	6	14	23	72	69	20	37	31
ENSMUSG00000036764	chr10	Dnajc12	6.3E+07	6.3E+07	2740	-0.73225821	3.426776652	0.0003756	0.001302236	0.04504	-1	234	147	213	197	208	184	212	110	180	151
ENSMUSG00000015568	chr8	Lpl	6.9E+07	6.9E+07	6810	-1.17637063	9.533688988	0.0003763	0.00130433	0.12707	-1	10583	3592	35918	16831	17737	10578	11020	7002	7826	10820
ENSMUSG00000047649	chr7	Cd3eap	1.9E+07	1.9E+07	1657	-0.73665265	3.340350868	0.0003765	0.001304379	0.04475	-1	179	148	267	178	178	173	199	127	145	135
ENSMUSG00000030654	chr7	Arl6ip1	1.2E+08	1.2E+08	2134	0.950759394	4.565724752	0.0003784	0.001310821	0.08148	1	206	168	172	159	536	969	536	482	621	635
ENSMUSG00000047497	chr15	Adamts12	1.1E+07	1.1E+07	6234	-1.51571538	0.929210343	0.0003827	0.001325445	0.17358	-1	56	46	34	30	31	21	42	11	8	19
ENSMUSG00000029913	chr6	Prdm5	6.6E+07	6.6E+07	3711	1.221268673	0.650021156	0.0003837	0.001328482	0.08953	1	17	8	17	10	13	62	27	34	38	47
ENSMUSG00000025968	chr1	Ndufs1	6.3E+07	6.3E+07	8086	-0.8948691	8.981634872	0.0003842	0.001329986	0.07471	-1	9035	5328	16902	11843	7894	7314	11154	5278	6225	6797
ENSMUSG00000021392	chr13	Nol8	5E+07	5E+07	4242	-0.76737491	3.52444585	0.0003849	0.001331942	0.05027	-1	225	162	263	246	183	218	216	144	124	175
ENSMUSG00000002731	chr2	Prkra	7.7E+07	7.7E+07	2028	0.917039823	3.012532869	0.000385	0.001332141	0.07109	1	70	54	103	49	152	303	197	186	200	187
ENSMUSG00000032342	chr9	Mto1	7.8E+07	7.8E+07	4078	-0.56833905	4.61771427	0.0003851	0.001332141	0.02818	-1	390	312	584	463	478	444	501	281	422	405
ENSMUSG00000073405	chr17	C920025E04Rik	3.6E+07	3.6E+07	1067	1.368971351	1.809168659	0.0003869	0.001337802	0.15025	1	28	20	18	15	62	186	61	50	107	112
ENSMUSG00000022680	chr16	Pdxdc1	1.4E+07	1.4E+07	7973	-0.62901867	5.444415509	0.000388	0.001341405	0.03605	-1	725	519	1052	892	847	765	936	483	711	665
ENSMUSG00000075054	chr13	Yae1d1	1.8E+07	1.8E+07	3436	-0.72044019	3.366832206	0.0003884	0.001342326	0.04324	-1	214	147	214	184	196	205	202	110	141	151
ENSMUSG00000061758	chr6	Akr1b10	3.4E+07	3.4E+07	3535	-0.70461996	5.913912558	0.0003886	0.001342826	0.04584	-1	1177	666	1727	1111	1065	1058	1277	666	869	906
ENSMUSG00000031197	chrX	Vbp1	7.6E+07	7.6E+07	2132	-0.66024252	4.934768194	0.0003902	0.001347967	0.03937	-1	651	477	613	486	544	564	650	352	468	429
ENSMUSG00000000605	chr7	Clcn4-2	7282316	7284274	4578	-0.71036705	6.054326386	0.0003908	0.001349816	0.04676	-1	1209	899	1659	1365	1091	1218	1438	717	917	976
ENSMUSG00000002266	chr7	Zim1	6675443	6678262	3641	-1.86877363	-0.02860303	0.0003937	0.001359343	0.24826	-1	27	26	30	18	3	17	10	4	4	7
ENSMUSG00000022019	chr14	Tdrd3	8.7E+07	8.7E+07	5643	-0.61038674	4.626994111	0.0003939	0.001359707	0.03301	-1	438	357	524	481	427	475	511	306	344	390
ENSMUSG00000054072	chr18	Iigp1	6E+07	6E+07	3121	1.594208568	3.923040763	0.0003968	0.001369398	0.22417	1	104	75	154	122	113	1575	259	107	211	399
ENSMUSG00000033416	chr10	Gucd1	7.5E+07	7.5E+07	8206	-0.71938645	5.759515188	0.0003971	0.001370168	0.04784	-1	985	641	1683	1007	864	965	1106	604	743	844
ENSMUSG00000031352	chrX	Hccs	1.7E+08	1.7E+08	5151	-0.83958741	4.946613104	0.0003979	0.001372728	0.06443	-1	507	291	1092	735	462	468	666	311	375	481
ENSMUSG00000031825	chr8	Crispld2	1.2E+08	1.2E+08	4777	0.675321129	4.782058622	0.0003995	0.001377749	0.04079	1	316	270	345	223	434	891	820	480	544	791
ENSMUSG00000030339	chr6	Ltbr	1.3E+08	1.3E+08	2354	0.680471007	4.903631268	0.0004006	0.001381242	0.04208	1	247	206	480	299	566	887	714	646	847	684
ENSMUSG00000032328	chr9	Tmem30a	8E+07	8E+07	5646	-0.69535516	6.780742003	0.0004008	0.001381688	0.04529	-1	2166	1521	2537	1947	2069	2030	2314	1266	1566	1567
ENSMUSG00000029461	chr7	Fam168a	1E+08	1E+08	6632	-0.65745427	5.59601266	0.0004021	0.001385458	0.03986	-1	856	658	1191	968	788	922	1003	537	707	747
ENSMUSG00000084329	chr11	Gm6733	7.3E+07	7.3E+07	1920	-1.19272464	0.765856361	0.0004021	0.001385458	0.09213	-1	30	16	55	34	41	17	31	13	26	15
ENSMUSG00000059108	chr7	Ifitm6	1.4E+08	1.4E+08	541	1.715367138	-0.09026215	0.000403	0.001387882	0.16636	1	5	5	4	5	9	34	9	29	37	16
ENSMUSG00000073468	chr17	Sft2d1	8311102	8311285	3580	1.000802719	2.85154208	0.000403	0.001387882	0.08374	1	74	58	45	48	130	235	169	147	216	211
ENSMUSG00000040584	chr5	Abcb1a	8660077	8660222	5480	-0.78931716	3.346053495	0.0004041	0.001391226	0.05307	-1	196	143	233	238	146	164	182	112	133	177
ENSMUSG00000056941	chr2	Commd7	1.5E+08	1.5E+08	5493	0.712636668	4.204196581	0.0004043	0.001391566	0.04456	1	198	174	194	174	303	549	374	373	570	479
ENSMUSG00000030519	chr7	Apba2	6.5E+07	6.5E+07	3746	1.893481721	0.301779843	0.0004064	0.001398325	0.24473	1	3	7	1	3	21	37	22	35	26	55
ENSMUSG00000068854	chr3	Hist2h2be	9.6E+07	9.6E+07	2620	-0.67232573	3.372943466	0.0004069	0.001399683	0.03724	-1	194	141	235	165	223	178	192	128	157	165
ENSMUSG00000026213	chr1	Stk11ip	7.6E+07	7.6E+07	5743	0.632445515	3.97240056	0.0004083	0.001404293	0.03433	1	175	106	256	195	209	478	401	272	448	375

ENSMUSG00000035181	chr12	Heatr5a	5.2E+07	5.2E+07	7761	-0.86163918	4.886986726	0.0004085	0.001404567	0.06819	-1	458	367	854	799	427	591	675	291	334	316
ENSMUSG00000035835	chr10	Lppr3	8E+07	8E+07	4357	1.821109897	0.645522334	0.000409	0.00140612	0.2447	1	7	9	2	5	24	54	14	42	50	66
ENSMUSG00000048732	chr11	Klhl11	1E+08	1E+08	2393	-1.41621765	0.127311156	0.0004096	0.001407633	0.12613	-1	16	24	36	17	18	9	12	8	7	21
ENSMUSG00000056612	chr19	Ppp1r14b	6975048	6975506	919	0.694004725	6.07390251	0.0004106	0.001410797	0.04493	1	547	538	961	706	1227	1937	1693	1361	1841	1753
ENSMUSG00000045193	chr10	Cirbp	8E+07	8E+07	2604	0.708805715	5.343657048	0.0004134	0.001419791	0.04637	1	373	314	642	343	718	1284	808	781	1017	1324
ENSMUSG00000079144	chr1	A130010J15Rik	1.9E+08	1.9E+08	4403	-0.89871206	2.765217757	0.0004134	0.001419791	0.06714	-1	140	93	179	135	115	105	139	76	105	61
ENSMUSG00000024642	chr19	Tle4	1.4E+07	1.4E+07	4640	-0.75758247	4.174900117	0.000414	0.001421399	0.05108	-1	290	195	581	357	336	257	388	230	224	277
ENSMUSG00000028134	chr3	Ptbp2	1.2E+08	1.2E+08	3364	-0.68697109	3.825493571	0.0004146	0.001423094	0.04092	-1	288	174	319	289	244	275	266	158	178	251
ENSMUSG00000033006	chr15	Sox10	7.9E+07	7.9E+07	2713	1.132025885	1.472445873	0.0004149	0.001424048	0.09253	1	19	26	25	18	35	120	77	35	63	90
ENSMUSG00000021068	chr12	Nin	7E+07	7E+07	10345	-0.75678889	4.996213478	0.0004155	0.001425397	0.0527	-1	632	559	685	650	401	507	664	355	440	494
ENSMUSG00000029061	chr4	Mmp23	1.6E+08	1.6E+08	2340	1.47676475	2.235335022	0.0004155	0.001425397	0.18255	1	22	37	15	16	92	216	96	106	147	134
ENSMUSG00000021583	chr13	Erap1	7.5E+07	7.5E+07	4014	-0.64584472	4.505418019	0.0004158	0.001425801	0.03732	-1	379	325	468	469	432	528	433	277	310	297
ENSMUSG00000056952	chr6	Tatdn2	1.1E+08	1.1E+08	3548	-0.67097127	4.980546823	0.0004159	0.001425806	0.0411	-1	465	377	921	647	574	549	714	311	466	509
ENSMUSG00000021022	chr12	Ppp2r3c	5.5E+07	5.5E+07	2395	-0.69617785	4.113780331	0.000417	0.001429216	0.04292	-1	277	317	398	304	279	327	277	216	288	253
ENSMUSG00000078716	chr4	Tmem8b	4.4E+07	4.4E+07	5553	-0.85856185	4.930708719	0.0004171	0.001429216	0.06785	-1	415	249	1163	772	514	497	516	300	442	502
ENSMUSG00000040280	chr10	Ndufa4l2	1.3E+08	1.3E+08	960	0.976849159	3.450709956	0.0004179	0.001431662	0.08475	1	77	46	132	111	212	346	194	198	388	363
ENSMUSG00000043259	chr10	Fam13c	7E+07	7E+07	3520	-0.7207995	3.034199358	0.0004182	0.001432234	0.04201	-1	145	98	209	147	176	165	139	96	107	131
ENSMUSG00000063605	chr8	Ccdc102a	9.5E+07	9.5E+07	2504	0.968352871	2.837737053	0.0004184	0.001432897	0.07913	1	40	60	73	61	129	239	149	142	251	181
ENSMUSG00000032097	chr9	Ddx6	4.5E+07	4.5E+07	6065	-0.6777114	6.8053271	0.0004186	0.001432937	0.0433	-1	2141	1600	2512	2060	2008	2084	2067	1428	1585	1738
ENSMUSG00000029290	chr5	Zfp326	1.1E+08	1.1E+08	7217	-0.69224223	3.268030824	0.00042	0.001437657	0.03936	-1	165	131	212	177	210	165	172	127	125	164
ENSMUSG00000046768	chr12	Rhoj	7.5E+07	7.5E+07	6484	0.676045924	4.333272749	0.0004213	0.001441671	0.04065	1	165	175	298	179	374	665	531	347	496	540
ENSMUSG00000051022	chr5	Hs3st1	4E+07	4E+07	2230	1.12089891	1.196886487	0.0004217	0.001442641	0.08572	1	14	18	31	17	23	70	42	47	57	89
ENSMUSG00000022119	chr14	Rbm26	1.1E+08	1.1E+08	7649	-0.63735385	4.431267196	0.0004258	0.001456338	0.03638	-1	410	310	423	433	375	492	345	232	318	379
ENSMUSG00000025782	chr2	Taf3	9914552	9916466	6389	-0.72781382	3.546245159	0.0004261	0.001456905	0.04553	-1	181	159	285	259	213	183	256	132	165	171
ENSMUSG00000057605	chr19	Gm6807	4.5E+07	4.5E+07	888	1.769314936	0.500699446	0.0004263	0.001457336	0.22748	1	5	2	3	11	24	27	30	22	61	63
ENSMUSG00000018398	chr11	Sept8	5.4E+07	5.4E+07	6087	0.732066817	4.796012897	0.0004283	0.001463913	0.04889	1	243	267	288	229	552	922	694	515	751	716
ENSMUSG00000055670	chr11	Zzef1	7.3E+07	7.3E+07	16363	-0.5923809	4.549951037	0.0004291	0.001466311	0.03123	-1	365	304	600	469	397	460	440	277	379	383
ENSMUSG00000029406	chr5	Pitpnm2	1.2E+08	1.2E+08	12843	-0.61954733	5.207610807	0.0004304	0.001470361	0.03522	-1	586	426	942	783	689	563	691	436	663	655
ENSMUSG00000029763	chr6	Exoc4	3.3E+07	3.3E+07	12640	-0.74615168	5.784281578	0.0004319	0.001474962	0.05221	-1	977	790	1413	1242	751	858	1140	592	879	807
ENSMUSG00000008892	chr8	Vdac3	2.3E+07	2.3E+07	1423	-0.6773585	8.557546229	0.0004335	0.001480076	0.04385	-1	6779	4920	9185	7056	7288	6548	6904	4498	5827	6283
ENSMUSG00000024081	chr17	Cebpz	7.9E+07	7.9E+07	4074	-0.5699017	4.787300471	0.0004341	0.001481951	0.02915	-1	506	341	639	507	504	557	495	346	398	508
ENSMUSG00000036820	chr17	Amdhd2	2.4E+07	2.4E+07	2728	0.746632687	3.264496216	0.0004344	0.001482421	0.04691	1	93	68	141	86	160	348	217	169	255	255
ENSMUSG00000041949	chr8	Tango6	1.1E+08	1.1E+08	4409	-0.78507717	3.163905556	0.0004348	0.001483357	0.05236	-1	146	144	221	191	139	139	176	92	138	134
ENSMUSG00000029999	chr6	Tgfa	8.6E+07	8.6E+07	8624	1.493558229	-0.21436146	0.000435	0.001483885	0.10972	1	9	2	10	4	4	26	22	24	20	18
ENSMUSG00000039529	chr18	Atp8b1	6.5E+07	6.5E+07	6440	0.869394354	2.150671744	0.0004362	0.00148754	0.05603	1	42	41	61	37	48	163	121	83	109	105
ENSMUSG00000027164	chr2	Traf6	1E+08	1E+08	7883	-0.63901947	4.335975581	0.0004366	0.001488462	0.03645	-1	329	270	484	347	439	370	472	210	317	279
ENSMUSG00000030562	chr7	Nox4	8.7E+07	8.7E+07	8471	0.988946728	2.458221545	0.0004371	0.001489861	0.07961	1	45	48	52	38	88	209	205	105	103	125
ENSMUSG00000040242	chr6	Fgfr1op2	1.5E+08	1.5E+08	4619	-0.63306824	5.803402537	0.0004379	0.001492117	0.03752	-1	1002	786	1300	1017	1003	1044	1119	695	783	898
ENSMUSG00000030304	chr6	Ergic2	1.5E+08	1.5E+08	6727	-0.65509202	5.632731483	0.000438	0.00149217	0.04012	-1	908	715	1165	933	827	939	1055	566	698	758
ENSMUSG00000031382	chrX	Asb11	1.6E+08	1.6E+08	2847	-0.74068958	7.144453514	0.0004381	0.00149217	0.05219	-1	2851	2068	3063	3028	2147	2702	2001	1689	2400	2186
ENSMUSG00000067547	chr15	Gm7666	6653923	6654741	819	-0.63461937	4.68070974	0.0004398	0.001497624	0.03636	-1	412	275	746	493	485	452	489	327	456	347
ENSMUSG00000064356	chrMT	mt-Atp8	7766	7969	204	-1.75988575	2.767809896	0.0004409	0.001501119	0.27187	-1	138	86	189	252	129	42	188	12	69	21
ENSMUSG00000032246	chr9	Calml4	6.3E+07	6.3E+07	861	1.161459955	1.933776667	0.0004441	0.001511384	0.10851	1	22	31	29	21	70	176	87	80	97	92
ENSMUSG00000024201	chr17	Kdm4b	5.6E+07	5.6E+07	4895	-0.61519465	4.683872633	0.0004446	0.001512883	0.03428	-1	393	314	620	587	446	483	485	278	456	412
ENSMUSG00000037548	chr17	H2-DMb2	3.4E+07	3.4E+07	1710	1.399588907	1.931666249	0.0004451	0.001514133	0.16196	1	34	21	16	17	65	219	86	65	64	133
ENSMUSG00000041481	chr12	Serpina3g	1E+08	1E+08	2105	2.243457925	1.527101574	0.0004481	0.001523905	0.41305	1	23	4	7	9	29	338	35	20	34	77
ENSMUSG00000034042	chr4	Gpbp1l1	1.2E+08	1.2E+08	4158	-0.5719697	4.71988875	0.0004488	0.001526058	0.02945	-1	439	304	615	502	547	512	559	292	386	462
ENSMUSG00000024526	chr18	Cidea	6.7E+07	6.7E+07	1164	-2.79997662	4.392662121	0.0004524	0.001537957	0.64512	-1	654	25	124	24	2255	184	100	68	65	140
ENSMUSG00000032216	chr9	Nedd4	7.3E+07	7.3E+07	10973	-0.72564922	8.672532891	0.0004546	0.00154511	0.05065	-1	7398	6052	9445	7234	8160	7322	9016	4325	5662	5845
ENSMUSG00000031508	chr8	Ankrd10	1.2E+07	1.2E+07	3950	0.598987608	4.394800394	0.0004564	0.001550843	0.03176	1	236	190	316	244	272	623	513	467	443	542
ENSMUSG00000038708	chr9	Golga4	1.2E+08	1.2E+08	7535	-0.87680052	9.017224249	0.0004569	0.001552032	0.07366	-1	8761	6219	16393	12663	7459	7277	11334	4848	7135	7579
ENSMUSG00000036478	chr10	Btg1	9.7E+07	9.7E+07	5010	1.035616978	5.038681515	0.0004581	0.001555765	0.10048	1	278	189	242	182	798	1250	681	767	841	1011
ENSMUSG00000094410	chr1	Zbed6	1.3E+08	1.3E+08	10156	-0.71213283	6.94245471	0.0004596	0.001560628	0.04856	-1	2292	2148	2454	2063	2305	2214	2343	1443	1759	1925
ENSMUSG00000003360	chr15	Ddx23	9.9E+07	9.9E+07	5452	-0.66567929	6.294417045	0.0004617	0.001567259	0.0422	-1	1371	1050	1798	1629	1415	1283	1533	858	1384	1250
ENSMUSG00000036779	chr8	Papd5	8.8E+07	8.8E+07	4937	-0.77872059	4.073907208	0.0004621	0.001568311	0.05507	-1	277	236	434	339	323	224	437	178	200	245
ENSMUSG00000007891	chr7	Ctsd	1.4E+08	1.4E+08	2519	0.733220722	10.227089	0.0004628	0.001570354	0.05193	1	11137	7714	19528	14080	17783	31656	31046	21303	35956	35453
ENSMUSG00000040522	chrX	Tlr8	1.7E+08	1.7E+08	3586	1.515197444	0.314319152	0.0004634	0.001571811	0.13687	1	8	12	7	9	5	53	49	22	18	30
ENSMUSG00000071711	chr15	Mpst	7.8E+07	7.8E+07	1509	-0.66126453	5.549337999	0.0004636	0.001572006	0.04118	-1	938	706	823	820	973	771	785	540	938	717
ENSMUSG00000002489	chr16	Tiam1	9E+07	9E+07	9911	-1.10455375	2.903272687	0.0004638	0.00157248	0.10774	-1	160	113	130	68	306	152	90	72	76	103
ENSMUSG00000036087	chr5	Slain2	7.3E+07	7.3E+07	8446	-0.73549534	6.861025335	0.0004681	0.00158652	0.0519	-1	1966	1566	3053	2487	1936	1904	2555	1252	1575	1805
ENSMUSG00000048376	chr13	F2r	9.6E+07	9.6E+07	3307	1.126482368	3.78076791	0.0004682	0.00158652	0.11696	1	73	36	311	158	118	525	408	307	295	405
ENSMUSG00000032633	chr11	Flcn	6E+07	6E+07	4322	-0.62948066	5.682189307	0.0004686	0.001587712	0.03743	-1	1016	735	1054	910	941	975	1018	586	779	841
ENSMUSG00000091373	chr17	Gm8810	3.6E+07	3.6E+07	754	1.395740732	3.354604935	0.0004689	0.001588344	0.17629	1	68	58	47	36	223	572	175	156	293	366
ENSMUSG00000030036	chr6	Mogs	8.3E+07	8.3E+07	2892	0.638526474	4.018738901	0.0004737	0.001604076	0.03608	1	161	114	231	209	254	481	353	313	476	404
ENSMUSG00000039316	chr17	Rftn1	5E+07	5E+07	4504	0.702919706	4.521024706	0.0004745	0.001606277	0.04565	1	203	136	478	251	303	779	632	387	648	521
ENSMUSG00000045251	chr7	Zfp688	1.3E+08	1.3E+08	2734	1.036241641	1.691022171	0.0004749	0.001607514	0.08076	1	27	24	24	28	50	99	63	72	112	81
ENSMUSG00000061175	chr3	Fnip2	7.9E+07	7.9E+07	8364	0.829731676	3.008829631	0.0004752	0.001608128	0.0577	1	63	87	99	67	110	200	260	143	215	233

ENSMUSG00000084145	chr11	Gm12263	5.9E+07	5.9E+07	1482	-1.3751491	0.005225382	0.0004756	0.001608885	0.10975	-1	17	18	31	16	19	8	17	12	10	5
ENSMUSG00000008813	chr14	Tppp2	5.2E+07	5.2E+07	741	-1.25412531	0.242780811	0.0004762	0.001608999	0.09467	-1	27	21	19	28	20	15	13	12	17	10
ENSMUSG00000020925	chr11	Ccdc43	1E+08	1E+08	3341	-0.65560263	6.170767126	0.0004762	0.001608999	0.04105	-1	1274	1092	1681	1160	1417	1274	1460	858	1134	1078
ENSMUSG00000021536	chr13	Adcy2	6.9E+07	6.9E+07	4211	-0.9774581	5.068669837	0.000476	0.001608999	0.09007	-1	517	371	1384	765	442	369	693	323	331	624
ENSMUSG00000033434	chr5	Gtpbp6	1.1E+08	1.1E+08	2825	0.700905613	3.558041449	0.0004761	0.001608999	0.04259	1	136	73	161	129	186	337	261	213	363	323
ENSMUSG00000075592	chr14	Nynrin	5.6E+07	5.6E+07	7436	0.765100947	2.720501011	0.0004762	0.001608999	0.04657	1	77	51	74	78	80	226	160	123	171	167
ENSMUSG00000098176	chr15	Ccdc166	7.6E+07	7.6E+07	2584	1.287189353	0.214068277	0.0004789	0.001617653	0.09224	1	12	5	10	8	10	33	23	28	41	24
ENSMUSG00000021870	chr14	Slmap	2.6E+07	2.6E+07	8054	-0.76115405	5.904214085	0.0004793	0.001618773	0.05531	-1	993	716	1772	1356	933	971	1275	571	773	1064
ENSMUSG00000022151	chr15	Ttc33	5185525	5185572	2163	-0.61591349	5.248131649	0.0004804	0.001622012	0.03551	-1	743	507	841	742	611	697	752	475	563	619
ENSMUSG00000031513	chr8	Leprotl1	3.4E+07	3.4E+07	2879	0.563932761	4.690641553	0.0004822	0.00162779	0.02878	1	285	206	371	300	429	721	606	438	710	716
ENSMUSG00000001029	chr11	Icam2	1.1E+08	1.1E+08	1904	0.803697434	3.260596365	0.000483	0.001630088	0.05646	1	76	68	161	96	133	388	207	212	239	202
ENSMUSG00000033396	chr2	Spg11	1.2E+08	1.2E+08	8042	-0.84048622	2.867659554	0.0004837	0.001632168	0.06054	-1	147	89	174	157	137	119	166	65	105	88
ENSMUSG00000063694	chr6	Cycs	5.1E+07	5.1E+07	3404	-0.89280925	8.21253851	0.0004858	0.001638606	0.07696	-1	4985	3151	11560	5959	4588	4861	6241	2994	3726	3869
ENSMUSG00000069806	chr7	Cacng7	3332955	3333036	2207	-0.8464563	2.119353702	0.0004866	0.001641189	0.0561	-1	79	62	90	71	115	80	74	34	67	66
ENSMUSG00000053453	chr14	Thoc7	1.4E+07	1.4E+07	883	-0.66489843	5.862095476	0.0004868	0.00164119	0.04218	-1	1220	806	1279	1059	967	1098	1117	751	875	810
ENSMUSG00000037110	chr2	Ralgapa2	1.5E+08	1.5E+08	18352	-0.64372484	4.350524215	0.0004881	0.00164522	0.03768	-1	416	250	341	342	530	403	373	238	340	298
ENSMUSG00000042426	chr13	Dhx29	1.1E+08	1.1E+08	4405	-0.62194307	4.473876858	0.0004882	0.001645335	0.0353	-1	361	323	508	441	384	432	465	262	349	309
ENSMUSG00000018861	chr11	Fdxr	1.2E+08	1.2E+08	2806	0.804690053	2.818026715	0.0004887	0.001646671	0.05452	1	67	38	116	69	104	231	161	124	196	207
ENSMUSG00000028268	chr3	Gbp3	1.4E+08	1.4E+08	3239	1.373512206	3.00755231	0.0004889	0.00164673	0.16917	1	76	42	61	62	91	666	171	71	135	221
ENSMUSG00000022799	chr16	Arhgap31	3.9E+07	3.9E+07	11141	-0.60862007	4.692588945	0.0004905	0.001651903	0.03388	-1	371	325	713	412	587	512	460	370	352	411
ENSMUSG00000051989	chr16	Smim11	9.2E+07	9.2E+07	972	0.587168809	5.249259679	0.0004927	0.001658864	0.03222	1	419	305	523	479	587	1083	796	771	980	1062
ENSMUSG00000025612	chr16	Bach1	8.8E+07	8.8E+07	6179	-0.71279286	4.473407452	0.0004934	0.001660863	0.04707	-1	414	296	590	381	412	389	548	236	249	334
ENSMUSG00000019373	chr11	Cops3	6E+07	6E+07	3454	-0.64576899	6.161178289	0.0004936	0.001660967	0.04003	-1	1347	958	1619	1367	1284	1278	1376	877	1174	1074
ENSMUSG00000034560	chr10	A230046K03Rik	8.4E+07	8.4E+07	5854	-0.71088656	3.907232426	0.0004945	0.001663628	0.0457	-1	282	234	312	304	244	276	331	164	211	200
ENSMUSG00000033904	chr7	Ccp110	1.2E+08	1.2E+08	8256	-0.87861061	1.942169436	0.0004951	0.001665441	0.06009	-1	77	58	91	70	71	66	70	29	60	54
ENSMUSG00000021962	chr14	Dcp1a	3E+07	3E+07	5616	-0.77085313	3.199088613	0.0004976	0.001673201	0.05197	-1	167	163	180	164	175	176	185	102	118	121
ENSMUSG00000044026	chr19	Slc35g1	3.8E+07	3.8E+07	3471	-1.00859733	1.743122776	0.0004977	0.001673201	0.07929	-1	57	46	60	56	116	44	47	41	55	35
ENSMUSG00000078348	chr10	Sf3b5	1.3E+07	1.3E+07	3841	0.612227633	4.919024462	0.0004989	0.001676857	0.03485	1	318	235	415	342	522	827	625	568	929	816
ENSMUSG00000099908	chr16	Gm28539	1.9E+07	1.9E+07	2982	-0.63876695	4.375368134	0.0005001	0.001680517	0.0373	-1	321	309	452	380	437	323	478	228	347	306
ENSMUSG00000061815	chr1	Rufy4	7.4E+07	7.4E+07	2329	-2.65440306	2.859175542	0.0005015	0.001684483	0.5908	-1	225	22	13	20	748	62	43	25	43	34
ENSMUSG00000096188	chr8	Cmtm4	1E+08	1E+08	7734	-0.62658984	4.315828999	0.0005015	0.001684483	0.03553	-1	338	195	439	365	534	364	378	227	295	361
ENSMUSG00000036718	chr5	Micall2	1.4E+08	1.4E+08	4147	1.014560053	1.580748525	0.0005025	0.001687442	0.0779	1	20	17	39	23	48	89	57	62	97	89
ENSMUSG00000037979	chr5	Ccdc92	1.2E+08	1.2E+08	2731	1.440222348	0.063592929	0.0005049	0.001695097	0.12238	1	6	4	10	11	6	21	23	18	49	26
ENSMUSG00000041684	chr1	Bivm	4.4E+07	4.4E+07	4206	-0.81738772	2.98824321	0.0005059	0.001697814	0.05813	-1	164	126	169	160	125	161	149	77	93	118
ENSMUSG00000067336	chr1	Bmpr2	6E+07	6E+07	17983	-0.71679555	6.461324847	0.000506	0.001697937	0.04974	-1	1596	1149	2417	1673	1502	1583	1951	970	1143	1310
ENSMUSG00000015095	chr2	Fbxw5	2.6E+07	2.6E+07	3052	-0.67504945	6.124463939	0.0005076	0.001702902	0.04397	-1	1170	940	1635	1400	1350	1134	1514	681	1203	1087
ENSMUSG00000044221	chr5	Grsf1	8.9E+07	8.9E+07	3036	-0.76519244	6.995213104	0.0005119	0.00171691	0.05697	-1	2071	1482	3890	2863	2062	2122	2659	1377	1786	1900
ENSMUSG00000010608	chr12	Rbm25	8.4E+07	8.4E+07	17376	-0.68174306	5.707538696	0.0005125	0.0017186	0.04467	-1	871	763	1324	1043	839	1005	1067	534	685	916
ENSMUSG00000040396	chr8	Abhd13	9977707	9978019	5191	-0.67663661	3.697883937	0.0005132	0.001720396	0.04028	-1	234	188	311	225	238	228	251	181	175	186
ENSMUSG00000040681	chr16	Hmgn1	9.6E+07	9.6E+07	3221	0.640027595	5.403463498	0.0005158	0.001728771	0.03898	1	422	353	588	437	732	1314	856	925	1103	1090
ENSMUSG00000023961	chr17	Enpp4	4.4E+07	4.4E+07	4560	-0.68349692	5.994131978	0.0005184	0.001737042	0.04515	-1	1084	916	1391	1298	1210	1084	1479	702	941	890
ENSMUSG00000007050	chr17	Lsm2	3.5E+07	3.5E+07	3152	0.783637153	3.438595226	0.0005189	0.0017382	0.05459	1	99	72	128	122	186	322	199	219	353	305
ENSMUSG00000002297	chr5	Dbf4	8396973	8398162	6571	1.456282342	0.084617432	0.0005212	0.001745687	0.13027	1	4	3	13	9	9	54	20	18	17	34
ENSMUSG00000046324	chr19	Ermp1	3E+07	3E+07	9338	-0.905816	4.591657112	0.0005219	0.001747494	0.07783	-1	407	254	480	308	1029	425	518	226	301	287
ENSMUSG00000029173	chr5	Sepsecs	5.3E+07	5.3E+07	5347	-0.70024856	3.395913748	0.000522	0.001747516	0.04281	-1	175	170	241	169	217	225	190	116	139	163
ENSMUSG00000027599	chr3	Armc1	1.9E+07	1.9E+07	3673	-0.64797413	4.545071127	0.000524	0.001753689	0.03902	-1	375	296	652	425	430	426	548	253	338	331
ENSMUSG00000056185	chr19	Snx32	5495278	5495648	1650	0.765189794	3.232708152	0.000525	0.001756679	0.05064	1	111	75	87	93	152	266	220	186	279	254
ENSMUSG00000005628	chr3	Tmod4	9.5E+07	9.5E+07	1717	-0.73827932	8.49274673	0.0005274	0.001764298	0.0536	-1	7413	5903	7036	6269	6658	5879	7213	4164	5747	4993
ENSMUSG00000030921	chr7	Trim30a	1E+08	1E+08	4419	0.971728667	2.508654103	0.0005288	0.00176853	0.07957	1	47	51	65	39	81	278	160	80	129	139
ENSMUSG00000020196	chr10	Cabin1	7.6E+07	7.6E+07	7460	0.604780021	4.418314224	0.0005293	0.00176961	0.03362	1	223	146	356	237	350	627	491	373	599	580
ENSMUSG00000021009	chr12	Ptpn21	9.9E+07	9.9E+07	5738	-0.62693717	5.537307165	0.0005298	0.001770896	0.03773	-1	767	678	989	878	919	740	1004	494	767	794
ENSMUSG00000003420	chr7	Fcgrt	4.5E+07	4.5E+07	1738	0.9049727	6.710423001	0.0005304	0.001772684	0.07975	1	899	651	908	937	2285	3509	2053	1986	3360	3283
ENSMUSG00000072596	chr14	Ear2	4.4E+07	4.4E+07	719	1.849129834	0.87580678	0.0005306	0.001772871	0.27417	1	4	10	8	1	34	95	35	55	37	50
ENSMUSG00000050552	chr5	Lamtor4	1.4E+08	1.4E+08	1176	0.655581718	5.654970117	0.0005312	0.001774456	0.04132	1	581	413	639	506	838	1422	1037	943	1569	1392
ENSMUSG00000018537	chr11	Pcgf2	9.8E+07	9.8E+07	3526	1.184485854	2.265684161	0.0005329	0.001779601	0.12159	1	39	36	43	16	84	159	84	96	136	197
ENSMUSG00000020737	chr11	Hn1	1.2E+08	1.2E+08	2149	0.705315469	6.015460531	0.0005346	0.001784821	0.04822	1	600	627	753	577	1163	1903	1608	1179	1914	1714
ENSMUSG00000020363	chr11	Gfpt2	5E+07	5E+07	5591	0.915660835	4.073517324	0.0005348	0.001784895	0.07885	1	117	109	145	133	403	512	490	308	428	538
ENSMUSG00000021048	chr12	Mthfd1	7.6E+07	7.6E+07	3324	-0.66148167	5.521731175	0.0005349	0.001784895	0.04208	-1	741	663	1103	1016	693	763	818	591	738	753
ENSMUSG00000014039	chr16	Prdm15	9.8E+07	9.8E+07	10547	-0.85511151	2.733158807	0.0005363	0.00178895	0.06344	-1	111	120	126	156	110	122	115	74	76	100
ENSMUSG00000061126	chr17	Cyp4f39	3.2E+07	3.2E+07	1599	-1.50052966	2.407837223	0.0005363	0.00178895	0.20285	-1	177	127	57	90	99	33	121	19	67	52
ENSMUSG00000035441	chr11	Myo1d	8E+07	8E+07	6465	0.680855669	3.522717436	0.0005377	0.00179287	0.0402	1	100	110	166	110	178	335	281	214	294	328
ENSMUSG00000035666	chr2	Gtf3c4	2.9E+07	2.9E+07	7230	-0.62980246	4.653675388	0.0005378	0.00179287	0.03701	-1	414	299	714	512	396	469	494	313	384	384
ENSMUSG00000050211	chr2	Pla2g4e	1.2E+08	1.2E+08	6960	-0.70703588	5.662447486	0.0005385	0.001795037	0.0484	-1	907	808	1047	1058	827	760	1112	571	842	700
ENSMUSG00000060671	chr3	Atp8b2	9E+07	9E+07	8561	0.687440506	3.69132033	0.0005395	0.001797733	0.04197	1	117	106	163	152	210	454	315	276	316	273
ENSMUSG00000040857	chr7	Erf	2.5E+07	2.5E+07	3607	0.780418303	3.336449932	0.0005397	0.001797959	0.05412	1	77	78	177	87	151	296	242	156	312	313
ENSMUSG00000021226	chr12	Acot2	8.4E+07	8.4E+07	2196	-1.34729639	4.094754254	0.0005406	0.001800543	0.17043	-1	204	117	1148	322	234	242	222	128	129	285
ENSMUSG00000041935	chr15	AW549877	3982036	3986479	5083	-0.59646659	4.264055226	0.0005407	0.001800543	0.03246	-1	338	264	410	343	383	359	404	213	272	343

ENSMUSG00000097530	chr7	Kansl2-ps	7.3E+07	7.3E+07	1461	-0.87007622	2.319679879	0.0005427	0.001806761	0.06239	-1	100	65	104	108	103	72	113	49	65	63
ENSMUSG00000025790	chr7	Slco3a1	7.4E+07	7.4E+07	8474	-0.81041079	6.038937415	0.0005456	0.001816122	0.06403	-1	963	754	2163	1515	1094	886	1491	689	914	975
ENSMUSG00000050966	chr4	Lin28a	1.3E+08	1.3E+08	3996	1.524574232	0.816506633	0.0005479	0.001823334	0.16983	1	10	17	6	4	24	36	74	34	55	49
ENSMUSG00000024134	chr17	Six2	8.6E+07	8.6E+07	2119	-1.77591136	2.844307727	0.0005486	0.00182497	0.28654	-1	276	218	40	44	189	149	48	44	57	49
ENSMUSG00000043535	chr2	Setx	2.9E+07	2.9E+07	11380	-0.75240755	5.700643504	0.0005487	0.00182497	0.05502	-1	821	637	1627	1151	770	824	1122	558	703	823
ENSMUSG00000020707	chr11	Rnf135	8E+07	8E+07	2140	0.835448217	2.13829165	0.0005491	0.001825783	0.05416	1	36	34	60	45	59	138	91	95	119	121
ENSMUSG00000024283	chr18	Wac	7868832	7869091	5962	-0.56435572	4.944255287	0.0005493	0.001826077	0.02996	-1	494	474	681	519	579	624	603	378	472	502
ENSMUSG00000070639	chr5	Lrrc8b	1.1E+08	1.1E+08	2841	-1.39725441	-0.12698142	0.0005499	0.001827815	0.12168	-1	20	12	27	10	24	10	19	3	8	8
ENSMUSG00000058331	chr13	Zfp85	6.8E+07	6.8E+07	2312	-1.13861505	1.040090704	0.0005512	0.001831347	0.09795	-1	42	41	31	39	48	39	35	18	15	23
ENSMUSG00000079588	chr1	Tmem182	4.1E+07	4.1E+07	2716	-0.77462888	8.256454109	0.0005513	0.001831347	0.05932	-1	5093	3854	8644	6835	5058	4639	6593	3276	3862	5108
ENSMUSG00000039004	chr13	Bmp6	3.8E+07	3.8E+07	2410	-0.86559873	3.074859256	0.0005594	0.001858055	0.06717	-1	162	77	235	169	198	143	182	66	89	145
ENSMUSG00000097565	chr13	Gm26965	6.7E+07	6.7E+07	1520	-1.03508816	1.404638283	0.0005618	0.001865347	0.08301	-1	49	50	53	49	56	51	52	17	28	31
ENSMUSG00000031278	chrX	Acsl4	1.4E+08	1.4E+08	5405	-0.64032845	4.696820756	0.0005626	0.001867577	0.03873	-1	544	369	556	390	505	484	539	347	313	407
ENSMUSG00000074802	chr10	Gas2l3	8.9E+07	8.9E+07	6748	1.304062255	0.561366225	0.0005635	0.001870206	0.10864	1	21	7	12	11	6	53	36	25	39	46
ENSMUSG00000021357	chr13	Exoc2	3.1E+07	3.1E+07	4427	-0.60811963	4.516133952	0.0005637	0.001870602	0.03456	-1	409	323	449	476	400	415	481	261	356	369
ENSMUSG00000041360	chr19	D19Bwg1357e	2.7E+07	2.7E+07	3462	0.628359794	4.20078545	0.0005684	0.001885465	0.03614	1	196	159	239	221	272	561	432	435	381	462
ENSMUSG00000037594	chr12	BC022687	1.1E+08	1.1E+08	1915	1.413258088	0.322686406	0.0005687	0.001886162	0.13357	1	6	6	11	3	21	43	22	20	41	43
ENSMUSG00000003153	chr6	Slc2a3	1.2E+08	1.2E+08	7245	-1.46709143	2.555313418	0.0005692	0.001887287	0.19601	-1	45	102	154	46	332	66	103	46	39	67
ENSMUSG00000021319	chr13	Sfrp4	2E+07	2E+07	1756	1.577037497	4.215201379	0.0005707	0.001891762	0.2328	1	106	160	28	78	305	978	217	433	640	617
ENSMUSG00000056917	chr19	Sipa1	5651185	5651562	3868	0.696013017	3.88168441	0.0005717	0.001894859	0.04459	1	110	106	220	170	262	482	319	305	378	386
ENSMUSG00000032261	chr9	Sh3bgrl2	8.4E+07	8.4E+07	7865	1.216277893	1.011728814	0.000572	0.001895406	0.1109	1	19	4	14	25	25	64	62	53	46	44
ENSMUSG00000049106	chr12	Dcaf5	8E+07	8E+07	5707	-0.63438822	5.912177906	0.0005753	0.001905956	0.03942	-1	974	847	1436	1115	1167	974	1300	675	985	968
ENSMUSG00000004071	chr16	Cdip1	4750348	4750601	5746	-0.65506354	6.659668706	0.0005765	0.001909019	0.04246	-1	1633	1241	2205	2115	2238	1636	1980	1087	1804	1663
ENSMUSG00000028126	chr3	Pip5k1a	9.5E+07	9.5E+07	4383	-0.52617995	5.072205848	0.0005765	0.001909019	0.02613	-1	574	424	733	562	723	669	660	426	522	582
ENSMUSG00000020053	chr10	Igf1	8.8E+07	8.8E+07	9904	1.064005843	5.234551818	0.0005794	0.001918003	0.10993	1	348	329	272	161	724	1737	639	918	974	998
ENSMUSG00000029713	chr5	Gnb2	1.4E+08	1.4E+08	3402	0.702503501	6.831844208	0.0005799	0.001919076	0.04895	1	1097	803	1639	1193	2000	3720	2383	2162	3348	3038
ENSMUSG00000035198	chr11	Tubg1	1E+08	1E+08	2266	-0.58292793	4.900891435	0.0005814	0.001923603	0.03223	-1	452	368	754	544	626	491	622	332	567	470
ENSMUSG00000074874	chr13	Ctla2b	6.1E+07	6.1E+07	1147	1.127330981	1.768469278	0.0005818	0.001924723	0.10337	1	26	27	35	23	44	167	63	93	63	77
ENSMUSG00000079111	chr5	Kdelr2	1.4E+08	1.4E+08	1846	0.621582342	4.767259281	0.0005823	0.001925644	0.03651	1	310	235	317	296	462	993	583	517	675	659
ENSMUSG00000062908	chr3	Acadm	1.5E+08	1.5E+08	2932	-0.94409288	8.622874457	0.0005854	0.001935715	0.08845	-1	6160	3022	15879	7892	8767	5670	8006	3716	4339	6433
ENSMUSG00000061046	chr17	Haghl	2.6E+07	2.6E+07	2643	0.676346677	3.834073501	0.000586	0.001937196	0.04195	1	150	95	202	140	258	460	303	276	379	387
ENSMUSG00000021373	chr13	Cap2	4.7E+07	4.7E+07	3322	-0.76487936	7.934695873	0.0005868	0.001939454	0.05838	-1	4669	3389	6232	5175	3713	4042	5458	2557	3555	3313
ENSMUSG00000059495	chr9	Arhgef12	4.3E+07	4.3E+07	10483	-0.68761662	6.198441828	0.0005875	0.001941185	0.04671	-1	1106	954	2158	1432	1297	1221	1490	841	1043	1246
ENSMUSG00000063511	chr7	Snrnp70	4.5E+07	4.5E+07	1676	0.691457714	5.96317807	0.0005885	0.001943901	0.04702	1	579	555	803	713	966	1997	1133	1170	1703	1986
ENSMUSG00000020850	chr11	Prpf8	7.5E+07	7.5E+07	7461	-0.71306238	7.154415154	0.0005897	0.001947468	0.05067	-1	2192	1763	3733	3349	2467	2478	2810	1531	2214	2223
ENSMUSG00000020390	chr11	Ube2b	5.2E+07	5.2E+07	2126	-0.73759033	8.691373779	0.0005899	0.0019477	0.05447	-1	7887	6899	8380	8337	6546	7060	7710	4726	5980	6719
ENSMUSG00000019907	chr10	Ppp1r12a	1.1E+08	1.1E+08	3403	-0.83725721	3.53260377	0.0005901	0.001947986	0.06552	-1	202	185	272	241	203	208	279	87	117	185
ENSMUSG00000003037	chr8	Rab8a	7.2E+07	7.2E+07	4678	0.616900225	4.480096135	0.0005911	0.001950659	0.03554	1	217	204	282	235	396	720	491	413	597	573
ENSMUSG00000082292	chr11	Gm12250	5.8E+07	5.8E+07	1274	2.598879677	0.648771069	0.0005913	0.001950813	0.52586	1	5	5	5	10	3	194	25	1	25	28
ENSMUSG00000042742	chr6	B630005N14Rik	1.4E+07	1.4E+07	4139	-0.90380229	3.338454112	0.0005945	0.00196098	0.0759	-1	208	169	216	224	149	150	247	72	130	141
ENSMUSG00000033715	chr13	Akr1c14	4049011	4049132	2973	-1.13192286	0.768412489	0.0005961	0.001965736	0.09318	-1	29	36	41	29	31	36	22	10	23	17
ENSMUSG00000031715	chr8	Smarca5	8.1E+07	8.1E+07	7777	-0.64219125	5.297394414	0.0005974	0.001969748	0.04014	-1	681	520	999	761	667	744	881	467	504	599
ENSMUSG00000085175	chr11	Gm11423	8.3E+07	8.3E+07	885	1.341539466	0.304990223	0.0005979	0.001970748	0.11413	1	13	6	9	5	14	45	17	31	35	34
ENSMUSG00000033717	chr19	Adra2a	5.4E+07	5.4E+07	3801	1.580584139	0.750152616	0.0005999	0.001976989	0.19148	1	1	15	12	6	24	46	41	33	74	44
ENSMUSG00000041598	chr11	Cdc42ep4	1.1E+08	1.1E+08	3643	0.805703557	4.231329771	0.0006006	0.001978903	0.06211	1	158	125	191	161	425	639	417	363	557	492
ENSMUSG00000047246	chr13	Hist1h2be	2.4E+07	2.4E+07	4374	-0.68736997	3.841176395	0.000601	0.001979879	0.04349	-1	269	180	309	293	280	242	257	175	291	163
ENSMUSG00000030748	chr7	Il4ra	1.3E+08	1.3E+08	5092	0.953794512	4.449661123	0.0006025	0.001984133	0.08718	1	133	296	189	222	214	767	416	568	659	516
ENSMUSG00000027463	chr2	Slc52a3	1.5E+08	1.5E+08	2767	1.166446477	0.948866752	0.0006026	0.001984163	0.10316	1	7	10	30	11	29	55	45	48	49	57
ENSMUSG00000007987	chr5	Ift22	1.4E+08	1.4E+08	911	0.906077506	1.894901058	0.0006031	0.001985082	0.06442	1	36	23	35	34	63	133	89	75	89	100
ENSMUSG00000027342	chr2	Pcna	1.3E+08	1.3E+08	2400	0.57700751	4.473832115	0.0006036	0.001986554	0.03104	1	217	173	319	294	359	708	551	427	497	566
ENSMUSG00000097666	chr18	A330094K24Rik	7.8E+07	7.8E+07	1027	-1.19314338	1.288012161	0.0006044	0.001988733	0.11264	-1	31	32	81	33	82	25	51	24	23	25
ENSMUSG00000034333	chr15	Zbed4	8.9E+07	8.9E+07	5764	-0.77602836	3.269075953	0.000605	0.001990197	0.05438	-1	161	154	203	231	147	183	174	115	133	127
ENSMUSG00000022614	chr15	Lmf2	8.9E+07	8.9E+07	2906	0.660848156	4.458499492	0.000611	0.002009435	0.04167	1	176	147	351	271	379	683	468	400	652	582
ENSMUSG00000034243	chr16	Golgb1	3.7E+07	3.7E+07	12639	-0.5917498	5.275287917	0.0006113	0.002009814	0.0341	-1	676	592	779	716	698	786	773	437	590	638
ENSMUSG00000026921	chr2	Egfl7	2.7E+07	2.7E+07	3581	0.74098965	5.695417716	0.0006116	0.002010031	0.05438	1	397	328	840	529	963	1630	1075	1027	1263	1711
ENSMUSG00000079669	chr9	Gm17396	1.2E+08	1.2E+08	1655	1.578082921	-0.36990716	0.0006116	0.002010031	0.13825	1	3	1	6	4	11	18	11	20	24	25
ENSMUSG00000021706	chr13	Zfyve16	9.2E+07	9.2E+07	7082	-0.73097321	3.194956364	0.0006123	0.00201177	0.04757	-1	169	130	221	170	165	198	171	104	105	136
ENSMUSG00000046567	chr10	4930430F08Rik	1E+08	1E+08	2419	-0.91227158	2.285656088	0.0006134	0.002014843	0.07049	-1	114	77	109	83	84	80	94	60	47	63
ENSMUSG00000034413	chr17	Neurl1b	2.6E+07	2.6E+07	6331	0.904008413	2.156171785	0.0006142	0.002017082	0.06803	1	46	21	46	45	75	148	99	100	122	112
ENSMUSG00000020895	chr11	Tmem107	6.9E+07	6.9E+07	1369	0.984064569	1.840380105	0.0006154	0.002020371	0.07547	1	28	38	41	23	42	124	83	57	113	102
ENSMUSG00000027534	chr3	Snx16	1E+07	1E+07	2632	-0.82561934	2.759807961	0.0006165	0.002023625	0.0594	-1	120	79	190	149	118	104	129	78	74	115
ENSMUSG00000094685	chr7	Gm5900	1E+08	1E+08	1266	0.602482672	3.793606702	0.0006171	0.002025149	0.03225	1	162	119	194	164	187	406	324	264	343	379
ENSMUSG00000055027	chr6	Smyd1	7.1E+07	7.1E+07	4546	-0.7412359	8.925848412	0.0006174	0.002025716	0.05541	-1	8186	6596	12097	11396	7639	7593	9509	5608	7693	7306
ENSMUSG00000030446	chr13	Zfp273	6.8E+07	6.8E+07	3799	-1.07482023	0.59512235	0.000618	0.002027106	0.07431	-1	33	25	33	28	26	24	22	12	16	22
ENSMUSG00000058997	chr14	Vwa8	7.9E+07	7.9E+07	6928	-0.86874678	7.327914781	0.0006183	0.002027729	0.07555	-1	2351	1598	5864	3927	2540	2331	3237	1657	2237	2354
ENSMUSG00000022387	chr15	Brd1	8.9E+07	8.9E+07	8138	-0.55048919	4.957028196	0.0006198	0.002032233	0.02896	-1	522	413	701	556	596	529	652	387	488	549
ENSMUSG00000011305	chr17	Plin5	5.6E+07	5.6E+07	2087	-1.4643847	5.410730737	0.0006207	0.002034621	0.20759	-1	459	204	2660	1005	884	498	687	257	195	749

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ENSMUSG00000047459	chr2	Dynlrb1	1.6E+08	1.6E+08	1009	0.722651485	6.05619204	0.0006213	0.002036062	0.05194	1	720	517	674	699	1214	1908	1379	1300	1985	1977
ENSMUSG00000052364	chrX	B630019K06Rik	8892382	8894964	2583	1.497657223	-0.31115734	0.0006215	0.002036155	0.11879	1	5	3	9	1	9	29	22	19	12	21
ENSMUSG00000034245	chr6	Hdac11	9.1E+07	9.1E+07	3849	-0.70101733	3.685654805	0.0006219	0.002036665	0.04539	-1	289	197	243	222	221	254	232	138	196	198
ENSMUSG00000046096	chr7	BC030336	1.2E+08	1.2E+08	4842	-0.61500448	4.005562342	0.0006219	0.002036665	0.03491	-1	255	246	343	291	316	285	336	187	234	271
ENSMUSG00000045983	chr16	Eif4g1	2.1E+07	2.1E+07	7227	-0.69730679	9.402877899	0.0006231	0.002040204	0.04921	-1	11866	8867	16780	13432	12677	11212	13919	7471	11184	9955
ENSMUSG00000002346	chr8	Slc25a42	7E+07	7E+07	5996	-0.65236944	5.777467138	0.000625	0.002045904	0.04216	-1	1030	625	1552	929	1021	943	1085	606	778	1028
ENSMUSG00000030469	chr7	Zfp719	4.4E+07	4.4E+07	4706	-0.91339742	2.32944971	0.0006254	0.002046791	0.07248	-1	97	92	106	96	87	91	109	42	59	61
ENSMUSG00000025956	chr1	Mettl21a	6.5E+07	6.5E+07	3005	0.621503323	3.730726313	0.0006258	0.002047339	0.03459	1	163	107	189	136	194	428	319	259	321	327
ENSMUSG00000019254	chr7	Ppp1r12c	4481520	4482158	4981	0.58939455	4.866332764	0.0006262	0.002048315	0.03335	1	287	232	438	309	527	948	667	492	728	816
ENSMUSG00000060224	chr19	Pyroxd2	4.3E+07	4.3E+07	3119	1.285496955	2.522579769	0.0006266	0.002049072	0.14931	1	56	52	27	15	90	216	115	118	183	194
ENSMUSG00000034892	chr12	Rps29	6.9E+07	6.9E+07	693	0.703104555	8.184247509	0.00063	0.00205985	0.04998	1	3143	2263	3983	3364	4134	8931	5484	5944	8845	7979
ENSMUSG00000074570	chr2	Cass4	1.7E+08	1.7E+08	5334	1.541678656	0.444169807	0.0006312	0.002063328	0.16411	1	7	10	1	7	21	52	47	21	33	38
ENSMUSG00000052151	chr10	Ppap2c	8E+07	8E+07	1645	1.023443798	2.005265649	0.0006315	0.002063644	0.09017	1	23	23	47	26	82	143	125	79	98	97
ENSMUSG00000020287	chr11	Mpg	3.2E+07	3.2E+07	3752	0.742860003	3.45547016	0.0006348	0.002074064	0.05069	1	116	71	154	95	194	348	224	203	308	328
ENSMUSG00000025485	chr7	Ric8	1.4E+08	1.4E+08	4742	0.564397192	4.748246282	0.0006361	0.00207768	0.03025	1	310	220	330	317	469	807	657	496	699	656
ENSMUSG00000024011	chr17	Pi16	2.9E+07	2.9E+07	3987	1.105440482	6.837983803	0.0006372	0.00208026	0.12161	1	668	749	614	924	2690	4193	2330	2364	3259	4090
ENSMUSG00000025537	chr5	Phkg1	1.3E+08	1.3E+08	3232	-0.77932296	8.728767899	0.000637	0.00208026	0.06147	-1	9187	7226	7570	7158	8265	5902	8427	4775	7437	5739
ENSMUSG00000011148	chr12	Adssl1	1.1E+08	1.1E+08	1861	-0.73401059	9.776241751	0.000639	0.002085925	0.0547	-1	14587	10279	21940	19832	17272	13781	18781	8556	14518	13229
ENSMUSG00000071662	chr19	Polr2g	8793129	8793404	868	0.54477028	5.065489475	0.0006411	0.002092048	0.02859	1	382	274	496	373	556	944	746	646	815	942
ENSMUSG00000029836	chr6	Cbx3	5.1E+07	5.1E+07	3229	-0.63775908	3.999748798	0.0006432	0.002098549	0.03786	-1	322	198	336	267	348	321	335	201	214	224
ENSMUSG00000026095	chr1	Asnsd1	5.3E+07	5.3E+07	3528	-0.67070706	6.639416416	0.0006436	0.00209934	0.04531	-1	1824	1235	2501	2033	1707	1770	2036	1052	1626	1550
ENSMUSG00000018965	chr5	Ywhah	3.3E+07	3.3E+07	2274	0.591221526	5.594708926	0.0006444	0.002101541	0.0345	1	471	396	661	591	832	1459	1194	905	1190	1270
ENSMUSG00000027304	chr2	Rtf1	1.2E+08	1.2E+08	5731	-0.63766771	5.567024419	0.0006456	0.002104716	0.04029	-1	807	560	1301	924	827	788	998	550	776	735
ENSMUSG00000023078	chr5	Cxcl13	9.6E+07	9.6E+07	1172	1.535354516	0.161183598	0.0006458	0.002104988	0.16027	1	1	6	9	3	20	31	32	17	34	38
ENSMUSG00000026608	chr1	Kctd3	1.9E+08	1.9E+08	8129	-0.63639045	3.896824967	0.0006468	0.00210729	0.03742	-1	262	184	315	233	388	257	312	171	252	214
ENSMUSG00000031133	chrX	Arhgef6	5.7E+07	5.7E+07	8552	-0.73325025	5.646230262	0.0006468	0.00210729	0.05364	-1	805	629	1351	1234	726	940	1076	498	677	755
ENSMUSG00000036568	chr17	Gltscr1l	4.7E+07	4.7E+07	6579	-0.67815916	3.583765238	0.0006485	0.002112406	0.04213	-1	213	172	227	237	251	227	253	126	154	199
ENSMUSG00000017344	chr11	Vtn	7.8E+07	7.8E+07	2030	0.73233504	5.098599895	0.0006488	0.002112937	0.05313	1	239	203	674	394	526	1015	697	634	1071	1005
ENSMUSG00000040121	chr6	Rep15	1.5E+08	1.5E+08	982	1.35097641	-0.20560241	0.0006512	0.00212031	0.09843	1	4	3	11	4	10	22	18	23	22	23
ENSMUSG00000028863	chr4	Meaf6	1.3E+08	1.3E+08	5211	0.664148159	3.717631644	0.000652	0.002122295	0.04024	1	154	101	181	131	204	415	283	224	326	420
ENSMUSG00000020803	chr11	Txndc17	7.2E+07	7.2E+07	1324	0.587345161	5.061866326	0.0006524	0.002122945	0.03353	1	401	273	441	350	566	1118	725	706	751	831
ENSMUSG00000027983	chr3	Cyp2u1	1.3E+08	1.3E+08	2331	-0.86428225	2.055720799	0.0006527	0.002122945	0.06057	-1	74	55	119	62	95	62	84	44	58	52
ENSMUSG00000047603	chr7	Zfp235	2.4E+07	2.4E+07	2466	-1.1120603	1.282869855	0.0006526	0.002122945	0.09871	-1	40	39	82	43	42	48	46	16	29	19
ENSMUSG00000097487	chr11	Ptges3l	1E+08	1E+08	2108	0.634885051	6.319119951	0.000654	0.002126898	0.04047	1	981	681	1152	880	1032	2155	1913	1714	2218	1953
ENSMUSG00000060992	chr15	Copz1	1E+08	1E+08	1669	0.628761046	5.956066035	0.0006573	0.002137054	0.03956	1	648	474	852	705	1068	1883	1355	1149	1686	1742
ENSMUSG00000022330	chr15	Osr2	3.5E+07	3.5E+07	1723	1.172324781	1.451525494	0.0006589	0.002141715	0.1129	1	8	15	30	36	34	57	78	54	78	103
ENSMUSG00000053004	chr6	Hrh1	1.1E+08	1.1E+08	4450	1.176813664	0.627682796	0.0006596	0.002143456	0.0889	1	7	12	11	14	21	55	35	26	50	38
ENSMUSG00000039530	chr8	Tusc3	3.9E+07	3.9E+07	1511	0.814399791	2.773593887	0.0006641	0.002157514	0.05812	1	75	48	80	59	110	273	170	120	188	147
ENSMUSG00000038214	chr10	Bend3	4.3E+07	4.3E+07	6028	-0.72981971	3.254427187	0.0006643	0.002157846	0.04755	-1	139	125	260	167	218	145	150	141	124	166
ENSMUSG00000074782	chr13	4833422C13Rik	9.2E+07	9.2E+07	5915	1.652591496	-0.35248978	0.000668	0.002169473	0.14709	1	11	3	6	1	2	26	18	11	24	24
ENSMUSG00000048965	chr7	Mrgpre	1.4E+08	1.4E+08	3759	1.15151857	1.456751044	0.000669	0.002172081	0.111	1	18	11	28	14	57	67	80	57	83	83
ENSMUSG00000044206	chrX	Vsig4	9.6E+07	9.6E+07	1484	1.399395512	0.171224402	0.0006715	0.002179666	0.13112	1	5	4	7	6	20	46	38	18	31	18
ENSMUSG00000001240	chr11	Ramp2	1E+08	1E+08	3301	0.666112134	6.322701102	0.0006745	0.002189055	0.04485	1	848	631	1030	846	1385	2365	1667	1557	2234	2322
ENSMUSG00000054150	chr12	Syne3	1E+08	1E+08	5532	-0.94915865	1.914155989	0.0006756	0.002192042	0.07644	-1	50	71	89	83	70	66	73	34	53	38
ENSMUSG00000040940	chr7	Arhgef1	2.5E+07	2.5E+07	7495	0.710365179	5.589679948	0.000676	0.002192771	0.0505	1	390	431	590	490	887	1511	1021	790	1290	1627
ENSMUSG00000029250	chr5	Polr2b	7.7E+07	7.7E+07	4667	-0.60343757	5.650231622	0.0006765	0.002193972	0.03636	-1	913	691	1126	930	891	960	1023	641	762	743
ENSMUSG00000070385	chr3	Ampd1	1E+08	1E+08	2921	-1.01928319	9.687207635	0.0006783	0.002199215	0.10527	-1	22977	17739	9452	14940	12674	10641	11481	8659	13642	11673
ENSMUSG00000022559	chr15	Fbxl6	7.7E+07	7.7E+07	1712	0.721175562	3.329011553	0.0006793	0.002201907	0.04672	1	89	93	126	122	134	329	200	180	306	270
ENSMUSG00000032527	chr9	Pccb	1E+08	1E+08	2771	-0.63586078	6.725660079	0.0006829	0.002212506	0.04111	-1	1884	1196	2305	1818	2712	1945	1888	1326	1783	1635
ENSMUSG00000038522	chr10	AI317395	4E+07	4E+07	2729	-1.159668	2.292919473	0.0006829	0.002212506	0.12316	-1	91	33	203	106	99	71	110	29	48	58
ENSMUSG00000040390	chr7	Map3k10	2.8E+07	2.8E+07	4142	-0.65631448	5.426442076	0.0006838	0.002214962	0.04303	-1	711	540	1057	893	800	609	912	457	846	637
ENSMUSG00000025856	chr5	Pdgfa	1.4E+08	1.4E+08	3119	0.540155183	4.809942308	0.0006848	0.002217816	0.02799	1	305	246	386	333	464	720	702	542	702	748
ENSMUSG00000040374	chr3	Pex2	5560188	5561764	2270	-0.55540151	4.882838782	0.0006854	0.002219039	0.02987	-1	490	360	691	535	598	586	622	389	437	438
ENSMUSG00000019261	chr8	Map1s	7.1E+07	7.1E+07	3271	0.712550896	3.684596322	0.0006888	0.002229712	0.04742	1	106	102	170	147	216	304	290	256	422	352
ENSMUSG00000022519	chr16	Srl	4480216	4483284	5325	-0.73676682	10.62627454	0.0006905	0.002234669	0.05583	-1	30657	20220	41164	31545	26320	24969	33885	16972	25025	22576
ENSMUSG00000040929	chr19	Rfx3	2.8E+07	2.8E+07	11034	-1.03045796	1.203081842	0.0006914	0.002237123	0.08083	-1	53	41	50	30	49	45	29	25	23	30
ENSMUSG00000021773	chr14	Comtd1	2.2E+07	2.2E+07	2464	0.987076093	2.594936245	0.0006921	0.0022387	0.08856	1	33	45	65	45	119	163	132	115	218	183
ENSMUSG00000022220	chr14	Adcy4	5.6E+07	5.6E+07	3500	0.739882472	3.234474216	0.0006938	0.002243742	0.05018	1	72	72	149	86	161	288	210	184	259	262
ENSMUSG00000055093	chr6	Gm8430	1.2E+08	1.2E+08	471	0.943819632	2.4876052	0.000694	0.002243748	0.07864	1	61	38	40	59	84	172	98	119	159	194
ENSMUSG00000049327	chr5	Setd8	1.2E+08	1.2E+08	4034	-0.76615627	7.24517125	0.0006947	0.002245655	0.06003	-1	2464	2493	3358	3468	2378	2196	3131	1611	2676	2045
ENSMUSG00000045036	chr17	Tmem232	6.5E+07	6.5E+07	2673	-1.02112523	3.459250032	0.0006961	0.002249742	0.10037	-1	248	266	175	173	179	100	163	139	197	132
ENSMUSG00000024897	chr19	Apba1	2.4E+07	2.4E+07	6632	0.849830313	1.935965026	0.0006967	0.002251105	0.05563	1	33	35	46	38	46	138	88	71	102	96
ENSMUSG00000041245	chrX	Wnk3	1.5E+08	1.5E+08	10589	-1.54679283	-0.17607129	0.000697	0.002251378	0.15911	-1	26	19	18	8	18	5	15	3	8	12
ENSMUSG00000069206	chr13	Zfp874a	6.7E+07	6.7E+07	5263	-0.86588543	2.636570257	0.0006984	0.002255447	0.06725	-1	147	99	117	117	106	109	115	76	86	64
ENSMUSG00000029177	chr5	Cenpa	3.1E+07	3.1E+07	2503	1.034538106	1.43771018	0.0007028	0.002269117	0.08696	1	21	12	44	21	34	98	47	48	78	90
ENSMUSG00000068823	chr3	Csde1	1E+08	1E+08	4201	-0.71796585	9.697539531	0.0007031	0.002269616	0.05317	-1	16895	11626	18105	15393	15480	13469	18275	8887	11763	13085
ENSMUSG00000001175	chr12	Calm1	1E+08	1E+08	4698	-0.80413555	9.06946387	0.0007041	0.002272217	0.06648	-1	10958	10380	7960	9396	10826	8407	10118	6046	8589	7379

ENSMUSG00000093273	chr11	Mir3064	1.1E+08	1.1E+08	67	-0.67621868	4.716019613	0.0007042	0.002272217	0.04525	-1	500	472	451	394	554	596	479	304	317	417
ENSMUSG00000028248	chr4	Pnisr	2.2E+07	2.2E+07	10187	-0.66664933	5.321422127	0.0007055	0.002275825	0.04466	-1	704	667	765	711	781	827	729	419	453	812
ENSMUSG00000025151	chrX	Maged1	9.5E+07	9.5E+07	4351	0.759577569	5.756033369	0.0007065	0.002278697	0.05847	1	488	392	653	441	1147	1923	1133	1044	1402	1562
ENSMUSG00000021759	chr13	Ppap2a	1.1E+08	1.1E+08	1635	0.644690587	6.029372289	0.0007104	0.002290628	0.0422	1	717	459	1148	835	759	2124	1562	1253	1740	1586
ENSMUSG00000018845	chr11	Unc45b	8.3E+07	8.3E+07	4493	-0.70156996	8.1619098	0.0007116	0.002292949	0.05076	-1	4988	3590	8677	4874	5162	5037	5529	3070	4881	4230
ENSMUSG00000031109	chrX	Enox2	4.9E+07	4.9E+07	4356	-0.68875011	3.414860006	0.0007115	0.002292949	0.0435	-1	197	151	190	175	273	188	187	143	148	169
ENSMUSG00000040033	chr10	Stat2	1.3E+08	1.3E+08	4397	0.823958505	3.360515287	0.0007114	0.002292949	0.06353	1	91	83	116	109	157	489	254	131	257	258
ENSMUSG00000027439	chr2	Gzf1	1.5E+08	1.5E+08	4472	-0.67158803	5.00625567	0.0007134	0.002298273	0.04492	-1	552	384	996	604	493	565	699	382	421	504
ENSMUSG00000024376	chr18	Epb4.1l4a	3.4E+07	3.4E+07	3853	0.802088856	2.532203821	0.0007138	0.00229877	0.05605	1	63	28	78	74	75	151	147	119	164	159
ENSMUSG00000023963	chr17	Cyp39a1	4.4E+07	4.4E+07	3053	-0.92707255	3.371465633	0.0007172	0.002309305	0.08285	-1	278	187	135	148	234	183	205	86	148	125
ENSMUSG00000053835	chr17	H2-T24	3.6E+07	3.6E+07	2182	0.98645343	3.061924571	0.0007219	0.002323987	0.09293	1	40	46	148	81	122	379	241	100	208	243
ENSMUSG00000071984	chr17	Fndc1	7738569	7739330	9903	0.837772088	6.33092898	0.0007221	0.002324097	0.07162	1	813	767	603	684	1441	3379	1891	1501	2114	1949
ENSMUSG00000025609	chr6	Mkln1	3.1E+07	3.1E+07	22296	-0.63653181	6.3575233	0.0007233	0.002326689	0.04146	-1	1387	1127	1962	1595	1464	1412	1671	918	1303	1376
ENSMUSG00000037936	chr5	Scarb1	1.3E+08	1.3E+08	6291	0.773973587	4.836117736	0.0007232	0.002326689	0.06008	1	207	208	386	209	642	787	702	595	806	807
ENSMUSG00000027378	chr2	Nphp1	1.3E+08	1.3E+08	2708	-0.57293634	4.672819905	0.0007239	0.002328252	0.03207	-1	461	394	507	437	464	458	526	287	424	435
ENSMUSG00000041777	chr2	Cir1	7.3E+07	7.3E+07	3159	-0.75849277	3.374494284	0.0007259	0.00233401	0.05403	-1	239	151	244	174	158	202	195	119	124	157
ENSMUSG00000048388	chr2	Fam171b	8.4E+07	8.4E+07	5744	0.967565377	1.12330233	0.0007272	0.00233762	0.06266	1	17	18	22	21	26	68	62	40	64	47
ENSMUSG00000040054	chr10	Baz2a	1.3E+08	1.3E+08	8372	-0.57730055	4.692684233	0.0007305	0.002347827	0.0326	-1	432	303	591	490	547	551	543	273	338	471
ENSMUSG00000003923	chr10	Tfam	7.1E+07	7.1E+07	4438	-0.60774812	5.663873357	0.0007364	0.002366177	0.03741	-1	839	637	1308	998	876	989	978	640	744	814
ENSMUSG00000034088	chr1	Hdlbp	9.3E+07	9.3E+07	11320	-0.74843839	8.578920206	0.0007381	0.002371132	0.0581	-1	6318	4662	10612	9048	5950	6388	7687	4046	6077	5552
ENSMUSG00000029570	chr5	Lfng	1.4E+08	1.4E+08	2282	1.332812432	3.237758751	0.0007408	0.002379158	0.17341	1	50	46	67	27	233	383	175	260	295	249
ENSMUSG00000068663	chr16	Clec16a	1.1E+07	1.1E+07	8368	-0.73398335	6.625628094	0.0007429	0.002385651	0.05552	-1	1447	1175	2861	2276	1730	1529	2159	998	1539	1511
ENSMUSG00000013076	chr9	Amotl1	1.5E+07	1.5E+07	9798	-0.76334002	8.73840198	0.0007433	0.00238636	0.06049	-1	7085	6351	10569	9787	6495	6020	8772	4456	6239	7429
ENSMUSG00000030527	chr7	Crtc3	8.1E+07	8.1E+07	9850	-0.59860869	4.300017569	0.0007438	0.00238716	0.03464	-1	327	311	386	350	388	312	387	223	351	346
ENSMUSG00000031864	chr8	Ints10	6.9E+07	6.9E+07	6706	-0.59056947	3.865919779	0.0007448	0.002389941	0.03251	-1	238	180	362	257	297	326	248	173	218	244
ENSMUSG00000041479	chr14	Syt15	3.4E+07	3.4E+07	5165	0.977729477	1.377293869	0.0007532	0.002416217	0.07077	1	21	22	28	28	25	70	51	57	72	85
ENSMUSG00000099059	chr15	Mir7676-2	7.8E+07	7.8E+07	62	1.733009081	-0.45844503	0.000754	0.002418361	0.17524	1	1	2	3	3	12	21	32	9	11	23
ENSMUSG00000024640	chr19	Psat1	1.6E+07	1.6E+07	4254	1.031873077	2.8860969	0.000755	0.002420881	0.10069	1	58	60	63	41	142	263	129	205	202	193
ENSMUSG00000032263	chr9	Bckdhb	8.4E+07	8.4E+07	1805	-0.77518635	4.973329954	0.000756	0.002423734	0.06078	-1	761	493	403	481	781	552	361	426	497	533
ENSMUSG00000027613	chr2	Eif6	1.6E+08	1.6E+08	2702	0.597311401	5.378282761	0.0007584	0.002430815	0.03603	1	410	320	570	534	704	1134	926	775	1209	1122
ENSMUSG00000024053	chr17	Emilin2	7.1E+07	7.1E+07	3910	1.008849173	4.733636062	0.0007633	0.002445918	0.10299	1	172	180	156	198	664	995	707	567	803	604
ENSMUSG00000021213	chr13	Akr1c13	4191184	4191310	1400	1.744062671	0.779606969	0.000766	0.002454035	0.25305	1	7	9	3	3	33	99	34	26	51	47
ENSMUSG00000037447	chr1	Arid5a	3.6E+07	3.6E+07	12540	0.819049104	3.049548609	0.0007685	0.002461365	0.06192	1	79	59	121	113	75	303	152	163	250	213
ENSMUSG00000022051	chr14	Bnip3l	6.7E+07	6.7E+07	3859	-0.64041927	5.759135907	0.0007703	0.002466754	0.04206	-1	1160	776	1011	949	1006	993	1086	661	765	885
ENSMUSG00000047379	chr19	B3gnt1	5038826	5040032	2035	0.533745922	5.011118451	0.0007719	0.002471419	0.02815	1	373	261	462	407	502	952	725	553	844	884
ENSMUSG00000030177	chr6	Ccdc77	1.2E+08	1.2E+08	6685	-0.89786498	1.905835105	0.0007772	0.002487545	0.06894	-1	75	47	100	74	68	73	70	24	48	57
ENSMUSG00000020886	chr11	Dlg4	7E+07	7E+07	4982	0.931185588	1.9827642	0.000782	0.002502531	0.07357	1	29	30	43	33	66	139	72	87	115	104
ENSMUSG00000034940	chr11	Synrg	8.4E+07	8.4E+07	8744	-0.6789764	5.896422265	0.0007896	0.002526311	0.04762	-1	998	863	1340	1344	933	920	1273	708	963	871
ENSMUSG00000022791	chr16	Tnk2	3.3E+07	3.3E+07	5496	-0.70953483	5.969979854	0.000792	0.002533228	0.05208	-1	819	663	1604	1152	1874	969	1288	614	1027	1067
ENSMUSG00000024132	chr17	Eci1	2.4E+07	2.4E+07	1091	-0.92579702	6.503316285	0.0007932	0.002536003	0.08886	-1	1424	631	3959	1856	1717	1456	1634	891	1130	1415
ENSMUSG00000050930	chr8	Map10	1.3E+08	1.3E+08	3542	-1.00322602	1.854434814	0.0007931	0.002536003	0.08812	-1	48	58	115	82	56	50	77	28	48	44
ENSMUSG00000018425	chr11	Dhx40	8.7E+07	8.7E+07	4233	-0.61662603	4.033376115	0.0007937	0.002536887	0.03681	-1	321	237	331	276	311	331	339	181	228	267
ENSMUSG00000033392	chr9	Clasp2	1.1E+08	1.1E+08	5690	-0.63819527	5.732408152	0.000794	0.002537455	0.04195	-1	922	636	1355	1136	875	958	1066	557	825	939
ENSMUSG00000002908	chr8	Kcnn1	7.1E+07	7.1E+07	4054	-0.64198693	4.148115317	0.0007952	0.002540641	0.04022	-1	305	195	466	368	318	279	372	187	314	284
ENSMUSG00000034271	chr12	Jdp2	8.6E+07	8.6E+07	1881	0.848245379	2.611178195	0.0007967	0.002544766	0.06634	1	44	33	87	58	114	206	137	131	162	159
ENSMUSG00000028189	chr3	Ctbs	1.5E+08	1.5E+08	2892	-0.86567138	2.475799105	0.0007974	0.002546404	0.06807	-1	120	89	93	99	126	122	105	52	65	66
ENSMUSG00000033308	chr3	Dpyd	1.2E+08	1.2E+08	8040	-1.10094638	1.576800923	0.0007977	0.002547004	0.10479	-1	52	32	108	37	84	50	61	27	25	30
ENSMUSG00000079737	chr16	3110001I22Rik	1.4E+07	1.4E+07	1722	-0.93636697	1.906148642	0.0007992	0.00255114	0.07628	-1	57	78	92	66	64	58	74	32	48	52
ENSMUSG00000033222	chr3	Ttf2	1E+08	1E+08	6564	-0.77116095	3.147954587	0.0008014	0.002557481	0.05614	-1	189	147	184	166	131	146	169	92	142	127
ENSMUSG00000042793	chr1	Lgr6	1.3E+08	1.3E+08	6851	-1.57811691	0.644537553	0.0008027	0.002560976	0.20657	-1	38	7	79	36	17	14	21	13	8	20
ENSMUSG00000026349	chr1	Ccnt2	1.3E+08	1.3E+08	12345	-0.57493694	4.814693809	0.0008056	0.002569139	0.03307	-1	551	404	586	457	515	572	552	345	380	499
ENSMUSG00000028559	chr4	Osbpl9	1.1E+08	1.1E+08	7006	-0.67917867	6.380387671	0.0008059	0.002569139	0.04811	-1	1727	1241	2012	1306	1385	1557	1693	953	1160	1310
ENSMUSG00000038014	chr13	Fam120a	4.9E+07	4.9E+07	5105	-0.65108852	7.043029913	0.0008059	0.002569139	0.04444	-1	2322	1704	3049	2732	2382	2360	2673	1482	2041	2134
ENSMUSG00000042558	chr4	Adprhl2	1.3E+08	1.3E+08	2475	0.697589439	3.709073912	0.0008057	0.002569139	0.04679	1	138	97	182	118	227	448	251	235	372	365
ENSMUSG00000021577	chr13	Sdha	7.4E+07	7.4E+07	3883	-0.77188068	10.04970331	0.0008062	0.002569518	0.06274	-1	18665	11163	32500	21662	19857	15637	24042	11331	14971	15463
ENSMUSG00000079012	chr12	Serpina3m	1E+08	1E+08	1719	1.744450249	1.549656913	0.0008078	0.002573906	0.27347	1	14	17	5	6	55	165	123	62	56	46
ENSMUSG00000074825	chr2	Itpripl1	1.3E+08	1.3E+08	3738	0.798826412	2.645476087	0.0008088	0.002576363	0.0569	1	60	48	74	55	105	205	144	150	163	136
ENSMUSG00000029478	chr5	Ncor2	1.3E+08	1.3E+08	10479	-0.74892498	6.266690491	0.000813	0.002589206	0.05847	-1	1138	792	2456	1720	1424	1097	1629	846	1267	1111
ENSMUSG00000039384	chr1	Dusp10	1.8E+08	1.8E+08	3042	-0.5840942	5.204986289	0.0008132	0.002589206	0.03454	-1	610	417	802	693	870	647	703	541	476	657
ENSMUSG00000038583	chr10	Pln	5.3E+07	5.3E+07	2480	1.274388488	2.311211098	0.0008146	0.002593238	0.15451	1	24	15	81	75	26	124	173	96	92	222
ENSMUSG00000036019	chr10	Tmtc2	1.1E+08	1.1E+08	7779	-1.21239371	1.093044093	0.000816	0.002597	0.12239	-1	26	23	72	70	31	25	39	16	23	26
ENSMUSG00000037362	chr15	Nov	5.5E+07	5.5E+07	2869	0.717481291	3.944578923	0.0008174	0.002601015	0.05073	1	181	79	176	235	216	445	347	328	393	442
ENSMUSG00000056579	chr11	Tug1	3639785	3645523	8325	-0.57197837	4.93614928	0.0008184	0.002603564	0.03299	-1	462	468	658	562	589	680	590	364	406	529
ENSMUSG00000028414	chr4	Fktn	5.4E+07	5.4E+07	6491	-0.62917876	4.247140282	0.0008198	0.002606798	0.03908	-1	335	277	443	337	335	311	442	207	278	310
ENSMUSG00000029998	chr6	Pcyox1	8.6E+07	8.6E+07	4797	-0.63354899	6.127301503	0.00082	0.002606798	0.04183	-1	1338	1038	1345	1225	1391	1318	1435	803	1107	1044
ENSMUSG00000040026	chr7	Saa3	4.7E+07	4.7E+07	531	2.087536085	0.442426253	0.00082	0.002606798	0.38139	1	0	0	16	6	16	55	34	15	84	18
ENSMUSG00000038780	chr5	Smurf1	1.4E+08	1.4E+08	6336	-0.60746189	4.745587645	0.0008207	0.00260853	0.03699	-1	337	303	767	525	583	500	542	306	408	455

ENSMUSG00000026111	chr1	Unc50	3.7E+07	3.7E+07	1579	0.62375071	4.158217119	0.0008221	0.002612167	0.03794	1	196	146	223	183	319	574	390	379	445	431
ENSMUSG00000038489	chr7	Polr2l	1.4E+08	1.4E+08	1650	0.556844547	5.315703144	0.0008223	0.002612419	0.03146	1	460	346	525	490	616	1028	931	800	1056	1048
ENSMUSG00000059475	chr9	Zfp426	2E+07	2E+07	4888	-0.70572779	3.361290813	0.0008231	0.002614171	0.04715	-1	199	162	197	192	189	190	206	106	131	178
ENSMUSG00000030987	chr7	Stim1	1E+08	1E+08	3597	-0.76101688	7.552787925	0.0008256	0.002621532	0.061	-1	3190	2265	5194	4306	3095	2842	4372	1892	2568	2878
ENSMUSG00000029208	chr5	Guf1	7E+07	7E+07	9114	-0.55794839	4.56091588	0.0008264	0.002622998	0.03065	-1	380	294	582	465	411	425	456	309	366	412
ENSMUSG00000060913	chr3	Trim55	2E+07	2E+07	2659	-0.71452035	5.92764644	0.0008262	0.002622998	0.0532	-1	1297	976	1360	1089	856	903	1218	750	959	917
ENSMUSG00000027710	chr3	Acad9	3.6E+07	3.6E+07	3913	-0.57719054	5.316419818	0.0008274	0.002625601	0.03399	-1	627	428	998	788	837	723	845	469	632	654
ENSMUSG00000027324	chr2	Rpusd2	1.2E+08	1.2E+08	2706	-0.964784	1.477352276	0.0008282	0.002627583	0.07568	-1	45	39	82	58	49	36	60	24	34	37
ENSMUSG00000051811	chr7	Cox6b2	4751792	4751975	1108	1.4351874	-0.17642318	0.000829	0.002629398	0.1193	1	5	3	7	5	11	36	11	19	19	29
ENSMUSG00000031066	chrX	Usp11	2.1E+07	2.1E+07	4732	0.847981301	2.330172675	0.0008327	0.002640721	0.06218	1	41	44	79	55	45	149	113	93	128	170
ENSMUSG00000039952	chr9	Dag1	1.1E+08	1.1E+08	6357	-0.72566405	8.157965364	0.0008335	0.002642651	0.05571	-1	4929	4045	6447	6520	4752	4665	6356	2967	4459	4027
ENSMUSG00000071337	chr6	Tia1	8.6E+07	8.6E+07	12945	-0.62543351	3.832741639	0.0008349	0.002646408	0.03785	-1	252	221	324	233	258	294	263	147	208	257
ENSMUSG00000021051	chr12	Ppp2r5e	7.5E+07	7.5E+07	4808	-0.58433534	5.23416603	0.0008381	0.002656051	0.03495	-1	605	553	821	761	633	712	784	463	565	600
ENSMUSG00000021327	chr13	Zkscan3	2.1E+07	2.1E+07	7817	-0.59854286	4.124612099	0.0008396	0.002659987	0.03492	-1	330	237	363	316	326	357	305	226	228	317
ENSMUSG00000024404	chr18	Riok3	1.2E+07	1.2E+07	3661	-0.69545177	7.210349027	0.0008404	0.002661825	0.05109	-1	2829	2324	3305	2620	2552	2469	3175	1726	2247	2119
ENSMUSG00000097891	chr18	Gm3650	4.3E+07	4.3E+07	747	1.353856758	-0.02382968	0.0008405	0.002661825	0.10442	1	4	5	6	11	10	37	19	24	28	18
ENSMUSG00000053038	chr8	Gm6180	4.2E+07	4.2E+07	501	1.358589185	1.06212677	0.0008411	0.002662929	0.15723	1	7	10	9	14	45	67	52	38	77	57
ENSMUSG00000001089	chr4	Luzp1	1.4E+08	1.4E+08	8112	-0.55387783	4.694989628	0.0008438	0.002669663	0.0304	-1	413	294	659	456	546	449	520	363	427	395
ENSMUSG00000036040	chr2	Adamtsl2	2.7E+07	2.7E+07	7993	0.919127674	1.843367041	0.0008436	0.002669663	0.07021	1	28	25	47	47	34	116	125	53	104	77
ENSMUSG00000040260	chr17	Daam2	4.9E+07	4.9E+07	6045	0.684874802	3.206687061	0.0008434	0.002669663	0.04264	1	91	87	124	91	135	296	203	164	241	265
ENSMUSG00000044345	chr19	Marveld1	4.2E+07	4.2E+07	4304	0.880221575	4.477685358	0.0008451	0.002673205	0.07943	1	138	144	213	184	551	787	578	473	550	591
ENSMUSG00000024812	chr19	Tjp2	2.4E+07	2.4E+07	4591	0.788281627	2.731259323	0.0008459	0.002675129	0.05718	1	58	37	105	70	103	180	155	163	167	176
ENSMUSG00000020268	chr11	Lyrm7	5.5E+07	5.5E+07	3597	-0.71894126	3.661514932	0.0008517	0.00269287	0.05023	-1	192	159	357	257	236	203	290	153	150	189
ENSMUSG00000024483	chr18	Ankhd1	3.7E+07	3.7E+07	9845	-0.5803945	5.138352492	0.0008542	0.002700307	0.03447	-1	539	495	832	723	585	608	690	400	574	659
ENSMUSG00000005615	chr16	Pcyt1a	3.2E+07	3.2E+07	5751	-0.68056652	7.065348671	0.0008559	0.002705108	0.04903	-1	2191	1723	3642	2541	2519	2147	2973	1463	2094	2035
ENSMUSG00000015869	chr11	Prpsap1	1.2E+08	1.2E+08	3407	0.70285779	3.722068624	0.0008562	0.002705453	0.04799	1	124	109	152	126	251	385	279	253	396	362
ENSMUSG00000005732	chr16	Ranbp1	1.8E+07	1.8E+07	1666	0.661831968	4.114488738	0.0008567	0.002705777	0.0436	1	184	116	258	173	304	550	361	414	410	423
ENSMUSG00000020576	chr12	Nbas	1.3E+07	1.3E+07	7239	-0.60573058	4.596490638	0.0008567	0.002705777	0.03693	-1	391	300	531	575	402	447	496	270	402	380
ENSMUSG00000001383	chr18	Zmat2	3.7E+07	3.7E+07	2257	0.624824395	6.512637729	0.0008575	0.002706986	0.04109	1	1091	815	1213	919	1394	2740	2131	1879	2268	2403
ENSMUSG00000040936	chr9	Ulk4	1.2E+08	1.2E+08	7984	2.51879256	-0.31777298	0.0008575	0.002706986	0.48737	1	0	0	5	6	4	8	22	1	29	58
ENSMUSG00000041261	chr4	Car8	8143362	8146216	3853	-1.03829157	1.8529139	0.0008579	0.002707574	0.09603	-1	55	35	147	78	59	59	58	41	34	47
ENSMUSG00000063457	chr10	Rps15	8E+07	8E+07	630	0.677597972	8.226423573	0.0008591	0.002710952	0.04886	1	3188	2514	3764	3615	4378	9176	5971	5665	8811	8588
ENSMUSG00000020335	chr11	Zfp354b	5.1E+07	5.1E+07	2888	-1.14290458	0.799664819	0.0008594	0.002711054	0.09944	-1	34	36	29	25	46	29	31	17	15	16
ENSMUSG00000038406	chr7	Scaf1	4.5E+07	4.5E+07	8368	-0.65964545	5.7002108	0.0008609	0.002715118	0.04544	-1	847	641	1283	1176	889	801	1039	531	1008	815
ENSMUSG00000043252	chr4	Tmem64	1.5E+07	1.5E+07	4670	-0.70894278	6.938366464	0.000861	0.002715118	0.05318	-1	2148	1557	3696	2275	1975	1760	2327	1568	1854	2055
ENSMUSG00000025511	chr7	Tspan4	1.4E+08	1.4E+08	2178	0.876932948	4.127919215	0.0008621	0.002718027	0.07841	1	171	102	180	123	383	633	322	450	436	459
ENSMUSG00000024194	chr17	Cuta	2.7E+07	2.7E+07	649	0.669144916	5.880534926	0.0008642	0.00272401	0.04687	1	651	468	685	654	1004	1490	1266	1045	1988	1681
ENSMUSG00000055485	chr2	Soga1	1.6E+08	1.6E+08	7984	-1.01846378	1.779287385	0.0008645	0.00272406	0.09261	-1	73	59	69	67	66	49	85	25	32	43
ENSMUSG00000092541	chr9	Gm20537	8.8E+07	8.8E+07	1009	-0.65188917	3.66194645	0.0008675	0.002733127	0.04093	-1	236	194	246	236	232	228	260	154	177	196
ENSMUSG00000020696	chr11	Rffl	8.3E+07	8.3E+07	5922	-0.69820672	3.096846807	0.0008701	0.002740655	0.04516	-1	142	100	178	148	240	156	161	87	125	147
ENSMUSG00000021186	chr12	Fbln5	1E+08	1E+08	5829	0.612608883	4.605761814	0.0008716	0.002744617	0.0377	1	264	220	302	223	451	822	548	447	579	658
ENSMUSG00000074283	chr7	Zfp109	2.4E+07	2.4E+07	1935	-1.9112488	-0.37997093	0.0008734	0.002749798	0.25735	-1	18	13	31	13	8	9	15	5	1	0
ENSMUSG00000027285	chr2	Haus2	1.2E+08	1.2E+08	3218	-0.76521054	3.470110667	0.0008759	0.002757168	0.05733	-1	215	153	242	233	198	199	268	116	147	123
ENSMUSG00000010376	chr14	Nedd8	5.6E+07	5.6E+07	604	0.623305057	6.236218822	0.000878	0.002762945	0.0409	1	933	644	954	862	1081	2200	1641	1524	2081	1971
ENSMUSG00000027330	chr2	Cdc25b	1.3E+08	1.3E+08	3728	1.1265767	2.181843614	0.0008783	0.002763469	0.11638	1	25	46	27	27	81	155	95	112	123	134
ENSMUSG00000042622	chr15	Maff	7.9E+07	7.9E+07	2119	0.886526784	2.183144133	0.000879	0.002764407	0.06995	1	40	27	67	46	59	104	149	76	96	170
ENSMUSG00000051007	chr7	Pddc1	1.4E+08	1.4E+08	2871	0.694272945	3.481598356	0.0008789	0.002764407	0.04609	1	125	80	136	115	191	348	238	188	339	311
ENSMUSG00000096768	chrY	Erdr1	9.1E+07	9.1E+07	1124	1.810008144	2.50097993	0.0008799	0.002766556	0.31296	1	20	49	30	29	48	289	10	136	192	264
ENSMUSG00000016477	chr13	E2f3	3E+07	3E+07	4794	-0.6492912	4.317474356	0.0008811	0.002769787	0.04239	-1	325	281	525	378	327	323	461	228	321	274
ENSMUSG00000029776	chr6	Hibadh	5.3E+07	5.3E+07	2226	-0.67128489	7.179456359	0.0008817	0.0027709	0.04797	-1	2762	1677	3888	2739	2565	2579	2832	1848	2070	2234
ENSMUSG00000026017	chr1	Carf	6E+07	6E+07	14557	-0.86072139	1.941083278	0.0008839	0.002777239	0.06397	-1	69	59	107	72	59	78	58	40	46	57
ENSMUSG00000021703	chr13	Serinc5	9.3E+07	9.3E+07	5316	0.679651391	3.186491504	0.0008863	0.002784074	0.04249	1	83	77	144	95	129	271	217	180	203	273
ENSMUSG00000035184	chr14	Fam124a	6.3E+07	6.3E+07	4406	0.994780199	2.471415245	0.000888	0.002788563	0.09376	1	38	33	60	33	120	178	133	103	138	198
ENSMUSG00000090125	chr4	Pou3f1	1.2E+08	1.2E+08	3849	1.405527052	0.107338045	0.0008881	0.002788563	0.13843	1	4	6	16	2	12	28	20	22	26	45
ENSMUSG00000073403	chr17	Gm10499	3.6E+07	3.6E+07	1762	1.320786621	3.458399174	0.0008914	0.002798207	0.1752	1	135	51	45	61	179	586	153	135	289	502
ENSMUSG00000022012	chr14	Enox1	7.7E+07	7.7E+07	3495	1.23044722	0.329141335	0.0008936	0.002804475	0.10172	1	16	5	13	4	13	44	34	27	33	25
ENSMUSG00000031537	chr8	Ikbkb	2.3E+07	2.3E+07	19078	0.545123603	4.567434056	0.000896	0.002811522	0.02949	1	281	195	308	283	395	750	607	407	531	630
ENSMUSG00000020889	chr11	Nr1d1	9.9E+07	9.9E+07	3077	-0.63871971	7.386896227	0.0008978	0.0028165	0.04363	-1	2809	2104	3470	3554	3521	2831	2939	1941	2893	2974
ENSMUSG00000037960	chr13	1110007C09Rik	4.9E+07	4.9E+07	804	0.663322439	6.041061025	0.0009023	0.002829918	0.0466	1	589	428	1213	776	984	1678	1805	1122	1896	1877
ENSMUSG00000000149	chr5	Gna12	1.4E+08	1.4E+08	3416	0.648444718	5.715118347	0.0009051	0.002838078	0.04435	1	464	326	906	630	885	1569	1534	865	1447	1282
ENSMUSG00000057777	chr3	Mab21l2	8.7E+07	8.7E+07	3049	1.443339677	-0.38479109	0.0009053	0.002838078	0.11117	1	2	2	5	8	9	16	23	14	17	26
ENSMUSG00000032228	chr9	Tcf12	7.2E+07	7.2E+07	15529	-0.58816766	4.578620392	0.0009064	0.002840871	0.03505	-1	395	332	563	445	425	500	525	276	368	321
ENSMUSG00000086605	chr2	Gm14290	1.7E+08	1.7E+08	1894	-0.76256209	3.223388763	0.0009082	0.002845956	0.05612	-1	143	129	181	209	220	115	188	102	179	125
ENSMUSG00000025025	chr19	Mxi1	5.3E+07	5.3E+07	5619	-0.6260769	5.582665068	0.0009124	0.002858311	0.04123	-1	874	668	957	1046	787	831	857	508	809	920
ENSMUSG00000006005	chr1	Tpr	1.5E+08	1.5E+08	10496	-0.69028347	6.561935293	0.0009149	0.002865644	0.05084	-1	1610	1266	2512	2008	1429	1763	1946	1095	1290	1434
ENSMUSG00000034422	chr16	Parp14	3.6E+07	3.6E+07	9306	0.749164039	3.99683037	0.0009161	0.002868125	0.05647	1	169	121	191	161	261	765	373	216	375	398
ENSMUSG00000047423	chr19	AI837181	5425157	5425308	1529	0.592071697	5.110050133	0.0009159	0.002868125	0.03626	1	339	284	494	394	599	890	767	666	1114	826

ENSMUSG00000035829	chr2	Ppp1r26	2.8E+07	2.8E+07	5619	-0.88313445	1.605254864	0.0009179	0.002873121	0.06244	-1	59	31	79	67	59	50	48	28	51	40
ENSMUSG00000027832	chr3	Ptx3	6.6E+07	6.6E+07	2682	0.902057349	3.466202341	0.000919	0.002875884	0.08136	1	117	81	117	107	155	291	191	361	366	204
ENSMUSG00000030330	chr6	Ing4	1.3E+08	1.3E+08	6675	0.574714549	5.253262254	0.0009197	0.002877504	0.03415	1	430	349	476	419	640	1094	813	711	1044	1049
ENSMUSG00000031928	chr9	Mre11a	1.5E+07	1.5E+07	5902	-0.64900074	3.917992408	0.0009218	0.00288332	0.04191	-1	256	256	308	269	272	291	320	179	219	210
ENSMUSG00000022412	chr15	Mief1	8E+07	8E+07	5541	-0.58310849	4.791768789	0.0009221	0.002883546	0.03474	-1	411	319	755	559	507	499	582	319	471	432
ENSMUSG00000022687	chr16	Boc	4.4E+07	4.4E+07	4456	0.848378556	3.554714413	0.0009223	0.002883649	0.07178	1	72	97	117	114	238	425	387	178	251	339
ENSMUSG00000061778	chrX	Mospd2	1.6E+08	1.6E+08	7914	-0.89496526	2.849228591	0.0009229	0.002884906	0.07776	-1	131	114	198	113	147	159	164	57	72	79
ENSMUSG00000074417	chr7	Gm14548	3884242	3884427	2128	1.411894306	0.494463297	0.0009236	0.002886595	0.15322	1	9	8	6	10	19	49	73	24	18	30
ENSMUSG00000028629	chr4	Exo5	1.2E+08	1.2E+08	2008	1.018661849	1.605581042	0.0009253	0.002891219	0.0884	1	26	22	25	22	51	127	69	72	74	61
ENSMUSG00000028284	chr4	Map3k7	3.2E+07	3.2E+07	6423	-0.6642662	6.117561608	0.0009282	0.002899573	0.04698	-1	1157	947	1779	1443	1105	1263	1488	761	991	1104
ENSMUSG00000038459	chr7	Abhd17c	8.4E+07	8.4E+07	2415	0.617365724	3.941302728	0.0009287	0.002900361	0.03765	1	172	107	214	164	272	401	391	338	376	385
ENSMUSG00000022789	chr16	Dnm1l	1.6E+07	1.6E+07	4107	-0.72602176	6.164200269	0.0009293	0.002900812	0.05617	-1	1133	897	2058	1627	1109	1246	1591	837	959	981
ENSMUSG00000049303	chr19	Syt12	4445908	4447860	5539	-1.03244496	2.285537462	0.0009294	0.002900812	0.10112	-1	36	77	97	149	131	77	67	53	62	67
ENSMUSG00000050954	chr13	Zfp169	4.8E+07	4.8E+07	8017	-1.15541597	0.321834405	0.0009294	0.002900812	0.09214	-1	25	22	22	28	23	17	24	7	14	14
ENSMUSG00000032845	chr18	Alpk2	6.5E+07	6.5E+07	7782	-0.91632645	5.860399927	0.0009302	0.002902422	0.08898	-1	1098	546	2124	1458	675	767	791	864	712	922
ENSMUSG00000020142	chr11	Slc1a4	2E+07	2E+07	3926	1.203582621	1.467070369	0.0009311	0.002904755	0.1241	1	10	24	14	32	38	110	61	59	89	61
ENSMUSG00000022641	chr16	Bbx	5E+07	5E+07	14205	-0.6810511	3.331880525	0.0009314	0.002905153	0.04447	-1	188	164	196	153	217	182	199	115	155	147
ENSMUSG00000093701	chr16	Gm21970	9.1E+07	9.1E+07	884	1.033182476	3.825500261	0.0009384	0.002926181	0.10995	1	107	74	103	81	366	528	355	314	373	386
ENSMUSG00000041355	chr3	Ssr2	8.9E+07	8.9E+07	1864	0.649747708	5.569297015	0.0009391	0.002927788	0.04453	1	563	387	556	494	805	1494	899	968	1401	1211
ENSMUSG00000057069	chr13	Ero1lb	1.3E+07	1.3E+07	4237	0.863444885	2.047996383	0.0009406	0.002931719	0.06369	1	47	30	34	40	63	144	98	74	107	116
ENSMUSG00000067369	chrX	Trmt2b	1.3E+08	1.3E+08	4648	-0.70439081	4.547732859	0.0009422	0.002936183	0.0513	-1	370	263	743	486	373	420	537	248	281	370
ENSMUSG00000081058	chr3	Hist2h3c2	9.6E+07	9.6E+07	1020	1.031594739	1.533836255	0.0009429	0.00293769	0.0887	1	15	20	23	34	46	80	62	58	99	83
ENSMUSG00000030189	chr6	Ybx3	1.3E+08	1.3E+08	1862	-0.66655474	9.420426784	0.0009446	0.002942118	0.04818	-1	10734	8838	16324	12799	15690	10971	13925	7095	11241	12037
ENSMUSG00000067869	chr15	Tcea1-ps1	9.1E+07	9.1E+07	904	-1.22382802	1.095899742	0.0009452	0.002943357	0.13066	-1	41	40	41	52	40	27	54	12	24	14
ENSMUSG00000035314	chr7	Gdpd5	9.9E+07	9.9E+07	3582	-0.66487678	3.472894426	0.0009458	0.002944677	0.04247	-1	196	137	240	157	310	210	189	140	175	169
ENSMUSG00000021877	chr14	Arf4	2.7E+07	2.7E+07	2813	0.724470924	5.633157037	0.0009479	0.002950015	0.05573	1	501	384	509	425	1059	1671	1169	1062	1219	1259
ENSMUSG00000025223	chr19	Ldb1	4.6E+07	4.6E+07	3583	0.638466353	4.905888506	0.0009479	0.002950015	0.04237	1	306	244	444	263	547	959	588	536	744	961
ENSMUSG00000022421	chr15	Nptxr	8E+07	8E+07	5169	0.933826919	1.990568228	0.0009515	0.002960241	0.07601	1	26	35	38	39	61	156	127	61	105	83
ENSMUSG00000067203	chr17	H2-K2	3.4E+07	3.4E+07	1049	1.159786214	2.825268783	0.0009516	0.002960241	0.13229	1	47	60	51	32	136	381	130	115	185	211
ENSMUSG00000022407	chr15	Adsl	8.1E+07	8.1E+07	4398	-0.70764024	6.661295541	0.0009531	0.002964098	0.05381	-1	1551	1197	2979	2177	1764	1434	2132	1153	1653	1580
ENSMUSG00000022474	chr15	Pmm1	8.2E+07	8.2E+07	2776	0.653746267	4.137628385	0.0009533	0.002964098	0.0435	1	168	106	304	180	311	569	385	351	430	481
ENSMUSG00000000318	chr11	Clec10a	7E+07	7E+07	2899	1.65350683	4.993008562	0.0009538	0.002964952	0.27927	1	178	307	27	99	484	1891	567	781	922	892
ENSMUSG00000044609	chr7	Gm9294	4.3E+07	4.3E+07	789	1.186535742	1.00718289	0.0009559	0.002971003	0.11342	1	19	8	15	21	24	60	26	41	74	67
ENSMUSG00000034751	chr13	Mast4	1E+08	1E+08	32204	-0.7390156	5.955369952	0.0009592	0.002980462	0.0584	-1	1260	1064	1110	1297	923	990	1217	823	977	765
ENSMUSG00000000759	chr8	Tubgcp3	1.3E+07	1.3E+07	8568	-0.66186536	3.478071271	0.0009599	0.002981202	0.04266	-1	201	153	289	190	195	230	221	124	165	156
ENSMUSG00000022199	chr14	Slc22a17	5.5E+07	5.5E+07	2294	1.023479866	1.969541504	0.0009598	0.002981202	0.0933	1	31	36	27	29	63	149	76	62	120	125
ENSMUSG00000039911	chr4	Spsb1	1.5E+08	1.5E+08	4396	0.826441119	3.662564544	0.0009605	0.002982409	0.06942	1	103	78	118	114	294	409	334	239	360	326
ENSMUSG00000005107	chr5	Slc2a9	3.8E+07	3.8E+07	5083	1.218545314	0.453317861	0.0009625	0.002987974	0.10362	1	15	3	12	9	18	56	33	20	32	41
ENSMUSG00000058093	chr13	AA987161	6.8E+07	6.8E+07	4861	-0.88618826	1.927960046	0.0009637	0.002991218	0.06901	-1	84	57	87	59	77	70	80	37	43	44
ENSMUSG00000031974	chr8	Abcb10	1.2E+08	1.2E+08	4306	-0.58774395	5.09337207	0.0009671	0.00300098	0.03599	-1	515	400	916	717	590	585	716	440	517	557
ENSMUSG00000019820	chr10	Utrn	1.2E+07	1.2E+07	12382	-0.55040836	5.025734379	0.0009703	0.003010352	0.03139	-1	567	407	604	547	814	674	646	403	459	566
ENSMUSG00000027667	chr3	Zfp639	3.3E+07	3.3E+07	5475	-0.5757871	4.203929333	0.0009742	0.00302169	0.03318	-1	274	277	403	349	347	362	357	237	279	293
ENSMUSG00000000420	chr18	Galnt1	2.4E+07	2.4E+07	5519	-0.64171149	6.623652216	0.0009744	0.003021803	0.04442	-1	1754	1303	2299	1849	1896	1676	2210	1158	1508	1449
ENSMUSG00000089782	chr1	Gm3531	9.8E+07	9.8E+07	489	0.718662269	2.801456535	0.000976	0.003025802	0.04734	1	69	54	91	91	87	176	166	148	194	189
ENSMUSG00000017765	chr8	Slc12a4	1.1E+08	1.1E+08	4297	0.713355444	4.683146376	0.0009767	0.003027434	0.05356	1	175	131	489	323	428	747	655	484	667	744
ENSMUSG00000060636	chr16	Rpl35a	3.3E+07	3.3E+07	3526	0.674817224	7.131423367	0.0009788	0.003033352	0.04931	1	1623	1195	1967	1466	1933	4808	2672	3131	3554	3586
ENSMUSG00000014355	chr2	Anapc1	1.3E+08	1.3E+08	16714	-0.64145964	5.866717502	0.0009792	0.003033713	0.044	-1	986	654	1639	1148	1046	1031	1293	663	857	902
ENSMUSG00000024927	chr19	Rela	5637483	5637841	2716	0.645890525	4.96517359	0.000982	0.003041448	0.04393	1	274	208	492	305	631	966	673	576	862	869
ENSMUSG00000090673	chr19	Gm340	4.2E+07	4.2E+07	3729	-1.39495813	0.207797292	0.0009821	0.003041448	0.14668	-1	20	16	24	41	16	10	22	6	7	17
ENSMUSG00000006273	chr8	Atp6v1b2	6.9E+07	6.9E+07	5305	0.660438276	6.983503841	0.000983	0.003043721	0.04725	1	1197	932	1850	1516	2082	3124	3251	2149	3756	3804
ENSMUSG00000063077	chr4	Kif1b	1.5E+08	1.5E+08	17608	-0.75021713	9.083051093	0.0009849	0.003048916	0.06129	-1	8995	6795	13998	13705	8080	8530	10790	5755	8267	8755
ENSMUSG00000036305	chr15	Rpl39-ps	1E+08	1E+08	355	0.793887642	2.235607064	0.0009861	0.003051782	0.05399	1	43	45	58	42	64	138	116	77	141	133
ENSMUSG00000026554	chr1	Dcaf8	1.7E+08	1.7E+08	12996	-0.64217132	8.056276869	0.000989	0.003060145	0.04497	-1	4890	3752	5746	5023	4947	4449	5055	3164	4444	4433
ENSMUSG00000027329	chr2	Spef1	1.3E+08	1.3E+08	2747	1.229683236	0.439403961	0.0009912	0.003066251	0.11228	1	4	6	14	8	25	49	33	23	38	36
ENSMUSG00000074829	chr9	2010315B03Rik	1.2E+08	1.2E+08	3914	-0.83415187	1.696769084	0.0009942	0.003074948	0.05724	-1	64	43	68	65	66	69	49	35	44	40
ENSMUSG00000025078	chr19	Nhlrc2	5.7E+07	5.7E+07	3934	-0.73378372	2.368770258	0.0009951	0.003076361	0.04684	-1	81	73	132	94	103	100	79	62	74	81
ENSMUSG00000040592	chr11	Cd79b	1.1E+08	1.1E+08	1431	1.788562045	-0.28930771	0.000995	0.003076361	0.23572	1	0	1	2	6	15	33	18	22	13	23
ENSMUSG00000020329	chr10	Polrmt	8E+07	8E+07	4685	-0.60923667	4.756144474	0.0009973	0.003082393	0.03853	-1	369	282	782	525	585	449	545	290	496	444
ENSMUSG00000038372	chr13	Gmds	3.2E+07	3.2E+07	3323	1.042190019	1.519517108	0.0009975	0.003082522	0.09344	1	26	17	31	14	50	111	67	71	64	66
ENSMUSG00000037242	chr4	Clic4	1.4E+08	1.4E+08	6572	0.698337056	6.625677359	0.001	0.003089307	0.05287	1	924	652	1278	998	2034	3195	2765	1835	2327	2608
ENSMUSG00000002396	chr8	Ocel1	7.1E+07	7.1E+07	7133	0.750889849	3.655554585	0.0010004	0.003089785	0.05738	1	96	66	233	164	174	387	261	237	376	363
ENSMUSG00000029249	chr5	Rest	7.7E+07	7.7E+07	7222	-0.60237682	4.135974227	0.0010006	0.003089785	0.03667	-1	281	284	341	330	333	323	349	220	293	255
ENSMUSG00000040774	chr3	Cept1	1.1E+08	1.1E+08	3116	-0.73324937	4.82032136	0.0010009	0.003090137	0.05689	-1	608	551	420	518	429	554	425	363	401	446
ENSMUSG00000048482	chr2	Bdnf	1.1E+08	1.1E+08	6217	1.561529864	0.944925448	0.0010011	0.003090186	0.22019	1	7	3	27	30	3	57	46	42	57	72
ENSMUSG00000014158	chr5	Trpv4	1.1E+08	1.1E+08	4076	1.145489866	1.697560874	0.0010014	0.003090416	0.12085	1	14	23	23	22	67	126	66	69	83	100
ENSMUSG00000021192	chr12	Golga5	1E+08	1E+08	2897	-0.52917387	4.689349619	0.0010035	0.003095509	0.02866	-1	441	319	596	474	480	529	532	287	443	413
ENSMUSG00000025420	chr18	Katnal2	7.7E+07	7.7E+07	4061	1.944184616	3.347361741	0.0010033	0.003095509	0.37537	1	98	40	6	6	164	420	404	248	315	267

ENSMUSG00000031299	chrX	Pdha1	1.6E+08	1.6E+08	3734	-0.85326152	9.468405471	0.0010043	0.003096562	0.07928	-1	12307	6980	25310	15184	11638	10500	16419	7255	8850	9604
ENSMUSG00000036112	chr10	Metap2	9.4E+07	9.4E+07	7588	-0.66552004	7.283954867	0.0010041	0.003096562	0.04824	-1	2749	1971	4198	2522	3227	2830	3305	1971	2164	2216
ENSMUSG00000086782	chr4	E130102H24Rik	1E+08	1E+08	918	-1.24945534	0.494557931	0.0010047	0.003097144	0.12171	-1	35	25	19	33	26	25	20	6	11	22
ENSMUSG00000020018	chr10	Snrpf	9.4E+07	9.4E+07	861	0.59015477	4.345124234	0.0010057	0.003099588	0.03519	1	222	197	285	215	298	582	428	471	502	497
ENSMUSG00000057265	chr12	Ccdc176	8.4E+07	8.4E+07	2234	-1.0151852	0.932060875	0.0010064	0.003100876	0.07592	-1	30	25	62	36	35	25	32	19	19	30
ENSMUSG00000013155	chr8	Enkd1	1.1E+08	1.1E+08	1272	1.276507714	0.570242413	0.0010098	0.003110936	0.12912	1	18	3	14	5	21	59	39	25	46	31
ENSMUSG00000079662	chr17	Ntn3	2.4E+07	2.4E+07	4894	1.191898677	0.637439855	0.0010119	0.003116653	0.10708	1	16	6	12	19	12	58	23	31	45	48
ENSMUSG00000047371	chr7	Zfp768	1.3E+08	1.3E+08	2245	-0.62211933	5.551427156	0.001013	0.003119408	0.04134	-1	715	494	1342	939	920	810	927	487	846	783
ENSMUSG00000034327	chr14	Kctd9	6.8E+07	6.8E+07	4746	-0.64968853	5.986370733	0.0010169	0.003130472	0.04555	-1	1109	855	1595	1276	1008	1214	1359	757	901	904
ENSMUSG00000059273	chr7	Zc3h4	1.6E+07	1.6E+07	6049	-0.53890792	5.108721712	0.0010171	0.003130661	0.03032	-1	599	395	890	602	643	617	661	446	552	629
ENSMUSG00000019054	chr5	Fis1	1.4E+08	1.4E+08	1714	0.628305225	7.015441191	0.0010179	0.003131555	0.04301	1	1474	1051	1771	1566	1863	3518	2857	2523	3696	3606
ENSMUSG00000075410	chr11	Gm11744	1.2E+08	1.2E+08	1534	1.530178921	-0.22555553	0.0010178	0.003131555	0.15603	1	1	2	8	4	14	28	14	12	30	28
ENSMUSG00000002771	chr7	Grin2d	4.6E+07	4.6E+07	5862	1.490434087	-0.3659121	0.0010214	0.003141761	0.13945	1	1	1	5	9	10	29	14	14	23	19
ENSMUSG00000022309	chr15	Angpt1	4.2E+07	4.2E+07	4256	-1.00592018	5.075296971	0.0010217	0.003142009	0.10808	-1	604	314	1354	933	297	420	690	338	453	416
ENSMUSG00000044927	chr6	H1fx	8.8E+07	8.8E+07	1217	1.663447484	0.520670472	0.0010226	0.003143927	0.22937	1	6	10	0	7	23	38	25	34	55	49
ENSMUSG00000044197	chr5	Gpr146	1.4E+08	1.4E+08	6786	-0.57243129	5.548698803	0.0010264	0.003154909	0.03498	-1	669	659	985	936	974	935	926	588	699	759
ENSMUSG00000024019	chr17	Cmtr1	3E+07	3E+07	7890	-0.56699737	5.542425863	0.0010267	0.003155301	0.03431	-1	710	651	1077	910	848	967	880	568	719	774
ENSMUSG00000039449	chr2	Prpf18	4622058	4624526	5310	-0.6223659	5.40991333	0.0010292	0.003162173	0.04142	-1	795	584	980	777	737	732	1007	491	607	644
ENSMUSG00000048920	chr7	Fkrp	1.7E+07	1.7E+07	2803	-0.67359526	5.831589581	0.0010303	0.003164806	0.04902	-1	888	826	1288	1200	1062	820	1352	581	998	818
ENSMUSG00000056999	chr19	Ide	3.7E+07	3.7E+07	5823	-0.68408139	6.863269409	0.001031	0.003166488	0.05106	-1	1946	1459	2806	2781	1869	1865	2288	1438	1836	1796
ENSMUSG00000037824	chr14	Tspan14	4.1E+07	4.1E+07	2475	0.774510599	4.714607065	0.0010339	0.003174616	0.06384	1	264	156	280	203	612	723	599	586	749	724
ENSMUSG00000021709	chr13	Erbb2ip	1E+08	1E+08	7939	-0.81077796	5.684313524	0.0010362	0.003181077	0.07101	-1	777	602	1719	1132	840	744	1275	547	519	799
ENSMUSG00000069939	chr11	Gm12070	2.7E+07	2.7E+07	1002	-1.58551132	0.031470901	0.0010376	0.003184418	0.19983	-1	23	26	9	23	22	2	16	6	15	10
ENSMUSG00000060798	chr3	Intu	4.1E+07	4.1E+07	7429	-0.88874012	1.603712941	0.0010406	0.003193002	0.06653	-1	45	35	90	70	56	42	49	30	45	49
ENSMUSG00000041341	chr12	Atg2b	1.1E+08	1.1E+08	10173	-0.57915293	4.933274668	0.0010409	0.003193158	0.03524	-1	535	416	648	654	480	568	603	407	475	473
ENSMUSG00000020409	chr11	Slu7	4.3E+07	4.3E+07	4050	-0.56490496	5.228940298	0.0010472	0.003212015	0.03394	-1	710	555	790	625	653	755	754	416	637	596
ENSMUSG00000053819	chr3	Camk2d	1.3E+08	1.3E+08	15928	0.597999488	6.014979214	0.0010507	0.003222081	0.03873	1	715	497	995	787	948	1584	1909	1322	1455	1730
ENSMUSG00000026867	chr2	Gapvd1	3.5E+07	3.5E+07	8287	-0.57100015	5.207153658	0.0010585	0.00324431	0.03471	-1	624	511	903	671	618	764	787	416	560	579
ENSMUSG00000044700	chr4	Tmem201	1.5E+08	1.5E+08	8944	-0.6889471	5.942191973	0.0010583	0.00324431	0.05155	-1	906	671	1762	1456	1059	909	1092	679	1163	1028
ENSMUSG00000049600	chr7	Zbtb45	1.3E+07	1.3E+07	2722	0.755420627	2.475862125	0.0010587	0.003244334	0.05223	1	47	35	82	64	85	156	137	95	167	155
ENSMUSG00000026516	chr1	Nvl	1.8E+08	1.8E+08	13488	-0.58593112	4.434261678	0.001063	0.003256866	0.0354	-1	360	312	487	430	348	395	367	310	315	383
ENSMUSG00000021711	chr13	Trappc13	1E+08	1E+08	5166	-0.5618879	4.613069686	0.0010638	0.003258508	0.03277	-1	433	340	562	444	408	510	495	317	366	359
ENSMUSG00000071177	chr12	Serpina1d	1E+08	1E+08	1394	1.465085238	0.007442738	0.0010683	0.003271534	0.15873	1	7	3	9	1	16	39	13	23	28	29
ENSMUSG00000023991	chr17	Foxp4	4.8E+07	4.8E+07	4926	0.65120978	3.438939193	0.0010694	0.003274167	0.04159	1	110	70	150	133	182	303	259	200	294	302
ENSMUSG00000021067	chr12	Sav1	7E+07	7E+07	2524	-0.66541973	5.567587303	0.0010738	0.003286984	0.04801	-1	960	801	757	711	1053	854	979	535	685	764
ENSMUSG00000047412	chr9	Zbtb44	3.1E+07	3.1E+07	8857	-0.55518395	5.387662896	0.0010757	0.003292238	0.0329	-1	732	474	999	747	863	716	833	551	637	759
ENSMUSG00000020978	chr12	Klhdc2	6.9E+07	6.9E+07	5438	-0.7002197	6.855871841	0.0010805	0.003305302	0.05394	-1	2253	1727	2685	2130	1917	1925	2593	1424	1747	1444
ENSMUSG00000027810	chr3	Eif2a	5.9E+07	5.9E+07	6118	-0.60488739	5.236007192	0.0010804	0.003305302	0.03928	-1	760	540	841	590	671	826	802	436	529	533
ENSMUSG00000017737	chr2	Mmp9	1.6E+08	1.6E+08	3539	1.636445401	2.4758499	0.0010815	0.003307814	0.26742	1	32	47	5	13	96	164	214	89	175	217
ENSMUSG00000034485	chr9	Uaca	6.1E+07	6.1E+07	4428	-0.77104504	7.688445126	0.0010825	0.003309981	0.06557	-1	3498	1967	6751	4519	3592	2929	4327	2139	3013	3442
ENSMUSG00000034160	chrX	Ogt	1E+08	1E+08	8045	-0.65785421	6.917787105	0.0010835	0.003312286	0.04769	-1	2164	2043	2380	1983	2388	2405	2242	1350	1647	2159
ENSMUSG00000097971	chr17	Gm26917	4E+07	4E+07	3329	0.831106092	4.992142758	0.001086	0.003319318	0.07481	1	329	106	561	413	404	1057	583	757	1010	753
ENSMUSG00000068747	chr3	Sort1	1.1E+08	1.1E+08	7560	-0.83519402	6.549505004	0.0010884	0.003325823	0.07656	-1	2114	1773	1227	1126	2542	1524	1635	961	1506	1377
ENSMUSG00000032898	chr5	Fbxo21	1.2E+08	1.2E+08	3909	-0.85079435	4.513794058	0.0010889	0.003326622	0.07734	-1	302	205	527	313	1009	381	402	228	323	361
ENSMUSG00000021608	chr13	Lpcat1	7.3E+07	7.3E+07	4131	0.737758308	3.153856347	0.0010907	0.003331598	0.05315	1	96	73	98	80	153	321	200	144	221	266
ENSMUSG00000062563	chr12	Cys1	2.5E+07	2.5E+07	2646	1.10348886	1.440768868	0.0010916	0.003333379	0.10517	1	20	21	19	21	42	127	60	33	69	86
ENSMUSG00000064202	chr19	4430402I18Rik	2.9E+07	2.9E+07	5420	-1.04845999	0.945640482	0.0010923	0.003334849	0.08655	-1	22	25	42	36	68	33	27	14	24	28
ENSMUSG00000057789	chr17	Bak1	2.7E+07	2.7E+07	2407	0.618457761	4.499294225	0.0010935	0.003337913	0.03971	1	235	224	258	240	378	644	523	362	728	584
ENSMUSG00000031985	chr8	Gnpat	1.2E+08	1.2E+08	3587	-0.80579204	7.495208128	0.0010957	0.003343879	0.07165	-1	2592	1821	6383	3829	3442	2571	4137	1833	2442	2695
ENSMUSG00000027420	chr2	Bfsp1	1.4E+08	1.4E+08	2390	1.441261799	-0.45559153	0.001096	0.003343897	0.10082	1	5	4	8	5	2	25	20	14	12	20
ENSMUSG00000050052	chr8	Tdrp	1.4E+07	1.4E+07	4694	-0.82388546	3.91087094	0.0010966	0.003345218	0.0712	-1	192	199	324	182	603	276	236	166	254	191
ENSMUSG00000003809	chr8	Gcdh	8.5E+07	8.5E+07	2754	-0.59189625	5.016642038	0.0010983	0.003349657	0.03731	-1	643	421	693	663	486	626	519	460	498	548
ENSMUSG00000104357	chr3	TTC14	3.4E+07	3.4E+07	2145	-0.79916698	2.7346912	0.001103	0.003363318	0.0621	-1	107	105	158	140	117	145	108	69	64	118
ENSMUSG00000017747	chr11	Ghdc	1E+08	1E+08	2692	0.641285997	3.463742571	0.0011036	0.003364255	0.04007	1	97	101	143	141	163	294	274	201	311	296
ENSMUSG00000026097	chr1	Ormdl1	5.3E+07	5.3E+07	4711	-0.6403802	3.459251986	0.0011055	0.003369238	0.04026	-1	215	157	226	173	229	191	199	151	159	178
ENSMUSG00000074129	chr7	Rpl13a	4.5E+07	4.5E+07	3034	0.642575048	8.12632402	0.0011057	0.003369238	0.04589	1	3005	2393	3791	3315	4054	8723	5800	5461	7781	7509
ENSMUSG00000026074	chr1	Map4k4	4E+07	4E+07	9579	0.665480351	5.155503955	0.0011061	0.003369436	0.04787	1	305	261	497	311	779	1116	928	696	826	958
ENSMUSG00000033184	chr18	Tmed7	4.7E+07	4.7E+07	8839	-0.57517662	5.137967137	0.0011062	0.003369436	0.03545	-1	647	510	736	602	654	746	767	420	472	545
ENSMUSG00000047343	chr1	Mettl21c	4.4E+07	4.4E+07	4300	-1.13760853	4.71976013	0.0011111	0.003383585	0.13907	-1	335	338	654	372	1167	123	488	339	458	233
ENSMUSG00000030057	chr6	Cnbp	8.8E+07	8.8E+07	2536	-0.65595734	8.96109763	0.0011191	0.003407103	0.04802	-1	9258	6993	11247	8332	10219	9363	10304	6243	7100	7150
ENSMUSG00000020290	chr11	Xpo1	2.3E+07	2.3E+07	7181	-0.58579161	4.846615617	0.0011207	0.003411203	0.03649	-1	552	393	649	508	486	618	596	375	374	424
ENSMUSG00000031226	chrX	Pbdc1	1.1E+08	1.1E+08	6098	0.817465905	3.88978731	0.0011288	0.003435015	0.0694	1	167	158	110	170	167	492	251	342	385	455
ENSMUSG00000064339	chrMT	mt-Rnr2	1094	2675	1582	-0.8921013	9.417237267	0.0011299	0.00343774	0.08829	-1	12181	5478	23839	17186	11226	9146	15071	6670	9273	9704
ENSMUSG00000018930	chr11	Ccl4	8.4E+07	8.4E+07	660	1.382396103	-0.37983562	0.0011305	0.003438916	0.10726	1	1	4	7	5	10	19	24	17	20	15
ENSMUSG00000030397	chr7	Mark4	1.9E+07	1.9E+07	2259	-0.69585521	3.554300518	0.0011387	0.003462949	0.04931	-1	184	137	322	240	228	176	253	115	224	161
ENSMUSG00000050891	chr15	Tatdn1	5.9E+07	5.9E+07	1366	-0.54583326	4.350278916	0.0011399	0.003466038	0.03073	-1	392	259	418	346	407	402	415	250	305	347
ENSMUSG00000103409	chr9	RP23-456B9.23	1.1E+08	1.1E+08	369	-0.7625347	3.400133355	0.0011441	0.0034779	0.05924	-1	222	167	203	221	159	177	211	134	158	122

ENSMUSG00000020513	chr11	Tubd1	8.7E+07	8.7E+07	2070	-0.77111909	3.0667397	0.0011455	0.003481452	0.06012	-1	159	163	155	121	171	158	158	76	117	136
ENSMUSG00000033237	chr15	Arid2	9.6E+07	9.6E+07	10737	-0.54735972	4.028767579	0.0011487	0.003490507	0.03026	-1	258	220	363	308	310	316	291	193	275	298
ENSMUSG00000026589	chr1	Sec16b	1.6E+08	1.6E+08	5410	1.089258212	1.426449428	0.001151	0.003496511	0.10296	1	31	21	14	16	39	110	77	42	63	74
ENSMUSG00000034674	chr10	Tdg	8.3E+07	8.3E+07	5374	-0.93178367	1.716887716	0.0011541	0.003505335	0.07734	-1	53	44	107	65	54	39	61	29	57	43
ENSMUSG00000025571	chr11	Tnrc6c	1.2E+08	1.2E+08	12843	-0.62202952	4.915817892	0.0011568	0.003512699	0.04173	-1	539	392	718	676	420	567	596	320	444	555
ENSMUSG00000099227	chr1	Mir8114	1.5E+08	1.5E+08	111	-0.80960435	3.375579492	0.0011591	0.003518809	0.06754	-1	248	172	126	209	201	175	161	125	166	146
ENSMUSG00000024127	chr17	Prepl	8.5E+07	8.5E+07	3830	-0.65250772	3.927135048	0.0011603	0.003521802	0.04391	-1	267	239	351	280	242	232	258	233	247	227
ENSMUSG00000024727	chr19	Trpm6	1.9E+07	1.9E+07	6508	1.489491172	-0.42220473	0.0011624	0.00352644	0.12098	1	8	4	6	2	4	21	11	18	18	25
ENSMUSG00000031486	chr8	Gpr124	2.7E+07	2.7E+07	5775	0.746484782	2.857949585	0.0011625	0.00352644	0.05297	1	64	68	89	87	91	244	181	170	170	152
ENSMUSG00000032826	chr3	Ank2	1.3E+08	1.3E+08	35218	-0.98754888	5.922585591	0.0011628	0.00352644	0.10739	-1	957	596	2520	1655	574	907	1166	611	709	834
ENSMUSG00000097141	chr18	Gm10524	8.3E+07	8.3E+07	1893	-1.05385357	1.947221197	0.0011627	0.00352644	0.10783	-1	58	40	153	86	63	55	69	21	44	71
ENSMUSG00000059412	chr9	Fxyd2	4.5E+07	4.5E+07	632	1.211819107	1.996655915	0.0011656	0.003534147	0.14284	1	28	31	18	17	82	158	88	76	106	134
ENSMUSG00000018428	chr11	Akap1	8.9E+07	8.9E+07	4390	-0.89550543	6.772408229	0.0011676	0.003539283	0.089	-1	1491	848	4546	2552	1957	1720	2037	1057	1316	1852
ENSMUSG00000101493	chr4	2810405F17Rik	1.4E+08	1.4E+08	1117	1.223980266	0.088631987	0.0011702	0.003546402	0.08896	1	5	7	10	10	10	39	22	19	20	36
ENSMUSG00000020782	chr11	Llgl2	1.2E+08	1.2E+08	4844	-0.75262526	2.800788576	0.0011724	0.003552345	0.0556	-1	118	81	176	148	140	123	130	51	118	120
ENSMUSG00000022526	chr15	Zfp251	7.7E+07	7.7E+07	3497	-0.7233919	3.355184735	0.0011751	0.003559842	0.05314	-1	158	135	271	222	177	153	237	103	150	156
ENSMUSG00000042700	chr12	Sipa1l1	8.2E+07	8.2E+07	7697	-0.7749962	3.613889363	0.0011761	0.003562144	0.06284	-1	193	206	198	176	384	212	239	104	217	172
ENSMUSG00000050471	chr9	Fam118b	3.5E+07	3.5E+07	5981	-0.53772599	4.589178902	0.0011781	0.003567272	0.03036	-1	401	342	544	388	470	412	514	295	417	391
ENSMUSG00000032314	chr9	Etfa	5.5E+07	5.5E+07	1835	-0.79206786	7.6642759	0.0011819	0.003578003	0.07021	-1	3375	1723	7110	4158	3985	3355	4281	2152	2431	3273
ENSMUSG00000028412	chr4	Slc44a1	5.3E+07	5.3E+07	6945	0.590169986	5.505648126	0.0011861	0.003589955	0.03817	1	572	325	664	449	783	1402	1280	893	1026	1049
ENSMUSG00000030835	chr7	Nomo1	4.6E+07	4.6E+07	5936	-0.62192133	6.287244405	0.0011864	0.003590198	0.04301	-1	1254	1070	1740	1660	1406	1207	1485	975	1363	1311
ENSMUSG00000021023	chr12	1110008L16Rik	5.5E+07	5.5E+07	4452	-0.62223441	3.297591159	0.0011875	0.00359279	0.03761	-1	181	107	230	180	209	187	172	117	169	153
ENSMUSG00000029064	chr4	Gnb1	1.6E+08	1.6E+08	4268	0.687528829	6.568698531	0.0011886	0.003595216	0.05277	1	890	719	1148	933	1938	3026	2181	1929	2508	2466
ENSMUSG00000028261	chr4	Ndufaf4	2.5E+07	2.5E+07	3902	-0.60906075	5.176392285	0.0011918	0.003604126	0.04035	-1	488	420	1045	768	646	655	745	441	512	616
ENSMUSG00000045140	chr11	Pigw	8.5E+07	8.5E+07	2733	-0.81937967	2.272315379	0.0011928	0.00360645	0.06315	-1	84	93	93	86	91	85	93	52	60	68
ENSMUSG00000000359	chr2	Rem1	1.5E+08	1.5E+08	2156	0.945310836	2.578190791	0.0011936	0.003608154	0.08993	1	44	35	65	42	127	215	108	128	177	167
ENSMUSG00000035078	chr14	Mtmr9	6.4E+07	6.4E+07	2402	-0.83300852	3.106040447	0.0011968	0.003616838	0.0713	-1	153	145	219	132	173	194	185	91	79	97
ENSMUSG00000026219	chr1	Trip12	8.5E+07	8.5E+07	16601	-0.6843507	7.191021075	0.0011971	0.003617222	0.05257	-1	2524	1996	3681	3158	2215	2606	2983	1770	2074	2197
ENSMUSG00000053877	chr7	Srcap	1.3E+08	1.3E+08	18791	-0.58319169	5.898085157	0.0011984	0.003620207	0.03759	-1	954	706	1358	1300	1125	1074	1072	759	1037	991
ENSMUSG00000014074	chr16	Rnf168	3.2E+07	3.2E+07	4462	-0.60854432	4.014469262	0.0011987	0.003620244	0.03843	-1	287	257	316	300	280	299	305	218	260	232
ENSMUSG00000041559	chr1	Fmod	1.3E+08	1.3E+08	3306	0.932159928	8.282546146	0.0012016	0.00362848	0.09715	1	4010	2224	3259	2249	4481	17755	5303	5237	6694	8734
ENSMUSG00000031539	chr8	Ap3m2	2.3E+07	2.3E+07	3467	0.853946905	3.01642793	0.001203	0.003631666	0.07351	1	83	72	71	54	148	308	182	156	228	195
ENSMUSG00000026433	chr1	Rab29	1.3E+08	1.3E+08	1468	0.771402816	2.910260143	0.0012039	0.00363365	0.05829	1	66	62	93	65	132	301	182	132	178	186
ENSMUSG00000030747	chr7	Dgat2	9.9E+07	9.9E+07	2251	-1.48607483	6.665014324	0.0012081	0.003645727	0.23927	-1	1513	658	2118	576	7643	1462	789	994	1206	1029
ENSMUSG00000033808	chr2	Tmem87a	1.2E+08	1.2E+08	7528	-0.65711872	5.601225876	0.00121	0.003650536	0.04783	-1	1035	805	843	716	972	889	1020	577	722	704
ENSMUSG00000093803	chr9	Ppp2r3d	1.2E+08	1.2E+08	1861	0.820111932	3.0076092	0.0012121	0.003656082	0.0681	1	86	47	139	76	96	284	131	142	259	238
ENSMUSG00000022442	chr15	Ttll1	8.3E+07	8.3E+07	2918	0.712396867	2.845380684	0.0012126	0.003656085	0.04769	1	81	68	77	73	101	212	191	130	204	173
ENSMUSG00000022489	chr15	Pde1b	1E+08	1E+08	2954	1.047985431	1.44347881	0.0012124	0.003656085	0.09867	1	17	14	33	23	44	114	48	39	72	95
ENSMUSG00000052248	chr2	Zeb2os	4.5E+07	4.5E+07	1388	1.057109352	1.609094777	0.0012132	0.003656933	0.1002	1	35	24	19	18	45	127	60	66	76	80
ENSMUSG00000029096	chr5	Htra3	3.6E+07	3.6E+07	3860	0.941216223	6.23084177	0.001215	0.003661682	0.09864	1	493	477	557	654	1850	2293	1775	1392	2109	2695
ENSMUSG00000032536	chr9	Trak1	1.2E+08	1.2E+08	4883	-0.90645774	7.126997734	0.0012184	0.003671115	0.09197	-1	2123	1309	5330	3213	2420	1787	3501	1349	1814	1681
ENSMUSG00000046364	chr7	Rpl27a	1.1E+08	1.1E+08	2774	0.66788898	7.237168364	0.0012193	0.003673017	0.05021	1	1738	1333	1858	1605	2260	4839	2866	3213	3998	4165
ENSMUSG00000032245	chr9	Cln6	6.3E+07	6.3E+07	2434	0.56688843	4.375200438	0.0012204	0.003675471	0.03378	1	257	156	342	202	325	592	459	374	571	560
ENSMUSG00000089837	chr15	Npcd	8E+07	8E+07	1453	-1.26514153	1.106619609	0.0012221	0.003679858	0.1457	-1	37	49	49	33	50	22	45	18	34	8
ENSMUSG00000021550	chr13	2210016F16Rik	5.8E+07	5.8E+07	2822	0.660961083	4.253388984	0.0012235	0.003683288	0.04663	1	197	137	261	183	360	626	345	409	534	479
ENSMUSG00000029649	chr5	Pomp	1.5E+08	1.5E+08	734	0.638566452	6.695947673	0.0012282	0.003696382	0.04578	1	1282	903	1383	1130	1414	3285	2075	2314	2643	2643
ENSMUSG00000076051	chr7	Mir707	4.5E+07	4.5E+07	73	-1.34239477	0.095057246	0.0012286	0.003696382	0.13651	-1	30	21	15	12	27	12	18	4	10	15
ENSMUSG00000081926	chr10	Gm15536	7038661	7038774	114	2.014668806	0.386980138	0.0012284	0.003696382	0.35656	1	4	6	0	8	16	17	25	10	82	60
ENSMUSG00000044496	chr4	2510039O18Rik	1.5E+08	1.5E+08	2731	0.529554305	4.914637173	0.0012294	0.003697869	0.0301	1	297	253	479	340	527	770	770	591	786	741
ENSMUSG00000037761	chr2	Actr5	1.6E+08	1.6E+08	4186	0.901048526	1.655660368	0.0012313	0.003702806	0.0688	1	25	28	30	31	44	108	60	67	80	91
ENSMUSG00000062604	chr5	Srpk2	2.4E+07	2.4E+07	6436	-0.55379995	4.913266084	0.0012318	0.003703649	0.03308	-1	520	459	590	458	652	588	611	415	453	450
ENSMUSG00000021876	chr14	Rnase4	5.1E+07	5.1E+07	1996	0.837644472	6.070741134	0.0012344	0.003710686	0.07827	1	586	692	499	569	1242	2902	1852	1271	1414	1623
ENSMUSG00000056493	chr5	Foxk1	1.4E+08	1.4E+08	7445	-0.56926129	4.554243451	0.0012367	0.003716711	0.03447	-1	377	293	555	391	528	422	558	287	323	371
ENSMUSG00000022570	chr15	Tsta3	7.6E+07	7.6E+07	1311	-0.55056662	4.092631828	0.0012372	0.00371753	0.03115	-1	306	207	378	318	323	331	303	217	312	265
ENSMUSG00000002625	chr17	Akap8l	3.2E+07	3.2E+07	2075	-0.54677833	4.721285549	0.0012379	0.003718617	0.03205	-1	459	403	578	429	465	511	457	305	413	541
ENSMUSG00000027082	chr2	Tfpi	8.4E+07	8.4E+07	5463	0.879915675	2.12327232	0.0012406	0.003726106	0.07136	1	47	39	40	30	67	148	99	101	112	103
ENSMUSG00000090015	chr5	Gm15446	1.1E+08	1.1E+08	3780	-0.86425134	2.09121147	0.0012452	0.003738966	0.06974	-1	101	66	88	70	77	85	62	57	47	55
ENSMUSG00000028890	chr4	Mtf1	1.2E+08	1.2E+08	8907	-0.61081917	4.193617776	0.0012497	0.003750989	0.03958	-1	329	266	419	363	268	351	362	204	285	303
ENSMUSG00000049764	chr10	Zfp280b	7.6E+07	7.6E+07	5097	-0.64842663	4.076171955	0.0012497	0.003750989	0.04444	-1	296	229	373	268	393	237	413	204	247	251
ENSMUSG00000063334	chr10	Krr1	1.1E+08	1.1E+08	5958	-0.54033923	4.954746778	0.0012509	0.003753832	0.03158	-1	497	424	668	607	566	587	689	378	485	484
ENSMUSG00000020460	chr11	Rps27a	3E+07	3E+07	1972	0.644473108	7.69322133	0.0012532	0.003760015	0.0471	1	2443	1940	2579	2312	2822	6759	4364	4213	5127	5660
ENSMUSG00000028049	chr3	Scamp3	8.9E+07	8.9E+07	2270	0.622265985	5.605835668	0.0012548	0.003763824	0.04302	1	452	388	620	592	890	1259	1106	853	1499	1388
ENSMUSG00000021866	chr14	Anxa11	2.6E+07	2.6E+07	4135	-0.68935206	5.918408488	0.0012555	0.003765185	0.05326	-1	963	817	1523	1304	1046	985	1498	566	967	841
ENSMUSG00000067780	chr1	Pi15	1.8E+07	1.8E+07	6923	1.031603761	2.089026004	0.0012558	0.003765185	0.09965	1	58	44	37	25	31	165	101	78	129	105
ENSMUSG00000036053	chr2	Fmnl2	5.3E+07	5.3E+07	6033	-0.78797987	3.015649229	0.0012613	0.00378091	0.06299	-1	157	133	152	144	168	163	156	110	95	83
ENSMUSG00000027255	chr2	Arfgap2	9.1E+07	9.1E+07	4129	-0.62746583	7.483905117	0.0012652	0.003791024	0.04472	-1	2707	2468	3987	3354	3998	2945	3652	2058	3106	2845
ENSMUSG00000036323	chr5	Srp72	7.7E+07	7.7E+07	5717	-0.565893	5.627942525	0.0012651	0.003791024	0.03554	-1	832	676	1038	975	912	978	1002	642	743	766

ENSMUSG00000028158	chr3	Mttp	1.4E+08	1.4E+08	4410	-0.78570445	2.330817848	0.0012657	0.003791698	0.05791	-1	95	73	129	85	92	92	77	56	55	98
ENSMUSG00000055633	chr7	Zfp580	5051532	5051714	1101	0.978316079	1.851747361	0.0012693	0.003801644	0.09124	1	31	16	49	31	56	81	77	59	145	115
ENSMUSG00000070871	chr1	Ccnyl1	6.5E+07	6.5E+07	3456	-0.58323043	4.158806759	0.0012709	0.003805756	0.03563	-1	335	237	374	277	392	335	360	254	242	276
ENSMUSG00000029823	chr6	Luc7l2	3.9E+07	3.9E+07	12084	-0.64615412	6.649850588	0.001272	0.003807324	0.04724	-1	1968	1595	2001	1602	1929	1873	1818	1129	1368	1974
ENSMUSG00000048058	chr2	Ldlrad3	1E+08	1E+08	6023	0.767080343	3.867250053	0.001272	0.003807324	0.06329	1	129	67	260	221	162	404	519	244	325	414
ENSMUSG00000020415	chr11	Pttg1	4.3E+07	4.3E+07	2000	0.872267089	1.392484379	0.0012725	0.003807894	0.05887	1	29	18	30	27	29	79	68	48	57	83
ENSMUSG00000049191	chrX	Rgag4	1E+08	1E+08	4761	1.100423428	1.297083224	0.0012732	0.003809143	0.10577	1	17	17	17	13	49	88	60	42	67	74
ENSMUSG00000050447	chr2	Lypd6	5E+07	5E+07	3729	-1.21220824	1.483442257	0.0012734	0.003809143	0.13877	-1	63	41	90	70	22	31	34	41	27	32
ENSMUSG00000024220	chr17	Zfp523	2.8E+07	2.8E+07	3991	-0.57578837	3.863639894	0.0012761	0.0038162	0.03394	-1	231	161	345	288	307	283	260	170	278	219
ENSMUSG00000038201	chr7	Kcna7	4.5E+07	4.5E+07	3494	-0.71321725	7.693664771	0.0012802	0.003827847	0.05787	-1	3493	2267	5745	4634	3662	3161	4589	2296	3429	2814
ENSMUSG00000028292	chr4	Rars2	3.5E+07	3.5E+07	2771	-0.57362689	3.973353953	0.0012814	0.003830505	0.03405	-1	276	228	343	244	317	318	270	216	221	273
ENSMUSG00000007880	chr4	Arid1a	1.3E+08	1.3E+08	11476	-0.53898749	5.241031135	0.0012824	0.003832757	0.0319	-1	609	479	874	675	771	714	858	419	586	642
ENSMUSG00000021676	chr13	Iqgap2	9.6E+07	9.6E+07	5771	0.944065718	2.00186247	0.0012831	0.003833178	0.08306	1	34	32	42	30	63	194	87	70	99	88
ENSMUSG00000029720	chr5	Gm20605	1.4E+08	1.4E+08	4464	0.575714306	5.119031497	0.0012829	0.003833178	0.03626	1	356	311	434	387	632	991	783	555	961	1038
ENSMUSG00000053128	chr9	Rnf26	4.4E+07	4.4E+07	4546	0.792139799	2.887928783	0.0012856	0.003839706	0.06283	1	71	53	85	58	144	251	165	154	177	208
ENSMUSG00000039831	chr3	Arhgap29	1.2E+08	1.2E+08	5088	-0.70690627	4.360137668	0.0012875	0.003844639	0.05431	-1	359	294	366	247	673	434	346	263	259	312
ENSMUSG00000036913	chr8	Trim67	1.2E+08	1.2E+08	8817	-2.7405652	1.441902711	0.0012896	0.003850149	0.70491	-1	29	16	50	0	295	15	34	9	7	6
ENSMUSG00000025193	chr19	Cutc	4.4E+07	4.4E+07	1422	-0.62141849	3.664457958	0.0012926	0.003858387	0.03987	-1	224	191	287	228	213	246	249	152	208	177
ENSMUSG00000006288	chr14	Ttc5	5.1E+07	5.1E+07	1841	0.691361746	3.182876917	0.0012946	0.003863488	0.04725	1	92	88	111	85	140	286	197	154	255	261
ENSMUSG00000000168	chr9	Dlat	5.1E+07	5.1E+07	4886	-0.77887354	7.783260377	0.0012964	0.003867874	0.06906	-1	3385	2031	7277	5124	4030	3205	4822	2317	3112	3417
ENSMUSG00000031438	chrX	Rnf128	1.4E+08	1.4E+08	3464	-0.67794898	4.84940206	0.0012973	0.003869864	0.0508	-1	527	409	625	697	372	433	520	292	493	565
ENSMUSG00000022540	chr16	Rogdi	5008730	5009252	1421	0.839065905	3.187915329	0.0012979	0.003870717	0.07409	1	63	55	108	86	194	284	182	169	263	299
ENSMUSG00000011263	chr7	Exoc3l2	1.9E+07	1.9E+07	2201	1.322333336	0.855777482	0.0013006	0.003876246	0.15856	1	5	5	28	24	13	51	30	46	71	45
ENSMUSG00000021643	chr13	Serf1	1E+08	1E+08	1315	1.101535241	2.155943362	0.0013002	0.003876246	0.11872	1	38	44	19	34	66	163	78	112	141	110
ENSMUSG00000026389	chr1	Steap3	1.2E+08	1.2E+08	5715	0.595933951	6.050709534	0.0013005	0.003876246	0.0399	1	700	631	861	718	1077	1967	1494	1227	1768	1809
ENSMUSG00000084416	chr1	Rpl10a-ps1	6.5E+07	6.5E+07	654	0.586801299	4.92220278	0.0013011	0.003877156	0.03735	1	340	315	341	355	447	860	650	498	893	875
ENSMUSG00000060143	chr14	Gm10076	1.1E+08	1.1E+08	384	0.703911607	3.808868236	0.0013029	0.003881593	0.05209	1	180	123	173	123	196	518	242	256	357	424
ENSMUSG00000056492	chr17	Gpr116	4.3E+07	4.3E+07	8535	-0.64481801	5.930145633	0.0013043	0.003884842	0.04682	-1	917	619	1834	1175	1265	1081	1216	664	851	1149
ENSMUSG00000005148	chr14	Klf5	9.9E+07	9.9E+07	1721	0.97658359	1.740004519	0.0013058	0.003888642	0.08605	1	43	24	41	31	22	94	117	79	84	62
ENSMUSG00000074873	chr19	AI606181	4.2E+07	4.2E+07	2796	0.957109046	2.108740059	0.0013119	0.003905885	0.09047	1	34	15	55	42	79	124	83	96	139	124
ENSMUSG00000006818	chr17	Sod2	1.3E+07	1.3E+07	3824	-0.74230073	8.01725861	0.0013144	0.003912519	0.06299	-1	4042	2647	8677	5431	4558	4069	5502	2867	3771	3937
ENSMUSG00000086968	chr3	4933431E20Rik	1.1E+08	1.1E+08	6821	-0.82581553	1.930023771	0.001316	0.003916515	0.06265	-1	78	63	74	54	88	78	63	37	52	52
ENSMUSG00000023912	chr17	Slc25a27	4.4E+07	4.4E+07	2687	-0.8194709	2.605998455	0.0013165	0.003917011	0.06769	-1	149	105	123	88	100	110	110	59	89	87
ENSMUSG00000062054	chr12	Iah1	2.1E+07	2.1E+07	924	1.165692176	3.102943147	0.0013169	0.00391734	0.14462	1	86	58	31	41	180	331	171	197	268	242
ENSMUSG00000031930	chr8	Wwp2	1.1E+08	1.1E+08	4280	0.524737411	4.668762107	0.0013176	0.003918782	0.02955	1	271	187	448	330	369	731	631	410	688	660
ENSMUSG00000040687	chr2	Madd	9.1E+07	9.1E+07	9086	0.59019178	3.539510943	0.0013188	0.003921411	0.03473	1	124	94	161	135	188	360	281	208	296	294
ENSMUSG00000029413	chr5	Naaa	9.2E+07	9.2E+07	3721	1.023229746	4.503740541	0.0013238	0.003935524	0.11613	1	233	139	131	120	530	949	432	461	564	754
ENSMUSG00000044477	chr17	Zfand3	3E+07	3E+07	2616	-0.61788531	6.987639156	0.0013265	0.003942585	0.0436	-1	2132	1495	2917	2254	3011	2184	2688	1428	2174	1949
ENSMUSG00000017686	chr11	Rhot1	8E+07	8E+07	7077	-0.59484292	5.503666873	0.0013268	0.003942869	0.0396	-1	808	638	1072	828	753	874	981	571	634	690
ENSMUSG00000027597	chr2	Ahcy	1.6E+08	1.6E+08	2805	-0.58442827	4.48188602	0.0013299	0.003951136	0.0369	-1	390	328	483	397	404	349	486	271	412	325
ENSMUSG00000024232	chr18	Bambi	3507957	3508285	5040	1.031817538	1.278864447	0.0013303	0.003951328	0.09295	1	28	14	28	13	32	96	43	57	53	69
ENSMUSG00000056592	chr7	Zfp658	4.4E+07	4.4E+07	3495	1.01687447	1.168534978	0.0013338	0.003959278	0.08609	1	20	12	18	19	38	84	59	37	44	73
ENSMUSG00000060548	chr14	Tnfrsf19	6.1E+07	6.1E+07	4777	-1.00564346	4.020326734	0.0013338	0.003959278	0.11147	-1	460	142	436	424	175	269	380	151	148	180
ENSMUSG00000098404	chr7	Gm8086	1.5E+07	1.5E+07	940	-1.91974785	0.294669862	0.0013337	0.003959278	0.34251	-1	23	20	45	35	16	6	34	0	5	7
ENSMUSG00000041977	chr3	Arhgef11	8.8E+07	8.8E+07	7918	-0.54004109	5.153658857	0.0013344	0.003960305	0.03218	-1	605	439	827	662	669	624	740	371	680	611
ENSMUSG00000051343	chr6	Rab11fip5	8.5E+07	8.5E+07	4104	0.79394934	5.627534813	0.0013435	0.00398656	0.07136	1	336	258	1007	769	472	1403	1483	863	1305	1470
ENSMUSG00000074682	chr2	Zcchc3	1.5E+08	1.5E+08	3073	1.024667728	1.136922263	0.0013476	0.003997777	0.08447	1	9	21	22	23	27	71	52	50	52	60
ENSMUSG00000021518	chr13	Ptdss1	6.7E+07	6.7E+07	3424	0.536152172	4.8967217	0.0013482	0.003998631	0.03144	1	301	213	492	435	428	825	714	563	773	759
ENSMUSG00000026883	chr2	Dab2ip	3.6E+07	3.6E+07	8366	-0.85634671	6.822682584	0.0013555	0.004019543	0.08371	-1	1632	2329	1653	3034	1830	1504	1735	1401	2047	1550
ENSMUSG00000038879	chr15	Nipal2	3.5E+07	3.5E+07	3825	1.543022017	-0.21675357	0.0013646	0.004045768	0.16151	1	3	4	1	5	15	33	15	14	29	22
ENSMUSG00000055862	chr10	Izumo4	8.1E+07	8.1E+07	938	1.229865604	1.52107965	0.001371	0.004063613	0.14582	1	18	20	18	17	51	120	44	42	68	130
ENSMUSG00000051705	chr9	Senp8	6E+07	6E+07	3792	-0.70195577	3.019967506	0.0013737	0.004070938	0.04977	-1	173	119	156	150	142	154	144	100	108	128
ENSMUSG00000016758	chr15	Bik	8.4E+07	8.4E+07	943	1.206165037	-0.05100909	0.0013752	0.004074457	0.08374	1	6	7	10	5	10	27	21	15	33	25
ENSMUSG00000043683	chr17	Fem1a	5.6E+07	5.6E+07	6816	-0.70549041	8.977760293	0.0013761	0.004076299	0.05754	-1	7885	6268	12990	11636	8904	7782	11002	5250	8666	7244
ENSMUSG00000033544	chr1	Angptl1	1.6E+08	1.6E+08	2841	0.964461572	4.672093042	0.0013795	0.004085608	0.10337	1	307	325	178	187	209	1351	671	416	514	634
ENSMUSG00000047090	chr10	Tmem198b	1.3E+08	1.3E+08	3363	0.74406109	3.020051213	0.0013803	0.004087042	0.0559	1	77	66	95	70	149	269	177	136	233	230
ENSMUSG00000022108	chr14	Itm2b	7.3E+07	7.3E+07	1773	0.693167375	8.492245871	0.001382	0.00409116	0.05556	1	3869	3022	4355	3048	6789	11938	8366	6995	9329	9619
ENSMUSG00000001741	chr7	Il16	8.4E+07	8.4E+07	7842	0.786715012	2.861593551	0.0013841	0.004096494	0.06236	1	78	55	69	76	119	299	151	135	173	189
ENSMUSG00000026603	chr1	Smyd2	1.9E+08	1.9E+08	2717	-0.66063588	7.630633575	0.0013849	0.004098058	0.05039	-1	2672	2609	4505	4490	4220	2902	3685	2310	3340	3638
ENSMUSG00000078713	chr4	Tomm5	4.5E+07	4.5E+07	868	0.550590007	5.347349288	0.001386	0.004100279	0.03395	1	465	277	713	544	548	1122	1022	801	1031	1006
ENSMUSG00000026311	chr1	Asb1	9.2E+07	9.2E+07	6432	-0.64840893	4.215819505	0.00139	0.004111423	0.04569	-1	335	207	506	406	272	304	384	213	290	306
ENSMUSG00000032965	chr16	Ift57	5E+07	5E+07	2862	0.811361376	2.344441976	0.0013964	0.004129475	0.06368	1	43	35	51	52	95	137	128	118	132	130
ENSMUSG00000028560	chr4	Usp1	9.9E+07	9.9E+07	3733	-0.57732357	4.142998385	0.0013975	0.004131832	0.03574	-1	276	237	389	346	347	356	385	181	250	311
ENSMUSG00000042446	chr4	Zmym4	1.3E+08	1.3E+08	8139	-0.5640296	4.274308298	0.0013979	0.004132183	0.03418	-1	341	251	473	355	321	362	406	217	310	328
ENSMUSG00000032503	chr9	Arpp21	1.1E+08	1.1E+08	17428	1.402619514	3.490217602	0.0013995	0.004135236	0.21503	1	65	30	251	125	17	330	363	269	299	394
ENSMUSG00000074505	chr9	Fat3	1.6E+07	1.6E+07	18456	-1.46276819	1.327623128	0.0013995	0.004135236	0.21426	-1	92	52	27	65	18	30	41	15	32	20
ENSMUSG00000037169	chr12	Mycn	1.3E+07	1.3E+07	3292	-1.71771369	1.035509922	0.0014049	0.004150304	0.29485	-1	39	75	23	65	7	21	18	11	28	21

ENSMUSG00000028397	chr4	Kdm4c	7.4E+07	7.4E+07	5823	-0.63618375	3.322734977	0.0014059	0.004152406	0.04117	-1	176	137	230	186	183	182	207	121	136	161
ENSMUSG00000030352	chr6	Tspan9	1.3E+08	1.3E+08	4732	0.724063635	6.062405735	0.0014075	0.004156153	0.06003	1	507	491	1090	1071	697	1691	1669	1331	2248	1616
ENSMUSG00000035390	chr7	Brsk1	4690604	4690720	3594	1.117013583	0.575993987	0.0014094	0.00416088	0.09087	1	18	10	15	8	13	59	31	23	36	46
ENSMUSG00000033530	chr12	Ttc7b	1E+08	1E+08	3441	-0.73832681	6.45662643	0.0014102	0.004162438	0.06269	-1	1415	1006	2484	1889	1672	1133	2232	842	1304	1357
ENSMUSG00000022191	chr15	Drosha	1.3E+07	1.3E+07	5934	-0.55459327	5.329834355	0.0014118	0.00416615	0.03451	-1	683	501	973	779	692	686	838	480	703	669
ENSMUSG00000021930	chr14	Spryd7	6.2E+07	6.2E+07	4002	-0.61103302	4.741744129	0.0014121	0.0041662	0.04148	-1	532	442	477	343	599	477	541	328	431	412
ENSMUSG00000028869	chr4	Gnl2	1.3E+08	1.3E+08	3683	-0.53414908	4.97844707	0.0014159	0.004176567	0.03155	-1	578	439	659	580	527	652	545	442	530	484
ENSMUSG00000019210	chr6	Atp6v1e1	1.2E+08	1.2E+08	1203	0.616721431	7.133360234	0.0014163	0.004176904	0.04398	1	1599	1171	1969	1720	1950	3638	3127	2854	3709	4137
ENSMUSG00000028270	chr3	Gbp2	1.4E+08	1.4E+08	2516	1.107795054	4.603971952	0.0014166	0.004176904	0.13761	1	182	177	251	210	348	1908	409	251	415	673
ENSMUSG00000031596	chr8	Slc7a2	4.1E+07	4.1E+07	9135	-0.73584792	5.26022436	0.0014223	0.004191951	0.06148	-1	919	607	687	798	470	602	549	544	638	595
ENSMUSG00000035585	chr7	Tsen34	3693375	3693889	2416	0.536060699	5.243147136	0.0014223	0.004191951	0.03215	1	360	292	629	501	601	1121	861	672	1021	972
ENSMUSG00000024085	chr17	Man2a1	6.5E+07	6.5E+07	7223	0.616716625	4.624705204	0.0014232	0.004193595	0.04184	1	289	224	266	229	460	867	550	467	608	604
ENSMUSG00000032193	chr9	Ldlr	2.2E+07	2.2E+07	4531	0.904292644	4.571454392	0.0014237	0.004194339	0.09238	1	137	121	245	202	616	772	755	544	520	591
ENSMUSG00000021824	chr14	Ap3m1	2.1E+07	2.1E+07	7015	-0.53937736	4.868468985	0.0014325	0.00421921	0.03218	-1	482	392	682	538	516	584	649	346	445	455
ENSMUSG00000036822	chr4	Topors	4E+07	4E+07	3856	-0.63106944	3.504059327	0.0014331	0.00422023	0.04143	-1	204	159	272	183	218	186	242	125	165	202
ENSMUSG00000001228	chr17	Uhrf1	5.6E+07	5.6E+07	4259	1.121249431	0.560111636	0.0014361	0.004228261	0.09544	1	14	5	18	11	17	65	39	26	38	25
ENSMUSG00000036644	chr11	Tbc1d9b	5E+07	5E+07	6429	-0.55754779	5.607927898	0.0014383	0.004233581	0.0353	-1	758	582	1191	964	944	983	992	525	823	807
ENSMUSG00000027509	chr2	Rae1	1.7E+08	1.7E+08	2554	0.557214725	4.395580995	0.0014394	0.004235973	0.03369	1	219	168	312	231	375	603	469	454	501	533
ENSMUSG00000028841	chr4	Cnksr1	1.3E+08	1.3E+08	2804	0.645696055	6.055909361	0.0014435	0.004247233	0.04797	1	625	425	1194	962	819	2090	1784	1391	1573	1541
ENSMUSG00000102918	chr18	PCDHGB6	3.8E+07	3.8E+07	5499	0.806089959	6.208493388	0.0014492	0.004263138	0.07481	1	688	663	604	601	1520	2460	1416	1555	2190	2089
ENSMUSG00000037221	chr5	Mospd3	1.4E+08	1.4E+08	1651	0.790016701	3.411603011	0.0014509	0.004266427	0.06644	1	98	86	108	93	204	295	210	179	369	331
ENSMUSG00000040952	chr7	Rps19	2.5E+07	2.5E+07	4685	0.645642775	7.394344487	0.0014507	0.004266427	0.04848	1	1789	1454	2257	1813	2671	5398	3261	3416	4638	4498
ENSMUSG00000027694	chr3	Gm8325	6.1E+07	6.1E+07	464	-1.06726814	0.42019196	0.0014544	0.004275757	0.08688	-1	27	17	37	29	19	21	22	8	19	15
ENSMUSG00000020798	chr11	Spns3	7.2E+07	7.2E+07	5508	-1.74031304	2.156835044	0.0014548	0.004275997	0.31749	-1	26	31	117	33	362	38	77	24	39	32
ENSMUSG00000032803	chr9	Cdv3	1E+08	1E+08	7403	-0.67284574	7.659177364	0.0014566	0.004280499	0.05275	-1	3405	2329	5338	4565	3361	3538	4151	2399	2790	3308
ENSMUSG00000010290	chr1	AI597479	4.3E+07	4.3E+07	3458	-0.57936894	4.817214373	0.0014589	0.004286205	0.03738	-1	488	347	649	587	481	483	662	343	423	430
ENSMUSG00000097284	chr14	4930480K23Rik	7E+07	7E+07	3755	-1.15249673	0.175597024	0.0014658	0.004305496	0.09665	-1	21	11	23	32	23	20	18	7	14	9
ENSMUSG00000022092	chr14	Ppp3cc	7E+07	7E+07	1948	-0.70744701	4.065057487	0.001467	0.004308233	0.05522	-1	274	188	497	356	278	296	410	156	215	255
ENSMUSG00000034903	chr2	Cobll1	6.5E+07	6.5E+07	8342	-1.18999575	2.129866211	0.0014796	0.004344241	0.14587	-1	40	49	104	69	217	61	45	59	33	67
ENSMUSG00000025586	chr7	Cpeb1	8.1E+07	8.1E+07	4192	-0.72334852	5.245886305	0.00148	0.004344675	0.05986	-1	776	603	630	422	1112	627	838	432	508	566
ENSMUSG00000046876	chr13	Atxn1	4.6E+07	4.6E+07	10605	-0.54063852	5.080595501	0.0014818	0.004349096	0.03275	-1	712	416	776	520	604	676	651	447	538	539
ENSMUSG00000079418	chrX	Atg4a	1.4E+08	1.4E+08	2661	-0.59195719	4.810414478	0.0014827	0.00435072	0.03934	-1	536	412	641	453	478	551	660	302	420	407
ENSMUSG00000002980	chr7	Bcam	2E+07	2E+07	3199	0.758665462	5.678116452	0.0014912	0.004374661	0.06651	1	321	265	1054	725	655	1538	1288	941	1377	1536
ENSMUSG00000032018	chr9	Sc5d	4.2E+07	4.2E+07	2328	-0.70841611	3.714985224	0.0014916	0.004375052	0.05432	-1	259	200	206	192	357	235	256	182	169	178
ENSMUSG00000024048	chr17	Myl12a	7.1E+07	7.1E+07	3201	0.812851419	7.954391484	0.0014958	0.004386324	0.07717	1	2019	1232	4859	3622	2432	6687	6169	5291	5912	8470
ENSMUSG00000041775	chr7	Mapk1ip1	1.4E+08	1.4E+08	1883	-0.57178214	4.189162026	0.0014961	0.004386476	0.03547	-1	290	227	479	328	338	341	332	189	290	377
ENSMUSG00000051890	chr12	Klhdc1	6.9E+07	6.9E+07	3137	-0.69607403	4.447890453	0.0015003	0.004397847	0.05438	-1	498	309	486	375	337	318	540	259	298	304
ENSMUSG00000004207	chr10	Psap	6E+07	6E+07	2744	0.632920102	10.70273181	0.0015007	0.004398132	0.04722	1	17093	12575	26525	18447	26458	45249	43748	28482	46531	46951
ENSMUSG00000027452	chr2	Acss1	1.5E+08	1.5E+08	4128	-0.92351305	5.307976144	0.0015069	0.004415282	0.09802	-1	784	254	1603	919	558	870	585	428	383	595
ENSMUSG00000036273	chr15	Lrrk2	9.2E+07	9.2E+07	11834	-0.66117085	3.367361916	0.0015083	0.004418441	0.04582	-1	190	157	237	170	187	207	215	124	146	134
ENSMUSG00000028124	chr3	Gclm	1.2E+08	1.2E+08	5543	-0.70587845	3.768960844	0.0015122	0.004428985	0.0542	-1	239	138	327	189	424	260	287	163	184	178
ENSMUSG00000042745	chr2	Id1	1.5E+08	1.5E+08	1160	0.817216276	3.996429489	0.0015156	0.004437897	0.07489	1	95	94	166	226	314	395	342	380	427	513
ENSMUSG00000047617	chr2	BC029214	2.5E+07	2.5E+07	2066	0.662028584	3.72254948	0.0015164	0.004439447	0.04732	1	123	90	177	153	242	409	254	292	339	353
ENSMUSG00000002910	chr8	Arrdc2	7.1E+07	7.1E+07	2329	-0.91210696	2.968535238	0.001517	0.004440305	0.08955	-1	83	84	246	229	146	140	145	71	76	133
ENSMUSG00000019866	chr10	Aim1	4.4E+07	4.4E+07	7416	0.803551077	2.28987376	0.0015178	0.004441656	0.06299	1	54	28	57	42	87	166	131	89	103	143
ENSMUSG00000028426	chr4	Rad23b	5.5E+07	5.5E+07	5733	-0.61940283	6.896924633	0.0015237	0.004457892	0.04492	-1	2037	1632	2837	2175	2240	2140	2613	1464	1777	1759
ENSMUSG00000002804	chr12	Nudt14	1.1E+08	1.1E+08	793	0.750761908	3.054145843	0.0015253	0.004461221	0.05926	1	64	54	153	97	107	243	159	171	252	232
ENSMUSG00000032315	chr9	Cyp1a1	5.8E+07	5.8E+07	2619	1.079703286	1.056242526	0.0015255	0.004461221	0.0954	1	21	20	14	20	16	54	41	50	68	56
ENSMUSG00000022803	chr16	Popdc2	3.8E+07	3.8E+07	2360	0.605287418	6.194500972	0.0015258	0.004461296	0.04245	1	789	740	917	922	957	1899	2149	1228	2064	1845
ENSMUSG00000006931	chr11	Leprel4	1E+08	1E+08	2178	0.898701123	2.901117439	0.0015272	0.004464523	0.08726	1	57	37	167	61	86	315	156	137	186	209
ENSMUSG00000020641	chr12	Rsad2	2.6E+07	2.6E+07	4328	0.933942717	1.968593631	0.001528	0.004465832	0.08409	1	29	25	35	42	68	167	126	56	91	87
ENSMUSG00000042647	chr5	Acad12	1.2E+08	1.2E+08	5007	-0.58807802	4.658932565	0.0015345	0.004483919	0.03875	-1	387	274	669	544	456	512	559	252	389	406
ENSMUSG00000045725	chr6	Prr15	5.4E+07	5.4E+07	1381	1.548071462	-0.26292283	0.0015372	0.00449084	0.19059	1	1	0	12	10	5	26	31	18	13	20
ENSMUSG00000051000	chr3	Fam160a1	8.6E+07	8.6E+07	7521	-0.79577662	5.977213836	0.0015399	0.004497908	0.0737	-1	1112	824	1634	1719	709	962	1376	665	964	820
ENSMUSG00000069539	chr10	Scyl2	9E+07	9E+07	10099	-0.67564641	3.714888777	0.0015408	0.004499402	0.04975	-1	222	182	353	242	219	237	315	133	169	200
ENSMUSG00000053472	chr2	Gm13534	5.8E+07	5.8E+07	513	-1.61410205	-0.1716895	0.0015431	0.00450526	0.22153	-1	22	16	16	26	10	8	21	4	8	1
ENSMUSG00000032042	chr9	Srpr	3.5E+07	3.5E+07	3364	-0.64758454	8.09777191	0.0015436	0.004505748	0.04949	-1	5408	3967	5104	4668	5863	4471	5472	3240	4920	4012
ENSMUSG00000050931	chr3	Sgms2	1.3E+08	1.3E+08	5873	0.95702289	1.826692815	0.0015453	0.004509816	0.08629	1	31	35	21	34	50	130	91	78	94	73
ENSMUSG00000034488	chr13	Edil3	8.9E+07	8.9E+07	13677	1.036792263	0.579355902	0.0015496	0.004520603	0.07627	1	12	7	19	17	13	49	50	23	33	37
ENSMUSG00000048720	chr19	Tbc1d12	3.9E+07	3.9E+07	4209	-0.77792104	2.305097821	0.0015495	0.004520603	0.05911	-1	86	70	127	79	106	95	95	48	86	51
ENSMUSG00000048701	chr10	Ccdc6	7E+07	7E+07	6385	-0.57140607	6.168069167	0.0015503	0.004521714	0.03801	-1	1257	978	1408	1286	1546	1251	1344	877	1297	1220
ENSMUSG00000043154	chr9	Ppp2r3a	1E+08	1E+08	12455	-0.71213383	7.910172679	0.0015517	0.004524886	0.05979	-1	4642	3029	6205	4989	3766	3452	5602	2584	3503	3821
ENSMUSG00000033256	chr2	Shf	1.2E+08	1.2E+08	2305	1.011287592	1.62184212	0.0015543	0.004531497	0.09799	1	25	15	26	29	56	83	52	65	95	109
ENSMUSG00000033294	chr5	Noc4l	1.1E+08	1.1E+08	2505	0.52812797	4.376718139	0.0015548	0.004531866	0.03032	1	239	173	322	253	304	552	444	418	547	548
ENSMUSG00000054894	chr12	Atp5s	7E+07	7E+07	1485	-0.66152356	3.582043485	0.0015558	0.004533905	0.04679	-1	224	166	297	232	177	205	237	157	160	192
ENSMUSG00000020074	chr10	Ccar1	6.3E+07	6.3E+07	4478	-0.55641616	4.704696859	0.0015669	0.004565427	0.03476	-1	441	407	575	472	408	524	527	322	386	431
ENSMUSG00000037577	chr17	Ephx3	3.2E+07	3.2E+07	2502	1.161753419	0.857185898	0.0015674	0.004565718	0.11832	1	16	7	20	14	23	72	21	50	43	51

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ENSMUSG00000039096	chr11	Rsad1	9.5E+07	9.5E+07	4391	-0.71646557	2.683540459	0.001569	0.004569417	0.0519	-1	121	80	173	92	140	127	120	62	83	112
ENSMUSG00000060538	chr7	Tmem219	1.3E+08	1.3E+08	2292	0.739639881	3.777856453	0.0015728	0.0045797	0.06023	1	112	100	137	151	286	486	288	241	414	348
ENSMUSG00000021936	chr14	Mapk8	3.3E+07	3.3E+07	9255	-0.60689348	5.277972308	0.0015742	0.004582687	0.04237	-1	703	542	919	797	538	668	780	495	569	663
ENSMUSG00000025234	chr9	Arih1	5.9E+07	5.9E+07	7707	-0.65086101	6.771737201	0.0015767	0.004588967	0.04987	-1	2060	1508	2593	2069	1806	1962	2427	1349	1594	1488
ENSMUSG00000050890	chr4	Pdik1l	1.3E+08	1.3E+08	5810	-0.86091043	1.471895373	0.001578	0.004590908	0.06547	-1	53	36	51	57	66	51	53	22	41	34
ENSMUSG00000052337	chr6	Immt	7.2E+07	7.2E+07	4964	-0.72733047	8.446380347	0.0015777	0.004590908	0.0626	-1	5615	3766	10355	8139	5709	5501	7657	3814	5186	5176
ENSMUSG00000096942	chr12	Rps19-ps6	1.1E+08	1.1E+08	438	0.820789143	3.191260506	0.0015799	0.004595545	0.0723	1	95	73	145	67	118	232	405	129	248	195
ENSMUSG00000024780	chr19	Cdc37l1	2.9E+07	2.9E+07	2517	-0.65212784	5.309397011	0.0015816	0.004599556	0.04917	-1	683	563	1076	810	507	711	847	467	574	603
ENSMUSG00000059070	chr7	Rpl18	4.6E+07	4.6E+07	4042	0.649598332	7.627309227	0.0015821	0.004600117	0.04991	1	1925	1827	2497	2437	2928	5842	3824	4080	5609	5513
ENSMUSG00000025465	chr7	Echs1	1.4E+08	1.4E+08	5274	-0.62708905	7.223560523	0.001587	0.004612506	0.04646	-1	2571	1493	3593	3150	3209	2546	2710	1848	2365	2682
ENSMUSG00000035413	chr11	Tmem98	8.1E+07	8.1E+07	1633	1.044011341	2.023242635	0.0015869	0.004612506	0.11348	1	27	18	43	23	93	145	91	76	132	107
ENSMUSG00000028044	chr3	Cks1b	8.9E+07	8.9E+07	1126	1.158803388	2.227905637	0.0015885	0.004615622	0.14149	1	49	34	28	21	80	199	66	128	150	100
ENSMUSG00000091264	chr13	Smim13	4.1E+07	4.1E+07	4464	-0.62439451	6.361920587	0.0015935	0.004629408	0.04581	-1	1472	1075	1988	1625	1378	1408	1825	968	1268	1253
ENSMUSG00000020482	chr11	Ccdc117	5528887	5531533	3372	-0.63527036	5.03085721	0.0015939	0.004629591	0.04643	-1	579	541	590	720	477	652	654	414	474	459
ENSMUSG00000039480	chr10	Nt5dc1	3.4E+07	3.4E+07	3192	-0.72461024	2.286960479	0.0015977	0.004639541	0.05026	-1	82	63	105	84	123	90	98	47	68	76
ENSMUSG00000036372	chr19	Tmem258	1E+07	1E+07	1611	0.564552167	5.001504983	0.001601	0.004647434	0.0361	1	401	288	400	377	473	999	608	626	945	759
ENSMUSG00000050222	chr14	Il17d	5.8E+07	5.8E+07	1221	1.246586561	1.187590762	0.0016011	0.004647434	0.1464	1	16	17	8	15	39	89	33	51	74	64
ENSMUSG00000099200	chr4	Mir7019	1.4E+08	1.4E+08	69	-0.6230973	3.768443126	0.0016048	0.004657442	0.04211	-1	229	162	326	297	236	224	266	143	264	214
ENSMUSG00000014426	chr17	Map3k4	1.2E+07	1.2E+07	5305	-0.59255697	5.358736444	0.0016061	0.004660181	0.04056	-1	638	467	1130	842	712	718	879	439	745	630
ENSMUSG00000037400	chr3	Atp11b	3.6E+07	3.6E+07	4859	-0.55175653	4.476354392	0.001608	0.004663747	0.03397	-1	404	329	477	372	390	481	432	266	309	391
ENSMUSG00000065126	chr11	Snord104	1.1E+08	1.1E+08	70	1.33005146	0.059486394	0.0016079	0.004663747	0.13678	1	2	3	14	14	7	33	20	28	21	31
ENSMUSG00000035547	chr7	Capn5	9.8E+07	9.8E+07	5485	0.983643874	2.575817513	0.0016112	0.004672151	0.10144	1	43	54	38	42	118	218	135	93	164	204
ENSMUSG00000024985	chr19	Tcf7l2	5.6E+07	5.6E+07	8739	0.835739972	3.064541386	0.0016177	0.004689217	0.07545	1	89	59	71	67	167	274	159	162	237	263
ENSMUSG00000037818	chr3	3110057O12Rik	4.1E+07	4.1E+07	5433	-1.13835199	3.561144637	0.0016178	0.004689217	0.14591	-1	225	85	473	386	93	170	171	138	100	173
ENSMUSG00000022621	chr15	Rabl2	9E+07	9E+07	2960	0.925503665	1.26998787	0.0016198	0.004693981	0.07464	1	27	12	25	17	40	74	66	53	58	57
ENSMUSG00000028957	chr4	Per3	1.5E+08	1.5E+08	9608	-0.68081012	3.610100226	0.0016243	0.004706057	0.05042	-1	251	190	226	155	297	240	174	171	183	191
ENSMUSG00000041187	chr7	Prkd2	1.7E+07	1.7E+07	3757	0.765343813	3.191284041	0.0016347	0.004735208	0.06332	1	68	56	138	87	176	341	187	181	232	240
ENSMUSG00000032712	chr6	2810474O19Rik	1.5E+08	1.5E+08	6802	0.650714231	3.688741317	0.0016356	0.004736883	0.04562	1	146	117	203	128	158	432	279	274	244	384
ENSMUSG00000032265	chr9	Fam46a	8.5E+07	8.5E+07	5703	0.921818885	3.127965289	0.0016429	0.004757101	0.09279	1	105	71	54	52	165	325	221	149	233	255
ENSMUSG00000093076	chr17	Mir3082	2.6E+07	2.6E+07	64	0.550690685	4.384040634	0.0016542	0.004788778	0.03375	1	230	150	344	284	288	601	433	424	535	550
ENSMUSG00000027669	chr3	Gnb4	3.3E+07	3.3E+07	12692	0.637971031	3.944146322	0.001655	0.004790048	0.04479	1	123	144	243	153	253	574	368	263	325	423
ENSMUSG00000069020	chr2	Urm1	3E+07	3E+07	4275	0.515036987	4.749069636	0.0016587	0.00479994	0.02976	1	299	222	503	307	365	779	652	443	700	713
ENSMUSG00000028010	chr3	Gar1	1.3E+08	1.3E+08	1714	0.690150603	3.16401048	0.0016624	0.004809668	0.04963	1	90	80	121	99	121	269	162	200	220	268
ENSMUSG00000063684	chr2	Gm13910	1.1E+08	1.1E+08	1428	-0.80058107	5.567132672	0.0016645	0.004814576	0.0753	-1	797	344	1770	923	975	771	1048	483	524	784
ENSMUSG00000004233	chr3	Wars2	9.9E+07	9.9E+07	5946	-0.69048914	3.015782998	0.0016679	0.00482191	0.04972	-1	154	106	179	166	140	133	174	93	118	118
ENSMUSG00000025980	chr1	Hspd1	5.5E+07	5.5E+07	2642	-0.62696597	8.053208447	0.001668	0.00482191	0.04706	-1	4448	3030	7555	4771	5105	5100	4935	3372	3951	4289
ENSMUSG00000028078	chr3	Dclk2	8.7E+07	8.7E+07	10553	1.125770094	0.565132071	0.001668	0.00482191	0.10417	1	9	5	16	12	24	49	24	38	40	38
ENSMUSG00000038608	chr1	Dock10	8.1E+07	8.1E+07	18267	0.855190084	2.531414032	0.0016685	0.004822238	0.07462	1	62	48	44	51	97	215	162	84	126	182
ENSMUSG00000056216	chr7	Cebpg	3.5E+07	3.5E+07	4935	-0.56572339	5.97909606	0.00167	0.004824632	0.03762	-1	881	741	1576	1185	1426	1144	1190	790	1022	1121
ENSMUSG00000062797	chr7	l7Rn6	9E+07	9E+07	2933	-0.56810699	5.34165572	0.0016699	0.004824632	0.03751	-1	793	594	723	740	737	723	807	508	722	617
ENSMUSG00000054003	chr12	Tdrd9	1.1E+08	1.1E+08	5415	1.246072066	0.239056196	0.001673	0.0048322	0.117	1	10	3	9	16	9	43	18	27	27	37
ENSMUSG00000058690	chr14	Ccser2	3.7E+07	3.7E+07	8715	-0.59844914	6.739993464	0.0016752	0.004837576	0.04261	-1	1926	1400	2355	2096	1929	1891	2161	1327	1583	1850
ENSMUSG00000009073	chr11	Nf2	4765845	4768273	6825	-0.64941479	6.775284137	0.0016912	0.004882885	0.0503	-1	1788	1365	2930	2271	1851	1765	2434	1177	1750	1761
ENSMUSG00000017132	chr11	Cyth1	1.2E+08	1.2E+08	3905	-0.62536816	5.436480881	0.0016916	0.004883023	0.04578	-1	698	440	1349	820	782	710	875	458	793	709
ENSMUSG00000034118	chr5	Tpst1	1.3E+08	1.3E+08	2789	0.815127164	4.00480108	0.0016948	0.004891179	0.07575	1	184	114	122	124	340	599	316	346	430	413
ENSMUSG00000041736	chr15	Tspo	8.4E+07	8.4E+07	854	1.2587333	6.231751826	0.0017051	0.004919786	0.18501	1	596	415	291	265	1908	2988	1413	1746	2764	2042
ENSMUSG00000028664	chr4	Ephb2	1.4E+08	1.4E+08	12608	1.077200831	1.793394242	0.0017157	0.004949467	0.1175	1	22	26	30	22	64	153	52	85	78	99
ENSMUSG00000039210	chr1	Gpatch2	1.9E+08	1.9E+08	7684	-0.65214958	3.433157738	0.0017226	0.004968322	0.0458	-1	213	148	253	191	181	172	211	136	143	199
ENSMUSG00000080935	chr5	Got2-ps1	1.4E+08	1.4E+08	1293	-1.02528113	3.675309252	0.0017247	0.004973309	0.12031	-1	149	101	498	423	175	164	274	106	171	160
ENSMUSG00000001604	chr4	Tcea3	1.4E+08	1.4E+08	1400	-0.65076786	7.189057897	0.0017263	0.004977048	0.05084	-1	2759	2035	3223	2854	2490	2121	2835	1582	2780	2460
ENSMUSG00000039285	chr9	Azi2	1.2E+08	1.2E+08	6439	-0.56402916	5.207504501	0.0017289	0.004983181	0.03697	-1	549	417	1029	743	654	702	761	462	535	632
ENSMUSG00000061479	chr7	Snrpa	2.7E+07	2.7E+07	1754	0.498248676	5.100183027	0.0017292	0.004983181	0.02837	1	384	305	522	446	497	931	751	640	964	850
ENSMUSG00000025723	chr7	Nmb	8.1E+07	8.1E+07	793	1.074411064	1.305989543	0.0017305	0.004985893	0.11201	1	10	13	23	19	53	65	78	47	67	71
ENSMUSG00000071533	chr16	Pcnp	5.6E+07	5.6E+07	3115	-0.52851263	5.098855482	0.0017408	0.005014679	0.0323	-1	630	468	692	562	687	728	709	449	449	577
ENSMUSG00000043733	chr5	Ptpn11	1.2E+08	1.2E+08	7492	-0.73607394	7.203032878	0.001742	0.005017096	0.06506	-1	2067	1675	4643	2932	3045	2286	3685	1496	2050	2037
ENSMUSG00000020594	chr12	Pum2	8674134	8674170	7260	-0.60609773	6.60232392	0.001747	0.005030583	0.04402	-1	1771	1392	2185	1815	1615	1688	1986	1165	1552	1602
ENSMUSG00000022142	chr15	Nup155	8109313	8109602	6402	-0.65111035	3.701964928	0.0017494	0.005036211	0.04712	-1	228	220	230	255	231	246	268	159	194	178
ENSMUSG00000047388	chr8	Atmin	1.2E+08	1.2E+08	4877	-0.53538208	5.246187647	0.0017521	0.005042991	0.03345	-1	665	523	763	730	678	727	766	400	711	634
ENSMUSG00000078480	chr4	Mrpl48-ps	8.9E+07	8.9E+07	636	0.579587029	3.778683909	0.0017558	0.005052789	0.03646	1	139	104	214	188	191	400	305	240	350	400
ENSMUSG00000020459	chr11	Mtif2	3E+07	3E+07	3868	-0.60496379	4.402735691	0.0017644	0.005076441	0.04173	-1	348	256	628	366	358	416	465	249	280	335
ENSMUSG00000018401	chr11	Mtmr4	8.8E+07	8.8E+07	6240	-0.56828196	4.121530476	0.0017649	0.00507668	0.03607	-1	302	221	424	328	295	366	359	195	283	258
ENSMUSG00000027907	chr3	S100a11	9.4E+07	9.4E+07	511	1.259751777	5.64625582	0.0017705	0.005090853	0.18629	1	331	238	198	201	1383	2043	954	1194	1566	1537
ENSMUSG00000051615	chr14	Rap2a	1.2E+08	1.2E+08	4174	0.603802402	3.794156581	0.0017704	0.005090853	0.03963	1	132	132	161	179	218	440	377	268	347	289
ENSMUSG00000003382	chr3	Etv3	8.8E+07	8.8E+07	10274	-0.54288329	3.97841655	0.0017711	0.00509136	0.03209	-1	230	211	341	270	365	276	290	214	252	284
ENSMUSG00000022415	chr15	Syngr1	8E+07	8E+07	4808	-0.54628053	5.32253	0.0017714	0.00509136	0.03501	-1	743	550	833	691	744	710	807	418	786	672
ENSMUSG00000054027	chr10	Nt5dc3	8.7E+07	8.7E+07	5952	-0.66773067	6.669469078	0.0017753	0.00510138	0.05363	-1	1380	1389	2729	1976	2091	1418	2245	983	1707	1853
ENSMUSG00000035311	chr10	Gnptab	8.8E+07	8.8E+07	5883	-0.63997509	4.01716004	0.0017774	0.005106543	0.04646	-1	292	255	316	252	353	301	391	162	258	210

ENSMUSG00000026356	chr1	Dars	1.3E+08	1.3E+08	4358	-0.6061408	5.904160131	0.0017811	0.005116109	0.04382	-1	1077	931	1316	1089	955	1103	1232	782	861	931
ENSMUSG00000037331	chr11	Larp1	5.8E+07	5.8E+07	6829	-0.62836638	7.178125549	0.0017819	0.005117331	0.04769	-1	2377	1989	3221	3077	2574	2321	3016	1650	2447	2378
ENSMUSG00000036737	chr9	Oxsr1	1.2E+08	1.2E+08	5350	-0.61894153	7.010779473	0.0017856	0.005126879	0.04625	-1	2367	1723	2709	2753	2152	2349	2529	1526	2086	2080
ENSMUSG00000040327	chr17	Cul9	4.7E+07	4.7E+07	12198	-0.55287362	4.522000728	0.0017865	0.005128536	0.03487	-1	364	289	537	478	398	423	440	237	467	374
ENSMUSG00000030424	chr7	Zfp939	3.9E+07	3.9E+07	2480	-1.1041289	0.673753245	0.0017881	0.005131926	0.10737	-1	34	25	25	45	24	21	29	10	23	18
ENSMUSG00000061330	chr13	Gm11361	2.8E+07	2.8E+07	459	0.754444678	3.112143052	0.0017897	0.005135413	0.06108	1	88	82	79	99	124	248	163	160	289	246
ENSMUSG00000047591	chr15	Mafa	7.6E+07	7.6E+07	1080	-0.8566095	3.607915406	0.001792	0.005141049	0.0839	-1	230	272	200	223	194	137	238	113	244	163
ENSMUSG00000028199	chr3	Cryz	1.5E+08	1.5E+08	6195	-0.60056318	4.276401047	0.0017942	0.005146248	0.04089	-1	370	180	503	360	389	389	422	230	275	285
ENSMUSG00000098923	chr1	Tmem185b	1.2E+08	1.2E+08	2824	0.694836745	3.102951958	0.0017968	0.005152654	0.05199	1	84	54	104	107	150	256	191	187	195	248
ENSMUSG00000028431	chr4	Ikbkap	5.7E+07	5.7E+07	7399	-0.52355969	5.081544008	0.0018039	0.00517202	0.03181	-1	555	436	787	643	598	582	742	451	521	568
ENSMUSG00000025154	chr19	Arhgap19	4.2E+07	4.2E+07	5140	-0.57742885	4.058878971	0.0018101	0.005188674	0.0376	-1	309	249	340	288	296	366	315	163	275	283
ENSMUSG00000018500	chr11	Adora2b	6.2E+07	6.2E+07	1845	1.09192351	0.472165704	0.0018115	0.005191245	0.09543	1	9	6	15	11	21	40	33	39	24	38
ENSMUSG00000042211	chr18	Fbxo38	6.3E+07	6.3E+07	4388	-0.5184682	4.663602999	0.0018117	0.005191245	0.03061	-1	413	324	598	477	445	467	546	334	394	410
ENSMUSG00000042684	chr1	Npl	1.5E+08	1.5E+08	2961	0.94199861	2.752220319	0.0018133	0.005194584	0.09593	1	63	65	37	54	116	277	153	149	173	150
ENSMUSG00000026639	chr1	Lamb3	1.9E+08	1.9E+08	6612	-1.15734357	1.273242679	0.0018139	0.005195261	0.13286	-1	32	14	65	88	54	28	35	19	29	39
ENSMUSG00000027427	chr2	Polr3f	1.4E+08	1.4E+08	7710	-0.66527941	3.191585759	0.0018182	0.0052066	0.04738	-1	134	134	227	190	153	164	175	115	123	148
ENSMUSG00000026926	chr2	Pmpca	2.6E+07	2.6E+07	4282	-0.61351156	7.431528266	0.0018256	0.00522664	0.04574	-1	3138	2347	3927	3273	3034	2856	3468	2110	2814	2878
ENSMUSG00000037410	chr9	Tbc1d2b	9E+07	9E+07	8799	0.642492139	4.107598111	0.0018284	0.00523303	0.04659	1	199	165	182	163	296	636	364	300	459	426
ENSMUSG00000057722	chr4	Lepr	1E+08	1E+08	7049	-0.71037069	2.661531039	0.0018285	0.00523303	0.05252	-1	126	88	131	121	116	137	97	58	88	119
ENSMUSG00000059201	chr6	Lep	2.9E+07	2.9E+07	3354	-2.86622145	4.864159705	0.0018295	0.005234685	0.84523	-1	325	763	9	14	2877	254	79	191	86	96
ENSMUSG00000026960	chr2	Arl6ip6	5.3E+07	5.3E+07	2703	-0.72914081	3.065766334	0.0018324	0.005242048	0.05785	-1	174	132	167	148	147	154	182	88	94	135
ENSMUSG00000024556	chr18	Me2	7.4E+07	7.4E+07	2455	0.874185376	3.001869688	0.0018422	0.005268862	0.08549	1	43	60	143	47	146	254	239	167	191	205
ENSMUSG00000062825	chr11	Actg1	1.2E+08	1.2E+08	2658	0.643097383	7.408083872	0.0018431	0.005270376	0.05029	1	1615	1542	2012	1830	3089	5392	3850	3145	4584	4558
ENSMUSG00000071637	chr16	Cebpd	1.6E+07	1.6E+07	1180	0.808739545	3.133738377	0.0018495	0.005287716	0.07242	1	67	63	113	90	153	220	166	181	354	207
ENSMUSG00000028552	chr4	Eps15	1.1E+08	1.1E+08	6931	-0.66344007	6.314990634	0.0018506	0.005289792	0.05324	-1	1654	1327	1306	1387	1474	1541	1658	928	1098	1197
ENSMUSG00000020424	chr11	Gatsl3	4218225	4218426	1574	1.086570815	1.905591321	0.0018527	0.005294746	0.12387	1	21	26	33	21	78	183	71	72	91	99
ENSMUSG00000012076	chr12	Brms1l	5.6E+07	5.6E+07	2566	-0.59990182	4.186082836	0.0018576	0.005306482	0.04114	-1	329	291	415	311	277	327	344	210	346	270
ENSMUSG00000064181	chr10	Rab3ip	1.2E+08	1.2E+08	2690	-0.65501696	4.640241032	0.0018574	0.005306482	0.05039	-1	357	361	591	627	341	416	524	249	404	427
ENSMUSG00000022842	chr16	Ece2	2.1E+07	2.1E+07	6547	0.73179098	2.64974725	0.0018585	0.00530699	0.05563	1	56	44	88	69	99	181	127	103	200	188
ENSMUSG00000094638	chr1	Gm21972	8.6E+07	8.6E+07	776	0.587184379	5.979253575	0.0018582	0.00530699	0.04138	1	758	517	743	845	941	1830	1340	1290	1601	1732
ENSMUSG00000039795	chr3	Zfand1	1E+07	1E+07	6267	-0.90863258	1.741005891	0.0018631	0.005318833	0.08346	-1	61	60	74	61	61	62	76	25	44	33
ENSMUSG00000042082	chr13	Arsb	9.4E+07	9.4E+07	3989	0.745131381	4.169672162	0.0018658	0.005325435	0.06441	1	191	150	163	130	387	662	498	337	415	430
ENSMUSG00000038188	chr11	Scarf1	7.6E+07	7.6E+07	2887	0.752225192	3.200198147	0.0018697	0.005335503	0.0628	1	60	62	137	96	174	258	192	173	272	282
ENSMUSG00000025555	chr14	Farp1	1.2E+08	1.2E+08	5524	0.759983701	2.762619028	0.0018711	0.005338633	0.06162	1	64	51	101	46	121	186	178	154	177	163
ENSMUSG00000074818	chr19	Pdzd7	4.5E+07	4.5E+07	4089	-1.04756377	2.418877599	0.0018719	0.005339658	0.12125	-1	117	120	75	58	149	57	96	33	92	84
ENSMUSG00000037957	chr12	Wdr20	1.1E+08	1.1E+08	5593	-0.67863081	3.264147346	0.0018729	0.005341419	0.05021	-1	170	109	213	197	208	197	219	102	116	135
ENSMUSG00000032340	chr9	Neo1	5.9E+07	5.9E+07	7387	-0.58512991	5.942232867	0.0018741	0.005343727	0.04124	-1	1142	912	1377	1004	1082	1187	1315	720	916	987
ENSMUSG00000030779	chr7	Rbbp6	1.2E+08	1.2E+08	8752	-0.51308236	5.003759433	0.0018767	0.005350091	0.03069	-1	488	415	695	644	609	561	690	379	527	586
ENSMUSG00000023886	chr17	Smoc2	1.4E+07	1.4E+07	2832	0.72193103	7.516268872	0.0018775	0.005351211	0.06349	1	2225	2038	1569	1828	2405	5696	4028	3694	5080	5073
ENSMUSG00000024528	chr18	Srfbp1	5.2E+07	5.2E+07	1463	-0.65707121	3.212742749	0.001881	0.005360307	0.04655	-1	188	127	197	157	177	186	191	114	118	133
ENSMUSG00000027981	chr3	Rnpc3	1.1E+08	1.1E+08	6627	-0.78992059	2.692935474	0.0018846	0.005369284	0.06691	-1	88	117	135	145	115	133	96	89	71	94
ENSMUSG00000041653	chr15	Pnpla3	8.4E+07	8.4E+07	4640	-1.67285334	4.771363433	0.0018855	0.005370796	0.32261	-1	517	349	119	199	2122	353	115	320	326	189
ENSMUSG00000024713	chr19	Pcsk5	1.7E+07	1.7E+07	9346	0.891632055	2.955762666	0.001888	0.005376821	0.0885	1	56	65	79	54	156	356	179	148	153	207
ENSMUSG00000018567	chr11	Gabarap	7E+07	7E+07	1844	0.591448888	7.628874402	0.0018901	0.005381831	0.04282	1	2156	1644	2746	2508	2969	6171	4451	3617	4984	5521
ENSMUSG00000022999	chr15	Lmbr1l	9.9E+07	9.9E+07	4217	0.743949952	2.65835867	0.0018932	0.005389595	0.05756	1	58	51	70	61	113	185	149	110	148	214
ENSMUSG00000037253	chr18	Mex3c	7.4E+07	7.4E+07	3738	-0.62064813	3.799838052	0.0018953	0.00539426	0.04344	-1	256	207	312	219	267	307	298	164	174	199
ENSMUSG00000071573	chr19	Rnls	3.3E+07	3.3E+07	1627	-0.76340132	2.883652835	0.0018962	0.005395958	0.06298	-1	146	91	194	165	99	128	146	79	105	106
ENSMUSG00000034881	chr10	Tbxa2r	8.1E+07	8.1E+07	1763	1.199564935	-0.09199535	0.0018967	0.00539606	0.10511	1	8	2	16	5	7	23	22	19	30	22
ENSMUSG00000056671	chr18	Prelid2	4.2E+07	4.2E+07	724	0.891336322	1.253772511	0.0019038	0.005415243	0.06809	1	24	14	30	27	25	73	46	50	57	76
ENSMUSG00000047757	chrX	Fancb	1.6E+08	1.6E+08	2983	-1.1582665	0.733136338	0.0019062	0.005420951	0.12447	-1	43	16	35	27	47	37	29	6	17	16
ENSMUSG00000047473	chr7	Zfp30	3E+07	3E+07	6078	-0.89530012	2.874174439	0.0019091	0.005428141	0.08913	-1	122	74	295	142	108	102	157	65	97	109
ENSMUSG00000021012	chr12	Zc3h14	9.9E+07	9.9E+07	4184	-0.53969056	5.601535999	0.0019101	0.005430016	0.03486	-1	794	645	1090	893	927	897	1063	570	766	822
ENSMUSG00000033161	chr3	Atp1a1	1E+08	1E+08	4487	0.635931591	7.171623525	0.0019161	0.005444733	0.04949	1	1370	1156	2228	2182	1647	3786	3620	2652	3894	4205
ENSMUSG00000038403	chr3	Hfe2	9.7E+07	9.7E+07	2021	-0.62850988	9.203981028	0.001916	0.005444733	0.04868	-1	10685	7978	14141	9854	11666	9521	12478	6468	9944	9824
ENSMUSG00000078864	chr2	Gm14322	1.8E+08	1.8E+08	1254	-1.07640093	0.32282123	0.0019182	0.005449687	0.08676	-1	25	19	31	26	18	14	22	14	15	12
ENSMUSG00000021982	chr14	Cdadc1	6E+07	6E+07	1901	-0.54039411	4.874977614	0.0019207	0.005455539	0.03424	-1	555	408	615	537	477	622	581	378	478	420
ENSMUSG00000076240	chr5	Mir702	1.4E+08	1.4E+08	109	0.920589867	1.771945051	0.0019219	0.005457776	0.086	1	41	15	35	23	62	121	77	62	96	92
ENSMUSG00000024253	chr17	Dync2li1	8.5E+07	8.5E+07	1324	0.775804885	2.814196091	0.0019297	0.005479051	0.06456	1	75	66	81	43	120	228	170	138	181	187
ENSMUSG00000031590	chr8	Frg1	4.1E+07	4.1E+07	1085	0.5540123	4.54915256	0.0019306	0.005480421	0.03518	1	313	232	314	220	336	755	508	464	562	580
ENSMUSG00000021460	chr13	Auh	5.3E+07	5.3E+07	9580	-0.58513466	5.959317672	0.0019326	0.005484321	0.04143	-1	1211	659	1553	1087	1224	1030	1311	742	997	1079
ENSMUSG00000047250	chr2	Ptgs1	3.6E+07	3.6E+07	3884	0.796097064	2.232812539	0.0019328	0.005484321	0.06386	1	30	39	67	43	78	147	116	74	128	142
ENSMUSG00000054000	chr4	Tusc1	9.3E+07	9.3E+07	1374	1.289387278	0.873558963	0.0019336	0.005485022	0.16559	1	8	4	16	9	42	60	35	35	57	62
ENSMUSG00000061207	chr17	Stk19	3.5E+07	3.5E+07	3155	0.726605849	2.961999649	0.0019338	0.005485022	0.05645	1	58	71	99	75	138	270	180	129	204	218
ENSMUSG00000006412	chr1	Pfdn2	1.7E+08	1.7E+08	1937	0.542838789	5.896556694	0.001935	0.005487207	0.0355	1	734	523	898	646	879	1571	1379	1114	1553	1671
ENSMUSG00000004837	chr11	Grap	6.2E+07	6.2E+07	1793	0.777392443	3.031410051	0.0019371	0.005492298	0.06656	1	71	63	91	68	164	278	158	175	208	231
ENSMUSG00000092827	chr2	Mir3091	1.8E+08	1.8E+08	76	1.727929648	-0.566229	0.0019409	0.005501745	0.18086	1	1	8	3	2	4	20	7	14	21	24
ENSMUSG00000096054	chr10	Syne1	5020203	5022247	11801	-0.58254302	5.665829054	0.0019431	0.00550688	0.04097	-1	845	699	1079	1037	909	943	1104	567	682	947

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ENSMUSG00000030868	chr7	Dctn5	1.2E+08	1.2E+08	2649	0.544466792	4.620982666	0.0019479	0.005519545	0.03431	1	293	210	319	247	453	801	537	448	603	636
ENSMUSG00000044730	chr4	9930104L06Rik	1.2E+08	1.2E+08	5592	-0.57428959	3.555974396	0.0019484	0.005519753	0.03574	-1	203	157	259	208	230	208	221	150	218	173
ENSMUSG00000019370	chr7	Calm3	1.7E+07	1.7E+07	2423	-0.69832116	8.216703629	0.001952	0.005528828	0.0601	-1	6131	4989	5191	4969	5796	4840	6114	3170	5641	3854
ENSMUSG00000024764	chr19	Naa40	7225668	7228091	3275	-0.54902237	4.426347283	0.0019545	0.005534194	0.03472	-1	361	251	549	405	381	390	473	243	374	334
ENSMUSG00000093930	chr13	Hmgcs1	1.2E+08	1.2E+08	3233	-0.73213709	5.927637921	0.0019547	0.005534194	0.06522	-1	970	720	1110	815	2307	1117	1248	677	848	877
ENSMUSG00000014763	chr17	Fam120b	1.5E+07	1.5E+07	4518	-0.54498794	4.340664897	0.0019551	0.005534346	0.03415	-1	347	292	465	352	343	397	435	235	307	339
ENSMUSG00000029392	chr5	Rilpl1	1.2E+08	1.2E+08	2247	-0.74929429	7.374768248	0.0019576	0.005540086	0.06896	-1	2489	1800	5502	3606	2805	2696	3903	1694	2064	2592
ENSMUSG00000027680	chr3	Fxr1	3.4E+07	3.4E+07	2323	-0.67246073	8.189588941	0.0019824	0.005608005	0.05592	-1	5781	4176	6616	5523	4729	5005	6760	3360	4213	4094
ENSMUSG00000037415	chr8	Ranbp10	1.1E+08	1.1E+08	5308	-0.57758725	5.374855417	0.0019822	0.005608005	0.04014	-1	675	602	941	798	707	675	962	497	661	654
ENSMUSG00000041712	chr12	Ubr7	1E+08	1E+08	3247	-0.51722429	4.578874214	0.0019865	0.005618685	0.03095	-1	382	319	559	402	468	472	525	290	412	342
ENSMUSG00000025369	chr10	Smarcc2	1.3E+08	1.3E+08	5027	-0.54147092	5.952705429	0.0019899	0.005627193	0.03562	-1	1013	743	1274	1107	1472	1224	1225	702	1057	1057
ENSMUSG00000073639	chr18	Rab18	6765205	6765332	2257	-0.62655391	6.48649566	0.0019933	0.005635471	0.0482	-1	1712	1292	1976	1517	1662	1621	2071	1091	1176	1367
ENSMUSG00000000531	chr15	Grasp	1E+08	1E+08	2013	0.858514242	2.591815085	0.0020032	0.005662383	0.08136	1	55	25	61	66	122	170	138	115	161	203
ENSMUSG00000047866	chr8	Lonp2	8.7E+07	8.7E+07	5346	-0.56087468	6.07196111	0.0020105	0.005681916	0.03841	-1	1228	835	1392	1282	1324	1370	1319	871	1060	1018
ENSMUSG00000031843	chr8	Mphosph6	1.2E+08	1.2E+08	1054	0.782259148	2.378947742	0.0020138	0.005690078	0.06473	1	44	30	82	47	89	184	106	95	148	136
ENSMUSG00000037822	chr5	Smim14	6.5E+07	6.5E+07	7460	0.55897863	5.754333616	0.0020151	0.005692548	0.03785	1	621	492	670	621	892	1623	1173	1021	1326	1509
ENSMUSG00000084067	chr2	Gm14269	1.7E+08	1.7E+08	306	-1.20900812	-0.09968481	0.0020159	0.005693725	0.10328	-1	20	11	28	20	11	11	11	12	8	10
ENSMUSG00000020601	chr12	Trib2	1.6E+07	1.6E+07	4290	0.497673059	4.592178598	0.0020196	0.005702905	0.02851	1	293	204	389	288	344	705	563	504	531	591
ENSMUSG00000032745	chr13	Gpbp1	1.1E+08	1.1E+08	3905	-0.58667342	6.05846356	0.0020301	0.005731386	0.04216	-1	1196	878	1569	1286	1102	1278	1371	829	955	1099
ENSMUSG00000039509	chr8	Nup133	1.2E+08	1.2E+08	5808	-0.51086912	4.646608021	0.0020315	0.005733403	0.03031	-1	450	284	581	487	431	454	489	322	448	419
ENSMUSG00000039994	chr10	Timeless	1.3E+08	1.3E+08	6115	0.765820127	2.838228086	0.0020316	0.005733403	0.06449	1	45	47	106	83	125	263	182	121	158	205
ENSMUSG00000051224	chrX	Tceanc	1.7E+08	1.7E+08	4201	-0.93839184	1.153263682	0.0020343	0.005739807	0.08358	-1	41	45	49	38	35	39	36	15	34	31
ENSMUSG00000103114	chr1	RP23-103B18.8	1.9E+08	1.9E+08	2385	-1.29391523	-0.24327229	0.0020359	0.005743224	0.12722	-1	16	14	18	10	24	7	19	3	7	10
ENSMUSG00000048280	chr13	Zfp738	6.8E+07	6.8E+07	5217	-0.91121077	1.479464357	0.0020383	0.005748818	0.08075	-1	57	58	54	43	47	47	38	34	41	34
ENSMUSG00000056260	chr3	Lrif1	1.1E+08	1.1E+08	9192	-0.6571012	3.059165908	0.0020399	0.005752375	0.04687	-1	159	121	156	161	157	140	171	93	123	139
ENSMUSG00000026048	chr1	Ercc5	4.4E+07	4.4E+07	5864	-0.55299074	3.852611378	0.0020503	0.005780364	0.03436	-1	225	188	346	281	257	304	278	169	223	242
ENSMUSG00000070284	chr9	Gmppb	1.1E+08	1.1E+08	2785	0.676843766	3.169792128	0.0020511	0.005781532	0.05016	1	65	71	138	119	132	267	204	181	266	209
ENSMUSG00000028689	chr4	Ccdc163	1.2E+08	1.2E+08	2519	0.894880943	1.83711752	0.0020527	0.005784917	0.07907	1	36	34	33	28	48	150	82	63	68	107
ENSMUSG00000023079	chr5	Gtf2ird1	1.3E+08	1.3E+08	4834	-0.55287991	3.674139951	0.0020535	0.005786066	0.03344	-1	215	155	303	207	275	245	237	161	196	228
ENSMUSG00000017677	chr11	Wsb1	7.9E+07	7.9E+07	3987	0.654176247	4.189101876	0.0020542	0.005786692	0.04964	1	147	206	208	232	251	578	421	368	357	570
ENSMUSG00000067873	chrX	Htatsf1	5.7E+07	5.7E+07	4879	-0.59994262	7.035696054	0.0020595	0.005800638	0.04466	-1	2422	1752	3072	2282	2421	2480	2763	1644	1905	2037
ENSMUSG00000079505	chr17	Gm11131	3.5E+07	3.5E+07	3122	1.349442289	0.034242194	0.0020668	0.005819901	0.14304	1	8	5	7	4	14	46	12	18	20	38
ENSMUSG00000030865	chr7	Chp2	1.2E+08	1.2E+08	1603	0.864593709	2.897060205	0.0020694	0.005825973	0.08265	1	56	83	66	69	109	300	267	103	164	171
ENSMUSG00000021670	chr13	Hmgcr	9.7E+07	9.7E+07	7275	0.6980571	2.979931804	0.0020762	0.00584416	0.05304	1	60	62	112	90	132	281	224	151	183	163
ENSMUSG00000067786	chr2	Nnat	1.6E+08	1.6E+08	1829	-3.18376319	5.094030341	0.0020805	0.005854831	1.03311	-1	532	569	12	10	3861	200	154	152	6	179
ENSMUSG00000042729	chr19	Wdr74	8735839	8735905	1203	0.573420837	3.896061431	0.0020822	0.005858692	0.03742	1	167	108	213	189	234	407	310	331	363	397
ENSMUSG00000029156	chr5	Sgcb	7.4E+07	7.4E+07	3709	-0.65579774	7.303504288	0.0020831	0.005859654	0.05355	-1	3469	2231	3242	2933	2480	2917	3218	1915	2402	2287
ENSMUSG00000029185	chr5	Fam114a1	6.5E+07	6.5E+07	2964	0.665885406	3.926529146	0.0020834	0.005859654	0.05121	1	200	125	139	151	264	580	376	269	356	360
ENSMUSG00000036111	chr7	Lmo1	1.1E+08	1.1E+08	1071	1.065576964	2.003028225	0.0020846	0.005860752	0.12347	1	26	23	29	28	89	116	74	71	154	128
ENSMUSG00000074896	chr19	Ifit3	3.5E+07	3.5E+07	1745	1.059873219	2.641336804	0.0020842	0.005860752	0.1275	1	81	36	50	28	107	351	152	90	147	145
ENSMUSG00000024259	chr18	Slc25a46	3.2E+07	3.2E+07	4371	-0.56863259	5.88100331	0.0021004	0.005903723	0.03969	-1	1036	674	1466	1143	1057	1093	1254	756	841	973
ENSMUSG00000042133	chr2	Ppig	7E+07	7E+07	8122	-0.53967768	4.949229666	0.0021017	0.005906339	0.03483	-1	549	415	786	523	488	607	657	388	458	502
ENSMUSG00000025034	chr19	Trim8	4.7E+07	4.7E+07	3230	0.562278947	5.179263747	0.0021032	0.00590924	0.03813	1	326	341	478	391	694	1018	809	714	1001	901
ENSMUSG00000032350	chr9	Gclc	7.8E+07	7.8E+07	3423	-0.65776527	3.302276514	0.0021045	0.005911955	0.0483	-1	158	105	264	171	233	197	217	111	123	146
ENSMUSG00000027397	chr2	Slc20a1	1.3E+08	1.3E+08	5580	0.700727992	3.852159029	0.0021064	0.005916104	0.05723	1	122	128	151	136	297	390	381	274	305	486
ENSMUSG00000076617	chr12	Ighm	1.1E+08	1.1E+08	1886	1.254482588	6.788919676	0.002107	0.005916366	0.19163	1	597	573	921	344	2827	2160	6111	2130	3208	2546
ENSMUSG00000073616	chr1	Myeov2	9.3E+07	9.3E+07	1499	0.568881209	5.679450507	0.0021186	0.005947963	0.03962	1	565	436	647	600	891	1391	1081	1074	1395	1330
ENSMUSG00000043881	chr14	Kbtbd7	7.9E+07	7.9E+07	4529	-0.72976662	2.87989293	0.0021243	0.005962634	0.05821	-1	124	93	179	152	144	93	164	84	95	130
ENSMUSG00000055994	chr8	Nod2	8.9E+07	8.9E+07	5014	1.043585175	0.417033261	0.0021252	0.005964031	0.08327	1	10	5	15	9	22	38	34	30	31	34
ENSMUSG00000033953	chr11	Ppp3r1	1.7E+07	1.7E+07	3228	-0.61097405	7.388370762	0.0021277	0.005969736	0.04671	-1	3344	2328	3338	2691	3507	3053	3389	2123	2738	2427
ENSMUSG00000019966	chr10	Kitl	1E+08	1E+08	5765	-0.61453185	4.304973519	0.0021307	0.005976961	0.04457	-1	303	216	613	355	365	372	425	224	246	358
ENSMUSG00000000301	chr11	Pemt	6E+07	6E+07	2104	0.906041174	1.591286524	0.0021331	0.005982486	0.07786	1	21	27	28	28	47	94	67	47	106	78
ENSMUSG00000021576	chr13	Pdcd6	7.4E+07	7.4E+07	1524	0.535333719	4.444840507	0.0021347	0.005985755	0.03356	1	236	174	316	225	414	613	551	410	497	585
ENSMUSG00000103212	chr1	Ptpn4	1.2E+08	1.2E+08	1788	0.692914888	3.069907045	0.0021441	0.006010939	0.05314	1	81	53	101	105	148	252	182	182	191	245
ENSMUSG00000027322	chr2	Siglec1	1.3E+08	1.3E+08	7143	1.443644811	2.741503646	0.0021471	0.006018225	0.23736	1	32	82	9	42	79	369	177	92	251	137
ENSMUSG00000024052	chr17	Lpin2	7.1E+07	7.1E+07	12233	0.732241679	2.656982386	0.0021492	0.006022927	0.05739	1	49	55	90	51	112	189	187	119	163	143
ENSMUSG00000045576	chr3	St7l	1E+08	1E+08	7583	-0.62568832	3.505073137	0.0021524	0.006030546	0.04406	-1	184	186	235	205	208	194	217	161	179	159
ENSMUSG00000045917	chr4	6330416G13Rik	6.4E+07	6.4E+07	3974	-0.52490014	4.250275919	0.0021586	0.006046756	0.03182	-1	270	239	411	377	408	348	356	224	377	310
ENSMUSG00000099112	chr15	Gm27406	1E+08	1E+08	182	-0.55751961	4.023173892	0.002163	0.006057831	0.036	-1	254	233	309	312	340	317	354	167	264	271
ENSMUSG00000031877	chr8	Ces2g	1E+08	1E+08	2859	1.490376386	1.924176358	0.0021668	0.006067482	0.245	1	24	35	10	16	54	224	31	87	139	83
ENSMUSG00000024782	chr19	Ak3	2.9E+07	2.9E+07	3120	-0.58753208	6.312480124	0.0021758	0.006091327	0.04299	-1	1304	903	1724	1274	2171	1495	1640	904	1294	1289
ENSMUSG00000066068	chr2	Gm13611	3.2E+07	3.2E+07	318	0.99548371	1.282402664	0.0021781	0.006096595	0.09542	1	21	13	31	24	29	72	32	64	79	64
ENSMUSG00000028496	chr4	Mllt3	8.8E+07	8.8E+07	12004	-0.67371062	6.829661345	0.0021794	0.006096957	0.05688	-1	2477	1800	2171	2098	1721	2131	2351	1268	1848	1546
ENSMUSG00000080741	chr13	Gm11398	2.4E+07	2.4E+07	320	-1.01220534	1.24905312	0.0021795	0.006096957	0.09909	-1	49	32	71	49	32	41	40	29	31	16
ENSMUSG00000092243	chr17	Gm7030	3.6E+07	3.6E+07	927	1.348673455	1.336994559	0.0021794	0.006096957	0.19469	1	20	14	13	7	49	144	40	37	65	79
ENSMUSG00000041483	chr1	Zfp281	1.4E+08	1.4E+08	4937	-0.64112755	3.46764738	0.0021831	0.006105643	0.04652	-1	207	128	274	228	181	201	214	143	139	191
ENSMUSG00000006941	chr9	Eif1b	1.2E+08	1.2E+08	917	0.495011876	5.02034555	0.0021844	0.006107598	0.02927	1	428	276	485	364	489	881	726	666	813	803

ENSMUSG00000037295	chr4	Ldlrap1	1.3E+08	1.3E+08	3829	0.644405379	3.546173685	0.0021846	0.006107598	0.0472	1	132	92	134	122	208	321	234	255	330	304
ENSMUSG00000031967	chr8	Afg3l1	1.2E+08	1.2E+08	4757	-0.57523295	6.149533223	0.0021865	0.006111519	0.04116	-1	1141	872	1723	1434	1299	1280	1497	809	1211	1140
ENSMUSG00000036450	chr19	Hif1an	4.5E+07	4.5E+07	6606	-0.70414262	7.945260192	0.0021889	0.006117004	0.06241	-1	4212	3190	6499	5572	3664	3614	5625	2615	4140	3509
ENSMUSG00000022822	chr16	Abcc5	2E+07	2E+07	10592	-0.6111719	5.955248969	0.0021914	0.006122715	0.04649	-1	1170	978	1356	1103	945	1107	1231	623	1102	1073
ENSMUSG00000040383	chr2	Aqr	1.1E+08	1.1E+08	11805	-0.60321115	4.022743763	0.0021975	0.006138702	0.0425	-1	276	218	370	338	267	316	336	228	198	248
ENSMUSG00000052609	chr12	Plekhg3	7.7E+07	7.7E+07	4955	0.669196039	3.563080383	0.0022032	0.006151988	0.05121	1	118	93	126	116	240	343	266	217	339	324
ENSMUSG00000070814	chr7	6330408A02Rik	1.3E+07	1.3E+07	11662	-0.57656541	4.912545498	0.0022028	0.006151988	0.04033	-1	523	308	721	658	550	561	682	287	531	476
ENSMUSG00000079478	chr19	Sssca1	5728088	5728868	3083	0.59523215	5.649607717	0.0022074	0.006162685	0.04384	1	511	384	667	537	988	1496	1131	834	1546	1280
ENSMUSG00000087090	chr7	Nctc1	1.4E+08	1.4E+08	3438	-0.65481299	6.258363461	0.0022131	0.00617722	0.05369	-1	1529	1297	1454	1060	1580	1294	1578	705	1285	1379
ENSMUSG00000059851	chr7	Suv420h2	4740115	4740181	4001	0.697812713	3.464873431	0.0022188	0.006192089	0.05583	1	118	79	123	111	209	361	228	170	297	361
ENSMUSG00000005779	chr3	Psmb4	9.5E+07	9.5E+07	1384	0.590402092	7.275630455	0.0022246	0.006206865	0.04396	1	1727	1251	2346	1839	2297	4471	3243	2983	4245	4301
ENSMUSG00000014776	chr8	Nol3	1.1E+08	1.1E+08	2869	0.629147879	6.661804379	0.0022297	0.006220032	0.04978	1	1038	611	1899	1300	1370	2607	2677	1751	2803	2925
ENSMUSG00000097632	chr19	4930552P12Rik	5.6E+07	5.6E+07	2496	-0.99065665	0.619952197	0.0022312	0.006222931	0.08054	-1	27	16	48	32	26	21	21	12	26	21
ENSMUSG00000030432	chr7	Rpl28	4792874	4792998	1138	0.636615699	7.768822929	0.0022349	0.006231812	0.05127	1	2109	1578	3233	2938	3303	5820	4430	4039	6650	6494
ENSMUSG00000019943	chr10	Atp2b1	9.9E+07	9.9E+07	7130	-0.68160822	6.074918454	0.0022486	0.006268957	0.05821	-1	1235	829	1786	1458	989	1098	1628	715	879	1084
ENSMUSG00000016024	chr2	Lbp	1.6E+08	1.6E+08	4831	0.88207276	4.863108313	0.0022495	0.006270114	0.09595	1	173	262	210	234	683	960	613	766	667	825
ENSMUSG00000030123	chr6	Plxnd1	1.2E+08	1.2E+08	7192	0.606337765	6.206963618	0.0022545	0.006282958	0.04611	1	718	562	1117	727	1429	2196	1705	1400	2025	1903
ENSMUSG00000027524	chr2	Edn3	1.7E+08	1.7E+08	4113	-1.29229729	0.142801258	0.0022576	0.00629007	0.14282	-1	27	17	38	8	21	15	19	11	10	6
ENSMUSG00000031862	chr8	Atp13a1	7E+07	7E+07	3915	0.512133968	4.278632894	0.002258	0.00629007	0.03036	1	225	164	282	234	308	508	452	327	535	533
ENSMUSG00000071796	chr8	6820431F20Rik	2E+07	2E+07	5006	-1.17390095	0.605139145	0.0022584	0.00629007	0.12809	-1	50	25	20	23	29	22	22	19	13	15
ENSMUSG00000040620	chr11	Dhx33	7.1E+07	7.1E+07	10031	-0.61438081	3.538572968	0.002261	0.006296089	0.04302	-1	221	176	201	190	253	240	177	164	174	185
ENSMUSG00000031511	chr8	Arhgef7	1.2E+07	1.2E+07	13075	-0.61395281	5.733325114	0.002263	0.006300389	0.04693	-1	778	528	1565	1155	979	898	1037	622	945	856
ENSMUSG00000044857	chr17	Lemd2	2.7E+07	2.7E+07	2595	0.536991511	5.434276718	0.0022641	0.006302004	0.03547	1	439	358	680	588	628	1200	943	752	1293	1112
ENSMUSG00000030980	chr7	Knop1	1.2E+08	1.2E+08	5871	-0.59820205	5.851420111	0.0022655	0.006302645	0.04469	-1	1014	783	1342	1169	915	903	1287	649	942	989
ENSMUSG00000043587	chr9	Pxylp1	9.7E+07	9.7E+07	6148	0.855712402	1.718126131	0.002265	0.006302645	0.07013	1	38	28	31	28	43	121	86	67	59	90
ENSMUSG00000062866	chr10	Phactr2	1.3E+07	1.3E+07	11688	-0.52263012	4.377571021	0.0022656	0.006302645	0.03224	-1	343	268	509	350	389	414	393	214	337	425
ENSMUSG00000031712	chr8	Il15	8.2E+07	8.2E+07	1908	-0.79251426	3.530164504	0.0022666	0.006304185	0.07439	-1	219	186	325	241	111	179	218	138	158	175
ENSMUSG00000034616	chr19	Ssh3	4261668	4262632	2740	0.768160332	2.778478883	0.0022676	0.006305626	0.06458	1	64	64	72	59	117	235	187	91	169	215
ENSMUSG00000030096	chr6	Slc6a6	9.2E+07	9.2E+07	6169	-0.6677167	6.448542369	0.0022721	0.006316964	0.05618	-1	1321	1284	2309	1716	1469	1442	2166	874	1190	1397
ENSMUSG00000078317	chrX	F8a	7.3E+07	7.3E+07	2505	0.650805949	3.535970573	0.0022729	0.006317851	0.04862	1	104	86	148	156	191	308	229	226	369	312
ENSMUSG00000001289	chr15	Pfdn5	1E+08	1E+08	1394	0.578667774	6.714204246	0.002274	0.006319642	0.04219	1	1229	939	1401	1224	1571	3050	2198	2026	2780	2939
ENSMUSG00000049232	chr6	Tigd2	5.9E+07	5.9E+07	3007	-0.62475204	3.815234234	0.0022763	0.006324867	0.04555	-1	234	183	421	228	235	283	280	185	183	211
ENSMUSG00000031543	chr8	Ank1	2.3E+07	2.3E+07	13527	-0.761366	9.237040072	0.002279	0.006331018	0.07357	-1	11379	11757	10366	12044	9263	7959	11153	6645	11639	8847
ENSMUSG00000026764	chr2	Kif5c	5E+07	5E+07	7142	1.212465927	2.074111051	0.0022814	0.006336526	0.16038	1	43	53	12	21	42	179	105	84	125	102
ENSMUSG00000070572	chr4	Trmt112-ps2	1.5E+08	1.5E+08	378	1.169370182	0.157764553	0.002289	0.006356382	0.09933	1	6	7	8	8	17	36	18	26	33	27
ENSMUSG00000048442	chr11	Smim5	1.2E+08	1.2E+08	1649	1.181807666	0.313623535	0.0022915	0.00636209	0.12081	1	8	3	14	11	17	43	24	37	19	34
ENSMUSG00000022833	chr16	Ccdc14	3.5E+07	3.5E+07	4107	-0.83832037	1.746962301	0.0022941	0.006367262	0.07171	-1	72	46	82	61	56	64	62	22	45	56
ENSMUSG00000024054	chr17	Smchd1	7.1E+07	7.1E+07	19319	-0.57882886	3.895408138	0.0022943	0.006367262	0.03911	-1	269	172	364	283	265	323	317	151	220	239
ENSMUSG00000021932	chr14	Rnaseh2b	6.2E+07	6.2E+07	6243	0.697155419	2.587464618	0.0022992	0.006379531	0.05064	1	61	56	67	60	94	193	142	127	144	145
ENSMUSG00000046791	chr12	2410016O06Rik	8.4E+07	8.4E+07	2346	0.743809101	2.402843683	0.0023078	0.006402234	0.059	1	48	36	77	59	77	174	92	114	143	143
ENSMUSG00000005371	chr17	Fbxo11	8.8E+07	8.8E+07	4144	-0.5586659	5.366938341	0.0023181	0.006428156	0.03866	-1	748	564	929	658	809	808	954	537	571	590
ENSMUSG00000038838	chr17	Vars2	3.6E+07	3.6E+07	5460	-0.59595802	3.916956037	0.0023179	0.006428156	0.04143	-1	262	139	426	285	296	255	300	178	254	255
ENSMUSG00000049107	chr6	Ntf3	1.3E+08	1.3E+08	1427	0.99861058	1.513347917	0.0023218	0.006437018	0.10364	1	29	17	38	16	40	85	42	81	66	93
ENSMUSG00000098416	chr15	Mir7117	2.8E+07	2.8E+07	65	-1.66337666	-0.11014318	0.0023234	0.006440427	0.25243	-1	22	10	32	22	13	7	21	10	2	1
ENSMUSG00000037190	chr9	Cyb561d2	1.1E+08	1.1E+08	1974	0.738171679	2.214770905	0.0023259	0.006443863	0.05567	1	41	35	59	43	82	153	117	87	124	106
ENSMUSG00000042472	chr12	Zfp410	8.4E+07	8.4E+07	2697	-0.53281898	4.276540183	0.0023253	0.006443863	0.03359	-1	336	267	395	374	339	412	373	240	269	350
ENSMUSG00000067377	chrX	Tspan6	1.3E+08	1.3E+08	2060	0.83901196	2.33868231	0.0023263	0.006443863	0.07649	1	40	35	75	48	75	229	96	108	99	128
ENSMUSG00000100455	chr1	Gm29170	1.4E+08	1.4E+08	3666	-0.8543098	2.188902695	0.0023265	0.006443863	0.07904	-1	78	84	122	81	64	59	57	65	76	67
ENSMUSG00000043889	chr13	Gm8399	8.1E+07	8.1E+07	1119	1.070324732	0.562245013	0.0023273	0.006444785	0.09673	1	10	7	9	18	22	41	44	35	27	40
ENSMUSG00000031570	chr8	Ppapdc1b	2.6E+07	2.6E+07	2546	0.750980168	3.072841718	0.0023283	0.006446151	0.06338	1	69	86	70	98	137	301	192	158	227	205
ENSMUSG00000028668	chr4	Tceb3	1.4E+08	1.4E+08	4708	-0.57867913	5.983800091	0.0023315	0.006453839	0.04209	-1	1078	825	1499	1215	1118	1087	1418	775	1058	922
ENSMUSG00000069237	chr13	C78339	4.7E+07	4.7E+07	3827	-0.56755434	5.563978838	0.0023362	0.006465469	0.04027	-1	898	727	851	788	922	947	994	510	719	820
ENSMUSG00000054364	chr12	Rhob	8497763	8499985	2223	0.647121459	5.697060706	0.0023377	0.006468498	0.05266	1	461	346	694	538	1128	1311	1306	980	1357	1575
ENSMUSG00000046027	chr7	Stard5	8.4E+07	8.4E+07	5450	0.839578003	2.493188687	0.002339	0.006470801	0.07774	1	45	50	50	41	114	185	149	101	132	169
ENSMUSG00000035399	chr2	Oser1	1.6E+08	1.6E+08	2600	-0.6537391	3.632247935	0.0023409	0.006474731	0.05005	-1	244	179	293	201	215	251	277	154	146	169
ENSMUSG00000054128	chr17	H2-T3	3.6E+07	3.6E+07	2728	1.601398713	-0.04698183	0.0023437	0.006481327	0.23728	1	6	2	3	1	20	46	15	13	25	33
ENSMUSG00000045667	chr11	Smtnl2	7.2E+07	7.2E+07	3815	-0.71562074	7.834156248	0.0023602	0.006525616	0.06539	-1	3340	3083	3733	4017	7558	4075	4630	2220	4192	2989
ENSMUSG00000028945	chr5	Rheb	2.5E+07	2.5E+07	5540	-0.55379546	5.95294354	0.0023661	0.0065407	0.03862	-1	1120	819	1262	1148	1194	1204	1347	753	980	938
ENSMUSG00000054252	chr5	Fgfr3	3.4E+07	3.4E+07	6907	0.883483796	1.597082165	0.0023675	0.006540714	0.07645	1	17	28	50	25	35	89	75	64	64	95
ENSMUSG00000057036	chr3	Gm7536	2.4E+07	2.4E+07	444	0.551415672	5.158448171	0.0023668	0.006540714	0.03735	1	449	351	504	370	495	1157	658	722	883	954
ENSMUSG00000065947	chrMT	mt-Nd4l	9877	10173	297	-1.69045923	1.461973303	0.0023671	0.006540714	0.32265	-1	51	23	58	109	76	10	85	7	22	11
ENSMUSG00000024327	chr17	Slc39a7	3.4E+07	3.4E+07	2594	0.558187868	6.403693526	0.0023698	0.00654574	0.03946	1	954	679	1210	1070	1317	2580	1850	1589	2244	2184
ENSMUSG00000098148	chr8	Gm20204	1.2E+08	1.2E+08	5220	0.68431969	3.303070765	0.0023735	0.006554456	0.05396	1	108	77	114	86	188	261	238	225	217	288
ENSMUSG00000038002	chr17	Cramp1l	2.5E+07	2.5E+07	7517	-0.61193323	3.087005058	0.002374	0.006554538	0.04124	-1	151	106	177	149	191	165	169	101	115	143
ENSMUSG00000018378	chr11	Cuedc1	8.8E+07	8.8E+07	5779	-0.60822231	7.885599827	0.0023746	0.006555091	0.0474	-1	3962	3290	5265	4426	4610	3450	4429	2741	4534	4220
ENSMUSG00000030730	chr7	Atp2a1	1.3E+08	1.3E+08	3483	-0.6697883	14.78099194	0.0023785	0.006564419	0.05768	-1	506765	388290	548247	610591	536328	384898	543816	302913	564798	455656
ENSMUSG00000026596	chr1	Abl2	1.6E+08	1.6E+08	10800	-0.57362417	4.730533657	0.0023791	0.006564998	0.04026	-1	420	350	695	557	374	478	564	317	422	431

ENSMUSG00000020108	chr10	Ddit4	6E+07	6E+07	1685	0.746127185	3.086174416	0.0023895	0.006592218	0.06449	1	58	61	164	77	130	298	212	182	225	168
ENSMUSG00000058729	chr1	Lin9	1.8E+08	1.8E+08	7244	-0.89308557	2.272540738	0.002399	0.006617166	0.08927	-1	140	59	101	54	114	72	100	40	64	73
ENSMUSG00000021668	chr13	Polk	9.6E+07	9.6E+07	4289	-0.93902202	3.103370272	0.0024003	0.006619472	0.10556	-1	177	117	170	105	291	126	243	66	93	89
ENSMUSG00000019986	chr10	Ahi1	2.1E+07	2.1E+07	5093	0.937754614	1.15760304	0.0024038	0.006627759	0.08007	1	20	17	21	16	35	92	55	33	52	59
ENSMUSG00000072720	chr5	Myo18b	1.1E+08	1.1E+08	10698	-0.73385488	8.415661342	0.0024171	0.00666311	0.06914	-1	5233	3997	9606	8617	5199	4565	6949	3250	5884	6085
ENSMUSG00000070056	chr8	Mfhas1	3.6E+07	3.6E+07	6666	0.638955164	3.039264767	0.0024195	0.006668609	0.0454	1	78	60	151	95	105	237	242	138	204	208
ENSMUSG00000022477	chr15	Aco2	8.2E+07	8.2E+07	3892	-0.77182925	10.85581684	0.0024202	0.006669052	0.07654	-1	27441	17389	62133	44876	31415	26138	40027	18658	27767	30026
ENSMUSG00000026098	chr1	Pms1	5.3E+07	5.3E+07	7542	-0.79822553	1.382816049	0.0024242	0.00667874	0.05773	-1	40	35	68	46	56	37	41	34	36	41
ENSMUSG00000029276	chr5	Glmn	1.1E+08	1.1E+08	2688	-0.84136982	2.509491419	0.0024294	0.006691707	0.08107	-1	120	119	95	92	96	128	77	50	93	77
ENSMUSG00000027194	chr2	Ttc17	9.4E+07	9.4E+07	8984	-0.55886591	4.627047973	0.0024315	0.006695638	0.03816	-1	414	350	534	523	371	410	515	301	448	389
ENSMUSG00000028873	chr4	Cdca8	1.2E+08	1.2E+08	5177	1.166453743	0.05184124	0.0024317	0.006695638	0.10668	1	7	2	10	11	13	43	23	19	29	17
ENSMUSG00000033166	chr14	Dis3	9.9E+07	9.9E+07	3722	-0.64960834	3.074890361	0.0024333	0.006697298	0.0476	-1	138	114	191	169	159	187	160	108	110	111
ENSMUSG00000069208	chr13	Zfp825	7.4E+07	7.4E+07	822	-0.86253901	2.21357537	0.0024331	0.006697298	0.08239	-1	99	93	89	81	66	88	83	56	55	54
ENSMUSG00000022528	chr16	Hes1	3E+07	3E+07	2037	0.922192688	4.046094632	0.0024371	0.006706569	0.10587	1	88	49	275	235	268	403	356	358	448	634
ENSMUSG00000049580	chr7	Tsku	9.8E+07	9.8E+07	2859	1.189743063	1.862202071	0.0024452	0.006727456	0.16108	1	25	12	18	25	89	134	68	87	108	103
ENSMUSG00000001517	chr6	Foxm1	1.3E+08	1.3E+08	5498	1.093142281	0.182588215	0.0024459	0.006727937	0.09181	1	9	4	7	11	18	27	35	23	29	27
ENSMUSG00000034040	chr5	Wbscr17	1.3E+08	1.3E+08	8989	0.800438869	4.019415863	0.0024498	0.006737478	0.07929	1	94	89	284	152	322	382	653	291	410	388
ENSMUSG00000021810	chr14	Ecd	2E+07	2E+07	3125	-0.52523775	5.358984299	0.0024532	0.006745363	0.03442	-1	685	541	872	822	720	747	856	550	700	618
ENSMUSG00000041729	chr9	Coro2b	6.2E+07	6.2E+07	5919	0.730984163	3.497074634	0.0024542	0.006746978	0.06367	1	77	88	130	114	242	371	266	184	334	304
ENSMUSG00000092203	chr17	1110038B12Rik	3.5E+07	3.5E+07	1811	0.692280196	2.798743191	0.0024595	0.006760086	0.05242	1	82	59	87	65	102	224	143	158	162	180
ENSMUSG00000032468	chr9	Armc8	9.9E+07	9.9E+07	6531	-0.53769436	5.289281283	0.0024707	0.006789566	0.03618	-1	688	570	787	718	686	746	858	479	557	674
ENSMUSG00000003500	chr6	Impdh1	2.9E+07	2.9E+07	3294	0.594344987	4.729672712	0.0024746	0.00679773	0.04385	1	261	176	351	285	573	726	601	525	751	674
ENSMUSG00000047714	chr16	Ppp1r2	3.1E+07	3.1E+07	4440	-0.58514055	6.822021337	0.0024744	0.00679773	0.044	-1	2037	1532	2375	2205	2046	2164	2384	1309	1658	1926
ENSMUSG00000026662	chr2	Sephs1	4881564	4881860	5925	-0.49256875	4.707566385	0.0024838	0.006821536	0.02947	-1	450	392	497	393	547	502	492	331	458	462
ENSMUSG00000028165	chr3	Cisd2	1.4E+08	1.4E+08	4360	-0.53129971	5.037980648	0.0024883	0.00683187	0.035	-1	529	401	819	672	525	591	663	398	497	637
ENSMUSG00000031274	chrX	Col4a5	1.4E+08	1.4E+08	6718	-0.93940627	2.003299786	0.0024885	0.00683187	0.09804	-1	75	96	67	61	74	62	84	39	41	56
ENSMUSG00000035226	chr2	Rims4	1.6E+08	1.6E+08	4962	-0.94852458	2.435664403	0.00249	0.006834494	0.104	-1	94	34	149	173	98	101	66	42	83	91
ENSMUSG00000072772	chr6	Grcc10	1.2E+08	1.2E+08	1988	0.593427966	6.231359283	0.0024978	0.006854602	0.04502	1	823	618	1029	890	1208	2079	1447	1410	2294	2094
ENSMUSG00000079215	chr5	Zfp664	1.2E+08	1.2E+08	5729	-0.53167208	4.920335109	0.0024989	0.006856304	0.0349	-1	468	376	757	551	578	597	708	387	437	440
ENSMUSG00000022901	chr16	Cd86	3.7E+07	3.7E+07	3661	1.297383392	1.524521712	0.0025	0.006858014	0.18164	1	19	31	7	15	42	149	61	58	83	58
ENSMUSG00000059447	chr5	Hadhb	3E+07	3E+07	6595	-0.80814986	8.856346773	0.0025059	0.006872954	0.08428	-1	7851	3481	17339	9015	9454	7890	9526	4783	4955	8081
ENSMUSG00000048807	chr11	Slc35e4	3907021	3907984	3063	0.521641366	5.251780571	0.0025123	0.006888975	0.03395	1	375	363	634	392	624	930	939	770	1000	959
ENSMUSG00000019362	chr8	D8Ertd738e	8.4E+07	8.4E+07	659	0.56862097	6.619588593	0.0025198	0.006907501	0.0416	1	1059	708	1435	1360	1528	2702	2371	1796	2656	2637
ENSMUSG00000038069	chr8	Cdkn2aip	4.8E+07	4.8E+07	3494	-0.65957556	2.783091363	0.00252	0.006907501	0.04803	-1	118	106	156	125	119	123	133	79	100	113
ENSMUSG00000002996	chr12	Hbp1	3.2E+07	3.2E+07	6167	-0.59347969	6.372303454	0.0025226	0.006913373	0.04525	-1	1638	1211	1725	1314	1555	1576	1802	1012	1214	1262
ENSMUSG00000029101	chr5	Rgs12	3.5E+07	3.5E+07	7910	0.763334869	2.719006484	0.0025237	0.006914816	0.06556	1	38	53	86	80	111	210	138	124	198	173
ENSMUSG00000026944	chr2	Abca2	2.5E+07	2.5E+07	8346	-0.57942861	5.142225614	0.0025242	0.006914951	0.04214	-1	475	411	1068	679	640	618	771	372	626	567
ENSMUSG00000034312	chr6	Iqsec1	9.1E+07	9.1E+07	7412	-0.59291775	6.263917446	0.0025278	0.006923455	0.04509	-1	1136	880	2068	1548	1491	1244	1601	882	1379	1252
ENSMUSG00000025538	chr5	Sumf2	1.3E+08	1.3E+08	2667	0.682527256	3.323468184	0.0025312	0.006930173	0.05495	1	99	68	143	83	199	284	226	177	297	281
ENSMUSG00000087119	chr3	Atg4a-ps	1E+08	1E+08	1185	-1.06353144	0.704728362	0.0025311	0.006930173	0.10901	-1	25	27	46	29	32	22	37	11	25	10
ENSMUSG00000038155	chr19	Gstp2	4040285	4040539	770	0.537506505	5.028893189	0.0025386	0.006948856	0.03576	1	401	332	476	331	453	835	690	604	1018	826
ENSMUSG00000020741	chr11	Cluh	7.5E+07	7.5E+07	6502	-0.73756704	7.510858549	0.0025408	0.006953515	0.07036	-1	2429	1591	6428	3826	3862	2884	3817	1867	2918	2777
ENSMUSG00000083061	chr11	Gm12191	5E+07	5E+07	348	0.877833155	2.016821954	0.002544	0.006960879	0.08164	1	33	36	30	40	68	87	133	69	115	121
ENSMUSG00000092781	chr10	Mir3057	8.1E+07	8.1E+07	91	-0.78140722	2.979285248	0.0025447	0.006961438	0.07095	-1	119	79	253	193	122	132	159	83	124	100
ENSMUSG00000030452	chr7	Nipa2	5.6E+07	5.6E+07	5386	-0.50331167	5.10233793	0.0025483	0.006968783	0.03155	-1	611	476	710	565	660	679	776	419	547	534
ENSMUSG00000037172	chr6	E330009J07Rik	4E+07	4E+07	7511	0.932046825	1.999803673	0.002548	0.006968783	0.09367	1	40	36	32	32	58	72	147	60	113	135
ENSMUSG00000005373	chr5	Mlxipl	1.4E+08	1.4E+08	5367	-0.61063846	5.93313243	0.0025491	0.006969436	0.04775	-1	871	804	1205	1474	1214	966	956	694	1124	1265
ENSMUSG00000018593	chr11	Sparc	5.5E+07	5.5E+07	3367	0.885331541	9.072007387	0.0025503	0.00697155	0.10121	1	4219	3781	5628	3233	12860	22268	12445	11778	14658	11536
ENSMUSG00000037736	chr5	Limch1	6.7E+07	6.7E+07	7411	-0.64954032	6.733625448	0.002554	0.006980145	0.05451	-1	1941	1347	2758	2250	1534	1950	2253	1367	1416	1593
ENSMUSG00000038812	chr19	Trmt112	6909698	6909855	1233	0.553968024	4.537952418	0.0025555	0.006981716	0.0373	1	282	232	273	250	366	669	456	453	669	589
ENSMUSG00000051495	chr8	Irf2bp2	1.3E+08	1.3E+08	5080	0.501514496	5.184604398	0.0025554	0.006981716	0.03118	1	409	360	494	433	567	1072	767	685	867	1009
ENSMUSG00000056900	chr3	Usp13	3.3E+07	3.3E+07	7599	-0.65397101	8.261341479	0.0025586	0.006988634	0.05564	-1	4939	3430	8747	6372	5461	5212	6956	3300	4588	4846
ENSMUSG00000019055	chr4	Plod1	1.5E+08	1.5E+08	6765	0.578772068	5.755153087	0.0025676	0.007011931	0.04284	1	490	363	929	752	836	1749	1189	966	1421	1405
ENSMUSG00000022802	chr16	Lmln	3.3E+07	3.3E+07	6511	-0.91826338	2.278019052	0.0025682	0.007012254	0.09612	-1	124	92	109	66	66	82	90	51	77	44
ENSMUSG00000057411	chr17	Fam173a	2.6E+07	2.6E+07	800	0.542077121	5.201084726	0.0025687	0.007012316	0.03682	1	410	320	454	464	619	988	752	667	1137	952
ENSMUSG00000028064	chr3	Sema4a	8.8E+07	8.8E+07	5406	1.342480774	3.460785023	0.0025777	0.007032734	0.22077	1	83	72	22	43	250	511	177	199	343	412
ENSMUSG00000038722	chr5	Bud31	1.5E+08	1.5E+08	1609	0.529377118	5.346719533	0.002577	0.007032734	0.03525	1	508	342	535	459	685	1278	827	766	1066	1036
ENSMUSG00000045094	chr18	Arhgef37	6.1E+07	6.1E+07	3234	-1.37792243	1.382972031	0.0025777	0.007032734	0.21524	-1	64	51	73	53	30	18	79	15	14	23
ENSMUSG00000025786	chr9	Zdhhc3	1.2E+08	1.2E+08	11846	-0.58830994	6.395390415	0.0025796	0.00703499	0.04468	-1	1569	1111	1815	1717	1369	1542	1696	976	1496	1285
ENSMUSG00000040287	chr10	Stac3	1.3E+08	1.3E+08	2543	-0.70228084	7.843455516	0.0025795	0.00703499	0.06414	-1	5173	4187	3723	3716	3791	3804	4027	2719	4033	3508
ENSMUSG00000098708	chr7	Gm27252	6.4E+07	6.4E+07	717	-1.07396493	0.426773982	0.0025808	0.007037114	0.10282	-1	18	27	27	32	23	22	25	11	17	10
ENSMUSG00000089857	chr8	Zfp882	7.2E+07	7.2E+07	3569	-0.95476165	1.200827046	0.0025867	0.007051754	0.09018	-1	59	26	59	35	44	31	51	21	30	24
ENSMUSG00000078349	chr4	AW011738	1.6E+08	1.6E+08	1848	-1.02197362	1.406054543	0.0025966	0.007077251	0.11473	-1	46	34	85	58	41	51	47	9	44	31
ENSMUSG00000022208	chr14	Jph4	5.5E+07	5.5E+07	6872	1.267992212	-0.15518238	0.0026025	0.007092111	0.10663	1	8	8	4	5	8	33	20	20	24	15
ENSMUSG00000035310	chr5	Lin54	1E+08	1E+08	5820	-0.77260173	2.171111882	0.0026068	0.007102335	0.06479	-1	62	54	119	85	112	79	103	40	60	61
ENSMUSG00000029338	chr5	Antxr2	9.8E+07	9.8E+07	5427	0.56859393	4.758405839	0.0026119	0.007114925	0.03999	1	356	260	271	275	463	744	810	474	666	654
ENSMUSG00000028291	chr4	Akirin2	3.5E+07	3.5E+07	1711	0.530491525	5.141512663	0.0026154	0.007122942	0.03533	1	434	276	560	489	432	1042	760	781	767	916

ENSMUSG00000028580	chr4	Pum1	1.3E+08	1.3E+08	6008	-0.49203156	5.219968648	0.0026192	0.007132094	0.03029	-1	585	456	807	749	704	706	735	510	636	607
ENSMUSG00000038695	chr7	Josd2	4.4E+07	4.4E+07	2466	0.48376293	5.114172927	0.0026261	0.007149508	0.02905	1	406	301	510	462	508	928	806	568	973	913
ENSMUSG00000032911	chr9	Cspg4	5.7E+07	5.7E+07	8050	0.762508341	4.596100593	0.0026366	0.007176571	0.07389	1	152	146	287	231	603	763	556	555	600	637
ENSMUSG00000032743	chr7	D430042O09Rik	1.3E+08	1.3E+08	7191	-0.68929788	2.791332211	0.0026381	0.00717841	0.05404	-1	135	103	159	113	124	147	140	77	92	92
ENSMUSG00000046764	chr6	A530053G22Rik	6E+07	6E+07	1526	-2.89974674	0.619428619	0.0026383	0.00717841	0.86089	-1	43	19	0	1	144	13	2	11	4	4
ENSMUSG00000027828	chr3	Ssr3	6.5E+07	6.5E+07	4172	-0.66969242	7.90944208	0.0026494	0.007206258	0.05869	-1	4344	4499	4034	4444	4120	4381	4591	3066	3602	3561
ENSMUSG00000062098	chr2	Btbd3	1.4E+08	1.4E+08	5776	-0.57297055	4.07157801	0.0026496	0.007206258	0.0399	-1	306	242	395	267	296	326	381	197	264	235
ENSMUSG00000048967	chr8	Yjefn3	7E+07	7E+07	808	0.699588858	3.351756783	0.0026504	0.007207119	0.05837	1	89	71	188	103	148	213	280	168	358	273
ENSMUSG00000030284	chr6	Creld1	1.1E+08	1.1E+08	3816	0.573250034	5.697526709	0.002654	0.007215679	0.04224	1	543	376	729	572	1013	1440	1163	971	1485	1349
ENSMUSG00000097451	chr12	Rian	1.1E+08	1.1E+08	17475	0.88390425	3.584731249	0.002655	0.00721682	0.09492	1	153	133	90	106	117	578	222	281	247	275
ENSMUSG00000029599	chr5	Ddx54	1.2E+08	1.2E+08	3929	0.510241217	5.157757855	0.0026599	0.007227512	0.03271	1	334	297	536	545	532	951	863	658	966	887
ENSMUSG00000031568	chr8	Rwdd4a	4.8E+07	4.8E+07	3352	-0.50247349	4.594535399	0.0026595	0.007227512	0.03093	-1	381	319	628	397	425	454	490	307	383	434
ENSMUSG00000041815	chr15	Poldip3	8.3E+07	8.3E+07	5679	0.512849742	4.905906213	0.0026722	0.007259384	0.03275	1	344	255	384	359	535	902	627	600	719	778
ENSMUSG00000070803	chr4	Cited4	1.2E+08	1.2E+08	1249	0.892969129	3.553720308	0.0026811	0.007282214	0.09901	1	95	70	173	54	255	284	328	223	450	272
ENSMUSG00000003429	chr7	Rps11	4.5E+07	4.5E+07	602	0.601963668	7.696465018	0.0026928	0.007312517	0.04757	1	2240	1862	2639	2441	3295	6148	4167	4295	5513	5629
ENSMUSG00000027932	chr3	Slc27a3	9E+07	9E+07	2569	0.873174237	2.245413565	0.0026944	0.007315414	0.08374	1	48	48	35	36	74	184	105	72	140	127
ENSMUSG00000026339	chr1	Ccdc93	1.2E+08	1.2E+08	11445	-0.5834559	4.213184359	0.0026955	0.0073169	0.04171	-1	303	224	532	351	286	382	338	259	264	285
ENSMUSG00000075585	chr5	6330403L08Rik	1.4E+08	1.4E+08	5522	-0.5608176	4.656157128	0.0026964	0.007317938	0.03938	-1	412	353	553	441	504	363	619	257	432	448
ENSMUSG00000025533	chr5	Asl	1.3E+08	1.3E+08	4563	0.722413313	3.368336962	0.0026971	0.007318583	0.06142	1	137	94	79	125	132	298	218	191	307	301
ENSMUSG00000048949	chrX	Gm6206	1E+08	1E+08	2199	-0.6521894	3.229655507	0.0027012	0.007328168	0.04973	-1	186	149	209	136	168	153	188	120	152	133
ENSMUSG00000048776	chr6	Pthlh	1.5E+08	1.5E+08	1603	1.212337663	0.644265813	0.0027053	0.007337877	0.15043	1	10	3	29	7	20	28	43	29	42	63
ENSMUSG00000036986	chr9	Pml	5.8E+07	5.8E+07	5571	0.747669063	3.046668627	0.002715	0.007362914	0.06588	1	74	56	91	94	153	298	179	118	280	200
ENSMUSG00000074657	chr10	Kif5a	1.3E+08	1.3E+08	6310	1.310883888	-0.43376722	0.0027156	0.007362914	0.09793	1	4	5	4	7	6	21	16	9	22	23
ENSMUSG00000033287	chr15	Kctd17	7.8E+07	7.8E+07	2134	0.841931019	3.857111631	0.0027204	0.007374632	0.08895	1	99	94	147	101	372	490	323	296	420	382
ENSMUSG00000026484	chr1	Rnf2	1.5E+08	1.5E+08	4127	-0.54316914	3.780732479	0.0027234	0.007381329	0.03505	-1	235	186	304	236	264	278	291	151	210	234
ENSMUSG00000043183	chr13	Simc1	5.5E+07	5.5E+07	5675	-0.90910926	1.742290846	0.002724	0.007381541	0.09058	-1	83	60	45	63	60	66	55	30	37	51
ENSMUSG00000021928	chr14	Ebpl	6.1E+07	6.1E+07	2077	0.82656466	3.380318462	0.0027278	0.007390342	0.0825	1	116	105	83	81	164	353	154	230	329	287
ENSMUSG00000021768	chr14	Dusp13	2.2E+07	2.2E+07	2744	-0.63698226	7.425940048	0.0027294	0.007393285	0.05337	-1	2986	2863	3160	3012	3467	2678	3617	1734	3099	2921
ENSMUSG00000031327	chrX	Chic1	1E+08	1E+08	7375	1.119094618	-0.06508831	0.0027465	0.007438323	0.09211	1	8	2	11	9	10	33	19	17	19	30
ENSMUSG00000035713	chr7	Usp35	9.7E+07	9.7E+07	5285	1.000954612	0.857203307	0.0027514	0.007450142	0.09405	1	10	12	22	15	27	69	37	44	30	51
ENSMUSG00000020454	chr11	Eif4enif1	3202392	3202556	6370	-0.53616425	4.976588483	0.002759	0.007469047	0.03643	-1	539	399	781	605	493	616	714	361	510	478
ENSMUSG00000020935	chr11	Dcakd	1E+08	1E+08	2556	0.684505413	4.432587643	0.0027696	0.007496426	0.05972	1	156	106	430	325	289	592	509	417	621	597
ENSMUSG00000053565	chr7	Eif3k	2.9E+07	2.9E+07	773	0.564907122	6.318320244	0.0027708	0.007498304	0.04171	1	841	618	1188	1016	1281	2210	1680	1497	2227	2220
ENSMUSG00000000934	chr15	Top1mt	7.6E+07	7.6E+07	1903	-0.59783233	3.52190766	0.0027799	0.007521392	0.04235	-1	206	167	199	187	272	191	180	153	214	195
ENSMUSG00000090248	chr2	Gm14027	1.3E+08	1.3E+08	622	-1.2046829	0.275565251	0.0027804	0.007521392	0.13106	-1	35	12	32	20	21	15	20	9	5	22
ENSMUSG00000063358	chr16	Mapk1	1.7E+07	1.7E+07	7110	-0.58762375	6.926718059	0.0027847	0.007531435	0.04548	-1	2225	1700	2484	2312	2215	2293	2583	1560	1751	1893
ENSMUSG00000031751	chr8	Amfr	9.4E+07	9.4E+07	3953	-0.60583223	7.592011023	0.002788	0.007538869	0.04853	-1	3413	2505	4312	3769	3608	3222	4422	2163	3157	2973
ENSMUSG00000022146	chr15	Osmr	6813577	6815928	12113	0.644505788	3.354461344	0.0027943	0.0075544	0.04912	1	97	82	143	101	184	377	281	192	199	240
ENSMUSG00000033016	chr18	Nfatc1	8.1E+07	8.1E+07	7433	-0.52757168	5.224165589	0.002796	0.00755757	0.03554	-1	588	442	964	721	657	633	821	446	649	625
ENSMUSG00000029191	chr5	Rfc1	6.5E+07	6.5E+07	6000	-0.47191926	4.947580253	0.0028055	0.00758191	0.02787	-1	513	382	731	483	623	590	645	381	501	566
ENSMUSG00000028017	chr3	Egf	1.3E+08	1.3E+08	4757	-0.7782996	5.45632183	0.0028062	0.007582255	0.079	-1	845	906	764	887	564	651	1068	379	689	607
ENSMUSG00000040447	chr11	Spns2	7.2E+07	7.2E+07	4083	-1.22157986	5.324750421	0.00282	0.00761826	0.19189	-1	295	379	1612	307	2086	477	901	267	429	458
ENSMUSG00000030101	chr6	Sumf1	1.1E+08	1.1E+08	3405	0.555606138	4.517096985	0.0028288	0.007640514	0.03853	1	249	211	312	200	439	760	573	415	525	555
ENSMUSG00000028949	chr5	Smarcd3	2.5E+07	2.5E+07	4545	-0.62022131	7.139601862	0.0028406	0.007670833	0.05094	-1	2148	1947	2895	2819	3115	2059	2940	1460	2827	2277
ENSMUSG00000034544	chr3	Rsrc1	6.7E+07	6.7E+07	12000	-0.60211963	4.115030458	0.0028445	0.007679917	0.04528	-1	356	287	267	279	338	375	300	209	268	276
ENSMUSG00000037411	chr5	Serpine1	1.4E+08	1.4E+08	3024	1.017299941	3.177725649	0.0028454	0.007680788	0.13023	1	71	26	125	91	161	316	141	333	204	190
ENSMUSG00000020056	chr10	Ccdc53	8.8E+07	8.8E+07	4536	0.525300808	4.516722411	0.0028466	0.007682573	0.03415	1	290	210	302	253	355	697	449	449	626	555
ENSMUSG00000020402	chr11	Vdac1	5.2E+07	5.2E+07	2620	-0.64303214	10.1526087	0.0028501	0.007689531	0.05514	-1	19521	11816	32074	23853	20001	18571	22795	13700	17863	19133
ENSMUSG00000027496	chr2	Aurka	1.7E+08	1.7E+08	2531	-0.93109526	3.083727046	0.0028503	0.007689531	0.10721	-1	231	178	92	119	168	126	121	113	140	91
ENSMUSG00000010048	chr9	Ifrd2	1.1E+08	1.1E+08	2637	-0.52275919	5.207847672	0.002852	0.007692842	0.03502	-1	536	453	814	827	673	727	706	456	707	550
ENSMUSG00000024143	chr17	Rhoq	8.7E+07	8.7E+07	4151	-0.60777638	7.695316152	0.0028537	0.007693434	0.04908	-1	3571	2483	4905	3792	4407	3368	4837	2563	3228	3013
ENSMUSG00000030649	chr7	Anapc15	1E+08	1E+08	4737	0.498721392	4.019565922	0.0028538	0.007693434	0.02955	1	174	142	254	209	238	459	416	306	392	379
ENSMUSG00000038533	chr2	Cbfa2t2	1.5E+08	1.5E+08	8650	-0.48981855	4.713228823	0.0028539	0.007693434	0.02996	-1	420	348	580	516	438	497	532	342	447	436
ENSMUSG00000080776	chr11	Gm12174	4.7E+07	4.7E+07	813	0.796824789	3.067195365	0.0028567	0.00769945	0.0755	1	73	80	61	98	137	240	159	149	266	272
ENSMUSG00000005533	chr7	Igf1r	6.8E+07	6.8E+07	4489	-0.97164534	1.76061166	0.0028584	0.007701854	0.10457	-1	79	50	78	84	34	48	44	50	40	45
ENSMUSG00000027281	chr2	Slx4ip	1.4E+08	1.4E+08	5905	-0.92096492	1.858782247	0.0028587	0.007701854	0.09709	-1	59	69	95	59	65	55	86	25	60	33
ENSMUSG00000031388	chrX	Naa10	7.4E+07	7.4E+07	4132	0.485333037	4.972004254	0.0028594	0.007702222	0.02976	1	332	263	510	370	531	796	712	605	864	780
ENSMUSG00000026072	chr1	Il1r1	4E+07	4E+07	6363	0.680294176	3.600129327	0.0028605	0.007703795	0.05602	1	136	122	131	97	206	459	296	246	285	252
ENSMUSG00000098374	chr17	Gm28043	3E+07	3E+07	6521	-0.51900164	5.863807308	0.0028668	0.007719301	0.03514	-1	874	785	1329	1113	1087	1201	1146	724	936	972
ENSMUSG00000028847	chr4	Trappc3	1.3E+08	1.3E+08	1737	0.514691582	4.679405412	0.0028698	0.007724452	0.03329	1	285	205	379	269	483	769	536	492	657	652
ENSMUSG00000030805	chr7	Stx4a	1.3E+08	1.3E+08	2364	0.524240202	5.991979866	0.0028697	0.007724452	0.0359	1	784	543	919	695	1035	1837	1549	1146	1614	1639
ENSMUSG00000033444	chr10	Specc1l	7.5E+07	7.5E+07	6075	-0.56515108	6.125699612	0.0028723	0.00772952	0.04199	-1	1191	958	1605	1386	1117	1250	1368	827	1194	1209
ENSMUSG00000020661	chr12	Dnmt3a	3806007	3806232	16642	-0.60409289	6.233792288	0.0028737	0.007732027	0.04804	-1	1260	827	2023	1598	1257	1146	1423	908	1292	1399
ENSMUSG00000037349	chr19	Nudt22	6993018	6993202	1195	0.689805677	3.050187802	0.0028874	0.007767299	0.05669	1	77	53	141	85	131	245	156	151	221	272
ENSMUSG00000028089	chr3	Chd1l	9.8E+07	9.8E+07	3008	-0.53845731	4.215766894	0.0028952	0.007786679	0.03586	-1	285	239	466	343	337	314	374	193	354	340
ENSMUSG00000031095	chrX	Cul4b	3.9E+07	3.9E+07	3873	-0.58946425	3.445829104	0.0028965	0.00778866	0.04127	-1	211	148	240	157	227	202	225	133	158	179
ENSMUSG00000021288	chr12	Klc1	1.1E+08	1.1E+08	4070	0.536247546	6.38427771	0.0028972	0.007789175	0.03788	1	946	765	1271	962	1228	2303	1980	1573	2289	2068

ENSMUSG00000074746	chr19	Pdzd8	5.9E+07	5.9E+07	7076	-0.62981059	4.006319141	0.0029036	0.007804776	0.04966	-1	241	205	432	359	241	335	354	164	216	252
ENSMUSG00000032513	chr9	Gorasp1	1.2E+08	1.2E+08	3483	-0.54899261	4.529637612	0.0029077	0.007814379	0.03794	-1	378	274	557	514	352	410	437	283	443	364
ENSMUSG00000020283	chr11	Pex13	2.4E+07	2.4E+07	4644	-0.47431159	4.722735105	0.0029249	0.007859197	0.02807	-1	427	327	551	412	622	590	485	360	428	425
ENSMUSG00000074582	chr2	Arfgef2	1.7E+08	1.7E+08	8770	-0.59224391	5.174245741	0.0029273	0.007864059	0.04546	-1	502	404	1060	794	585	586	785	432	560	618
ENSMUSG00000033478	chr19	Fam160b1	5.7E+07	5.7E+07	5630	-0.62108887	3.732703229	0.0029336	0.007879429	0.04724	-1	181	137	408	257	269	264	270	151	183	220
ENSMUSG00000028857	chr4	Tmem222	1.3E+08	1.3E+08	2003	0.554534355	4.90541254	0.0029383	0.007890553	0.03946	1	318	241	401	322	581	820	584	583	878	796
ENSMUSG00000010517	chr4	Faf1	1.1E+08	1.1E+08	5093	-0.57307977	6.179655781	0.0029412	0.007896771	0.04344	-1	1191	973	1641	1456	1275	1389	1620	826	1084	1165
ENSMUSG00000021115	chr12	Vrk1	1.1E+08	1.1E+08	3796	0.693713339	2.551878641	0.0029455	0.007906891	0.05352	1	61	42	82	75	74	215	119	120	133	149
ENSMUSG00000032419	chr9	Tbx18	8.8E+07	8.8E+07	4718	1.134426647	0.831188527	0.0029467	0.007907035	0.13414	1	10	8	18	7	38	67	52	37	30	49
ENSMUSG00000086841	chr11	2410006H16Rik	6.3E+07	6.3E+07	462	0.772724758	3.665799941	0.0029467	0.007907035	0.07432	1	159	120	106	101	204	519	220	237	289	395
ENSMUSG00000033793	chr1	Atp6v1h	5070018	5070144	9746	0.634772714	4.556677602	0.0029496	0.007913384	0.05168	1	261	181	283	183	512	711	517	447	570	709
ENSMUSG00000021635	chr13	Rad17	1E+08	1E+08	2846	-0.57141843	4.096117551	0.0029504	0.007913985	0.0404	-1	278	196	464	319	307	335	369	232	236	246
ENSMUSG00000075514	chr2	Gm13375	2.1E+07	2.1E+07	854	0.828779348	2.487939263	0.0029577	0.007932021	0.08084	1	27	36	81	59	107	184	138	96	175	139
ENSMUSG00000031198	chrX	Fundc2	7.5E+07	7.5E+07	2785	-0.62408489	7.230434821	0.002972	0.007968815	0.05209	-1	2867	1994	3645	2972	2217	2689	3141	1717	2301	2461
ENSMUSG00000010660	chr9	Plcd1	1.2E+08	1.2E+08	2651	0.569962692	3.859134563	0.0029732	0.007970504	0.03958	1	156	130	212	140	247	413	289	278	411	385
ENSMUSG00000085342	chr11	Gm12254	5.9E+07	5.9E+07	471	0.664261049	3.817567477	0.0029773	0.00798013	0.055	1	127	107	154	195	243	359	267	251	430	465
ENSMUSG00000028706	chr4	Nsun4	1.2E+08	1.2E+08	5993	-0.54656831	4.630585336	0.002981	0.007988406	0.03795	-1	356	288	745	460	416	531	486	301	371	406
ENSMUSG00000001482	chr8	Def8	1.2E+08	1.2E+08	3988	-0.58687782	5.686016138	0.0029817	0.007988896	0.04533	-1	782	596	1393	1063	910	844	1190	570	868	810
ENSMUSG00000021662	chr13	Arhgef28	9.8E+07	9.8E+07	6259	-0.83262582	2.360431543	0.0029865	0.008000248	0.08048	-1	96	63	98	62	182	92	103	45	70	72
ENSMUSG00000053898	chr7	Ech1	2.9E+07	2.9E+07	2284	-0.83883132	8.178336586	0.0029899	0.008007635	0.09392	-1	4336	2049	11514	6183	5792	4554	6419	2836	3289	4642
ENSMUSG00000020114	chr10	Cand1	1.2E+08	1.2E+08	8357	0.507744365	4.673116968	0.0029918	0.008009705	0.03259	1	281	211	372	295	451	800	531	533	555	657
ENSMUSG00000038022	chr6	Fam188b	5.5E+07	5.5E+07	4270	0.828831928	1.689550862	0.0029913	0.008009705	0.06912	1	34	29	34	27	43	98	66	51	87	111
ENSMUSG00000006457	chr19	Actn3	4861223	4861503	2894	-0.75776337	12.29411529	0.0030036	0.008039802	0.07714	-1	110834	84670	67868	95448	101576	69829	82249	53765	110380	69706
ENSMUSG00000024608	chr18	Rps14	6.1E+07	6.1E+07	1384	0.588161234	8.273680527	0.0030065	0.008045932	0.04656	1	3468	2804	4040	3523	4887	9490	6477	6035	7995	8478
ENSMUSG00000061894	chr4	Zscan20	1.3E+08	1.3E+08	8375	-0.70292384	1.895226449	0.0030082	0.008049025	0.04997	-1	56	48	90	72	78	69	68	41	54	56
ENSMUSG00000025209	chr19	Peo1	4.5E+07	4.5E+07	3488	-0.66587811	5.393705575	0.0030111	0.008055221	0.05844	-1	643	581	981	1139	502	716	737	481	739	695
ENSMUSG00000060904	chr10	Arl1	8.9E+07	8.9E+07	2369	-0.59130799	6.509415714	0.0030118	0.008055494	0.04666	-1	1850	1299	1884	1549	1584	1914	1853	1153	1330	1311
ENSMUSG00000036299	chr18	BC031181	7.5E+07	7.5E+07	1047	0.559730721	5.322420284	0.0030197	0.008075199	0.04092	1	439	351	526	384	771	1184	824	825	1059	1005
ENSMUSG00000058492	chr9	Scp2-ps2	1.2E+08	1.2E+08	432	-0.73389786	2.389205629	0.0030261	0.008090732	0.0604	-1	90	61	135	80	132	93	107	69	56	75
ENSMUSG00000090210	chr3	Itga10	9.7E+07	9.7E+07	5186	1.004837163	1.201574785	0.0030303	0.008100317	0.10339	1	18	16	38	19	19	71	45	47	39	97
ENSMUSG00000025583	chr11	Rptor	1.2E+08	1.2E+08	13471	-0.64574163	5.429791308	0.0030378	0.008117412	0.055	-1	616	508	1153	1111	617	689	935	517	666	670
ENSMUSG00000058446	chr6	Znrf2	5.5E+07	5.5E+07	6176	-0.53355936	5.294121753	0.0030373	0.008117412	0.03708	-1	647	407	1007	635	905	778	875	463	553	674
ENSMUSG00000023266	chr17	Frs3	4.8E+07	4.8E+07	3128	-0.73543603	2.299176243	0.0030408	0.008122351	0.06159	-1	116	70	89	81	95	95	89	49	83	64
ENSMUSG00000063268	chr15	Parp10	7.6E+07	7.6E+07	4275	0.579396248	3.88836047	0.0030405	0.008122351	0.04137	1	145	125	217	157	261	533	294	256	371	388
ENSMUSG00000020258	chr9	Glyctk	1.1E+08	1.1E+08	4229	-0.86322068	1.207288555	0.0030571	0.008164254	0.07381	-1	26	40	50	46	55	36	39	19	37	34
ENSMUSG00000073233	chr12	Gm9144	7859827	7860076	1265	-1.03873736	0.348631328	0.003058	0.008165097	0.09212	-1	20	21	36	23	21	12	21	12	23	12
ENSMUSG00000027088	chr2	Phospho2	7E+07	7E+07	4335	-0.53497386	4.376063848	0.0030715	0.00819804	0.03623	-1	367	292	469	365	345	463	440	251	310	302
ENSMUSG00000032440	chr9	Tgfbr2	1.2E+08	1.2E+08	4785	0.581689708	5.978603916	0.0030709	0.00819804	0.04496	1	581	569	863	693	1157	2319	1610	1101	1483	1407
ENSMUSG00000042572	chr3	Ube2q1	9E+07	9E+07	3081	0.492818651	4.953686939	0.0030979	0.008266901	0.03115	1	323	279	415	366	577	861	751	553	718	864
ENSMUSG00000104348	chr1	RP23-59N15.4	1.9E+08	1.9E+08	2573	-1.02395819	0.856047524	0.0031025	0.008277689	0.10529	-1	33	18	69	35	25	25	31	16	29	17
ENSMUSG00000021578	chr13	Ccdc127	7.4E+07	7.4E+07	9559	-0.52675661	5.480799526	0.0031048	0.008282204	0.03656	-1	855	608	939	781	760	831	950	545	750	722
ENSMUSG00000031078	chr7	Cttn	1.4E+08	1.4E+08	4192	0.589433054	5.328974156	0.0031163	0.008311418	0.04588	1	399	312	521	385	868	1376	966	735	990	959
ENSMUSG00000034687	chr5	Fras1	9.6E+07	9.6E+07	15848	1.068046149	1.798910546	0.0031181	0.00831443	0.13029	1	59	20	38	26	17	93	65	95	110	95
ENSMUSG00000061013	chr18	Mkx	6910459	6910633	3925	1.119983525	0.645338798	0.0031289	0.008341862	0.12165	1	14	9	16	14	15	83	21	34	32	35
ENSMUSG00000090862	chr7	Rps13	1.2E+08	1.2E+08	582	0.585181591	7.237778893	0.0031327	0.008350408	0.04627	1	1674	1371	2229	1699	2182	4593	2940	3029	4060	4070
ENSMUSG00000051579	chrX	Tceal8	1.4E+08	1.4E+08	2563	0.592185532	3.750905488	0.0031343	0.008352871	0.04274	1	173	139	163	121	198	367	317	281	329	354
ENSMUSG00000027115	chr2	Kif18a	1.1E+08	1.1E+08	9832	-1.35199297	-0.27051168	0.0031515	0.008397088	0.15256	-1	8	13	31	19	11	6	17	6	9	5
ENSMUSG00000009030	chr2	Pdcl	3.7E+07	3.7E+07	3751	-0.56732908	3.707754767	0.0031545	0.008403524	0.03951	-1	233	154	323	234	240	251	293	148	196	205
ENSMUSG00000001870	chr17	Ltbp1	7.5E+07	7.5E+07	10480	0.559516468	4.471750409	0.0031674	0.00843314	0.04018	1	204	187	299	235	452	610	590	447	466	601
ENSMUSG00000029036	chr4	Atad3a	1.6E+08	1.6E+08	3765	-0.52445956	5.120593514	0.0031669	0.00843314	0.03579	-1	495	351	951	596	812	646	533	478	633	644
ENSMUSG00000036966	chr15	Spryd3	1E+08	1E+08	2927	0.542514135	4.048453068	0.0031669	0.00843314	0.03667	1	166	133	244	193	294	525	389	284	476	358
ENSMUSG00000030134	chr6	Rasgef1a	1.2E+08	1.2E+08	3236	1.286038048	-0.17552232	0.0031684	0.008434136	0.13503	1	10	1	8	10	4	29	31	9	20	24
ENSMUSG00000041035	chr19	Dpcd	4.6E+07	4.6E+07	1995	0.521418207	3.810006005	0.0031716	0.008441278	0.03289	1	157	115	216	158	230	418	335	231	356	371
ENSMUSG00000033068	chr2	Entpd6	1.5E+08	1.5E+08	4775	-0.6182145	3.648498886	0.0031723	0.0084414	0.04755	-1	204	163	217	208	359	242	189	126	259	212
ENSMUSG00000028639	chr4	Ybx1	1.2E+08	1.2E+08	2531	-0.5778956	8.840312993	0.0031749	0.008445051	0.04555	-1	7832	5805	11013	8290	8860	8521	9579	5255	7156	7854
ENSMUSG00000040093	chr2	Bmf	1.2E+08	1.2E+08	5253	0.750454903	2.429471448	0.0031746	0.008445051	0.06438	1	62	42	83	43	69	204	113	98	106	169
ENSMUSG00000026674	chr1	Ddr2	1.7E+08	1.7E+08	9264	0.688701223	5.410896099	0.0031758	0.008445901	0.06299	1	512	437	369	373	721	1613	869	932	841	1172
ENSMUSG00000097867	chr16	1110054M08Rik	2.4E+07	2.4E+07	1603	0.585012305	4.245809065	0.0031772	0.008448064	0.04338	1	205	173	236	246	276	542	321	373	590	504
ENSMUSG00000083773	chr2	Gm13394	2.9E+07	2.9E+07	1000	-0.69959328	9.561247249	0.0031905	0.008481801	0.06666	-1	11981	10060	16400	18707	13302	10484	16056	7442	15537	10443
ENSMUSG00000032181	chr9	Scg3	7.6E+07	7.6E+07	2249	1.086487033	1.314357017	0.0031962	0.008495411	0.12681	1	17	25	28	14	28	103	29	44	89	69
ENSMUSG00000039908	chr11	Slc26a11	1.2E+08	1.2E+08	3610	0.857631598	1.587184579	0.003197	0.008495915	0.07384	1	30	27	22	37	35	92	98	45	71	82
ENSMUSG00000020246	chr10	Hcfc2	8.3E+07	8.3E+07	5485	-0.49892285	4.730443659	0.0031981	0.008497248	0.03211	-1	468	396	506	446	494	531	583	314	424	437
ENSMUSG00000048249	chr17	Crebrf	2.7E+07	2.7E+07	8564	-0.52435203	4.537621854	0.0032044	0.0085123	0.03525	-1	450	329	438	411	405	445	423	319	318	456
ENSMUSG00000054723	chr17	Vmac	5.7E+07	5.7E+07	2276	0.799974736	2.539355281	0.0032097	0.008524692	0.07564	1	53	47	55	45	117	207	116	111	164	153
ENSMUSG00000029186	chr5	Pi4k2b	5.3E+07	5.3E+07	3751	1.134552448	1.160352163	0.0032121	0.008529561	0.14144	1	20	13	13	8	47	92	59	48	52	49
ENSMUSG00000002043	chr7	Trappc6a	2E+07	2E+07	1317	1.015615348	1.415133108	0.003218	0.008543524	0.11304	1	16	18	23	20	52	102	41	46	85	80
ENSMUSG00000036501	chr18	Fam13b	3.4E+07	3.4E+07	3343	-0.68662648	3.062650027	0.0032258	0.008562668	0.05787	-1	154	119	202	131	167	197	182	86	100	104

ENSMUSG00000059974	chr9	Ntm	2.9E+07	2.9E+07	8079	1.138283035	0.174033148	0.0032283	0.008567674	0.11465	1	10	3	16	10	9	22	21	21	32	45
ENSMUSG00000009876	chr2	Cox4i2	1.5E+08	1.5E+08	788	1.016785045	1.751281013	0.0032328	0.008577867	0.12392	1	21	10	48	30	62	122	51	58	119	101
ENSMUSG00000069601	chr10	Ank3	7E+07	7E+07	33152	-0.70789709	6.105140276	0.0032334	0.008578031	0.06766	-1	1254	866	1764	1714	826	1069	1556	744	931	1140
ENSMUSG00000023050	chr15	Map3k12	1E+08	1E+08	8986	0.754773352	2.187374452	0.0032343	0.008578724	0.06428	1	40	31	72	36	77	138	124	64	130	128
ENSMUSG00000026849	chr2	Tor1a	3.1E+07	3.1E+07	1995	0.708048713	2.808372014	0.0032403	0.008593012	0.0595	1	85	53	73	60	127	230	155	143	172	183
ENSMUSG00000022707	chr16	Gbe1	7E+07	7E+07	5352	-0.78362871	6.147111587	0.0032627	0.008650885	0.083	-1	1067	569	2360	1871	1181	1113	1698	696	883	1058
ENSMUSG00000042834	chr18	Nrep	3.3E+07	3.3E+07	2513	-0.6869409	6.78437717	0.0032678	0.008662596	0.06411	-1	2487	1220	2252	1855	2550	1623	1717	1732	2240	1223
ENSMUSG00000043518	chrX	Rai2	1.6E+08	1.6E+08	2403	-0.49521121	4.35829969	0.0032706	0.008668447	0.03108	-1	347	271	381	399	398	391	406	239	383	347
ENSMUSG00000061816	chr1	Myl1	6.7E+07	6.7E+07	2074	-0.68001395	12.15082492	0.003277	0.008683779	0.06344	-1	89802	76093	95502	74754	77396	71691	101455	52605	80530	56251
ENSMUSG00000057835	chr17	Zfp119a	5.6E+07	5.6E+07	2018	-0.97767541	1.393430078	0.0032801	0.008688623	0.10361	-1	63	39	73	37	43	29	58	32	23	34
ENSMUSG00000095677	chr17	Dynlt1f	6648941	6649337	807	1.04178225	1.025129828	0.00328	0.008688623	0.10817	1	19	17	12	11	34	85	57	38	47	41
ENSMUSG00000037907	chr11	Ankrd13b	7.7E+07	7.7E+07	3839	-0.64527485	4.005458838	0.0032873	0.008706134	0.05378	-1	246	229	436	348	211	269	308	149	260	321
ENSMUSG00000031976	chr8	Urb2	1.2E+08	1.2E+08	6153	-0.69965889	2.877547404	0.0032964	0.008728623	0.05901	-1	122	123	144	158	118	129	142	98	104	98
ENSMUSG00000025178	chr19	Pi4k2a	4.2E+07	4.2E+07	3771	0.477678288	4.784628885	0.0032975	0.008729853	0.02931	1	327	237	409	347	428	648	698	462	770	733
ENSMUSG00000020063	chr10	Sirt1	6.3E+07	6.3E+07	5331	-0.63167226	3.114579981	0.0032997	0.008734037	0.04776	-1	161	92	213	177	155	155	175	104	118	147
ENSMUSG00000029416	chr5	Slc15a4	1.3E+08	1.3E+08	5312	0.524999159	4.247939186	0.0033063	0.008749842	0.03477	1	187	187	285	182	341	538	505	341	453	477
ENSMUSG00000035596	chr7	Mboat7	3677790	3678849	7716	0.518909442	4.051513786	0.0033095	0.008756791	0.03372	1	159	128	258	215	285	498	395	304	422	395
ENSMUSG00000024359	chr18	Hspa9	3.5E+07	3.5E+07	3932	-0.65559845	9.270041961	0.0033107	0.008758122	0.05906	-1	9897	6213	18710	13072	10864	10549	12861	7239	8946	10229
ENSMUSG00000029676	chr6	Pot1a	2.6E+07	2.6E+07	8669	-0.54558126	3.542228334	0.0033159	0.008770251	0.03636	-1	206	165	256	182	226	233	230	131	197	191
ENSMUSG00000001588	chr11	Acap1	7E+07	7E+07	4878	1.210167548	0.547696081	0.0033272	0.008798611	0.14277	1	14	13	10	6	16	41	27	27	25	72
ENSMUSG00000015451	chr17	C4a	3.5E+07	3.5E+07	6206	1.482596858	1.996523022	0.0033315	0.008806652	0.27216	1	11	20	15	10	105	196	143	46	97	125
ENSMUSG00000023027	chr15	Atf1	1E+08	1E+08	3060	-0.52899384	5.582154621	0.0033313	0.008806652	0.03752	-1	869	720	963	802	854	936	973	644	743	758
ENSMUSG00000024538	chr18	Ppic	5.3E+07	5.3E+07	1286	0.66503373	4.740571711	0.0033369	0.008819087	0.05824	1	366	291	261	223	371	1013	511	599	650	599
ENSMUSG00000027223	chr2	Mapk8ip1	9.2E+07	9.2E+07	4644	0.661125883	3.176105703	0.0033487	0.008848595	0.05236	1	86	94	100	94	143	272	211	157	291	204
ENSMUSG00000021109	chr12	Hif1a	7.4E+07	7.4E+07	5896	-0.55727537	4.394809657	0.0033518	0.008855276	0.04014	-1	343	292	469	348	438	383	502	290	255	323
ENSMUSG00000059975	chr7	Zfp74	3E+07	3E+07	5628	-0.73456976	2.257035088	0.0033592	0.008873037	0.06222	-1	85	78	96	85	94	89	105	53	53	68
ENSMUSG00000023104	chr5	Rfc2	1.3E+08	1.3E+08	1518	0.511261268	4.170492814	0.0033638	0.008883552	0.03279	1	230	147	233	216	296	521	406	317	474	466
ENSMUSG00000026088	chr1	Mitd1	3.8E+07	3.8E+07	2770	0.925944427	1.328715179	0.0033721	0.008903747	0.09189	1	18	14	32	17	47	94	53	45	52	82
ENSMUSG00000078486	chr4	Perm1	1.6E+08	1.6E+08	3901	-1.24620287	7.994682074	0.0033781	0.00891791	0.20831	-1	2436	1382	13626	9029	2734	2509	5005	1896	2792	3594
ENSMUSG00000024941	chr19	Scyl1	5758427	5758696	2637	-0.55857878	6.460312743	0.0033809	0.008923778	0.04261	-1	1413	1051	2116	1696	1744	1626	1970	966	1486	1393
ENSMUSG00000024735	chr19	Prpf19	1.1E+07	1.1E+07	7278	-0.61367566	7.395854333	0.0033829	0.0089267	0.05178	-1	2807	2130	4455	3502	2580	2727	3271	2122	2905	2716
ENSMUSG00000051098	chr13	Mblac2	8.2E+07	8.2E+07	3881	-0.90582532	1.014066672	0.0033833	0.0089267	0.08041	-1	53	28	39	25	45	34	28	20	31	27
ENSMUSG00000027889	chr3	Ampd2	1.1E+08	1.1E+08	5069	0.839018483	3.32874083	0.0033847	0.008928726	0.09013	1	76	79	73	85	234	351	203	194	283	292
ENSMUSG00000045377	chr11	Tmem88	6.9E+07	6.9E+07	1582	0.77139995	3.321349061	0.0033869	0.008932717	0.07661	1	76	53	208	104	138	300	163	234	264	312
ENSMUSG00000031425	chrX	Plp1	1.4E+08	1.4E+08	5551	0.757868756	2.528566709	0.0033931	0.008947364	0.0675	1	72	45	66	50	84	226	107	95	135	182
ENSMUSG00000044792	chr13	Isca1	6E+07	6E+07	4288	-0.64410381	7.577360911	0.0033946	0.00894815	0.05711	-1	3004	2053	5898	3557	3624	3075	4419	2133	2948	2938
ENSMUSG00000056666	chr6	Retsat	7.3E+07	7.3E+07	3537	-0.83384619	5.559118188	0.0033943	0.00894815	0.09425	-1	639	308	2024	1088	809	844	841	399	664	819
ENSMUSG00000039007	chr15	Cpq	3.3E+07	3.3E+07	1923	0.574496117	4.951424852	0.0033957	0.00894933	0.04372	1	359	290	364	273	595	1086	676	592	795	689
ENSMUSG00000050069	chr1	Grem2	1.7E+08	1.7E+08	3745	-0.76615075	2.79627939	0.0034005	0.008960297	0.07254	-1	95	126	148	82	203	119	139	70	111	92
ENSMUSG00000090733	chr3	Rps27	9E+07	9E+07	255	0.609002488	7.782984668	0.0034014	0.008960869	0.05111	1	2726	2117	2829	2303	3094	7319	4149	4310	5681	6129
ENSMUSG00000022237	chr15	Ankrd33b	3.1E+07	3.1E+07	8706	-0.68098246	5.273055506	0.0034083	0.00897734	0.06266	-1	795	459	1141	812	396	728	744	437	561	622
ENSMUSG00000020354	chr11	Sgcd	4.7E+07	4.7E+07	8257	-0.69033707	3.964014061	0.0034097	0.008979467	0.06211	-1	317	208	337	386	176	292	239	211	270	211
ENSMUSG00000028687	chr4	Mutyh	1.2E+08	1.2E+08	2612	0.931644799	1.300875952	0.0034184	0.00900072	0.08782	1	29	22	17	16	35	71	66	41	82	58
ENSMUSG00000025776	chr1	Crispld1	1.8E+07	1.8E+07	4515	0.799096466	1.793670871	0.003431	0.009032118	0.06677	1	29	35	51	36	31	123	77	61	95	86
ENSMUSG00000031993	chr9	Snx19	3E+07	3E+07	5541	-0.5379793	5.410981547	0.0034325	0.00903441	0.03893	-1	714	577	947	867	672	777	918	535	717	647
ENSMUSG00000026504	chr1	Sdccag8	1.8E+08	1.8E+08	4129	-0.67907618	3.33359132	0.0034389	0.009048434	0.05866	-1	192	164	175	148	239	203	228	85	138	160
ENSMUSG00000031201	chrX	Brcc3	7.5E+07	7.5E+07	7887	-0.52971574	4.206213577	0.0034395	0.009048434	0.03603	-1	311	259	420	343	298	355	387	216	329	280
ENSMUSG00000038803	chr5	Ost4	3.1E+07	3.1E+07	1272	0.566117481	5.706472144	0.0034398	0.009048434	0.04329	1	647	523	551	580	833	1561	1171	999	1477	1230
ENSMUSG00000044018	chr4	Mrpl50	5E+07	5E+07	2114	-0.52769017	5.741903908	0.0034422	0.009053017	0.03768	-1	933	669	1293	975	921	995	1094	724	797	916
ENSMUSG00000038007	chr4	Acer2	8.7E+07	8.7E+07	7159	-0.85336053	2.514579636	0.0034493	0.009070085	0.08936	-1	83	59	124	90	215	122	106	57	49	88
ENSMUSG00000033031	chr16	C330027C09Rik	4.9E+07	4.9E+07	5688	-1.17716276	0.405430089	0.0034571	0.009088851	0.14215	-1	25	22	48	12	25	25	22	6	8	20
ENSMUSG00000002944	chr5	Cd36	1.8E+07	1.8E+07	3927	-0.77471664	8.807920674	0.0034589	0.009091887	0.08286	-1	6421	3521	15553	7868	12154	8032	9651	4349	4871	7851
ENSMUSG00000045973	chr4	Slc25a51	4.5E+07	4.5E+07	5510	-0.52323329	6.29314992	0.0034601	0.009093443	0.03742	-1	1266	960	1721	1355	1764	1445	1564	1011	1364	1276
ENSMUSG00000027787	chr3	Nmd3	7E+07	7E+07	10155	-0.50403316	4.623685002	0.0034654	0.009105479	0.03303	-1	386	326	563	479	424	490	512	357	360	378
ENSMUSG00000037754	chr2	Ppp1r16b	1.6E+08	1.6E+08	8844	-0.60138746	3.206487572	0.0034808	0.00914423	0.04386	-1	152	103	236	176	181	173	193	93	138	165
ENSMUSG00000064317	chr10	Gm10146	7.8E+07	7.8E+07	448	1.075228513	0.808055445	0.0034848	0.009153262	0.11776	1	21	8	15	13	22	57	22	29	66	54
ENSMUSG00000030838	chr7	Ush1c	4.6E+07	4.6E+07	3849	-1.01380906	1.448872834	0.0034872	0.00915763	0.1201	-1	63	60	43	32	61	26	39	21	44	53
ENSMUSG00000023020	chr15	Cox14	1E+08	1E+08	723	0.54980738	6.664864603	0.0034935	0.0091725	0.04163	1	1105	840	1547	1263	1541	2580	2297	1977	2971	2574
ENSMUSG00000021116	chr12	Eif2s1	7.9E+07	7.9E+07	3405	-0.52366039	5.293457134	0.0034965	0.009177133	0.03689	-1	744	588	787	628	688	811	794	533	597	593
ENSMUSG00000025597	chrX	Klhl4	1.1E+08	1.1E+08	3584	-1.13847142	0.147139028	0.0034963	0.009177133	0.11031	-1	12	14	43	15	26	12	20	8	12	14
ENSMUSG00000007817	chr14	Zmiz1	2.5E+07	2.5E+07	12523	-0.50149304	5.334205113	0.0034989	0.009181494	0.03374	-1	597	510	793	837	840	737	865	493	644	727
ENSMUSG00000049285	chr5	Mblac1	1.4E+08	1.4E+08	1308	1.044906104	0.900889974	0.003503	0.009190753	0.10947	1	18	11	14	13	30	71	26	31	61	55
ENSMUSG00000027692	chr3	Tnik	2.8E+07	2.8E+07	19282	-0.64520701	5.051309627	0.0035041	0.009191781	0.05613	-1	627	286	945	801	458	533	671	413	508	542
ENSMUSG00000043190	chr13	Rfesd	7.6E+07	7.6E+07	2906	-0.55537909	3.801569758	0.0035082	0.009200923	0.03914	-1	253	193	293	229	275	308	307	152	206	206
ENSMUSG00000000938	chr6	Hoxa10	5.2E+07	5.2E+07	3270	-0.52963288	4.19211352	0.0035129	0.009211502	0.03603	-1	319	273	340	292	384	286	355	245	329	317
ENSMUSG00000032116	chr9	Stt3a	3.7E+07	3.7E+07	8948	0.551082194	5.470861032	0.0035217	0.009230927	0.04106	1	522	391	530	498	783	1605	1021	865	983	1003
ENSMUSG00000034127	chr10	Tspan8	1.2E+08	1.2E+08	1522	-0.78986047	6.29828647	0.0035213	0.009230927	0.08584	-1	2214	1446	958	1061	1474	1480	1408	941	1087	1067

ENSMUSG00000069171	chr13	Nr2f1	7.8E+07	7.8E+07	4752	0.953495715	0.757750433	0.0035229	0.009232362	0.08596	1	14	9	28	13	18	55	27	37	46	47
ENSMUSG00000070305	chr9	Mpzl3	4.5E+07	4.5E+07	6987	0.686866261	2.801270375	0.0035241	0.009233988	0.05595	1	82	60	95	57	104	226	173	152	187	132
ENSMUSG00000014353	chr2	Tmem87b	1.3E+08	1.3E+08	8395	-0.46064895	5.057620722	0.0035259	0.009236924	0.02805	-1	542	448	641	606	659	670	691	433	524	587
ENSMUSG00000040653	chr10	Ppp1r14c	3366150	3366969	2524	-0.7288987	6.580425953	0.0035294	0.009244319	0.07334	-1	2282	1848	1235	1484	1699	1775	1581	1221	1436	1425
ENSMUSG00000009633	chr1	G0s2	1.9E+08	1.9E+08	871	-0.89156441	5.112220265	0.0035311	0.00924572	0.10805	-1	383	353	556	500	1802	588	504	377	627	409
ENSMUSG00000021461	chr13	Fancc	6.3E+07	6.3E+07	7884	0.863044196	1.346831298	0.0035313	0.00924572	0.07491	1	19	20	26	25	40	80	44	53	71	73
ENSMUSG00000026718	chr2	Stam	1.4E+07	1.4E+07	8386	-0.55191638	3.776498193	0.0035341	0.009251529	0.0386	-1	235	218	277	208	271	264	276	157	206	249
ENSMUSG00000006058	chr11	Snf8	9.6E+07	9.6E+07	2677	0.495506981	4.729051271	0.0035651	0.00933082	0.03238	1	279	200	433	332	452	720	549	503	756	661
ENSMUSG00000018474	chr11	Chd3	6.9E+07	6.9E+07	8443	0.579663124	4.358617619	0.0035706	0.009343392	0.044	1	224	186	255	182	402	665	478	311	511	603
ENSMUSG00000019814	chr10	Ltv1	1.3E+07	1.3E+07	1766	-0.48151802	4.602972537	0.0035738	0.009350182	0.03023	-1	438	339	456	404	477	543	429	339	374	410
ENSMUSG00000025142	chr11	Aspscr1	1.2E+08	1.2E+08	4770	0.515424559	4.963968159	0.0035757	0.009353356	0.0353	1	345	285	413	388	510	905	573	581	913	812
ENSMUSG00000022661	chr16	Cd200	4.5E+07	4.5E+07	3321	0.598050282	4.943339929	0.003581	0.009365373	0.04848	1	252	195	557	323	607	802	796	565	679	984
ENSMUSG00000024976	chr19	Shoc2	5.4E+07	5.4E+07	4203	-0.50721451	4.73243089	0.0035838	0.009369271	0.03398	-1	482	342	623	460	445	509	608	341	399	417
ENSMUSG00000098652	chr16	Gm27671	1.4E+07	1.4E+07	66	-1.95911815	-0.31468621	0.0035837	0.009369271	0.41461	-1	15	17	27	16	12	4	25	0	2	1
ENSMUSG00000021065	chr12	Fut8	7.7E+07	7.7E+07	3543	-0.59112679	4.31537092	0.0035869	0.009373978	0.04619	-1	318	265	538	325	376	393	514	200	283	276
ENSMUSG00000024921	chr19	Smarca2	2.7E+07	2.7E+07	7854	-0.50900544	5.632373464	0.0035863	0.009373978	0.0353	-1	881	623	1123	893	886	1027	1048	554	790	865
ENSMUSG00000089989	chr7	Flt3l	4.5E+07	4.5E+07	3712	0.939914736	2.657277743	0.0035879	0.009374891	0.11046	1	62	56	33	52	112	294	118	125	131	184
ENSMUSG00000020941	chr11	Map3k14	1E+08	1E+08	6550	0.588617995	3.47535312	0.0035923	0.009384468	0.0428	1	109	100	167	165	121	323	268	205	268	306
ENSMUSG00000060733	chr10	Ipmk	7.1E+07	7.1E+07	7093	-0.56422773	4.75112758	0.0035946	0.009388728	0.04256	-1	401	340	701	588	405	488	619	312	396	444
ENSMUSG00000048120	chr19	Entpd1	4.1E+07	4.1E+07	5580	0.505332431	4.045157113	0.0036101	0.009427462	0.0322	1	185	141	293	200	217	523	401	276	397	413
ENSMUSG00000051934	chr15	Spats2	9.9E+07	9.9E+07	3065	0.624562686	3.050717873	0.0036117	0.009429958	0.04725	1	84	71	106	89	139	233	174	185	206	216
ENSMUSG00000025366	chr10	Esyt1	1.3E+08	1.3E+08	3687	0.693663537	5.907317219	0.0036191	0.009447426	0.06641	1	508	457	589	570	1433	1888	1424	1097	1691	1606
ENSMUSG00000086859	chr11	2810008D09Rik	1.2E+08	1.2E+08	2166	0.874334824	2.022812945	0.003622	0.009453222	0.08918	1	36	33	67	30	46	136	54	88	115	131
ENSMUSG00000017679	chr2	Ttpal	1.6E+08	1.6E+08	5951	0.644538666	3.163760131	0.0036347	0.009484823	0.0512	1	85	86	135	82	136	299	195	201	179	236
ENSMUSG00000026029	chr1	Casp8	5.9E+07	5.9E+07	2893	0.756716671	2.744679838	0.003636	0.009486309	0.07094	1	59	52	79	53	134	243	141	131	140	205
ENSMUSG00000037896	chr12	Rcor1	1.1E+08	1.1E+08	5684	-0.57889058	3.754667632	0.0036476	0.009514725	0.04319	-1	216	212	306	213	260	262	307	129	220	214
ENSMUSG00000025738	chr17	Fbxl16	2.6E+07	2.6E+07	3478	0.769280399	2.12497975	0.0036505	0.00951893	0.06694	1	41	31	55	55	56	139	142	59	138	84
ENSMUSG00000090115	chr17	Usp49	4.8E+07	4.8E+07	8581	-0.64438974	2.764205692	0.0036502	0.00951893	0.04944	-1	99	78	164	148	139	108	132	78	105	120
ENSMUSG00000037032	chr7	Apbb1	1.1E+08	1.1E+08	4404	0.514885421	3.999341512	0.0036579	0.009536432	0.0337	1	178	123	261	186	260	476	417	239	441	386
ENSMUSG00000034639	chr6	Setmar	1.1E+08	1.1E+08	1765	-0.68916252	2.389255158	0.0036684	0.009560159	0.05588	-1	95	81	108	99	92	90	107	59	88	66
ENSMUSG00000098955	chr11	Mir6935	1.2E+08	1.2E+08	64	-1.10246878	1.202746298	0.0036683	0.009560159	0.14402	-1	36	61	32	40	50	42	32	9	43	26
ENSMUSG00000052727	chr13	Map1b	9.9E+07	9.9E+07	11852	0.506876007	4.474941239	0.0036778	0.009582988	0.03354	1	216	207	418	274	281	613	642	408	499	532
ENSMUSG00000006800	chr2	Sulf2	1.7E+08	1.7E+08	5818	0.920423775	4.822218466	0.0036831	0.009593108	0.11589	1	218	190	173	167	779	1065	671	536	804	777
ENSMUSG00000033658	chr8	Ddx19b	1.1E+08	1.1E+08	6742	-0.55137787	4.780905507	0.0036826	0.009593108	0.04093	-1	527	398	572	531	391	478	592	312	493	440
ENSMUSG00000040297	chr1	Suco	1.6E+08	1.6E+08	8928	-0.51179699	3.815597009	0.0036839	0.009593503	0.03281	-1	243	188	293	235	284	268	276	194	215	239
ENSMUSG00000020721	chr11	Helz	1.1E+08	1.1E+08	15044	-0.49505331	4.36973341	0.0036926	0.009614255	0.03181	-1	362	251	510	360	350	410	414	272	325	352
ENSMUSG00000032299	chr9	Commd4	5.7E+07	5.7E+07	824	0.536218948	4.298323152	0.0037023	0.009637808	0.03744	1	232	178	232	200	371	591	456	345	534	482
ENSMUSG00000023259	chr9	Slc26a6	1.1E+08	1.1E+08	5411	-0.58544265	3.334051173	0.0037149	0.009668823	0.04239	-1	141	136	236	188	214	189	221	115	166	143
ENSMUSG00000074211	chr7	Sdhaf1	3E+07	3E+07	2490	0.545338885	4.463427398	0.0037259	0.009695524	0.03972	1	210	146	388	250	407	642	482	418	523	633
ENSMUSG00000027219	chr2	Slc28a2	1.2E+08	1.2E+08	4208	-0.58769199	3.502608739	0.0037272	0.009697151	0.04339	-1	197	129	297	179	240	255	232	126	149	182
ENSMUSG00000025747	chr5	Tyms	3E+07	3E+07	6089	1.328807331	0.74634421	0.0037294	0.009701229	0.20386	1	13	2	9	15	30	71	18	47	54	35
ENSMUSG00000035069	chr4	Oma1	1E+08	1E+08	2144	-0.51655124	4.946951741	0.003731	0.00970344	0.03587	-1	515	337	724	683	501	563	643	401	507	508
ENSMUSG00000044447	chr14	Dock5	6.8E+07	6.8E+07	10335	0.846313312	1.707090241	0.0037326	0.009705967	0.07911	1	21	27	32	30	61	76	101	57	95	88
ENSMUSG00000028398	chr4	Tmem261	7.5E+07	7.5E+07	741	0.484474498	5.079850252	0.0037399	0.009723096	0.03162	1	419	256	545	405	538	1019	693	657	922	773
ENSMUSG00000002477	chr18	Snrpd1	1.1E+07	1.1E+07	837	0.597970405	3.911470138	0.0037466	0.009738758	0.04616	1	163	160	190	146	230	487	306	358	355	333
ENSMUSG00000087440	chr3	4930577N17Rik	5.1E+07	5.1E+07	1625	-1.02284235	0.514822638	0.0037647	0.009783934	0.1005	-1	24	13	44	22	38	20	31	8	15	19
ENSMUSG00000020831	chr11	0610010K14Rik	7E+07	7E+07	1896	0.532085368	4.334052749	0.0037666	0.00978702	0.03731	1	223	149	315	237	343	593	408	317	606	552
ENSMUSG00000031495	chr8	Cd209d	3871827	3872110	916	1.275378041	3.274557957	0.0037703	0.0097947	0.21526	1	58	92	18	41	205	458	207	236	256	246
ENSMUSG00000059049	chr4	Frem1	8.3E+07	8.3E+07	13978	1.012179263	1.010673105	0.0037723	0.009798134	0.10164	1	22	22	25	12	10	69	55	33	51	55
ENSMUSG00000028708	chr4	Mknk1	1.2E+08	1.2E+08	4502	-0.5329389	4.6320609	0.0037742	0.009801369	0.03812	-1	488	370	439	476	382	470	491	311	422	402
ENSMUSG00000097188	chr19	Snhg1	8723496	8725256	2947	0.704609265	3.101894588	0.0037753	0.009802315	0.06278	1	93	67	120	81	131	321	150	213	172	220
ENSMUSG00000071660	chr19	Ttc9c	8809075	8811838	3984	-0.55323281	3.543193326	0.003782	0.009817873	0.03864	-1	230	148	235	202	223	252	234	129	180	188
ENSMUSG00000032534	chr9	Cep63	1E+08	1E+08	9588	-0.48759977	5.188562447	0.0037951	0.009850228	0.0323	-1	751	482	688	573	687	737	662	469	626	651
ENSMUSG00000033227	chr1	Wnt6	7.5E+07	7.5E+07	2192	1.226589174	-0.07971101	0.0038017	0.0098654	0.12721	1	4	5	12	11	5	24	15	21	38	19
ENSMUSG00000027004	chr2	Frzb	8E+07	8E+07	3237	-1.01614417	4.33691066	0.0038068	0.009876879	0.14097	-1	245	120	1016	527	283	205	435	201	280	253
ENSMUSG00000089682	chr14	Bcl2l2	5.5E+07	5.5E+07	4462	-0.49354421	5.668957075	0.00381	0.009883392	0.03355	-1	815	586	1187	919	1049	1064	1048	619	817	856
ENSMUSG00000042677	chr4	Zc3h12a	1.3E+08	1.3E+08	2882	0.839832406	2.101826798	0.0038195	0.009906014	0.08602	1	23	20	71	46	77	128	117	83	92	134
ENSMUSG00000101086	chr14	Gm28651	3.3E+07	3.3E+07	644	-1.12441054	1.146475102	0.0038242	0.009916446	0.14599	-1	42	15	83	47	44	25	57	16	17	25
ENSMUSG00000020921	chr11	Tmem101	1E+08	1E+08	2021	0.502613986	3.954749855	0.0038281	0.009924762	0.03212	1	173	132	226	174	270	426	387	277	411	370
ENSMUSG00000063972	chr2	Nr6a1	3.9E+07	3.9E+07	7488	-0.80709953	2.111345331	0.0038339	0.00993792	0.0787	-1	96	69	56	95	80	67	62	48	78	64
ENSMUSG00000061062	chr17	Gm10093	7.8E+07	7.8E+07	1977	0.884907996	2.182853764	0.0038357	0.00994067	0.0961	1	33	32	40	32	103	164	100	91	128	111
ENSMUSG00000039068	chr3	Zzz3	1.5E+08	1.5E+08	8401	-0.47087527	4.679603194	0.0038442	0.009961012	0.02935	-1	392	354	535	448	511	470	530	367	380	460
ENSMUSG00000007411	chr12	Mark3	1.1E+08	1.1E+08	3388	-0.52739285	5.770180834	0.0038467	0.009965721	0.03865	-1	978	742	1267	950	909	1075	1172	661	866	879
ENSMUSG00000004100	chr9	Ppan	2.1E+07	2.1E+07	2504	0.732396986	3.21987255	0.0038476	0.00996607	0.06902	1	76	83	112	105	148	278	131	209	296	260
ENSMUSG00000091811	chr7	Inafm1	1.6E+07	1.6E+07	1679	0.523357312	4.398997731	0.0038491	0.009968231	0.03604	1	229	187	272	296	318	536	463	347	646	576
ENSMUSG00000021832	chr14	Psmc6	4.5E+07	4.5E+07	1564	-0.58320238	6.619245375	0.0038725	0.01002695	0.04794	-1	1945	1401	2183	1690	1586	1873	2101	1261	1451	1475
ENSMUSG00000104372	chr11	AL663030.1	1.2E+08	1.2E+08	495	-0.7226077	2.9647663	0.0038952	0.010083918	0.06653	-1	140	93	222	141	143	119	191	79	134	85

ENSMUSG00000046275	chr11	Tusc5	7.7E+07	7.7E+07	3302	-2.40560732	4.793873774	0.003897	0.010086708	0.72458	-1	351	218	36	21	3304	326	79	181	168	150
ENSMUSG00000074221	chr7	Zfp568	3E+07	3E+07	7183	-0.56820254	4.161471579	0.0038979	0.010087201	0.04297	-1	324	279	362	352	255	354	344	239	279	269
ENSMUSG00000002326	chr14	Gmpr2	5.6E+07	5.6E+07	1543	0.842893136	2.379351146	0.0039101	0.010116799	0.08846	1	29	47	53	43	106	196	111	103	127	141
ENSMUSG00000028522	chr4	Mier1	1E+08	1E+08	12513	-0.506229	4.240744695	0.0039111	0.010117542	0.03363	-1	323	228	465	320	351	365	402	222	270	364
ENSMUSG00000038204	chr5	Asb10	2.5E+07	2.5E+07	2806	-0.60691734	6.74582411	0.0039244	0.010150067	0.05211	-1	1800	1264	2921	2126	1810	1680	2420	1204	1946	1588
ENSMUSG00000000326	chr16	Comt	1.8E+07	1.8E+07	2532	-0.56201082	5.788020179	0.003927	0.010153741	0.04417	-1	976	715	996	797	1532	1219	1086	681	856	810
ENSMUSG00000031774	chr8	Fam192a	9.5E+07	9.5E+07	1797	0.447076815	4.999447761	0.0039273	0.010153741	0.02683	1	379	273	508	393	511	834	747	568	790	870
ENSMUSG00000052293	chr13	Taf9	1E+08	1E+08	2120	-0.5384981	4.82774492	0.0039315	0.010162846	0.03954	-1	499	421	616	513	453	607	608	395	378	406
ENSMUSG00000035248	chr13	Zcchc6	6E+07	6E+07	5551	-0.49743782	5.134532748	0.0039346	0.010167555	0.03392	-1	531	477	794	677	620	798	756	408	528	559
ENSMUSG00000078441	chr10	Scamp4	8.1E+07	8.1E+07	1863	0.496540265	4.99233396	0.0039348	0.010167555	0.03346	1	365	270	395	388	590	899	704	566	904	777
ENSMUSG00000021224	chr12	Numb	8.4E+07	8.4E+07	3823	-0.52436523	4.068783153	0.0039392	0.010173227	0.03606	-1	286	232	337	308	317	334	357	200	306	230
ENSMUSG00000036362	chr3	P2ry13	5.9E+07	5.9E+07	2524	1.157453583	0.839111528	0.0039389	0.010173227	0.14021	1	15	17	6	10	27	75	43	25	60	38
ENSMUSG00000094989	chr13	Rpl9-ps4	7.2E+07	7.2E+07	579	1.301061635	-0.07301539	0.0039385	0.010173227	0.13378	1	7	9	3	9	6	26	20	10	33	33
ENSMUSG00000024206	chr17	Rfx2	5.7E+07	5.7E+07	3353	0.747756757	2.104466684	0.0039409	0.010174038	0.06615	1	39	21	68	45	71	122	117	65	132	111
ENSMUSG00000038264	chr9	Sema7a	5.8E+07	5.8E+07	3296	0.656106747	3.975345122	0.0039403	0.010174038	0.05804	1	105	121	340	148	240	385	384	351	418	413
ENSMUSG00000024378	chr18	Stard4	3.3E+07	3.3E+07	5586	0.618850616	3.438267164	0.0039533	0.010204045	0.04947	1	99	79	160	117	201	394	306	188	214	261
ENSMUSG00000026526	chr1	Fh1	1.8E+08	1.8E+08	3392	-0.62069128	8.153494196	0.0039587	0.010216178	0.05495	-1	4603	2853	8264	5988	5082	4942	6051	3246	4585	4539
ENSMUSG00000047963	chr5	Stbd1	9.3E+07	9.3E+07	1985	0.654394576	6.990505198	0.0039594	0.010216178	0.06065	1	1209	1490	1327	1819	1337	3578	3149	2405	3685	3273
ENSMUSG00000019850	chr10	Tnfaip3	1.9E+07	1.9E+07	7226	0.59150595	3.247723127	0.0039602	0.010216199	0.04353	1	82	85	157	112	136	239	281	153	235	266
ENSMUSG00000020472	chr11	Zkscan17	5.9E+07	5.9E+07	4573	-0.48852722	4.583756606	0.0039617	0.01021829	0.0318	-1	422	302	599	380	420	421	501	317	423	394
ENSMUSG00000035370	chr10	Adat3	8.1E+07	8.1E+07	4586	0.494785784	5.022924439	0.0039769	0.010255651	0.03333	1	369	279	409	392	604	916	720	577	923	795
ENSMUSG00000038068	chr13	Rnf144b	4.7E+07	4.7E+07	4694	-0.47776029	4.439404603	0.0039823	0.01026757	0.03012	-1	369	246	521	401	385	449	393	270	351	418
ENSMUSG00000020777	chr11	Acox1	1.2E+08	1.2E+08	5082	-0.55274181	7.355865007	0.0039833	0.010268383	0.04352	-1	2658	1719	3773	3175	3716	3354	2909	2113	2504	2905
ENSMUSG00000001039	chr11	B9d1	6.2E+07	6.2E+07	1593	0.959774673	1.336399253	0.0039882	0.010279151	0.1018	1	30	18	16	24	33	111	46	53	69	50
ENSMUSG00000028692	chr4	Akr1a1	1.2E+08	1.2E+08	2750	0.579125562	8.065125265	0.0039977	0.010301678	0.04794	1	3212	2527	3277	2703	4490	7869	6248	5190	6989	6901
ENSMUSG00000020134	chr11	Peli1	2.1E+07	2.1E+07	6553	-0.69497729	3.601490748	0.0040042	0.010314684	0.06418	-1	175	141	410	212	224	211	308	121	157	169
ENSMUSG00000035007	chr11	Rundc1	1E+08	1E+08	3223	0.517317707	3.957024335	0.0040041	0.010314684	0.03482	1	170	108	264	213	224	467	386	270	414	353
ENSMUSG00000023018	chr15	Smarcd1	1E+08	1E+08	3153	0.568814342	3.770011613	0.0040072	0.010318554	0.04176	1	136	125	166	164	235	394	293	217	390	391
ENSMUSG00000040296	chr4	Ddx58	4E+07	4E+07	7050	0.72456074	2.890428583	0.0040072	0.010318554	0.06662	1	67	47	89	77	147	271	180	100	213	197
ENSMUSG00000031429	chrX	Psmd10	1.4E+08	1.4E+08	1469	0.540014766	3.577671991	0.0040099	0.010323547	0.037	1	143	95	177	121	203	319	297	233	301	295
ENSMUSG00000038702	chr1	Dsel	1.1E+08	1.1E+08	5763	0.738166443	2.661274576	0.0040248	0.010360076	0.06652	1	72	65	64	54	90	248	159	135	133	130
ENSMUSG00000028766	chr4	Alpl	1.4E+08	1.4E+08	4033	-1.00861187	3.516113854	0.0040286	0.010367788	0.13867	-1	145	62	523	283	222	143	247	71	134	202
ENSMUSG00000005150	chr8	Wdr83	8.5E+07	8.5E+07	2818	0.497920269	4.235970019	0.0040371	0.010387768	0.03268	1	193	158	333	209	305	472	451	332	509	506
ENSMUSG00000029577	chr5	Ube3b	1.1E+08	1.1E+08	5264	-0.62201996	7.847805862	0.0040388	0.010390411	0.05538	-1	3628	2757	6017	5065	3868	3542	5115	2469	4044	3724
ENSMUSG00000022024	chr14	Sugt1	8E+07	8E+07	1951	-0.54735372	5.914124317	0.0040442	0.010402273	0.04226	-1	1129	925	1193	1017	1043	1135	1268	769	878	1029
ENSMUSG00000031796	chr8	Cfap20	9.5E+07	9.5E+07	1292	0.775591922	2.930484943	0.0040525	0.010421307	0.07787	1	82	48	96	49	156	286	175	132	162	238
ENSMUSG00000032492	chr9	Pth1r	1.1E+08	1.1E+08	2484	1.319023002	2.840466892	0.0040531	0.010421307	0.23032	1	73	71	17	21	107	333	80	177	215	233
ENSMUSG00000057541	chr5	Pus7	2.4E+07	2.4E+07	5171	-0.59494119	3.465876583	0.0040584	0.010433136	0.04543	-1	185	164	227	199	214	202	192	182	153	161
ENSMUSG00000087014	chr10	Gm16364	4E+07	4E+07	1313	-1.22180846	0.842482684	0.0040655	0.010449364	0.17497	-1	23	18	60	36	52	11	48	6	20	23
ENSMUSG00000015943	chr3	Bola1	9.6E+07	9.6E+07	1082	0.529774075	4.123583615	0.0040705	0.010460384	0.03688	1	190	162	215	206	300	497	357	335	473	450
ENSMUSG00000028878	chr4	Fam76a	1.3E+08	1.3E+08	3088	-0.48479715	4.738653329	0.0040726	0.010463781	0.03167	-1	414	311	631	443	589	496	608	368	389	434
ENSMUSG00000035142	chr12	Nubpl	5.2E+07	5.2E+07	4954	-0.57671252	3.073447965	0.0040742	0.010466082	0.04094	-1	146	109	174	139	190	168	168	106	123	130
ENSMUSG00000091985	chr4	Gm17354	1.1E+08	1.1E+08	3039	-0.74940626	1.978141966	0.0040762	0.010469247	0.06552	-1	72	47	78	76	96	68	82	27	63	64
ENSMUSG00000018171	chr11	Vmp1	8.7E+07	8.7E+07	3862	-0.51153538	5.764485731	0.0040796	0.01047612	0.0368	-1	895	760	1159	1019	958	1049	1141	659	845	968
ENSMUSG00000030842	chr7	Lamtor1	1E+08	1E+08	1366	0.532838647	6.968289737	0.0040814	0.010478733	0.04056	1	1432	993	2005	1550	1871	3308	3027	2364	3356	3232
ENSMUSG00000029674	chr5	Limk1	1.3E+08	1.3E+08	7154	0.889029475	2.252750429	0.0040898	0.010498573	0.10091	1	39	23	57	28	111	156	125	104	133	103
ENSMUSG00000052496	chr15	Pkdrej	8.6E+07	8.6E+07	7058	-1.47026809	0.257367555	0.0040942	0.010507942	0.24617	-1	21	9	40	47	9	13	25	2	9	14
ENSMUSG00000099552	chr1	9830004L10Rik	8E+07	8E+07	2333	-1.66587475	0.423755005	0.0040998	0.010520204	0.32427	-1	8	22	24	15	83	5	30	8	14	5
ENSMUSG00000059920	chr16	4930453N24Rik	6.5E+07	6.5E+07	5948	-0.49691998	5.842817465	0.004103	0.010526526	0.03474	-1	906	731	1216	1030	1218	1113	1240	718	948	926
ENSMUSG00000015957	chr7	Wnt11	9.9E+07	9.9E+07	3633	0.63010147	3.507088108	0.0041038	0.010526664	0.05251	1	102	72	188	119	212	313	231	238	282	341
ENSMUSG00000044199	chr10	S1pr4	8.1E+07	8.2E+07	2388	1.095523565	0.638533751	0.0041095	0.010537707	0.12876	1	7	8	26	11	19	40	19	36	48	55
ENSMUSG00000074264	chr3	Amy1	1.1E+08	1.1E+08	3446	-0.66915838	5.707469933	0.0041096	0.010537707	0.06336	-1	838	613	1252	722	1568	839	1404	601	721	629
ENSMUSG00000066036	chr4	Ubr4	1.4E+08	1.4E+08	17997	-0.59638524	7.206435813	0.0041113	0.010540082	0.05098	-1	2337	1647	3841	3365	2425	2586	2777	1794	2568	2461
ENSMUSG00000027303	chr2	Ptpra	1.3E+08	1.3E+08	3335	0.541343309	4.901647825	0.0041279	0.010580851	0.04026	1	299	298	340	313	588	990	704	514	741	740
ENSMUSG00000006241	chr9	Ccdc159	2.2E+07	2.2E+07	1545	0.952307775	0.459010451	0.004139	0.010607213	0.07508	1	12	10	14	11	17	49	29	20	39	35
ENSMUSG00000028756	chr4	Pink1	1.4E+08	1.4E+08	2673	-0.61591654	9.724910214	0.0041442	0.010618665	0.0548	-1	15567	9834	22212	17258	13212	13714	16913	9744	14768	14236
ENSMUSG00000031791	chr8	Tmem38a	7.3E+07	7.3E+07	2094	-0.64389485	10.0812848	0.0041474	0.010624944	0.05987	-1	18859	13556	28184	22336	17520	15218	23992	12422	19674	16230
ENSMUSG00000040441	chr10	Slc26a10	1.3E+08	1.3E+08	2215	0.827298531	2.980353362	0.004159	0.01065264	0.08995	1	46	57	116	122	87	262	165	109	179	332
ENSMUSG00000092192	chr9	Dyx1c1	7.3E+07	7.3E+07	1975	-0.90231008	0.944826667	0.0041656	0.010667546	0.08423	-1	46	22	32	39	42	26	39	19	29	20
ENSMUSG00000025931	chr1	Paqr8	2.1E+07	2.1E+07	5488	0.982875724	0.673059397	0.0041681	0.01067212	0.09599	1	14	4	24	21	13	48	49	29	42	34
ENSMUSG00000002068	chr7	Ccne1	3.8E+07	3.8E+07	2662	1.257959552	-0.00203044	0.0041728	0.01068223	0.13639	1	12	5	2	7	12	32	25	27	26	15
ENSMUSG00000022041	chr14	Chrna2	6.6E+07	6.6E+07	3527	-2.34628927	1.237223898	0.004174	0.010683256	0.67811	-1	14	1	266	29	22	18	18	8	2	31
ENSMUSG00000025742	chrX	Prps2	1.7E+08	1.7E+08	3873	0.800689072	2.165405732	0.004189	0.010719859	0.07652	1	39	42	42	40	76	165	151	61	111	98
ENSMUSG00000027684	chr3	Mecom	3E+07	3E+07	12427	-0.7242679	2.394565119	0.0042052	0.01075931	0.06498	-1	82	77	121	84	127	109	120	48	56	79
ENSMUSG00000017561	chr11	Crlf3	8E+07	8E+07	4261	0.640393301	2.797264854	0.0042437	0.010855856	0.05041	1	73	56	113	61	107	202	158	151	155	189
ENSMUSG00000020868	chr11	Xylt2	9.5E+07	9.5E+07	3979	0.659863215	3.333354377	0.0042501	0.010869648	0.05769	1	93	71	157	86	196	327	194	186	297	263
ENSMUSG00000024712	chr19	Rfk	1.7E+07	1.7E+07	2603	-0.55268662	6.605704682	0.0042507	0.010869648	0.04392	-1	1774	1228	2275	1631	1890	1788	2244	1180	1474	1527

ENSMUSG00000024544	chr18	Ldlrad4	6.8E+07	6.8E+07	2493	-0.71019539	2.423273892	0.0042528	0.010873177	0.06154	-1	103	68	145	105	76	90	103	58	71	95
ENSMUSG00000037536	chr14	Fbxo34	4.7E+07	4.7E+07	3726	-0.56432206	3.65339755	0.0042635	0.010898495	0.04152	-1	180	172	268	238	274	218	288	149	219	174
ENSMUSG00000012117	chr4	Dhdds	1.3E+08	1.3E+08	3784	0.539624226	4.126718233	0.0042748	0.010923463	0.0391	1	202	130	239	195	324	541	371	281	488	468
ENSMUSG00000083678	chr4	Gm12989	1.4E+08	1.4E+08	731	1.065826139	-0.10250443	0.0042747	0.010923463	0.08031	1	6	7	9	8	9	22	23	23	23	20
ENSMUSG00000036985	chrX	Zdhhc9	4.8E+07	4.8E+07	6733	0.52541877	3.868873951	0.0043085	0.011007365	0.03606	1	165	126	181	174	258	381	375	238	408	377
ENSMUSG00000025487	chr7	Psmd13	1.4E+08	1.4E+08	3395	0.52188467	6.736782258	0.0043184	0.01103078	0.03929	1	1263	905	1607	1282	1616	3086	2391	2002	2792	2738
ENSMUSG00000074876	chr2	Spata5l1	1.2E+08	1.2E+08	1547	-0.77191193	1.902297553	0.0043253	0.011046312	0.07066	-1	67	53	89	61	80	63	86	44	52	35
ENSMUSG00000033417	chr19	Cacul1	6.1E+07	6.1E+07	5790	-0.47456437	5.353748315	0.0043265	0.011047455	0.0316	-1	707	555	860	715	731	733	827	536	720	718
ENSMUSG00000085411	chr2	Gm14319	1.7E+08	1.7E+08	703	-1.41612429	0.521797186	0.004336	0.011069604	0.23582	-1	28	48	17	36	9	20	14	10	25	10
ENSMUSG00000031828	chr8	Klhl36	1.2E+08	1.2E+08	2141	0.867419788	1.397940367	0.0043368	0.011069779	0.07937	1	32	22	24	16	39	76	63	42	73	83
ENSMUSG00000046139	chr19	Patl1	1.2E+07	1.2E+07	4221	-0.5110842	4.845557489	0.0043466	0.011092702	0.03621	-1	473	327	710	568	498	467	671	351	468	496
ENSMUSG00000022214	chr14	Dcaf11	5.6E+07	5.6E+07	8070	-0.58470252	7.38059248	0.0043498	0.011098812	0.04968	-1	2902	2140	4024	3298	2767	2670	3618	1929	2850	2775
ENSMUSG00000006307	chr7	Kmt2b	3.1E+07	3.1E+07	9596	-0.44917324	4.677326208	0.0043513	0.011098971	0.02745	-1	408	364	502	438	498	514	521	316	431	463
ENSMUSG00000019933	chr10	2310015B20Rik	7E+07	7E+07	1180	-0.66778412	5.807411095	0.0043528	0.011098971	0.06411	-1	1038	1132	765	727	1320	1011	935	648	857	1040
ENSMUSG00000020420	chr7	Zfp607	2.8E+07	2.8E+07	2061	-1.05231155	0.422752625	0.0043532	0.011098971	0.1146	-1	32	29	18	26	18	20	20	14	15	16
ENSMUSG00000036748	chr19	Cuedc2	4.6E+07	4.6E+07	1941	0.527953801	5.735459821	0.0043516	0.011098971	0.03981	1	602	354	882	738	798	1469	1173	963	1475	1426
ENSMUSG00000036941	chr18	Elac1	7.4E+07	7.4E+07	4971	-0.49984556	4.138781356	0.0043538	0.011098971	0.03342	-1	312	215	403	331	295	381	336	205	279	318
ENSMUSG00000029247	chr5	Paics	7.7E+07	7.7E+07	3139	-0.52533926	6.612104559	0.0043568	0.01110461	0.03987	-1	1544	1291	2237	1759	1928	1870	2050	1262	1570	1564
ENSMUSG00000025626	chrX	Phf6	5.3E+07	5.3E+07	6946	-0.79697401	2.444651348	0.0043711	0.01113892	0.08155	-1	99	90	126	101	92	113	129	57	47	66
ENSMUSG00000023919	chr17	Cenpq	4.1E+07	4.1E+07	2604	-0.75275844	1.875581931	0.0043797	0.011158956	0.06538	-1	71	54	86	72	54	71	54	51	47	52
ENSMUSG00000000628	chr6	Hk2	8.3E+07	8.3E+07	5969	-0.73979903	8.152054725	0.0043939	0.011193068	0.07961	-1	3900	2372	10007	6998	4861	4590	5833	3515	3796	4284
ENSMUSG00000031320	chrX	Rps4x	1E+08	1E+08	1631	0.586479635	8.505275313	0.0043976	0.011200545	0.05027	1	4188	3393	4632	4267	5389	11802	6893	7044	9451	10039
ENSMUSG00000002147	chr10	Stat6	1.3E+08	1.3E+08	4402	0.495341936	5.268086645	0.0044041	0.011214981	0.03454	1	396	335	545	421	757	1171	979	669	918	950
ENSMUSG00000042608	chr4	Stk40	1.3E+08	1.3E+08	4117	-0.60414431	7.248327935	0.0044094	0.011225167	0.05316	-1	2140	1952	3816	3456	2587	2656	3092	1715	2886	2206
ENSMUSG00000091277	chr12	Gm1818	4.9E+07	4.9E+07	2399	-0.79491715	1.531423903	0.0044097	0.011225167	0.07003	-1	69	37	56	54	51	42	50	37	35	47
ENSMUSG00000014503	chr18	Pkd2l2	3.4E+07	3.4E+07	2666	-1.0278547	0.099045321	0.0044231	0.011252986	0.08847	-1	18	14	28	18	23	12	24	9	13	9
ENSMUSG00000015709	chr7	Arnt2	8.4E+07	8.4E+07	5988	1.009543947	0.474065583	0.004423	0.011252986	0.09316	1	14	10	22	9	8	42	26	26	41	39
ENSMUSG00000037997	chr6	Parp11	1.3E+08	1.3E+08	5720	0.723119062	2.638102244	0.0044215	0.011252986	0.06611	1	45	51	73	73	110	256	139	112	149	141
ENSMUSG00000022971	chr16	Ifnar2	9.1E+07	9.1E+07	3329	1.026114671	4.188650585	0.004424	0.011253236	0.14879	1	152	90	116	76	518	689	382	436	525	471
ENSMUSG00000005683	chr10	Cs	1.3E+08	1.3E+08	2828	-0.65542909	9.854977736	0.0044264	0.011257508	0.0629	-1	13856	8655	29337	19179	17979	14247	19427	10685	14694	15540
ENSMUSG00000086915	chr10	Gm16365	4E+07	4E+07	1408	1.082476574	0.789831736	0.0044283	0.011260129	0.13284	1	9	8	28	8	28	41	27	40	49	64
ENSMUSG00000002107	chr2	Celf2	6539694	6545675	25884	-0.64399125	6.069707776	0.0044372	0.011280768	0.06002	-1	1466	1107	944	1077	1399	1013	1416	720	1089	1211
ENSMUSG00000038811	chr11	Gngt2	9.6E+07	9.6E+07	1877	1.006546857	2.627868396	0.004459	0.011334076	0.13783	1	44	25	44	47	160	256	108	132	167	176
ENSMUSG00000015970	chr14	Chdh	3E+07	3E+07	6156	-2.28751399	2.012603634	0.0044735	0.011367394	0.66875	-1	98	43	5	3	384	43	21	36	17	18
ENSMUSG00000044788	chr11	Fads6	1.2E+08	1.2E+08	6653	-1.02176339	3.844760194	0.0044737	0.011367394	0.14655	-1	204	97	783	305	167	187	324	120	159	197
ENSMUSG00000027207	chr2	Galk2	1.3E+08	1.3E+08	6088	0.829864407	2.721250396	0.0044824	0.011387505	0.09062	1	72	43	45	55	142	236	142	132	192	157
ENSMUSG00000031731	chr8	Ap1g1	1.1E+08	1.1E+08	7681	-0.50093767	5.828163677	0.0044883	0.011398329	0.03606	-1	904	732	1283	1124	987	1145	1157	696	950	947
ENSMUSG00000035109	chr2	Shc4	1.3E+08	1.3E+08	8263	0.939213459	0.960784553	0.004488	0.011398329	0.0894	1	17	13	22	29	12	50	68	36	50	43
ENSMUSG00000043795	chr7	Prr33	1.4E+08	1.4E+08	2348	-0.56737023	7.546080807	0.0044957	0.011414014	0.04718	-1	3185	2588	3867	3576	3554	3025	3976	2127	3516	3004
ENSMUSG00000059775	chr8	Rps26-ps1	1.1E+08	1.1E+08	410	0.635466603	3.145276465	0.0044961	0.011414014	0.05181	1	91	85	121	94	124	236	158	170	266	263
ENSMUSG00000021671	chr13	Poc5	9.6E+07	9.6E+07	3033	-0.63532835	2.58687363	0.0045014	0.0114254	0.04942	-1	91	85	158	105	109	117	119	67	95	86
ENSMUSG00000096606	chr7	Gm4980	1E+08	1E+08	3022	0.661612263	4.887323416	0.0045062	0.011435469	0.06183	1	294	339	264	438	323	695	806	452	1044	763
ENSMUSG00000029436	chr5	Mmp17	1.3E+08	1.3E+08	4395	0.883395853	0.507360862	0.0045085	0.011439333	0.06594	1	14	9	16	12	18	36	40	28	36	33
ENSMUSG00000031603	chr8	Fgf20	4E+07	4E+07	1678	-1.24986337	0.046053629	0.0045115	0.011444856	0.1624	-1	23	26	12	25	10	8	14	11	11	14
ENSMUSG00000063953	chr10	Amd2	3.6E+07	3.6E+07	3201	-1.43876006	3.795422441	0.0045191	0.011462097	0.28728	-1	151	124	454	117	827	90	444	87	82	78
ENSMUSG00000074521	chr2	Gm14327	1.8E+08	1.8E+08	1451	-1.02278291	0.559852379	0.0045212	0.011465163	0.10835	-1	30	36	22	24	23	23	22	13	20	18
ENSMUSG00000097245	chr10	Gm5421	2.2E+07	2.2E+07	2354	-0.93280003	2.272126559	0.0045244	0.011471373	0.113	-1	65	41	166	136	81	41	95	56	77	64
ENSMUSG00000020079	chr10	Supv3l1	6.2E+07	6.2E+07	2969	-0.5970358	4.180511882	0.004527	0.011475856	0.04923	-1	237	206	578	367	299	355	379	223	269	269
ENSMUSG00000042419	chr17	Nfkbil1	3.5E+07	3.5E+07	1746	0.638110183	3.163212474	0.0045388	0.011501507	0.05351	1	71	61	155	97	157	234	205	158	255	263
ENSMUSG00000052102	chr18	Gnpda1	3.8E+07	3.8E+07	2392	0.487640615	3.884995434	0.0045383	0.011501507	0.03088	1	171	136	223	171	226	456	357	243	368	363
ENSMUSG00000007815	chr9	Rhoa	1.1E+08	1.1E+08	7494	0.569829486	7.304313766	0.00454	0.011502567	0.04762	1	1651	1324	2120	1690	2991	4756	3597	3069	3904	4221
ENSMUSG00000023439	chr6	Gnb3	1.2E+08	1.2E+08	2632	1.031730016	0.335182802	0.0045503	0.011526472	0.09771	1	11	7	18	8	13	24	28	37	32	32
ENSMUSG00000024854	chr19	Pold4	4231899	4232188	910	0.591757719	4.016575092	0.0045614	0.011552512	0.04747	1	199	164	166	154	275	536	360	250	456	424
ENSMUSG00000027284	chr2	Cdan1	1.2E+08	1.2E+08	11421	-0.57535681	3.574983897	0.0045658	0.011561651	0.04427	-1	204	170	278	233	177	266	223	127	189	193
ENSMUSG00000027335	chr2	Adra1d	1.3E+08	1.3E+08	1899	-1.50378263	0.58274993	0.0045667	0.011561949	0.26531	-1	25	15	24	7	97	24	9	16	11	15
ENSMUSG00000029363	chr5	Rfc5	1.2E+08	1.2E+08	4669	0.809544964	1.739822938	0.0045763	0.011584044	0.07696	1	27	20	44	31	59	84	96	46	82	120
ENSMUSG00000057335	chr1	Cep170	1.8E+08	1.8E+08	18049	-0.60648541	3.659590667	0.0045777	0.011585454	0.04999	-1	224	207	199	187	311	256	261	142	171	211
ENSMUSG00000015766	chr6	Eps8	1.4E+08	1.4E+08	5731	0.628108981	3.014205486	0.0045816	0.011593358	0.04984	1	96	71	97	77	132	266	233	152	158	197
ENSMUSG00000027776	chr3	Il12a	6.9E+07	6.9E+07	1701	-1.10255084	1.992991262	0.0045847	0.011599105	0.16177	-1	106	83	50	50	99	29	102	25	57	48
ENSMUSG00000028274	chr4	Rngtt	3.3E+07	3.3E+07	7094	-0.6303747	3.545761018	0.0045861	0.011600431	0.05341	-1	188	111	343	238	217	195	266	113	181	199
ENSMUSG00000102014	chr1	2900009J06Rik	1.3E+08	1.3E+08	503	1.169371153	0.273552265	0.0045913	0.01161157	0.14462	1	4	5	25	9	9	38	18	23	45	30
ENSMUSG00000004631	chr6	Sgce	4674350	4674632	3086	0.772748686	3.926092231	0.0045934	0.011614857	0.08325	1	181	152	111	94	292	565	305	308	385	414
ENSMUSG00000064068	chr3	Mtx1	8.9E+07	8.9E+07	3584	0.537214914	4.353091661	0.0046129	0.011661832	0.04026	1	196	130	324	260	388	587	437	392	543	529
ENSMUSG00000039103	chr3	Nexn	1.5E+08	1.5E+08	2562	-0.62375093	8.55715192	0.0046176	0.011671763	0.05747	-1	6470	4655	9808	7320	6601	6040	8500	4302	4641	7370
ENSMUSG00000040586	chrX	Ofd1	1.7E+08	1.7E+08	4453	-0.64711875	3.138277679	0.0046257	0.011690103	0.05545	-1	155	154	178	162	135	174	178	96	117	146
ENSMUSG00000027332	chr2	Ivd	1.2E+08	1.2E+08	5505	-0.5487561	7.071883346	0.0046305	0.011700237	0.04429	-1	2431	1477	2995	2741	2545	2293	2458	1719	2440	2373
ENSMUSG00000031358	chrX	Msl3	1.7E+08	1.7E+08	2877	-0.51718177	5.153089008	0.0046317	0.011701112	0.03817	-1	631	440	859	716	512	693	761	422	568	602

ENSMUSG00000027875	chr3	Hmgcs2	9.8E+07	9.8E+07	3290	1.029627682	1.694462333	0.0046352	0.011707762	0.1339	1	21	20	25	17	76	88	123	59	60	103
ENSMUSG00000068134	chr2	Zfp120	1.5E+08	1.5E+08	4376	-0.56288516	3.64213579	0.0046441	0.011727218	0.04244	-1	245	180	253	221	203	270	235	147	172	222
ENSMUSG00000069008	chr3	Gm5537	5.8E+07	5.8E+07	1661	1.484540129	0.209187297	0.0046446	0.011727218	0.23926	1	6	6	0	9	19	22	33	11	51	40
ENSMUSG00000020183	chr10	Cpm	1.2E+08	1.2E+08	5964	-0.82836946	1.917811613	0.004648	0.011733854	0.08526	-1	56	31	132	73	82	74	72	29	58	48
ENSMUSG00000030032	chr6	Wdr54	8.3E+07	8.3E+07	6562	1.002623058	0.234773285	0.0046509	0.0117389	0.08141	1	7	8	13	10	15	24	29	21	39	31
ENSMUSG00000031701	chr8	Dnaja2	8.6E+07	8.6E+07	2839	-0.56361994	7.520306554	0.004664	0.011769842	0.04693	-1	3264	2650	3831	3321	3315	3264	3899	2446	2840	2858
ENSMUSG00000030815	chr7	Phkg2	1.3E+08	1.3E+08	3998	0.5532272	3.534864799	0.0046653	0.011771148	0.04027	1	121	93	163	137	199	330	245	192	328	325
ENSMUSG00000001802	chr7	Lrp3	3.5E+07	3.5E+07	4571	0.550609236	3.239949024	0.0046725	0.011787095	0.03849	1	104	73	137	108	159	285	240	166	237	226
ENSMUSG00000040771	chr17	Oard1	4.8E+07	4.8E+07	1336	-0.48105995	4.244896515	0.0046765	0.011795223	0.03149	-1	363	253	385	295	358	394	350	245	299	349
ENSMUSG00000029686	chr6	Cul1	4.7E+07	4.7E+07	4058	-0.53463327	6.466785202	0.0046795	0.011800521	0.04193	-1	1588	1148	1962	1643	1548	1738	1862	1143	1342	1411
ENSMUSG00000026387	chr1	Sctr	1.2E+08	1.2E+08	2012	0.647308947	3.577688756	0.0046936	0.011833942	0.05772	1	127	59	197	111	236	393	333	206	270	308
ENSMUSG00000041921	chr2	Metap1d	7.1E+07	7.1E+07	4537	-0.45786861	4.996381552	0.0046993	0.011846153	0.02953	-1	522	415	734	597	514	653	598	402	567	570
ENSMUSG00000033728	chr15	Lrrc14	7.7E+07	7.7E+07	5647	0.530655623	4.09608782	0.0047041	0.011854082	0.03881	1	157	122	303	203	300	460	387	309	477	446
ENSMUSG00000036241	chr4	Ube2r2	4.1E+07	4.1E+07	4189	-0.62044838	7.914438753	0.0047041	0.011854082	0.05704	-1	4268	4256	4091	4818	3859	4260	4145	2870	4370	4072
ENSMUSG00000022992	chr15	Kansl2	9.9E+07	9.9E+07	2417	-0.50883826	5.559967475	0.0047217	0.011894647	0.03747	-1	772	701	1030	818	820	845	1022	603	798	761
ENSMUSG00000028345	chr4	Tex10	4.8E+07	4.8E+07	4382	-0.54389885	3.620574314	0.0047227	0.011894647	0.03964	-1	223	172	246	232	211	246	259	137	203	194
ENSMUSG00000028898	chr4	Trnau1ap	1.3E+08	1.3E+08	2710	0.580412786	3.690752414	0.0047222	0.011894647	0.04541	1	120	117	180	126	243	394	263	268	327	328
ENSMUSG00000098754	chr2	Gm28045	1.3E+08	1.3E+08	3370	-0.58111156	3.549213071	0.0047241	0.011895895	0.04535	-1	210	184	247	180	219	173	244	163	194	181
ENSMUSG00000036208	chr16	BC027231	4.5E+07	4.5E+07	5741	-0.73661637	1.642462981	0.0047262	0.011898948	0.06179	-1	44	51	72	57	62	57	63	35	41	41
ENSMUSG00000040918	chr1	Slc19a2	1.6E+08	1.6E+08	3838	-0.74187677	2.338826415	0.0047332	0.011914508	0.06931	-1	100	59	135	104	76	76	115	55	64	77
ENSMUSG00000022295	chr15	Atp6v1c1	3.9E+07	3.9E+07	2097	0.462663001	5.236838219	0.0047454	0.011943005	0.03047	1	485	301	613	448	577	917	1022	621	965	1003
ENSMUSG00000020109	chr10	Dnajb12	6E+07	6E+07	3369	-0.49333359	5.8680776	0.004758	0.011972611	0.03545	-1	978	732	1207	1083	1169	1056	1213	675	1109	994
ENSMUSG00000027966	chr3	Col11a1	1.1E+08	1.1E+08	9657	0.89510022	2.331559443	0.0047743	0.012010004	0.10523	1	48	36	73	37	69	292	92	83	90	124
ENSMUSG00000075391	chr2	Gm13443	3.5E+07	3.5E+07	555	-0.66080318	3.393012549	0.0047745	0.012010004	0.05937	-1	238	135	219	195	169	152	223	125	204	130
ENSMUSG00000045573	chr4	Penk	4133531	4134507	1634	1.09265585	3.746839496	0.0047773	0.012014882	0.1702	1	97	65	123	30	370	449	456	248	368	370
ENSMUSG00000020722	chr11	Cacng1	1.1E+08	1.1E+08	1249	0.58837614	8.442657989	0.0047842	0.012027914	0.05156	1	4289	3268	3975	3659	5709	8875	8277	6846	10296	8724
ENSMUSG00000045534	chr6	Kcna5	1.3E+08	1.3E+08	2834	-0.81583079	2.251362814	0.0047842	0.012027914	0.08506	-1	62	55	181	100	67	87	75	57	60	72
ENSMUSG00000025192	chr19	Entpd7	4.4E+07	4.4E+07	8963	1.11230666	1.192945383	0.0047856	0.012029217	0.14556	1	14	20	15	8	46	92	47	39	73	57
ENSMUSG00000001435	chr10	Col18a1	7.7E+07	7.7E+07	7021	0.827822667	4.959752727	0.0047869	0.012030262	0.09962	1	272	228	244	182	817	1151	644	631	935	761
ENSMUSG00000073987	chr4	Ggh	2E+07	2E+07	1965	0.6578067	3.709259034	0.0047968	0.012052979	0.05931	1	153	119	126	99	265	418	313	231	349	342
ENSMUSG00000015522	chr3	Arnt	9.5E+07	9.5E+07	8007	-0.48503848	5.496254332	0.004801	0.012061523	0.03404	-1	712	633	1029	785	804	921	893	574	680	839
ENSMUSG00000054793	chr7	Cadm4	2.4E+07	2.4E+07	2161	0.883189295	1.800773919	0.0048033	0.012065002	0.09905	1	17	17	71	42	39	129	70	66	88	100
ENSMUSG00000030259	chr6	Rassf8	1.5E+08	1.5E+08	5559	-0.57997171	4.260212214	0.0048176	0.01209875	0.04719	-1	282	195	580	386	336	337	442	216	277	324
ENSMUSG00000026840	chr2	Lamc3	3.2E+07	3.2E+07	6091	-1.69381324	-0.00504668	0.0048324	0.012133665	0.32064	-1	4	16	31	3	58	11	9	7	4	13
ENSMUSG00000095385	chr9	D630033O11Rik	4.3E+07	4.3E+07	574	1.181681392	0.140920603	0.0048403	0.012151521	0.13885	1	4	5	10	9	18	31	13	26	25	43
ENSMUSG00000026924	chr2	Sec16a	2.6E+07	2.6E+07	9189	-0.46935653	5.378183891	0.0048424	0.012154489	0.03169	-1	692	495	905	814	753	801	804	565	727	704
ENSMUSG00000028675	chr4	Pnrc2	1.4E+08	1.4E+08	2213	-0.52123439	5.606258422	0.0048509	0.012173207	0.03959	-1	743	593	1221	912	919	905	1146	617	721	762
ENSMUSG00000035923	chr10	Myf6	1.1E+08	1.1E+08	1248	0.544444515	6.210415379	0.0048516	0.012173207	0.04367	1	855	653	1045	958	1042	1646	1765	1691	1972	1839
ENSMUSG00000063317	chr7	Usp31	1.2E+08	1.2E+08	10198	-0.53402536	3.88770226	0.0048547	0.012178972	0.03878	-1	255	217	291	274	262	228	284	215	243	261
ENSMUSG00000032691	chr11	Nlrp3	6E+07	6E+07	4057	1.193499996	0.008665806	0.0048795	0.012238961	0.12929	1	3	7	4	10	16	35	18	16	34	24
ENSMUSG00000039997	chr1	Ifi203	1.7E+08	1.7E+08	6706	0.655692546	3.000594798	0.0048832	0.01224384	0.05595	1	80	71	136	80	99	303	182	122	164	246
ENSMUSG00000079108	chr12	Srp54b	5.5E+07	5.5E+07	5603	-0.7063452	3.459080293	0.0048832	0.01224384	0.06944	-1	273	133	212	200	197	189	288	107	155	132
ENSMUSG00000022193	chr14	Psmb5	5.5E+07	5.5E+07	871	0.519158441	6.129107618	0.0048982	0.012279318	0.03975	1	827	571	1160	800	1051	1879	1508	1409	1925	1746
ENSMUSG00000066037	chr4	Hnrnpr	1.4E+08	1.4E+08	8733	-0.50388642	4.718026137	0.0049006	0.012283109	0.03606	-1	405	353	640	438	505	516	654	316	373	407
ENSMUSG00000020473	chr11	Aebp1	5861947	5862398	4058	0.784456674	7.111206632	0.0049052	0.012292405	0.09129	1	1988	1421	817	1523	1548	4718	2918	2821	4506	3151
ENSMUSG00000009097	chr16	Tbx1	1.9E+07	1.9E+07	1777	0.649837256	4.720665305	0.0049097	0.012301348	0.06129	1	221	157	520	408	290	537	611	498	880	765
ENSMUSG00000039738	chr16	Slx4	3979105	3980172	7657	-0.60653981	2.688713076	0.0049164	0.012315986	0.04606	-1	125	73	129	127	129	138	109	72	109	99
ENSMUSG00000057093	chr7	C030039L03Rik	2.8E+07	2.8E+07	5508	1.040214583	0.140569762	0.0049312	0.012350791	0.09218	1	12	5	10	10	11	48	23	16	23	28
ENSMUSG00000023971	chr17	Rrp36	4.7E+07	4.7E+07	1195	0.488491288	3.916501534	0.0049653	0.01243406	0.03208	1	168	127	245	187	227	442	322	283	395	369
ENSMUSG00000097908	chr5	4933404O12Rik	1.4E+08	1.4E+08	4101	-0.6669945	3.114893433	0.0049717	0.012447795	0.06053	-1	183	146	151	148	145	154	181	86	154	119
ENSMUSG00000061665	chr17	Cd2ap	4.3E+07	4.3E+07	5399	-0.50186581	4.192120852	0.0049762	0.012456868	0.03501	-1	323	264	367	266	384	393	377	224	264	314
ENSMUSG00000002844	chr16	Adprh	3.8E+07	3.8E+07	1583	0.471668877	5.465511179	0.0049839	0.01247386	0.03233	1	504	365	683	588	686	1290	985	857	1120	1041
ENSMUSG00000039357	chr14	Fut11	2.1E+07	2.1E+07	3344	0.815949936	2.283448347	0.0049858	0.012476444	0.08634	1	56	30	51	34	94	176	120	123	109	92
ENSMUSG00000062373	chr15	Tmem65	5.9E+07	5.9E+07	3747	-1.01745368	7.496297858	0.0049929	0.012491999	0.15308	-1	2544	1000	8886	4818	2367	2317	4101	1663	1896	2477
ENSMUSG00000020413	chr11	Hus1	8993137	8996346	6450	-0.59188627	3.363457998	0.0049984	0.012503692	0.04745	-1	163	146	210	222	179	200	229	114	166	142
ENSMUSG00000092329	chr8	Gm20388	1.2E+08	1.2E+08	3953	-0.52727866	6.438082792	0.0050218	0.012559919	0.04144	-1	1418	1089	1957	1406	1952	1804	1869	980	1505	1276
ENSMUSG00000046603	chr9	Tcaim	1.2E+08	1.2E+08	3126	-0.65043038	5.197562853	0.0050227	0.012559995	0.06213	-1	597	361	1195	825	494	532	816	430	517	657
ENSMUSG00000006494	chr2	Pdk1	7.2E+07	7.2E+07	7779	-0.6555057	6.368954393	0.005031	0.012578389	0.0641	-1	1445	821	2462	1973	1080	1408	1689	955	1282	1332
ENSMUSG00000037519	chr7	Ppfia1	1.4E+08	1.4E+08	10105	-0.47167939	4.591079863	0.0050331	0.012581492	0.03133	-1	359	309	545	479	423	466	477	309	359	479
ENSMUSG00000025558	chr14	Dock9	1.2E+08	1.2E+08	8199	-0.52017704	4.89153378	0.005037	0.012588937	0.03899	-1	403	314	717	511	777	540	655	302	469	586
ENSMUSG00000032702	chr19	Kank1	2.5E+07	2.5E+07	6166	-0.47474123	4.931022435	0.0050503	0.012619829	0.03235	-1	479	453	596	453	682	654	641	400	462	492
ENSMUSG00000019528	chr3	Gyg	2E+07	2E+07	2344	-0.55775668	8.467517433	0.0050834	0.012700393	0.04704	-1	6409	4716	7750	6686	6157	6488	7492	4115	5694	6057
ENSMUSG00000040738	chr4	Ints8	1.1E+07	1.1E+07	7472	-0.62588208	3.963917906	0.0050954	0.012728157	0.05584	-1	329	250	238	273	294	341	351	181	199	207
ENSMUSG00000028191	chr3	Bcl10	1.5E+08	1.5E+08	1760	0.490303299	4.097361289	0.0050979	0.012731964	0.03299	1	184	146	237	213	301	475	392	297	419	480
ENSMUSG00000027618	chr2	Nfs1	1.6E+08	1.6E+08	3612	-0.53769555	6.77311548	0.0051096	0.012758919	0.04341	-1	1922	1392	2525	2042	1918	1973	2374	1347	1816	1752
ENSMUSG00000002997	chr12	Prkar2b	3.2E+07	3.2E+07	3652	-2.31690484	4.755593072	0.0051299	0.012802956	0.7196	-1	781	224	13	22	2614	340	128	162	164	145
ENSMUSG00000036526	chr5	Card11	1.4E+08	1.4E+08	4112	1.133564189	1.341282713	0.0051296	0.012802956	0.15988	1	28	21	17	11	34	52	131	30	84	49

ENSMUSG00000076432	chr12	Ywhaq	2.1E+07	2.1E+07	3061	0.68129408	4.441225001	0.0051283	0.012802956	0.06756	1	211	167	231	168	511	826	471	465	465	535
ENSMUSG00000079480	chrX	Pin4	1E+08	1E+08	651	0.527718454	3.844835572	0.0051426	0.012832368	0.03802	1	164	130	186	165	240	438	295	308	344	345
ENSMUSG00000032652	chr6	Crebl2	1.3E+08	1.3E+08	3923	-0.50898922	4.349293595	0.0051525	0.01285461	0.0368	-1	395	283	327	337	439	434	409	229	315	368
ENSMUSG00000027357	chr2	Crls1	1.3E+08	1.3E+08	2082	-0.52422771	4.167756787	0.0051537	0.0128553	0.03856	-1	334	228	312	259	470	381	329	237	302	274
ENSMUSG00000103671	chr11	AL603913.1	4.5E+07	4.5E+07	453	1.319377147	0.172088373	0.0051606	0.012870365	0.19693	1	9	2	9	2	23	33	14	26	38	34
ENSMUSG00000029598	chr5	Plbd2	1.2E+08	1.2E+08	6620	0.606997094	5.789590302	0.0051621	0.012871801	0.05508	1	449	335	1207	680	801	1406	1466	936	1609	1509
ENSMUSG00000001053	chr11	N4bp3	5.2E+07	5.2E+07	2728	0.755665983	2.727377145	0.0051665	0.012880322	0.07782	1	50	38	106	64	123	192	126	152	224	140
ENSMUSG00000038305	chr1	Spats2l	5.8E+07	5.8E+07	8041	0.709857961	2.27121622	0.0051683	0.012882689	0.06161	1	55	37	56	59	62	191	95	78	133	116
ENSMUSG00000021993	chr14	Mipep	6.1E+07	6.1E+07	2403	-0.5027985	5.887032197	0.0051997	0.012958605	0.03761	-1	992	676	1353	1195	1066	1075	1227	725	1083	970
ENSMUSG00000032515	chr9	Csrnp1	1.2E+08	1.2E+08	2870	0.833111449	2.098093192	0.0052024	0.012962924	0.09026	1	22	24	55	69	61	142	83	85	105	136
ENSMUSG00000032415	chr9	Ube2cbp	8.6E+07	8.6E+07	1790	-0.75406385	2.444864806	0.0052045	0.012966012	0.07521	-1	102	93	101	113	87	80	82	55	126	71
ENSMUSG00000026574	chr1	Dpt	1.6E+08	1.6E+08	1724	1.066213408	7.344821866	0.0052089	0.012974589	0.16928	1	1376	1131	728	692	4228	7952	3603	3397	4172	3998
ENSMUSG00000058064	chr18	Gm10036	1.6E+07	1.6E+07	537	1.810296757	0.048013754	0.0052227	0.013006601	0.38575	1	6	1	2	3	19	9	70	10	40	16
ENSMUSG00000028651	chr4	Ppie	1.2E+08	1.2E+08	1719	0.498120859	4.195309629	0.0052274	0.013016106	0.0345	1	233	166	241	199	304	514	391	360	483	449
ENSMUSG00000032725	chr7	Folr2	1E+08	1E+08	1079	1.306955374	4.131783199	0.005231	0.013022824	0.24674	1	122	165	28	62	363	915	420	294	695	309
ENSMUSG00000020840	chr11	Blmh	7.7E+07	7.7E+07	5891	0.514743263	5.432036297	0.0052385	0.013038529	0.03901	1	590	399	571	511	589	1292	838	920	1085	1070
ENSMUSG00000037525	chr15	Bcdin3d	9.9E+07	9.9E+07	1271	0.673620661	2.427315051	0.0052392	0.013038529	0.05849	1	53	32	103	60	67	144	121	102	159	141
ENSMUSG00000001056	chr11	Nhp2	5.2E+07	5.2E+07	1146	0.497816446	4.343645143	0.0052454	0.013049412	0.03481	1	213	191	284	268	311	595	386	409	544	500
ENSMUSG00000028228	chr4	Cpne3	2E+07	2E+07	7131	-0.51224564	4.082361441	0.0052453	0.013049412	0.03686	-1	304	254	346	263	314	367	348	211	240	283
ENSMUSG00000010307	chr7	Tmem86a	4.7E+07	4.7E+07	1791	1.046806929	3.431543653	0.0052509	0.013060649	0.15994	1	66	21	294	59	144	354	297	238	265	329
ENSMUSG00000039497	chr10	Dse	3.4E+07	3.4E+07	4224	0.806343061	3.717200227	0.005256	0.013071099	0.09311	1	170	128	87	74	245	520	370	241	292	317
ENSMUSG00000036381	chr3	P2ry14	5.9E+07	5.9E+07	1797	0.837992173	1.088114171	0.0052606	0.01308027	0.06997	1	18	20	24	22	23	77	47	38	43	62
ENSMUSG00000068697	chr14	Myoz1	2.1E+07	2.1E+07	1294	-0.58621612	10.78599702	0.0052754	0.013114549	0.05251	-1	31986	25654	33330	28188	40026	27645	34026	21099	35767	27506
ENSMUSG00000031709	chr8	Tbc1d9	8.3E+07	8.3E+07	5887	0.912444651	1.572992541	0.0052791	0.013117209	0.10446	1	21	15	29	26	63	89	94	34	96	79
ENSMUSG00000033114	chr13	Slc35d2	6.4E+07	6.4E+07	2276	0.961503896	0.882845206	0.0052779	0.013117209	0.10223	1	19	9	11	14	36	56	49	33	57	40
ENSMUSG00000059022	chr6	Kcp	2.9E+07	2.9E+07	7806	0.705599476	2.625664363	0.0052792	0.013117209	0.06543	1	62	45	87	51	110	163	117	110	204	181
ENSMUSG00000000275	chr11	Trim25	8.9E+07	8.9E+07	5754	0.531800088	4.370557722	0.0052808	0.013118666	0.04014	1	232	205	285	180	376	700	513	317	490	538
ENSMUSG00000027868	chr3	Tbx15	9.9E+07	9.9E+07	3747	-0.59825842	8.205590818	0.0052817	0.013118666	0.05452	-1	5918	4542	5790	4320	5898	4782	6728	3402	4774	4728
ENSMUSG00000026803	chr2	Ttf1	2.9E+07	2.9E+07	6023	-0.58819352	3.099727235	0.0052882	0.013132387	0.04628	-1	160	116	197	142	155	174	188	91	121	137
ENSMUSG00000042185	chr9	Nfrkb	3.1E+07	3.1E+07	9953	-0.48447608	3.826482665	0.0052975	0.013153212	0.03193	-1	230	180	297	268	270	312	258	180	235	239
ENSMUSG00000036061	chr15	Smug1	1E+08	1E+08	3281	-0.56756329	3.303353053	0.0053005	0.013158426	0.04331	-1	173	117	210	174	218	203	209	122	166	121
ENSMUSG00000048799	chr18	Cep120	5.4E+07	5.4E+07	4553	-0.53688884	4.508974625	0.005312	0.013184556	0.04156	-1	352	265	596	465	378	429	541	288	309	358
ENSMUSG00000074219	chr8	Gm10644	8.4E+07	8.4E+07	2798	-1.2636316	0.277310667	0.0053186	0.013198704	0.18644	-1	37	28	11	26	12	15	10	9	15	21
ENSMUSG00000036167	chr15	Pphln1	9.3E+07	9.3E+07	4264	-0.56505285	3.723663272	0.0053294	0.013223075	0.0444	-1	239	164	345	209	239	214	306	162	228	187
ENSMUSG00000040865	chr1	Ino80d	6.3E+07	6.3E+07	17713	-0.50967636	4.052229384	0.0053386	0.01324357	0.03654	-1	287	265	324	268	295	326	300	214	257	315
ENSMUSG00000072694	chr5	1500011B03Rik	1.1E+08	1.1E+08	1746	0.931342923	2.438980129	0.0053479	0.013264218	0.11996	1	41	35	35	37	135	199	110	111	159	141
ENSMUSG00000002393	chr8	Nr2f6	7.1E+07	7.1E+07	2983	0.528439283	4.553037859	0.0053492	0.013265222	0.04056	1	201	178	443	303	364	595	538	468	724	510
ENSMUSG00000027387	chr2	Zc3h8	1.3E+08	1.3E+08	1624	-0.58595339	2.996001119	0.005366	0.013304511	0.04523	-1	135	103	200	123	163	140	169	84	136	130
ENSMUSG00000028032	chr3	Papss1	1.3E+08	1.3E+08	2599	0.655740563	3.528782496	0.0053703	0.013308168	0.06043	1	116	90	129	95	255	392	254	220	281	306
ENSMUSG00000036099	chr10	Vezt	9.4E+07	9.4E+07	20631	-0.45961207	5.187135468	0.0053701	0.013308168	0.03099	-1	640	464	795	647	632	711	800	437	604	640
ENSMUSG00000046519	chr3	Golph3l	9.6E+07	9.6E+07	2841	-0.55758034	3.809141126	0.00537	0.013308168	0.04396	-1	268	209	226	247	282	285	282	140	209	269
ENSMUSG00000008429	chr9	Herpud2	2.5E+07	2.5E+07	2744	-0.48087596	5.352261071	0.0053766	0.013321393	0.03421	-1	739	542	810	717	761	755	925	524	639	690
ENSMUSG00000003779	chr18	Kif20a	3.5E+07	3.5E+07	3796	0.973093133	0.80410627	0.005387	0.013344702	0.10215	1	9	10	19	26	19	58	45	41	50	26
ENSMUSG00000021557	chr13	Agtpbp1	5.9E+07	5.9E+07	12833	-0.54844613	5.911531353	0.005391	0.013352316	0.04534	-1	1025	818	1320	1259	931	1178	1352	713	863	991
ENSMUSG00000066235	chr9	Pomgnt2	1.2E+08	1.2E+08	2369	-0.4784262	3.991097995	0.0053976	0.013366426	0.03168	-1	273	202	324	276	319	307	313	185	313	259
ENSMUSG00000063652	chr11	Slc22a21	5.4E+07	5.4E+07	3645	1.104527283	0.017498048	0.0054007	0.013369243	0.10262	1	8	9	12	3	10	35	20	20	18	32
ENSMUSG00000086889	chr13	Phf2os1	4.9E+07	4.9E+07	498	1.177687083	-0.22983704	0.0054003	0.013369243	0.10874	1	6	6	4	8	9	26	11	20	22	24
ENSMUSG00000072591	chr5	5930412G12Rik	1.3E+08	1.3E+08	3394	1.374415366	0.810874922	0.0054076	0.013383862	0.23995	1	17	2	24	23	3	57	25	27	55	79
ENSMUSG00000036097	chr19	Fam178a	4.5E+07	4.5E+07	6880	-0.49838192	4.328585402	0.0054201	0.013412588	0.03545	-1	374	272	432	352	327	361	445	256	312	346
ENSMUSG00000050900	chrX	Gm7327	6.2E+07	6.2E+07	652	-0.97264512	0.953195815	0.0054321	0.013439808	0.11025	-1	45	29	56	30	25	30	41	20	25	14
ENSMUSG00000018666	chr11	Cbx1	9.7E+07	9.7E+07	4273	-0.48013384	4.950032059	0.0054388	0.013454003	0.0338	-1	589	453	575	487	568	577	675	389	498	535
ENSMUSG00000061979	chr5	Wbscr16	1.3E+08	1.3E+08	2874	-0.46662014	4.92013459	0.0054418	0.013459162	0.03165	-1	431	368	793	535	563	562	654	382	530	505
ENSMUSG00000036275	chr11	9530068E07Rik	5.2E+07	5.2E+07	3296	0.528412158	6.457937151	0.0054564	0.013492937	0.04237	1	1094	782	1067	1034	1461	2688	1963	1703	2203	2182
ENSMUSG00000014226	chr1	Cacybp	1.6E+08	1.6E+08	2390	-0.50259421	5.877190469	0.0054598	0.013495708	0.03804	-1	1094	750	1319	1030	1001	1200	1249	741	917	951
ENSMUSG00000017969	chr2	Ptgis	1.7E+08	1.7E+08	2567	0.917743027	2.240270881	0.0054604	0.013495708	0.11324	1	28	38	54	41	83	238	71	110	89	118
ENSMUSG00000024018	chr17	Ccdc167	3E+07	3E+07	4896	-0.68630727	2.617588037	0.0054594	0.013495708	0.06312	-1	127	103	110	111	98	121	103	73	110	75
ENSMUSG00000029684	chr6	Wasl	2.5E+07	2.5E+07	4923	-0.54572114	4.200921036	0.0054778	0.013536121	0.04269	-1	287	238	488	279	375	403	406	251	233	254
ENSMUSG00000027318	chr2	Adam33	1.3E+08	1.3E+08	5394	1.124681733	2.064126636	0.0054791	0.013536933	0.17256	1	23	42	20	24	80	186	62	62	105	172
ENSMUSG00000032388	chr9	Spg21	6.5E+07	6.5E+07	2690	0.739987731	4.250125769	0.0054813	0.013540199	0.08077	1	196	145	151	135	466	698	435	353	502	483
ENSMUSG00000003549	chr7	Ercc1	1.9E+07	1.9E+07	3111	0.503649546	4.083557275	0.0054871	0.013552063	0.03571	1	225	125	224	196	297	462	396	303	435	451
ENSMUSG00000019970	chr10	Sgk1	2.2E+07	2.2E+07	4903	-0.71172246	6.696352177	0.0055154	0.013619545	0.0773	-1	1349	1144	3316	2034	2250	1103	2575	1196	1336	1893
ENSMUSG00000037316	chr8	Bag4	2.6E+07	2.6E+07	4798	-0.5967982	3.019321572	0.0055224	0.013634518	0.0474	-1	151	106	160	113	205	148	156	94	144	122
ENSMUSG00000022280	chr15	Rnf19a	3.6E+07	3.6E+07	4276	-0.50744675	4.27133616	0.0055282	0.013646333	0.03693	-1	301	284	431	312	373	358	462	237	308	287
ENSMUSG00000040037	chr3	Negr1	1.6E+08	1.6E+08	6725	-1.77185827	0.46955411	0.0055318	0.013652946	0.39053	-1	34	19	4	8	93	15	5	16	13	10
ENSMUSG00000031494	chr8	Cd209a	3743395	3744234	1484	1.305679431	3.104037978	0.0055381	0.013665913	0.24381	1	81	89	10	33	136	340	169	276	193	243
ENSMUSG00000056394	chr7	Lig1	1.3E+07	1.3E+07	4268	0.930437086	1.951048768	0.0055411	0.013670865	0.11487	1	23	29	37	25	85	157	81	71	127	76
ENSMUSG00000083836	chr4	Ldha-ps2	1.2E+08	1.2E+08	1057	-0.70802603	2.480801961	0.0055421	0.013671093	0.06708	-1	105	77	116	105	111	77	119	52	120	67

ENSMUSG00000040219	chr9	Ttc12	4.9E+07	4.9E+07	4545	0.706560495	2.337917638	0.0055625	0.01371648	0.06475	1	41	36	95	49	70	173	154	74	138	105
ENSMUSG00000049124	chr17	Gm8186	2.6E+07	2.6E+07	386	0.75246355	2.024234277	0.0055621	0.01371648	0.06999	1	47	35	50	41	47	151	76	74	131	83
ENSMUSG00000082922	chr7	Gm6939	1.3E+08	1.3E+08	864	0.86874323	0.971519505	0.0055646	0.013719397	0.08054	1	18	13	28	9	32	53	56	37	47	52
ENSMUSG00000021978	chr14	Extl3	6.5E+07	6.5E+07	5977	-0.52494478	6.337057075	0.0055657	0.013719539	0.04203	-1	1457	1110	1589	1371	1637	1413	1702	982	1541	1236
ENSMUSG00000050908	chr16	Tvp23a	1E+07	1E+07	3971	1.015797717	0.27379311	0.0055694	0.013726402	0.09539	1	7	8	11	13	15	42	23	22	42	21
ENSMUSG00000028223	chr4	Decr1	1.6E+07	1.6E+07	3879	-0.65186039	7.629656673	0.0055719	0.013730068	0.06534	-1	3296	1589	6634	3551	4143	3618	3933	2207	2628	3690
ENSMUSG00000028902	chr4	Sf3a3	1.2E+08	1.2E+08	2785	0.491601964	4.313377032	0.0056052	0.013809692	0.0347	1	204	164	345	239	314	582	398	430	476	485
ENSMUSG00000025793	chr11	Hgs	1.2E+08	1.2E+08	2991	0.494129008	4.79304526	0.0056197	0.013843005	0.03595	1	287	205	463	348	476	699	604	456	855	738
ENSMUSG00000067148	chr17	Polr1c	4.6E+07	4.6E+07	2278	0.587504438	3.82957854	0.0056265	0.013857222	0.04903	1	145	142	180	116	273	422	317	272	407	333
ENSMUSG00000046351	chr13	Zfp322a	2.3E+07	2.3E+07	5197	-0.56052879	3.704392978	0.0056278	0.013857953	0.04432	-1	220	202	291	232	206	275	235	187	170	214
ENSMUSG00000022860	chr16	Chodl	7.9E+07	7.9E+07	3820	0.61711913	3.768946946	0.0056298	0.013860676	0.05418	1	129	141	243	140	152	458	278	290	251	413
ENSMUSG00000025525	chrX	Apool	1.1E+08	1.1E+08	3486	-0.4938107	5.168987367	0.0056311	0.013861268	0.03635	-1	643	429	855	696	559	666	809	422	605	606
ENSMUSG00000022110	chr14	Sucla2	7.4E+07	7.4E+07	3988	-0.59764294	9.067361407	0.0056379	0.013873413	0.05533	-1	9849	5983	14533	9844	9418	9020	12421	6476	7911	8507
ENSMUSG00000032777	chr7	Gtf3c1	1.3E+08	1.3E+08	6960	-0.5276792	5.673140139	0.0056389	0.013873413	0.04219	-1	819	665	1130	1063	862	856	1116	567	1003	805
ENSMUSG00000058655	chr15	Eif4b	1E+08	1E+08	3853	-0.54577577	8.129833657	0.005639	0.013873413	0.04611	-1	4973	3944	6034	5146	4810	5258	5546	3253	4543	5139
ENSMUSG00000018572	chr11	Phf23	7E+07	7E+07	3273	0.463727531	4.840972765	0.0056478	0.013892617	0.03141	1	304	251	401	366	513	888	591	540	697	715
ENSMUSG00000097589	chr14	Dleu2	6.2E+07	6.2E+07	11334	0.732023255	2.592937866	0.0056514	0.01389912	0.07007	1	69	57	49	68	86	233	138	103	119	181
ENSMUSG00000029466	chr5	Anapc7	1.2E+08	1.2E+08	5119	0.451080206	4.807061689	0.0056749	0.013954424	0.02976	1	278	227	498	355	465	771	661	542	641	711
ENSMUSG00000028788	chr4	Ptp4a2	1.3E+08	1.3E+08	4377	-0.59556361	9.654563855	0.0056771	0.013957447	0.05508	-1	15808	11868	15412	15032	13861	13816	17636	9454	14010	11810
ENSMUSG00000038525	chr5	Armc10	2.2E+07	2.2E+07	3407	0.678543681	3.055769965	0.0056809	0.013964223	0.064	1	85	60	101	73	168	277	196	168	151	254
ENSMUSG00000030621	chr7	Me3	9E+07	9E+07	14624	-0.5683154	6.729928408	0.0056834	0.013965473	0.04973	-1	1858	1357	2540	2230	1572	1911	2247	1233	1862	1644
ENSMUSG00000087367	chr19	Gm15491	4.6E+07	4.6E+07	751	-0.90525389	0.926377326	0.0056825	0.013965473	0.09221	-1	20	34	42	43	39	23	34	26	26	20
ENSMUSG00000024678	chr19	Ms4a4d	1.2E+07	1.2E+07	1513	0.759996745	3.286373362	0.0056897	0.013978535	0.08201	1	87	102	82	75	190	361	269	218	233	172
ENSMUSG00000033055	chr15	Ankrd54	7.9E+07	7.9E+07	4270	0.627183115	2.78272971	0.0056917	0.013979104	0.05175	1	75	51	85	74	122	218	152	142	182	153
ENSMUSG00000080836	chr5	Gm6444	1.2E+08	1.2E+08	458	1.018882056	1.450728961	0.0056919	0.013979104	0.1333	1	20	13	29	34	36	42	78	29	114	100
ENSMUSG00000028080	chr3	Lrba	8.6E+07	8.6E+07	18270	-0.5371627	5.279695504	0.0057011	0.013999349	0.04343	-1	599	422	1048	845	612	659	836	469	597	724
ENSMUSG00000055436	chr3	Srsf11	1.6E+08	1.6E+08	7135	-0.46421817	5.147843234	0.0057143	0.014029164	0.03212	-1	584	531	672	579	697	712	682	445	533	721
ENSMUSG00000012609	chr12	Ttll5	8.6E+07	8.6E+07	15833	-0.64300972	2.525727712	0.0057173	0.014034056	0.05444	-1	91	82	136	120	92	98	103	59	88	114
ENSMUSG00000016637	chr15	Ift27	7.8E+07	7.8E+07	1012	0.665661273	3.451940007	0.0057364	0.014078548	0.06324	1	131	78	118	88	230	322	236	241	302	261
ENSMUSG00000086965	chr16	Gm16314	1.8E+07	1.8E+07	865	-1.02258199	-0.05382347	0.00574	0.01408485	0.08193	-1	11	12	23	20	24	12	9	11	12	15
ENSMUSG00000022698	chr16	Naa50	4.4E+07	4.4E+07	4648	-0.59952023	8.291850356	0.0057442	0.014092629	0.05584	-1	5762	4096	8005	4989	5883	4610	7609	3706	4639	5272
ENSMUSG00000029851	chr6	Fam115c	4.3E+07	4.3E+07	4775	0.820263422	1.918732117	0.0057566	0.014120338	0.08616	1	42	28	28	32	70	137	82	89	84	88
ENSMUSG00000041594	chr14	Tmtc4	1.2E+08	1.2E+08	7367	-0.94077391	1.388851369	0.0057575	0.014120338	0.11322	-1	61	23	66	34	76	61	44	21	18	40
ENSMUSG00000027677	chr3	Ttc14	3.4E+07	3.4E+07	11072	-0.5541311	3.856339065	0.0057586	0.014120733	0.04401	-1	196	225	322	287	254	316	250	186	181	281
ENSMUSG00000012535	chr6	Tnpo3	3E+07	3E+07	10246	-0.51438786	5.828635273	0.0057719	0.014150883	0.04041	-1	984	774	1206	1094	950	1067	1294	661	876	981
ENSMUSG00000029071	chr4	Dvl1	1.6E+08	1.6E+08	4996	-0.55127604	7.196265679	0.0057762	0.014158746	0.04711	-1	2210	1837	3640	2886	2732	2579	3217	1663	2607	2329
ENSMUSG00000035575	chr11	Utp6	8E+07	8E+07	4517	-0.51944944	5.40287595	0.0057915	0.014193817	0.04089	-1	834	651	830	697	664	801	789	606	675	703
ENSMUSG00000029502	chr5	Golga3	1.1E+08	1.1E+08	12671	-0.58296358	5.867202445	0.005843	0.014315188	0.05223	-1	963	648	1572	1318	846	1082	1304	599	888	1025
ENSMUSG00000089704	chr8	Galnt2	1.2E+08	1.2E+08	4282	-0.51722289	6.423852849	0.005843	0.014315188	0.04131	-1	1391	1080	1933	1390	1928	1789	1861	971	1498	1273
ENSMUSG00000021222	chr12	Dcaf4	8.4E+07	8.4E+07	2081	-0.44363164	4.810242123	0.0058485	0.014323348	0.02888	-1	453	352	603	488	552	493	595	332	549	496
ENSMUSG00000024121	chr17	Atp6v0c	2.4E+07	2.4E+07	3384	0.472591699	5.133494375	0.0058494	0.014323348	0.03339	1	390	286	556	457	561	829	876	537	1055	936
ENSMUSG00000046417	chr11	Lrrc75a	6.3E+07	6.3E+07	2089	0.62529495	2.759088297	0.0058487	0.014323348	0.05112	1	73	58	85	94	83	230	143	123	187	156
ENSMUSG00000030970	chr7	Ctbp2	1.3E+08	1.3E+08	6220	-0.63607656	3.349580162	0.0058795	0.01439446	0.05738	-1	119	135	247	227	213	162	247	116	158	140
ENSMUSG00000070939	chr1	Tgfbrap1	4.3E+07	4.3E+07	10972	-0.46912515	4.571677598	0.0058827	0.014399705	0.0322	-1	321	321	536	441	471	477	534	294	353	414
ENSMUSG00000005481	chr8	Ddx39	8.4E+07	8.4E+07	5155	0.472474565	4.194708063	0.0058914	0.014418594	0.03175	1	220	160	263	246	266	476	436	385	410	462
ENSMUSG00000084845	chr4	Tmem240	1.6E+08	1.6E+08	5514	1.279392443	-0.30803241	0.005899	0.014434655	0.15549	1	2	1	6	6	16	21	16	11	26	26
ENSMUSG00000028980	chr4	H6pd	1.5E+08	1.5E+08	5236	-0.61624196	5.730034725	0.0059016	0.014438422	0.05842	-1	901	660	915	716	1749	970	1227	625	792	746
ENSMUSG00000020282	chr11	Rhbdf1	3.2E+07	3.2E+07	5433	0.530622002	4.747715847	0.0059085	0.014452852	0.0421	1	243	219	359	333	535	706	544	480	821	719
ENSMUSG00000041596	chr7	Nlrp5-ps	1.5E+07	1.5E+07	4335	1.356241715	-0.31011018	0.0059156	0.014467744	0.16956	1	8	4	6	8	2	30	6	20	19	25
ENSMUSG00000002825	chr9	Qtrt1	2.1E+07	2.1E+07	1319	0.63264536	2.428955291	0.005945	0.014537042	0.05102	1	51	39	83	71	72	145	115	110	133	155
ENSMUSG00000039473	chr16	Ubn1	5050068	5050781	6455	-0.47987872	5.654268071	0.0059692	0.014593603	0.03521	-1	794	650	1150	970	869	958	1061	609	858	887
ENSMUSG00000084896	chr11	Gm11632	9.8E+07	9.8E+07	674	-0.81233892	1.440053143	0.0059744	0.014603827	0.08275	-1	49	40	77	33	57	53	58	19	36	36
ENSMUSG00000031775	chr8	Pllp	9.5E+07	9.5E+07	1889	1.009688951	0.869755667	0.0059787	0.014611723	0.12463	1	6	7	27	17	32	66	36	25	57	54
ENSMUSG00000059040	chr18	Eno1b	4.8E+07	4.8E+07	1757	0.745998133	4.825481689	0.005984	0.014622141	0.08528	1	262	158	300	215	740	773	561	632	936	716
ENSMUSG00000071477	chr6	Zfp777	4.8E+07	4.8E+07	3588	-0.49272766	4.463092015	0.0059876	0.014628446	0.03561	-1	328	252	485	483	411	375	418	267	456	376
ENSMUSG00000040621	chrX	Gemin8	1.7E+08	1.7E+08	2487	0.900211295	0.410742663	0.0060012	0.014659196	0.07287	1	13	10	11	11	18	42	32	26	27	35
ENSMUSG00000025521	chr8	Tmem192	6.5E+07	6.5E+07	1123	0.459664375	4.280958303	0.0060134	0.014686474	0.03038	1	203	166	302	233	347	519	470	338	500	495
ENSMUSG00000038086	chr9	Hspb2	5.1E+07	5.1E+07	840	0.52651352	6.271703239	0.0060185	0.014696275	0.04291	1	903	749	975	1096	998	2043	1826	1384	2208	1971
ENSMUSG00000036371	chr6	Serbp1	6.7E+07	6.7E+07	6685	-0.56223757	8.009113114	0.0060277	0.014714133	0.04968	-1	4449	3851	5385	5142	4000	4678	4952	3318	4154	4430
ENSMUSG00000041000	chr4	Trim62	1.3E+08	1.3E+08	5015	1.063238617	0.70196973	0.0060279	0.014714133	0.13397	1	8	6	20	7	36	40	44	33	39	52
ENSMUSG00000010453	chr1	Kansl3	3.6E+07	3.6E+07	6742	-0.50196155	5.798725714	0.006032	0.014721625	0.03879	-1	892	620	1449	1040	1011	1164	1176	663	845	962
ENSMUSG00000096401	chr8	Gm21811	2E+07	2E+07	930	-1.21741016	0.099015561	0.0060426	0.014744816	0.16294	-1	26	25	22	15	13	23	12	13	4	10
ENSMUSG00000032288	chr9	Imp3	5.7E+07	5.7E+07	924	0.470854706	5.140294425	0.0060594	0.014783402	0.03336	1	427	323	484	435	563	977	671	716	897	937
ENSMUSG00000031446	chr8	Cul4a	1.3E+07	1.3E+07	6408	-0.56051002	6.694854761	0.0060644	0.014792867	0.0491	-1	1821	1343	2627	1917	1639	1878	2353	1320	1539	1590
ENSMUSG00000070583	chr4	Fv1	1.5E+08	1.5E+08	1380	-0.9238128	1.130268464	0.0060733	0.014812044	0.10588	-1	46	44	35	44	32	34	44	18	20	37
ENSMUSG00000041841	chr15	Rpl37	5116613	5116684	867	0.548302983	6.882878198	0.0060907	0.014851951	0.04708	1	1316	1018	1833	1392	1752	3523	2118	2371	3302	3126
ENSMUSG00000025815	chr2	Dhtkd1	5896115	5898812	6333	-1.07606621	1.151413507	0.0060977	0.014866384	0.15179	-1	64	37	36	19	61	42	20	22	16	44

ENSMUSG00000048550	chr2	Thnsl1	2.1E+07	2.1E+07	4043	-0.69115323	2.903359719	0.0061021	0.0148719	0.06741	-1	166	82	169	117	165	144	181	82	105	80
ENSMUSG00000054893	chr7	Zfp667	6286579	6286654	4755	-0.61774868	2.610249357	0.0061012	0.0148719	0.05016	-1	110	85	130	120	102	128	114	76	90	86
ENSMUSG00000028701	chr4	Lurap1	1.2E+08	1.2E+08	5886	-0.58530872	3.023680684	0.0061241	0.014923057	0.04641	-1	110	101	196	141	196	138	172	100	135	122
ENSMUSG00000031286	chr3	Glt28d2	8.6E+07	8.6E+07	2732	-0.67427523	3.015527177	0.0061354	0.014948009	0.06435	-1	133	115	191	184	115	140	182	96	93	130
ENSMUSG00000008167	chr8	Fbxw9	8.5E+07	8.5E+07	3383	0.744338021	2.559032589	0.0061496	0.014979787	0.07633	1	55	49	72	35	121	170	142	112	180	143
ENSMUSG00000062997	chr2	Rpl35	3.9E+07	3.9E+07	1241	0.55702002	7.01779882	0.0061529	0.014985341	0.04873	1	1546	1201	1896	1504	1764	3828	2313	2673	3527	3526
ENSMUSG00000032449	chr9	Slc25a36	9.7E+07	9.7E+07	9594	-0.47581603	5.36199134	0.0061616	0.015003953	0.03466	-1	620	622	920	698	720	768	856	488	717	747
ENSMUSG00000026925	chr2	Inpp5e	2.6E+07	2.6E+07	4301	-0.5389278	3.926475398	0.0061644	0.015008203	0.04234	-1	213	198	418	297	241	280	292	161	256	300
ENSMUSG00000040464	chr5	Gtpbp10	5537454	5539451	4744	-0.47452293	3.772296067	0.0061837	0.015052565	0.03149	-1	220	164	312	235	275	276	247	170	231	258
ENSMUSG00000044068	chr11	Zrsr1	2.3E+07	2.3E+07	3282	-0.57673124	3.775435955	0.0061901	0.01506382	0.04846	-1	310	148	307	218	257	230	306	161	183	256
ENSMUSG00000058443	chr9	Rpl10-ps3	5E+07	5E+07	742	1.404821822	1.475278005	0.0061905	0.01506382	0.2682	1	11	26	2	23	43	55	56	48	122	114
ENSMUSG00000002496	chr17	Tsc2	2.5E+07	2.5E+07	6018	-0.58631618	6.18764228	0.0062161	0.015123451	0.05379	-1	1054	762	2063	1654	1229	1149	1456	814	1400	1229
ENSMUSG00000016409	chrX	Nkap	3.7E+07	3.7E+07	4326	-0.55500448	3.650184872	0.0062281	0.015150032	0.04475	-1	237	154	258	242	230	265	258	104	216	227
ENSMUSG00000039137	chr4	Whrn	6.3E+07	6.3E+07	7337	0.910361287	0.814682202	0.0062315	0.01515569	0.09261	1	13	11	30	8	26	50	54	39	36	40
ENSMUSG00000029348	chr5	Asphd2	1.1E+08	1.1E+08	1584	1.170827828	0.008663381	0.0062333	0.015157536	0.14089	1	7	7	7	1	19	34	23	19	20	30
ENSMUSG00000038366	chr11	Lasp1	9.8E+07	9.8E+07	6495	0.824951826	5.671658362	0.0062398	0.015170648	0.10618	1	411	308	418	334	1442	1631	1167	1041	1446	1446
ENSMUSG00000050071	chrX	Bex1	1.4E+08	1.4E+08	1186	0.725954415	4.622907944	0.0062437	0.015177562	0.08019	1	380	265	169	293	212	777	493	418	738	762
ENSMUSG00000057406	chr5	Whsc1	3.4E+07	3.4E+07	15898	-0.51746654	3.824298734	0.0062505	0.015191463	0.03864	-1	240	209	319	246	227	289	286	188	222	216
ENSMUSG00000041889	chr1	Shisa4	1.4E+08	1.4E+08	2418	0.548200826	7.244906028	0.0062688	0.015233152	0.04751	1	1866	1184	2057	1749	2576	3852	3581	2663	4627	3924
ENSMUSG00000039450	chr11	Dcxr	1.2E+08	1.2E+08	1144	0.61418633	3.268343015	0.0062751	0.015245881	0.05336	1	116	76	113	109	157	252	178	180	317	259
ENSMUSG00000020076	chr10	Ddx50	6.3E+07	6.3E+07	2527	-0.46055162	5.444477522	0.0062814	0.015256142	0.03255	-1	772	525	978	712	845	954	866	580	686	719
ENSMUSG00000021408	chr13	Ripk1	3.4E+07	3.4E+07	6138	0.630621016	3.139616927	0.0062815	0.015256142	0.05591	1	90	78	97	85	169	317	198	145	204	244
ENSMUSG00000001520	chr6	Nrip2	1.3E+08	1.3E+08	3602	0.746481062	2.170248212	0.0062974	0.01529118	0.07182	1	55	39	35	43	72	143	95	78	136	118
ENSMUSG00000002365	chr17	Snx9	5841328	5841546	2411	-0.45816426	4.82858836	0.0062988	0.01529118	0.03162	-1	503	392	532	471	561	637	610	362	434	448
ENSMUSG00000062960	chr5	Kdr	7.6E+07	7.6E+07	7278	-0.60452698	5.962184798	0.0062992	0.01529118	0.0572	-1	716	553	1927	1155	1643	1151	1174	732	952	1133
ENSMUSG00000022105	chr14	Rb1	7.3E+07	7.3E+07	6015	-0.49810737	4.839192051	0.0063028	0.015297327	0.03765	-1	504	409	548	569	454	506	635	395	443	463
ENSMUSG00000002778	chr7	Kdelr1	4.6E+07	4.6E+07	1873	0.515076839	6.150741345	0.0063075	0.015305952	0.04155	1	846	576	1024	837	1192	2187	1440	1279	1986	1781
ENSMUSG00000034269	chr6	Setd5	1.1E+08	1.1E+08	12481	-0.42890122	5.127545664	0.0063113	0.01531262	0.02787	-1	583	462	716	586	673	774	700	423	587	624
ENSMUSG00000029364	chr5	Wsb2	1.2E+08	1.2E+08	5857	0.543053432	7.400459432	0.006322	0.01533605	0.04677	1	1922	1328	3032	1857	2477	4322	5332	2769	4329	4130
ENSMUSG00000057092	chr7	Fxyd3	3.1E+07	3.1E+07	4850	1.143078446	0.07954228	0.0063262	0.015343558	0.1199	1	6	9	12	9	7	36	11	20	34	31
ENSMUSG00000030770	chr7	Parva	1.1E+08	1.1E+08	10157	0.560413559	4.951312902	0.0063298	0.01534682	0.04827	1	327	240	342	323	692	1060	664	594	751	751
ENSMUSG00000032280	chr9	Tle3	6.1E+07	6.1E+07	11653	0.92840876	4.215696099	0.0063292	0.01534682	0.13263	1	145	112	129	99	521	621	350	497	423	573
ENSMUSG00000014778	chr8	Fhod1	1.1E+08	1.1E+08	4666	0.526660429	6.088636766	0.0063353	0.015356252	0.04352	1	740	481	1117	903	1072	1809	1853	1183	2058	1425
ENSMUSG00000035863	chr10	Palm	8E+07	8E+07	2651	0.678075775	4.428854866	0.0063358	0.015356252	0.07044	1	156	170	229	195	535	678	459	364	604	647
ENSMUSG00000007836	chr13	Hnrnpa0	5.8E+07	5.8E+07	2678	0.536541536	5.646798552	0.0063437	0.015372707	0.04501	1	501	325	907	578	898	1313	1045	1009	1407	1309
ENSMUSG00000022996	chr15	Wnt10b	9.9E+07	9.9E+07	2334	-1.30880502	0.288165102	0.006368	0.015428892	0.21514	-1	14	20	10	17	64	13	13	8	9	25
ENSMUSG00000042492	chr7	Tbc1d10b	1.3E+08	1.3E+08	4690	0.500802943	5.649849023	0.0063733	0.015438982	0.03904	1	522	371	781	683	852	1307	1251	755	1468	1352
ENSMUSG00000003929	chr17	Zfp81	3.3E+07	3.3E+07	6639	-0.6743979	2.094899146	0.0063761	0.015443053	0.05762	-1	78	61	100	73	76	84	61	64	56	66
ENSMUSG00000015942	chr5	Gtf2ird2	1.3E+08	1.3E+08	5572	-0.62524884	2.828101446	0.0063829	0.01545692	0.05287	-1	112	76	151	155	159	127	123	104	123	89
ENSMUSG00000024401	chr17	Tnf	3.5E+07	3.5E+07	1639	1.245215104	0.339507051	0.0063881	0.015466955	0.1889	1	6	1	7	22	16	30	22	27	35	49
ENSMUSG00000036989	chr7	Trim3	1.1E+08	1.1E+08	4569	0.488514105	4.509202393	0.0063905	0.015469975	0.0353	1	238	250	291	249	388	608	528	383	588	641
ENSMUSG00000032966	chr2	Fkbp1a	1.5E+08	1.5E+08	3857	0.554520789	7.330401279	0.0063929	0.015473203	0.04885	1	1768	1434	1974	1833	2907	4455	3462	2972	4608	4310
ENSMUSG00000024792	chr19	Zfpl1	6080762	6081214	1798	0.55179435	3.760451617	0.0064022	0.015493084	0.04393	1	135	124	155	174	237	429	286	213	381	362
ENSMUSG00000021906	chr14	Oxnad1	3.2E+07	3.2E+07	5769	-0.64555743	4.949080584	0.0064038	0.015494176	0.06453	-1	453	264	1172	612	478	553	678	356	456	460
ENSMUSG00000024581	chr18	Napg	6.3E+07	6.3E+07	5139	-0.46925239	4.417135067	0.0064088	0.01550361	0.0327	-1	378	297	425	366	385	372	467	269	375	367
ENSMUSG00000098021	chr15	Gm9522	3.9E+07	3.9E+07	931	-1.08166434	0.944642085	0.0064106	0.015505337	0.15136	-1	59	29	41	36	20	32	43	19	13	17
ENSMUSG00000002808	chr13	Epdr1	2E+07	2E+07	2386	-0.57398416	7.326935697	0.0064202	0.015525725	0.05243	-1	3010	2188	3427	3386	2310	2801	3109	1925	2908	2641
ENSMUSG00000098134	chr12	Rnf113a2	8.4E+07	8.4E+07	1383	-0.57292458	3.076166762	0.0064288	0.015543221	0.04566	-1	137	112	195	124	195	177	180	91	117	139
ENSMUSG00000104049	chr12	AC120402.1	8.4E+07	8.4E+07	1383	-0.57292464	3.076166762	0.0064296	0.015543221	0.04566	-1	137	112	195	124	195	177	180	91	117	139
ENSMUSG00000030077	chr6	Chl1	1E+08	1E+08	7751	1.106007059	0.403194289	0.0064437	0.01557449	0.13543	1	12	9	10	9	17	42	39	45	18	20
ENSMUSG00000032422	chr9	Snx14	8.8E+07	8.8E+07	6107	-0.46392228	4.254804961	0.0064493	0.015585362	0.0316	-1	349	260	367	317	359	399	372	263	294	327
ENSMUSG00000058594	chr2	Fbxo18	1.2E+07	1.2E+07	5115	-0.44196959	5.061016289	0.0064505	0.015585634	0.02978	-1	567	476	615	573	635	694	713	431	534	566
ENSMUSG00000012483	chr6	Rpa3	8255936	8256247	1136	0.648881885	2.273152376	0.0064543	0.015590391	0.05376	1	47	34	63	60	77	161	105	102	117	109
ENSMUSG00000074925	chr19	Ptar1	2.4E+07	2.4E+07	2064	-1.12049328	0.581455258	0.0064547	0.015590391	0.15331	-1	28	28	35	39	13	10	25	9	27	22
ENSMUSG00000029833	chr6	Trim24	3.8E+07	3.8E+07	8521	-0.56397685	5.312053205	0.0064642	0.015610435	0.0495	-1	566	488	1033	549	1041	635	1014	499	555	613
ENSMUSG00000053470	chr6	Kdm3a	7.2E+07	7.2E+07	4921	-0.51020982	4.063582323	0.0064652	0.015610435	0.0385	-1	260	247	350	316	290	345	356	206	222	302
ENSMUSG00000018736	chr11	Ndel1	6.9E+07	6.9E+07	3253	-0.51302015	5.743231122	0.0064777	0.015637985	0.04127	-1	914	665	1263	883	1074	1002	1308	578	928	802
ENSMUSG00000031482	chr8	Slc25a15	2.2E+07	2.2E+07	3451	-0.54937965	4.020318589	0.0064849	0.01565249	0.04484	-1	266	169	424	357	256	321	357	185	255	252
ENSMUSG00000096687	chr10	AA474331	4E+07	4E+07	3833	-0.65405873	2.3362012	0.0064953	0.015674937	0.05588	-1	92	65	133	74	100	98	101	65	63	73
ENSMUSG00000055128	chr14	Cgrrf1	4.7E+07	4.7E+07	3291	-0.45060663	5.083180802	0.006504	0.015693326	0.03107	-1	558	447	657	636	640	634	767	418	623	530
ENSMUSG00000046909	chr11	Tefm	8E+07	8E+07	1570	-0.5356031	3.920456095	0.006518	0.015724372	0.04209	-1	249	145	427	288	275	281	328	181	246	244
ENSMUSG00000032459	chr9	Mrps22	9.9E+07	9.9E+07	3991	-0.46213967	4.152401207	0.0065273	0.015744047	0.03119	-1	277	230	397	300	355	359	388	219	304	281
ENSMUSG00000028621	chr4	Cyb5rl	1.1E+08	1.1E+08	7430	-0.56305797	3.129234778	0.0065379	0.015766904	0.04406	-1	147	94	213	179	159	166	162	93	152	158
ENSMUSG00000021713	chr13	Ppwd1	1E+08	1E+08	2367	-0.66952252	2.24705588	0.0065463	0.015781678	0.05955	-1	91	69	105	87	77	94	102	46	67	69
ENSMUSG00000073647	chr18	Gm10557	4198216	4198611	750	-1.26317254	0.351858051	0.0065452	0.015781678	0.19174	-1	36	27	35	18	8	12	24	16	9	11
ENSMUSG00000036707	chr1	Cab39	8.6E+07	8.6E+07	7077	-0.61993579	7.729427914	0.0065481	0.015783322	0.06149	-1	3223	2363	6219	4628	3393	3617	4949	2354	2925	3614
ENSMUSG00000074794	chr13	Arrdc3	8.1E+07	8.1E+07	6259	-0.47377642	5.035449834	0.0065537	0.015794126	0.03443	-1	597	332	829	606	559	647	666	381	527	640

ENSMUSG00000020122	chr11	Egfr	1.7E+07	1.7E+07	11326	0.551578341	4.150066437	0.006568	0.015823706	0.0456	1	166	151	252	208	322	596	578	321	308	391
ENSMUSG00000078937	chr15	Cpt1b	8.9E+07	8.9E+07	3372	-0.70689371	8.509310651	0.0065682	0.015823706	0.07996	-1	5365	3071	13395	8017	5938	6305	7473	3776	4800	6605
ENSMUSG00000024561	chr18	Mbd1	7.4E+07	7.4E+07	2689	-0.48952101	3.777654458	0.006576	0.01583975	0.03449	-1	226	173	307	237	267	284	297	164	206	233
ENSMUSG00000041654	chr11	Slc39a11	1.1E+08	1.1E+08	3359	0.626532408	2.515424798	0.0065937	0.015874162	0.05174	1	59	45	71	62	99	158	164	97	166	121
ENSMUSG00000075232	chr10	Amd1	4E+07	4E+07	3206	-1.39762474	7.869308084	0.0065923	0.015874162	0.30143	-1	2332	1813	8965	2050	13294	1421	7783	1267	1694	1441
ENSMUSG00000075376	chr2	Rc3h2	3.7E+07	3.7E+07	11688	-0.46726993	5.315341052	0.006593	0.015874162	0.03386	-1	664	539	863	647	771	725	929	507	665	637
ENSMUSG00000050945	chr18	Zfp438	5210031	5211198	3209	-0.64634368	2.347393388	0.0065994	0.015885171	0.05443	-1	80	64	128	104	89	84	106	65	74	74
ENSMUSG00000009470	chr13	Tnpo1	9.9E+07	9.9E+07	8579	-0.46524394	5.439287776	0.0066015	0.015887541	0.03372	-1	734	615	886	738	792	903	889	570	657	763
ENSMUSG00000037788	chr6	Vopp1	5.8E+07	5.8E+07	9661	0.676752695	3.594889681	0.0066156	0.015918762	0.06936	1	110	54	280	143	147	313	367	222	283	341
ENSMUSG00000025271	chrX	Pfkfb1	1.5E+08	1.5E+08	4017	-0.62359673	5.439436983	0.0066178	0.015921237	0.06115	-1	669	322	1548	829	820	763	853	547	697	669
ENSMUSG00000048661	chr10	Lemd3	1.2E+08	1.2E+08	4809	-0.50934356	3.79282307	0.0066286	0.015942035	0.03743	-1	227	172	297	270	260	255	260	216	233	200
ENSMUSG00000098802	chr7	Mir7046	2.5E+07	2.5E+07	66	0.768706336	1.435367316	0.0066287	0.015942035	0.06891	1	22	21	31	29	42	60	63	47	87	78
ENSMUSG00000071281	chr13	Zfp65	6.8E+07	6.8E+07	4124	-0.68085295	2.035680379	0.0066456	0.015979958	0.05965	-1	83	56	91	72	70	86	62	49	49	75
ENSMUSG00000033720	chr6	Sfxn5	8.5E+07	8.5E+07	5743	-0.92689213	2.547802236	0.0066531	0.015992417	0.12639	-1	134	69	75	53	254	91	73	63	87	97
ENSMUSG00000053334	chr5	Ficd	1.1E+08	1.1E+08	3154	-0.48869296	3.634112447	0.0066527	0.015992417	0.03385	-1	200	162	264	216	249	255	236	174	202	194
ENSMUSG00000022533	chr16	Atp13a3	3E+07	3E+07	9559	-0.60001252	5.188074379	0.0066597	0.016002393	0.05655	-1	776	650	645	492	636	534	793	522	485	628
ENSMUSG00000028096	chr3	Gpr89	9.7E+07	9.7E+07	5365	-0.49020047	4.431894407	0.0066616	0.016002393	0.03633	-1	361	316	435	427	329	389	431	271	359	404
ENSMUSG00000046516	chr16	Cox17	3.8E+07	3.8E+07	5773	0.540150658	6.223876701	0.0066618	0.016002393	0.04639	1	965	628	1006	844	1178	2090	1388	1648	1942	1981
ENSMUSG00000082809	chr2	Gm14150	1.5E+08	1.5E+08	1354	1.00653618	1.087615822	0.0066597	0.016002393	0.12771	1	14	13	12	15	48	71	68	39	60	39
ENSMUSG00000034932	chr10	Mrpl54	8.1E+07	8.1E+07	825	0.484056224	5.869909225	0.0066681	0.016014828	0.03695	1	632	489	935	794	876	1624	1242	1036	1685	1470
ENSMUSG00000032009	chr9	Sesn3	1.4E+07	1.4E+07	2162	-0.95848116	1.893787312	0.0066753	0.016029416	0.12957	-1	71	57	99	102	28	51	82	32	41	53
ENSMUSG00000047446	chr12	Arl4a	4E+07	4E+07	7701	-0.62052581	4.647712801	0.0066848	0.01604684	0.05979	-1	494	282	359	339	855	549	446	315	319	423
ENSMUSG00000061079	chr7	Zfp143	1.1E+08	1.1E+08	3013	-0.59734186	3.348422794	0.006684	0.01604684	0.05171	-1	179	155	182	213	172	176	179	145	129	197
ENSMUSG00000028266	chr3	Lmo4	1.4E+08	1.4E+08	3295	-0.49001696	4.827483033	0.006704	0.016089959	0.03686	-1	407	409	503	416	774	518	531	387	468	527
ENSMUSG00000005982	chr16	Naa60	3872375	3872581	3815	-0.48685809	5.562643461	0.0067145	0.016112578	0.03726	-1	719	604	959	900	997	966	1086	591	764	689
ENSMUSG00000071335	chr10	G630090E17Rik	4E+07	4E+07	1787	-0.89877194	1.697191378	0.0067267	0.016138918	0.11101	-1	74	35	94	73	37	65	68	28	27	45
ENSMUSG00000021598	chr13	Med10	7E+07	7E+07	862	0.589931887	3.296562633	0.0067565	0.016207708	0.05011	1	104	88	110	94	194	303	226	175	241	268
ENSMUSG00000018481	chr11	Appbp2	8.5E+07	8.5E+07	6463	-0.42946812	4.523719497	0.0067678	0.016230268	0.02754	-1	376	299	465	379	472	476	482	294	364	417
ENSMUSG00000064061	chr16	Dzip3	4.9E+07	4.9E+07	9081	-0.83070394	1.597958645	0.0067682	0.016230268	0.09033	-1	63	56	72	44	44	63	57	36	30	35
ENSMUSG00000004451	chr1	Ralb	1.2E+08	1.2E+08	4930	0.546020082	4.278515994	0.0067836	0.016261611	0.04583	1	190	112	352	230	354	649	411	391	457	465
ENSMUSG00000036376	chr13	Abt1	2.3E+07	2.3E+07	1278	0.542607485	3.656726765	0.0067833	0.016261611	0.04321	1	140	83	176	176	209	342	260	263	342	314
ENSMUSG00000063903	chr7	Klk1	4.4E+07	4.4E+07	876	1.037559037	0.685771324	0.0067989	0.016295555	0.11558	1	10	23	11	13	12	50	51	27	40	39
ENSMUSG00000098465	chr8	Mir1668	8.4E+07	8.4E+07	107	0.651946139	2.44743873	0.0068285	0.016363708	0.05848	1	48	33	88	58	97	181	120	98	131	149
ENSMUSG00000041846	chr12	Smek1	1E+08	1E+08	4594	-0.47884948	4.269074564	0.0068319	0.016369106	0.03427	-1	312	235	429	327	403	358	461	253	292	300
ENSMUSG00000028854	chr4	Slc9a1	1.3E+08	1.3E+08	5324	0.512062816	4.181209695	0.0068416	0.016389399	0.03967	1	155	150	361	197	294	466	450	353	432	484
ENSMUSG00000043872	chr4	Zmym1	1.3E+08	1.3E+08	4164	-0.63671882	2.455084813	0.0068626	0.016436949	0.05455	-1	118	71	116	89	101	103	114	63	84	76
ENSMUSG00000030528	chr7	Blm	8E+07	8E+07	4946	-0.84822134	0.781437422	0.0068807	0.016475213	0.07911	-1	36	27	42	30	22	26	28	17	26	24
ENSMUSG00000031209	chrX	Heph	9.6E+07	9.6E+07	7662	-1.50238288	1.738939635	0.0068809	0.016475213	0.32838	-1	57	64	24	10	219	50	28	35	22	40
ENSMUSG00000015776	chr2	Med22	2.7E+07	2.7E+07	3614	0.471508166	4.634902358	0.0068867	0.016486228	0.03386	1	296	217	306	291	469	679	534	458	672	628
ENSMUSG00000016918	chr1	Sulf1	1.3E+07	1.3E+07	11294	0.516029249	3.950027201	0.0069029	0.016522153	0.03975	1	166	119	232	159	302	511	375	274	329	396
ENSMUSG00000042073	chr9	Abhd14b	1.1E+08	1.1E+08	1820	0.785616633	2.806530741	0.0069061	0.016527072	0.09021	1	47	68	57	63	147	215	136	131	200	219
ENSMUSG00000071176	chr8	Arhgef10	1.5E+07	1.5E+07	9210	-0.59643356	3.531898154	0.0069179	0.016552473	0.05343	-1	176	179	239	175	275	283	241	91	186	174
ENSMUSG00000001100	chr11	Poldip2	7.9E+07	7.9E+07	3783	-0.53540712	6.882426497	0.0069202	0.016555229	0.04631	-1	1789	1251	3154	2339	2267	2135	2477	1380	2048	1986
ENSMUSG00000003644	chr4	Rps6ka1	1.3E+08	1.3E+08	4258	0.685766875	3.495701363	0.0069311	0.016575626	0.07093	1	156	81	114	78	226	343	250	182	335	327
ENSMUSG00000075271	chr2	Ttc30a1	7.6E+07	7.6E+07	3721	-0.70384247	1.387130307	0.0069309	0.016575626	0.05685	-1	40	30	68	48	55	49	38	32	44	36
ENSMUSG00000069727	chr7	Gm5595	4.3E+07	4.3E+07	3148	-1.0147018	0.73942743	0.0069478	0.016612555	0.1264	-1	52	29	22	26	26	31	26	17	14	22
ENSMUSG00000006527	chr14	Sfmbt1	3.1E+07	3.1E+07	8629	-0.50399625	3.966474777	0.00695	0.016615165	0.03786	-1	268	217	308	308	262	264	329	204	245	287
ENSMUSG00000058454	chr7	Dhcr7	1.4E+08	1.4E+08	3784	0.551275871	3.709465762	0.0069599	0.016636027	0.04484	1	145	121	170	116	250	331	328	221	354	365
ENSMUSG00000058298	chr10	Mcm9	5.4E+07	5.4E+07	4868	0.961075193	0.991737934	0.0069687	0.016654201	0.11515	1	23	7	21	12	35	85	36	43	43	48
ENSMUSG00000002748	chr5	Baz1b	1.4E+08	1.4E+08	10794	-0.48700561	6.017227663	0.0069749	0.016666193	0.03795	-1	1024	747	1579	1186	1256	1274	1388	800	1094	1054
ENSMUSG00000067365	chr5	Tmem128	3.8E+07	3.8E+07	1942	0.602888516	3.284279375	0.0069776	0.016669715	0.05283	1	86	90	113	99	195	313	220	192	226	251
ENSMUSG00000038005	chr8	2700029M09Rik	6.1E+07	6.1E+07	1701	0.589123488	3.32838868	0.0070008	0.016722165	0.05085	1	116	77	117	100	198	311	211	202	239	269
ENSMUSG00000041161	chr4	Otud3	1.4E+08	1.4E+08	1668	-0.66846854	2.484423303	0.0070125	0.016747471	0.06285	-1	101	87	118	114	83	95	124	56	89	81
ENSMUSG00000008206	chr8	Cers4	4493026	4493068	12268	0.706973212	3.168597213	0.0070162	0.016753251	0.07491	1	100	55	112	63	197	317	206	169	185	270
ENSMUSG00000047793	chr1	Sned1	9.3E+07	9.3E+07	9491	0.832611164	4.021031866	0.0070602	0.016855554	0.10737	1	193	230	107	104	181	659	284	331	383	494
ENSMUSG00000087387	chr17	Gm15420	2.8E+07	2.8E+07	382	0.980375547	0.406242882	0.0070629	0.016859236	0.10054	1	13	7	17	13	11	26	32	22	28	56
ENSMUSG00000008035	chrX	Mid1ip1	1.1E+07	1.1E+07	2128	0.895348281	5.416707332	0.0070682	0.016868866	0.12882	1	174	133	1025	385	770	1314	1151	1007	1221	992
ENSMUSG00000030224	chr6	Strap	1.4E+08	1.4E+08	3090	-0.52300959	6.787763193	0.0070724	0.016876176	0.04442	-1	1976	1587	2181	1993	1983	1964	2353	1464	1775	1815
ENSMUSG00000035107	chr16	Dcbld2	5.8E+07	5.8E+07	8401	0.674136888	3.441159867	0.0070951	0.016927379	0.06834	1	84	96	96	112	245	327	288	194	272	293
ENSMUSG00000025130	chr11	P4hb	1.2E+08	1.2E+08	2861	0.51309646	8.189032306	0.0071025	0.016942192	0.0431	1	3279	2494	4472	3750	4351	9237	6785	5590	7333	6656
ENSMUSG00000029178	chr5	Klf3	6.5E+07	6.5E+07	2479	-0.71017345	2.301118375	0.0071079	0.016952188	0.07105	-1	72	74	112	88	110	114	112	52	56	53
ENSMUSG00000034154	chr2	Ino80	1.2E+08	1.2E+08	6803	-0.4437098	4.343200053	0.0071111	0.016956925	0.02945	-1	320	264	458	352	371	389	377	299	343	355
ENSMUSG00000076270	chr14	Mir719	6E+07	6E+07	110	-1.12923279	0.710350087	0.0071396	0.017021933	0.16668	-1	33	34	35	32	23	28	44	11	13	8
ENSMUSG00000030095	chr6	Tmem43	9.1E+07	9.1E+07	3741	0.626669865	5.905714433	0.0071457	0.017033583	0.06349	1	580	474	680	503	1419	2046	1644	1074	1542	1289
ENSMUSG00000073557	chr1	Ppp1r12b	1.3E+08	1.3E+08	14983	-0.78069442	7.977536123	0.0071516	0.017044851	0.09925	-1	3453	2633	9209	6524	2995	3310	5689	2516	3416	4377
ENSMUSG00000028967	chr4	Errfi1	1.5E+08	1.5E+08	3582	0.499164122	4.538083188	0.0071554	0.017050809	0.03864	1	212	198	369	295	401	602	519	559	478	594
ENSMUSG00000044017	chr5	Gpr133	1.3E+08	1.3E+08	8321	0.748202999	4.277186307	0.0071634	0.017067047	0.08828	1	125	172	155	169	487	723	576	336	457	447

ENSMUSG00000005803	chr2	Sqrdl	1.2E+08	1.2E+08	4084	-0.47221853	5.651444172	0.0071747	0.017085184	0.03566	-1	976	580	929	832	1110	1148	917	629	859	836
ENSMUSG00000021704	chr13	Mtx3	9.3E+07	9.3E+07	6275	-0.61805087	3.115555705	0.0071739	0.017085184	0.05621	-1	152	127	165	111	233	196	160	82	123	154
ENSMUSG00000026150	chr1	Mff	8.3E+07	8.3E+07	9757	-0.52465195	6.734393856	0.007174	0.017085184	0.04484	-1	1909	1459	2291	1958	1800	2007	2346	1341	1724	1649
ENSMUSG00000020471	chr11	Pold2	5872180	5872418	1896	-0.45693402	4.522637929	0.0071856	0.017106981	0.03191	-1	320	302	525	401	471	389	522	290	398	402
ENSMUSG00000024773	chr19	Atg2a	6241668	6241966	7693	-0.49931883	4.816146682	0.0071862	0.017106981	0.03905	-1	395	309	768	591	473	515	580	301	531	507
ENSMUSG00000021838	chr14	Samd4	4.7E+07	4.7E+07	8529	-0.6263465	5.73706285	0.007222	0.01718905	0.06348	-1	861	600	1481	1289	707	897	1307	564	740	873
ENSMUSG00000021057	chr12	Akap5	7.6E+07	7.6E+07	6824	-1.02541721	0.929856381	0.0072501	0.017253023	0.13199	-1	31	11	83	36	34	26	30	24	24	18
ENSMUSG00000032719	chr1	Sbspon	1.6E+07	1.6E+07	2748	1.003164612	0.028842289	0.0072522	0.017254042	0.09338	1	9	6	16	8	6	25	23	14	26	36
ENSMUSG00000062785	chr7	Kcnc3	4.5E+07	4.5E+07	5344	-0.73075447	2.634652322	0.0072529	0.017254042	0.07803	-1	122	104	105	128	103	81	136	77	113	67
ENSMUSG00000009487	chr7	Otog	4.6E+07	4.6E+07	10043	1.019626059	1.231250964	0.0072575	0.017261937	0.1378	1	14	22	24	18	32	34	52	57	47	110
ENSMUSG00000047731	chr19	Wbp1l	4.7E+07	4.7E+07	4463	-0.54054159	6.435024549	0.0072594	0.017263586	0.04767	-1	1386	1301	1594	1745	1595	1545	1924	894	1510	1507
ENSMUSG00000004698	chr12	Hdac9	3.4E+07	3.4E+07	4422	-0.84959143	2.855751972	0.007267	0.017278578	0.10922	-1	159	72	202	198	68	97	155	74	83	122
ENSMUSG00000004098	chr9	Col5a3	2.1E+07	2.1E+07	6809	0.804035547	6.653774735	0.0072932	0.017332719	0.10531	1	734	858	715	777	2568	3282	2208	1893	3361	2555
ENSMUSG00000021733	chr14	Slc4a7	1.5E+07	1.5E+07	7389	-0.79330923	3.51687383	0.0072953	0.017332719	0.09761	-1	155	118	475	225	165	151	284	124	125	179
ENSMUSG00000054434	chr5	Tmem120b	1.2E+08	1.2E+08	2852	-0.69951406	3.780324835	0.0072959	0.017332719	0.07583	-1	187	112	371	172	520	238	222	151	227	244
ENSMUSG00000086567	chr13	Gm2830	5.4E+07	5.5E+07	385	0.440998461	4.995573195	0.0072959	0.017332719	0.03039	1	325	295	556	416	469	831	669	625	795	847
ENSMUSG00000091931	chr12	AK010878	1E+08	1E+08	1417	-0.50545706	3.604349842	0.0072911	0.017332719	0.03723	-1	212	144	282	228	211	235	247	162	190	200
ENSMUSG00000101939	chr1	Gm28438	2.5E+07	2.5E+07	345	-0.74842921	3.132848332	0.0073069	0.017355899	0.0852	-1	141	74	272	188	181	94	214	74	135	160
ENSMUSG00000033365	chr4	Ipo13	1.2E+08	1.2E+08	4207	-0.57813298	7.786179323	0.0073091	0.017358215	0.055	-1	3612	2444	6002	4756	3463	3555	4277	2425	3923	4243
ENSMUSG00000026198	chr1	Abcb6	7.5E+07	7.5E+07	5315	-0.46777021	4.923436282	0.0073161	0.01737185	0.03429	-1	407	343	748	657	540	554	584	386	551	558
ENSMUSG00000015542	chr11	Nat9	1.2E+08	1.2E+08	2066	0.50659884	3.821677152	0.0073245	0.017388907	0.03828	1	169	107	224	166	225	432	308	213	420	351
ENSMUSG00000028042	chr3	Zbtb7b	8.9E+07	8.9E+07	5591	-0.50438955	5.455017026	0.00734	0.017422769	0.04091	-1	637	569	795	748	1170	851	891	452	884	719
ENSMUSG00000070498	chr5	Tmem132b	1.3E+08	1.3E+08	8238	-1.75290082	2.77699306	0.0073664	0.017482447	0.46538	-1	28	137	294	132	232	16	244	22	30	19
ENSMUSG00000033257	chr1	Ttll4	7.5E+07	7.5E+07	11527	-0.51952702	3.995633723	0.0073713	0.017491183	0.04117	-1	279	259	320	250	278	320	314	234	221	255
ENSMUSG00000030105	chr6	Arl8b	1.1E+08	1.1E+08	2928	-0.51604273	7.000451222	0.0073781	0.017504339	0.04378	-1	2404	1763	2587	2248	2270	2556	2604	1627	2085	2077
ENSMUSG00000024614	chr18	Tmx3	9.1E+07	9.1E+07	4611	-0.46695713	4.631482055	0.0073817	0.017509854	0.03406	-1	405	365	506	429	438	539	570	294	377	391
ENSMUSG00000004609	chr7	Cd33	4.4E+07	4.4E+07	2571	1.011808386	1.114644364	0.0073897	0.017525793	0.12862	1	13	22	13	15	37	89	66	26	41	67
ENSMUSG00000028073	chr3	Pear1	8.8E+07	8.8E+07	6781	0.497777376	3.973122977	0.0073987	0.017541357	0.03751	1	156	130	288	161	267	462	344	272	387	434
ENSMUSG00000038437	chr11	Mllt6	9.8E+07	9.8E+07	7451	-0.54580556	6.554145037	0.0073975	0.017541357	0.04884	-1	1443	1104	2710	1778	1541	1784	1975	1022	1495	1716
ENSMUSG00000029432	chr5	Gbas	1.3E+08	1.3E+08	2750	-0.61890481	9.119725258	0.0074395	0.017635139	0.06343	-1	9142	6119	16103	12284	8135	8869	12173	6451	8566	9510
ENSMUSG00000036620	chr11	Mgat4b	5E+07	5E+07	2719	0.555329467	6.009322499	0.0074725	0.017710265	0.05048	1	649	438	1005	629	1376	1831	1823	1065	1696	1576
ENSMUSG00000093445	chr5	Lrch4	1.4E+08	1.4E+08	3925	0.452893154	4.901441305	0.0074749	0.017712918	0.03213	1	330	274	401	362	549	812	666	487	816	800
ENSMUSG00000034647	chr17	Ankrd12	6.6E+07	6.6E+07	11508	-0.61805311	3.348525729	0.0074806	0.01772335	0.05768	-1	198	153	216	191	151	204	231	127	118	150
ENSMUSG00000027665	chr3	Pik3ca	3.2E+07	3.2E+07	9088	-0.564609	6.134185944	0.0074925	0.017748176	0.05227	-1	1384	961	1345	1551	959	1291	1368	842	1113	1272
ENSMUSG00000029144	chr5	Gtf3c2	3.1E+07	3.1E+07	6359	-0.41492482	5.067002762	0.0074936	0.017748176	0.02706	-1	548	445	753	537	607	727	629	441	549	635
ENSMUSG00000020441	chr11	2310033P09Rik	5.9E+07	5.9E+07	1285	0.628125974	2.544659296	0.0075009	0.017762587	0.05504	1	61	40	76	62	107	170	121	122	138	163
ENSMUSG00000031706	chr8	Rfx1	8.4E+07	8.4E+07	4172	0.699027547	2.664559248	0.0075056	0.01776826	0.07187	1	66	34	85	65	120	175	120	107	223	173
ENSMUSG00000058881	chr18	Zfp516	8.3E+07	8.3E+07	7817	-0.46594168	4.350704394	0.0075058	0.01776826	0.03353	-1	348	289	399	382	341	398	436	250	348	344
ENSMUSG00000025494	chr7	Sigirr	1.4E+08	1.4E+08	1990	0.720959429	1.831695434	0.0075132	0.017779654	0.06864	1	38	21	51	36	54	102	62	65	112	101
ENSMUSG00000030357	chr6	Fkbp4	1.3E+08	1.3E+08	2795	-0.53260931	7.139947718	0.007513	0.017779654	0.04688	-1	2021	1627	3607	2940	2615	2570	2762	1612	2635	2428
ENSMUSG00000001349	chr9	Cnn1	2.2E+07	2.2E+07	2368	0.907472481	1.427493251	0.0075227	0.01779317	0.10408	1	21	36	34	19	19	101	62	46	79	61
ENSMUSG00000015087	chr2	Rabl6	2.6E+07	2.6E+07	6379	-0.56638926	6.896168694	0.0075215	0.01779317	0.05297	-1	1785	1481	2919	2564	2073	1958	2800	1233	2168	1876
ENSMUSG00000045733	chr7	Sprn	1.4E+08	1.4E+08	3374	1.336151972	-0.25176141	0.0075212	0.01779317	0.19834	1	7	3	2	1	18	24	17	21	16	26
ENSMUSG00000021814	chr14	Anxa7	2E+07	2E+07	2965	0.599782162	6.796198501	0.0075279	0.017802463	0.05936	1	1254	896	1575	837	2282	3806	2968	2172	2460	2522
ENSMUSG00000045962	chr6	Wnk1	1.2E+08	1.2E+08	15780	-0.52903192	8.183538253	0.0075338	0.017811678	0.04651	-1	5260	3857	6488	5354	4884	5332	6098	3651	4685	4937
ENSMUSG00000086096	chr4	Gm12688	1E+08	1E+08	701	0.951656015	0.224176515	0.0075343	0.017811678	0.0903	1	7	7	10	12	18	31	19	24	33	34
ENSMUSG00000093467	chr11	Gm20659	1E+08	1E+08	604	2.206906076	-0.74708306	0.0075455	0.017834956	0.60606	1	0	0	8	2	3	0	23	1	27	28
ENSMUSG00000022574	chr15	Naprt	7.6E+07	7.6E+07	1890	0.60362875	3.197415075	0.0075795	0.017909402	0.05432	1	125	60	139	95	133	305	166	153	267	249
ENSMUSG00000050714	chr2	Zbtb26	3.7E+07	3.7E+07	5267	-0.74028656	2.199928277	0.0075792	0.017909402	0.0778	-1	80	74	84	115	63	92	78	60	53	67
ENSMUSG00000019278	chr8	Dpep1	1.2E+08	1.2E+08	2241	0.667888692	4.633029574	0.0075817	0.017911542	0.07168	1	216	223	236	185	609	729	765	379	577	733
ENSMUSG00000018433	chr11	Nol11	1.1E+08	1.1E+08	5357	-0.45338394	4.140423555	0.007596	0.017940196	0.03101	-1	258	229	393	327	332	354	336	252	282	306
ENSMUSG00000023235	chr8	Ccl25	4325210	4325288	2668	-0.82859951	1.178732121	0.0075967	0.017940196	0.08532	-1	54	38	42	30	43	35	38	23	42	25
ENSMUSG00000027668	chr3	Mfn1	3.3E+07	3.3E+07	6114	-0.68377918	7.422771911	0.0075977	0.017940196	0.07742	-1	2460	1676	5963	4071	2347	2820	3554	1935	2393	2988
ENSMUSG00000034723	chr2	Tmx4	1.3E+08	1.3E+08	10907	-0.48406034	4.449741814	0.0076131	0.01797367	0.03663	-1	406	301	452	385	354	429	484	293	314	362
ENSMUSG00000054321	chr18	Taf4b	1.5E+07	1.5E+07	5149	-0.82399593	1.431960143	0.0076195	0.017985756	0.08648	-1	45	38	87	40	46	39	48	38	24	44
ENSMUSG00000025766	chr3	D3Ertd751e	4.2E+07	4.2E+07	5813	-0.64977682	2.081947693	0.0076274	0.018001412	0.05511	-1	69	56	94	65	103	94	65	56	54	66
ENSMUSG00000062554	chr4	Gm12751	3.4E+07	3.4E+07	381	0.977512944	0.515382932	0.0076305	0.018005538	0.10506	1	12	7	15	21	11	59	27	27	25	42
ENSMUSG00000058809	chr11	Gm12141	4.1E+07	4.2E+07	1722	-0.6844303	2.359272769	0.0076655	0.018085225	0.0656	-1	88	52	161	87	96	87	111	59	81	64
ENSMUSG00000027540	chr2	Ptpn1	1.7E+08	1.7E+08	5533	0.462388498	4.73053503	0.0076738	0.018101616	0.03353	1	225	272	468	338	391	688	717	471	697	601
ENSMUSG00000026436	chr1	Elk4	1.3E+08	1.3E+08	6407	0.470310392	5.286106064	0.0076758	0.018103368	0.0356	1	444	332	570	484	666	1139	724	736	1021	1053
ENSMUSG00000039427	chr16	Alg1	5233621	5233857	2682	0.523326778	4.057898297	0.0076812	0.018113009	0.04262	1	168	126	264	165	334	463	357	334	449	406
ENSMUSG00000038286	chr13	Bphl	3.4E+07	3.4E+07	1209	-0.45732986	4.3928471	0.0077015	0.018157861	0.03241	-1	356	266	493	319	410	426	440	245	414	316
ENSMUSG00000020834	chr11	Dhrs13	7.8E+07	7.8E+07	1967	0.921871705	0.998698866	0.0077097	0.018174094	0.1092	1	25	5	27	20	23	62	39	37	75	40
ENSMUSG00000053907	chr6	Mat2a	7.2E+07	7.2E+07	2804	-0.52712777	6.995487712	0.0077234	0.018203486	0.04619	-1	1865	1862	2724	1881	3104	2615	2463	1790	2002	1932
ENSMUSG00000071604	chr19	Fam189a2	2.4E+07	2.4E+07	2547	0.476141624	5.278247745	0.007735	0.018227684	0.0364	1	468	373	569	580	431	1150	928	715	1009	867
ENSMUSG00000027163	chr2	Commd9	1E+08	1E+08	1602	0.4334524	4.915210867	0.0077552	0.018266107	0.02964	1	388	261	455	353	494	842	617	549	791	776
ENSMUSG00000042790	chr9	Rnf214	4.6E+07	4.6E+07	5922	-0.57904899	3.944440559	0.0077542	0.018266107	0.05253	-1	241	200	415	340	192	277	325	168	255	257

ENSMUSG00000059486	chr6	Kbtbd2	5.7E+07	5.7E+07	4083	-0.45528074	4.576978639	0.0077548	0.018266107	0.03253	-1	429	352	464	386	417	520	447	338	363	409
ENSMUSG00000084168	chr11	Atp5l2-ps	9.8E+07	9.8E+07	312	1.105766106	1.907560038	0.0077698	0.018297324	0.18238	1	21	21	12	41	81	89	103	42	152	132
ENSMUSG00000020541	chr11	Tom1l1	9.1E+07	9.1E+07	7749	-0.60367701	3.383980354	0.0077817	0.018322273	0.05572	-1	192	134	236	205	176	182	274	105	159	142
ENSMUSG00000032968	chr1	Inha	7.6E+07	7.6E+07	1475	0.693208497	1.923925028	0.0077847	0.01832631	0.06024	1	44	38	38	46	41	100	99	67	102	101
ENSMUSG00000036733	chr7	Rbm42	3.1E+07	3.1E+07	2193	0.471720797	5.260522292	0.0077881	0.018331336	0.03604	1	371	295	669	511	639	1003	831	661	1119	990
ENSMUSG00000003559	chr19	As3mt	4.7E+07	4.7E+07	1751	-0.55935394	5.7332237	0.007798	0.018348304	0.05146	-1	817	549	1780	947	850	1014	1087	629	861	884
ENSMUSG00000068856	chr3	Sf3b4	9.6E+07	9.6E+07	2162	0.517740006	3.426792346	0.0077967	0.018348304	0.03917	1	122	87	158	140	160	294	248	180	320	259
ENSMUSG00000044080	chr3	S100a1	9.1E+07	9.1E+07	694	0.543621661	7.53182494	0.0078192	0.018395083	0.04946	1	1934	1292	3415	2209	2902	4490	5035	3043	4714	5539
ENSMUSG00000067261	chr4	Foxd3	1E+08	1E+08	2324	0.959595448	0.595974023	0.0078362	0.018432013	0.0968	1	13	13	13	21	9	40	34	26	36	53
ENSMUSG00000021003	chr12	Galc	9.8E+07	9.8E+07	3822	0.524419772	3.273402037	0.0078521	0.01846296	0.04034	1	111	70	165	103	157	297	256	162	229	233
ENSMUSG00000027184	chr2	Caprin1	1E+08	1E+08	10219	-0.48823103	6.137480888	0.0078533	0.01846296	0.03939	-1	1122	913	1548	1283	1358	1439	1450	1001	1081	1081
ENSMUSG00000074358	chr7	Ccdc61	1.9E+07	1.9E+07	2122	0.633545516	2.31666	0.0078512	0.01846296	0.05465	1	54	41	78	45	73	146	121	101	145	96
ENSMUSG00000048234	chr1	Rnf149	4E+07	4E+07	2838	0.517985967	3.738118676	0.0078776	0.01851705	0.04085	1	126	113	256	149	196	315	349	222	343	387
ENSMUSG00000042320	chr12	Prox2	8.5E+07	8.5E+07	3335	-1.01730071	0.994925063	0.0079039	0.018575677	0.14157	-1	49	37	37	35	30	18	56	17	21	20
ENSMUSG00000026615	chr1	Eprs	1.9E+08	1.9E+08	18102	-0.55673489	7.494827709	0.0079106	0.018588419	0.05198	-1	2967	2036	4620	3923	2857	3082	3717	2315	2914	3068
ENSMUSG00000016995	chr2	Matn4	1.6E+08	1.6E+08	5174	1.003277435	1.726118793	0.007924	0.018616776	0.14735	1	20	17	21	34	72	181	63	58	71	76
ENSMUSG00000042589	chr5	Cux2	1.2E+08	1.2E+08	8015	-1.21813218	1.436912356	0.0079431	0.018658579	0.2151	-1	38	10	149	63	40	26	54	27	23	31
ENSMUSG00000021725	chr13	Parp8	1.2E+08	1.2E+08	3088	-0.54076563	4.086637385	0.0079456	0.018661246	0.04607	-1	243	252	413	346	250	341	373	213	229	278
ENSMUSG00000025504	chr7	Eps8l2	1.4E+08	1.4E+08	4370	0.718674943	2.032286163	0.0079488	0.018665535	0.07036	1	25	36	72	43	54	94	126	83	91	113
ENSMUSG00000051373	chr2	Ppapdc3	3.2E+07	3.2E+07	2078	-0.55645908	7.129936072	0.0079525	0.018671286	0.05192	-1	2499	1930	2674	2404	3037	2179	3086	1627	2901	1960
ENSMUSG00000073471	chr17	Rsph3a	7945653	7946303	2189	-0.5528877	3.478816321	0.0079614	0.018688996	0.04635	-1	181	128	299	218	182	228	239	131	154	185
ENSMUSG00000003752	chr7	Itpkc	2.7E+07	2.7E+07	3644	0.613811074	2.939447541	0.0079723	0.018708233	0.05476	1	91	66	114	80	101	247	128	165	206	193
ENSMUSG00000023938	chr17	Aars2	4.6E+07	4.6E+07	3348	-0.50086437	4.609832617	0.0079717	0.018708233	0.03997	-1	352	253	622	522	452	382	522	284	494	409
ENSMUSG00000038612	chr3	Mcl1	9.6E+07	9.6E+07	3485	0.55532096	7.623398142	0.0079785	0.018719693	0.05189	1	1897	1324	3853	2756	2630	5478	4816	3776	4649	5550
ENSMUSG00000038302	chr10	Lace1	4.2E+07	4.2E+07	2705	-0.56817299	4.403664898	0.0080108	0.018792316	0.05175	-1	332	170	670	414	400	438	449	213	327	361
ENSMUSG00000097180	chr5	2700038G22Rik	2.4E+07	2.4E+07	1261	0.901302927	0.89829381	0.0080454	0.018870396	0.0949	1	14	16	13	16	32	59	31	38	52	53
ENSMUSG00000050323	chr4	Ndufaf6	1.1E+07	1.1E+07	1235	-0.52718699	3.571112352	0.0080498	0.018877575	0.04175	-1	187	153	315	197	212	217	258	160	171	194
ENSMUSG00000028156	chr3	Eif4e	1.4E+08	1.4E+08	2882	-0.54880454	6.598726341	0.0080532	0.018882289	0.05045	-1	1726	1127	2589	1722	1646	1667	2220	1266	1662	1318
ENSMUSG00000015932	chr2	Dstn	1.4E+08	1.4E+08	1911	0.503888325	4.996663415	0.0080925	0.018971327	0.04112	1	367	327	412	281	606	1087	758	590	669	786
ENSMUSG00000035392	chr2	Dennd1a	3.8E+07	3.8E+07	5740	-0.43038261	4.765891033	0.0081023	0.018991016	0.02945	-1	415	351	543	542	497	524	552	340	520	465
ENSMUSG00000022758	chr16	P2rx6	1.8E+07	1.8E+07	3995	-0.45274155	4.597296767	0.0081158	0.019019486	0.03256	-1	443	302	397	432	524	441	518	296	423	439
ENSMUSG00000024529	chr18	Lox	5.3E+07	5.3E+07	4810	0.857216381	4.89038174	0.0081247	0.019037212	0.1213	1	228	253	266	175	700	1553	751	703	463	517
ENSMUSG00000021318	chr13	Gli3	1.5E+07	1.5E+07	9589	0.719228395	1.586960003	0.0081309	0.019048514	0.06521	1	27	22	30	32	55	100	70	53	74	76
ENSMUSG00000031023	chr7	Akip1	1.1E+08	1.1E+08	1305	0.568432735	3.430554778	0.0081364	0.019058218	0.04901	1	130	93	132	100	199	320	221	227	265	277
ENSMUSG00000057329	chr1	Bcl2	1.1E+08	1.1E+08	9157	-0.59632528	3.832128227	0.0081603	0.019111147	0.05596	-1	268	146	388	212	309	204	370	182	207	201
ENSMUSG00000036934	chr8	4921524J17Rik	8.5E+07	8.5E+07	1595	-0.59822073	2.811678099	0.0081785	0.019150548	0.05248	-1	138	110	118	106	149	138	122	92	108	111
ENSMUSG00000094130	chr14	Rpp14	8090078	8090554	477	-0.47294243	3.708183669	0.0081799	0.019150548	0.03355	-1	216	162	274	240	252	252	241	177	245	209
ENSMUSG00000031669	chr8	Gins3	9.6E+07	9.6E+07	2412	0.902568867	0.605856138	0.0081882	0.01916693	0.08161	1	15	13	15	17	12	57	37	28	39	28
ENSMUSG00000015597	chr17	Zfp318	4.6E+07	4.6E+07	8594	-0.46731848	3.914904777	0.0082094	0.019213208	0.03341	-1	266	194	342	253	261	331	275	204	230	267
ENSMUSG00000025213	chr19	Kazald1	4.5E+07	4.5E+07	1681	-1.04410962	3.248595899	0.0082116	0.019215126	0.17583	-1	312	238	65	112	151	153	90	92	163	144
ENSMUSG00000024258	chr18	Polr2d	3.2E+07	3.2E+07	956	0.493563098	3.740901814	0.0082204	0.019229404	0.03708	1	148	121	214	131	229	384	313	272	314	314
ENSMUSG00000032040	chr9	Dcps	3.5E+07	3.5E+07	1451	0.48920022	3.776263868	0.0082197	0.019229404	0.03645	1	139	118	214	175	219	416	273	264	343	345
ENSMUSG00000039629	chr6	Strip2	3E+07	3E+07	8328	-1.10597468	0.370295962	0.0082469	0.019288192	0.15813	-1	46	21	22	10	23	21	23	9	11	17
ENSMUSG00000042772	chr1	Smg7	1.5E+08	1.5E+08	6341	-0.47143826	5.92058554	0.0082483	0.019288238	0.03705	-1	932	801	1428	1123	1038	1200	1194	763	1004	1111
ENSMUSG00000032402	chr9	Smad3	6.4E+07	6.4E+07	5542	-0.59711297	6.929210746	0.0082832	0.019366624	0.06029	-1	1475	1678	3100	2627	2298	1526	2370	1790	1923	2256
ENSMUSG00000050014	chr15	Apol10b	7.8E+07	7.8E+07	1986	0.869381126	2.616545699	0.0082943	0.019389365	0.11692	1	67	39	67	54	98	386	130	85	100	138
ENSMUSG00000037275	chr11	Gemin5	5.8E+07	5.8E+07	6618	-0.52191967	3.649181752	0.0082986	0.019396138	0.04168	-1	181	160	313	262	200	229	239	161	229	201
ENSMUSG00000003269	chr7	Cyth2	4.6E+07	4.6E+07	3515	0.447627863	4.394269873	0.0083024	0.019401714	0.03152	1	240	167	323	298	327	548	454	370	540	587
ENSMUSG00000005949	chr11	Ctns	7.3E+07	7.3E+07	3391	0.599894847	3.2191181	0.0083131	0.019423495	0.05549	1	107	59	132	82	190	287	207	173	225	258
ENSMUSG00000025226	chr19	Fbxl15	4.6E+07	4.6E+07	1348	0.688076317	2.367852183	0.008319	0.019434049	0.06943	1	40	34	89	66	70	147	93	85	163	158
ENSMUSG00000097799	chr2	Gm26899	1.2E+08	1.2E+08	3328	-2.84210269	1.592207226	0.0083439	0.019488901	1.1294	-1	4	4	327	100	8	1	45	0	11	19
ENSMUSG00000025584	chr7	Pde8a	8.1E+07	8.1E+07	4045	-0.60819571	4.310961222	0.0083608	0.019525208	0.05997	-1	271	138	599	444	446	377	423	227	270	338
ENSMUSG00000019832	chr10	Rab32	1.1E+07	1.1E+07	2108	1.255146295	2.529781508	0.0083719	0.019541379	0.24861	1	34	39	23	10	154	264	127	153	150	125
ENSMUSG00000052428	chr1	Tmco1	1.7E+08	1.7E+08	4764	-0.48613654	5.370157275	0.0083694	0.019541379	0.03919	-1	741	625	784	592	856	893	897	548	598	642
ENSMUSG00000096056	chrX	Gm21986	1E+08	1E+08	5560	0.69972527	2.472349396	0.008371	0.019541379	0.07191	1	46	37	60	62	115	145	120	99	149	182
ENSMUSG00000091549	chr17	Gm6548	7.9E+07	7.9E+07	1165	0.690241986	2.264604564	0.0083744	0.019544066	0.06745	1	46	37	59	37	97	161	116	77	133	118
ENSMUSG00000024481	chr18	4833403I15Rik	4.7E+07	4.7E+07	3219	-1.13897382	0.606551454	0.0083759	0.019544216	0.17273	-1	25	30	30	13	52	21	40	6	14	15
ENSMUSG00000040183	chr4	Ankrd6	3.3E+07	3.3E+07	5477	-0.6999842	1.605594291	0.0083791	0.019548491	0.06398	-1	42	43	73	50	72	70	56	26	42	44
ENSMUSG00000005034	chr3	Prkacb	1.5E+08	1.5E+08	5451	-0.45080014	5.634564868	0.0083808	0.019549142	0.03372	-1	737	631	1196	872	932	970	1041	641	857	844
ENSMUSG00000092360	chr10	Gm20441	7.6E+07	7.6E+07	756	0.506902634	4.312174685	0.0083975	0.019584953	0.04125	1	234	143	295	221	370	580	355	375	542	545
ENSMUSG00000045625	chr16	Pigz	3.2E+07	3.2E+07	2541	1.20396803	0.27441908	0.0084227	0.019640315	0.18518	1	9	4	8	2	28	50	30	17	36	25
ENSMUSG00000042784	chr3	Muc1	8.9E+07	8.9E+07	2346	1.040372693	-0.08911483	0.0084303	0.019654794	0.10723	1	6	3	9	7	16	38	17	13	25	22
ENSMUSG00000085156	chr11	Gm11974	6525591	6525817	1359	1.019077427	0.552288381	0.0084317	0.019654794	0.12807	1	7	10	16	10	25	46	16	35	41	45
ENSMUSG00000034875	chr7	Nudt19	3.6E+07	3.6E+07	2680	-0.44320995	5.25915183	0.0084456	0.019683953	0.03229	-1	626	462	935	666	669	753	816	464	725	617
ENSMUSG00000020829	chr11	Slc46a1	7.8E+07	7.8E+07	3080	1.130963178	1.43830322	0.008461	0.01971659	0.18786	1	27	19	16	5	56	95	48	50	103	71
ENSMUSG00000024366	chr18	Gfra3	3.5E+07	3.5E+07	1992	1.21301774	-0.29705589	0.0084742	0.019744068	0.14872	1	8	1	6	3	14	27	11	16	26	19
ENSMUSG00000079677	chr9	Fdx1l	2.1E+07	2.1E+07	782	0.423350767	5.371405258	0.0084779	0.01974948	0.02943	1	481	368	684	534	626	1108	976	718	1075	1030

ENSMUSG00000022194	chr14	Pabpn1	5.5E+07	5.5E+07	3035	0.502210185	5.318293051	0.0084879	0.019769428	0.04178	1	436	391	522	455	688	1194	713	697	1007	1237
ENSMUSG00000026565	chr1	Pou2f1	1.7E+08	1.7E+08	16597	-0.56961745	3.322370257	0.0085009	0.019796325	0.04986	-1	154	177	235	154	160	184	173	116	169	188
ENSMUSG00000019158	chr7	Tmem160	1.6E+07	1.6E+07	814	0.509061552	5.037532143	0.0085394	0.019882729	0.04273	1	334	298	417	448	553	806	669	547	1146	812
ENSMUSG00000060935	chr10	Tmem263	8.5E+07	8.5E+07	3778	0.490520868	3.945642287	0.0085458	0.019894396	0.03723	1	174	159	253	168	205	490	321	311	378	345
ENSMUSG00000026425	chr1	Srgap2	1.3E+08	1.3E+08	12560	0.528818624	4.399502778	0.0085517	0.019904854	0.04501	1	212	232	260	179	415	625	541	368	508	539
ENSMUSG00000033773	chr5	Rpap2	1.1E+08	1.1E+08	3893	-0.6771606	2.826560906	0.0085652	0.019932798	0.07032	-1	159	130	113	110	115	152	113	85	111	101
ENSMUSG00000029195	chr5	Klb	6.5E+07	6.5E+07	3464	-2.16521182	1.284794934	0.0085943	0.019997238	0.69509	-1	92	33	0	4	171	35	10	13	18	15
ENSMUSG00000025102	chr7	3110040N11Rik	8.2E+07	8.2E+07	1231	0.498414764	3.630071922	0.0086009	0.020009395	0.03783	1	153	110	184	137	188	353	243	238	327	321
ENSMUSG00000053134	chr5	Supt7l	3.2E+07	3.2E+07	5347	-0.52701226	3.71822619	0.0086101	0.020027454	0.04353	-1	213	198	281	218	248	215	305	164	242	183
ENSMUSG00000103309	chr18	RP23-407E2.27	3.8E+07	3.8E+07	2205	1.246508955	-0.15911989	0.0086157	0.020037121	0.18368	1	6	4	4	1	20	36	18	18	17	23
ENSMUSG00000034926	chr4	Dhcr24	1.1E+08	1.1E+08	4028	0.615059846	3.683329147	0.0086403	0.020091011	0.06026	1	98	108	143	144	282	395	272	260	292	372
ENSMUSG00000093593	chr17	Gm20683	2.6E+07	2.6E+07	2790	-0.57905535	6.861556158	0.0086419	0.020091317	0.05734	-1	1616	1314	3194	2578	2029	1704	2468	1218	2243	2070
ENSMUSG00000096956	chr15	Snhg18	3.2E+07	3.2E+07	1482	0.747571272	2.958297536	0.0086441	0.020093227	0.08665	1	94	69	59	63	143	317	135	145	213	192
ENSMUSG00000038351	chr11	Sgsm2	7.5E+07	7.5E+07	6884	0.601845583	3.257352178	0.0086669	0.020142725	0.05475	1	89	106	105	102	158	337	207	151	262	237
ENSMUSG00000031959	chr8	Wdr59	1.1E+08	1.1E+08	5222	-0.48535198	3.898485542	0.0086835	0.020178013	0.03683	-1	260	188	303	286	267	284	332	202	239	222
ENSMUSG00000026062	chr1	Slc9a2	4.1E+07	4.1E+07	6984	-0.54251466	5.450288141	0.0086892	0.020187881	0.04955	-1	657	534	1192	976	579	773	896	540	696	782
ENSMUSG00000000838	chrX	Fmr1	6.9E+07	6.9E+07	8966	-0.57392354	3.571080096	0.0087179	0.020249497	0.05188	-1	200	198	201	196	251	170	245	153	167	242
ENSMUSG00000074824	chr13	Rslcan18	6.7E+07	6.7E+07	8039	-1.03370923	0.378976618	0.0087186	0.020249497	0.13224	-1	33	24	31	17	16	28	23	8	9	17
ENSMUSG00000098950	chr2	Gm28036	1.6E+08	1.6E+08	5823	-0.44948477	5.422935001	0.0087311	0.020275176	0.03378	-1	674	588	877	681	920	929	948	507	713	693
ENSMUSG00000062480	chr17	Acat3	1.3E+07	1.3E+07	2345	1.585090927	0.109618389	0.008744	0.020301845	0.34666	1	2	1	11	12	11	7	29	6	46	59
ENSMUSG00000087412	chr7	Gm15501	9.3E+07	9.3E+07	687	0.62322712	3.748467259	0.0087533	0.020319965	0.0621	1	162	115	129	169	212	342	245	204	475	414
ENSMUSG00000042532	chr19	Golga7b	4.2E+07	4.2E+07	2988	0.857775613	2.952872588	0.0087551	0.020320856	0.11626	1	151	56	43	61	84	208	193	169	260	176
ENSMUSG00000018395	chr11	Kif3a	5.4E+07	5.4E+07	3586	0.556322445	3.208540273	0.0087624	0.020331034	0.04638	1	101	92	127	79	161	261	221	173	218	251
ENSMUSG00000019782	chr10	Rwdd1	3.4E+07	3.4E+07	1136	-0.48375464	5.951812607	0.0087617	0.020331034	0.03973	-1	1151	834	1228	1062	1130	1313	1329	771	898	1069
ENSMUSG00000005267	chr11	Zfp287	6.3E+07	6.3E+07	7632	0.849648875	0.628712283	0.0087651	0.020333972	0.07769	1	13	12	25	11	16	56	41	21	38	36
ENSMUSG00000031776	chr8	Arl2bp	9.5E+07	9.5E+07	1905	0.503715941	6.075921806	0.0087713	0.02034501	0.04321	1	680	554	1317	668	1120	1893	1648	1238	1736	1673
ENSMUSG00000026519	chr1	Tmem63a	1.8E+08	1.8E+08	4492	0.460666889	4.719363169	0.0087755	0.020351492	0.03443	1	296	254	315	304	505	800	599	444	686	638
ENSMUSG00000025350	chr10	Rdh5	1.3E+08	1.3E+08	2809	0.500392659	6.29708014	0.0087799	0.020358336	0.04264	1	979	750	977	947	1239	2092	1672	1468	2150	2120
ENSMUSG00000029587	chr5	Zfp12	1.4E+08	1.4E+08	5821	-0.53088161	3.404405333	0.0087881	0.020370595	0.04333	-1	175	142	251	188	183	211	214	152	142	168
ENSMUSG00000044562	chr7	Rasip1	4.6E+07	4.6E+07	3202	0.64373049	4.088966663	0.0087878	0.020370595	0.06876	1	126	94	296	171	368	430	334	351	522	476
ENSMUSG00000040139	chr7	9430038I01Rik	1.4E+08	1.4E+08	5752	0.710038239	2.049531617	0.0087917	0.020373775	0.07282	1	32	22	81	48	56	130	85	71	107	126
ENSMUSG00000044768	chr1	D1Ertd622e	9.8E+07	9.8E+07	41324	-0.59238409	3.746374131	0.0087924	0.020373775	0.05635	-1	282	212	230	157	313	210	267	182	240	194
ENSMUSG00000097352	chr10	C920009B18Rik	2.2E+07	2.2E+07	6564	1.243247276	-0.60269922	0.0087955	0.020377539	0.12922	1	3	2	5	7	7	21	12	16	7	21
ENSMUSG00000030275	chr6	Etnk1	1.4E+08	1.4E+08	6429	-0.43184773	5.389334835	0.0087996	0.020383641	0.03105	-1	665	493	976	723	818	868	881	530	680	752
ENSMUSG00000091900	chr7	Gm4353	1.2E+08	1.2E+08	1559	-1.02262537	0.628834956	0.0088188	0.020424676	0.13634	-1	30	23	35	36	23	32	37	13	10	10
ENSMUSG00000021597	chr13	Ankrd32	7.7E+07	7.7E+07	5881	-0.80319705	3.332862244	0.008833	0.020454363	0.1051	-1	178	130	293	259	100	142	272	111	119	113
ENSMUSG00000022607	chr15	Ptk2	7.3E+07	7.3E+07	4991	-0.42946479	4.927251925	0.0088479	0.020485329	0.03015	-1	441	379	719	509	616	561	674	405	562	476
ENSMUSG00000070822	chr7	Zscan18	1.3E+07	1.3E+07	3626	0.843845988	0.569235117	0.0088614	0.020513203	0.07202	1	14	11	16	16	16	47	37	30	40	26
ENSMUSG00000073295	chrX	Nudt11	6047453	6048404	3036	-0.91190798	0.064398592	0.0088646	0.0205172	0.07687	-1	22	13	25	15	20	17	12	8	17	15
ENSMUSG00000084098	chr2	Gm13422	2.3E+07	2.3E+07	504	-0.9717588	0.320243081	0.0089021	0.020600796	0.10687	-1	16	20	34	23	24	9	23	14	23	11
ENSMUSG00000072761	chr17	Gm6712	1.7E+07	1.7E+07	594	-0.94345009	0.496238446	0.0089091	0.020613447	0.10638	-1	24	25	36	29	16	27	22	17	10	18
ENSMUSG00000008301	chr18	Phax	5.7E+07	5.7E+07	2223	0.480260037	4.274805715	0.0089275	0.020652645	0.03727	1	220	152	285	235	344	595	375	408	421	509
ENSMUSG00000021268	chr12	Meg3	1.1E+08	1.1E+08	18089	0.978683314	3.605567439	0.0089378	0.020669642	0.157	1	124	155	59	79	158	596	133	217	287	455
ENSMUSG00000045248	chr8	Med26	7.2E+07	7.2E+07	3040	-0.62816095	3.27396194	0.0089372	0.020669642	0.06224	-1	131	120	227	263	140	160	195	112	157	158
ENSMUSG00000052295	chr5	8030423F21Rik	5.3E+07	5.3E+07	2850	1.118077968	-0.36453588	0.008965	0.020729046	0.10854	1	4	3	3	9	12	23	23	11	17	19
ENSMUSG00000031984	chr8	2810004N23Rik	1.2E+08	1.2E+08	1382	-0.46412533	4.738041107	0.0089699	0.020737076	0.03544	-1	475	333	676	453	402	569	551	362	393	447
ENSMUSG00000038126	chr5	Mphosph9	1.2E+08	1.2E+08	8544	-0.63004269	2.035217234	0.0089773	0.020750853	0.05388	-1	63	51	80	94	81	80	65	49	65	68
ENSMUSG00000014349	chr11	Ube2z	9.6E+07	9.6E+07	3997	0.44686526	5.856523452	0.0089894	0.02077185	0.03389	1	645	498	988	775	841	1736	1417	977	1466	1363
ENSMUSG00000033411	chr2	Ctdspl2	1.2E+08	1.2E+08	9251	-0.70478148	2.196333982	0.008988	0.02077185	0.07312	-1	76	61	134	74	82	90	101	50	42	75
ENSMUSG00000039308	chr14	Ndst2	2.1E+07	2.1E+07	3305	0.525744011	3.597700428	0.0089959	0.020783472	0.04277	1	140	114	144	126	220	362	258	228	291	326
ENSMUSG00000063316	chr11	Rpl27	1E+08	1E+08	1535	0.523959372	7.012862949	0.0090237	0.020844306	0.04748	1	1588	1198	1814	1583	1795	3995	2414	2755	3280	3212
ENSMUSG00000055850	chr6	Rnf181	7.2E+07	7.2E+07	2070	0.498576267	5.71354973	0.0090294	0.020853951	0.04229	1	603	493	684	571	946	1437	1024	1055	1387	1404
ENSMUSG00000048772	chr4	Tmem53	1.2E+08	1.2E+08	1713	0.784615209	2.489408797	0.0090459	0.020888637	0.09716	1	40	18	105	76	83	143	129	92	177	180
ENSMUSG00000040234	chr6	Tm7sf3	1.5E+08	1.5E+08	3438	0.452189054	4.246826544	0.00905	0.020894637	0.03243	1	200	190	294	205	324	606	470	308	457	441
ENSMUSG00000022452	chr15	Smdt1	8.2E+07	8.2E+07	1077	0.482646598	6.597441255	0.0090667	0.02092978	0.0402	1	1170	810	1678	1115	1418	2562	2206	1834	2617	2419
ENSMUSG00000022427	chr15	Tomm22	8E+07	8E+07	1113	0.471939654	5.676111448	0.0090695	0.020932789	0.03797	1	507	389	907	649	873	1496	1166	1043	1175	1233
ENSMUSG00000048486	chr2	Fitm2	1.6E+08	1.6E+08	3967	-0.616727	7.197857497	0.0090888	0.02097388	0.06598	-1	2060	1267	4615	3333	2705	2439	3160	1582	2301	2606
ENSMUSG00000028709	chr4	Mob3c	1.2E+08	1.2E+08	2975	0.675344808	2.406850949	0.0090964	0.020988085	0.06688	1	58	47	58	51	87	199	95	102	113	154
ENSMUSG00000006717	chr13	Acot13	2.5E+07	2.5E+07	721	-0.56321085	6.169541922	0.0091015	0.020996099	0.05466	-1	1094	754	2224	1474	1105	1304	1540	808	1144	1263
ENSMUSG00000038733	chr1	Wdr26	1.8E+08	1.8E+08	7848	-0.53215039	7.096946933	0.0091029	0.020996099	0.04917	-1	2371	1862	3193	2518	2238	2681	3039	1770	1853	2284
ENSMUSG00000058704	chr17	Memo1	7.4E+07	7.4E+07	1513	-0.43171315	5.004448289	0.0091106	0.021010504	0.03094	-1	530	413	674	607	546	665	687	427	564	488
ENSMUSG00000039942	chr15	Ptger4	5206661	5209784	6648	0.682566238	2.003007752	0.0091315	0.021055036	0.06524	1	35	24	44	52	75	121	111	68	92	107
ENSMUSG00000031891	chr8	Hsd11b2	1.1E+08	1.1E+08	1845	1.762665038	-0.71691031	0.0091348	0.021059308	0.29663	1	4	7	0	1	3	24	4	16	24	8
ENSMUSG00000072692	chr5	Rpl37rt	1.2E+08	1.2E+08	682	0.453795491	4.891715217	0.0091399	0.021067502	0.03389	1	366	296	331	407	465	868	680	560	668	763
ENSMUSG00000025404	chr10	R3hdm2	1.3E+08	1.3E+08	5987	-0.56865388	7.093616501	0.009151	0.021086174	0.05622	-1	2302	1510	3501	2899	2276	2089	3257	1477	2326	2310
ENSMUSG00000038677	chr17	Scube3	2.8E+07	2.8E+07	8660	1.008294239	0.312395306	0.0091508	0.021086174	0.11282	1	6	11	11	6	22	27	31	19	37	40
ENSMUSG00000048379	chr14	Socs4	4.7E+07	4.7E+07	6873	-0.50558249	3.339531484	0.009169	0.021124227	0.039	-1	175	129	221	170	198	189	193	139	141	195

ENSMUSG00000007908	chr9	Hmgcll1	7.6E+07	7.6E+07	5449	1.084418501	0.266199747	0.0091796	0.021145298	0.1224	1	8	15	7	5	15	40	29	15	36	33
ENSMUSG00000026482	chr1	Rgl1	1.5E+08	1.5E+08	6907	0.635212412	4.659739247	0.0092066	0.021203862	0.06811	1	252	225	229	199	606	926	640	396	675	589
ENSMUSG00000028333	chr4	Anp32b	4.6E+07	4.6E+07	1716	0.492896859	6.342626038	0.0092123	0.021210459	0.04196	1	1025	721	1092	922	1353	2423	1775	1611	1775	2209
ENSMUSG00000032599	chr9	Ip6k2	1.1E+08	1.1E+08	4067	0.456707117	3.889764203	0.0092125	0.021210459	0.03249	1	172	132	203	189	246	382	350	270	349	408
ENSMUSG00000035949	chr2	Fbxw2	3.5E+07	3.5E+07	6661	-0.4654329	5.775532608	0.0092353	0.021259434	0.03708	-1	992	710	1094	912	1076	1030	1188	728	987	826
ENSMUSG00000021360	chr13	Gcnt2	4.1E+07	4.1E+07	7038	-0.68635299	3.242896557	0.0092388	0.02126421	0.07531	-1	128	95	323	143	228	155	208	144	114	114
ENSMUSG00000026797	chr2	Stxbp1	3.3E+07	3.3E+07	4991	0.659764965	2.797086836	0.0092432	0.021267855	0.06663	1	68	62	85	57	132	212	162	91	205	210
ENSMUSG00000063873	chr2	Slc24a3	1.5E+08	1.5E+08	4564	-1.28182611	2.851709626	0.0092435	0.021267855	0.26941	-1	102	73	63	44	539	126	69	82	78	72
ENSMUSG00000028007	chr3	Snx7	1.2E+08	1.2E+08	2171	0.853767329	2.529797963	0.0092476	0.021273968	0.11459	1	69	40	35	37	126	204	147	147	113	134
ENSMUSG00000038534	chr11	Osbpl7	9.7E+07	9.7E+07	5920	0.620694484	2.733659064	0.0092707	0.021323578	0.05725	1	53	67	94	82	92	179	132	113	196	200
ENSMUSG00000030956	chr7	Fam53b	1.3E+08	1.3E+08	6911	-0.52775163	5.626992371	0.0092878	0.021357586	0.04777	-1	770	447	1214	803	1350	800	1098	536	909	871
ENSMUSG00000041423	chr3	Paqr6	8.8E+07	8.8E+07	2429	1.05979839	-0.13106033	0.0092886	0.021357586	0.10474	1	9	7	10	4	8	30	22	8	29	23
ENSMUSG00000029484	chr5	Anxa3	9.7E+07	9.7E+07	1597	0.568620944	4.389043555	0.009293	0.021364411	0.05405	1	175	180	242	205	497	639	521	405	485	530
ENSMUSG00000015189	chr6	Casd1	4600840	4601301	4062	-0.47231994	4.902991996	0.0093029	0.021383633	0.03729	-1	555	330	642	570	539	536	702	434	430	474
ENSMUSG00000026819	chr2	Slc25a25	3.2E+07	3.2E+07	7862	-0.79231544	4.336036574	0.0093214	0.021422605	0.10654	-1	169	256	283	709	516	246	285	213	382	393
ENSMUSG00000004044	chr11	Ptrf	1E+08	1E+08	3587	0.660868068	8.048314571	0.0093239	0.021422817	0.07643	1	2413	1918	2982	2487	6220	8967	4860	5499	7390	6810
ENSMUSG00000004655	chr6	Aqp1	5.5E+07	5.5E+07	2627	-0.62392385	7.93362255	0.0093246	0.021422817	0.06815	-1	3826	2157	8173	5274	3840	3938	4779	2852	4410	3966
ENSMUSG00000062611	chr14	Rps3a2	8.8E+07	8.8E+07	792	0.483864545	4.757599237	0.0093281	0.021427435	0.03883	1	338	274	359	301	414	941	502	513	565	746
ENSMUSG00000037347	chrX	Chst7	2E+07	2E+07	2206	0.739208641	1.84698128	0.0093355	0.02144091	0.07946	1	28	23	54	37	60	95	72	85	121	69
ENSMUSG00000021219	chr12	Rgs6	8.3E+07	8.3E+07	8145	-1.189725	0.398446138	0.0093419	0.021448583	0.19216	-1	18	36	10	22	39	27	7	14	13	18
ENSMUSG00000032434	chr9	Cmtm6	1.1E+08	1.1E+08	3352	0.54409254	4.589490903	0.0093419	0.021448583	0.0497	1	237	208	292	214	555	799	558	439	582	584
ENSMUSG00000033147	chr3	Slc22a15	1E+08	1E+08	11085	0.98961034	0.487297423	0.0093455	0.021453446	0.11231	1	15	11	9	6	23	46	31	33	25	39
ENSMUSG00000032311	chr9	Nrg4	5.5E+07	5.5E+07	6075	-2.2834621	1.974690052	0.0093789	0.021526494	0.79516	-1	72	44	2	2	403	32	10	25	46	20
ENSMUSG00000026455	chr1	Klhl12	1.3E+08	1.3E+08	11395	-0.4071284	4.963525381	0.0093806	0.021526864	0.02747	-1	503	373	651	564	605	600	687	395	551	549
ENSMUSG00000031703	chr8	Itfg1	8.6E+07	8.6E+07	3355	-0.47736352	5.861537268	0.0094252	0.021622076	0.03935	-1	1082	782	1095	1012	1090	1222	1248	792	898	878
ENSMUSG00000040209	chr3	Zfp704	9427020	9438898	15255	-0.49879209	3.575397737	0.0094244	0.021622076	0.0393	-1	238	157	245	191	210	244	237	145	182	214
ENSMUSG00000004931	chr10	Apba3	8.1E+07	8.1E+07	2106	-0.59378848	5.998955048	0.0094544	0.021682011	0.0613	-1	889	625	1961	1498	1008	1069	1317	660	1266	1005
ENSMUSG00000028399	chr4	Ptprd	7.6E+07	7.6E+07	22702	-0.9934264	2.882529403	0.0094538	0.021682011	0.16201	-1	131	78	113	57	393	163	117	78	67	86
ENSMUSG00000039176	chr7	Polg	7.9E+07	7.9E+07	6843	-0.49021582	5.590085405	0.0094877	0.021754776	0.04135	-1	811	516	1109	1062	785	865	987	593	905	802
ENSMUSG00000020719	chr11	Ddx5	1.1E+08	1.1E+08	5775	-0.52834606	8.601644213	0.0095212	0.021828147	0.04934	-1	6484	6274	7352	6200	7762	8182	7271	4987	5627	7027
ENSMUSG00000035559	chr8	Mpv17l2	7.1E+07	7.1E+07	955	0.548931306	3.983557046	0.0095243	0.021831698	0.04996	1	163	103	251	177	303	350	332	280	487	474
ENSMUSG00000040007	chr2	Bahd1	1.2E+08	1.2E+08	4664	0.517109919	3.657737696	0.0095323	0.021846337	0.04244	1	101	118	207	159	203	352	317	190	359	321
ENSMUSG00000090266	chr11	Mettl23	1.2E+08	1.2E+08	2697	-0.41039027	4.950077039	0.0095347	0.021848289	0.02811	-1	547	401	608	524	566	599	574	391	561	624
ENSMUSG00000036817	chr5	Sun1	1.4E+08	1.4E+08	7596	-0.47472462	5.644987215	0.009541	0.021859188	0.03888	-1	948	690	1068	831	810	1025	1053	674	788	798
ENSMUSG00000039428	chr7	Tmem135	8.9E+07	8.9E+07	6104	-0.56226467	4.941812795	0.0095576	0.021893675	0.05403	-1	517	360	495	380	1077	593	530	380	528	539
ENSMUSG00000024234	chr18	Mtpap	4375592	4375778	2651	-0.46041728	4.094556835	0.009563	0.021902465	0.03399	-1	277	187	391	331	320	362	309	257	280	267
ENSMUSG00000017299	chr2	Dnttip1	1.6E+08	1.6E+08	2122	0.439477546	4.204321133	0.0095657	0.021904966	0.03117	1	206	156	311	235	284	503	399	370	453	445
ENSMUSG00000020864	chr11	Ankrd40	9.4E+07	9.4E+07	4255	-0.52664625	8.05663383	0.0095779	0.021929464	0.04902	-1	4145	3158	6604	5319	4805	4617	5962	3127	4603	4392
ENSMUSG00000021765	chr13	Fst	1.1E+08	1.1E+08	2337	0.811442443	3.747364517	0.0095812	0.021933422	0.10924	1	146	196	79	77	185	470	331	293	295	365
ENSMUSG00000071451	chr13	Psmg4	3.4E+07	3.4E+07	554	0.587797422	2.962592164	0.0095938	0.021958668	0.05356	1	86	61	105	81	137	208	147	150	240	204
ENSMUSG00000064363	chrMT	mt-Nd4	10167	11544	1378	-0.67001009	12.78531375	0.0096003	0.02196991	0.07935	-1	113725	56696	214081	162003	135481	110366	176825	69927	94632	119298
ENSMUSG00000040697	chr4	Dnajc16	1.4E+08	1.4E+08	6510	-0.4887649	4.767796124	0.0096053	0.021977778	0.04027	-1	395	303	697	593	443	481	618	331	493	426
ENSMUSG00000026617	chr1	Bpnt1	1.9E+08	1.9E+08	2263	-0.49855827	4.093084531	0.0096098	0.021984483	0.04065	-1	285	232	306	234	453	362	310	242	291	250
ENSMUSG00000020894	chr11	Vamp2	6.9E+07	6.9E+07	3809	0.473150218	6.085612415	0.0096218	0.022008311	0.03898	1	774	544	1060	867	1121	1839	1522	1171	1676	1979
ENSMUSG00000034522	chr14	Zfp395	6.5E+07	6.5E+07	4229	-0.41561214	4.685535313	0.0096248	0.022011648	0.02863	-1	424	337	463	451	533	511	515	296	483	490
ENSMUSG00000022672	chr16	Prkdc	1.6E+07	1.6E+07	13187	-0.53675763	3.403919526	0.0096353	0.022032006	0.0461	-1	191	152	166	199	218	224	216	112	170	177
ENSMUSG00000033319	chr18	Fem1c	4.7E+07	4.7E+07	5726	-0.51659018	4.264760889	0.0096597	0.022084233	0.04435	-1	267	236	536	373	316	348	461	240	279	309
ENSMUSG00000030867	chr7	Plk1	1.2E+08	1.2E+08	2203	1.508212638	-0.36536532	0.0096679	0.022099462	0.26083	1	2	6	1	3	13	33	5	21	23	16
ENSMUSG00000028468	chr4	Rgp1	4.4E+07	4.4E+07	6199	-0.44298087	5.642907372	0.0096833	0.022131113	0.03384	-1	774	613	1226	880	894	1015	928	608	964	890
ENSMUSG00000020453	chr11	Patz1	3288874	3289347	5904	-0.4804508	3.675687523	0.0096904	0.022143569	0.0367	-1	208	184	256	221	240	222	254	152	242	230
ENSMUSG00000029386	chr5	Tctn2	1.2E+08	1.2E+08	8318	0.829138476	1.758330081	0.0096967	0.022154474	0.09914	1	37	26	25	21	69	124	73	56	90	93
ENSMUSG00000046836	chr1	Brox	1.8E+08	1.8E+08	5010	-0.43156109	4.850285716	0.0096995	0.022157162	0.03125	-1	468	386	663	510	463	602	605	389	486	460
ENSMUSG00000036057	chr9	Ptpn23	1.1E+08	1.1E+08	5336	0.495066552	4.168418293	0.0097072	0.022171232	0.04042	1	200	143	274	198	329	444	397	281	566	485
ENSMUSG00000044252	chr18	Osbpl1a	1.3E+07	1.3E+07	7392	-0.53325066	5.561689488	0.0097182	0.022192644	0.04932	-1	744	460	1469	931	737	900	916	641	701	827
ENSMUSG00000027435	chr2	Cd93	1.5E+08	1.5E+08	6677	0.515522162	5.772683506	0.0097276	0.022210648	0.04641	1	440	402	1014	719	944	1756	1237	1083	1296	1280
ENSMUSG00000029428	chr5	Stx2	1.3E+08	1.3E+08	4164	0.520401292	3.596961303	0.0097451	0.022246865	0.04304	1	111	118	147	151	219	362	322	218	310	255
ENSMUSG00000005417	chr11	Mprip	6E+07	6E+07	13327	-0.47469715	6.798814444	0.0097509	0.022256465	0.03973	-1	1693	1376	2490	2044	2268	2255	2301	1321	1868	1980
ENSMUSG00000044949	chr11	Ubtd2	3.2E+07	3.2E+07	1012	-0.83637713	1.410667932	0.0097564	0.022265309	0.10203	-1	45	61	45	35	55	51	55	27	33	28
ENSMUSG00000024875	chr19	Yif1a	5088538	5088748	1493	0.475287643	5.388463194	0.0097621	0.022274864	0.03907	1	444	280	820	569	617	1090	1087	677	1130	1078
ENSMUSG00000055240	chr17	Zfp101	3.3E+07	3.3E+07	7424	-0.74544242	1.957765332	0.0097834	0.022319858	0.08289	-1	83	57	67	88	57	89	70	43	39	57
ENSMUSG00000015804	chr5	Med28	4.6E+07	4.6E+07	5010	0.434570892	5.576258152	0.0097863	0.022322679	0.03245	1	592	465	692	556	756	1362	1103	865	1180	1163
ENSMUSG00000054836	chr9	Elp6	1.1E+08	1.1E+08	2054	0.668069368	2.358906114	0.0097993	0.02234885	0.06711	1	57	39	55	44	101	148	113	113	141	115
ENSMUSG00000057667	chr7	Bloc1s3	2E+07	2E+07	1824	0.588882968	2.982954675	0.009801	0.022349	0.05365	1	93	69	121	69	122	241	141	157	210	216
ENSMUSG00000001583	chr11	Tnk1	7E+07	7E+07	3329	1.422015436	-0.5456808	0.0098202	0.02238561	0.21492	1	3	4	3	1	12	26	6	19	10	22
ENSMUSG00000097412	chr10	1810014B01Rik	8.7E+07	8.7E+07	1661	-0.57105184	3.593992368	0.0098188	0.02238561	0.05344	-1	188	160	296	253	187	171	237	116	240	242
ENSMUSG00000054203	chr1	Ifi205	1.7E+08	1.7E+08	4177	1.008844752	1.676631929	0.0098366	0.022419342	0.15903	1	20	23	39	14	62	105	167	54	55	49
ENSMUSG00000031622	chr8	Sin3b	7.3E+07	7.3E+07	4298	0.446666835	4.969142921	0.0098665	0.022483707	0.03402	1	325	231	478	427	587	876	650	591	794	810

ENSMUSG00000034757	chr11	Tmub2	1E+08	1E+08	2544	0.420773226	4.826588071	0.009873	0.022494873	0.02944	1	326	300	422	323	452	779	623	488	754	713
ENSMUSG00000090641	chr13	Zfp712	6.7E+07	6.7E+07	3970	-0.83058353	0.463166157	0.0098845	0.022517374	0.07702	-1	23	17	35	26	25	24	28	12	13	20
ENSMUSG00000024120	chr17	Lrpprc	8.5E+07	8.5E+07	8504	-0.53678448	6.744445779	0.0099087	0.022565275	0.05102	-1	1595	1091	3167	2094	1928	1942	2295	1336	1630	1878
ENSMUSG00000037062	chr3	Sh3glb1	1.4E+08	1.4E+08	3949	-0.58055568	7.94335293	0.0099103	0.022565275	0.06003	-1	3793	2527	7592	4753	4313	3950	5623	2836	3593	4513
ENSMUSG00000072837	chr10	Mir546	1.3E+08	1.3E+08	121	-0.47878251	3.960999044	0.0099099	0.022565275	0.03742	-1	263	170	386	271	296	371	320	167	229	277
ENSMUSG00000048027	chr17	Rgmb	1.6E+07	1.6E+07	2633	-0.45719061	4.666155829	0.0099223	0.022588852	0.03533	-1	429	382	485	455	423	467	583	331	423	407
ENSMUSG00000023883	chr17	Phf10	1.5E+07	1.5E+07	4914	-0.47617037	5.743761872	0.0099692	0.022692038	0.03967	-1	911	835	1054	915	900	1027	1024	760	924	880
ENSMUSG00000078238	chr4	Gm12854	1.2E+08	1.2E+08	297	1.105595603	-0.04505777	0.0099905	0.022736782	0.1442	1	3	3	9	5	22	36	21	20	20	22
ENSMUSG00000001946	chr9	Esam	3.8E+07	3.8E+07	2867	0.52050449	5.15788709	0.0099968	0.022747523	0.04724	1	320	229	632	429	698	1070	665	739	927	917
ENSMUSG00000025393	chr10	Atp5b	1.3E+08	1.3E+08	4237	-0.61642634	11.62875605	0.0100045	0.022757553	0.06803	-1	48079	29192	99182	69896	53498	49928	70086	35929	51309	52660
ENSMUSG00000099066	chr17	Mir6978	5.7E+07	5.7E+07	57	1.179264529	-0.00156919	0.0100029	0.022757553	0.15095	1	4	12	5	3	15	25	29	12	33	27
ENSMUSG00000024413	chr18	Npc1	1.2E+07	1.2E+07	10725	-0.54748526	5.376672535	0.0100109	0.022768352	0.05234	-1	612	401	1221	581	1081	842	993	417	647	651
ENSMUSG00000028944	chr5	Prkag2	2.5E+07	2.5E+07	6480	0.622469704	4.253734491	0.010018	0.022780915	0.06659	1	176	134	271	134	463	531	445	410	541	432
ENSMUSG00000079065	chr5	BC005561	1E+08	1E+08	5181	-0.81949549	1.965607659	0.0101336	0.023039959	0.10314	-1	82	79	84	61	50	50	81	58	43	50
ENSMUSG00000046879	chr11	Irgm1	4.9E+07	4.9E+07	5810	0.57555726	4.52660185	0.0101417	0.023054688	0.05686	1	280	189	411	246	282	1100	443	380	440	552
ENSMUSG00000002010	chrX	Idh3g	7.4E+07	7.4E+07	2701	-0.58752434	8.422565768	0.0101459	0.023056663	0.06193	-1	5170	3232	10055	6989	6799	5229	8179	3852	5545	5714
ENSMUSG00000024471	chr18	Myot	4.4E+07	4.4E+07	2209	-0.72804131	9.894570178	0.0101456	0.023056663	0.09481	-1	14326	8496	30657	26361	12555	14912	22694	9281	12799	15401
ENSMUSG00000000094	chr11	Tbx4	8.6E+07	8.6E+07	3401	0.936433068	0.532643073	0.0101557	0.023075228	0.09981	1	19	11	18	12	7	56	36	21	32	37
ENSMUSG00000026525	chr1	Opn3	1.8E+08	1.8E+08	1913	1.198831703	0.515445445	0.0101626	0.023085995	0.18872	1	18	9	5	8	18	49	12	23	49	55
ENSMUSG00000054199	chr3	Gon4l	8.9E+07	8.9E+07	7564	-0.45447825	4.250288236	0.0101653	0.023085995	0.03446	-1	276	277	413	335	347	389	377	202	386	321
ENSMUSG00000096981	chr9	Gm16845	2.2E+07	2.2E+07	1415	1.11806858	-0.27444227	0.0101648	0.023085995	0.13245	1	4	2	12	8	8	27	14	7	23	30
ENSMUSG00000027001	chr2	Dusp19	8.1E+07	8.1E+07	2992	-0.55587873	2.915949446	0.0101834	0.023119489	0.04778	-1	146	105	144	127	143	141	148	105	118	111
ENSMUSG00000038976	chr11	Ppp1r9b	9.5E+07	9.5E+07	5083	0.673374389	5.783826543	0.0101834	0.023119489	0.08047	1	493	324	626	452	1476	1624	1283	989	1572	1558
ENSMUSG00000029501	chr5	Ankle2	1.1E+08	1.1E+08	5259	-0.42878309	4.890023102	0.0102071	0.023169598	0.03141	-1	483	409	616	544	491	599	654	366	500	508
ENSMUSG00000019822	chr10	Smpd2	4.1E+07	4.1E+07	4468	0.491935741	3.649459609	0.0102379	0.023235786	0.03922	1	135	87	185	163	230	382	290	214	305	324
ENSMUSG00000025484	chr7	Bet1l	1.4E+08	1.4E+08	1552	0.508991222	3.987279709	0.0102463	0.023250963	0.04327	1	186	112	215	171	323	528	379	307	363	344
ENSMUSG00000037443	chr4	Cep85	1.3E+08	1.3E+08	5269	-0.48867069	5.574055762	0.0102485	0.023252252	0.04197	-1	750	569	1195	877	857	811	1138	557	696	922
ENSMUSG00000036825	chr3	Ssx2ip	1.5E+08	1.5E+08	4195	-0.5342872	4.798420202	0.0102581	0.023270251	0.04941	-1	474	297	830	463	479	410	709	305	441	496
ENSMUSG00000026723	chr2	Trdmt1	1.4E+07	1.4E+07	3835	-0.67031704	2.296830106	0.0102762	0.023307591	0.06843	-1	105	48	131	96	74	83	104	60	68	71
ENSMUSG00000079550	chr1	Mpp4	5.9E+07	5.9E+07	7063	0.629065317	2.179510377	0.0102905	0.023336113	0.05827	1	52	31	72	40	72	145	96	96	107	108
ENSMUSG00000042298	chr11	Ttc19	6.2E+07	6.2E+07	4675	-0.52176729	5.648428434	0.0102956	0.023344031	0.04808	-1	655	601	1435	1031	822	879	1160	591	841	810
ENSMUSG00000020175	chr10	Rab36	7.5E+07	7.5E+07	6175	1.194059058	0.202528655	0.0103071	0.023366255	0.17469	1	8	10	6	3	19	61	19	14	27	30
ENSMUSG00000071415	chr11	Rpl23	9.8E+07	9.8E+07	1770	0.524001577	8.21422255	0.0103225	0.023397404	0.04951	1	3738	2888	3978	3354	4337	9005	5636	5797	7738	8032
ENSMUSG00000072941	chr5	Sod3	5.2E+07	5.2E+07	3570	0.971766313	5.846097916	0.0103279	0.023405886	0.16698	1	341	287	382	278	1856	2050	1277	1214	1590	1759
ENSMUSG00000071647	chr19	Eml3	8929694	8929952	3161	0.658418946	3.390627793	0.0103387	0.023426588	0.07214	1	106	80	113	84	239	347	193	188	287	306
ENSMUSG00000020455	chr11	Trim11	5.9E+07	5.9E+07	3580	0.529244591	3.47724093	0.0103685	0.023490396	0.04546	1	117	82	167	121	212	327	242	179	277	334
ENSMUSG00000084289	chrX	Gm6977	9.1E+07	9.1E+07	512	0.670565732	2.200131498	0.0103804	0.023513467	0.06741	1	34	33	64	52	84	98	137	75	130	129
ENSMUSG00000051278	chr3	Zgrf1	1.3E+08	1.3E+08	7046	-0.87177157	0.319191275	0.0104079	0.023572072	0.08377	-1	27	21	27	17	20	20	15	12	16	22
ENSMUSG00000043964	chr7	Orai3	1.3E+08	1.3E+08	2141	0.444544683	4.364733387	0.0104149	0.023583925	0.03292	1	247	182	270	243	381	647	462	353	494	507
ENSMUSG00000051726	chr12	Kcnf1	1.7E+07	1.7E+07	4789	0.972500657	2.13537727	0.01042	0.023591867	0.15446	1	15	31	111	37	33	85	176	78	133	111
ENSMUSG00000090386	chr16	Mir99ahg	7.7E+07	7.7E+07	14045	0.814047911	1.372854447	0.0104285	0.023607149	0.09414	1	17	19	42	21	39	99	43	49	50	86
ENSMUSG00000038267	chr13	Slc22a23	3.4E+07	3.4E+07	6386	-0.69061816	4.046317871	0.0104362	0.023620909	0.08204	-1	222	110	620	371	303	228	336	218	245	263
ENSMUSG00000058396	chr10	Gpr182	1.3E+08	1.3E+08	3954	0.99977942	0.25878365	0.0104478	0.023643225	0.11276	1	4	10	9	9	22	40	27	21	36	24
ENSMUSG00000037887	chr7	Dusp8	1.4E+08	1.4E+08	4870	-0.59006227	5.282389459	0.0104551	0.02365602	0.06151	-1	466	371	1120	885	819	462	784	428	794	736
ENSMUSG00000039199	chr8	Zdhhc1	1.1E+08	1.1E+08	1737	0.48338451	4.159121679	0.010481	0.023710658	0.03926	1	179	149	305	216	292	481	329	316	507	509
ENSMUSG00000019857	chr10	Asf1a	5.4E+07	5.4E+07	2180	-0.50621459	3.647050644	0.0104881	0.02372296	0.04198	-1	214	181	306	197	201	268	250	169	183	197
ENSMUSG00000033629	chr9	Ptplad1	6.5E+07	6.5E+07	2731	0.469380509	4.076741366	0.0104998	0.023745492	0.03637	1	226	150	208	188	292	473	417	326	356	439
ENSMUSG00000085783	chr16	Gm9816	6.3E+07	6.3E+07	1414	-0.63654473	2.206635579	0.0105286	0.023806806	0.05982	-1	67	66	97	95	91	72	106	56	71	62
ENSMUSG00000031681	chr8	Smad1	7.9E+07	7.9E+07	5814	0.487180013	3.838993467	0.0105312	0.023808944	0.03909	1	166	126	219	148	245	411	298	320	318	349
ENSMUSG00000025352	chr10	Gdf11	1.3E+08	1.3E+08	4062	0.814896388	4.064866851	0.0105353	0.023814394	0.11516	1	319	151	109	91	204	644	462	402	362	317
ENSMUSG00000000093	chr11	Tbx2	8.6E+07	8.6E+07	3626	0.810202065	2.219186245	0.0105592	0.02386455	0.10562	1	30	36	67	27	97	174	74	95	119	136
ENSMUSG00000026049	chr1	Tex30	4.4E+07	4.4E+07	1926	-0.76508146	1.358740087	0.0105716	0.023888633	0.08166	-1	45	41	64	40	45	44	45	30	50	21
ENSMUSG00000042333	chr4	Tnfrsf14	1.5E+08	1.5E+08	1158	1.075787395	0.552323183	0.0105775	0.023898275	0.14547	1	13	15	12	8	15	74	17	32	29	37
ENSMUSG00000035469	chr14	Rcbtb1	5.9E+07	5.9E+07	6010	-0.44417475	4.392931362	0.0105972	0.02393875	0.03333	-1	373	294	405	360	370	439	436	297	318	345
ENSMUSG00000029201	chr5	Ugdh	6.5E+07	6.5E+07	6799	0.588984827	4.22079915	0.0105997	0.023940709	0.05978	1	198	162	193	159	423	704	479	323	412	420
ENSMUSG00000025876	chr13	Unc5a	5.5E+07	5.5E+07	4168	-0.80494095	1.098228805	0.0106026	0.023943353	0.08544	-1	30	24	53	41	54	40	18	26	44	26
ENSMUSG00000098917	chr8	Mir7654	8690093	8690162	70	-0.86955547	0.707284533	0.0106098	0.023955771	0.09516	-1	25	25	44	33	24	24	22	21	32	13
ENSMUSG00000041046	chr11	Ramp3	6658521	6658627	1380	1.192961638	0.579191142	0.0106306	0.023998748	0.20998	1	10	1	34	16	5	38	37	24	41	56
ENSMUSG00000028447	chr4	Dctn3	4.2E+07	4.2E+07	1042	0.478138529	4.284622819	0.0106453	0.024024333	0.03869	1	214	167	248	217	396	544	442	328	556	475
ENSMUSG00000090247	chr10	Bloc1s1	1.3E+08	1.3E+08	1288	0.486129274	6.322765372	0.0106452	0.024024333	0.04239	1	998	760	1007	968	1283	2115	1711	1493	2156	2157
ENSMUSG00000024145	chr17	Pigf	8.7E+07	8.7E+07	988	0.835479005	1.246192822	0.010663	0.024060269	0.10276	1	30	8	29	16	43	68	56	60	58	51
ENSMUSG00000032235	chr9	Ice2	6.9E+07	6.9E+07	7736	-0.62894934	2.461251054	0.0106961	0.024131247	0.06104	-1	81	78	129	121	87	118	93	69	64	99
ENSMUSG00000019996	chr10	Map7	2E+07	2E+07	4351	-1.01562698	1.525680143	0.0107081	0.02415433	0.16145	-1	31	21	146	41	66	36	63	21	29	44
ENSMUSG00000018547	chr11	Pip4k2b	9.8E+07	9.8E+07	5204	-0.51681081	6.860947211	0.0107446	0.024232832	0.04844	-1	1888	1568	2527	2390	1902	2099	2653	1276	2002	1963
ENSMUSG00000028840	chr4	Zfp593	1.3E+08	1.3E+08	2088	0.635758633	3.191517929	0.0107613	0.024266608	0.06661	1	112	81	102	73	167	314	167	214	228	202
ENSMUSG00000045114	chr7	Prrt2	1.3E+08	1.3E+08	3272	0.583181409	3.09104776	0.010771	0.024284539	0.05371	1	95	93	104	86	123	278	187	122	207	265
ENSMUSG00000021519	chr13	Mterf3	6.7E+07	6.7E+07	4652	-0.46841496	3.932690949	0.01078	0.024300881	0.03658	-1	276	204	307	233	310	371	310	189	227	237

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ENSMUSG00000024238	chr18	Zeb1	5591860	5591967	10112	-0.43782168	5.537343936	0.0107892	0.024317674	0.03399	-1	723	637	951	865	832	939	959	617	739	834
ENSMUSG00000033124	chr1	Atg9a	7.5E+07	7.5E+07	5762	-0.54435221	7.479405512	0.0107913	0.024318585	0.05397	-1	3140	2455	3422	3828	2931	2788	3615	2002	3600	3070
ENSMUSG00000021900	chr14	Btd	3.2E+07	3.2E+07	2353	0.640896594	3.620545203	0.0108118	0.02436077	0.07022	1	115	95	164	95	272	396	203	235	367	336
ENSMUSG00000021466	chr13	Ptch1	6.4E+07	6.4E+07	8745	-0.49503508	3.672536214	0.0108181	0.024367127	0.04035	-1	228	148	243	236	270	259	284	161	168	223
ENSMUSG00000087574	chr11	C030037D09Rik	8.9E+07	8.9E+07	4199	-0.75814346	1.282656566	0.0108177	0.024367127	0.07729	-1	53	30	56	43	41	42	51	32	25	30
ENSMUSG00000041225	chr18	Arhgap12	6024427	6026730	8016	-0.43519367	4.832174974	0.0108506	0.024436441	0.03289	-1	465	357	643	543	461	653	606	335	432	507
ENSMUSG00000013629	chr5	Cad	3.1E+07	3.1E+07	8164	-0.46569226	3.672111461	0.0108741	0.024485468	0.03512	-1	185	148	281	235	277	284	238	168	225	191
ENSMUSG00000024687	chr19	Osbp	1.2E+07	1.2E+07	4578	-0.49352977	6.852778167	0.010876	0.024485738	0.04429	-1	2048	1529	2456	2059	2079	1929	2523	1411	2093	1997
ENSMUSG00000029104	chr5	Htt	3.5E+07	3.5E+07	18808	-0.42788383	4.216246155	0.0108892	0.024509235	0.0306	-1	283	250	401	318	353	418	347	251	334	289
ENSMUSG00000035275	chr4	Raver2	1E+08	1E+08	6342	-1.00792462	1.529195868	0.0108899	0.024509235	0.1624	-1	47	17	114	86	31	50	56	18	32	41
ENSMUSG00000021196	chr13	Pfkp	6579768	6581592	9395	0.733329148	4.101574949	0.0108948	0.024516279	0.09464	1	163	128	145	103	459	574	398	314	438	495
ENSMUSG00000015053	chr6	Gata2	8.8E+07	8.8E+07	3351	0.58923616	2.910659276	0.0108991	0.024518113	0.05682	1	70	48	139	73	134	207	167	154	188	199
ENSMUSG00000050174	chr3	Nudt6	3.7E+07	3.7E+07	1635	-0.50143281	3.20934804	0.0108983	0.024518113	0.03972	-1	129	122	222	167	178	179	173	123	164	146
ENSMUSG00000027854	chr3	Sike1	1E+08	1E+08	4627	0.434860715	4.235623775	0.0109128	0.02454502	0.03124	1	252	186	259	238	258	571	439	334	447	446
ENSMUSG00000036977	chr8	Anapc10	8E+07	8E+07	2802	-0.60871654	2.369978859	0.010921	0.024559578	0.0568	-1	80	83	110	83	105	128	93	57	74	71
ENSMUSG00000036980	chr5	Taf6	1.4E+08	1.4E+08	3779	-0.43226878	5.207823411	0.0109419	0.02460252	0.03286	-1	597	446	800	708	662	617	821	471	675	667
ENSMUSG00000024066	chr17	Xdh	7.4E+07	7.4E+07	4587	0.529007883	5.375276919	0.0109466	0.024609276	0.05015	1	323	330	722	439	845	1492	1007	671	905	1072
ENSMUSG00000044950	chr11	Pwwp2a	4.4E+07	4.4E+07	5508	-0.60921893	2.497505378	0.0109521	0.024617679	0.05682	-1	109	73	127	90	110	112	105	76	59	104
ENSMUSG00000034601	chr12	2700049A03Rik	7.1E+07	7.1E+07	5879	-0.65022445	2.252993369	0.0109554	0.024621076	0.06479	-1	90	67	110	85	78	58	101	51	86	81
ENSMUSG00000030317	chr6	Timp4	1.2E+08	1.2E+08	1416	-0.6067422	4.870814975	0.0109781	0.024668279	0.06553	-1	293	363	807	339	988	577	542	303	537	465
ENSMUSG00000052419	chr6	2610001J05Rik	1.4E+07	1.4E+07	3784	0.421764282	5.163716875	0.0109879	0.024686313	0.03107	1	432	357	521	437	559	1086	733	717	836	850
ENSMUSG00000028820	chr4	Sfpq	1.3E+08	1.3E+08	4743	0.454099182	5.792805318	0.0110034	0.024717227	0.03702	1	612	465	825	747	927	1573	1169	1151	1330	1352
ENSMUSG00000006235	chr9	Epor	2.2E+07	2.2E+07	1829	1.282292895	0.772762243	0.0110081	0.024723723	0.2483	1	10	9	2	6	44	57	36	39	51	46
ENSMUSG00000029223	chr5	Uchl1	6.7E+07	6.7E+07	1616	0.962968248	1.696490623	0.0110165	0.02473461	0.15227	1	18	5	66	38	44	107	67	52	82	121
ENSMUSG00000100551	chr1	Gm19503	1.5E+08	1.5E+08	241	-1.21234436	0.930524904	0.0110165	0.02473461	0.22879	-1	40	19	106	28	8	30	22	20	18	23
ENSMUSG00000057842	chr13	Zfp595	6.7E+07	6.7E+07	5430	-0.76329894	1.283804599	0.0110198	0.024738203	0.08096	-1	45	48	41	33	51	42	37	34	31	35
ENSMUSG00000085334	chr4	Gm12940	1.3E+08	1.3E+08	2680	0.680948179	3.102911779	0.0110284	0.024753349	0.07834	1	81	62	111	81	169	314	139	174	158	298
ENSMUSG00000041733	chr5	Coq5	1.2E+08	1.2E+08	2037	-0.65913638	6.931783428	0.0110495	0.02479695	0.07929	-1	1676	1064	4417	2746	1903	1898	2780	1343	1939	1886
ENSMUSG00000042453	chr5	Reln	2.2E+07	2.2E+07	19834	0.722460485	2.373857884	0.0110724	0.024840349	0.08203	1	33	42	85	76	55	129	153	77	106	193
ENSMUSG00000046329	chr17	Slc25a23	5.7E+07	5.7E+07	5294	-0.51004363	4.579662845	0.0110719	0.024840349	0.04551	-1	381	280	378	369	744	507	370	298	381	490
ENSMUSG00000042106	chr9	Fam212a	1.1E+08	1.1E+08	1156	0.814706863	2.138078744	0.011085	0.024864604	0.1065	1	38	30	39	26	108	134	94	93	122	118
ENSMUSG00000055116	chr7	Arntl	1.1E+08	1.1E+08	2904	-0.57559999	4.758913548	0.0110943	0.024881553	0.05912	-1	425	425	481	673	369	468	678	276	420	431
ENSMUSG00000033938	chr8	Ndufb7	8.4E+07	8.4E+07	4522	0.518188844	7.696616899	0.0111086	0.024909484	0.04936	1	2222	1522	3855	2822	2777	5029	4815	3896	5815	5614
ENSMUSG00000022008	chr14	Gpalpp1	7.6E+07	7.6E+07	5448	-0.44864383	3.907702113	0.0111146	0.024918983	0.03338	-1	284	180	311	257	270	329	295	197	234	258
ENSMUSG00000028530	chr4	Jak1	1E+08	1E+08	7227	-0.52725261	6.942985233	0.0111312	0.024952167	0.05093	-1	2218	1740	2705	2116	2106	2460	2898	1597	1859	1661
ENSMUSG00000036975	chr1	Tmem177	1.2E+08	1.2E+08	3341	-0.4539548	4.137477339	0.0111332	0.024952785	0.0347	-1	283	191	447	265	381	334	363	205	345	294
ENSMUSG00000020694	chr11	Tlk2	1.1E+08	1.1E+08	8070	-0.44345312	5.577994334	0.0111417	0.024967773	0.03526	-1	774	634	1053	885	794	989	999	609	776	835
ENSMUSG00000026171	chr1	Rnf25	7.5E+07	7.5E+07	2181	0.431309703	4.303308253	0.0111459	0.024973316	0.03129	1	210	187	263	267	341	547	442	366	483	493
ENSMUSG00000067038	chr19	Rps12-ps3	5.9E+07	5.9E+07	494	0.907175371	0.393258999	0.0111501	0.024978696	0.09247	1	16	8	9	11	18	39	21	28	35	36
ENSMUSG00000033721	chr3	Vav3	1.1E+08	1.1E+08	6005	0.658739664	2.139268873	0.0111547	0.024985043	0.06389	1	48	40	60	46	56	159	120	97	85	81
ENSMUSG00000017478	chr8	Zc3h18	1.2E+08	1.2E+08	9190	-0.45354236	4.907713433	0.0111753	0.025027149	0.03614	-1	406	367	743	615	510	508	628	377	586	518
ENSMUSG00000058624	chr19	Gda	2.1E+07	2.1E+07	6135	0.626469953	4.257259998	0.0111883	0.02505211	0.06944	1	178	150	245	142	451	700	442	443	368	426
ENSMUSG00000029730	chr5	Mcm7	1.4E+08	1.4E+08	4426	0.486015736	3.47722747	0.0112083	0.025092885	0.03796	1	133	98	148	139	178	351	244	187	282	277
ENSMUSG00000020250	chr10	Txnrd1	8.3E+07	8.3E+07	3417	-0.49753729	6.398603251	0.0112583	0.025200983	0.0452	-1	1363	1020	2264	1329	1610	1481	1837	1210	1383	1283
ENSMUSG00000073435	chr17	Nme3	2.5E+07	2.5E+07	876	0.527996281	3.086341026	0.011264	0.025209594	0.04454	1	101	70	112	93	147	244	178	170	219	208
ENSMUSG00000074513	chr3	Arfip1	8.4E+07	8.4E+07	2986	0.429054851	4.343200858	0.0113056	0.025298674	0.03134	1	228	173	301	267	347	592	455	409	426	507
ENSMUSG00000022466	chr15	Rpap3	9.8E+07	9.8E+07	2260	-0.48784944	4.088137491	0.0113116	0.025304484	0.04084	-1	359	203	337	305	280	360	362	221	244	279
ENSMUSG00000059995	chr11	Atxn7l3	1E+08	1E+08	4121	0.39712635	4.657303925	0.0113118	0.025304484	0.02701	1	285	219	394	332	431	625	641	423	648	626
ENSMUSG00000042369	chr2	Rbm45	7.6E+07	7.6E+07	1898	0.521516384	3.807352817	0.0113268	0.025334007	0.04594	1	175	135	202	131	219	440	256	314	315	353
ENSMUSG00000021256	chr12	Vash1	8.7E+07	8.7E+07	2599	-0.98764046	1.645040735	0.0113452	0.025371113	0.15724	-1	50	24	113	81	50	49	86	17	41	24
ENSMUSG00000026888	chr2	Grb14	6.5E+07	6.5E+07	7185	-0.63770721	5.076668023	0.0113562	0.025391623	0.07331	-1	456	211	1211	667	763	519	751	433	477	538
ENSMUSG00000024767	chr19	Otub1	7198202	7199239	2545	0.426147318	5.475949949	0.0113969	0.025478535	0.03254	1	497	391	732	583	696	1076	1119	805	1212	1044
ENSMUSG00000032998	chr4	Foxj3	1.2E+08	1.2E+08	10973	-0.41076273	5.379950734	0.0114059	0.025492903	0.03007	-1	648	522	934	725	775	878	793	575	693	760
ENSMUSG00000064337	chrMT	mt-Rnr1	70	1024	955	-0.57210423	8.662322685	0.0114069	0.025492903	0.06068	-1	7808	3573	10567	8877	6565	6963	8450	5057	6572	6717
ENSMUSG00000046207	chr11	Pik3r6	6.9E+07	6.9E+07	3622	0.644759725	2.148819799	0.0114167	0.025510628	0.06249	1	32	37	62	51	76	162	99	80	104	104
ENSMUSG00000028138	chr3	Adh5	1.4E+08	1.4E+08	2801	-0.45241386	5.852379399	0.0114223	0.025519215	0.03714	-1	932	681	1451	981	1062	1062	1236	742	1073	940
ENSMUSG00000034587	chr11	8430429K09Rik	3452365	3452434	2649	-0.71460895	1.171916346	0.0114321	0.025536976	0.06419	-1	38	22	59	40	49	34	38	27	40	30
ENSMUSG00000041528	chr9	Rnf123	1.1E+08	1.1E+08	6754	-0.52896824	6.809144915	0.0114363	0.02554237	0.05159	-1	1871	1443	2263	2316	2085	1620	2420	1296	2370	1797
ENSMUSG00000022884	chr16	Eif4a2	2.3E+07	2.3E+07	5338	-0.51117549	8.575135239	0.0114509	0.025563224	0.04857	-1	6798	5456	7918	7052	6208	7989	7479	4776	5718	6811
ENSMUSG00000030615	chr7	Tmem126a	9E+07	9E+07	1018	-0.44334751	5.76202533	0.0114476	0.025563224	0.03564	-1	957	724	1115	970	918	1095	1039	742	948	931
ENSMUSG00000102976	chr1	Zc3h11a	1.3E+08	1.3E+08	6031	-0.48497544	6.784395063	0.0114511	0.025563224	0.04337	-1	1853	1693	2097	1732	2206	2188	2239	1440	1745	1920
ENSMUSG00000021594	chr13	Srd5a1	7E+07	7E+07	2881	1.484850653	-0.47263039	0.0114573	0.025572955	0.24617	1	3	6	2	0	12	36	9	14	20	12
ENSMUSG00000022617	chr15	Chkb	8.9E+07	8.9E+07	5805	-0.64018389	8.618355316	0.0114942	0.025651095	0.076	-1	5701	3301	13972	8340	6588	7123	7998	4244	5325	7429
ENSMUSG00000042524	chr15	Sun2	8E+07	8E+07	4969	-0.50608205	7.356681571	0.0115144	0.025692072	0.04746	-1	2702	1965	3448	2757	3845	2634	3738	1865	2966	2886
ENSMUSG00000044442	chr16	N6amt1	8.7E+07	8.7E+07	6135	-0.48970677	3.621888516	0.0115293	0.025717253	0.03998	-1	220	176	264	193	218	261	191	187	197	210
ENSMUSG00000051359	chr15	Ncald	3.7E+07	3.7E+07	6987	0.610637064	2.475094987	0.0115276	0.025717253	0.05682	1	60	52	86	64	62	203	106	104	134	137
ENSMUSG00000000631	chr11	Myo18a	7.8E+07	7.8E+07	14864	-0.59346418	7.662948955	0.0115333	0.025721975	0.06533	-1	2721	2528	5035	5286	2909	3255	4063	2139	3594	3790

ENSMUSG00000029817	chr6	Tra2a	4.9E+07	4.9E+07	1828	0.473442176	4.41574567	0.0115633	0.02578492	0.0395	1	214	142	384	281	369	593	465	443	449	589
ENSMUSG00000022507	chr16	1810013L24Rik	8830100	8830685	4066	-0.48272968	5.33995772	0.0115771	0.025804678	0.04205	-1	605	423	1159	735	737	772	924	535	566	703
ENSMUSG00000022550	chr15	Adck5	7.7E+07	7.7E+07	3452	0.586570306	2.407800316	0.0115762	0.025804678	0.0528	1	54	40	75	55	95	160	118	86	154	131
ENSMUSG00000032178	chr9	Ilf3	2.1E+07	2.1E+07	4754	-0.42582017	4.772867257	0.0115777	0.025804678	0.03177	-1	465	323	664	495	428	529	528	373	507	469
ENSMUSG00000040943	chr3	Tet2	1.3E+08	1.3E+08	9179	-0.58648059	3.874864414	0.011589	0.025825672	0.06034	-1	293	172	275	365	203	276	236	150	217	342
ENSMUSG00000040274	chr5	Cdk6	3343893	3343971	3735	1.231177113	-0.29559475	0.0115953	0.025835737	0.16929	1	2	4	13	9	3	28	21	5	29	19
ENSMUSG00000030064	chr6	Frmd4b	9.7E+07	9.7E+07	11521	0.64531975	3.213600933	0.0116075	0.02585874	0.07038	1	100	89	111	61	182	358	231	178	185	215
ENSMUSG00000087095	chr19	Emx2os	5.9E+07	5.9E+07	5023	1.143925375	-0.33248658	0.0116321	0.025909506	0.13205	1	5	6	3	6	11	25	9	20	17	23
ENSMUSG00000040029	chr6	Ipo8	1.5E+08	1.5E+08	10623	-0.43076013	4.902334146	0.0116519	0.025949326	0.03284	-1	484	426	623	509	524	580	631	453	500	449
ENSMUSG00000028188	chr3	Spata1	1.5E+08	1.5E+08	4114	-0.89094914	1.017433183	0.0116781	0.026003748	0.11751	-1	39	38	51	33	26	35	40	10	20	40
ENSMUSG00000078941	chr13	Ak6	1E+08	1E+08	2769	-0.46994872	5.668195417	0.0116895	0.02602488	0.04035	-1	910	757	990	869	854	1106	1050	693	803	769
ENSMUSG00000085665	chr11	Gm12059	2.3E+07	2.3E+07	3105	-0.97802829	0.324425752	0.0117093	0.026064873	0.12288	-1	21	20	43	15	19	16	26	9	9	22
ENSMUSG00000076012	chr6	Mir705	8.5E+07	8.5E+07	82	0.890749326	1.544940507	0.0117296	0.026105886	0.12587	1	16	11	64	36	28	57	111	48	78	81
ENSMUSG00000066415	chr9	Msl2	1E+08	1E+08	5627	-0.42230531	4.906256767	0.0117377	0.026119784	0.03158	-1	516	406	649	498	505	589	636	438	472	502
ENSMUSG00000027425	chr2	Csrp2bp	1.4E+08	1.4E+08	4699	-0.46664072	4.543697641	0.0117519	0.026147207	0.03844	-1	295	291	648	392	455	496	537	252	375	391
ENSMUSG00000031879	chr8	Fam96b	1E+08	1E+08	1075	0.466190789	4.5886018	0.0117712	0.026181904	0.03871	1	203	173	456	326	417	616	559	470	615	601
ENSMUSG00000039783	chr1	Kmo	1.8E+08	1.8E+08	4724	1.493977081	0.298927245	0.0117695	0.026181904	0.31678	1	5	11	0	3	23	55	14	22	33	45
ENSMUSG00000028597	chr4	Gpx7	1.1E+08	1.1E+08	1289	0.624147432	3.672760388	0.011798	0.026237263	0.06716	1	142	144	100	140	205	433	223	257	339	333
ENSMUSG00000031918	chr9	Mtmr2	1.4E+07	1.4E+07	4913	-0.45208098	4.33695072	0.0118019	0.026241866	0.03558	-1	309	238	477	337	424	485	457	243	305	294
ENSMUSG00000024290	chr18	Rock1	1E+07	1E+07	6187	-0.48511018	3.992308951	0.0118087	0.026252893	0.04071	-1	267	223	347	239	319	349	377	195	206	253
ENSMUSG00000079260	chr9	Tmppe	1.1E+08	1.1E+08	6855	0.672836638	2.34591397	0.0118157	0.026264206	0.07305	1	48	32	60	45	113	161	110	103	127	129
ENSMUSG00000042428	chr15	Mgat3	8E+07	8E+07	4665	0.635906493	1.699028324	0.0118179	0.026264991	0.05476	1	35	25	45	36	45	108	72	49	87	82
ENSMUSG00000066315	chr4	Gm12918	1.1E+07	1.1E+07	636	0.569081278	2.833778719	0.0118204	0.026266368	0.05085	1	68	67	89	98	103	183	180	106	204	200
ENSMUSG00000074121	chr7	Ntf5	4.5E+07	4.5E+07	1962	0.618566965	2.692261861	0.0118367	0.026298276	0.06146	1	45	60	95	83	98	170	177	127	198	119
ENSMUSG00000058638	chr7	Zfp110	1.3E+07	1.3E+07	4116	-0.43813224	3.94421757	0.0118481	0.026315402	0.03248	-1	235	190	325	299	287	324	321	180	261	273
ENSMUSG00000093264	chr11	Gm23419	1.2E+08	1.2E+08	84	0.437209289	5.237568108	0.0118477	0.026315402	0.03432	1	398	396	527	415	685	1143	815	679	901	957
ENSMUSG00000077450	chr17	Rab11b	3.4E+07	3.4E+07	6109	0.484653048	6.804795223	0.0118558	0.026328385	0.04373	1	1274	857	1957	1423	1679	2844	2440	2099	2837	3222
ENSMUSG00000030083	chr6	Abtb1	8.9E+07	8.9E+07	1879	0.428478306	4.88009253	0.0118829	0.026384246	0.03252	1	394	249	394	391	469	830	595	516	825	724
ENSMUSG00000079020	chr15	Slc45a4	7.4E+07	7.4E+07	8471	-0.47286334	4.730588169	0.0118951	0.026407157	0.03995	-1	455	342	666	365	521	495	664	317	472	363
ENSMUSG00000042548	chr2	Asxl1	1.5E+08	1.5E+08	7428	-0.43121613	4.127794856	0.0119019	0.026413981	0.03174	-1	276	236	362	304	328	321	366	237	286	322
ENSMUSG00000075224	chr2	Lrrc55	8.5E+07	8.5E+07	4080	0.995062583	0.21716232	0.0119005	0.026413981	0.10912	1	14	9	9	10	9	25	19	19	40	39
ENSMUSG00000031924	chr8	Cyb5b	1.1E+08	1.1E+08	4294	-0.47417215	6.458971787	0.0119249	0.026460868	0.04173	-1	1421	984	1894	1339	2258	1751	1796	1139	1529	1427
ENSMUSG00000037071	chr19	Scd1	4.4E+07	4.4E+07	4836	-2.22783146	10.02565337	0.0119304	0.026468892	0.82863	-1	22589	14632	325	850	99493	10431	3665	10932	8889	2143
ENSMUSG00000000732	chr10	Icosl	7.8E+07	7.8E+07	2756	0.761730156	2.178365055	0.0119331	0.026470529	0.0913	1	42	54	35	36	73	153	86	94	100	139
ENSMUSG00000031389	chrX	Arhgap4	7.4E+07	7.4E+07	8105	0.427006339	4.271968781	0.011945	0.026492887	0.03134	1	221	175	316	208	336	549	420	338	472	508
ENSMUSG00000023852	chr17	Chd1	1.6E+07	1.6E+07	8721	-0.45624616	4.140208865	0.0119556	0.026512079	0.03577	-1	275	228	421	291	329	315	376	272	261	294
ENSMUSG00000097167	chr3	Gm16740	9.5E+07	9.5E+07	956	0.913240199	0.561871555	0.0119609	0.026519746	0.10835	1	12	7	19	14	20	30	24	22	51	55
ENSMUSG00000007216	chr6	Zfp775	4.9E+07	4.9E+07	4083	-0.56105579	3.550866885	0.0120141	0.026633377	0.05415	-1	186	115	333	254	184	205	261	120	193	205
ENSMUSG00000040010	chr8	Slc7a5	1.2E+08	1.2E+08	3708	0.841582986	2.764038091	0.0120511	0.026711223	0.1252	1	33	38	161	42	113	160	164	195	186	153
ENSMUSG00000002210	chr7	Smg9	2.4E+07	2.4E+07	3702	0.450434033	3.928271765	0.0120579	0.026722194	0.03412	1	175	151	237	193	207	412	318	276	427	370
ENSMUSG00000038759	chr6	Nup205	3.5E+07	3.5E+07	6406	-0.47132438	3.903343483	0.0121133	0.026840724	0.03815	-1	195	221	283	261	344	290	309	206	258	226
ENSMUSG00000032033	chr9	Barx2	3.2E+07	3.2E+07	1968	-1.55512434	3.017091563	0.0121478	0.026912891	0.42294	-1	38	17	671	208	91	75	184	41	40	89
ENSMUSG00000097052	chr2	Snhg7	2.7E+07	2.7E+07	2465	0.814109368	1.816516915	0.0121608	0.026937312	0.10638	1	38	23	28	24	76	125	62	59	94	112
ENSMUSG00000021236	chr12	Entpd5	8.4E+07	8.4E+07	6039	-0.45287509	4.635745726	0.0121925	0.027002352	0.03653	-1	408	291	504	330	673	531	508	316	355	471
ENSMUSG00000024247	chr17	Pkdcc	8.3E+07	8.3E+07	2712	-0.55157349	6.778022564	0.012194	0.027002352	0.05709	-1	1444	1154	3190	1940	2498	1756	2666	1170	1956	1740
ENSMUSG00000103565	chr15	Sgsm3	8.1E+07	8.1E+07	2283	-0.52644798	3.82219742	0.0122099	0.027033259	0.04842	-1	195	173	358	284	261	229	341	145	280	209
ENSMUSG00000029359	chr5	Tesc	1.2E+08	1.2E+08	1591	0.963419289	0.619299918	0.0122171	0.027045031	0.12946	1	11	5	28	19	11	61	22	23	45	44
ENSMUSG00000028194	chr3	Ddah1	1.5E+08	1.5E+08	3983	-0.76853437	3.997943321	0.0122193	0.027045554	0.10687	-1	178	118	574	401	331	158	400	195	182	271
ENSMUSG00000032320	chr9	Rcn2	5.6E+07	5.6E+07	4745	0.414070945	4.987073391	0.0122528	0.027115368	0.03067	1	399	293	437	381	547	1007	677	606	716	737
ENSMUSG00000038546	chr13	Ranbp9	4.3E+07	4.3E+07	3064	-0.44497033	5.390990681	0.0122601	0.027127403	0.03631	-1	703	537	943	723	750	779	1014	516	672	713
ENSMUSG00000029640	chr5	Usp12	1.5E+08	1.5E+08	4639	-0.49419221	4.653410374	0.0122718	0.027148863	0.04405	-1	408	261	705	491	398	473	625	287	388	405
ENSMUSG00000024810	chr19	Il33	3E+07	3E+07	2886	0.627123739	3.007798424	0.0122797	0.027162198	0.06651	1	89	67	83	95	137	281	178	200	135	191
ENSMUSG00000095464	chr16	Gm21987	3.8E+07	3.8E+07	456	0.486702755	6.261046868	0.0122817	0.027162242	0.04426	1	1016	667	1075	887	1195	2112	1479	1651	1964	1947
ENSMUSG00000047766	chr9	Lrrc49	6.1E+07	6.1E+07	6310	0.674495908	2.134619062	0.0122887	0.027173381	0.07161	1	31	34	67	71	47	124	115	93	85	123
ENSMUSG00000023791	chr16	Pigx	3.2E+07	3.2E+07	2394	0.541784537	2.762580402	0.012296	0.027185216	0.04617	1	68	60	98	77	111	203	159	106	162	196
ENSMUSG00000066456	chr9	Hmgn3	8.3E+07	8.3E+07	1869	1.043663312	1.756214811	0.0123109	0.027214012	0.18395	1	23	18	13	21	91	110	60	88	86	101
ENSMUSG00000041202	chr4	Pla2g2d	1.4E+08	1.4E+08	2243	1.093764857	3.003119143	0.0123236	0.027237766	0.21045	1	84	95	16	28	136	293	227	121	204	289
ENSMUSG00000079084	chr9	Ccdc82	1.3E+07	1.3E+07	1847	-1.06508783	0.904910765	0.0123301	0.027247829	0.17732	-1	47	33	38	26	36	35	54	12	9	14
ENSMUSG00000063952	chr17	Brpf3	2.9E+07	2.9E+07	7194	-0.46760364	3.949096356	0.0123455	0.027277492	0.03761	-1	208	180	324	242	425	325	279	209	255	269
ENSMUSG00000002413	chr6	Braf	4E+07	4E+07	13862	-0.51633534	3.349212355	0.0123562	0.02728827	0.04502	-1	173	158	184	152	222	210	166	125	152	212
ENSMUSG00000032115	chr9	Hyou1	4.4E+07	4.4E+07	7230	0.478469437	5.663944911	0.0123538	0.02728827	0.04243	1	517	399	722	834	758	1728	1092	928	1178	1214
ENSMUSG00000068959	chr7	Zfp619	4E+07	4E+07	5964	-0.92619623	0.624987996	0.012356	0.02728827	0.115	-1	39	20	35	30	19	20	26	20	10	27
ENSMUSG00000075324	chr2	Fign	6.4E+07	6.4E+07	9969	-0.7528277	1.420556952	0.0123581	0.02728827	0.08511	-1	40	51	42	46	62	44	37	22	57	42
ENSMUSG00000070923	chr4	Klhl9	8.9E+07	8.9E+07	4174	-0.47024877	5.576966202	0.0123977	0.027371316	0.04091	-1	801	474	1185	1002	792	1065	900	633	769	790
ENSMUSG00000082145	chr11	Gm12312	7E+07	7E+07	644	-0.9239258	0.310444222	0.0124715	0.027529911	0.10724	-1	20	21	33	26	13	15	25	14	12	16
ENSMUSG00000036862	chr7	Dchs1	1.1E+08	1.1E+08	11070	0.64066197	2.945554435	0.0124756	0.02753476	0.07151	1	64	39	164	91	112	225	152	158	228	188
ENSMUSG00000059027	chr4	9630013D21Rik	1.1E+08	1.1E+08	3142	-1.21382713	0.711221967	0.0125052	0.027591384	0.23056	-1	27	25	18	8	91	29	15	12	23	19

ENSMUSG00000059834	chr3	Sclt1	4.2E+07	4.2E+07	7569	-0.71385467	1.416083996	0.0125041	0.027591384	0.07154	-1	51	40	60	49	40	46	49	38	30	38
ENSMUSG00000073771	chr4	Btbd19	1.2E+08	1.2E+08	3883	0.812974217	1.157827639	0.0125253	0.02763126	0.09681	1	18	14	23	17	46	63	38	44	71	60
ENSMUSG00000009535	chr18	Rnmt	6.8E+07	6.8E+07	7339	-0.46348038	5.134275124	0.01253	0.027637269	0.03961	-1	661	564	545	575	636	677	705	422	631	632
ENSMUSG00000075318	chr2	Scn2a1	6.6E+07	6.6E+07	9259	1.23244762	1.664820516	0.0125501	0.027677279	0.25464	1	10	14	22	79	9	125	86	64	57	112
ENSMUSG00000024787	chr19	Snx15	6119399	6119954	2184	0.494369521	3.775368845	0.0125575	0.027689379	0.04167	1	126	154	179	182	201	373	307	239	388	338
ENSMUSG00000027131	chr2	Emc4	1.1E+08	1.1E+08	1052	-0.46543589	5.406609106	0.0125786	0.027731509	0.04018	-1	822	611	679	650	891	804	888	552	772	671
ENSMUSG00000023088	chr16	Abcc1	1.4E+07	1.4E+07	12366	-0.40980993	5.152051587	0.0125917	0.027755957	0.03046	-1	483	413	793	621	805	639	735	500	612	658
ENSMUSG00000060244	chr1	Alyref2	1.7E+08	1.7E+08	1273	0.660302712	1.499166582	0.0126007	0.027771543	0.059	1	29	24	39	26	41	87	55	55	73	72
ENSMUSG00000037622	chr4	Wdtc1	1.3E+08	1.3E+08	4800	-0.52950674	6.929582256	0.0126134	0.027795051	0.05319	-1	1888	1422	2920	2384	2420	1729	2626	1258	2621	2148
ENSMUSG00000026610	chr1	Esrrg	1.9E+08	1.9E+08	6208	-1.29001366	3.745622281	0.0126521	0.027875855	0.30132	-1	186	29	805	429	113	176	274	103	66	193
ENSMUSG00000039178	chr5	Tbc1d19	5.4E+07	5.4E+07	2688	-0.44713164	3.905171569	0.0126638	0.027897387	0.03458	-1	257	210	281	233	310	288	329	191	258	243
ENSMUSG00000001630	chr6	Stk38l	1.5E+08	1.5E+08	4571	-0.47416474	3.870517341	0.0126686	0.027903579	0.03932	-1	203	216	299	248	309	353	306	180	205	231
ENSMUSG00000022246	chr15	Rai14	1.1E+07	1.1E+07	5008	0.484440211	3.614426825	0.0126748	0.027908531	0.04013	1	138	98	216	171	150	371	359	208	279	260
ENSMUSG00000066278	chr5	Vps37b	1.2E+08	1.2E+08	2512	0.494624286	3.474469006	0.0126748	0.027908531	0.04104	1	116	102	163	133	181	269	240	194	321	305
ENSMUSG00000092118	chr7	Fancf	5.2E+07	5.2E+07	1691	0.828122077	0.539274549	0.0127216	0.028007053	0.0814	1	19	9	12	12	20	48	28	27	36	37
ENSMUSG00000003948	chr11	Mmd	9E+07	9E+07	5386	-1.13748631	5.659079298	0.0127308	0.028022923	0.2401	-1	964	772	308	274	3072	958	477	535	770	531
ENSMUSG00000085945	chr7	2310014F06Rik	1.1E+08	1.1E+08	659	-1.26199477	0.237821582	0.0127417	0.028042552	0.2236	-1	16	4	55	30	19	10	22	16	6	10
ENSMUSG00000003380	chr7	Rabac1	2.5E+07	2.5E+07	875	0.483730684	7.021052904	0.0127483	0.028046114	0.04453	1	1391	1089	1925	1682	2216	3346	3032	2133	3834	3385
ENSMUSG00000092659	chr7	Mir3100	1.9E+07	1.9E+07	65	-0.7790206	1.307525891	0.0127493	0.028046114	0.09093	-1	43	38	62	47	37	38	64	20	28	35
ENSMUSG00000097758	chr12	Dio3os	1.1E+08	1.1E+08	1281	0.992360538	0.516314165	0.0127493	0.028046114	0.13066	1	8	13	13	6	26	49	44	32	19	35
ENSMUSG00000029312	chr5	Klhl8	1E+08	1E+08	3489	-0.55525447	5.435931592	0.0127593	0.028063621	0.05793	-1	876	828	612	658	723	783	825	542	778	698
ENSMUSG00000027227	chr2	Sord	1.2E+08	1.2E+08	2352	-0.39843196	5.196831989	0.0127679	0.028078062	0.02907	-1	656	477	696	603	696	757	712	459	647	713
ENSMUSG00000040463	chr11	Mybbp1a	7.2E+07	7.2E+07	5803	-0.47722336	6.243679931	0.01279	0.028122319	0.04305	-1	1101	976	1735	1590	1267	1341	1447	1000	1416	1336
ENSMUSG00000052062	chr1	Pard3b	6.2E+07	6.2E+07	13153	-0.62602301	2.756223996	0.0128042	0.028149191	0.06631	-1	116	77	177	154	92	128	145	84	86	102
ENSMUSG00000061288	chr5	Taok3	1.2E+08	1.2E+08	10952	0.491893809	3.157436682	0.0128321	0.028206079	0.03944	1	95	79	133	118	131	245	202	150	230	242
ENSMUSG00000028848	chr4	Gpn2	1.3E+08	1.3E+08	1482	0.496105295	3.09093894	0.0128501	0.02824133	0.04024	1	89	70	135	107	133	244	189	163	219	201
ENSMUSG00000036282	chr14	Naa30	4.9E+07	4.9E+07	6970	-0.40976414	4.648825766	0.012854	0.028245443	0.02998	-1	445	298	523	455	436	505	500	380	392	435
ENSMUSG00000066724	chr7	Gm10175	2.4E+07	2.4E+07	589	1.040285881	1.305386225	0.0128839	0.02830662	0.17581	1	10	17	8	32	49	57	51	45	88	83
ENSMUSG00000037103	chr8	Dcaf15	8.4E+07	8.4E+07	2320	0.529403873	3.405846055	0.0129007	0.028339087	0.04805	1	97	93	175	116	179	305	201	176	293	313
ENSMUSG00000022336	chr15	Eif3e	4.3E+07	4.3E+07	1541	-0.51242789	6.874708235	0.0129035	0.028340778	0.05013	-1	2228	1815	2275	1831	2071	2527	2183	1723	1586	1965
ENSMUSG00000021028	chr12	Mbip	5.6E+07	5.6E+07	1509	-0.58578867	2.221692008	0.0129074	0.028344952	0.05327	-1	85	63	106	71	91	94	90	63	58	74
ENSMUSG00000028911	chr4	Srsf4	1.3E+08	1.3E+08	3561	0.42566346	4.949602661	0.0129162	0.028359784	0.03317	1	314	250	543	402	525	737	730	490	815	897
ENSMUSG00000019143	chr18	Hars2	3.7E+07	3.7E+07	4279	-0.41424795	4.303700456	0.0129524	0.028434767	0.03024	-1	320	240	429	292	437	432	415	239	312	365
ENSMUSG00000029624	chr5	Ptcd1	1.5E+08	1.5E+08	3271	-0.45610382	4.077947812	0.0129669	0.028461285	0.03664	-1	239	203	442	321	283	314	317	210	298	332
ENSMUSG00000037166	chr7	Ppp1r14a	2.9E+07	2.9E+07	531	0.888083512	1.416035955	0.0129685	0.028461285	0.1231	1	18	22	28	19	49	104	31	47	70	92
ENSMUSG00000022881	chr16	Rfc4	2.3E+07	2.3E+07	1534	-0.52922107	2.922862849	0.0129723	0.028465167	0.04641	-1	139	89	153	141	150	172	142	78	140	113
ENSMUSG00000016984	chr11	Etaa1	1.8E+07	1.8E+07	4185	-0.67757195	1.494459011	0.0129754	0.028467478	0.06543	-1	54	33	69	50	50	68	46	31	41	34
ENSMUSG00000025358	chr10	Cdk2	1.3E+08	1.3E+08	2432	0.609472226	2.714240423	0.0129895	0.02849391	0.06189	1	73	55	79	55	128	207	137	121	195	147
ENSMUSG00000092397	chr2	C130080G10Rik	1.1E+08	1.1E+08	2586	1.048825347	-0.03116953	0.012995	0.028501691	0.12738	1	15	4	8	3	12	24	23	24	29	17
ENSMUSG00000001666	chr10	Ddt	7.6E+07	7.6E+07	773	0.494322221	4.42985612	0.0129988	0.02850554	0.04471	1	258	143	343	239	404	614	373	403	580	622
ENSMUSG00000014773	chr17	Dll1	1.5E+07	1.5E+07	4219	0.60881828	2.628298394	0.0130238	0.028555897	0.05987	1	50	66	72	85	85	142	145	122	159	183
ENSMUSG00000051499	chr6	Zfp786	4.8E+07	4.8E+07	3191	-1.04378197	-0.1571775	0.0130303	0.02856557	0.12976	-1	18	16	9	23	14	11	10	12	7	14
ENSMUSG00000044952	chr7	Kctd21	9.7E+07	9.7E+07	2966	-0.58321528	2.710908446	0.0130395	0.028581351	0.05713	-1	127	97	130	111	113	135	135	59	125	91
ENSMUSG00000044456	chr12	Rin3	1E+08	1E+08	6835	0.610375568	3.192492043	0.0130614	0.028624813	0.06578	1	95	50	151	84	184	253	175	166	273	261
ENSMUSG00000043088	chr6	Il17re	1.1E+08	1.1E+08	2992	1.07501011	1.772767472	0.0130671	0.028632857	0.19921	1	15	19	20	15	99	68	101	71	115	100
ENSMUSG00000037784	chr9	Dzip1l	1E+08	1E+08	7984	0.760047053	1.171103568	0.0130711	0.028637289	0.08131	1	28	14	27	20	31	90	47	34	66	44
ENSMUSG00000015850	chr3	Adamtsl4	9.6E+07	9.6E+07	4198	0.497555255	4.027557655	0.0130764	0.028644216	0.04445	1	143	108	279	262	252	501	398	245	401	445
ENSMUSG00000060771	chr1	Tsga10	3.8E+07	3.8E+07	10662	-0.56227185	2.726173022	0.0130844	0.028657332	0.05198	-1	108	67	137	145	140	140	119	70	92	132
ENSMUSG00000091580	chr16	Gm6467	2.2E+07	2.2E+07	609	0.739976276	1.418444265	0.0130913	0.028667939	0.08034	1	17	17	42	36	35	91	61	33	78	73
ENSMUSG00000060096	chr18	Amd-ps3	6.4E+07	6.4E+07	1496	-1.88618737	1.360133438	0.0131313	0.028751154	0.60106	-1	22	19	115	18	154	11	80	9	10	1
ENSMUSG00000074141	chr7	Il4i1	4.5E+07	4.5E+07	4097	-0.77527332	1.760170302	0.0131446	0.028775631	0.0965	-1	73	56	70	51	60	28	72	36	48	67
ENSMUSG00000021567	chr13	Nkd2	7.4E+07	7.4E+07	4728	0.777138014	1.914857622	0.0131925	0.028876201	0.09701	1	38	39	33	21	70	116	101	64	73	126
ENSMUSG00000027513	chr2	Pck1	1.7E+08	1.7E+08	3429	-2.6587444	6.929771836	0.0132083	0.028906192	1.15759	-1	2659	821	13	12	14091	1499	146	627	625	586
ENSMUSG00000009549	chr2	Srp14	1.2E+08	1.2E+08	1195	0.456132235	6.487935284	0.0132204	0.02892812	0.03974	1	1151	843	1315	1058	1349	2416	1962	1749	2277	2283
ENSMUSG00000028145	chr3	Them4	9.4E+07	9.4E+07	1730	-0.52423884	3.090007622	0.0132341	0.028953562	0.04618	-1	133	93	229	152	160	158	167	103	121	170
ENSMUSG00000028647	chr4	Mycbp	1.2E+08	1.2E+08	2934	-0.49421045	3.775365584	0.0132506	0.028985217	0.04317	-1	262	190	266	236	234	249	309	191	223	194
ENSMUSG00000027243	chr2	Harbi1	9.2E+07	9.2E+07	5588	-0.59486672	2.559876601	0.0132641	0.029005582	0.05887	-1	118	78	114	110	104	131	123	76	77	75
ENSMUSG00000041319	chr17	Thoc6	2.4E+07	2.4E+07	2026	0.500839525	3.348930845	0.0132621	0.029005582	0.04195	1	101	111	149	126	138	290	231	201	268	226
ENSMUSG00000008140	chr7	Emc10	4.4E+07	4.4E+07	2917	0.465798951	6.208539192	0.0132989	0.029075051	0.04142	1	810	612	1173	1016	1143	1981	1642	1183	2212	1902
ENSMUSG00000024462	chr17	Gabbr1	3.7E+07	3.7E+07	7764	0.587000867	3.139483332	0.0133047	0.029075051	0.06034	1	85	62	182	75	141	260	192	174	182	271
ENSMUSG00000028453	chr4	Fancg	4.3E+07	4.3E+07	3795	0.766330159	1.620077024	0.0133062	0.029075051	0.08954	1	33	26	27	21	58	124	71	47	78	71
ENSMUSG00000038323	chr1	1700066M21Rik	5.7E+07	5.7E+07	3235	-0.68190227	1.694185247	0.0133013	0.029075051	0.07043	-1	53	45	84	53	60	66	56	51	39	36
ENSMUSG00000043801	chr17	Oaz1-ps	1.7E+07	1.7E+07	681	0.476367979	5.827019107	0.0133061	0.029075051	0.04306	1	707	532	714	614	1024	1316	1297	1106	1658	1389
ENSMUSG00000021548	chr13	Ccnh	8.5E+07	8.5E+07	3105	-0.43456153	4.155549329	0.0133138	0.029087231	0.03356	-1	310	259	351	276	328	357	323	248	343	287
ENSMUSG00000043987	chr9	Cep164	4.6E+07	4.6E+07	5980	0.587356995	2.554826714	0.0133289	0.029115569	0.05594	1	51	57	97	55	91	158	129	95	176	160
ENSMUSG00000019927	chr10	Ube2d1	7.1E+07	7.1E+07	4371	-0.60522868	7.657955837	0.0133888	0.029241876	0.07087	-1	4287	3812	2743	3219	3442	3248	3462	2711	3579	3457
ENSMUSG00000085180	chr4	Al838599	3242055	3242190	4243	1.065013491	2.492026663	0.013433	0.029333762	0.20281	1	51	49	22	26	118	236	65	99	119	261

ENSMUSG00000034832	chr6	Tet3	8.3E+07	8.3E+07	11999	-0.4072151	4.412976467	0.0134749	0.02942066	0.0296	-1	345	257	428	340	474	443	413	298	319	417
ENSMUSG00000090958	chr7	Lrrc32	9.8E+07	9.8E+07	3817	0.478235339	3.304019441	0.0134969	0.029464292	0.03847	1	108	85	140	119	171	256	257	162	266	240
ENSMUSG00000036529	chr15	Sbf1	8.9E+07	8.9E+07	6826	-0.4566736	6.060376825	0.0135039	0.029474864	0.03992	-1	1110	766	1394	1343	1248	1228	1329	772	1328	1198
ENSMUSG00000034994	chr10	Eef2	8.1E+07	8.1E+07	3098	-0.49474862	10.57221214	0.0135084	0.029480188	0.0478	-1	24177	18292	37502	28809	27244	28278	30754	17420	27383	28035
ENSMUSG00000028717	chr4	Tal1	1.2E+08	1.2E+08	4379	0.66223057	1.532767362	0.0135465	0.029558776	0.0602	1	26	31	34	31	38	93	68	50	65	77
ENSMUSG00000020308	chr10	Tpgs1	8E+07	8E+07	1101	0.487000816	4.1079899	0.0135899	0.029648778	0.04309	1	182	130	271	231	286	488	316	317	552	393
ENSMUSG00000038721	chr11	Hoxb7	9.6E+07	9.6E+07	1544	0.752450036	1.029534388	0.0135973	0.029660357	0.07438	1	23	15	23	18	29	78	37	39	50	46
ENSMUSG00000043833	chr5	2900005J15Rik	2.5E+07	2.5E+07	2928	1.514553046	-0.08871681	0.0136068	0.029676364	0.3469	1	0	7	3	1	21	39	15	20	14	36
ENSMUSG00000024777	chr19	Ppp2r5b	6227765	6228531	2895	-0.43877965	5.465153154	0.0136186	0.029697565	0.03647	-1	665	531	1066	783	838	836	1005	476	831	774
ENSMUSG00000027642	chr2	Rpn2	1.6E+08	1.6E+08	4430	0.505549937	6.798731678	0.0136261	0.029709358	0.04947	1	1269	1058	1225	1394	1986	3446	2382	2171	2968	2539
ENSMUSG00000059409	chr17	Ppp2r5d	4.7E+07	4.7E+07	2926	-0.40415491	5.142244573	0.0136408	0.029736789	0.03035	-1	526	370	767	705	715	676	726	446	670	634
ENSMUSG00000104279	chr1	RP24-252K15.4	1.8E+08	1.8E+08	1870	0.659987284	1.327083056	0.013645	0.029741208	0.05872	1	23	17	38	34	29	68	61	50	61	61
ENSMUSG00000026566	chr1	Mpzl1	1.7E+08	1.7E+08	3550	0.516661134	3.395608155	0.0136475	0.029742042	0.04641	1	103	88	189	123	156	352	194	199	248	279
ENSMUSG00000049553	chr6	Polr1a	7.2E+07	7.2E+07	6105	-0.44237492	4.98121646	0.0136607	0.029766199	0.03648	-1	546	385	662	663	473	602	521	479	602	536
ENSMUSG00000020522	chr11	Mfap3	5.8E+07	5.8E+07	5801	-0.46725454	3.640909795	0.013666	0.02977314	0.03842	-1	224	184	244	191	231	270	255	149	206	206
ENSMUSG00000097101	chr13	1810034E14Rik	6.4E+07	6.4E+07	1805	1.161943861	0.134364178	0.0136871	0.029814442	0.19432	1	7	1	11	7	21	51	24	7	25	36
ENSMUSG00000021418	chr13	Rpp40	3.6E+07	3.6E+07	6540	-0.5966661	3.254514002	0.0137072	0.029848897	0.06357	-1	177	180	159	130	187	189	184	134	154	116
ENSMUSG00000026999	chr2	Nup35	8.1E+07	8.1E+07	3366	-0.49324696	3.594783087	0.013706	0.029848897	0.0431	-1	184	180	218	223	244	285	246	142	205	166
ENSMUSG00000083282	chr19	Ctsf	4855129	4855486	1975	0.412313415	5.111694252	0.0137131	0.02985717	0.03167	1	407	302	508	491	542	984	680	654	798	951
ENSMUSG00000028195	chr3	Cyr61	1.5E+08	1.5E+08	2028	0.599828112	5.803712753	0.013725	0.029878556	0.06949	1	478	332	996	704	995	1079	1280	1204	1153	2128
ENSMUSG00000003421	chr7	Nosip	4.5E+07	4.5E+07	2920	0.397862028	5.065819133	0.0137441	0.029915327	0.02947	1	374	261	572	506	503	886	794	629	847	763
ENSMUSG00000020785	chr11	Camkk1	7.3E+07	7.3E+07	3728	0.793286672	1.231441	0.0137679	0.029956281	0.09502	1	13	15	31	25	42	98	48	49	50	48
ENSMUSG00000026208	chr1	Des	7.5E+07	7.5E+07	3754	0.54027254	11.99312836	0.0137736	0.029956281	0.05728	1	40099	25970	83251	57514	53574	119854	99789	75158	105705	101059
ENSMUSG00000026821	chr2	Ralgds	2.9E+07	2.9E+07	6159	0.452178161	4.594890574	0.0137664	0.029956281	0.03776	1	276	211	313	264	493	653	495	469	636	610
ENSMUSG00000062456	chr19	Rpl9-ps6	3.2E+07	3.2E+07	691	0.704384831	2.574195575	0.013771	0.029956281	0.08544	1	60	49	50	68	108	176	95	94	171	217
ENSMUSG00000071708	chrX	Sms	1.6E+08	1.6E+08	6010	-0.53858815	7.108785491	0.0137717	0.029956281	0.05654	-1	2724	2249	2327	1804	2980	2758	2953	1629	2355	2048
ENSMUSG00000026966	chr2	Ssna1	2.5E+07	2.5E+07	1276	0.395120175	4.57501217	0.0137804	0.029966424	0.02818	1	266	221	379	309	388	709	503	426	605	554
ENSMUSG00000031137	chrX	Fgf13	5.9E+07	5.9E+07	4019	-0.42549081	4.859100845	0.0137951	0.029989212	0.03366	-1	522	356	617	509	502	510	692	358	520	487
ENSMUSG00000094935	chr12	Gm9726	9.4E+07	9.4E+07	2099	0.766770596	0.670699391	0.0137942	0.029989212	0.07198	1	12	10	19	18	24	41	33	28	42	47
ENSMUSG00000054611	chr19	Kdm2a	4314419	4319281	14294	-0.42239684	5.905451849	0.0138011	0.029997572	0.03419	-1	992	782	1220	1043	1135	1206	1187	776	1031	1116
ENSMUSG00000033885	chr14	Pxk	8098213	8098416	2840	-0.46219739	3.858065557	0.0138068	0.03000524	0.03823	-1	209	197	327	274	256	327	318	159	242	228
ENSMUSG00000038000	chr8	Acd	1.1E+08	1.1E+08	1425	0.648513858	3.043471011	0.0138131	0.030009739	0.07548	1	69	58	132	55	185	264	187	151	227	202
ENSMUSG00000042408	chr4	Zmym6	1.3E+08	1.3E+08	7692	-0.62583668	2.505126084	0.0138124	0.030009739	0.0652	-1	107	52	175	89	106	125	106	65	71	93
ENSMUSG00000051451	chr7	Crebzf	9E+07	9E+07	4989	-0.46301727	3.796569305	0.0138238	0.030028268	0.03775	-1	187	157	326	279	281	274	269	183	201	278
ENSMUSG00000007038	chr17	Neu1	3.5E+07	3.5E+07	3733	0.390248688	4.58728275	0.0138372	0.030052792	0.02758	1	282	205	385	299	419	712	537	407	584	587
ENSMUSG00000026000	chr1	Lancl1	6.7E+07	6.7E+07	6863	0.408543786	4.361160285	0.0138697	0.030118582	0.03001	1	215	193	343	239	356	589	464	377	499	486
ENSMUSG00000030532	chr7	Hddc3	8E+07	8E+07	860	0.413837876	5.00149822	0.0138894	0.030152158	0.03191	1	424	281	448	359	575	859	702	602	871	729
ENSMUSG00000036570	chr7	Fxyd1	3.1E+07	3.1E+07	709	0.513774767	8.092739653	0.0138887	0.030152158	0.05175	1	3031	2240	4064	3838	3983	6118	5829	4876	7941	8333
ENSMUSG00000057672	chr8	Pkn1	8.4E+07	8.4E+07	7386	-0.43830819	5.094715665	0.0138976	0.030165136	0.03607	-1	481	333	797	610	838	649	811	410	589	561
ENSMUSG00000031488	chr8	Rab11fip1	2.7E+07	2.7E+07	7965	1.048509661	0.768868625	0.0139062	0.030179284	0.18045	1	3	4	39	18	19	41	42	36	38	60
ENSMUSG00000021901	chr14	Bap1	3.1E+07	3.1E+07	4682	-0.4659809	6.007513213	0.0139186	0.030201529	0.04194	-1	990	785	1457	1292	1140	1164	1480	723	1161	1109
ENSMUSG00000072946	chr12	Ptgr2	8.4E+07	8.4E+07	5929	-0.55655219	6.391028166	0.0139471	0.030258546	0.06022	-1	1255	748	2800	1588	1477	1528	1789	1028	1174	1538
ENSMUSG00000031493	chr7	Ggn	2.9E+07	2.9E+07	2643	0.99904682	-0.18894113	0.0139598	0.030281438	0.11642	1	5	2	14	7	11	37	16	14	22	16
ENSMUSG00000044156	chr6	Hepacam2	3457089	3457916	5775	1.079731688	0.170651837	0.0139648	0.030287571	0.14493	1	8	12	8	5	14	33	18	12	30	49
ENSMUSG00000006958	chr16	Chrd	2.1E+07	2.1E+07	5838	0.707239298	2.285808683	0.0139741	0.030303108	0.08473	1	51	33	53	33	110	174	107	94	110	128
ENSMUSG00000024613	chr18	Tcof1	6.1E+07	6.1E+07	5266	-0.40195955	4.758023166	0.0139804	0.030312037	0.02969	-1	374	324	653	449	560	494	565	353	532	464
ENSMUSG00000027596	chr2	a	1.5E+08	1.5E+08	1169	-0.71561105	1.492468153	0.0140633	0.030487114	0.07774	-1	35	41	76	56	50	48	51	39	47	27
ENSMUSG00000014550	chr6	Zfyve20	9.2E+07	9.2E+07	5757	-0.38463689	4.688868536	0.0140797	0.030517944	0.02703	-1	360	314	580	463	506	551	530	342	452	444
ENSMUSG00000022890	chr16	Atp5j	8.5E+07	8.5E+07	3130	-0.52560914	8.602929361	0.0140915	0.030538772	0.05445	-1	6538	4374	10317	7854	6030	7279	8485	5112	5862	6298
ENSMUSG00000039354	chr1	Smarcal1	7.3E+07	7.3E+07	5728	-0.41901573	4.650313469	0.0141012	0.030555223	0.03257	-1	360	339	549	512	394	544	485	310	451	444
ENSMUSG00000026281	chr1	Dtymk	9.4E+07	9.4E+07	2631	0.560911769	3.618145359	0.0141095	0.030568416	0.05703	1	138	109	140	116	246	404	211	231	311	347
ENSMUSG00000027774	chr3	Gfm1	6.7E+07	6.7E+07	4419	-0.54556734	7.272206375	0.0141505	0.030652581	0.05846	-1	2248	1526	4722	3268	2519	2838	3205	1939	2315	2747
ENSMUSG00000031878	chr8	Nae1	1E+08	1E+08	7792	-0.43519449	4.802834732	0.0141547	0.030656938	0.0356	-1	513	412	564	445	444	638	558	375	410	482
ENSMUSG00000010914	chr2	Pdhx	1E+08	1E+08	3930	-0.56413536	6.702422386	0.0141706	0.030686581	0.06232	-1	1590	943	3391	2082	1739	1705	2356	1224	1699	1742
ENSMUSG00000048668	chr6	Rhno1	1.3E+08	1.3E+08	2486	0.525074038	3.01720689	0.01422	0.030788718	0.04661	1	84	72	118	90	135	264	162	161	182	205
ENSMUSG00000047648	chr10	Fbxo30	1.1E+07	1.1E+07	5197	-0.61321647	3.955275422	0.0142487	0.030846198	0.0704	-1	296	156	493	287	210	297	387	186	167	236
ENSMUSG00000012519	chr8	Mlkl	1.1E+08	1.1E+08	2303	0.889370896	1.54744454	0.0142667	0.03088043	0.1315	1	30	20	25	16	59	133	39	54	76	78
ENSMUSG00000019734	chr7	Tmc4	3665790	3666008	3859	0.885714536	0.323137876	0.0142717	0.030886512	0.09092	1	9	11	9	12	18	48	27	19	24	35
ENSMUSG00000020495	chr11	Smg8	8.7E+07	8.7E+07	3218	-0.52886644	3.474327433	0.0142819	0.030903754	0.05035	-1	251	153	218	177	169	222	212	132	165	210
ENSMUSG00000000441	chr6	Raf1	1.2E+08	1.2E+08	6363	-0.47595092	7.261359247	0.0142944	0.030926078	0.04466	-1	2509	2063	3450	2832	2591	2869	3266	1916	2617	2665
ENSMUSG00000025630	chrX	Hprt	5.3E+07	5.3E+07	1289	0.420418797	5.101873049	0.0143069	0.030948286	0.03338	1	463	313	456	373	618	1014	737	685	789	817
ENSMUSG00000026784	chr2	Pdss1	2.3E+07	2.3E+07	4248	-0.69972003	2.843247518	0.0143141	0.030954199	0.08788	-1	115	62	258	145	110	126	175	70	89	107
ENSMUSG00000074217	chr8	2210011C24Rik	8.4E+07	8.4E+07	1413	0.92766765	0.91944921	0.014312	0.030954199	0.12953	1	26	12	18	8	28	36	41	37	79	43
ENSMUSG00000026317	chr8	Cln8	1.5E+07	1.5E+07	7606	0.390724318	4.785102264	0.014361	0.031036485	0.02807	1	305	277	435	357	427	736	725	419	720	654
ENSMUSG00000027695	chr3	Pld1	2.8E+07	2.8E+07	12961	0.558191797	2.304900216	0.0143603	0.031036485	0.04873	1	50	41	77	56	74	141	118	73	140	128
ENSMUSG00000028996	chr4	Rbp7	1.5E+08	1.5E+08	718	0.574791193	3.969711649	0.0143582	0.031036485	0.06229	1	158	93	295	128	319	457	300	267	457	454
ENSMUSG00000042507	chr12	Elmsan1	8.4E+07	8.4E+07	7611	-0.48412889	4.083528573	0.0143601	0.031036485	0.04313	-1	189	211	396	363	349	337	348	198	246	340

ENSMUSG00000030188	chr6	Magohb	1.3E+08	1.3E+08	1720	0.661611559	2.107262858	0.0143747	0.031061503	0.07356	1	54	23	58	42	74	126	78	95	96	131
ENSMUSG00000036086	chr1	Zranb3	1.3E+08	1.3E+08	9079	-0.51501242	3.420439771	0.0143806	0.03106937	0.04731	-1	214	127	269	167	173	222	225	132	179	153
ENSMUSG00000021131	chr12	Erh	8.1E+07	8.1E+07	1350	0.424555584	4.458896081	0.0144003	0.031107089	0.03299	1	288	219	306	247	347	650	463	444	531	495
ENSMUSG00000033763	chr8	Mtss1l	1.1E+08	1.1E+08	5311	-0.49930192	6.389119141	0.0144084	0.031119769	0.04893	-1	1332	1148	1790	1581	1536	1124	1608	1034	1679	1705
ENSMUSG00000029171	chr5	Pgm1	6.4E+07	6.4E+07	2608	0.614437883	1.998241876	0.0144142	0.031126116	0.05944	1	46	24	65	39	63	134	107	74	84	89
ENSMUSG00000042675	chr7	Ypel3	1.3E+08	1.3E+08	1848	0.496327848	5.962651131	0.0144157	0.031126116	0.04802	1	920	542	730	657	1049	1723	1276	1070	1714	1783
ENSMUSG00000026319	chr1	2310035C23Rik	1.1E+08	1.1E+08	9500	-0.52819214	3.168370231	0.0144371	0.031167389	0.04908	-1	140	140	189	141	179	200	199	110	120	133
ENSMUSG00000045980	chr11	Tmem104	1.2E+08	1.2E+08	4610	0.490557393	3.851850709	0.0144423	0.031173849	0.04425	1	166	84	237	201	240	331	377	255	413	353
ENSMUSG00000036214	chr17	Znrd1as	3.7E+07	3.7E+07	1360	-0.43634305	3.859397884	0.0144523	0.031190652	0.03414	-1	253	200	272	246	272	296	308	180	236	257
ENSMUSG00000043542	chr3	Zc2hc1a	7503483	7503527	3508	0.549544267	3.235821074	0.0144915	0.031270491	0.05355	1	88	83	143	113	150	180	287	203	194	263
ENSMUSG00000014294	chr18	Ndufa2	3.7E+07	3.7E+07	572	0.487090312	7.573762482	0.0145086	0.031302506	0.04704	1	2161	1529	3075	2598	2795	4629	4164	3481	5740	4908
ENSMUSG00000028382	chr4	Ptbp3	5.9E+07	5.9E+07	7480	0.509550039	4.372906386	0.0145334	0.031351131	0.04908	1	203	165	290	185	483	602	546	370	444	556
ENSMUSG00000025103	chr7	Btbd1	8.2E+07	8.2E+07	3000	-0.54595737	7.740701691	0.0145463	0.031371021	0.05915	-1	3748	2431	6089	4307	2824	3915	4387	2706	3185	3844
ENSMUSG00000029635	chr5	Cdk8	1.5E+08	1.5E+08	3881	-0.53017137	3.422896536	0.0145471	0.031371021	0.05086	-1	161	183	227	154	213	197	253	117	172	171
ENSMUSG00000042396	chr9	Rbm7	4.8E+07	4.8E+07	1798	-0.5022516	3.386151259	0.0145588	0.031391485	0.04493	-1	176	163	182	154	233	216	218	120	158	185
ENSMUSG00000022972	chr16	1110004E09Rik	9.1E+07	9.1E+07	1360	-0.38902572	4.838986019	0.0145697	0.031410249	0.02824	-1	455	361	580	494	560	523	629	386	534	485
ENSMUSG00000097177	chr9	9330159M07Rik	8.9E+07	8.9E+07	6831	-0.8444566	0.793982508	0.0145904	0.031450068	0.10137	-1	32	32	46	17	32	31	28	25	17	20
ENSMUSG00000048232	chr4	Fbxo10	4.5E+07	4.5E+07	4691	0.60410578	2.747574312	0.014609	0.031485301	0.06369	1	62	57	113	51	122	174	204	130	182	131
ENSMUSG00000044847	chr11	Lsm11	4.6E+07	4.6E+07	6453	-0.69181652	2.377464166	0.0146151	0.031493466	0.08382	-1	75	105	100	114	65	91	71	58	96	90
ENSMUSG00000078234	chr4	Klhdc7a	1.4E+08	1.4E+08	7807	-2.08465021	3.292094877	0.0146487	0.031561185	0.7706	-1	248	121	3	5	884	124	37	73	65	83
ENSMUSG00000036885	chr3	Arhgef26	6.2E+07	6.2E+07	10116	-0.86989525	0.22975465	0.0146638	0.031588709	0.09413	-1	25	15	25	19	22	32	15	9	13	12
ENSMUSG00000003808	chr8	Farsa	8.5E+07	8.5E+07	4538	0.403438827	4.99391485	0.0146853	0.031625466	0.03072	1	332	299	453	455	540	830	675	579	818	834
ENSMUSG00000014813	chr14	Stc1	6.9E+07	6.9E+07	3743	-1.45180112	-0.12001403	0.0146838	0.031625466	0.31523	-1	11	40	12	3	21	9	6	14	7	10
ENSMUSG00000040220	chr8	Gas8	1.2E+08	1.2E+08	1679	0.625644652	2.158797646	0.0147453	0.031749812	0.0643	1	48	33	48	42	91	137	106	75	118	113
ENSMUSG00000005483	chr8	Dnajb1	8.4E+07	8.4E+07	2263	0.491151018	3.420990168	0.0147508	0.031751887	0.04259	1	104	85	149	133	208	296	271	178	262	282
ENSMUSG00000030204	chr6	Ddx47	1.4E+08	1.4E+08	4952	0.394981575	4.78907307	0.0147492	0.031751887	0.02932	1	339	219	448	343	484	745	592	519	683	691
ENSMUSG00000041974	chr16	Spidr	1.6E+07	1.6E+07	3279	0.775217779	1.491889283	0.0147836	0.031817576	0.09439	1	25	24	26	18	58	97	63	64	64	61
ENSMUSG00000044712	chr12	Slc38a6	7.3E+07	7.3E+07	7783	0.819373792	1.962523132	0.0148201	0.031891224	0.11333	1	41	38	21	27	76	143	77	80	90	109
ENSMUSG00000091449	chr18	Gm10269	2.1E+07	2.1E+07	372	0.609687912	2.156838209	0.014863	0.031978676	0.05986	1	52	35	58	54	61	117	86	95	139	99
ENSMUSG00000057751	chr4	Megf6	1.5E+08	1.5E+08	7877	1.00734006	0.474348975	0.0148838	0.032018508	0.14021	1	1	12	15	19	16	47	35	21	38	35
ENSMUSG00000026872	chr2	Zeb2	4.5E+07	4.5E+07	19658	-0.50194344	4.560841207	0.0149016	0.032046886	0.04839	-1	403	371	358	352	568	524	572	261	322	369
ENSMUSG00000068551	chr6	Zfp467	4.8E+07	4.8E+07	4255	-0.53399578	4.765055442	0.0149002	0.032046886	0.05517	-1	538	383	353	367	764	536	417	317	586	448
ENSMUSG00000028410	chr4	Dnaja1	4.1E+07	4.1E+07	8629	0.463453013	5.395333087	0.0149236	0.03208432	0.04173	1	541	379	464	537	742	1361	919	859	967	923
ENSMUSG00000087298	chr7	Gm9392	4.7E+07	4.7E+07	554	-0.720017	2.003239488	0.0149216	0.03208432	0.08861	-1	71	77	85	55	73	67	105	39	52	48
ENSMUSG00000033126	chr10	Ybey	7.6E+07	7.6E+07	4520	-0.52486254	3.152631278	0.0149333	0.032100272	0.04878	-1	167	113	206	153	146	166	198	120	141	122
ENSMUSG00000054942	chr3	Fam73a	1.5E+08	1.5E+08	5355	-0.50607337	3.504042602	0.0149387	0.032107071	0.04644	-1	222	158	245	182	182	208	246	137	157	220
ENSMUSG00000030256	chr6	Bhlhe41	1.5E+08	1.5E+08	6262	-0.6016801	5.545391798	0.014965	0.032158668	0.07126	-1	666	427	1227	541	1636	685	1047	531	780	800
ENSMUSG00000078812	chr11	Eif5a	7E+07	7E+07	2377	0.481118331	8.766288418	0.0149737	0.032172357	0.0465	1	5082	4084	5947	5538	6833	11082	9551	8258	12030	11364
ENSMUSG00000036469	chr8	March1	6.6E+07	6.6E+07	7146	0.973661931	0.933544243	0.0150016	0.032227415	0.13963	1	11	23	9	18	26	92	46	29	36	47
ENSMUSG00000019087	chrX	Atp6ap1	7.4E+07	7.4E+07	3026	0.461175459	7.613593235	0.0150337	0.032286447	0.04259	1	2420	1912	2771	2319	3003	5446	4548	3549	5174	4784
ENSMUSG00000030138	chr6	Bms1	1.2E+08	1.2E+08	4286	-0.39962611	5.151072711	0.0150334	0.032286447	0.0307	-1	571	500	691	653	596	757	684	485	620	625
ENSMUSG00000024384	chr18	Iws1	3.2E+07	3.2E+07	9623	-0.41482279	4.813627167	0.0150574	0.032332409	0.03281	-1	481	381	589	495	456	606	626	358	422	495
ENSMUSG00000058503	chr5	Fam133b	3543844	3543947	1555	-0.53724298	2.835039966	0.015088	0.032393213	0.05008	-1	145	93	146	118	125	158	128	96	98	117
ENSMUSG00000052821	chrX	Cysltr1	1.1E+08	1.1E+08	5142	0.86349872	0.977805294	0.0150905	0.03239343	0.10247	1	16	26	16	21	15	67	56	41	37	45
ENSMUSG00000031711	chr8	Zfp330	8.3E+07	8.3E+07	1675	-0.43791749	4.280003147	0.0151102	0.032430822	0.03588	-1	377	275	351	311	341	416	391	269	307	320
ENSMUSG00000039263	chr2	Npepl1	1.7E+08	1.7E+08	2998	-0.46019775	6.769002507	0.0151237	0.032454809	0.04226	-1	1573	1194	2609	2088	2273	2033	2195	1329	2110	1873
ENSMUSG00000022637	chr16	Cblb	5.2E+07	5.2E+07	6323	-0.42352791	4.099403789	0.0151506	0.032507587	0.03303	-1	248	246	378	301	297	366	334	216	304	297
ENSMUSG00000004667	chr10	Polr2e	8E+07	8E+07	2670	0.406399021	5.497417821	0.0151915	0.032590462	0.03214	1	541	400	724	591	701	1211	967	839	1168	1120
ENSMUSG00000027884	chr3	Clcc1	1.1E+08	1.1E+08	4368	-0.43469484	4.96395577	0.0152202	0.03264698	0.03656	-1	562	453	611	571	455	660	658	400	484	555
ENSMUSG00000043770	chr4	Gm12481	4.4E+07	4.4E+07	297	0.399121593	5.229119692	0.0152435	0.032691965	0.03055	1	486	380	602	437	527	999	882	591	1000	960
ENSMUSG00000024472	chr18	Dcp2	4.4E+07	4.4E+07	8643	-0.43058412	3.889444159	0.0152529	0.032707001	0.03363	-1	254	197	332	209	290	294	302	194	270	242
ENSMUSG00000040794	chr2	C1qtnf4	9.1E+07	9.1E+07	1290	-0.70116729	1.99788775	0.0152618	0.032721099	0.08388	-1	78	76	80	49	74	57	60	43	90	58
ENSMUSG00000075227	chr19	Znhit2	6061192	6062472	1281	0.556057121	3.355094532	0.0152905	0.032777749	0.0567	1	90	73	149	128	196	262	196	175	333	280
ENSMUSG00000043090	chr8	Zfp866	7E+07	7E+07	5601	-0.49503172	3.64139265	0.0152963	0.03278505	0.04519	-1	224	192	197	237	219	252	233	172	182	225
ENSMUSG00000038696	chr2	Mapkap1	3.4E+07	3.4E+07	4059	-0.46523195	5.561203086	0.0153037	0.032796058	0.04267	-1	755	524	1229	887	803	927	1117	519	862	725
ENSMUSG00000054676	chr7	1600014C10Rik	3.8E+07	3.8E+07	3931	-0.4110057	5.629421449	0.0153322	0.03285193	0.0331	-1	769	570	1095	763	1143	941	966	628	927	944
ENSMUSG00000021846	chr14	Peli2	4.8E+07	4.8E+07	5849	-0.60933494	3.785714741	0.0153544	0.032894602	0.07073	-1	233	129	263	179	499	309	291	128	190	231
ENSMUSG00000002733	chr2	Plekha3	7.7E+07	7.7E+07	3126	-0.47357949	3.415855734	0.015366	0.032913866	0.03975	-1	173	126	234	180	228	219	243	130	157	176
ENSMUSG00000019846	chr10	Lama4	3.9E+07	3.9E+07	12068	0.514964001	5.490333471	0.0153681	0.032913866	0.05252	1	427	358	557	491	1034	1527	957	854	1131	1017
ENSMUSG00000036752	chr2	Tubb4b	2.5E+07	2.5E+07	2088	0.512609008	7.963821385	0.0153775	0.032928922	0.05308	1	3080	1927	3725	3221	3799	6567	7402	4099	7912	4582
ENSMUSG00000033960	chr18	9430020K01Rik	4634929	4635031	6730	-0.43540507	4.773785265	0.0153815	0.03293255	0.03619	-1	353	267	720	499	614	619	538	365	464	428
ENSMUSG00000048186	chr2	Bend7	4717831	4718292	4194	-1.01344311	0.655189253	0.0153857	0.032936389	0.15327	-1	24	11	67	30	26	13	35	19	14	19
ENSMUSG00000002329	chr14	Mdp1	5.6E+07	5.6E+07	1733	0.38951127	5.234633179	0.0153944	0.032950141	0.02924	1	420	351	613	536	551	1031	867	687	975	845
ENSMUSG00000027011	chr2	Ube2e3	7.9E+07	7.9E+07	4390	-0.38054172	4.629919435	0.0154406	0.033043877	0.02713	-1	423	302	502	390	501	504	537	334	432	418
ENSMUSG00000031386	chrX	Hcfc1	7.4E+07	7.4E+07	8360	-0.42965202	6.061427166	0.0154514	0.033061977	0.0367	-1	1071	848	1448	1226	1200	1327	1251	931	1159	1209
ENSMUSG00000023307	chr19	March5	3.7E+07	3.7E+07	2396	-0.44623426	5.944934779	0.0154788	0.033115536	0.03956	-1	839	753	1373	956	1552	1174	1324	794	1069	1047
ENSMUSG00000032555	chr9	Topbp1	1E+08	1E+08	11122	-0.46966883	3.412609596	0.015494	0.033143113	0.03944	-1	190	132	230	176	202	241	222	129	172	162

ENSMUSG00000025724	chr7	Sec11a	8.1E+07	8.1E+07	4614	0.465934259	4.594082619	0.015509	0.033170127	0.04141	1	328	253	293	248	386	789	522	529	514	515
ENSMUSG00000038763	chr7	Alpk3	8.1E+07	8.1E+07	6445	-0.73426701	7.982860119	0.0155694	0.033294252	0.10868	-1	3556	2221	8287	7762	2713	3611	5342	2429	3899	4554
ENSMUSG00000033623	chr5	Pcgf3	1.1E+08	1.1E+08	9544	-0.44622826	5.487401877	0.015574	0.033298948	0.03936	-1	838	622	925	729	747	764	1024	573	783	784
ENSMUSG00000071347	chr14	C1qtnf9	6.1E+07	6.1E+07	1903	-0.4223278	4.566204662	0.0155766	0.033299352	0.03377	-1	349	233	609	361	562	504	493	282	409	422
ENSMUSG00000021326	chr13	Trim27	2.1E+07	2.1E+07	4702	0.396937723	4.629825094	0.0155869	0.033316292	0.02957	1	282	239	387	372	325	695	539	446	625	596
ENSMUSG00000081824	chr16	BC002163	4.3E+07	4.3E+07	319	0.469090208	3.363695531	0.0155917	0.033321546	0.03844	1	129	89	142	124	164	244	256	178	268	276
ENSMUSG00000097243	chr14	Gm26908	7E+07	7E+07	1637	-0.78761991	0.817559811	0.0155953	0.033324105	0.09134	-1	28	20	53	34	28	23	43	15	24	23
ENSMUSG00000044378	chr6	Slc15a5	1.4E+08	1.4E+08	3088	-2.70646663	0.838374774	0.0156067	0.033343416	1.1929	-1	4	0	229	5	24	2	35	3	6	0
ENSMUSG00000063628	chr18	Gm7665	1.6E+07	1.6E+07	297	1.239910624	-0.24080505	0.0157136	0.033566663	0.20902	1	5	3	2	2	21	27	17	12	30	19
ENSMUSG00000063663	chrX	Brwd3	1.1E+08	1.1E+08	12692	-0.69824102	1.680549805	0.0157258	0.033587666	0.07926	-1	47	49	65	72	56	49	78	40	37	42
ENSMUSG00000024766	chr19	Lipo1	3.4E+07	3.4E+07	3431	-0.5612016	2.607151143	0.0157297	0.033590892	0.05414	-1	106	76	138	107	117	88	144	74	89	107
ENSMUSG00000069835	chr11	Sat2	7E+07	7E+07	1424	0.656876954	2.281539355	0.0157461	0.033620811	0.07472	1	45	39	80	33	88	129	99	103	106	158
ENSMUSG00000033327	chr17	Tnxb	3.5E+07	3.5E+07	12209	0.532525521	7.003696653	0.0158497	0.033836846	0.05757	1	1194	1044	1546	1535	2783	4321	2922	2178	3508	2937
ENSMUSG00000031684	chr8	Slc10a7	7.9E+07	7.9E+07	3630	-0.56901477	2.701495512	0.0158637	0.033861564	0.05677	-1	92	103	101	121	156	128	114	91	110	90
ENSMUSG00000057657	chr8	Rps18-ps3	1.1E+08	1.1E+08	432	1.082403572	-0.04060323	0.0158785	0.033888019	0.15041	1	15	6	3	4	12	23	17	18	36	24
ENSMUSG00000022565	chr15	Plec	7.6E+07	7.6E+07	18113	-0.66316116	9.457283421	0.0159128	0.03395076	0.0896	-1	9831	6550	23360	18892	8430	11583	13235	8482	12580	10417
ENSMUSG00000032010	chr9	Usp2	4.4E+07	4.4E+07	4807	-0.52502423	6.792199425	0.0159127	0.03395076	0.05591	-1	1643	1042	3363	1891	2349	1743	2463	1283	1808	2142
ENSMUSG00000037752	chr4	Xkr8	1.3E+08	1.3E+08	4312	0.822129523	1.696194682	0.0159654	0.034057985	0.11816	1	19	25	34	19	78	90	78	59	112	72
ENSMUSG00000022367	chr15	Has2	5.7E+07	5.7E+07	4237	1.020013451	0.540922548	0.0159688	0.034059927	0.15393	1	11	13	12	9	20	44	71	12	21	41
ENSMUSG00000029097	chr5	Trmt44	3.6E+07	3.6E+07	4151	-0.78699245	0.912418608	0.0159771	0.034072407	0.09507	-1	27	39	31	23	49	31	36	16	30	25
ENSMUSG00000085566	chr2	A730017L22Rik	1.3E+08	1.3E+08	6012	-0.68558115	1.532016594	0.0159883	0.034091255	0.07628	-1	57	50	51	45	53	65	53	22	42	46
ENSMUSG00000023764	chr11	Sfi1	3131850	3132131	7559	0.547622545	5.97084208	0.0160075	0.034126904	0.06035	1	938	649	673	624	872	2405	1228	941	1459	1828
ENSMUSG00000039706	chr5	Ldb2	4.4E+07	4.4E+07	2485	0.604919418	2.522618196	0.0160195	0.034147246	0.06172	1	67	66	63	58	75	174	120	103	176	130
ENSMUSG00000025060	chr19	Slk	4.8E+07	4.8E+07	8284	-0.51555737	5.777829244	0.0160282	0.034160764	0.05351	-1	875	630	1488	1209	713	1158	1162	713	815	845
ENSMUSG00000087679	chr2	C330006A16Rik	2.6E+07	2.6E+07	2483	0.460288598	4.85393351	0.0160374	0.03417506	0.04182	1	264	202	487	339	616	817	628	531	687	794
ENSMUSG00000030555	chr7	Ttc23	6.8E+07	6.8E+07	6343	-0.51676424	3.385837958	0.0160941	0.034290764	0.04988	-1	189	168	190	191	161	216	221	112	175	170
ENSMUSG00000027314	chr2	Dll4	1.2E+08	1.2E+08	3852	-0.49929684	3.485557824	0.0161022	0.034302766	0.04546	-1	175	121	250	183	277	178	218	164	155	230
ENSMUSG00000035824	chr8	Tk2	1E+08	1E+08	2400	0.525592782	3.439595956	0.016117	0.034329165	0.05046	1	109	105	119	119	215	354	242	185	257	284
ENSMUSG00000067847	chr2	Romo1	1.6E+08	1.6E+08	747	0.503506865	6.286776469	0.016157	0.03440907	0.05141	1	862	698	1023	1061	1245	1830	1556	1382	2705	1953
ENSMUSG00000027605	chr2	Acss2	1.6E+08	1.6E+08	10163	-0.64177278	5.549252498	0.0161798	0.034452298	0.08304	-1	719	237	1651	910	1100	841	947	564	701	739
ENSMUSG00000019039	chr9	Dalrd3	1.1E+08	1.1E+08	2458	0.45642999	3.814010868	0.0162222	0.034537382	0.03899	1	154	105	210	176	264	344	313	251	387	372
ENSMUSG00000027651	chr2	Rprd1b	1.6E+08	1.6E+08	6499	-0.40407978	5.413373745	0.0162868	0.034669692	0.03245	-1	671	559	858	788	773	832	911	572	709	773
ENSMUSG00000057716	chr6	Tmem178b	4E+07	4E+07	9729	-0.90794544	0.94919353	0.0163164	0.034727335	0.13782	-1	27	15	61	50	35	43	45	10	20	19
ENSMUSG00000040549	chr2	Ckap5	9.2E+07	9.2E+07	9462	-0.45381047	5.471064127	0.0163235	0.034734162	0.04126	-1	705	502	1124	922	650	885	909	583	748	754
ENSMUSG00000041781	chr12	Cpsf2	1E+08	1E+08	5315	-0.43375479	4.879932902	0.0163245	0.034734162	0.03694	-1	472	396	694	503	483	641	665	425	410	448
ENSMUSG00000023008	chr15	Fmnl3	9.9E+07	9.9E+07	5021	0.534444496	3.858189686	0.0163289	0.034738136	0.05556	1	135	81	328	150	243	416	342	243	397	375
ENSMUSG00000041538	chr17	H2-Ob	3.4E+07	3.4E+07	3153	1.104638371	-0.36842783	0.0163433	0.034763573	0.13013	1	7	8	3	4	8	30	12	15	13	22
ENSMUSG00000020745	chr11	Pafah1b1	7.5E+07	7.5E+07	9620	-0.46253467	7.238310694	0.016352	0.034771624	0.0439	-1	2595	1942	3188	2691	2791	2988	3324	1944	2457	2485
ENSMUSG00000043822	chr10	Adamtsl5	8E+07	8E+07	4722	0.776971519	5.993580171	0.0163506	0.034771624	0.12278	1	383	196	1546	1054	621	1815	1717	1032	1865	1968
ENSMUSG00000024958	chr19	Gpr137	6938069	6938529	2768	0.487060186	4.068855295	0.0163626	0.034788726	0.04584	1	168	112	320	207	280	441	351	256	515	465
ENSMUSG00000019795	chr10	Pcmt1	7629373	7630976	4718	-0.46786018	6.85945443	0.0163875	0.03483641	0.04484	-1	2105	1623	2345	2060	1920	2141	2371	1608	2029	1905
ENSMUSG00000029407	chr5	Uso1	9.2E+07	9.2E+07	3897	-0.49275512	6.68225445	0.0163962	0.034844443	0.04971	-1	1786	1450	1947	2098	1637	2110	2312	1327	1566	1559
ENSMUSG00000057506	chr19	Bloc1s2	4.4E+07	4.4E+07	878	0.47616266	3.59530487	0.0163941	0.034844443	0.04101	1	157	128	184	116	166	395	280	213	280	283
ENSMUSG00000018001	chr5	Cyth3	1.4E+08	1.4E+08	4682	0.392334109	4.252779977	0.0164195	0.034888678	0.02887	1	225	158	309	257	307	528	486	357	430	425
ENSMUSG00000024527	chr18	Afg3l2	6.7E+07	6.7E+07	3085	-0.56436811	6.787289116	0.0164279	0.034901222	0.06525	-1	1530	974	3537	2451	1855	1991	2489	1318	1732	1740
ENSMUSG00000043251	chr8	Exoc3l	1.1E+08	1.1E+08	2497	0.598811285	1.86104106	0.0164431	0.034928156	0.0563	1	33	27	46	50	57	109	87	71	93	77
ENSMUSG00000022957	chr16	Itsn1	9.2E+07	9.2E+07	22539	-0.46707235	6.517533864	0.0164467	0.034930542	0.0446	-1	1478	1179	2154	1766	1453	1710	2031	1129	1546	1580
ENSMUSG00000040824	chr7	Snrpd2	1.9E+07	1.9E+07	613	0.421393746	5.229052552	0.0164567	0.03494661	0.03506	1	480	393	507	448	566	1027	734	698	1046	914
ENSMUSG00000021559	chr13	Dapk1	6.1E+07	6.1E+07	5934	0.769141646	4.106750143	0.0164606	0.034949568	0.11686	1	178	219	87	94	344	582	421	357	395	480
ENSMUSG00000048040	chrX	Arxes2	1.4E+08	1.4E+08	1532	-2.00172461	1.995015955	0.0164718	0.034967899	0.73159	-1	135	26	4	1	339	51	21	32	23	33
ENSMUSG00000031697	chr8	Orc6	8.5E+07	8.5E+07	1653	0.616182619	2.121722611	0.0164799	0.034979904	0.06357	1	57	30	50	48	69	136	111	96	77	107
ENSMUSG00000028830	chr4	AU040320	1.3E+08	1.3E+08	6259	-0.43260737	5.493146875	0.0165159	0.035051062	0.03764	-1	661	552	988	893	832	848	942	467	923	831
ENSMUSG00000026087	chr1	Mrpl30	3.8E+07	3.8E+07	3226	-0.44378615	6.42835717	0.0165291	0.035073689	0.04023	-1	1426	1064	1940	1605	1480	1678	1786	1166	1454	1469
ENSMUSG00000037992	chr11	Rara	9.9E+07	9.9E+07	4365	0.432056485	4.397767471	0.0165375	0.035086262	0.03581	1	187	203	317	331	316	535	504	395	557	492
ENSMUSG00000024537	chr18	Psmg2	6.8E+07	6.8E+07	1059	0.429536194	4.65886697	0.0165418	0.035090089	0.03581	1	362	246	350	251	406	699	514	528	611	609
ENSMUSG00000068036	chr17	Mllt4	1.4E+07	1.4E+07	10223	-0.43066092	5.80735853	0.0165487	0.035099437	0.03746	-1	846	574	1313	947	1304	1200	1118	707	847	1097
ENSMUSG00000086863	chr6	Gm15543	1.5E+08	1.5E+08	361	-1.43168239	2.651986013	0.0165638	0.035126114	0.39242	-1	73	11	404	172	98	25	184	51	35	49
ENSMUSG00000029924	chr6	Slc37a3	3.9E+07	3.9E+07	4065	-0.4434887	4.051441937	0.0165941	0.035185104	0.03765	-1	311	229	328	256	300	409	297	188	313	261
ENSMUSG00000003039	chr8	Fam32a	7.2E+07	7.2E+07	1910	0.45719563	4.973269294	0.0166094	0.035212109	0.0416	1	380	255	387	321	690	979	697	552	766	778
ENSMUSG00000060459	chr16	Kng2	2.3E+07	2.3E+07	2509	1.655077481	0.968222779	0.0166285	0.035247254	0.48605	1	15	7	1	0	45	109	29	42	41	67
ENSMUSG00000032377	chr9	Plscr4	9.2E+07	9.2E+07	3590	0.653776488	2.596142737	0.0166381	0.035262268	0.07528	1	47	75	59	62	97	204	168	87	127	177
ENSMUSG00000028950	chr4	Tas1r1	1.5E+08	1.5E+08	4776	0.63724511	1.782091977	0.016646	0.03527381	0.0619	1	39	33	41	37	44	117	63	63	88	88
ENSMUSG00000024505	chr18	Dtwd2	5E+07	5E+07	3520	-0.63073108	2.257677991	0.0166719	0.035323279	0.07011	-1	81	78	86	98	79	69	106	60	85	60
ENSMUSG00000026520	chr1	Pycr2	1.8E+08	1.8E+08	2958	0.462380982	3.847168347	0.0166891	0.035349108	0.04026	1	167	127	192	149	284	431	303	262	362	358
ENSMUSG00000084786	chr9	Ubl5	2.1E+07	2.1E+07	3468	0.456984317	6.342194979	0.0166869	0.035349108	0.04271	1	1015	769	1142	1023	1202	2161	1585	1574	2237	2094
ENSMUSG00000100801	chr5	Gm15459	5781615	5783555	1941	-0.51207724	7.63427983	0.0167149	0.035398393	0.05427	-1	2814	2506	5263	4258	2931	3641	4189	2506	3352	3304
ENSMUSG00000002500	chr17	Rpl3l	2.5E+07	2.5E+07	1643	-0.50570755	8.848821194	0.0167328	0.035430956	0.05312	-1	7404	5118	11661	9430	7853	7460	9909	5643	8793	7672

ENSMUSG00000021592	chr13	Arsk	7.6E+07	7.6E+07	5681	-0.6268915	2.509477949	0.0167606	0.035484375	0.0719	-1	96	111	85	104	99	122	112	56	90	84
ENSMUSG00000040811	chr7	Eml2	1.9E+07	1.9E+07	3540	0.401342646	4.205179071	0.0168001	0.035562751	0.03006	1	225	188	293	222	264	496	428	308	474	461
ENSMUSG00000071652	chr19	Ints5	8888926	8888964	3889	0.381175067	4.835459349	0.0168257	0.035611567	0.02829	1	322	266	454	347	500	781	608	519	729	691
ENSMUSG00000030662	chr14	Ipo5	1.2E+08	1.2E+08	4591	-0.53361459	7.390031765	0.0168852	0.035732015	0.05903	-1	2432	1753	4736	3815	2570	2957	3619	2064	2728	2858
ENSMUSG00000047153	chr14	Khnyn	5.6E+07	5.6E+07	3876	-0.46992048	3.362451664	0.0168995	0.035756869	0.04055	-1	163	136	211	206	175	208	214	125	160	184
ENSMUSG00000020628	chr12	Trappc12	2.9E+07	2.9E+07	4257	-0.46256312	4.818657771	0.0169337	0.03582377	0.04258	-1	389	283	758	640	448	550	605	343	475	493
ENSMUSG00000049482	chr8	Ctu2	1.2E+08	1.2E+08	5164	0.50131534	3.245566644	0.0169443	0.035840876	0.04627	1	97	73	157	101	173	244	196	184	254	252
ENSMUSG00000028657	chr4	Ppt1	1.2E+08	1.2E+08	3674	0.433951493	5.372388225	0.0169565	0.035861307	0.03807	1	474	334	743	435	742	1415	910	738	915	980
ENSMUSG00000025340	chr5	Rabgef1	1.3E+08	1.3E+08	4168	-0.45197482	6.636543455	0.0169853	0.03591682	0.04223	-1	1528	1476	1922	1838	1804	1919	2015	1296	1796	1684
ENSMUSG00000045078	chr5	Rnf216	1.4E+08	1.4E+08	4671	-0.38154756	4.788153497	0.0170071	0.035957509	0.02843	-1	403	361	612	459	531	529	599	359	526	470
ENSMUSG00000038777	chr3	Sema6c	9.5E+07	9.5E+07	5935	-0.49462522	7.002575484	0.0170229	0.035985379	0.05076	-1	2155	1542	2751	2519	2412	1805	2735	1465	2589	2434
ENSMUSG00000095438	chr18	Gm21747	1.1E+07	1.1E+07	395	-0.54869022	2.474912858	0.017037	0.036009765	0.05248	-1	94	86	113	91	102	117	117	61	90	80
ENSMUSG00000026646	chr2	Suv39h2	3455815	3458729	4410	-0.77551067	0.890882483	0.0170637	0.03606082	0.08939	-1	33	20	50	43	24	39	31	15	31	21
ENSMUSG00000038388	chr6	Mpp6	5E+07	5E+07	2843	-0.46585251	6.035866144	0.0170708	0.036070464	0.04465	-1	1267	877	1297	1199	1030	1345	1417	859	961	1142
ENSMUSG00000027167	chr2	Elp4	1.1E+08	1.1E+08	3318	-0.53983892	2.469247458	0.0171043	0.036135793	0.04963	-1	89	77	124	105	91	95	101	74	88	100
ENSMUSG00000040225	chr1	Prrc2c	1.6E+08	1.6E+08	16092	-0.41372168	5.445181536	0.017119	0.036155793	0.03467	-1	709	596	957	749	724	915	902	570	681	812
ENSMUSG00000071350	chr14	Setdb2	5.9E+07	5.9E+07	4047	-0.68838707	1.868228752	0.0171186	0.036155793	0.08356	-1	69	66	72	55	63	85	81	37	44	41
ENSMUSG00000025036	chr19	Sfxn2	4.7E+07	4.7E+07	3210	-0.99980635	2.408843676	0.0171297	0.036173099	0.19335	-1	115	163	31	71	99	92	51	50	70	104
ENSMUSG00000028005	chr3	Gucy1b3	8.2E+07	8.2E+07	3951	-0.51360571	2.760663845	0.0171753	0.03626377	0.04674	-1	105	80	174	120	124	149	134	80	104	109
ENSMUSG00000084910	chr4	C630043F03Rik	7.2E+07	7.2E+07	2581	-0.75790373	1.819243286	0.0172188	0.036350287	0.10235	-1	75	51	68	85	41	56	84	44	43	38
ENSMUSG00000030107	chr6	Usp18	1.2E+08	1.2E+08	1770	0.674316713	1.846453685	0.0172654	0.036443148	0.07745	1	39	26	35	36	68	130	100	57	98	63
ENSMUSG00000075000	chr10	Nrbf2	6.7E+07	6.7E+07	1860	-0.45605275	3.626531014	0.0172815	0.036471617	0.03889	-1	209	149	257	219	243	220	293	163	204	191
ENSMUSG00000075590	chr15	Nrbp2	7.6E+07	7.6E+07	2495	0.666826291	4.046517004	0.0172916	0.036487477	0.08933	1	144	132	148	126	435	528	347	283	369	575
ENSMUSG00000020284	chr10	1810043G02Rik	7.8E+07	7.8E+07	6627	0.69764693	2.899989941	0.017295	0.036489076	0.09317	1	78	56	72	49	178	259	142	129	207	211
ENSMUSG00000028081	chr3	Rps3a1	8.6E+07	8.6E+07	977	0.492114302	8.331214252	0.0173188	0.036533408	0.05077	1	3977	3268	4046	3890	4838	9860	6124	6212	7914	8842
ENSMUSG00000042726	chr5	Trafd1	1.2E+08	1.2E+08	4486	0.430920918	5.7824738	0.0173212	0.036533408	0.03804	1	632	476	1029	738	706	1542	1217	899	1424	1490
ENSMUSG00000042380	chr4	Smim12	1.3E+08	1.3E+08	1022	0.382957832	5.027823816	0.0174039	0.036702278	0.02923	1	366	277	567	424	538	794	757	561	904	792
ENSMUSG00000032366	chr9	Tpm1	6.7E+07	6.7E+07	6485	-0.51792686	14.04436666	0.0174265	0.036738984	0.05653	-1	323066	251731	303333	267140	334159	262741	346622	224949	339834	256063
ENSMUSG00000039615	chr17	Stub1	2.6E+07	2.6E+07	1672	0.46827838	6.807128135	0.0174245	0.036738984	0.04576	1	1167	870	1801	1658	1731	2909	2344	2019	3062	3095
ENSMUSG00000004880	chr1	Lbr	1.8E+08	1.8E+08	4761	-0.44911543	4.252705894	0.0174327	0.036742211	0.03979	-1	332	288	373	297	342	467	416	228	267	307
ENSMUSG00000017286	chr11	Glod4	7.6E+07	7.6E+07	6005	-0.38854727	5.031287058	0.0174333	0.036742211	0.03022	-1	533	467	663	522	585	786	604	445	569	537
ENSMUSG00000023828	chr17	Slc22a3	1.2E+07	1.2E+07	3501	-1.33188631	2.323871298	0.0174594	0.036780549	0.34368	-1	68	74	38	14	368	93	45	58	41	51
ENSMUSG00000041168	chr17	Lonp1	5.7E+07	5.7E+07	2963	-0.47901705	6.884835252	0.017459	0.036780549	0.04791	-1	1726	1209	2952	2450	2299	2023	2577	1478	2154	1999
ENSMUSG00000047216	chr1	Cdh19	1.1E+08	1.1E+08	4280	-0.90416238	0.087970895	0.0174555	0.036780549	0.11829	-1	16	23	21	15	19	20	16	5	9	22
ENSMUSG00000024369	chr17	Nelfe	3.5E+07	3.5E+07	2076	0.505647125	3.560338199	0.0174829	0.036819042	0.04868	1	137	93	143	135	232	334	241	223	358	259
ENSMUSG00000034863	chr8	Ano8	7.1E+07	7.1E+07	3753	-0.41160086	4.60048595	0.0174807	0.036819042	0.03342	-1	396	268	582	458	405	470	549	279	455	415
ENSMUSG00000032872	chr9	Cyb5r4	8.7E+07	8.7E+07	6736	-0.42910577	5.107888531	0.0175028	0.036849997	0.0372	-1	552	391	842	632	604	739	824	458	467	567
ENSMUSG00000062328	chr18	Rpl17	7.5E+07	7.5E+07	775	0.490191353	7.564079979	0.0175019	0.036849997	0.05037	1	2349	2113	2373	2152	2677	5973	3839	3653	4702	4727
ENSMUSG00000031380	chrX	Figf	1.6E+08	1.6E+08	2408	0.548626121	2.531817149	0.0175144	0.036868869	0.0523	1	54	55	86	55	101	151	172	103	144	127
ENSMUSG00000024104	chr6	Fam21	1.2E+08	1.2E+08	4294	-0.41192264	5.316399235	0.017523	0.036881318	0.03455	-1	671	586	771	605	760	937	809	516	603	699
ENSMUSG00000039270	chr4	Megf9	7E+07	7E+07	8226	-0.7631956	2.931131867	0.0175257	0.036881536	0.11332	-1	147	94	115	64	317	167	126	91	101	98
ENSMUSG00000042251	chr1	Pm20d1	1.3E+08	1.3E+08	7028	-0.7195165	1.758330681	0.0175982	0.037028499	0.08882	-1	55	27	95	45	103	49	42	47	52	64
ENSMUSG00000063931	chr7	Pepd	3.5E+07	3.5E+07	3079	0.41689214	5.54602804	0.0176092	0.03704621	0.03544	1	595	460	641	534	786	1383	1034	812	1249	1063
ENSMUSG00000067787	chr2	Blcap	1.6E+08	1.6E+08	3043	-0.45318253	5.491892545	0.0176161	0.03705519	0.04206	-1	770	437	920	641	1276	869	786	625	796	840
ENSMUSG00000092686	chr10	Gm25745	8.7E+07	8.7E+07	133	-0.75425254	2.339972387	0.0176232	0.037064506	0.10757	-1	80	90	112	98	84	127	123	55	46	41
ENSMUSG00000070394	chr11	Tmem256	7E+07	7E+07	1105	0.442233012	5.782930812	0.0176402	0.037094673	0.04023	1	749	552	763	657	767	1763	1107	1037	1414	1245
ENSMUSG00000030493	chr7	C230052I12Rik	3.5E+07	3.5E+07	1824	0.866558367	0.722322669	0.0176447	0.037098531	0.1133	1	14	12	12	12	32	58	25	34	51	35
ENSMUSG00000097577	chr14	6230400D17Rik	2.1E+07	2.1E+07	1554	-0.66746455	1.784245993	0.0176583	0.037121682	0.07609	-1	65	40	77	81	48	77	65	34	40	57
ENSMUSG00000045438	chr5	Cox19	1.4E+08	1.4E+08	3539	0.421354653	5.048658522	0.0176884	0.037179291	0.03607	1	356	223	522	491	601	872	724	577	810	933
ENSMUSG00000028776	chr4	Tinagl1	1.3E+08	1.3E+08	4358	0.556257761	4.760098825	0.0177143	0.037228234	0.06355	1	226	186	392	252	673	856	515	574	746	616
ENSMUSG00000030671	chr7	Pde3b	1.1E+08	1.1E+08	6899	-1.51876905	3.392404971	0.0177743	0.03734865	0.4544	-1	252	116	28	17	822	143	85	91	117	121
ENSMUSG00000019787	chr10	Trdn	3.3E+07	3.3E+07	4514	-0.52995073	10.26126144	0.0177795	0.037352828	0.05949	-1	26635	18197	21265	21913	18490	23484	21558	15776	19337	23971
ENSMUSG00000021432	chr13	Slc35b3	3.9E+07	3.9E+07	2214	0.7216311	1.738077668	0.0177816	0.037352828	0.08634	1	30	37	35	30	48	146	68	65	63	76
ENSMUSG00000018548	chr11	Trim37	8.7E+07	8.7E+07	7214	-0.47602673	3.280849289	0.0177947	0.037374676	0.04231	-1	180	140	164	156	196	211	172	117	170	170
ENSMUSG00000073888	chr4	Ccl27a	4.2E+07	4.2E+07	2377	0.556934756	2.950213913	0.0178178	0.037417554	0.0564	1	95	77	88	79	122	198	145	152	229	206
ENSMUSG00000068452	chr2	Duox2	1.2E+08	1.2E+08	6403	1.154227241	-0.09037951	0.0178525	0.037484903	0.2035	1	6	2	2	7	22	27	21	16	14	38
ENSMUSG00000043067	chr9	Dpy19l1	2.4E+07	2.4E+07	6350	0.611599016	3.459181647	0.0178644	0.037504282	0.0731	1	117	93	111	91	248	431	269	214	211	249
ENSMUSG00000037493	chr9	Cib2	5.5E+07	5.5E+07	1433	-0.61673364	6.900727931	0.0179232	0.037622021	0.0801	-1	2591	2090	1435	1547	2896	2181	1726	1658	2461	1652
ENSMUSG00000049755	chr11	Zfp672	5.8E+07	5.8E+07	6674	-0.42344595	4.607049344	0.0179388	0.037649261	0.03569	-1	369	248	624	480	425	525	541	318	370	408
ENSMUSG00000070705	chr7	Eid2b	2.8E+07	2.8E+07	2424	-0.58294956	2.812476547	0.0179781	0.037726117	0.06391	-1	131	93	193	102	114	156	159	78	103	87
ENSMUSG00000032557	chr9	Uba5	1E+08	1E+08	5243	0.433438653	4.617859073	0.0179818	0.037728065	0.03751	1	303	236	331	242	470	784	513	483	532	595
ENSMUSG00000086316	chrX	2210013O21Rik	1.5E+08	1.5E+08	1880	0.530398911	3.689978318	0.0179873	0.037734043	0.05409	1	171	141	115	162	179	366	260	245	340	349
ENSMUSG00000029787	chr6	Avl9	5.7E+07	5.7E+07	7463	-0.57841816	2.55496895	0.0179907	0.037735625	0.06076	-1	93	91	104	108	122	112	140	69	92	71
ENSMUSG00000023348	chr5	Trip6	1.4E+08	1.4E+08	1760	0.735003485	3.55296555	0.018031	0.037814431	0.10864	1	87	92	111	69	324	361	228	247	339	319
ENSMUSG00000026239	chr1	Pde6d	8.7E+07	8.7E+07	2178	0.363959314	4.707951808	0.0180905	0.037933629	0.02589	1	336	251	423	327	388	746	631	436	650	586
ENSMUSG00000021794	chr14	Glud1	3.4E+07	3.4E+07	4089	-0.45450395	7.162362848	0.0180979	0.03794339	0.04372	-1	2351	1672	3265	2759	2560	3251	2818	1847	2226	2462
ENSMUSG00000022175	chr14	Lrp10	5.4E+07	5.4E+07	4201	0.443856557	5.940887225	0.0181193	0.037976942	0.04122	1	607	457	1118	821	1047	1563	1623	1042	1690	1420

ENSMUSG00000053754	chr14	Chd8	5.2E+07	5.2E+07	12599	-0.38796696	5.233261971	0.0181173	0.037976942	0.03065	-1	543	476	845	722	638	776	701	506	663	727
ENSMUSG00000020526	chr11	Znhit3	8.5E+07	8.5E+07	2136	-0.44582698	3.484436426	0.0181719	0.038081527	0.03713	-1	203	148	222	179	212	234	229	137	186	194
ENSMUSG00000039656	chr17	Rxrb	3.4E+07	3.4E+07	3698	-0.41180389	5.562785336	0.0181973	0.038128968	0.03506	-1	738	529	1123	893	840	948	940	590	939	797
ENSMUSG00000041147	chr5	Brca2	1.5E+08	1.5E+08	10724	-0.70209348	0.819895381	0.0182083	0.038146362	0.06998	-1	31	30	38	27	29	29	26	20	26	31
ENSMUSG00000051950	chr5	B3glct	1.5E+08	1.5E+08	4798	0.52592782	2.934187564	0.0182124	0.038148416	0.05051	1	79	65	98	89	140	258	175	149	152	188
ENSMUSG00000055692	chr16	Tmem191c	1.7E+07	1.7E+07	2441	0.810321729	0.757108346	0.0182147	0.038148416	0.09826	1	14	8	26	16	24	55	34	23	31	66
ENSMUSG00000028101	chr3	Pias3	9.7E+07	9.7E+07	3918	0.509400492	3.421047836	0.0182322	0.038179267	0.04957	1	118	90	118	127	214	346	261	200	262	224
ENSMUSG00000029166	chr5	Mapre3	3.1E+07	3.1E+07	3407	0.458585666	6.428877529	0.0182352	0.038179838	0.04431	1	1067	777	1349	997	1329	1855	2131	1514	2635	2135
ENSMUSG00000074771	chr2	Ankef1	1.4E+08	1.4E+08	7185	-1.88111933	2.060718572	0.0183115	0.038334	0.6768	-1	76	81	1	5	341	58	31	32	27	34
ENSMUSG00000022475	chr15	Hdac7	9.8E+07	9.8E+07	5530	0.442083039	4.598794914	0.0183235	0.03834765	0.03946	1	243	223	378	229	507	771	570	405	533	626
ENSMUSG00000103104	chr17	Riok2	1.7E+07	1.7E+07	3196	-0.42540036	4.278011338	0.0183217	0.03834765	0.03588	-1	288	263	494	314	322	405	437	235	317	328
ENSMUSG00000025453	chr13	Nnt	1.2E+08	1.2E+08	7037	-0.87069166	6.821910951	0.0183303	0.038356008	0.15938	-1	1535	808	4950	3487	815	1704	2028	1310	1222	1999
ENSMUSG00000029705	chr5	Cux1	1.4E+08	1.4E+08	20024	-0.46559713	6.439726753	0.0183417	0.038374185	0.04579	-1	1383	956	2132	1637	1620	1484	2075	1052	1534	1429
ENSMUSG00000039109	chr13	F13a1	3.7E+07	3.7E+07	3927	0.879042468	5.675895341	0.0183463	0.038378077	0.16155	1	384	597	261	277	1145	2842	1351	940	1109	802
ENSMUSG00000069919	chr11	Hba-a1	3.2E+07	3.2E+07	812	0.932953408	5.563109429	0.0183846	0.038452438	0.18212	1	87	214	555	744	1005	1146	931	1098	1897	1227
ENSMUSG00000026788	chr2	Zbtb43	3.3E+07	3.3E+07	5225	-0.44778549	3.754178154	0.018422	0.038524956	0.03852	-1	224	179	311	229	225	240	252	201	204	268
ENSMUSG00000036304	chr16	Zdhhc23	4.4E+07	4.4E+07	1389	-2.51227048	0.26982101	0.0184298	0.038535458	1.09205	-1	7	0	86	61	3	1	29	1	0	4
ENSMUSG00000071866	chr11	Ppia	6415443	6415979	3508	0.693391142	7.154243542	0.0184861	0.038647398	0.10209	1	1566	1350	1143	845	3369	5071	3025	3207	3427	3423
ENSMUSG00000036144	chr12	Meox2	3.7E+07	3.7E+07	2360	0.422010632	4.138487832	0.018505	0.038681192	0.03508	1	187	137	277	221	336	525	491	292	389	397
ENSMUSG00000098812	chr2	Mir7578	2.7E+07	2.7E+07	82	-0.80752006	0.601850931	0.0185248	0.038716964	0.09746	-1	20	25	35	30	27	27	37	9	19	18
ENSMUSG00000021094	chr12	Dhrs7	7.3E+07	7.3E+07	1301	0.599884344	4.808740024	0.0185371	0.038736751	0.07515	1	354	174	312	202	698	920	528	582	679	765
ENSMUSG00000027820	chr3	Mme	6.3E+07	6.3E+07	11542	-0.92265809	3.960366052	0.0185679	0.03879538	0.17622	-1	323	225	100	140	764	373	268	132	182	184
ENSMUSG00000036916	chrX	Zfp280c	4.9E+07	4.9E+07	5236	-0.6794656	1.652025876	0.0186049	0.038866905	0.07883	-1	45	50	64	63	60	66	43	43	28	63
ENSMUSG00000081128	chr2	Gm13328	2E+07	2E+07	1020	-0.73095009	1.414499206	0.0186205	0.038893742	0.08837	-1	44	26	98	45	38	44	44	29	37	47
ENSMUSG00000040720	chr4	1110037F02Rik	1.1E+07	1.1E+07	7138	-0.40352505	4.136436724	0.0186517	0.038953009	0.03181	-1	310	219	340	313	319	356	366	245	291	302
ENSMUSG00000026857	chr2	Ntmt1	3.1E+07	3.1E+07	2798	0.468777573	3.975924559	0.0187314	0.03911375	0.04397	1	127	131	306	169	291	412	370	304	387	397
ENSMUSG00000051339	chr5	2900026A02Rik	1.1E+08	1.1E+08	5876	0.393636864	5.610788433	0.0187428	0.039131612	0.03232	1	562	420	843	626	787	1207	1206	888	1214	1204
ENSMUSG00000034192	chr6	Lsm3	9.2E+07	9.2E+07	1257	0.466181276	4.130198543	0.018798	0.039241162	0.04395	1	170	124	375	220	254	533	370	365	383	429
ENSMUSG00000027367	chr2	Stard7	1.3E+08	1.3E+08	5567	-0.56854525	7.227927983	0.0188156	0.039271894	0.06924	-1	2163	1360	5034	3152	2351	2567	3279	1805	2185	2704
ENSMUSG00000066441	chr12	Rdh11	7.9E+07	7.9E+07	3455	0.654031247	2.618465777	0.0188287	0.039293381	0.08135	1	66	57	59	44	129	183	118	140	157	155
ENSMUSG00000024286	chr18	Ccny	9314044	9316672	4017	-0.44194341	6.45883891	0.0188431	0.039317577	0.04158	-1	1412	1033	2164	1551	1584	1746	1930	1190	1399	1465
ENSMUSG00000057969	chr9	Sema3b	1.1E+08	1.1E+08	4777	0.465654995	4.431378136	0.0188542	0.039334962	0.04418	1	182	175	443	321	274	708	467	352	507	573
ENSMUSG00000040591	chr2	1110051M20Rik	9.1E+07	9.1E+07	5202	0.424096571	3.952875729	0.0188642	0.039350057	0.03454	1	198	163	210	166	249	415	385	260	405	364
ENSMUSG00000039236	chr7	Isg20	7.9E+07	7.9E+07	1826	0.840031372	1.268155027	0.0188973	0.039413216	0.11857	1	18	24	16	14	51	85	51	42	67	60
ENSMUSG00000028329	chr4	Xpa	4.6E+07	4.6E+07	1894	0.51836018	2.618718044	0.0190035	0.039628745	0.04816	1	66	49	100	64	102	210	140	106	140	145
ENSMUSG00000039501	chr2	Znfx1	1.7E+08	1.7E+08	8189	-0.42393149	5.012966567	0.0190081	0.039632397	0.03725	-1	438	364	824	641	571	734	671	331	631	533
ENSMUSG00000025129	chr11	Ppp1r27	1.2E+08	1.2E+08	771	0.627688412	7.238121251	0.0190205	0.039652439	0.08467	1	1173	790	3049	2608	1723	3563	3109	3366	4232	4399
ENSMUSG00000022604	chr16	Cep97	5.6E+07	5.6E+07	9163	-0.55752908	2.595578841	0.0190904	0.03979231	0.05711	-1	106	85	146	104	93	96	127	72	118	86
ENSMUSG00000057604	chr6	Lmcd1	1.1E+08	1.1E+08	1730	0.858081042	7.701942927	0.0191434	0.039896762	0.15731	1	1406	785	4209	4308	904	6486	5134	4398	5541	6172
ENSMUSG00000042308	chr7	Setd1a	1.3E+08	1.3E+08	6795	-0.38040149	4.586835902	0.0191527	0.039910321	0.02909	-1	385	299	470	414	483	417	508	300	476	457
ENSMUSG00000010066	chr9	Cacna2d2	1.1E+08	1.1E+08	7947	-0.9305189	-0.14600975	0.0191908	0.03998369	0.11154	-1	17	14	23	17	9	13	15	8	16	6
ENSMUSG00000032640	chr7	Chsy1	6.6E+07	6.6E+07	4167	0.621016036	2.428066913	0.0192401	0.040080524	0.0704	1	65	53	44	53	94	168	111	114	129	134
ENSMUSG00000046441	chr8	Cmtr2	1.1E+08	1.1E+08	4115	-0.62112448	2.422072214	0.0192639	0.040124004	0.07286	-1	94	100	89	89	96	105	118	71	64	73
ENSMUSG00000031987	chr8	Egln1	1.2E+08	1.2E+08	3515	-0.62272366	8.249306089	0.019301	0.04018348	0.08388	-1	4054	2677	10734	6571	5145	4612	7777	3239	4709	4661
ENSMUSG00000087385	chr4	AA415398	1.2E+08	1.2E+08	2760	-0.66720191	1.142027885	0.0192996	0.04018348	0.0691	-1	27	34	42	38	56	41	35	25	28	41
ENSMUSG00000102340	chr9	RP24-496O17.2	2.1E+07	2.1E+07	2696	-1.04554276	0.437595753	0.0192984	0.04018348	0.17603	-1	21	22	25	35	25	5	38	14	11	17
ENSMUSG00000046733	chr6	Gprc5a	1.4E+08	1.4E+08	2083	0.805723129	0.754922743	0.0193375	0.040247421	0.10862	1	10	6	38	17	19	46	41	40	36	40
ENSMUSG00000100774	chr1	Gm7329	6.5E+07	6.5E+07	210	-0.86239376	0.340048428	0.019337	0.040247421	0.11196	-1	33	18	12	19	31	19	19	11	21	17
ENSMUSG00000026012	chr1	Cd28	6.1E+07	6.1E+07	6122	-0.7554663	1.608925239	0.0193948	0.040360659	0.10418	-1	61	48	84	37	51	37	84	29	37	43
ENSMUSG00000103009	chr2	RP23-160G19.10	1.3E+08	1.3E+08	1943	1.000435212	0.362120331	0.0194153	0.04039747	0.16794	1	4	3	24	10	21	49	33	34	18	24
ENSMUSG00000038446	chr10	Cdc40	4.1E+07	4.1E+07	3361	-0.49988494	3.315347458	0.0194361	0.040434608	0.04827	-1	190	120	216	177	171	192	239	129	152	137
ENSMUSG00000056679	chrX	Gpr173	1.5E+08	1.5E+08	5109	0.857426102	0.137121066	0.0194539	0.040465711	0.0939	1	13	4	10	9	17	39	22	23	21	25
ENSMUSG00000026028	chr1	Trak2	5.9E+07	5.9E+07	7088	-0.677974	7.020994211	0.0194707	0.04049134	0.09925	-1	1802	1139	4951	2968	1761	2072	3419	1292	1643	2046
ENSMUSG00000030802	chr7	Bckdk	1.3E+08	1.3E+08	3063	-0.46131037	7.645775755	0.019472	0.04049134	0.04622	-1	3178	2221	4760	3883	3740	3477	4310	2445	3801	3461
ENSMUSG00000018661	chr11	Cog1	1.1E+08	1.1E+08	4987	0.378413164	4.723801629	0.0194962	0.040535673	0.02927	1	288	209	478	360	435	653	648	452	693	636
ENSMUSG00000037313	chr5	Tacc3	3.4E+07	3.4E+07	3551	0.654493996	1.48386186	0.0195117	0.040561968	0.06883	1	24	23	33	31	47	105	57	44	64	73
ENSMUSG00000092650	chr13	Gm25241	8.1E+07	8.1E+07	84	0.88877546	-0.00532395	0.0195186	0.040570163	0.09529	1	8	6	5	12	15	24	25	22	18	27
ENSMUSG00000092137	chr9	Gcom1	7.1E+07	7.1E+07	1726	-0.43904021	5.983194181	0.0195291	0.040585939	0.04126	-1	994	734	1576	1152	1110	1175	1470	767	1134	1041
ENSMUSG00000001415	chr3	Smg5	8.8E+07	8.8E+07	6956	-0.44948271	6.35383788	0.0195406	0.040603952	0.04353	-1	1282	1124	1896	1484	1319	1634	1744	997	1551	1274
ENSMUSG00000037938	chr2	Chchd5	1.3E+08	1.3E+08	1727	0.429793159	3.760912952	0.0195478	0.040612787	0.0357	1	168	124	201	160	217	402	279	220	363	344
ENSMUSG00000006641	chr5	Slc5a6	3.1E+07	3.1E+07	3991	-0.48165849	3.165722366	0.0195756	0.04066462	0.04392	-1	111	100	214	160	218	184	162	107	163	157
ENSMUSG00000037358	chrX	4930578C19Rik	1.8E+07	1.8E+07	3499	-0.78800092	1.541586557	0.0195807	0.040669257	0.1111	-1	55	55	71	55	27	53	38	39	29	55
ENSMUSG00000017405	chr11	Nek8	7.8E+07	7.8E+07	5222	0.829858423	0.848662253	0.0195907	0.040683927	0.10882	1	13	15	16	10	38	60	35	30	55	43
ENSMUSG00000044715	chr12	Gskip	1.1E+08	1.1E+08	2776	0.414108869	3.963438448	0.0196012	0.040699703	0.03334	1	183	162	216	186	253	415	385	286	410	332
ENSMUSG00000078153	chr11	Psme2b	4.9E+07	4.9E+07	837	0.63643947	1.743721176	0.0196044	0.040700286	0.06926	1	36	24	38	35	60	112	61	54	84	99
ENSMUSG00000044791	chr9	Setd2	1.1E+08	1.1E+08	8350	-0.39816535	5.105357458	0.019608	0.040701708	0.03303	-1	593	405	856	539	588	679	734	460	520	683
ENSMUSG00000003135	chr1	Cnot11	4E+07	4E+07	3508	-0.37366537	4.894226905	0.0196244	0.040729847	0.02868	-1	450	399	630	522	521	560	568	415	580	544

ENSMUSG00000007415	chr5	Gatad1	3632932	3634030	4125	-0.41069804	6.01150813	0.0196397	0.040755551	0.03608	-1	1003	768	1442	1141	1258	1240	1394	862	1123	1117
ENSMUSG00000041720	chr16	Pi4ka	1.7E+07	1.7E+07	11257	-0.38756465	4.928906815	0.0197122	0.040893788	0.03108	-1	444	346	627	518	710	611	708	351	568	516
ENSMUSG00000101249	chr1	Gm29216	2.5E+07	2.5E+07	492	-0.56723551	4.339817061	0.0197113	0.040893788	0.06718	-1	287	155	689	431	345	310	470	220	310	383
ENSMUSG00000068270	chrX	Shroom4	6399854	6400261	8880	-0.51088921	3.176985087	0.0197625	0.040992232	0.05018	-1	135	102	240	183	147	157	157	134	134	176
ENSMUSG00000063253	chr8	Scoc	8.3E+07	8.3E+07	2062	-0.47486853	3.251978204	0.0197845	0.041031611	0.04367	-1	152	145	180	143	203	184	205	118	167	147
ENSMUSG00000017376	chr11	Nlk	7.9E+07	7.9E+07	5447	-0.45919344	3.633685283	0.0197972	0.041051997	0.04179	-1	212	169	212	236	238	240	289	151	209	192
ENSMUSG00000027799	chr3	Nbea	5.6E+07	5.6E+07	10976	-0.62213625	1.804447076	0.0198194	0.041091935	0.06438	-1	61	46	66	56	84	64	50	59	45	55
ENSMUSG00000001518	chr6	Itfg2	1.3E+08	1.3E+08	5069	-0.43198356	3.797786042	0.0198237	0.041094702	0.03696	-1	226	198	287	200	286	277	316	171	226	236
ENSMUSG00000024360	chr18	Etf1	3.5E+07	3.5E+07	3709	-0.44809343	6.946955372	0.0198422	0.04112702	0.04369	-1	1838	1568	2946	2234	2248	2368	2703	1660	1900	2182
ENSMUSG00000033389	chr11	Arhgap44	6.5E+07	6.5E+07	5819	-0.50509026	3.682122821	0.019864	0.041166093	0.05131	-1	210	136	304	307	181	223	266	156	221	228
ENSMUSG00000027185	chr2	Nat10	1E+08	1E+08	7199	-0.41769004	4.380284921	0.019868	0.041168391	0.03553	-1	288	311	453	375	350	419	370	328	353	352
ENSMUSG00000037890	chr5	Wdr19	6.5E+07	6.5E+07	4403	0.729457105	1.39930168	0.0199068	0.041242653	0.08766	1	28	31	20	20	40	82	55	51	62	74
ENSMUSG00000020458	chr11	Rtn4	3E+07	3E+07	6991	-0.52922592	9.498483121	0.0199284	0.041281341	0.06147	-1	15833	10041	13898	10267	13738	13761	16874	9735	11450	9510
ENSMUSG00000044938	chr9	Klhl31	7.8E+07	7.8E+07	6494	-0.55282519	8.56750577	0.0199406	0.041300485	0.06698	-1	8480	6112	5156	5959	7190	6388	7748	4658	7107	5957
ENSMUSG00000036845	chr7	Lin37	3.1E+07	3.1E+07	1388	0.481943293	3.264447391	0.019954	0.041322102	0.04418	1	117	94	130	90	169	265	236	157	260	233
ENSMUSG00000041460	chr6	Cacna2d4	1.2E+08	1.2E+08	9478	-1.4138339	0.504827848	0.020001	0.041413336	0.37787	-1	14	9	63	8	66	22	39	5	4	7
ENSMUSG00000041891	chr18	Lman1	6.6E+07	6.6E+07	6411	-0.41363734	5.805534125	0.0200475	0.041503424	0.0368	-1	973	717	1168	1006	936	1185	1202	674	976	969
ENSMUSG00000006587	chr8	Snai3	1.2E+08	1.2E+08	1589	0.816922393	3.438024479	0.020068	0.041539761	0.14061	1	98	25	260	163	77	244	318	197	374	277
ENSMUSG00000024851	chr19	Pitpnm1	4099998	4100213	6889	0.706458493	3.049428183	0.0201132	0.041627267	0.10335	1	50	40	123	72	215	218	203	135	228	268
ENSMUSG00000024370	chr18	Cdc23	3.5E+07	3.5E+07	9500	-0.37967298	4.536104094	0.0201197	0.041634441	0.02934	-1	382	317	479	364	424	507	424	354	378	409
ENSMUSG00000031204	chrX	Asb12	9.5E+07	9.5E+07	1258	-0.42930788	5.028297329	0.0201229	0.04163492	0.03902	-1	613	398	693	651	446	629	634	385	664	578
ENSMUSG00000029142	chr5	Mrpl33	3.2E+07	3.2E+07	7473	0.432013241	6.292292558	0.0201619	0.041708351	0.04047	1	1003	707	1119	1076	1130	2181	1617	1537	1976	1953
ENSMUSG00000094483	chr11	Purb	6467599	6475917	8319	-0.39221598	5.636666873	0.0201643	0.041708351	0.03288	-1	766	617	943	879	1073	1101	1016	673	822	856
ENSMUSG00000021692	chr13	Dimt1	1.1E+08	1.1E+08	2545	-0.63502944	1.711873839	0.0201763	0.041727046	0.07119	-1	61	44	84	46	60	75	53	26	65	45
ENSMUSG00000022350	chr15	E430025E21Rik	5.9E+07	5.9E+07	4032	-0.3707228	5.025063981	0.0202214	0.041812564	0.02874	-1	529	407	717	577	539	752	640	414	570	582
ENSMUSG00000031641	chr8	Cbr4	6.1E+07	6.1E+07	3047	-0.42251651	4.553570408	0.0202236	0.041812564	0.03678	-1	389	217	613	432	427	494	499	329	343	409
ENSMUSG00000049517	chr13	Rps23	9.1E+07	9.1E+07	756	0.465602124	7.647860625	0.020234	0.041827815	0.04763	1	2560	2042	2695	2363	2954	6442	3980	3731	4745	5260
ENSMUSG00000052253	chr15	Zfp622	2.6E+07	2.6E+07	2803	0.373271442	4.822523663	0.0202562	0.041867687	0.0289	1	310	236	464	380	502	732	626	501	706	727
ENSMUSG00000071078	chr8	Nr2c2ap	7E+07	7E+07	1175	0.5654907	3.197008782	0.0202726	0.04189523	0.06329	1	74	95	114	84	189	283	191	177	262	204
ENSMUSG00000022419	chr15	Deptor	5.5E+07	5.5E+07	8874	-0.51177523	6.391274447	0.0202882	0.041921345	0.05723	-1	1396	1252	1415	1087	2283	1406	2026	1042	1354	1347
ENSMUSG00000032185	chr9	Carm1	2.2E+07	2.2E+07	4324	-0.41985382	5.967316441	0.0202921	0.041923232	0.03812	-1	939	766	1360	1058	1341	1034	1312	786	1244	1160
ENSMUSG00000020085	chr10	Aifm2	6.2E+07	6.2E+07	4121	-0.64982579	5.003611052	0.0202997	0.041932845	0.09087	-1	459	224	726	374	1389	716	465	393	472	549
ENSMUSG00000072872	chr6	Rybp	1E+08	1E+08	4458	-0.81280238	1.559596662	0.020328	0.041985135	0.12542	-1	44	73	40	51	54	68	59	30	25	38
ENSMUSG00000097119	chr17	B230354K17Rik	4.5E+07	4.5E+07	4897	-0.48127092	3.386164316	0.0203386	0.042000828	0.04587	-1	172	150	208	201	171	208	238	132	172	150
ENSMUSG00000027762	chr3	Sucnr1	6E+07	6E+07	1640	-2.05229748	-0.0436955	0.0203509	0.042019904	0.74961	-1	18	16	0	0	79	10	6	7	10	2
ENSMUSG00000020132	chr10	Rab21	1.2E+08	1.2E+08	1823	-0.44459635	5.4053111	0.0203714	0.042056077	0.04244	-1	713	502	1115	736	656	765	1020	539	652	747
ENSMUSG00000034037	chr6	Fgd5	9.2E+07	9.2E+07	6292	-0.42768946	3.845786731	0.0203961	0.042101007	0.03647	-1	191	171	375	251	274	299	291	165	247	273
ENSMUSG00000031953	chr8	Tmem170	1.1E+08	1.1E+08	1943	-0.86747915	0.551841615	0.0204123	0.042128139	0.12218	-1	25	21	32	25	32	27	41	11	15	9
ENSMUSG00000028953	chr5	Abcf2	2.5E+07	2.5E+07	2573	-0.44613489	7.079198851	0.0204626	0.04222585	0.0438	-1	2100	1812	2779	2563	2486	2419	2927	1744	2453	2316
ENSMUSG00000008958	chr3	Vps72	9.5E+07	9.5E+07	3639	-0.41930873	5.448979228	0.020511	0.042319346	0.03774	-1	650	610	858	625	1040	774	803	596	917	757
ENSMUSG00000036225	chr18	Kctd1	1.5E+07	1.5E+07	3587	0.917280293	1.598506483	0.0205435	0.042373927	0.16782	1	21	3	66	37	36	93	60	69	68	98
ENSMUSG00000036918	chr17	Ttc7	8.7E+07	8.7E+07	6315	0.524848572	4.52141776	0.0205431	0.042373927	0.05866	1	239	145	486	384	197	667	544	422	556	608
ENSMUSG00000022941	chr16	Ripply3	9.4E+07	9.4E+07	1531	0.974583937	0.838969228	0.0206005	0.042485357	0.17034	1	12	7	18	6	46	59	29	31	53	56
ENSMUSG00000069744	chr11	Psmb3	9.8E+07	9.8E+07	2300	0.426578782	6.788455387	0.0206857	0.042654819	0.04005	1	1252	992	1781	1433	1740	2950	2404	2061	2841	2824
ENSMUSG00000052942	chr19	Glis3	2.8E+07	2.8E+07	8842	1.103704007	0.272689747	0.0206918	0.042661093	0.19994	1	19	6	3	5	18	54	27	31	22	18
ENSMUSG00000049858	chr10	Suox	1.3E+08	1.3E+08	2349	-0.41691214	5.743688286	0.020732	0.042737661	0.03772	-1	930	635	941	961	1166	1056	1219	685	899	909
ENSMUSG00000003378	chr7	Grik5	2.5E+07	2.5E+07	3836	0.626616133	2.222163948	0.0207642	0.042797698	0.07311	1	38	37	84	53	63	172	85	62	142	121
ENSMUSG00000029146	chr5	Snx17	3.1E+07	3.1E+07	2791	0.410751347	5.775271344	0.0208395	0.042946653	0.03662	1	660	500	797	640	985	1427	1220	956	1507	1351
ENSMUSG00000030374	chr7	Strn4	1.7E+07	1.7E+07	7958	0.433514847	4.627616031	0.0208518	0.042965657	0.03989	1	198	193	449	313	487	666	560	451	596	654
ENSMUSG00000061535	chr5	C1qtnf7	4.4E+07	4.4E+07	4136	0.828585196	1.282633653	0.0208563	0.042968629	0.12044	1	16	26	22	13	48	103	60	45	48	53
ENSMUSG00000003437	chr7	Paf1	2.8E+07	2.8E+07	3438	0.383528235	5.190940911	0.0208712	0.042992919	0.0314	1	378	311	654	473	626	984	787	660	836	1001
ENSMUSG00000039195	chr2	1110008P14Rik	3.2E+07	3.2E+07	2694	0.485098925	4.618860381	0.0208885	0.043016018	0.05023	1	225	210	313	254	578	590	592	436	743	586
ENSMUSG00000075225	chr10	Ccdc162	4.2E+07	4.2E+07	5572	0.92316176	0.157939541	0.0208878	0.043016018	0.13028	1	14	4	15	2	18	35	21	21	29	28
ENSMUSG00000076431	chr13	Sox4	2.9E+07	2.9E+07	4795	0.505782206	2.893746033	0.0209023	0.043038132	0.0485	1	88	70	101	74	125	215	191	154	150	174
ENSMUSG00000015668	chrX	Pdzd11	1E+08	1E+08	2127	0.456958089	3.697463043	0.0209147	0.043057302	0.04166	1	171	114	154	166	213	436	282	247	288	292
ENSMUSG00000002017	chr17	Fam98a	7.6E+07	7.6E+07	3479	-0.39533593	5.263040342	0.0209365	0.043095941	0.03352	-1	544	501	893	738	618	822	733	498	731	659
ENSMUSG00000098808	chr3	Mir7009	3.6E+07	3.6E+07	64	1.063249664	-0.08613558	0.0210034	0.043227237	0.16147	1	5	7	4	3	21	22	26	11	30	26
ENSMUSG00000074733	chr19	5830428H23Rik	6.1E+07	6.1E+07	6503	0.690559187	1.766218215	0.0210391	0.04329427	0.08533	1	35	31	31	29	63	136	74	57	63	95
ENSMUSG00000022010	chr14	Tsc22d1	7.6E+07	7.6E+07	8994	0.465177214	7.281174324	0.0210593	0.043329678	0.04815	1	1544	1176	2990	2154	2285	4795	3959	3011	3564	3362
ENSMUSG00000025781	chr2	Atp5c1	1E+07	1E+07	1908	-0.50383643	9.43839941	0.0210643	0.043333411	0.05676	-1	11024	7311	20078	13673	10774	12938	14423	8797	11143	12279
ENSMUSG00000022032	chr14	Scara5	6.6E+07	6.6E+07	6093	0.517909994	5.008163796	0.0210966	0.043393657	0.05827	1	273	258	417	322	791	956	1062	463	701	798
ENSMUSG00000022144	chr15	Gdnf	7811011	7811114	3509	1.163320017	-0.35068757	0.0211105	0.043415725	0.19236	1	9	4	7	9	1	8	14	18	29	23
ENSMUSG00000070372	chr3	Capza1	1E+08	1E+08	3532	-0.45521624	3.866950285	0.021117	0.043422871	0.04271	-1	220	195	332	231	298	358	346	154	200	235
ENSMUSG00000025730	chr17	Rab40c	2.6E+07	2.6E+07	3094	0.451335068	3.452670376	0.0211221	0.043426999	0.04021	1	139	87	153	135	185	295	231	197	304	267
ENSMUSG00000054641	chr6	Mmrn1	6.1E+07	6.1E+07	5868	0.951735991	1.910536295	0.021145	0.043467601	0.17826	1	13	43	41	59	23	117	139	37	65	152
ENSMUSG00000042496	chr9	Prdm10	3.1E+07	3.1E+07	6075	-0.72384247	1.115809849	0.0211696	0.043511898	0.08725	-1	46	36	43	34	33	37	38	31	35	20
ENSMUSG00000029544	chr5	Cabp1	1.2E+08	1.2E+08	2413	0.89796823	0.05909619	0.0211876	0.043542456	0.10051	1	7	11	17	5	8	27	19	19	28	30

ENSMUSG00000048458	chr3	Fam212b	1.1E+08	1.1E+08	4781	-0.49145372	3.640306113	0.0212217	0.043606068	0.04945	-1	174	127	365	260	195	246	244	142	216	227
ENSMUSG00000025245	chr9	Lztfl1	1.2E+08	1.2E+08	9249	-0.44365247	3.699437364	0.0212249	0.04360626	0.03985	-1	213	190	267	194	253	293	279	174	194	198
ENSMUSG00000095432	chr13	Zfp748	6.8E+07	6.8E+07	4970	-0.60397756	1.497636119	0.0212368	0.043624296	0.05963	-1	50	36	67	43	55	54	49	39	33	49
ENSMUSG00000051034	chr5	Zfp11	1.3E+08	1.3E+08	3929	-0.65094345	1.516823357	0.0212452	0.04363534	0.0715	-1	47	30	80	54	50	52	46	37	30	58
ENSMUSG00000016831	chr14	Tox4	5.2E+07	5.2E+07	6940	-0.40471901	5.703516538	0.0212978	0.043728207	0.03579	-1	826	654	1164	942	905	979	1156	662	944	912
ENSMUSG00000024730	chr19	Ms4a8a	1.1E+07	1.1E+07	1795	1.146653499	0.082607614	0.0212992	0.043728207	0.19383	1	5	12	3	6	16	55	13	18	23	26
ENSMUSG00000035958	chr13	Tdp2	2.5E+07	2.5E+07	2095	-0.50720306	3.161133444	0.0212998	0.043728207	0.05062	-1	112	120	245	148	173	195	181	124	124	135
ENSMUSG00000019845	chr10	Tube1	3.9E+07	3.9E+07	2929	-0.83422708	0.043240664	0.0213466	0.043817955	0.09226	-1	19	13	20	20	19	21	16	6	20	8
ENSMUSG00000048707	chr2	Tprn	2.5E+07	2.5E+07	2932	0.661104252	2.10514283	0.0213709	0.043861356	0.08308	1	27	29	94	53	50	105	100	72	137	116
ENSMUSG00000002055	chr11	Spag5	7.8E+07	7.8E+07	5624	0.625420565	1.896403946	0.021423	0.043950183	0.07069	1	37	22	55	64	38	102	92	72	81	104
ENSMUSG00000078249	chr11	Hmga1-rs1	1.2E+08	1.2E+08	1626	0.390124038	4.285336605	0.0214231	0.043950183	0.03115	1	234	170	341	265	271	504	559	291	476	469
ENSMUSG00000079071	chr2	Gm14085	1.2E+08	1.2E+08	4996	0.640927773	2.756747998	0.0214236	0.043950183	0.08347	1	65	35	108	65	137	270	116	139	140	176
ENSMUSG00000026766	chr2	Mmadhc	5E+07	5E+07	2012	-0.43405119	6.801523512	0.0215359	0.044173943	0.04203	-1	1891	1355	2589	1941	1961	2195	2309	1602	1858	1828
ENSMUSG00000038718	chr2	Pbx3	3.4E+07	3.4E+07	6109	0.617407059	1.600198972	0.021539	0.044173943	0.06302	1	28	27	45	34	40	90	58	71	66	75
ENSMUSG00000028907	chr4	Utp11l	1.2E+08	1.2E+08	4711	0.412059079	4.290303041	0.0215925	0.044277224	0.03545	1	226	167	355	200	342	603	433	345	399	533
ENSMUSG00000049038	chr10	Mterf2	8.5E+07	8.5E+07	1565	-0.51055159	3.963652139	0.0216472	0.04438296	0.05472	-1	258	146	472	320	217	294	324	218	225	261
ENSMUSG00000073079	chr12	Srp54a	5.5E+07	5.5E+07	1515	-0.79150986	1.054908282	0.0216611	0.044405005	0.11234	-1	31	47	31	41	33	35	47	20	30	21
ENSMUSG00000021693	chr13	Kif2a	1.1E+08	1.1E+08	7046	-0.45123372	4.06886265	0.0216722	0.044421169	0.04271	-1	329	242	263	270	326	364	350	236	254	258
ENSMUSG00000030664	chr7	Sox6os	1.2E+08	1.2E+08	420	-0.75442355	1.158108565	0.0216841	0.044439195	0.09833	-1	42	33	34	26	69	31	26	30	43	33
ENSMUSG00000054708	chr10	Ankrd24	8.2E+07	8.2E+07	8142	-0.49808783	3.054139358	0.021691	0.044446671	0.04924	-1	181	107	147	124	162	178	154	104	144	129
ENSMUSG00000032243	chr9	Itga11	6.3E+07	6.3E+07	5131	0.519363009	3.245144436	0.0216979	0.044454352	0.05302	1	98	109	117	122	124	346	218	143	199	256
ENSMUSG00000028466	chr4	Creb3	4.4E+07	4.4E+07	2372	0.383808751	5.109969537	0.0217061	0.044464732	0.03145	1	452	346	482	420	550	1054	729	535	889	871
ENSMUSG00000050821	chr16	Fam131a	2.1E+07	2.1E+07	2853	-0.56942231	6.317809307	0.0217329	0.044513132	0.07239	-1	1140	832	2403	1064	2087	1015	1990	869	1633	1149
ENSMUSG00000029458	chr5	Brap	1.2E+08	1.2E+08	6284	-0.38137084	5.19093315	0.0217465	0.044534368	0.0314	-1	599	432	808	655	638	675	838	461	678	638
ENSMUSG00000024843	chr19	Chka	3851773	3852413	12024	0.648746025	1.470820377	0.0217786	0.044587161	0.06985	1	30	22	42	26	37	96	51	52	53	84
ENSMUSG00000069844	chr11	Sco1	6.7E+07	6.7E+07	3925	-0.46282441	3.343087882	0.0217785	0.044587161	0.0422	-1	161	111	265	189	169	204	204	125	164	184
ENSMUSG00000020827	chr11	Mink1	7.1E+07	7.1E+07	6286	-0.41446067	5.156416985	0.0218232	0.044671979	0.03743	-1	516	495	857	617	587	619	816	400	711	636
ENSMUSG00000040046	chr7	Tph1	4.7E+07	4.7E+07	3682	0.989962897	0.716143399	0.021848	0.044716199	0.16653	1	22	16	21	5	10	86	33	20	39	37
ENSMUSG00000006906	chr6	Stambp	8.4E+07	8.4E+07	2157	0.462620689	3.369664195	0.0219337	0.044885135	0.04274	1	123	88	139	114	193	337	239	188	215	254
ENSMUSG00000001962	chrX	Fam50a	7.4E+07	7.4E+07	2288	0.390497169	4.447880195	0.0219371	0.044885501	0.03185	1	223	217	338	270	384	589	458	386	569	548
ENSMUSG00000041801	chr1	Phlda3	1.4E+08	1.4E+08	1559	0.636972192	7.320736696	0.0219645	0.04493494	0.0914	1	1136	637	3554	2071	2773	5425	3543	2953	3799	4564
ENSMUSG00000036850	chr2	Mrpl41	2.5E+07	2.5E+07	888	0.4385032	4.217134278	0.0219836	0.044967397	0.04078	1	187	134	367	265	267	582	368	343	418	498
ENSMUSG00000101856	chr5	1700096K18Rik	2.6E+07	2.6E+07	1454	-0.68513212	1.513851399	0.0220144	0.045023833	0.08219	-1	47	22	75	42	83	43	56	31	36	54
ENSMUSG00000023034	chr15	Nr4a1	1E+08	1E+08	2474	-0.64570795	6.660426998	0.022019	0.045026734	0.09368	-1	1387	1281	1611	2658	2383	901	2125	914	2187	2054
ENSMUSG00000039463	chr2	Slc9a8	1.7E+08	1.7E+08	9095	-0.38781708	5.386871566	0.0220523	0.045088372	0.03291	-1	588	541	876	788	792	790	852	518	843	758
ENSMUSG00000000532	chr15	Acvr1b	1E+08	1E+08	4413	-0.4599507	5.459894301	0.0220839	0.045127836	0.04678	-1	788	536	879	519	1182	766	1005	574	688	799
ENSMUSG00000016181	chr1	Diexf	1.9E+08	1.9E+08	6530	-0.44567693	3.287589149	0.0220812	0.045127836	0.03849	-1	138	126	217	172	196	184	172	146	174	166
ENSMUSG00000024426	chr17	Atat1	3.6E+07	3.6E+07	4586	0.61725519	2.610652223	0.022086	0.045127836	0.07579	1	65	46	55	57	140	176	136	119	169	148
ENSMUSG00000055322	chr1	Tns1	7.4E+07	7.4E+07	16010	-0.58094749	8.509272416	0.0220756	0.045127836	0.07638	-1	4393	2993	12121	7008	8408	5779	8662	4280	5250	6368
ENSMUSG00000097093	chr15	C330013E15Rik	1E+08	1E+08	878	1.002655653	-0.23726566	0.0220877	0.045127836	0.13663	1	11	3	15	2	6	23	18	19	14	25
ENSMUSG00000020023	chr10	Tmcc3	9.4E+07	9.4E+07	7153	-0.36694524	5.176572199	0.0221378	0.045223527	0.0291	-1	606	423	715	567	787	721	801	479	598	676
ENSMUSG00000050043	chr2	Tmx2	8.5E+07	8.5E+07	2330	-0.43538976	5.664070743	0.0221458	0.04523337	0.04206	-1	719	599	1204	1112	794	1051	1062	659	819	887
ENSMUSG00000017417	chr11	Plxdc1	9.8E+07	9.8E+07	4836	0.616680439	3.090240944	0.0222185	0.04537516	0.07982	1	69	44	206	99	110	234	186	143	201	293
ENSMUSG00000022204	chr14	Ngdn	5.5E+07	5.5E+07	1198	0.402130489	4.141373364	0.0222261	0.045384127	0.03359	1	201	149	268	235	304	470	353	324	433	482
ENSMUSG00000020780	chr11	Srp68	1.2E+08	1.2E+08	2737	-0.43166314	6.532965299	0.0222544	0.045435158	0.04193	-1	1437	1118	2184	1808	1531	1797	1845	1194	1731	1611
ENSMUSG00000032333	chr9	Stoml1	5.8E+07	5.8E+07	1987	0.40312562	3.945003043	0.0222914	0.045504152	0.03301	1	205	145	242	177	228	458	341	291	378	333
ENSMUSG00000024049	chr17	Myom1	7.1E+07	7.1E+07	5672	-0.55884326	10.1332464	0.0223525	0.04562223	0.07113	-1	15550	11531	32680	27258	16406	17273	24446	13272	18632	20565
ENSMUSG00000052560	chr15	Cpne8	9E+07	9E+07	4164	0.707761748	2.9091125	0.022412	0.045737066	0.10465	1	81	75	60	49	157	274	173	189	122	182
ENSMUSG00000030393	chr7	Zik1	1E+07	1E+07	4199	-0.81239616	0.609129943	0.0224432	0.045794128	0.1076	-1	37	27	33	22	16	19	28	16	22	23
ENSMUSG00000074578	chr2	1500012F01Rik	1.7E+08	1.7E+08	2929	0.470247112	3.392275944	0.0224495	0.045800167	0.04472	1	120	98	144	118	181	331	219	223	212	257
ENSMUSG00000066798	chr2	Zbtb6	3.7E+07	3.7E+07	5080	-0.59115654	2.521914226	0.0225044	0.045905589	0.06864	-1	109	72	101	106	125	113	86	80	56	131
ENSMUSG00000038784	chr6	Cnot4	3.5E+07	3.5E+07	7185	-0.37594757	4.353701403	0.022543	0.04597756	0.02964	-1	336	242	434	381	349	430	397	257	360	402
ENSMUSG00000063412	chr8	Gm10131	3.4E+07	3.4E+07	594	0.668066343	1.014973225	0.0225564	0.045998247	0.06629	1	22	18	20	20	30	49	44	40	53	53
ENSMUSG00000037344	chr5	Slc12a9	1.4E+08	1.4E+08	5020	0.639158505	3.037601196	0.0225859	0.046051707	0.08423	1	84	89	58	80	159	239	180	119	219	275
ENSMUSG00000050332	chrX	Amer1	9.5E+07	9.5E+07	8496	-0.50760553	3.517254565	0.0225909	0.0460552	0.05383	-1	227	170	161	186	244	258	204	158	146	208
ENSMUSG00000031480	chr8	Thsd1	2.2E+07	2.2E+07	4422	0.598779548	2.123149844	0.0225973	0.046061638	0.06862	1	51	25	78	49	58	95	90	90	135	111
ENSMUSG00000089942	chr7	Pira2	3837057	3838339	3217	1.25913278	-0.13667112	0.0226432	0.046148406	0.23357	1	5	16	2	4	4	30	29	13	12	32
ENSMUSG00000027942	chr3	4933434E20Rik	9E+07	9E+07	6826	-0.42066285	6.197248281	0.022666	0.046175882	0.03992	-1	1299	988	1392	1239	1371	1444	1592	938	1309	1235
ENSMUSG00000041482	chr18	Piezo2	6.3E+07	6.3E+07	14566	0.827936496	1.354847027	0.0226665	0.046175882	0.12241	1	28	28	15	26	30	95	56	46	35	93
ENSMUSG00000050565	chr1	Tor1aip2	1.6E+08	1.6E+08	9218	-0.40410865	5.993474432	0.0226641	0.046175882	0.03665	-1	1034	873	1263	1069	1208	1369	1225	920	1014	1140
ENSMUSG00000003721	chr1	Insig2	1.2E+08	1.2E+08	3473	-0.42744782	5.843166876	0.0227268	0.046291857	0.04103	-1	1001	681	1361	962	1002	1123	1409	684	896	998
ENSMUSG00000022962	chr16	Gart	9.2E+07	9.2E+07	3992	-0.39410237	5.726147606	0.0227327	0.046297193	0.03467	-1	847	681	1076	962	961	1013	1103	698	1011	911
ENSMUSG00000028973	chr5	Abcb8	2.4E+07	2.4E+07	4739	-0.44219045	5.888770006	0.0227562	0.046338268	0.04389	-1	885	551	1608	1078	1205	1028	1299	771	1112	984
ENSMUSG00000074384	chr8	AI429214	3.7E+07	3.7E+07	1957	0.891762322	0.487369408	0.0228157	0.04645278	0.12895	1	16	6	11	6	30	50	26	26	37	33
ENSMUSG00000028988	chr4	Ctnnbip1	1.5E+08	1.5E+08	2792	0.470356818	4.456118595	0.0228537	0.046523458	0.04807	1	220	220	302	277	366	526	388	487	706	470
ENSMUSG00000084838	chr16	Gm10241	2E+07	2E+07	286	-0.85524921	0.331209293	0.0228575	0.04652442	0.11228	-1	29	12	33	22	19	13	29	16	16	11
ENSMUSG00000073002	chr6	Vamp5	7.2E+07	7.2E+07	1648	0.431684322	6.523299577	0.0228714	0.04654595	0.0423	1	1158	792	1473	1181	1361	2233	1943	1622	2475	2630

ENSMUSG00000031979	chr8	Cog2	1.2E+08	1.2E+08	4778	-0.42811436	4.461353141	0.022878	0.04655265	0.03957	-1	326	255	591	416	341	466	486	262	409	333
ENSMUSG00000048915	chr17	Efna5	6.3E+07	6.3E+07	4032	-1.19875843	0.348682488	0.022942	0.046675981	0.25656	-1	18	18	12	11	70	29	6	16	13	10
ENSMUSG00000039114	chr13	Nrn1	3.7E+07	3.7E+07	1766	0.927164413	0.193321857	0.0229794	0.046745322	0.12867	1	6	7	12	6	23	45	22	12	27	35
ENSMUSG00000042410	chr2	Agps	7.6E+07	7.6E+07	9421	-0.37192734	4.950417231	0.0229828	0.04674539	0.03004	-1	505	349	696	566	534	638	692	422	517	522
ENSMUSG00000043415	chr2	Otud1	2E+07	2E+07	2832	0.620828759	3.811756992	0.0229885	0.046750354	0.08465	1	129	86	148	147	352	251	329	300	368	468
ENSMUSG00000035776	chrX	Cd99l2	7.1E+07	7.1E+07	4902	-0.45769252	7.23618592	0.0229997	0.046766345	0.04799	-1	2663	1986	3006	2601	2869	3121	3629	1789	2232	2524
ENSMUSG00000060288	chr4	Ppih	1.2E+08	1.2E+08	1894	0.502818427	2.586645616	0.0230115	0.046783527	0.04781	1	81	44	86	68	93	181	129	112	151	142
ENSMUSG00000017756	chr13	Slc12a7	7.4E+07	7.4E+07	5131	0.535097878	3.947354045	0.023035	0.04682457	0.06272	1	126	87	256	174	353	549	331	260	378	381
ENSMUSG00000066705	chr9	Fxyd6	4.5E+07	4.5E+07	1791	1.022359295	6.97545446	0.0230567	0.046861858	0.23504	1	981	182	3288	1851	475	3788	4351	2342	2437	4686
ENSMUSG00000019923	chr10	Zwint	7.3E+07	7.3E+07	4434	-0.40349727	5.535318052	0.0230638	0.046869461	0.03639	-1	884	563	810	677	1056	949	905	629	820	830
ENSMUSG00000075273	chr2	Ttc30b	7.6E+07	7.6E+07	2737	-0.57348905	2.151476896	0.0230693	0.046873884	0.06227	-1	72	51	126	56	99	90	90	49	59	78
ENSMUSG00000046546	chr16	Fam43a	3.1E+07	3.1E+07	3075	0.575433245	3.989335242	0.023075	0.046878641	0.07312	1	154	92	266	119	380	483	322	326	466	347
ENSMUSG00000022075	chr14	Rhobtb2	7E+07	7E+07	5216	-0.39957957	4.846981743	0.0230793	0.046880645	0.03483	-1	441	332	772	427	546	527	629	344	599	477
ENSMUSG00000087687	chr8	Pet100	3621551	3621611	1189	0.402980083	4.162246175	0.0230853	0.046881186	0.03393	1	209	180	289	225	255	528	344	322	471	434
ENSMUSG00000096974	chr4	Gm26881	4.3E+07	4.3E+07	592	0.537279206	2.638119866	0.0230863	0.046881186	0.05711	1	70	42	98	77	97	160	126	150	166	132
ENSMUSG00000052139	chr5	Bre	3.2E+07	3.2E+07	4781	0.375660553	4.833970023	0.0231845	0.047073722	0.03078	1	308	231	474	402	492	695	620	542	694	751
ENSMUSG00000053173	chr6	Rpl18-ps2	1.3E+08	1.3E+08	604	0.671236559	1.431671486	0.0232144	0.047127698	0.08123	1	27	12	41	29	46	79	47	49	84	68
ENSMUSG00000051748	chr11	Wfdc21	8.4E+07	8.4E+07	434	1.525909696	-0.07244162	0.023219	0.047130181	0.42589	1	6	6	0	1	19	46	9	39	16	12
ENSMUSG00000018566	chr11	Slc2a4	7E+07	7E+07	3478	-0.55084704	9.027188592	0.023254	0.047187667	0.06998	-1	7036	4519	15205	12644	9143	8508	11462	5797	8914	9419
ENSMUSG00000032171	chr9	Pin1	2.1E+07	2.1E+07	3808	0.379936655	5.567202164	0.0232533	0.047187667	0.03225	1	574	422	774	603	770	1212	1083	885	1218	1119
ENSMUSG00000040859	chr4	Bsdc1	1.3E+08	1.3E+08	5630	-0.38736329	5.689263267	0.0233069	0.047288184	0.03372	-1	874	635	1077	905	924	1004	1066	689	958	911
ENSMUSG00000031889	chr8	D230025D16Rik	1.1E+08	1.1E+08	4704	-0.35846191	4.70270491	0.0233678	0.04740486	0.02768	-1	416	343	530	457	447	530	527	359	489	451
ENSMUSG00000019173	chr11	Rab5c	1E+08	1E+08	2194	0.453815605	5.781960472	0.0233835	0.047429777	0.04676	1	580	449	744	602	1217	1741	1291	942	1427	1224
ENSMUSG00000039759	chr4	Thap3	1.5E+08	1.5E+08	1334	0.368070575	5.059648952	0.0233993	0.047454979	0.02959	1	441	324	490	397	544	871	693	565	907	846
ENSMUSG00000026112	chr1	Coa5	3.7E+07	3.7E+07	5220	-0.45505927	7.388298414	0.0234269	0.047504148	0.04774	-1	2809	1937	4217	3043	2790	3116	3734	2167	2880	2763
ENSMUSG00000037523	chr2	Mavs	1.3E+08	1.3E+08	3345	-0.62777987	5.711232799	0.023469	0.047582493	0.08984	-1	666	413	1962	1309	680	802	1077	597	798	992
ENSMUSG00000014075	chr16	Tctex1d2	3.2E+07	3.2E+07	2385	0.487165607	2.948109003	0.0234827	0.047603374	0.04608	1	102	71	94	101	106	230	166	134	201	190
ENSMUSG00000039637	chr16	Coro7	4626133	4627499	7420	0.416478267	4.035398964	0.0235211	0.047674475	0.03667	1	180	131	246	218	299	516	390	227	427	401
ENSMUSG00000047514	chr10	Tspyl1	3.4E+07	3.4E+07	3086	-0.43102981	6.276770247	0.0235278	0.047681064	0.04252	-1	1383	1025	1524	1357	1383	1494	1818	969	1288	1301
ENSMUSG00000031821	chr8	Gins2	1.2E+08	1.2E+08	4097	0.941990328	0.198777303	0.0236228	0.047866695	0.14511	1	6	5	16	4	24	26	29	13	40	32
ENSMUSG00000021275	chr12	Tecpr2	1.1E+08	1.1E+08	7830	-0.59155549	2.676325623	0.0236771	0.047969833	0.07066	-1	93	62	180	144	108	111	158	77	80	97
ENSMUSG00000032123	chr9	Dpagt1	4.4E+07	4.4E+07	1905	0.381851587	4.330397796	0.0237106	0.048030845	0.03122	1	205	167	342	269	359	534	465	334	508	512
ENSMUSG00000021506	chr13	Pitx1	5.6E+07	5.6E+07	2656	1.300839077	0.134581733	0.023731	0.048065228	0.32241	1	2	1	11	2	30	27	16	17	50	31
ENSMUSG00000017499	chr11	Cdc6	9.9E+07	9.9E+07	5229	0.99589133	-0.24902849	0.0237803	0.048158058	0.14	1	5	3	9	4	16	35	14	8	20	24
ENSMUSG00000057280	chr4	Musk	5.8E+07	5.8E+07	3776	-0.65961602	2.679124068	0.0237849	0.04816041	0.0904	-1	92	100	193	105	97	69	173	77	84	102
ENSMUSG00000040723	chr1	Rcsd1	1.7E+08	1.7E+08	10131	-0.44824899	6.874401167	0.023792	0.048167813	0.04642	-1	1958	1352	2632	2110	2282	1974	2858	1408	2128	1947
ENSMUSG00000020604	chr11	Arsg	1.1E+08	1.1E+08	3906	0.665606274	1.443470974	0.0238231	0.048223774	0.07408	1	26	26	31	26	42	88	57	34	69	87
ENSMUSG00000005705	chr8	Agrp	1.1E+08	1.1E+08	1013	1.321803421	-0.09231224	0.0238382	0.048240382	0.30729	1	9	0	8	16	2	29	11	23	12	43
ENSMUSG00000038055	chr16	Dexi	1.1E+07	1.1E+07	3353	0.392939552	5.260144162	0.0238356	0.048240382	0.03469	1	492	285	701	494	581	899	883	680	1086	929
ENSMUSG00000021294	chr12	Kif26a	1.1E+08	1.1E+08	6918	-0.52313662	3.316436958	0.0238562	0.048266081	0.05774	-1	151	93	253	133	288	194	219	100	176	162
ENSMUSG00000098269	chr17	Mir8094	3.5E+07	3.5E+07	117	0.422116471	4.142450814	0.0238577	0.048266081	0.03795	1	196	174	222	236	304	479	342	308	464	488
ENSMUSG00000018196	chr1	Glrx2	1.4E+08	1.4E+08	8772	-0.37092388	5.14375475	0.0238836	0.04831141	0.03054	-1	573	471	646	609	688	661	649	528	709	614
ENSMUSG00000026792	chr2	Lrsam1	3.3E+07	3.3E+07	5145	-0.39262092	4.158670098	0.0239424	0.048417601	0.03311	-1	284	247	344	293	349	391	360	195	359	307
ENSMUSG00000028247	chr4	Coq3	2.2E+07	2.2E+07	2997	-0.4301056	5.213161756	0.023943	0.048417601	0.04161	-1	576	348	1035	727	613	705	835	467	605	669
ENSMUSG00000033809	chr16	Alg3	2.1E+07	2.1E+07	1451	0.473693219	3.802918971	0.0239579	0.048440717	0.04807	1	141	112	202	218	212	284	350	221	451	359
ENSMUSG00000034066	chr1	Farp2	9.4E+07	9.4E+07	5235	-0.53114625	3.443461867	0.0240156	0.04854348	0.06031	-1	200	111	282	245	134	187	216	130	199	184
ENSMUSG00000079334	chr9	Nat6	1.1E+08	1.1E+08	3154	0.410731473	4.711038933	0.0240155	0.04854348	0.03732	1	255	220	392	385	469	657	524	439	783	680
ENSMUSG00000029209	chr5	Gnpda2	7E+07	7E+07	6858	-0.55592704	2.316726467	0.0240764	0.048653549	0.05972	-1	102	57	77	84	121	103	100	63	70	76
ENSMUSG00000037661	chr3	Gpr160	3.1E+07	3.1E+07	4227	1.121053076	1.038255873	0.024077	0.048653549	0.24735	1	13	14	4	8	54	84	33	49	57	48
ENSMUSG00000030983	chr7	Bccip	1.3E+08	1.3E+08	2038	-0.38954505	5.863822505	0.0240871	0.048666898	0.03465	-1	959	730	1117	995	1188	1193	1292	748	991	1019
ENSMUSG00000017615	chr11	Tnfaip1	7.9E+07	7.9E+07	3781	-0.41384298	6.336761651	0.0240926	0.048670938	0.03947	-1	1153	1003	1817	1473	1589	1476	1677	1025	1577	1430
ENSMUSG00000017119	chr11	Nbr1	1E+08	1E+08	6871	-0.42870109	6.483098047	0.0240969	0.048672729	0.04246	-1	1398	1043	2155	1736	1489	1757	1905	1170	1478	1604
ENSMUSG00000067430	chr17	Zfp763	3.3E+07	3.3E+07	3557	-0.67328308	1.610415632	0.0241118	0.048695861	0.08633	-1	75	38	51	56	52	64	61	35	28	51
ENSMUSG00000051456	chr13	Hspb3	1.1E+08	1.1E+08	781	0.392892775	4.989889468	0.0241277	0.048720848	0.03422	1	423	316	462	423	429	808	619	666	829	753
ENSMUSG00000028347	chr4	Tmeff1	4.9E+07	4.9E+07	2549	-1.20419196	0.922997358	0.0241354	0.048729436	0.29614	-1	19	21	18	11	134	34	19	12	20	30
ENSMUSG00000021102	chr12	Glrx5	1.1E+08	1.1E+08	930	0.456734845	6.143375185	0.0241393	0.048730254	0.04821	1	685	485	1353	989	1147	1773	1497	1326	1875	1946
ENSMUSG00000006019	chr7	Dhx34	1.6E+07	1.6E+07	4596	0.506112132	2.970248441	0.0243849	0.049218966	0.05184	1	75	68	122	81	145	212	173	116	211	234
ENSMUSG00000033377	chr3	Palmd	1.2E+08	1.2E+08	3812	-0.59040326	5.096310309	0.0244004	0.049236141	0.07974	-1	379	229	1200	530	1010	581	766	394	470	625
ENSMUSG00000062933	chr9	Gm10123	9.7E+07	9.7E+07	490	0.65454547	3.917018094	0.0243978	0.049236141	0.09607	1	185	120	126	83	383	508	366	272	426	339
ENSMUSG00000060098	chr8	Prmt7	1.1E+08	1.1E+08	6125	-0.39928654	5.568705077	0.0244091	0.049246593	0.03637	-1	722	591	969	937	855	855	962	606	993	819
ENSMUSG00000025813	chr7	Homer2	8.2E+07	8.2E+07	11149	-1.14902391	5.01369837	0.0244184	0.049257279	0.29868	-1	319	148	1704	1294	123	322	558	306	248	634
ENSMUSG00000035847	chrX	Ids	7E+07	7E+07	5101	-0.39900623	4.843162046	0.0244214	0.049257279	0.0356	-1	503	345	568	461	594	532	722	311	449	574
ENSMUSG00000049086	chr2	Bmyc	2.6E+07	2.6E+07	983	0.579548322	3.265257161	0.0244794	0.049367052	0.072	1	111	81	118	92	179	339	127	171	258	290
ENSMUSG00000064080	chr6	Fbln2	9.1E+07	9.1E+07	5876	0.474356475	6.46865708	0.0245199	0.049441711	0.05242	1	734	635	1406	1398	1595	2740	2341	1427	2318	1947
ENSMUSG00000060427	chr8	Zfp868	7E+07	7E+07	2893	-0.48905226	2.637758194	0.0245469	0.04948905	0.04635	-1	100	70	129	117	131	136	111	90	86	105
ENSMUSG00000037526	chr14	Atg14	4.8E+07	4.8E+07	3450	-0.45739296	3.343017977	0.0245576	0.049503419	0.04376	-1	169	131	230	181	169	212	218	108	149	203
ENSMUSG00000075595	chr11	Zfp652	9.6E+07	9.6E+07	15444	-0.46518828	8.158769142	0.0245784	0.049531215	0.05087	-1	4556	3355	6912	4831	5779	4486	6356	3252	6102	4756

ENSMUSG00000080921	chr6	Rpl38-ps2	1.4E+08	1.4E+08	213	0.477592214	4.137226015	0.024576	0.049531215	0.04983	1	243	184	206	202	250	544	280	369	453	445
ENSMUSG00000074340	chr3	Ovgp1	1.1E+08	1.1E+08	3561	-0.83187104	1.008348495	0.0245922	0.049551828	0.12928	-1	35	51	22	29	40	38	21	25	26	34
ENSMUSG00000025733	chr17	Rhot2	2.6E+07	2.6E+07	4442	-0.53143979	7.126171379	0.0246404	0.049641831	0.06614	-1	1915	1408	4206	3104	2195	2073	3093	1533	2643	2534
ENSMUSG00000057123	chr3	Gja5	9.7E+07	9.7E+07	3166	0.540553769	2.654767006	0.0246795	0.049713509	0.0586	1	53	51	90	92	99	216	113	114	150	169
ENSMUSG00000053897	chr3	Slc39a8	1.4E+08	1.4E+08	7664	0.843244417	0.081293707	0.0247045	0.049756634	0.10002	1	10	3	16	6	17	34	30	13	23	26
ENSMUSG00000024217	chr17	Snrpc	2.8E+07	2.8E+07	6217	0.363865044	4.967708518	0.0247315	0.0497948	0.02927	1	385	325	432	395	516	816	701	540	842	735
ENSMUSG00000028969	chr5	Cdk5	2.4E+07	2.4E+07	2050	0.4392052	3.859530375	0.0247331	0.0497948	0.04162	1	177	105	195	176	291	462	330	229	375	340
ENSMUSG00000032463	chr9	Faim	9.9E+07	9.9E+07	5745	0.808627825	1.597258317	0.0247341	0.0497948	0.13119	1	27	18	26	14	80	98	75	59	80	70
ENSMUSG00000026380	chr1	Tfcp2l1	1.2E+08	1.2E+08	9438	-1.07649776	2.690040696	0.0247631	0.049838858	0.2547	-1	64	47	304	51	255	45	210	47	61	64
ENSMUSG00000083669	chr7	Gm10169	3E+07	3E+07	348	0.908939467	0.977017322	0.0247621	0.049838858	0.15992	1	27	2	15	19	37	41	52	38	61	54
ENSMUSG00000031848	chr8	Lsm4	7.1E+07	7.1E+07	1038	0.368322849	5.127520816	0.0247825	0.049870829	0.03048	1	417	316	611	453	528	858	752	647	976	811
ENSMUSG00000078572	chr11	1810043H04Rik	1.2E+08	1.2E+08	834	0.396905042	4.37187444	0.0248212	0.049941409	0.03444	1	251	178	309	268	352	552	402	361	611	496
ENSMUSG00000058173	chr9	Smco4	1.6E+07	1.6E+07	988	0.445395044	3.505687805	0.0248439	0.049979902	0.04133	1	148	109	179	115	170	331	223	215	300	270
ENSMUSG00000030591	chr7	Psmd8	2.9E+07	2.9E+07	1540	0.496285282	7.816489438	0.02485	0.04998508	0.05807	1	2435	1602	3728	2017	4942	6531	6018	4093	5279	5486
ENSMUSG00000045790	chr5	Ccdc149	5.2E+07	5.2E+07	3317	0.734131229	1.436214387	0.0248555	0.049989047	0.10016	1	29	20	31	14	55	95	47	53	68	71
ENSMUSG00000040205	chr7	Cuzd1	1.3E+08	1.3E+08	2256	-0.89470877	2.120178712	0.0248643	0.049999561	0.17325	-1	94	113	42	93	43	51	67	47	97	47
ENSMUSG00000055775	chr11	Myh8	6.7E+07	6.7E+07	11772	0.81179806	8.941771825	0.0248877	0.050032233	0.15398	0	3708	1928	5197	11185	5539	6939	11693	12130	20397	11701
ENSMUSG00000070304	chr9	Scn2b	4.5E+07	4.5E+07	4562	0.80144705	0.624795927	0.0248862	0.050032233	0.10804	0	10	12	28	6	24	34	38	25	48	41
ENSMUSG00000006850	chr18	Tmco6	3.7E+07	3.7E+07	1817	0.512626509	2.850646891	0.0249494	0.050149015	0.05201	0	99	73	84	85	93	187	182	144	192	152
ENSMUSG00000094595	chr4	Fsbp	1.2E+07	1.2E+07	4358	-1.27126824	0.023646951	0.0249656	0.050174452	0.29715	0	25	33	3	17	14	24	7	9	13	6
ENSMUSG00000020758	chr11	Itgb4	1.2E+08	1.2E+08	7015	0.63186897	3.059154201	0.0249723	0.050180763	0.08729	0	61	48	140	170	77	234	247	126	221	217
ENSMUSG00000030045	chr6	Mrpl19	8.2E+07	8.2E+07	5450	-0.43904146	4.577386929	0.0249768	0.050182569	0.04313	0	352	258	697	451	355	409	523	311	446	401
ENSMUSG00000022186	chr15	Oxct1	4026383	4026849	3701	-0.68233419	8.81462469	0.0250101	0.050240784	0.10956	0	7807	3626	17958	9894	4440	7489	9751	5176	6294	7234
ENSMUSG00000054690	chr3	Emcn	1.4E+08	1.4E+08	5409	0.457676192	4.128359235	0.0250129	0.050240784	0.04675	0	154	116	362	250	267	515	359	312	472	429
ENSMUSG00000005802	chr2	Slc30a4	1.2E+08	1.2E+08	5482	-0.38513092	4.747733485	0.0250378	0.050276271	0.03319	0	424	374	555	473	447	586	603	373	441	409
ENSMUSG00000034826	chr5	Nup54	9.2E+07	9.2E+07	2867	-0.45674747	3.189701405	0.0250372	0.050276271	0.04357	0	133	139	186	135	194	204	183	113	138	157
ENSMUSG00000017817	chr2	Jph2	1.6E+08	1.6E+08	4255	-0.49752928	9.811891888	0.0250596	0.050308862	0.0587	0	15944	13374	15044	16934	16610	14624	18882	10287	19789	13859
ENSMUSG00000068396	chr6	Rpl34-ps1	7.1E+07	7.1E+07	354	0.582205421	2.453934793	0.0250612	0.050308862	0.06759	0	57	51	71	56	90	207	95	111	104	150
ENSMUSG00000053716	chr9	Dusp7	1.1E+08	1.1E+08	3356	-0.54804915	3.92228107	0.0250823	0.050344085	0.06691	0	235	113	531	296	243	297	334	174	249	225
ENSMUSG00000039661	chr8	Dusp26	3.1E+07	3.1E+07	2305	-0.88199536	4.142644511	0.0250952	0.050362715	0.17821	0	274	75	840	466	192	212	465	125	257	244
ENSMUSG00000020272	chr11	Stk10	3.3E+07	3.3E+07	5187	0.592710873	2.599741627	0.025126	0.050404404	0.07465	0	64	27	91	62	131	152	145	111	156	174
ENSMUSG00000029319	chr5	Coq2	1E+08	1E+08	2624	-0.38750443	5.689179242	0.0251248	0.050404404	0.03468	0	865	663	955	939	966	1009	1069	653	980	930
ENSMUSG00000035632	chr7	Cnot3	3645290	3645584	4340	0.377209715	4.359601241	0.0251267	0.050404404	0.03099	0	231	183	323	255	370	538	444	341	545	527
ENSMUSG00000038848	chr2	Ythdf1	1.8E+08	1.8E+08	3316	-0.37423081	5.364740508	0.0251404	0.050424539	0.03192	0	671	476	925	759	699	852	841	582	702	732
ENSMUSG00000029376	chr5	Mthfd2l	9.1E+07	9.1E+07	2235	-0.60677487	1.505523515	0.0251685	0.05047383	0.06518	0	56	32	60	58	45	51	54	30	53	39
ENSMUSG00000020642	chr12	Rnf144a	2.6E+07	2.6E+07	5163	-0.66744507	3.503726206	0.025252	0.050633896	0.09984	0	208	141	150	110	459	259	156	122	194	181
ENSMUSG00000022828	chr16	Gtf2e1	3.8E+07	3.8E+07	6285	-0.43493023	3.372112822	0.0252602	0.050643127	0.03931	0	201	128	203	168	189	224	191	134	162	197
ENSMUSG00000021947	chr14	Cryl1	5.7E+07	5.7E+07	1410	0.612928945	2.908964475	0.0252731	0.05065459	0.08002	0	106	53	70	60	158	246	153	127	215	191
ENSMUSG00000071649	chr19	B3gat3	8920374	8920648	1601	0.387811342	5.543665715	0.0252705	0.05065459	0.03453	0	550	462	720	555	774	1274	992	769	1295	1154
ENSMUSG00000036333	chr12	Kidins220	2.5E+07	2.5E+07	7402	-0.39266462	5.48572037	0.0252919	0.050685014	0.0356	0	737	655	905	738	752	1034	883	591	722	802
ENSMUSG00000045257	chr17	Morn2	8E+07	8E+07	644	0.523475506	2.352111724	0.0253109	0.050715722	0.05377	0	62	34	69	63	86	131	108	94	127	147
ENSMUSG00000019861	chr10	Gopc	5.2E+07	5.2E+07	4317	-0.41523556	3.993113208	0.0253299	0.050746721	0.03758	0	265	233	333	214	316	359	339	215	252	247
ENSMUSG00000026170	chr1	Cyp27a1	7.5E+07	7.5E+07	2173	-0.40620394	5.347425011	0.0253468	0.050773154	0.03801	0	589	540	753	634	1005	750	977	469	728	726
ENSMUSG00000048240	chr10	Gng7	8.1E+07	8.1E+07	3786	-0.58235832	2.227299814	0.0253671	0.050806696	0.06807	0	90	59	62	89	114	84	78	47	98	77
ENSMUSG00000033105	chr10	Lss	7.7E+07	7.7E+07	10787	-0.67520207	2.252229384	0.0253819	0.050829128	0.09435	0	102	57	68	54	159	98	84	58	51	84
ENSMUSG00000038393	chr3	Txnip	9.7E+07	9.7E+07	3031	-0.50824352	9.470133817	0.0254079	0.050873864	0.06151	0	14437	9610	10073	11113	16987	14082	10927	10862	10786	13410
ENSMUSG00000079671	chr1	2610203C22Rik	9560832	9561778	4910	0.678805772	1.40133394	0.0254312	0.050913161	0.08461	0	31	12	37	21	50	81	83	46	49	64
ENSMUSG00000051116	chr5	Gm8121	5.8E+07	5.8E+07	501	-0.59909916	1.68500584	0.0254638	0.050971123	0.06685	0	57	58	58	48	57	57	50	40	59	51
ENSMUSG00000078879	chr2	Gm14306	1.8E+08	1.8E+08	2709	-0.91884302	-0.20667327	0.0254916	0.051019647	0.12518	0	22	15	13	11	14	22	10	5	9	11
ENSMUSG00000030917	chr7	Tmem159	1.2E+08	1.2E+08	1926	0.457801648	3.663580871	0.0255504	0.051130052	0.04586	0	110	92	232	148	248	344	342	202	294	335
ENSMUSG00000025958	chr1	Creb1	6.5E+07	6.5E+07	13742	-0.3901545	4.214946648	0.0255583	0.051138434	0.03328	0	329	209	346	336	370	411	392	253	274	334
ENSMUSG00000057234	chr2	Mettl15	1.1E+08	1.1E+08	2275	-0.71319415	1.983747702	0.0255666	0.051147729	0.10431	0	70	41	114	88	56	54	112	36	42	63
ENSMUSG00000034586	chr11	Hid1	1.2E+08	1.2E+08	4595	0.683333852	1.518246042	0.025588	0.051183264	0.08841	0	25	21	24	29	62	80	59	46	79	87
ENSMUSG00000024491	chr18	Rbm27	4.2E+07	4.2E+07	6431	-0.44059719	3.868430703	0.0256016	0.051203178	0.04223	0	248	180	351	255	234	267	334	219	201	247
ENSMUSG00000027475	chr2	Kif3b	1.5E+08	1.5E+08	5635	0.478575596	3.615048427	0.0256125	0.051217776	0.04993	0	120	108	145	134	272	370	291	211	279	321
ENSMUSG00000050148	chrX	Ubqln2	1.5E+08	1.5E+08	3344	-0.39847755	4.201430563	0.0256381	0.05126158	0.03486	0	335	196	382	311	366	364	409	216	371	289
ENSMUSG00000043671	chr7	Dpy19l3	3.6E+07	3.6E+07	11173	0.549759988	2.755701572	0.0256439	0.051265792	0.06207	0	69	68	91	95	79	187	122	166	158	167
ENSMUSG00000025135	chr11	Anapc11	1.2E+08	1.2E+08	5057	0.370859613	4.93201471	0.0256503	0.05126662	0.03094	0	379	289	477	419	444	731	682	531	899	699
ENSMUSG00000048832	chr19	Vps37c	1.1E+07	1.1E+07	2415	0.38047484	5.463104891	0.0256516	0.05126662	0.03338	0	506	376	717	682	636	1150	1072	772	1127	1036
ENSMUSG00000035529	chr10	Prdm4	8.6E+07	8.6E+07	3917	-0.35149631	4.5369867	0.0256645	0.051285057	0.0272	0	359	286	490	387	448	495	506	288	435	397
ENSMUSG00000039765	chr5	Cc2d2a	4.4E+07	4.4E+07	6776	-0.45726765	3.453369315	0.0256987	0.051346168	0.04495	0	174	141	252	191	196	228	262	115	155	203
ENSMUSG00000029108	chr5	Pcdh7	5.8E+07	5.8E+07	10478	0.554863193	3.140155457	0.0257264	0.051394219	0.06466	0	93	119	107	82	114	282	271	150	163	216
ENSMUSG00000026289	chr1	Atg16l1	8.8E+07	8.8E+07	9628	-0.35104558	4.739772331	0.0257332	0.051396281	0.0274	0	433	335	576	455	458	551	531	384	498	456
ENSMUSG00000041220	chr3	Elovl6	1.3E+08	1.3E+08	5951	-1.5574189	3.682593905	0.0257348	0.051396281	0.53872	0	646	164	15	36	554	213	50	155	184	54
ENSMUSG00000074151	chr8	Nlrc5	9.4E+07	9.4E+07	7646	0.912256389	2.10741062	0.0257443	0.051407983	0.17829	0	41	30	33	31	86	282	79	39	68	129
ENSMUSG00000022390	chr15	Zc3h7b	8.2E+07	8.2E+07	5958	-0.37793457	5.62595283	0.0257667	0.051445316	0.03308	0	722	551	1129	894	982	948	1029	677	898	887
ENSMUSG00000032727	chr13	Mier3	1.1E+08	1.1E+08	5846	-0.47604233	3.090173115	0.0258059	0.051516323	0.04714	0	154	93	175	161	163	193	169	122	111	136

ENSMUSG00000036636	chr17	Clcn7	2.5E+07	2.5E+07	5292	0.371770015	4.672046041	0.0258231	0.051543393	0.031	0	258	222	421	336	469	582	659	423	647	656
ENSMUSG00000027374	chr2	Mrps5	1.3E+08	1.3E+08	6578	-0.37516712	5.102178005	0.0258503	0.051590221	0.03205	0	586	325	850	599	631	687	720	434	628	637
ENSMUSG00000030852	chr7	Tacc2	1.3E+08	1.3E+08	9537	-0.64712778	9.262276795	0.0258704	0.051622981	0.09987	0	7433	5650	24094	14350	7723	11903	10924	8275	7202	11171
ENSMUSG00000071178	chr12	Serpina1b	1E+08	1E+08	2415	0.777126532	3.094121248	0.0258785	0.051631831	0.13723	0	60	47	76	65	246	269	116	182	256	269
ENSMUSG00000102644	chr5	THAP6	9.2E+07	9.2E+07	4119	-0.57234997	1.624230488	0.0259285	0.05172423	0.059	0	49	32	82	55	58	61	63	31	49	48
ENSMUSG00000071419	chr6	Rps15-ps2	5.8E+07	5.8E+07	438	0.45836134	4.042779355	0.0260174	0.051894274	0.04708	0	160	119	269	239	282	493	318	243	529	400
ENSMUSG00000093485	chr11	Gm20708	1.2E+08	1.2E+08	1780	-0.44476827	4.265400178	0.0260484	0.051948733	0.04485	0	359	264	376	360	283	377	418	208	414	280
ENSMUSG00000100309	chr1	Gm6644	5.5E+07	5.5E+07	951	-0.64780098	2.29092951	0.0260587	0.051961745	0.08732	0	84	80	97	107	65	63	119	61	86	57
ENSMUSG00000060843	chr10	Ctnna3	6.3E+07	6.3E+07	7227	-0.84053231	2.894270517	0.0260794	0.051995712	0.15967	0	126	86	242	224	38	90	145	85	136	86
ENSMUSG00000083844	chr11	2210015D19Rik	5762129	5762240	3102	-0.39818063	4.936468004	0.026109	0.05204727	0.03622	0	484	368	642	619	512	501	665	470	573	489
ENSMUSG00000028403	chr4	Zdhhc21	8.3E+07	8.3E+07	12972	-0.4354651	4.264312629	0.0261409	0.052103583	0.04266	0	356	288	384	311	291	363	398	308	294	303
ENSMUSG00000007030	chr17	Vwa7	3.5E+07	3.5E+07	4313	0.569899612	3.834221799	0.0261707	0.052155536	0.07453	0	153	66	332	170	185	365	521	225	382	273
ENSMUSG00000022103	chr14	Gfra2	7.1E+07	7.1E+07	3462	0.60073105	2.125168211	0.0262055	0.052209895	0.07109	0	41	42	48	49	74	159	76	93	97	103
ENSMUSG00000030965	chr7	Fam175b	1.3E+08	1.3E+08	5427	-0.3725496	5.038643922	0.0262049	0.052209895	0.03182	0	580	422	643	587	541	658	733	461	546	561
ENSMUSG00000058317	chr14	Ube2e2	1.9E+07	1.9E+07	4671	0.671107273	2.554946361	0.0262231	0.052237572	0.09655	0	64	51	49	42	132	184	99	125	146	173
ENSMUSG00000015405	chrX	Ace2	1.6E+08	1.6E+08	3762	-0.7723194	0.039790542	0.0262657	0.052315076	0.07809	0	16	10	28	17	20	15	17	7	14	19
ENSMUSG00000038538	chr6	Ubn2	3.8E+07	3.8E+07	21438	-0.39698213	4.826385267	0.0262957	0.052367351	0.0362	0	506	443	531	434	461	622	476	401	471	558
ENSMUSG00000003546	chr17	Klc4	4.7E+07	4.7E+07	2322	0.409596172	4.56855729	0.0263137	0.052395699	0.03808	0	233	196	445	372	313	572	581	360	672	621
ENSMUSG00000021177	chr12	Tdp1	1E+08	1E+08	5464	0.623503707	1.9102182	0.0263199	0.052400618	0.07699	0	33	31	63	23	72	119	92	59	100	91
ENSMUSG00000034574	chr12	Daam1	7.2E+07	7.2E+07	6004	-0.37027344	4.329622404	0.026337	0.052427351	0.03023	0	316	259	397	333	402	386	426	289	309	394
ENSMUSG00000040302	chr5	Rbm48	3583978	3584807	3071	-0.48925681	2.377699083	0.0263415	0.052428858	0.04587	0	83	58	122	87	108	114	93	64	78	94
ENSMUSG00000039217	chr9	Il18	5.1E+07	5.1E+07	714	1.105985134	0.815977294	0.0263868	0.052511584	0.23351	0	18	17	0	15	24	77	32	37	36	50
ENSMUSG00000021591	chr13	Glrx	7.6E+07	7.6E+07	1345	-0.37845316	5.102655514	0.0264846	0.052698614	0.03288	0	509	346	839	671	623	681	729	499	593	577
ENSMUSG00000030089	chr6	Slc41a3	9.1E+07	9.1E+07	2812	-0.48906653	6.71489801	0.0265028	0.05271989	0.05737	0	1790	1526	1912	2147	1714	1415	2265	1208	2110	2046
ENSMUSG00000059277	chr7	R74862	1.4E+08	1.4E+08	3889	0.742994814	0.706718927	0.0265	0.05271989	0.09062	0	15	10	19	11	32	43	30	33	38	50
ENSMUSG00000019948	chr10	Actr6	9E+07	9E+07	1703	-0.54049534	2.380391936	0.0265183	0.052743241	0.05884	0	92	67	112	68	124	114	117	59	69	78
ENSMUSG00000024151	chr17	Msh2	8.8E+07	8.8E+07	5518	-0.39315608	3.970925496	0.0265899	0.052878175	0.03377	0	224	188	384	263	298	343	344	192	269	261
ENSMUSG00000029103	chr5	Lrpap1	3.5E+07	3.5E+07	4127	0.40065939	5.941233161	0.0266042	0.052899235	0.0379	0	772	630	774	764	1031	1699	1502	1037	1545	1477
ENSMUSG00000069899	chr11	Gm12166	4.6E+07	4.6E+07	968	0.804123013	0.74517467	0.0266095	0.05290217	0.10798	0	13	18	10	13	30	48	34	38	34	48
ENSMUSG00000021241	chr12	Isca2	8.5E+07	8.5E+07	868	0.365990525	5.075960542	0.0266481	0.052971469	0.03102	0	405	244	568	437	629	924	758	604	780	858
ENSMUSG00000090031	chr1	4732440D04Rik	6209866	6215293	5428	-0.77648742	0.404508593	0.0266589	0.052985402	0.0943	0	27	16	36	24	15	28	14	12	20	21
ENSMUSG00000018809	chr11	Smyd4	7.5E+07	7.5E+07	4329	-0.5014216	2.711594779	0.0267192	0.053097655	0.05065	0	127	66	146	90	155	135	120	90	97	112
ENSMUSG00000020866	chr11	Cacna1g	9.4E+07	9.4E+07	10137	0.703545136	2.097766092	0.0267855	0.053221843	0.10102	0	43	51	50	34	55	165	56	64	135	121
ENSMUSG00000022595	chr15	Lypd2	7.5E+07	7.5E+07	679	1.03860409	-0.24080368	0.0267991	0.053233902	0.1823	0	4	1	6	7	19	20	15	9	23	34
ENSMUSG00000024747	chr19	Aldh1a7	2.1E+07	2.1E+07	2066	-1.57792948	2.044719033	0.0267954	0.053233902	0.54566	0	109	41	5	15	313	56	18	51	60	18
ENSMUSG00000041193	chr4	Pla2g5	1.4E+08	1.4E+08	2884	-0.97640732	0.603311898	0.026806	0.053239966	0.18602	0	19	23	12	53	34	36	13	13	28	12
ENSMUSG00000063410	chr14	Stk24	1.2E+08	1.2E+08	2676	-0.3733039	4.48046804	0.0268144	0.053249171	0.03145	0	346	307	491	366	380	472	486	288	406	365
ENSMUSG00000038178	chr11	Slc43a2	7.6E+07	7.6E+07	10042	0.506700504	5.392161101	0.0268772	0.053358716	0.06122	0	363	248	892	708	506	906	1074	869	1037	1142
ENSMUSG00000051977	chr17	Prdm9	1.6E+07	1.6E+07	4308	-0.71507419	1.565164117	0.0268762	0.053358716	0.10017	0	71	44	57	35	60	43	32	46	35	65
ENSMUSG00000050295	chr13	Foxc1	3.2E+07	3.2E+07	3953	0.69734769	0.698358807	0.0269561	0.053507799	0.07432	0	16	11	27	18	15	55	38	25	32	44
ENSMUSG00000098530	chr12	Gm28051	1E+08	1E+08	445	-0.6416036	2.219834607	0.0269874	0.053562444	0.08609	0	78	50	134	97	69	68	109	69	72	47
ENSMUSG00000026031	chr1	Cflar	5.9E+07	5.9E+07	12669	-0.36992447	5.324469545	0.0270176	0.053614655	0.03209	0	669	517	761	651	803	944	812	481	628	794
ENSMUSG00000027620	chr2	Rbm39	1.6E+08	1.6E+08	6946	-0.40270648	6.277953078	0.0270559	0.053683073	0.03888	0	1231	969	1683	1365	1448	1807	1518	1077	1188	1355
ENSMUSG00000041881	chr17	Ndufa7	3.4E+07	3.4E+07	1701	0.445419536	7.085269977	0.0270658	0.053695266	0.04801	0	1498	1092	1981	1981	2259	3260	2986	2324	4081	3536
ENSMUSG00000025010	chr19	Ccnj	4.1E+07	4.1E+07	4355	-0.53615868	2.487069853	0.0270773	0.053705166	0.05785	0	67	60	132	114	133	107	117	72	96	75
ENSMUSG00000034593	chr9	Myo5a	7.5E+07	7.5E+07	14803	0.543805748	3.948107019	0.0270785	0.053705166	0.0675	0	188	156	160	123	313	492	560	225	316	325
ENSMUSG00000029545	chr5	Acads	1.2E+08	1.2E+08	2269	-0.46986604	7.118701138	0.0271674	0.053873874	0.05348	0	2103	1187	3958	2631	2799	2514	2841	1752	2609	2366
ENSMUSG00000041263	chr3	Rusc1	8.9E+07	8.9E+07	3840	0.443076078	4.311796392	0.0271967	0.053916686	0.04542	0	199	119	425	285	289	535	477	310	512	541
ENSMUSG00000041769	chr7	Ppp2r2d	1.4E+08	1.4E+08	5903	-0.35457345	5.125330221	0.0271949	0.053916686	0.02904	0	486	413	820	566	716	680	760	481	629	616
ENSMUSG00000030265	chr6	Kras	1.5E+08	1.5E+08	5347	-0.42317287	4.379397531	0.027202	0.053919594	0.04095	0	289	264	502	424	322	400	483	283	296	374
ENSMUSG00000011832	chr8	Evi5l	4166567	4166763	8524	-0.42130789	4.49555427	0.0272354	0.053978117	0.04079	0	350	236	559	416	422	374	532	239	485	377
ENSMUSG00000039982	chr19	Dtx4	1.2E+07	1.2E+07	5765	0.569182292	3.973414796	0.0272629	0.054017475	0.07487	0	161	153	140	115	389	455	384	289	379	425
ENSMUSG00000060703	chr2	Cd302	6E+07	6E+07	1354	0.745195971	3.708375167	0.0272616	0.054017475	0.12893	0	141	127	73	66	324	538	290	248	322	301
ENSMUSG00000036591	chr2	Arhgap21	2.1E+07	2.1E+07	9271	-0.36643476	4.297167216	0.0273274	0.054137607	0.02989	0	314	218	437	357	357	438	414	264	327	337
ENSMUSG00000032387	chr9	Rbpms2	6.6E+07	6.6E+07	2041	0.805922065	2.62356393	0.0273349	0.054144883	0.14802	0	62	32	54	24	177	171	140	117	177	188
ENSMUSG00000071497	chr19	Nutf2-ps1	5.4E+07	5.4E+07	864	-0.80463891	0.610537095	0.0273444	0.054156016	0.11439	0	34	22	38	19	25	10	33	18	22	24
ENSMUSG00000019731	chr8	Slc35e1	7.2E+07	7.2E+07	4470	-0.47983504	6.084330622	0.027382	0.054222828	0.0555	0	971	718	1975	1421	1015	1259	1606	794	1114	1135
ENSMUSG00000079427	chr9	Mthfsl	8.9E+07	8.9E+07	4728	0.545024849	2.212985249	0.0274022	0.054255202	0.05704	0	63	41	50	48	74	140	98	85	115	117
ENSMUSG00000025337	chr5	Sbds	1.3E+08	1.3E+08	2033	0.368076296	5.181942165	0.0274495	0.054341059	0.03165	0	430	331	624	411	630	1119	789	620	748	977
ENSMUSG00000001150	chr10	Mcm3ap	7.6E+07	7.6E+07	6382	-0.40714689	4.449939705	0.0274839	0.054401512	0.03795	0	298	238	533	475	358	456	468	281	369	375
ENSMUSG00000021087	chr12	Rtn1	7.2E+07	7.2E+07	4003	0.696639697	1.032555853	0.0275859	0.054595762	0.0861	0	13	12	21	35	31	56	45	36	52	57
ENSMUSG00000089755	chr17	0610012D04Rik	8.7E+07	8.7E+07	531	-0.91108617	1.088991251	0.0276226	0.054660649	0.16899	0	24	18	38	51	78	26	64	14	17	28
ENSMUSG00000065990	chr4	Aurkaip1	1.6E+08	1.6E+08	1766	0.40603453	6.427618934	0.0277054	0.05481672	0.03996	0	964	728	1390	1153	1447	2146	1991	1544	2364	2079
ENSMUSG00000028683	chr4	Eif2b3	1.2E+08	1.2E+08	6520	-0.38705874	4.374220911	0.0277282	0.054854072	0.03415	0	281	313	375	326	462	393	395	288	397	375
ENSMUSG00000040188	chr9	Scamp2	5.8E+07	5.8E+07	2341	0.384850745	5.846155573	0.0277362	0.054862216	0.03544	0	623	560	873	757	976	1587	1274	992	1544	1352
ENSMUSG00000039943	chr2	Plcb4	1.4E+08	1.4E+08	8970	-0.42098421	3.852655253	0.0277662	0.054913737	0.03957	0	241	184	311	207	308	282	351	188	201	255
ENSMUSG00000044770	chr10	Scml4	4.3E+07	4.3E+07	7725	0.745946547	0.400469355	0.0278138	0.055000228	0.0802	0	14	8	18	13	15	29	30	34	26	33

ENSMUSG00000032006	chr9	Pdgfd	6168612	6168918	3119	-0.67016719	1.956647283	0.0278236	0.055003969	0.09261	0	47	48	71	57	139	85	68	51	38	62
ENSMUSG00000032076	chr9	Cadm1	4.8E+07	4.8E+07	9684	0.653154944	3.310877073	0.0278221	0.055003969	0.09664	0	148	107	87	50	171	292	260	131	274	305
ENSMUSG00000026134	chr1	Prim2	3.3E+07	3.3E+07	5938	0.753913009	0.633300037	0.0278561	0.055054247	0.09378	0	12	8	14	15	33	54	39	26	33	35
ENSMUSG00000030967	chr7	Zranb1	1.3E+08	1.3E+08	5431	-0.41164713	6.643898216	0.0278568	0.055054247	0.04126	0	1668	1243	2194	1671	1883	1781	2053	1214	1748	2123
ENSMUSG00000025580	chr11	Eif4a3	1.2E+08	1.2E+08	2122	0.371387664	5.220426845	0.0278674	0.05506727	0.03255	0	464	323	620	441	640	1114	765	751	866	826
ENSMUSG00000038646	chr7	Fam103a1	8.2E+07	8.2E+07	1741	-0.46935126	3.381590102	0.0279455	0.055213906	0.04859	0	202	149	223	139	187	235	230	126	147	169
ENSMUSG00000008763	chr3	Man1a2	1E+08	1E+08	7969	-0.40254931	4.254299349	0.0279522	0.055219438	0.03724	0	302	293	323	360	320	434	360	254	329	325
ENSMUSG00000066058	chr4	Cldn19	1.2E+08	1.2E+08	4263	0.601077197	1.303808205	0.0279983	0.055302736	0.06081	0	24	23	30	31	32	84	59	38	53	62
ENSMUSG00000018442	chr11	Derl2	7.1E+07	7.1E+07	8049	0.402865321	4.319120598	0.0280207	0.055339178	0.03704	0	229	201	303	210	357	617	440	426	416	426
ENSMUSG00000097994	chr6	Gm26982	1.1E+08	1.1E+08	1151	0.666559471	1.008677133	0.028026	0.05534188	0.08078	0	15	11	25	25	37	45	44	42	58	48
ENSMUSG00000024844	chr19	Banf1	5364641	5365158	820	0.420504726	6.63651304	0.0280406	0.055347291	0.04313	0	1262	923	1511	1198	1559	2511	2028	1830	2891	2469
ENSMUSG00000027878	chr3	Notch2	9.8E+07	9.8E+07	10506	0.45937676	4.3258944	0.0280367	0.055347291	0.04853	0	231	227	192	240	357	690	435	354	416	516
ENSMUSG00000051184	chr7	Zfp524	5015501	5015560	1110	0.491483673	3.348666238	0.0280333	0.055347291	0.05368	0	122	74	156	115	179	333	166	193	294	233
ENSMUSG00000015290	chrX	Ubl4	7.4E+07	7.4E+07	3142	-0.42232137	6.429560377	0.0280715	0.055390716	0.04348	0	1462	1060	1887	1653	1385	1743	1898	1090	1563	1370
ENSMUSG00000028617	chr4	Lrrc42	1.1E+08	1.1E+08	2139	0.415720355	3.64884658	0.0280745	0.055390716	0.03774	0	154	119	190	144	201	362	250	249	323	279
ENSMUSG00000079491	chr17	H2-T10	3.6E+07	3.6E+07	3419	0.72670237	3.216904134	0.0280732	0.055390716	0.12165	0	149	49	66	99	162	392	117	145	230	323
ENSMUSG00000025155	chr11	Dus1l	1.2E+08	1.2E+08	3758	-0.35308611	4.823519891	0.0280853	0.055396537	0.02883	0	449	330	589	540	493	624	566	379	545	464
ENSMUSG00000027411	chr2	Vps16	1.3E+08	1.3E+08	3727	0.40667449	4.250009694	0.0280846	0.055396537	0.03756	0	213	183	232	240	366	592	392	334	452	473
ENSMUSG00000026027	chr1	Stradb	5.9E+07	5.9E+07	7256	-0.43457608	6.750893741	0.0281068	0.055431087	0.04619	0	1728	1178	2578	2098	1893	1926	2536	1339	1884	1831
ENSMUSG00000015247	chr4	Nipsnap3b	5.3E+07	5.3E+07	1687	0.737918895	2.188245745	0.0281227	0.055454614	0.12012	0	29	36	37	35	121	163	101	100	107	101
ENSMUSG00000033044	chr11	Dhrs7c	6.8E+07	6.8E+07	1880	-0.50279804	7.704649804	0.028168	0.055536206	0.06224	0	3666	3303	3548	4016	3435	3120	3493	2659	4965	3516
ENSMUSG00000020952	chr12	Scfd1	5.1E+07	5.1E+07	2091	-0.42564797	4.002533549	0.0282323	0.055650433	0.04123	0	305	211	295	245	316	392	310	243	237	227
ENSMUSG00000029335	chr5	Bmp3	9.9E+07	9.9E+07	3112	-1.17163807	0.609119458	0.0282363	0.055650433	0.28556	0	28	22	5	13	86	30	18	16	14	14
ENSMUSG00000042178	chr7	Armc5	1.3E+08	1.3E+08	3834	0.421128194	4.19866661	0.0282379	0.055650433	0.04064	0	183	161	273	251	328	514	372	284	579	429
ENSMUSG00000037210	chr5	Fam193a	3.4E+07	3.4E+07	7418	-0.38743455	3.830052746	0.0282535	0.055673359	0.03293	0	207	166	305	266	278	276	294	196	230	272
ENSMUSG00000037149	chr12	Ddx1	1.3E+07	1.3E+07	2507	-0.41874411	7.03458284	0.0282607	0.055679719	0.04308	0	2353	1742	2529	2252	2359	2607	2809	1716	2220	2300
ENSMUSG00000070392	chr3	Gm20634	9.6E+07	9.6E+07	2956	-0.52477538	2.07798325	0.0282725	0.055695274	0.05319	0	64	56	98	75	77	74	88	49	79	62
ENSMUSG00000074480	chr3	Mex3a	8.9E+07	8.9E+07	5778	0.9517514	-0.17969842	0.0282834	0.055708849	0.12505	0	15	5	4	8	6	22	17	21	22	20
ENSMUSG00000039345	chr16	Mettl22	8470788	8470865	2665	-0.4394571	6.319210219	0.0282876	0.055709397	0.04721	0	1404	1113	1421	1542	1344	1429	1576	985	1744	1290
ENSMUSG00000096929	chr1	A330023F24Rik	1.9E+08	1.9E+08	9354	-0.7505108	2.11636648	0.0282969	0.05571987	0.12509	0	95	66	62	69	105	92	58	39	28	118
ENSMUSG00000037035	chr1	Inhbb	1.2E+08	1.2E+08	4255	-1.03037213	1.867507498	0.0283127	0.055743193	0.23588	0	65	40	31	25	218	61	43	49	30	56
ENSMUSG00000026003	chr1	Acadl	6.7E+07	6.7E+07	2005	-0.68668148	8.706481479	0.0283493	0.055807363	0.1159	0	5378	2460	17345	9279	7315	7209	9049	4521	4562	8114
ENSMUSG00000010110	chr19	Stx5a	8741413	8741575	5808	0.395963282	4.471160572	0.0283767	0.055846861	0.03614	0	272	202	301	249	431	724	468	359	510	564
ENSMUSG00000094365	chr7	Gm21982	3.1E+07	3.1E+07	3821	0.396516651	5.390945789	0.0283773	0.055846861	0.03777	0	407	342	763	566	726	1068	913	707	1195	1048
ENSMUSG00000028885	chr4	Smpdl3b	1.3E+08	1.3E+08	2006	0.714370107	1.66519846	0.0283888	0.055861645	0.10856	0	22	12	45	31	74	120	80	53	63	81
ENSMUSG00000035234	chr5	Fam175a	1E+08	1E+08	3011	-0.52489921	2.1192893	0.0284081	0.055883801	0.05412	0	75	45	113	71	83	91	83	47	79	65
ENSMUSG00000040263	chr8	Klhdc4	1.2E+08	1.2E+08	3708	0.438993732	3.714520584	0.0284072	0.055883801	0.04323	0	108	131	248	143	220	375	290	232	327	330
ENSMUSG00000050079	chr8	Rspry1	9.5E+07	9.5E+07	6425	-0.46231787	3.297874958	0.0284301	0.055919365	0.04762	0	178	142	172	168	181	224	218	122	133	160
ENSMUSG00000024177	chr17	Nme4	2.6E+07	2.6E+07	1418	0.651212523	1.897814727	0.0284506	0.055951783	0.08484	0	50	42	36	35	42	95	73	72	130	82
ENSMUSG00000023206	chr2	Il15ra	1.2E+07	1.2E+07	4446	-0.43909486	3.58515447	0.028466	0.055974192	0.04258	0	205	132	251	158	312	277	213	165	192	204
ENSMUSG00000042303	chr15	Sgsm3	8.1E+07	8.1E+07	4358	-0.42969448	3.996900033	0.0284792	0.055992251	0.04219	0	215	196	384	308	289	269	377	182	328	253
ENSMUSG00000028693	chr4	Nasp	1.2E+08	1.2E+08	7518	0.432082043	3.56884051	0.0285053	0.056023854	0.04059	0	154	120	200	133	146	367	260	231	253	285
ENSMUSG00000030846	chr7	Tial1	1.3E+08	1.3E+08	5861	-0.37023022	5.390458205	0.0285112	0.056023854	0.03283	0	710	591	823	681	721	898	789	566	737	802
ENSMUSG00000038991	chr13	Txndc5	3.9E+07	3.9E+07	4298	0.469071514	6.261230401	0.02851	0.056023854	0.05376	0	823	870	1012	1050	1010	2645	1343	1484	2065	1690
ENSMUSG00000057522	chr11	Spop	9.5E+07	9.5E+07	3159	-0.42949625	8.080469986	0.0285046	0.056023854	0.0457	0	5149	3623	5381	4351	4755	5182	5241	3655	4817	4976
ENSMUSG00000035901	chr7	Dennd5a	1.1E+08	1.1E+08	8677	-0.40687956	5.898289512	0.0285196	0.056032566	0.04025	0	801	733	1397	1102	1161	1203	1420	707	980	1047
ENSMUSG00000021806	chr14	Nid2	2E+07	2E+07	4884	0.484724818	4.028905287	0.0285361	0.05605704	0.05414	0	208	182	188	146	284	543	317	364	381	337
ENSMUSG00000050621	chr9	Rps27rt	1.1E+08	1.1E+08	370	0.504196376	3.826950558	0.028548	0.056072599	0.0578	0	183	166	116	154	236	459	317	255	328	359
ENSMUSG00000028173	chr3	Wls	1.6E+08	1.6E+08	3304	0.402898583	5.284297226	0.0285909	0.056149013	0.03904	0	440	314	714	398	741	1119	1152	662	767	918
ENSMUSG00000027363	chr2	Usp8	1.3E+08	1.3E+08	4193	-0.35343512	4.642612375	0.0285987	0.056156451	0.02878	0	381	293	533	424	500	550	563	338	372	453
ENSMUSG00000003545	chr7	Fosb	1.9E+07	1.9E+07	3751	1.048093915	0.708087375	0.0286616	0.056272069	0.21697	0	8	12	9	10	36	22	25	24	70	67
ENSMUSG00000024219	chr17	Anks1	2.8E+07	2.8E+07	7143	-0.4957414	4.259494262	0.0286759	0.056292222	0.05766	0	244	146	644	384	356	392	342	240	313	359
ENSMUSG00000026705	chr1	Klhl20	1.6E+08	1.6E+08	12847	-0.48958571	3.259320362	0.0287268	0.056384328	0.05363	0	187	135	192	145	170	191	243	113	130	148
ENSMUSG00000031633	chr8	Slc25a4	4.6E+07	4.6E+07	2353	-0.49727838	12.04762748	0.028747	0.056415986	0.06159	0	63131	46196	127343	81558	65211	72481	97017	50297	71944	73554
ENSMUSG00000031442	chr8	Mcf2l	1.3E+07	1.3E+07	12760	-0.57864976	3.29179331	0.0287625	0.056436361	0.07571	0	114	102	330	202	162	182	142	156	116	199
ENSMUSG00000032401	chr9	Lctl	6.4E+07	6.4E+07	2604	-1.99144906	1.684654011	0.0287654	0.056436361	0.86806	0	77	22	1	2	309	57	9	32	17	13
ENSMUSG00000073702	chr1	Rpl31	3.9E+07	3.9E+07	1662	0.423931718	7.248855124	0.0287944	0.056485378	0.04445	0	1924	1517	2080	2002	2218	4524	3174	2772	3919	3675
ENSMUSG00000021708	chr13	Rasgrf2	9.2E+07	9.2E+07	8810	-0.47362267	3.066103904	0.0288181	0.05652388	0.04873	0	124	86	176	134	228	178	170	97	122	159
ENSMUSG00000038416	chr8	Cdc16	1.4E+07	1.4E+07	3103	-0.3680661	5.115138146	0.0288303	0.056539936	0.03222	0	646	410	668	617	592	782	717	488	601	546
ENSMUSG00000026307	chr1	Scly	9.1E+07	9.1E+07	4549	0.40468408	3.959879748	0.0288376	0.056546465	0.03723	0	169	122	310	193	237	420	381	226	421	394
ENSMUSG00000062006	chr3	Rpl34	1.3E+08	1.3E+08	1179	0.434311255	6.472717473	0.028856	0.056574448	0.04634	0	1145	981	1201	1087	1189	2784	1742	1724	2134	2167
ENSMUSG00000034152	chr13	Exoc3	7.4E+07	7.4E+07	4596	-0.39616734	5.766901932	0.0288798	0.056613276	0.03816	0	872	589	1346	1011	920	1132	1166	701	986	903
ENSMUSG00000018574	chr11	Acadvl	7E+07	7E+07	2686	-0.6391927	8.826611652	0.028891	0.05662741	0.1013	0	5823	2804	17940	9777	8374	7498	9487	4749	6517	8842
ENSMUSG00000042216	chr5	Sgsm1	1.1E+08	1.1E+08	7466	0.806042799	0.010193773	0.0289137	0.056663815	0.09569	0	5	4	16	9	16	33	28	13	25	19
ENSMUSG00000084347	chr11	Akt2-ps	1.7E+07	1.7E+07	1449	-0.63408134	2.014586981	0.0289271	0.056682188	0.0832	0	63	44	85	83	94	41	104	54	58	60
ENSMUSG00000031360	chrX	Ctps2	1.6E+08	1.6E+08	4720	0.588097059	3.093225287	0.0289596	0.056730704	0.07915	0	87	54	99	75	212	305	181	158	177	233
ENSMUSG00000031835	chr8	Mbtps1	1.2E+08	1.2E+08	4370	-0.35450588	5.484822722	0.0289599	0.056730704	0.0302	0	692	560	891	746	916	971	894	610	790	811

ENSMUSG00000050666	chr14	Vstm4	3.3E+07	3.3E+07	2741	0.639385947	2.816584174	0.0290312	0.056862465	0.09135	0	81	68	70	43	148	244	121	126	194	193
ENSMUSG00000037816	chr13	Fbxw17	5E+07	5E+07	3818	0.73991029	2.448657526	0.0290365	0.056864842	0.12006	0	43	73	37	60	75	206	70	95	160	166
ENSMUSG00000023031	chr15	Cela1	1E+08	1E+08	1103	1.03986468	1.19920308	0.0291379	0.057055476	0.23468	0	17	14	4	12	62	94	46	38	71	56
ENSMUSG00000063146	chr5	Clip2	1.3E+08	1.3E+08	4995	0.48384938	2.905128771	0.0291443	0.057059971	0.04991	0	87	58	103	86	138	254	174	112	174	190
ENSMUSG00000052748	chr1	Swt1	1.5E+08	1.5E+08	12865	-0.5393419	2.244030158	0.0291751	0.057112321	0.06008	0	83	66	74	95	93	110	83	57	60	86
ENSMUSG00000032875	chr7	Arhgef17	1E+08	1E+08	10250	-0.37108617	5.280110063	0.0291928	0.057131045	0.03307	0	559	491	908	578	811	721	862	486	771	675
ENSMUSG00000040725	chr7	Hnrnpul1	2.6E+07	2.6E+07	3589	-0.41540411	6.128944654	0.0291905	0.057131045	0.04246	0	1029	758	1832	1244	1311	1333	1541	807	1299	1278
ENSMUSG00000020755	chr11	Sap30bp	1.2E+08	1.2E+08	3708	0.35667772	4.321430667	0.0292114	0.057159396	0.02891	0	221	187	297	272	352	551	479	362	466	454
ENSMUSG00000097915	chr15	A330009N23Rik	1E+08	1E+08	1392	0.81764852	0.524807707	0.0293046	0.057333937	0.10548	0	14	17	13	8	18	55	24	28	31	36
ENSMUSG00000022538	chr16	Lsg1	3.1E+07	3.1E+07	5555	-0.36712574	4.122116173	0.0293125	0.057341374	0.03043	0	259	213	392	304	317	341	332	238	336	319
ENSMUSG00000032409	chr9	Atr	9.6E+07	9.6E+07	23492	-0.45969123	3.059611685	0.0293421	0.057391296	0.04572	0	153	104	193	135	138	180	175	108	122	138
ENSMUSG00000032656	chr18	March3	5.7E+07	5.7E+07	6006	-0.66530793	1.262165494	0.0293505	0.057399562	0.08485	0	37	30	36	36	78	56	38	22	36	36
ENSMUSG00000024101	chr17	Wash	6.6E+07	6.6E+07	2986	0.344566656	4.65104025	0.029459	0.057596762	0.02744	0	298	246	433	320	379	696	530	432	656	589
ENSMUSG00000098986	chr19	Gm28006	5844916	5845037	122	-0.59923204	4.876150944	0.0294595	0.057596762	0.08818	0	583	546	353	325	774	735	463	260	347	674
ENSMUSG00000063171	chr6	Rps4l	1.5E+08	1.5E+08	943	0.816656923	1.240376917	0.0294714	0.057611972	0.14133	0	33	6	27	14	47	78	49	29	64	80
ENSMUSG00000020994	chr12	Pnn	5.9E+07	5.9E+07	3469	-0.3521914	4.726118031	0.0294958	0.057651592	0.02922	0	423	376	499	401	519	558	541	344	431	538
ENSMUSG00000028550	chr4	Atg4c	9.9E+07	9.9E+07	3351	-0.4992573	3.086883844	0.0295552	0.057759624	0.05626	0	169	126	144	144	146	191	193	100	117	129
ENSMUSG00000029474	chr5	Rnf34	1.2E+08	1.2E+08	1954	-0.3746699	4.353409979	0.0295742	0.05778875	0.03267	0	359	273	436	330	327	427	441	272	344	358
ENSMUSG00000059237	chr9	Ppp1r2-ps4	6.7E+07	6.7E+07	633	-0.86760056	0.053097582	0.0295822	0.057796372	0.12257	0	17	15	32	16	13	20	19	14	11	5
ENSMUSG00000039321	chr11	Uts2r	1.2E+08	1.2E+08	1703	0.67197836	1.634451298	0.0295956	0.057814565	0.0888	0	34	24	49	36	31	147	57	54	62	66
ENSMUSG00000031792	chr8	Usb1	9.5E+07	9.5E+07	2791	0.440706291	3.223667436	0.0296118	0.057838085	0.04232	0	110	85	123	113	163	254	200	191	230	216
ENSMUSG00000051149	chr2	Adnp	1.7E+08	1.7E+08	5350	-0.35671005	5.269598549	0.0296341	0.057865543	0.03056	0	610	439	854	609	801	775	871	540	666	646
ENSMUSG00000051639	chr17	Gm5812	6121208	6122164	957	0.685009211	0.982090327	0.0296327	0.057865543	0.08678	0	14	9	27	30	30	60	46	46	43	39
ENSMUSG00000043079	chr18	Synpo	6.1E+07	6.1E+07	9533	-0.58395678	7.363825294	0.0296796	0.057946287	0.0853	0	2339	1254	5610	3901	2508	2553	3699	1716	2652	3137
ENSMUSG00000049709	chr7	Nlrp10	1.1E+08	1.1E+08	4476	0.954297955	0.64245519	0.0297322	0.058040828	0.18275	0	11	7	31	22	4	26	66	30	33	39
ENSMUSG00000011960	chr15	Ccnt1	9.9E+07	9.9E+07	9157	-0.37087225	4.303668804	0.0297707	0.058107888	0.03168	0	285	269	412	316	395	409	385	316	310	342
ENSMUSG00000060301	chr10	2610008E11Rik	7.9E+07	7.9E+07	4229	-0.39842092	4.251144083	0.0298089	0.058171278	0.03713	0	331	259	371	341	308	435	343	283	265	366
ENSMUSG00000062929	chr12	Cfl2	5.5E+07	5.5E+07	2940	-0.45837195	8.485648566	0.0298114	0.058171278	0.05294	0	6180	4483	8544	6674	5494	6882	8460	4578	5295	6202
ENSMUSG00000039298	chr4	Cdk5rap2	7E+07	7E+07	13012	-0.52986502	3.253549683	0.0298828	0.058302387	0.06464	0	166	89	232	224	145	192	222	82	162	160
ENSMUSG00000041629	chr11	Fam104a	1.1E+08	1.1E+08	2619	0.372124172	5.577211575	0.0298977	0.058323454	0.03381	0	560	457	741	608	793	1149	1121	876	1298	1094
ENSMUSG00000017307	chr2	Acot8	1.6E+08	1.6E+08	1994	0.488206074	2.795164821	0.0300189	0.058548622	0.051	0	64	68	102	86	111	187	144	113	208	175
ENSMUSG00000020009	chr10	Ifngr1	2E+07	2E+07	2847	0.462334488	5.298859575	0.0300215	0.058548622	0.05275	0	383	317	559	357	968	1213	986	729	913	886
ENSMUSG00000064090	chr11	Vrk2	2.6E+07	2.6E+07	6591	0.542108964	2.254391086	0.0300352	0.058567227	0.06051	0	64	40	68	46	69	155	93	87	141	96
ENSMUSG00000066979	chr7	Bub3	1.3E+08	1.3E+08	2055	0.366929453	5.406310373	0.030103	0.058691172	0.03278	0	488	383	609	598	738	1078	954	741	1097	1061
ENSMUSG00000022718	chr16	Dgcr8	1.8E+07	1.8E+07	7286	-0.39534112	3.824607768	0.0301173	0.058710907	0.03543	0	188	192	307	241	286	289	304	203	232	230
ENSMUSG00000026584	chr1	Scyl3	1.6E+08	1.6E+08	5802	-0.48346812	2.665837665	0.0301489	0.058764357	0.05039	0	101	93	124	120	107	115	130	67	107	126
ENSMUSG00000055835	chr8	Zfp1	1.1E+08	1.1E+08	1871	-0.43434395	3.058755248	0.0302005	0.058856715	0.04036	0	139	107	188	133	151	156	161	115	150	142
ENSMUSG00000024661	chr19	Fth1	9982703	9982983	866	0.438811753	10.61033868	0.0302075	0.058862213	0.04889	0	17560	13514	24997	18815	27152	35527	43140	24992	41556	41759
ENSMUSG00000096370	chr19	Gm21992	4742913	4744867	5780	0.412726657	3.714271304	0.0302926	0.059019846	0.03883	0	126	109	203	191	229	350	287	224	358	322
ENSMUSG00000032897	chr4	Nfyc	1.2E+08	1.2E+08	2942	-0.35893721	5.013252737	0.0303334	0.059091162	0.03098	0	458	395	670	656	561	622	585	445	651	614
ENSMUSG00000007850	chr11	Hnrnph1	5E+07	5E+07	5842	-0.40622269	6.765065925	0.0303791	0.059171984	0.04154	0	1801	1500	2180	1631	2224	2185	2349	1295	1883	2054
ENSMUSG00000041429	chr17	Nthl1	2.5E+07	2.5E+07	1080	0.627745064	1.503748579	0.030385	0.059175163	0.07255	0	27	32	40	26	34	84	61	37	85	78
ENSMUSG00000036560	chr7	Lgi4	3.1E+07	3.1E+07	4584	0.536330665	3.005812101	0.0303993	0.059194818	0.06407	0	83	99	104	64	131	293	182	128	181	200
ENSMUSG00000027014	chr2	Cwc22	7.8E+07	7.8E+07	6822	-0.44274599	3.455010095	0.0304402	0.059266317	0.04404	0	209	140	257	147	197	248	199	157	184	167
ENSMUSG00000029095	chr5	Ablim2	3.6E+07	3.6E+07	7047	0.400868091	5.979696643	0.0304645	0.059305289	0.04005	0	844	531	1137	803	833	1592	1557	1282	1592	1334
ENSMUSG00000072568	chr15	Fam84b	6.1E+07	6.1E+07	5926	-0.52977553	2.583491405	0.0305132	0.05939188	0.05974	0	107	67	167	72	127	118	111	88	80	101
ENSMUSG00000025857	chr5	Heatr2	1.4E+08	1.4E+08	3514	-0.39411049	4.056357406	0.0305738	0.059501671	0.03606	0	250	193	358	324	306	334	388	217	298	250
ENSMUSG00000029547	chr5	Ints1	1.4E+08	1.4E+08	7113	-0.43344458	5.431197939	0.0306042	0.059552489	0.04653	0	609	467	963	980	765	643	906	523	941	778
ENSMUSG00000004032	chr3	Gstm5	1.1E+08	1.1E+08	1278	-0.38802285	5.791460525	0.0306137	0.05956275	0.03748	0	974	767	987	890	1067	1059	990	710	1113	1097
ENSMUSG00000058258	chr13	Idi1	8885501	8885996	3505	-0.70730255	1.856787321	0.0306226	0.059571768	0.11077	0	54	66	65	43	101	82	92	36	34	40
ENSMUSG00000033487	chr14	Fndc3a	7.3E+07	7.3E+07	9944	-0.4709439	3.394999969	0.030644	0.059596889	0.05135	0	181	135	211	171	220	217	282	114	143	163
ENSMUSG00000042423	chr7	Fbrs	1.3E+08	1.3E+08	2650	0.400164453	4.59451971	0.0306403	0.059596889	0.03851	0	222	213	392	303	473	648	497	370	638	701
ENSMUSG00000030264	chr6	Thumpd3	1.1E+08	1.1E+08	3888	-0.40301887	4.179078563	0.0306598	0.059619439	0.03841	0	312	277	365	282	288	416	336	265	295	295
ENSMUSG00000026828	chr2	Galnt5	5.8E+07	5.8E+07	4462	1.031172093	0.119326134	0.0307375	0.059762186	0.19642	0	9	3	17	17	2	32	45	23	16	17
ENSMUSG00000022521	chr16	Crebbp	4081328	4086198	12920	-0.33712701	4.758440816	0.0307428	0.059764211	0.02687	0	414	327	549	468	529	520	495	386	502	558
ENSMUSG00000022760	chr16	Thap7	1.8E+07	1.8E+07	1880	0.43605727	3.667761812	0.030768	0.059804921	0.04372	0	150	107	164	146	253	340	318	188	371	296
ENSMUSG00000027371	chr2	Fahd2a	1.3E+08	1.3E+08	1463	-0.34994875	4.846131792	0.0307976	0.05985402	0.0292	0	425	291	692	500	578	587	582	370	577	507
ENSMUSG00000064357	chrMT	mt-Atp6	7927	8607	681	-0.81600799	4.636056846	0.0308057	0.059861565	0.16553	0	374	211	432	816	602	198	845	116	457	293
ENSMUSG00000027466	chr2	Rbck1	1.5E+08	1.5E+08	4601	0.379794913	5.627721465	0.0308143	0.059870059	0.0358	0	545	400	844	674	849	1318	1107	768	1317	1308
ENSMUSG00000037058	chr18	Paip2	3.6E+07	3.6E+07	2789	-0.41982749	6.916398976	0.030822	0.059876655	0.04466	0	2347	1529	2389	2055	2041	2489	2576	1594	1975	2103
ENSMUSG00000022721	chr16	Trmt2a	1.8E+07	1.8E+07	4952	0.413784591	3.854624351	0.0308618	0.059945602	0.03963	0	152	137	213	155	286	402	297	259	355	385
ENSMUSG00000087269	chr2	D330023K18Rik	3.1E+07	3.1E+07	1249	0.684016629	1.398414271	0.0308727	0.059958468	0.09231	0	22	23	36	22	44	58	55	32	86	92
ENSMUSG00000022000	chr14	Zc3h13	7.5E+07	7.5E+07	6151	-0.40610488	4.218602362	0.0308849	0.059973916	0.03904	0	264	208	510	339	306	389	419	219	303	338
ENSMUSG00000029621	chr5	Arpc1a	1.5E+08	1.5E+08	2567	0.372328359	5.32764075	0.0308976	0.059990347	0.03415	0	453	339	661	458	791	1194	917	674	993	932
ENSMUSG00000050234	chr4	Gja4	1.3E+08	1.3E+08	1685	0.577080975	2.58861156	0.0309059	0.059998044	0.07521	0	45	48	124	54	99	162	113	126	190	132
ENSMUSG00000038888	chr7	Ctu1	4.4E+07	4.4E+07	2475	0.549110567	1.892890804	0.0309304	0.060037307	0.05901	0	46	30	37	46	61	106	82	70	86	97
ENSMUSG00000036199	chr8	Ndufa13	7E+07	7E+07	1243	0.432238936	8.767466492	0.0309363	0.060040548	0.04776	0	5501	3580	7414	6048	5782	10532	10264	8236	12120	10371

ENSMUSG00000030347	chr6	D6Wsu163e	1.3E+08	1.3E+08	2238	-0.47053259	2.925960156	0.0309563	0.060071045	0.04889	0	147	98	148	118	146	179	152	101	107	117
ENSMUSG00000068115	chr2	Ninl	1.5E+08	1.5E+08	5952	0.767144967	0.439339566	0.0310239	0.06019384	0.09568	0	6	14	17	10	22	45	39	22	27	29
ENSMUSG00000071632	chr16	2510002D24Rik	1.9E+07	1.9E+07	1486	-0.37442262	3.987085185	0.0310815	0.060297322	0.03232	0	267	193	371	251	271	328	291	203	288	318
ENSMUSG00000022403	chr15	St13	8.1E+07	8.1E+07	3457	-0.41317698	6.438101501	0.0311202	0.060364049	0.04317	0	1306	902	2327	1465	1680	1912	1823	1096	1426	1502
ENSMUSG00000051586	chr6	Mical3	1.2E+08	1.2E+08	7398	-0.34469875	4.868295234	0.0311345	0.060383415	0.0285	0	422	339	677	536	514	585	552	397	551	574
ENSMUSG00000032554	chr9	Trf	1E+08	1E+08	3320	1.083167529	6.592154988	0.0311878	0.060478289	0.29165	0	965	932	150	228	2326	3327	1536	2522	3199	2783
ENSMUSG00000000253	chr13	Gmpr	4.6E+07	4.6E+07	1871	-0.45805699	7.573006348	0.0312038	0.060501028	0.05359	0	3035	2075	4767	3833	3178	2900	3936	2388	4020	3323
ENSMUSG00000067344	chr6	Rps25-ps1	1.5E+08	1.5E+08	378	0.707833628	1.83848994	0.0312557	0.060593251	0.10804	0	28	32	23	57	55	74	79	55	118	117
ENSMUSG00000092252	chr5	Gm20499	1.1E+08	1.1E+08	444	0.773854405	0.897913969	0.0312714	0.060615374	0.11589	0	17	13	11	14	43	65	42	38	40	42
ENSMUSG00000039148	chr19	Sart1	5377523	5380135	5091	0.350087815	5.126395225	0.03133	0.060720558	0.03004	0	392	278	630	484	584	930	763	610	875	866
ENSMUSG00000020659	chr12	Cbll1	3.1E+07	3.1E+07	4007	-0.41300041	3.336301912	0.0314214	0.060880867	0.03792	0	172	121	217	165	194	182	218	137	170	181
ENSMUSG00000036503	chr3	Rnf13	5.8E+07	5.8E+07	2676	-0.43326764	5.187928293	0.031418	0.060880867	0.04696	0	714	551	692	570	558	786	929	420	538	576
ENSMUSG00000028149	chr3	Rap1gds1	1.4E+08	1.4E+08	3663	-0.42536927	6.332792142	0.0314361	0.060900879	0.04594	0	1219	1044	1795	1495	1436	1296	1956	968	1433	1490
ENSMUSG00000030766	chr7	Arhgap17	1.2E+08	1.2E+08	3583	0.351011111	4.501551029	0.0314792	0.060976041	0.02908	0	267	209	326	309	397	610	509	374	584	549
ENSMUSG00000027931	chr3	Npr1	9E+07	9E+07	4783	0.473817763	4.430267996	0.0314888	0.060986269	0.05522	0	211	172	309	191	521	759	473	346	538	503
ENSMUSG00000024400	chr18	Wdr33	3.2E+07	3.2E+07	6413	-0.33267857	5.072258895	0.0315037	0.06100652	0.02692	0	511	403	740	579	614	753	716	416	610	611
ENSMUSG00000019810	chr10	Fuca2	1.3E+07	1.3E+07	6161	-0.34848821	5.167923298	0.0315376	0.0610554	0.02982	0	570	441	781	625	628	721	813	447	675	633
ENSMUSG00000082896	chr3	Gm5844	1.8E+07	1.8E+07	2191	0.918923292	-0.16023516	0.0315356	0.0610554	0.13316	0	4	6	16	4	11	30	33	11	20	12
ENSMUSG00000011837	chr8	Snapc2	4253102	4253304	1513	0.368007018	4.177765327	0.0315701	0.061109926	0.03173	0	206	157	293	259	285	461	398	331	485	416
ENSMUSG00000022801	chr16	Lrch3	3.3E+07	3.3E+07	6610	-0.36255185	4.363503251	0.0315938	0.061140668	0.0312	0	289	293	403	325	428	438	396	285	326	415
ENSMUSG00000026667	chr1	Uhmk1	1.7E+08	1.7E+08	8101	-0.36678288	5.172449311	0.0315947	0.061140668	0.03322	0	538	455	677	555	862	726	837	420	691	613
ENSMUSG00000027245	chr2	Hypk	1.2E+08	1.2E+08	5278	0.410697322	6.400489611	0.0316173	0.061175881	0.04292	0	1015	685	1312	1201	1335	2248	1632	1639	2147	2247
ENSMUSG00000055923	chr5	Aasdh	7.7E+07	7.7E+07	6287	-0.44684701	3.225242489	0.0316753	0.061279769	0.04543	0	177	133	167	161	156	171	196	118	162	166
ENSMUSG00000038507	chr6	Parp12	3.9E+07	3.9E+07	3995	0.475396365	3.708577348	0.0316883	0.061296339	0.0541	0	150	80	223	148	249	501	312	177	286	325
ENSMUSG00000020676	chr11	Ccl11	8.2E+07	8.2E+07	1082	0.517388448	4.324465119	0.0317004	0.06131127	0.06576	0	222	201	201	202	411	708	384	449	317	560
ENSMUSG00000089872	chr1	Rps6kc1	1.9E+08	1.9E+08	9741	-0.40105681	4.967779402	0.0317464	0.061391906	0.03987	0	643	448	579	476	481	610	686	434	559	494
ENSMUSG00000031732	chr8	Phlpp2	1.1E+08	1.1E+08	8449	-0.51297541	2.473808828	0.0317928	0.061473103	0.05806	0	111	77	97	85	111	123	124	63	80	82
ENSMUSG00000031824	chr8	6430548M08Rik	1.2E+08	1.2E+08	6626	0.475221615	4.790357155	0.031807	0.061491999	0.05625	0	197	212	516	521	333	823	773	423	610	735
ENSMUSG00000000976	chr11	Heatr6	8.4E+07	8.4E+07	6419	-0.4036925	3.533773692	0.0318332	0.061534224	0.03712	0	171	142	234	223	223	229	258	136	197	213
ENSMUSG00000033849	chr1	B3galt2	1.4E+08	1.4E+08	9288	-0.79536533	3.043877105	0.0318612	0.061579969	0.15422	0	219	85	72	70	352	160	117	99	104	139
ENSMUSG00000041718	chrX	Alg13	1.4E+08	1.4E+08	5964	-0.51691787	2.005796691	0.0318806	0.061608897	0.05499	0	67	53	76	65	89	71	76	38	71	82
ENSMUSG00000033760	chr19	Rbm4b	4756543	4756661	9886	0.50512865	2.426107462	0.0319069	0.061651251	0.0537	0	60	45	68	56	103	142	115	101	134	144
ENSMUSG00000062542	chr7	Syt9	1.1E+08	1.1E+08	3979	-0.95060908	-0.02152413	0.0319399	0.06170645	0.15486	0	11	6	39	14	24	21	18	10	8	6
ENSMUSG00000040146	chr9	Rgl3	2.2E+07	2.2E+07	2550	0.705332068	1.672689825	0.0319602	0.061737173	0.1107	0	20	15	69	22	61	103	99	46	69	82
ENSMUSG00000009739	chr15	Pou6f1	1E+08	1E+08	6987	-0.3564318	4.439062605	0.0319746	0.06175654	0.03024	0	332	235	515	359	426	435	479	256	400	410
ENSMUSG00000056429	chr6	Tgoln1	7.3E+07	7.3E+07	5013	-0.40926584	6.213526268	0.0319799	0.061758254	0.04272	0	1297	940	1330	1086	1758	1723	1568	931	1199	1242
ENSMUSG00000033970	chr5	Rfc3	1.5E+08	1.5E+08	3611	0.575150969	2.102092358	0.0319844	0.061758493	0.07082	0	41	35	75	35	73	132	76	75	133	102
ENSMUSG00000025507	chr7	Pidd1	1.4E+08	1.4E+08	4528	0.881608883	0.16142951	0.0320195	0.061817754	0.1441	0	3	3	12	13	24	36	20	17	30	31
ENSMUSG00000001444	chr11	Tbx21	9.7E+07	9.7E+07	2488	0.89553552	0.018838474	0.0320708	0.061908227	0.12775	0	14	8	9	6	9	25	11	18	28	37
ENSMUSG00000049624	chr9	Slc17a5	7.9E+07	7.9E+07	3356	0.503907531	2.681551617	0.0320997	0.061955402	0.0562	0	86	45	71	75	121	189	173	115	158	132
ENSMUSG00000052794	chr8	1700030K09Rik	7.2E+07	7.2E+07	2970	-0.53322697	2.132625366	0.032139	0.062022764	0.06015	0	64	65	89	69	97	91	101	43	74	60
ENSMUSG00000038425	chr18	Poli	7.1E+07	7.1E+07	3863	0.68453475	1.148605265	0.0321681	0.062070333	0.09221	0	22	14	26	17	45	82	38	43	47	58
ENSMUSG00000020067	chr10	Mypn	6.3E+07	6.3E+07	5246	-0.44682011	8.266165584	0.0321848	0.062089281	0.05172	0	4921	3838	7138	6271	4670	5226	6569	3971	5835	5359
ENSMUSG00000029775	chr6	Klhdc10	3E+07	3E+07	8443	-0.38385742	5.873071474	0.0321867	0.062089281	0.03735	0	842	697	1358	1063	1106	1064	1353	741	1039	1081
ENSMUSG00000063524	chr4	Eno1	1.5E+08	1.5E+08	5379	0.604694195	6.691771739	0.0322375	0.062178629	0.09413	0	1176	565	1069	884	2800	2696	2133	2094	3247	2629
ENSMUSG00000023505	chr6	Cdca3	1.2E+08	1.2E+08	2866	0.747774017	0.540219178	0.0322549	0.062203578	0.08888	0	13	13	23	11	15	48	22	25	44	34
ENSMUSG00000021501	chr13	Caml	5.6E+07	5.6E+07	1755	0.441818345	3.137575351	0.0322909	0.062253138	0.04321	0	103	82	133	98	144	289	193	170	196	189
ENSMUSG00000024176	chr17	Sox8	2.6E+07	2.6E+07	3118	0.786631354	0.179315562	0.0322953	0.062253138	0.09358	0	11	7	16	12	10	47	18	17	27	25
ENSMUSG00000081406	chr2	Rps6-ps4	7.5E+07	7.5E+07	750	0.406184967	4.386617827	0.0322983	0.062253138	0.03981	0	270	209	289	270	305	678	401	438	390	538
ENSMUSG00000102101	chr16	2310061J03Rik	5.6E+07	5.6E+07	1350	0.709270179	1.80290134	0.0322962	0.062253138	0.11562	0	24	12	62	36	71	93	61	63	88	126
ENSMUSG00000038295	chr5	Atg9b	2.4E+07	2.4E+07	3946	0.934220381	-0.36101167	0.0323357	0.062316612	0.1326	0	4	4	10	2	15	22	16	19	12	19
ENSMUSG00000020812	chr11	1810032O08Rik	1.2E+08	1.2E+08	2776	0.728665561	1.261946225	0.0323466	0.06232915	0.1059	0	29	24	32	13	30	79	31	50	61	71
ENSMUSG00000029710	chr5	Ephb4	1.4E+08	1.4E+08	4640	0.436274057	4.557966291	0.0323619	0.062350071	0.04759	0	210	146	496	298	431	715	489	472	578	529
ENSMUSG00000045282	chr7	Tmem86b	4628042	4628753	1220	0.839081679	0.313887639	0.0323731	0.062363024	0.12001	0	10	7	19	13	12	45	34	8	24	42
ENSMUSG00000035242	chr10	Oaz1	8.1E+07	8.1E+07	2558	0.431576929	8.351709816	0.0323966	0.062399744	0.04838	0	4048	2978	4407	3719	6037	8276	7390	5815	9202	8102
ENSMUSG00000056947	chr3	Mab21l1	5.6E+07	5.6E+07	2776	-0.79484177	0.765630402	0.0324347	0.062464577	0.12597	0	31	36	18	21	44	37	29	13	28	18
ENSMUSG00000039634	chr4	Zfp189	5E+07	5E+07	3006	-0.59072337	1.772248579	0.03246	0.062504734	0.07234	0	63	51	90	42	56	69	62	49	41	53
ENSMUSG00000047804	chr11	Akap10	6.2E+07	6.2E+07	6451	-0.44673429	3.333782741	0.0324822	0.062538906	0.0465	0	173	123	213	193	169	214	238	111	141	184
ENSMUSG00000036452	chr18	Arhgap26	3.9E+07	3.9E+07	17331	-0.59813582	2.787902644	0.0325123	0.062588125	0.08422	0	127	116	75	103	186	116	157	82	95	114
ENSMUSG00000025967	chr1	Eef1b2	6.3E+07	6.3E+07	2532	0.432164774	7.731178849	0.0325509	0.062653968	0.04847	0	2786	2134	3025	2729	2864	6434	4151	4309	4791	5472
ENSMUSG00000074604	chr3	Mgst2	5.2E+07	5.2E+07	3703	1.390442505	0.454296524	0.0325694	0.062680897	0.41581	0	9	9	0	1	33	43	15	36	36	52
ENSMUSG00000020832	chr11	Eral1	7.8E+07	7.8E+07	2268	-0.34482904	4.695290648	0.0325767	0.062686287	0.02878	0	375	283	575	472	512	525	580	330	496	438
ENSMUSG00000020312	chr10	Shc2	8E+07	8E+07	5537	0.593075059	2.997577667	0.0326417	0.062802783	0.08312	0	82	77	85	52	183	245	191	175	157	205
ENSMUSG00000052371	chr2	Hoxd3os1	7.5E+07	7.5E+07	2872	0.777479454	1.040597676	0.0326825	0.062872728	0.11986	0	21	23	23	17	21	28	42	51	74	50
ENSMUSG00000002948	chr8	Map2k7	4238740	4239033	5359	-0.41500595	6.552997448	0.0327022	0.06290203	0.04447	0	1405	1156	2156	1777	1659	1627	1891	1069	1987	1801
ENSMUSG00000067242	chr19	Lgi1	3.8E+07	3.8E+07	7833	-1.61974647	1.060816689	0.0327287	0.062944306	0.60801	0	17	1	145	81	6	9	20	12	10	49
ENSMUSG00000020549	chr11	Elac2	6.5E+07	6.5E+07	3479	-0.33682358	4.803401807	0.0327339	0.062945666	0.02753	0	440	315	598	494	522	527	579	399	536	499

ENSMUSG00000063052	chr3	Lrrc40	1.6E+08	1.6E+08	4575	-0.42876348	3.145822153	0.0327762	0.063018294	0.04115	0	145	98	188	145	195	195	179	95	168	147
ENSMUSG00000058756	chr11	Thra	9.9E+07	9.9E+07	4614	-0.39663366	6.41987323	0.0327807	0.063018402	0.04057	0	1334	1054	1687	1471	1846	1638	1683	986	1849	1549
ENSMUSG00000010086	chr11	Rnf112	6.1E+07	6.1E+07	3923	1.100409127	-0.14914465	0.0328559	0.063147797	0.19147	0	12	11	3	2	7	34	22	23	12	18
ENSMUSG00000074748	chr10	Atxn7l3b	1.1E+08	1.1E+08	3572	0.414562468	4.881895946	0.032857	0.063147797	0.04297	0	362	276	347	296	640	883	653	574	703	656
ENSMUSG00000085095	chr7	Gm15635	1E+08	1E+08	1056	-0.67963676	2.169133989	0.032883	0.063189127	0.10852	0	103	78	54	73	88	76	57	31	103	91
ENSMUSG00000024498	chr18	Tcerg1	4.3E+07	4.3E+07	4246	-0.36370344	4.76131252	0.0328976	0.063208392	0.03259	0	417	372	586	458	455	594	542	403	382	525
ENSMUSG00000044548	chr12	Dact1	7.1E+07	7.1E+07	3761	0.666449212	2.895290825	0.0329272	0.06325671	0.108	0	56	41	92	57	206	234	149	169	203	165
ENSMUSG00000028970	chr5	Abcb1b	8798147	8798289	4344	-0.49565656	2.964850567	0.0329401	0.063272686	0.05715	0	168	91	178	123	123	182	160	78	113	143
ENSMUSG00000008153	chr6	Clstn3	1.2E+08	1.2E+08	4968	-1.45592404	2.543511438	0.0329743	0.063329718	0.51391	0	142	27	13	20	489	93	29	38	101	60
ENSMUSG00000020928	chr11	Higd1b	1E+08	1E+08	847	0.694173808	1.544087717	0.0330249	0.063409712	0.10673	0	22	11	61	42	32	100	49	51	76	83
ENSMUSG00000028234	chr4	Rps20	3831334	3834683	4080	0.420456704	7.733110627	0.0330239	0.063409712	0.04614	0	2632	2072	3138	2661	3237	6501	4058	3997	5359	5300
ENSMUSG00000039934	chr5	Gsap	2.1E+07	2.1E+07	3745	0.629953032	1.917313064	0.0331048	0.063554367	0.08566	0	36	34	62	31	56	139	93	50	58	130
ENSMUSG00000024807	chr19	Syvn1	6046576	6047128	4772	0.365270335	5.231067676	0.0331253	0.063584893	0.03361	0	395	303	575	562	688	970	862	618	1002	928
ENSMUSG00000023262	chr9	Acy1	1.1E+08	1.1E+08	2966	0.495290026	3.129955235	0.0331349	0.063594723	0.05753	0	93	67	154	133	101	204	170	182	206	271
ENSMUSG00000021240	chr12	Abcd4	8.5E+07	8.5E+07	2527	0.433304279	3.52024463	0.033241	0.063782287	0.04383	0	108	115	170	137	206	333	223	225	260	305
ENSMUSG00000074899	chr2	Sptbn5	1.2E+08	1.2E+08	10292	-0.79146079	0.294077269	0.0332417	0.063782287	0.11084	0	21	19	18	13	38	20	24	10	11	22
ENSMUSG00000024500	chr18	Ppp2r2b	4.3E+07	4.3E+07	3985	0.974353312	-0.45813379	0.0332793	0.063845707	0.10827	0	8	6	4	5	7	22	14	7	20	21
ENSMUSG00000019066	chr9	Rab3d	2.2E+07	2.2E+07	4196	0.656868626	4.218448298	0.0332959	0.063859957	0.10956	0	160	149	146	119	547	658	374	353	500	471
ENSMUSG00000040025	chr4	Ythdf2	1.3E+08	1.3E+08	4572	-0.3568429	4.435239296	0.0332921	0.063859957	0.03071	0	333	254	455	407	388	429	448	332	382	354
ENSMUSG00000040543	chr11	Pitpnm3	7.2E+07	7.2E+07	9815	-0.65636717	1.289625435	0.0333062	0.063870956	0.08606	0	36	26	52	60	46	37	40	17	42	56
ENSMUSG00000042271	chrX	Nxt2	1.4E+08	1.4E+08	3176	-0.63970205	1.668790802	0.0333207	0.06389002	0.08823	0	73	49	45	44	68	70	54	46	33	47
ENSMUSG00000032846	chr13	Zswim6	1.1E+08	1.1E+08	5456	0.571704489	1.267006391	0.0333401	0.063918567	0.05954	0	23	19	32	28	38	62	58	52	50	58
ENSMUSG00000026409	chr1	Pfkfb2	1.3E+08	1.3E+08	7254	-0.5195217	3.202711667	0.0333595	0.063947094	0.06457	0	138	100	290	172	131	195	208	88	134	166
ENSMUSG00000003131	chr9	Pafah1b2	4.6E+07	4.6E+07	4241	0.363757824	4.687164291	0.0334265	0.064066687	0.03254	0	271	264	375	299	500	709	560	475	581	660
ENSMUSG00000023805	chr17	Synj2	5941280	5941577	8342	-0.51255497	4.92976536	0.0334587	0.064119596	0.06699	0	484	226	985	666	451	558	598	385	378	682
ENSMUSG00000046711	chr17	Hmga1	2.8E+07	2.8E+07	1990	-0.51933322	2.934451199	0.033529	0.064245662	0.06315	0	124	111	201	132	102	133	184	79	125	129
ENSMUSG00000009076	chr11	Zmat5	4704678	4704721	1248	0.363153207	4.367673677	0.0335373	0.064252712	0.03155	0	270	216	291	266	303	513	473	339	559	511
ENSMUSG00000066894	chr5	Vsig10	1.2E+08	1.2E+08	5122	0.513011406	2.978078229	0.0335756	0.06431738	0.06129	0	98	59	133	66	139	243	183	123	149	258
ENSMUSG00000026675	chr1	Hsd17b7	1.7E+08	1.7E+08	5104	-0.63417193	2.902824505	0.0335865	0.064329454	0.09821	0	156	147	112	91	147	130	203	76	80	120
ENSMUSG00000024666	chr19	Tmem138	1.1E+07	1.1E+07	1590	0.725167927	1.146223396	0.033597	0.064340737	0.10616	0	19	21	21	15	43	69	36	31	68	68
ENSMUSG00000025737	chr17	Wdr24	2.6E+07	2.6E+07	3432	-0.43323338	3.981817149	0.0336881	0.064497633	0.04609	0	270	224	333	296	222	263	334	188	346	256
ENSMUSG00000079884	chr9	Gm10698	3.4E+07	3.4E+07	604	-0.64159058	2.04140713	0.0336859	0.064497633	0.09395	0	54	59	99	69	94	86	118	28	49	55
ENSMUSG00000002658	chr17	Gtf2f1	5.7E+07	5.7E+07	1717	0.33404664	4.776689779	0.033696	0.064503844	0.02737	0	311	260	473	375	423	743	633	492	693	590
ENSMUSG00000028850	chr4	Gpatch3	1.3E+08	1.3E+08	2086	0.52378024	2.301747295	0.0338529	0.064795426	0.05921	0	41	42	77	54	90	134	95	88	127	143
ENSMUSG00000020926	chr11	Adam11	1E+08	1E+08	5669	1.002319596	0.223555186	0.0338892	0.064856044	0.19264	0	5	9	6	7	26	31	11	29	28	42
ENSMUSG00000037089	chr17	Slc35b2	4.6E+07	4.6E+07	2326	0.368377484	4.747099224	0.0339044	0.064860272	0.0335	0	378	282	334	327	422	677	627	521	681	592
ENSMUSG00000042156	chr14	Dzip1	1.2E+08	1.2E+08	4744	0.651797371	1.87074618	0.0339046	0.064860272	0.09095	0	34	41	29	35	65	143	86	63	64	97
ENSMUSG00000051124	chr6	Gimap9	4.9E+07	4.9E+07	1642	0.666325172	1.150138763	0.0339053	0.064860272	0.08433	0	22	19	29	26	26	73	31	53	48	58
ENSMUSG00000020646	chr12	Mboat2	2.5E+07	2.5E+07	2802	0.843025296	-0.05958751	0.0339558	0.064939259	0.11059	0	6	3	17	14	6	31	19	14	25	23
ENSMUSG00000038587	chr10	Akap12	4266329	4266668	6244	-0.38914781	4.454783174	0.0339517	0.064939259	0.03744	0	264	271	395	395	572	485	390	295	360	436
ENSMUSG00000004535	chr6	Tax1bp1	5.3E+07	5.3E+07	6609	-0.40069018	6.46772574	0.0340155	0.065031083	0.04202	0	1554	1100	1856	1493	1602	1911	1992	1217	1363	1440
ENSMUSG00000027102	chr2	Hoxd8	7.5E+07	7.5E+07	2744	0.507327887	4.587789876	0.0340178	0.065031083	0.06533	0	204	277	343	334	315	375	668	487	841	484
ENSMUSG00000027412	chr2	Lpin3	1.6E+08	1.6E+08	3694	0.599631708	2.136966895	0.0340176	0.065031083	0.08108	0	36	35	61	35	97	128	144	60	96	114
ENSMUSG00000025224	chr19	Gbf1	4.6E+07	4.6E+07	9062	-0.39253631	6.123617886	0.0340361	0.06505737	0.04013	0	1066	835	1503	1392	1199	1324	1357	876	1408	1291
ENSMUSG00000015478	chr17	Rnf5	3.5E+07	3.5E+07	1483	0.353068162	4.80453481	0.0340982	0.065167019	0.0312	0	348	220	477	366	474	694	591	488	784	670
ENSMUSG00000096433	chr17	Gm4944	2.2E+07	2.2E+07	4880	-0.59428944	1.747360442	0.0341214	0.065202624	0.07701	0	50	62	54	58	66	67	75	39	39	52
ENSMUSG00000046387	chr18	Pcdhb17	3.7E+07	3.7E+07	4660	0.597743068	1.195369423	0.0341534	0.065254813	0.0663	0	23	18	33	20	38	51	70	43	49	56
ENSMUSG00000026839	chr2	Upp2	5.9E+07	5.9E+07	7053	0.682006809	0.759807033	0.0341938	0.065323162	0.07719	0	21	15	13	15	26	47	40	30	46	37
ENSMUSG00000079435	chrX	Rpl36a	1.3E+08	1.3E+08	1655	0.420200231	6.363473557	0.0342568	0.065434622	0.04621	0	1054	858	1052	1035	1259	2492	1521	1632	2029	2037
ENSMUSG00000062081	chr14	Gm6055	4.8E+07	4.8E+07	378	-0.53299625	1.998368651	0.0342894	0.065487809	0.05971	0	70	59	94	61	63	67	86	48	64	66
ENSMUSG00000031154	chrX	Otud5	7841364	7841400	5200	0.339895499	4.535691227	0.0343159	0.065524889	0.02799	0	278	246	381	274	362	688	510	399	525	560
ENSMUSG00000040928	chr4	S100pbp	1.3E+08	1.3E+08	9448	0.45684603	2.963279222	0.0343181	0.065524889	0.04685	0	90	77	109	78	137	241	173	144	167	197
ENSMUSG00000021103	chr12	Mnat1	7.3E+07	7.3E+07	5385	-0.36926845	3.862642816	0.0343332	0.065544723	0.03228	0	231	193	270	243	290	313	268	218	253	250
ENSMUSG00000024045	chr17	Akap8	3.2E+07	3.2E+07	3695	-0.35330901	5.142453907	0.0344398	0.065735163	0.0318	0	547	476	742	539	683	863	662	448	526	740
ENSMUSG00000040855	chrX	Reps2	1.6E+08	1.6E+08	8296	0.688875854	2.203714723	0.0344423	0.065735163	0.1087	0	57	49	38	26	85	196	106	61	118	107
ENSMUSG00000061371	chr10	Zfp873	8.2E+07	8.2E+07	1893	-0.65210693	0.883252413	0.0344574	0.065755002	0.07602	0	31	28	38	23	42	29	28	29	31	22
ENSMUSG00000028444	chr4	Cntfr	4.2E+07	4.2E+07	2782	-0.55447589	3.866627286	0.0344792	0.065787685	0.07774	0	273	258	200	215	317	175	209	176	379	266
ENSMUSG00000090639	chr9	Gm20425	1E+08	1E+08	3028	0.797468034	6.702338284	0.0345209	0.06585822	0.16671	0	1188	1089	426	485	2474	3361	1722	2532	3160	2721
ENSMUSG00000049299	chr11	Trappc1	6.9E+07	6.9E+07	1112	0.34882709	5.316971387	0.0345697	0.065942334	0.031	0	526	368	612	541	603	1085	820	736	940	1020
ENSMUSG00000069135	chr17	Fgfr1op	8165501	8165698	4008	-0.39664578	4.444604802	0.0346191	0.066027689	0.03932	0	280	299	558	372	365	396	487	300	326	428
ENSMUSG00000030990	chr7	Pgap2	1E+08	1E+08	4531	0.395205168	3.799777161	0.0346456	0.066069284	0.03778	0	157	104	251	163	253	366	344	210	357	362
ENSMUSG00000098579	chr12	Mir6937	2.9E+07	2.9E+07	65	-0.75845222	0.573145603	0.0346546	0.066077443	0.10759	0	31	16	32	17	39	15	38	16	17	21
ENSMUSG00000071723	chrX	Gspt2	9.5E+07	9.5E+07	3781	0.977148651	0.17775433	0.034682	0.066120621	0.17503	0	3	13	7	9	18	47	14	21	19	38
ENSMUSG00000030244	chr6	Gys2	1.4E+08	1.4E+08	2657	-1.54168021	1.253440618	0.0347233	0.066190351	0.5634	0	63	16	4	4	189	31	28	10	38	17
ENSMUSG00000042148	chr11	Cox10	6.4E+07	6.4E+07	3037	-0.51283107	5.742957761	0.0347377	0.06620888	0.06903	0	664	468	1731	1271	802	865	1192	627	965	929
ENSMUSG00000035235	chr14	Trim13	6.2E+07	6.2E+07	1699	-0.45169264	3.207298989	0.0347723	0.066265739	0.04805	0	154	136	199	158	142	202	143	143	143	164
ENSMUSG00000029321	chr5	Slc10a6	1E+08	1E+08	2124	0.761401977	0.760259196	0.0348512	0.066407159	0.11209	0	7	13	20	15	35	41	29	35	46	51

ENSMUSG00000004085	chr2	Zak	7.2E+07	7.2E+07	10175	-0.46508214	8.323926157	0.0348793	0.066451575	0.05777	0	5731	4278	7304	6312	4160	5802	7143	4248	4996	5696
ENSMUSG00000035967	chrX	Ddx26b	5.6E+07	5.6E+07	7173	-0.51220219	3.352138273	0.03495	0.066577312	0.06477	0	186	175	179	187	142	268	175	111	132	195
ENSMUSG00000027879	chr3	Sec22b	9.8E+07	9.8E+07	3709	0.377095968	5.30564668	0.0350579	0.066773761	0.03663	0	512	393	540	455	694	1213	761	773	915	942
ENSMUSG00000023968	chr17	Crip3	4.6E+07	4.6E+07	1520	0.981674982	1.062009323	0.0351396	0.066920242	0.22335	0	14	7	25	7	53	36	91	36	27	78
ENSMUSG00000016624	chr15	Phf21b	8.5E+07	8.5E+07	4264	0.936791201	-0.31705981	0.0351603	0.066950649	0.1272	0	5	6	10	6	8	26	11	6	27	24
ENSMUSG00000020064	chr10	Herc4	6.3E+07	6.3E+07	4019	-0.38023082	4.525641607	0.0351742	0.066967963	0.03642	0	426	324	456	345	385	507	486	352	351	363
ENSMUSG00000021062	chr12	Rab15	7.7E+07	7.7E+07	4614	1.100705053	3.095096789	0.0351883	0.066979708	0.30906	0	38	12	174	186	16	253	213	160	189	376
ENSMUSG00000021400	chr13	Wrnip1	3.3E+07	3.3E+07	2633	0.427880452	3.301571583	0.0351899	0.066979708	0.04319	0	123	77	198	108	135	280	243	192	208	232
ENSMUSG00000020359	chr11	Phykpl	5.2E+07	5.2E+07	9699	-0.44885782	3.869015978	0.0352316	0.06704991	0.05003	0	219	147	452	227	265	281	308	142	248	313
ENSMUSG00000014554	chr6	Dguok	8.3E+07	8.3E+07	2191	0.388010247	4.107414625	0.0352648	0.067104048	0.03712	0	218	151	287	183	299	539	332	327	380	433
ENSMUSG00000031478	chr8	Nek3	2.2E+07	2.2E+07	2153	0.641715885	1.221547486	0.035298	0.067158192	0.07896	0	35	21	31	16	26	69	50	44	66	49
ENSMUSG00000028567	chr4	Txndc12	1.1E+08	1.1E+08	2253	0.442176494	3.587583853	0.0353196	0.0671902	0.04777	0	121	96	181	144	239	365	239	221	350	246
ENSMUSG00000007458	chr6	M6pr	1.2E+08	1.2E+08	4170	0.378879767	5.537409564	0.0353459	0.067227969	0.03738	0	565	448	611	536	903	1371	1083	863	1057	1055
ENSMUSG00000019790	chr10	Stxbp5	9755547	9760954	12871	-0.4225157	3.923984672	0.0353491	0.067227969	0.04462	0	294	213	279	269	226	294	341	167	244	304
ENSMUSG00000022031	chr14	Elp3	6.6E+07	6.6E+07	2891	-0.38255333	6.106518307	0.0353787	0.067275142	0.03868	0	1145	916	1299	1221	1261	1324	1438	910	1330	1194
ENSMUSG00000041491	chr19	Cep78	1.6E+07	1.6E+07	2548	-0.53186823	1.706464738	0.0354121	0.067329579	0.05783	0	48	43	88	54	53	63	55	37	55	60
ENSMUSG00000024293	chr18	Esco1	1.1E+07	1.1E+07	4572	-0.3911922	3.830476956	0.0354222	0.06733954	0.03745	0	257	193	278	239	232	340	278	181	223	256
ENSMUSG00000068114	chr15	Ccdc134	8.2E+07	8.2E+07	2043	0.503423839	3.780015622	0.0354304	0.067346161	0.06228	0	165	187	114	158	189	412	315	257	345	325
ENSMUSG00000025279	chr14	Dnase1l3	7964533	7967875	5151	1.202776086	1.00652254	0.0354915	0.067443882	0.33221	0	7	22	3	6	46	54	30	35	44	108
ENSMUSG00000089764	chr17	Gm16580	2.6E+07	2.6E+07	1044	1.014126316	0.062516308	0.0354871	0.067443882	0.19433	0	11	6	8	3	18	17	53	8	27	24
ENSMUSG00000035726	chr14	Supt16	5.2E+07	5.2E+07	4491	0.343957287	4.701645156	0.0355011	0.067453063	0.02975	0	300	239	449	324	438	765	558	516	521	631
ENSMUSG00000025702	chr6	March8	1.2E+08	1.2E+08	6536	-0.38073176	5.480459576	0.0355266	0.067492366	0.03788	0	739	520	1004	777	798	882	1128	560	725	743
ENSMUSG00000024969	chr19	Mark2	7275396	7277450	7942	-0.36564699	5.493674724	0.0355469	0.067521711	0.03483	0	686	526	988	753	921	785	963	549	959	827
ENSMUSG00000036523	chr12	Greb1	1.7E+07	1.7E+07	9580	-1.40544831	0.743865876	0.0355624	0.06754203	0.46187	0	15	23	17	112	2	28	10	11	19	25
ENSMUSG00000006362	chr8	Cbfa2t3	1.2E+08	1.2E+08	4775	-0.42872403	4.363766225	0.0355704	0.067548079	0.04667	0	284	207	432	510	367	336	468	242	377	394
ENSMUSG00000100009	chr1	Gm7967	9.9E+07	9.9E+07	5950	-0.84951348	0.441527441	0.0356108	0.067615673	0.15118	0	31	31	14	16	26	29	19	11	26	11
ENSMUSG00000055653	chrX	Gpc3	5.2E+07	5.2E+07	2690	0.555518279	4.055011743	0.0356868	0.067750845	0.07877	0	194	192	168	164	270	608	199	367	456	392
ENSMUSG00000015889	chr10	Lta4h	9.3E+07	9.3E+07	2066	0.336009477	4.708131658	0.0357939	0.067944885	0.0282	0	324	264	441	301	418	808	588	471	576	575
ENSMUSG00000020823	chr11	Sec14l1	1.2E+08	1.2E+08	7176	0.373209125	5.965885167	0.0358186	0.067964299	0.03683	0	826	536	1025	703	1083	1746	1503	1011	1611	1471
ENSMUSG00000055839	chr17	Tceb2	2.4E+07	2.4E+07	508	0.427158609	7.199252168	0.0358123	0.067964299	0.04896	0	1853	1554	1910	1913	2110	3674	3235	2582	4453	3468
ENSMUSG00000089714	chr1	Gm16092	8.6E+07	8.6E+07	2405	-0.66773322	0.673963219	0.0358161	0.067964299	0.08344	0	31	15	38	32	25	30	35	13	20	24
ENSMUSG00000045268	chr4	Zfp691	1.2E+08	1.2E+08	2399	-0.4750709	3.873955612	0.0358493	0.06801327	0.05698	0	222	142	441	277	237	266	371	136	249	263
ENSMUSG00000022314	chr15	Rad21	5.2E+07	5.2E+07	3604	-0.39418786	6.172421683	0.0358951	0.068090888	0.04133	0	1171	798	1682	1208	1423	1333	1703	904	1162	1378
ENSMUSG00000078584	chr4	AU022252	1.2E+08	1.2E+08	9570	-0.38084425	4.221143688	0.0359035	0.068097712	0.03629	0	328	258	327	338	310	346	381	267	360	308
ENSMUSG00000022300	chr15	Dcaf13	3.9E+07	3.9E+07	1551	0.374599909	4.148493765	0.0359641	0.068175736	0.03479	0	196	156	280	224	322	493	340	323	426	476
ENSMUSG00000022517	chr16	Mgrn1	4886100	4886473	3293	-0.48517832	6.19873025	0.0359631	0.068175736	0.06291	0	858	688	2313	1472	1420	1257	1718	764	1393	1269
ENSMUSG00000032518	chr9	Rpsa	1.2E+08	1.2E+08	1861	0.421441573	8.097448583	0.0359589	0.068175736	0.04797	0	3213	2757	4344	3567	3771	8352	5163	5246	6992	6675
ENSMUSG00000038195	chr11	Rilp	7.6E+07	7.6E+07	1583	0.358902834	5.360100394	0.03595	0.068175736	0.0337	0	483	313	770	547	671	958	1046	736	974	1039
ENSMUSG00000025417	chr10	Pip4k2c	1.3E+08	1.3E+08	3374	0.342262385	4.683048121	0.0360863	0.068398201	0.02966	0	283	230	446	301	480	656	578	444	593	692
ENSMUSG00000020520	chr11	Galnt10	5.8E+07	5.8E+07	5965	0.377157882	4.017078365	0.0360942	0.06840107	0.03455	0	178	173	288	196	223	472	388	267	427	338
ENSMUSG00000030878	chr7	Cdr2	1.2E+08	1.2E+08	2782	0.680563965	2.922767522	0.0360976	0.06840107	0.11671	0	72	56	66	40	214	240	183	144	196	190
ENSMUSG00000034157	chr12	Cipc	8.7E+07	8.7E+07	4863	-0.35298131	5.559587075	0.0361214	0.068436993	0.03265	0	707	542	1095	818	880	937	961	605	913	883
ENSMUSG00000029330	chr5	Cds1	1E+08	1E+08	3939	-1.06246037	1.633661298	0.0361409	0.068464705	0.27652	0	29	13	195	17	92	42	63	22	37	39
ENSMUSG00000038765	chr2	Lmx1b	3.4E+07	3.4E+07	4880	0.859113487	-0.16766307	0.0361604	0.068483131	0.11016	0	4	9	10	5	13	22	17	11	22	31
ENSMUSG00000039770	chr17	Ypel5	7.3E+07	7.3E+07	2869	0.389101504	5.597777481	0.0361594	0.068483131	0.03997	0	613	445	711	502	930	1443	1036	983	1058	1128
ENSMUSG00000028037	chr3	Ifi44	1.5E+08	1.5E+08	6116	0.924813272	0.460527321	0.0361789	0.068499633	0.17483	0	14	5	13	11	23	74	40	8	32	23
ENSMUSG00000033174	chr6	Mgll	8.9E+07	8.9E+07	4868	-0.63656265	7.131707562	0.0361788	0.068499633	0.10894	0	2030	1137	2761	1433	6415	2411	2214	1624	2422	2712
ENSMUSG00000026727	chr2	Rsu1	1.3E+07	1.3E+07	9299	0.362128981	4.597910998	0.0362031	0.068526889	0.03302	0	290	243	306	294	464	720	618	417	557	511
ENSMUSG00000029168	chr5	Dpysl5	3.1E+07	3.1E+07	6867	-0.97265863	0.053778118	0.0361983	0.068526889	0.18631	0	26	20	17	16	13	9	33	5	9	12
ENSMUSG00000034853	chr4	Acot11	1.1E+08	1.1E+08	6056	-0.83164881	3.057042669	0.0362232	0.06852937	0.1769	0	180	19	342	172	142	124	188	80	97	129
ENSMUSG00000040712	chr11	Camta2	7.1E+07	7.1E+07	5207	-0.40089083	5.792500146	0.0362109	0.06852937	0.04267	0	760	607	1366	1035	1093	969	1209	593	1167	1049
ENSMUSG00000060397	chr7	Zfp128	1.3E+07	1.3E+07	4087	-0.60104434	1.312166335	0.0362153	0.06852937	0.07423	0	39	32	51	45	52	55	50	28	21	45
ENSMUSG00000081051	chr1	Gm15427	9.5E+07	9.5E+07	531	0.37131303	4.192591933	0.0362239	0.06852937	0.03405	0	205	170	311	264	255	496	386	283	502	469
ENSMUSG00000033862	chr8	Cdk10	1.2E+08	1.2E+08	1643	0.442604426	3.698256283	0.0362361	0.068543255	0.04775	0	142	149	151	148	224	355	256	212	345	372
ENSMUSG00000057614	chr5	Gnai1	1.8E+07	1.8E+07	3193	-1.05755137	3.232162256	0.0362567	0.068572883	0.28776	0	213	148	64	25	518	208	92	112	105	111
ENSMUSG00000017188	chr11	Coa3	1E+08	1E+08	886	0.388161798	6.041843763	0.0362947	0.06863419	0.04019	0	695	544	1119	955	1077	1697	1469	1099	1827	1647
ENSMUSG00000018822	chr19	Sfrp5	4.2E+07	4.2E+07	1900	0.640218949	4.094167421	0.0363038	0.06863419	0.10763	0	97	99	183	215	460	408	434	210	510	609
ENSMUSG00000028901	chr4	Gmeb1	1.3E+08	1.3E+08	7857	-0.41285332	3.640933898	0.0362999	0.06863419	0.04131	0	192	161	294	216	209	223	261	200	187	217
ENSMUSG00000042190	chr5	Cmklr1	1.1E+08	1.1E+08	3408	0.485258646	4.113906074	0.0364084	0.068822652	0.06002	0	160	206	164	172	371	511	412	327	436	391
ENSMUSG00000078656	chr11	Vps25	1E+08	1E+08	1642	0.377822859	5.717027804	0.0364659	0.068922036	0.03779	0	687	505	735	621	911	1417	1069	1007	1250	1372
ENSMUSG00000059714	chr17	Flot1	3.6E+07	3.6E+07	2893	0.379852315	6.104471376	0.0365008	0.068978814	0.03858	0	799	587	1141	839	1235	1947	1628	1215	1799	1474
ENSMUSG00000031826	chr8	Usp10	1.2E+08	1.2E+08	5456	-0.35322723	5.340538322	0.0365562	0.069074169	0.03267	0	594	540	871	658	770	749	802	551	874	694
ENSMUSG00000033916	chr7	Chmp2a	1.3E+07	1.3E+07	927	0.37935879	6.262437095	0.0365891	0.069126907	0.03853	0	983	739	1153	984	1181	2190	1650	1488	1728	1892
ENSMUSG00000020917	chr11	Acly	1E+08	1E+08	5279	-1.11625036	6.310057281	0.0366925	0.069312975	0.32844	0	2032	740	352	331	5156	1372	729	998	1407	603
ENSMUSG00000086290	chr4	Snhg12	1.3E+08	1.3E+08	1626	0.495856443	2.309158541	0.036755	0.069421805	0.05401	0	56	42	73	55	80	142	102	115	106	113
ENSMUSG00000033732	chr8	Sf3b3	1.1E+08	1.1E+08	4299	0.34271821	5.21129614	0.0368612	0.069611103	0.03066	0	433	320	652	544	544	1043	770	694	885	876
ENSMUSG00000051403	chr7	Ppp1r37	2E+07	2E+07	2971	-0.39238284	5.97240422	0.0368652	0.069611103	0.04124	0	922	631	1605	1163	1195	1206	1292	727	1264	1172

ENSMUSG00000042605	chr5	Atxn2	1.2E+08	1.2E+08	7161	-0.40805209	5.485332052	0.036886	0.069640939	0.04425	0	624	469	1144	935	757	735	968	555	924	801
ENSMUSG00000049823	chr17	Zbtb12	3.5E+07	3.5E+07	2020	-0.45503611	3.123687836	0.0368963	0.069651158	0.05001	0	135	115	164	187	147	171	175	99	183	131
ENSMUSG00000002949	chr8	Timm44	4259731	4260255	3664	-0.42031784	6.191332064	0.0369194	0.069685345	0.04758	0	1150	691	2021	1376	1254	1460	1595	891	1327	1239
ENSMUSG00000102426	chrX	RP23-330G24.3	1.5E+08	1.5E+08	1477	0.881631312	0.599096249	0.0369402	0.069715106	0.16198	0	15	8	10	8	34	52	30	16	29	63
ENSMUSG00000029505	chr5	Ep400	1.1E+08	1.1E+08	13971	-0.3368514	4.641691217	0.0369508	0.069725769	0.02884	0	359	312	541	469	421	539	525	339	425	457
ENSMUSG00000020219	chr10	Timm13	8.1E+07	8.1E+07	1225	0.392650618	6.087277019	0.0369702	0.069743561	0.04145	0	787	599	1107	879	1125	1636	1472	1198	2055	1593
ENSMUSG00000030725	chr7	Lipt2	1E+08	1E+08	1663	-0.44810947	2.833530867	0.0369674	0.069743561	0.04655	0	119	96	130	105	164	146	145	97	113	116
ENSMUSG00000042770	chr6	Hebp1	1.4E+08	1.4E+08	1061	0.704394967	3.789467315	0.0370052	0.06980026	0.13059	0	92	107	120	89	413	502	223	336	339	341
ENSMUSG00000032977	chr10	Fam207a	7.7E+07	7.7E+07	2427	0.388644828	3.686743732	0.0370379	0.06985255	0.03668	0	120	118	211	186	211	368	303	213	315	308
ENSMUSG00000052031	chr17	Tagap1	6954965	6957024	2358	-0.39498579	3.854580894	0.037169	0.070090314	0.03874	0	222	180	351	255	233	296	333	198	232	230
ENSMUSG00000026437	chr1	Cdk18	1.3E+08	1.3E+08	4764	0.557096981	3.389701905	0.0371898	0.070120182	0.07891	0	99	69	211	164	106	186	318	145	288	347
ENSMUSG00000073968	chr7	Trim68	1E+08	1E+08	2389	-0.45156154	3.13877152	0.0372244	0.070176	0.04908	0	176	118	168	118	177	190	166	124	120	163
ENSMUSG00000048897	chr7	Zfp710	8E+07	8E+07	4803	-0.42236358	4.821011837	0.0372588	0.070231469	0.04705	0	309	369	727	624	428	553	581	307	541	540
ENSMUSG00000019189	chr11	Rnf145	4.5E+07	4.5E+07	7786	0.511773332	4.080275831	0.037272	0.070246805	0.06846	0	151	143	213	129	446	505	444	297	410	400
ENSMUSG00000026457	chr1	Adipor1	1.3E+08	1.3E+08	5025	-0.40353451	8.218926252	0.0373751	0.070431694	0.04469	0	4963	3898	6029	4861	5868	5485	6610	3815	5615	5104
ENSMUSG00000031785	chr8	Gpr56	9.5E+07	9.5E+07	3864	0.537295487	4.70436296	0.0374065	0.070481404	0.0775	0	157	143	598	335	474	582	552	468	845	718
ENSMUSG00000038335	chr11	Tsr1	7.5E+07	7.5E+07	3837	-0.39080814	5.125581677	0.0374335	0.070522779	0.04052	0	565	575	613	577	573	787	606	558	564	585
ENSMUSG00000042167	chr13	Papd4	9.3E+07	9.3E+07	1873	-0.48273446	2.831136719	0.037444	0.070533152	0.05609	0	131	97	134	109	145	178	148	95	96	95
ENSMUSG00000013622	chr5	Atraid	3.1E+07	3.1E+07	2092	0.381311694	5.749826563	0.0374911	0.070612404	0.03905	0	672	477	809	614	1002	1548	1060	1049	1279	1331
ENSMUSG00000029287	chr5	Tgfbr3	1.1E+08	1.1E+08	6545	0.478792306	5.41691875	0.0375262	0.070669019	0.06174	0	444	382	479	388	1054	1417	1005	854	823	1047
ENSMUSG00000066607	chr9	6030419C18Rik	5.8E+07	5.8E+07	2139	-0.4190916	4.641547287	0.0375363	0.070678588	0.0461	0	363	298	617	532	352	447	595	297	511	366
ENSMUSG00000048755	chr15	Mcat	8.4E+07	8.4E+07	1893	-0.34023008	4.719336302	0.0376404	0.070864924	0.02951	0	402	264	585	433	585	503	546	384	515	443
ENSMUSG00000025613	chr16	Cct8	8.7E+07	8.7E+07	3088	0.395887534	7.355031002	0.0376762	0.070922937	0.04298	0	1958	1405	2771	2218	2465	4530	3506	3233	3782	4104
ENSMUSG00000057147	chr2	Dph6	1.1E+08	1.1E+08	7407	-0.54340181	2.352902746	0.0376949	0.0709485	0.07018	0	92	92	73	69	112	117	86	57	85	83
ENSMUSG00000020362	chr11	Cnot6	5E+07	5E+07	6610	-0.35162025	4.158644206	0.0377224	0.070990764	0.03093	0	258	236	382	294	339	414	350	255	290	312
ENSMUSG00000001211	chr10	Agpat3	7.8E+07	7.8E+07	7577	-0.48839081	7.262035827	0.0377892	0.071106946	0.06545	0	2039	1320	4959	3125	2697	2828	3082	1811	2367	3219
ENSMUSG00000022793	chr16	B4galt4	3.9E+07	3.9E+07	3032	0.560883172	2.063872188	0.0378369	0.071187192	0.07181	0	31	31	75	42	77	141	78	77	97	110
ENSMUSG00000085455	chr5	1810059H22Rik	1.5E+08	1.5E+08	2897	0.720248481	0.166488264	0.0378772	0.071253512	0.08378	0	6	7	17	13	15	25	27	26	24	25
ENSMUSG00000021453	chr13	Gadd45g	5.2E+07	5.2E+07	1173	0.487888006	4.428525124	0.0379077	0.07130118	0.06361	0	179	136	423	204	484	499	666	418	569	422
ENSMUSG00000033703	chr8	Fuk	1.1E+08	1.1E+08	3838	-0.47104113	2.473732719	0.0379189	0.071312668	0.05039	0	71	76	135	93	109	100	110	65	108	93
ENSMUSG00000025470	chr7	Zfp511	1.4E+08	1.4E+08	1100	0.486538998	2.575964906	0.0379256	0.071315847	0.05403	0	58	60	78	82	88	190	111	109	157	140
ENSMUSG00000025199	chr19	Chuk	4.4E+07	4.4E+07	5087	-0.35712502	3.994495474	0.0379913	0.071420212	0.03155	0	248	178	349	268	320	366	317	220	240	303
ENSMUSG00000035757	chr15	Selo	8.9E+07	8.9E+07	3744	-0.35668359	4.339174164	0.0379899	0.071420212	0.03232	0	298	227	450	409	340	429	399	273	385	349
ENSMUSG00000098974	chr19	Gm27505	5844638	5844747	110	-0.5485972	4.749017434	0.0380423	0.071506527	0.08122	0	534	514	352	263	658	635	444	277	339	603
ENSMUSG00000057134	chr10	Ado	6.8E+07	6.8E+07	4444	-0.35456124	5.271190132	0.0380801	0.071567919	0.03335	0	568	435	903	707	698	715	887	513	724	668
ENSMUSG00000042508	chr5	Dmtf1	9118801	9120138	11041	-0.43630447	3.261394155	0.0380987	0.071593324	0.04658	0	153	135	177	190	160	206	200	123	131	181
ENSMUSG00000063281	chr18	Zfp35	2.4E+07	2.4E+07	3040	-0.41500537	3.399558456	0.0381676	0.07171317	0.0422	0	176	122	193	207	207	244	205	155	163	162
ENSMUSG00000023885	chr17	Thbs2	1.5E+07	1.5E+07	5922	0.55881773	5.482584857	0.038189	0.071743807	0.08467	0	479	582	436	321	840	1993	1054	765	822	991
ENSMUSG00000048310	chr8	Pskh1	1.1E+08	1.1E+08	3255	-0.35001185	4.451110285	0.0382239	0.071799783	0.03125	0	343	225	471	347	499	413	470	268	404	440
ENSMUSG00000006276	chr8	Eps15l1	7.2E+07	7.2E+07	3141	-0.42094457	4.244797141	0.0382352	0.071811254	0.04585	0	225	201	567	359	331	368	405	246	288	370
ENSMUSG00000022656	chr16	Pvrl3	4.6E+07	4.6E+07	12747	0.50300775	2.315118185	0.0382706	0.071868124	0.05448	0	64	51	55	59	70	163	112	89	115	113
ENSMUSG00000060601	chr7	Nr1h2	4.5E+07	4.5E+07	3366	-0.35483911	5.406629606	0.0382779	0.071872286	0.03379	0	653	566	837	730	791	844	904	478	870	791
ENSMUSG00000026974	chr2	Zmynd19	2.5E+07	2.5E+07	4168	-0.37418613	4.055511062	0.0384047	0.072100627	0.03545	0	257	237	348	263	297	287	354	238	318	286
ENSMUSG00000029648	chr5	Flt1	1.5E+08	1.5E+08	11583	-0.45719284	5.673079697	0.0384128	0.072106239	0.05686	0	602	438	1630	1022	976	1056	1097	616	781	936
ENSMUSG00000032666	chr1	1700025G04Rik	1.5E+08	1.5E+08	11788	-0.4367047	6.75686481	0.0384365	0.072141021	0.05255	0	1827	1194	2327	2404	1665	2074	2591	1424	1668	1783
ENSMUSG00000021279	chr12	Cdc42bpb	1.1E+08	1.1E+08	6718	-0.34155259	4.995612826	0.0384431	0.072143755	0.03065	0	439	344	730	544	690	637	657	366	677	597
ENSMUSG00000045039	chr7	Megf8	2.5E+07	2.5E+07	10159	-0.38228367	5.928560678	0.0384503	0.072147644	0.03982	0	955	726	1298	1225	1006	1228	1283	723	1224	1056
ENSMUSG00000001891	chr11	Ugp2	2.1E+07	2.1E+07	3069	-0.50450589	9.526805584	0.0385217	0.072272014	0.0707	0	10656	7404	23627	15176	10489	16060	16071	9279	9936	12359
ENSMUSG00000025602	chr9	Zfp202	4E+07	4E+07	3877	-0.51649614	1.640062717	0.0385959	0.072401579	0.05424	0	43	45	63	54	64	67	48	41	51	51
ENSMUSG00000032313	chr9	AI118078	5.5E+07	5.5E+07	4714	-1.01866601	1.742771082	0.0386238	0.072444071	0.26449	0	89	64	18	114	22	54	30	23	73	49
ENSMUSG00000031485	chr8	Prosc	2.7E+07	2.7E+07	4534	-0.39672437	5.115648119	0.0386782	0.072536422	0.04209	0	490	305	974	696	606	712	767	451	579	599
ENSMUSG00000052214	chr7	Opa3	1.9E+07	1.9E+07	4554	-0.4279851	6.674725114	0.038684	0.072537737	0.05054	0	1480	1177	2753	1987	1586	1845	2309	1352	1879	1631
ENSMUSG00000001657	chr15	Hoxc8	1E+08	1E+08	2832	-0.87543481	2.672300543	0.0387253	0.072595654	0.20021	0	119	67	86	43	329	195	62	51	65	103
ENSMUSG00000032621	chr13	Srek1	1E+08	1E+08	3985	-0.38680133	4.232928521	0.0387245	0.072595654	0.03895	0	312	298	346	291	322	396	420	255	282	332
ENSMUSG00000054728	chr13	Phactr1	4.3E+07	4.3E+07	9611	0.569729564	2.032244623	0.038773	0.072675393	0.0753	0	33	30	52	42	91	129	83	66	100	117
ENSMUSG00000021615	chr13	Xrcc4	9E+07	9E+07	4213	-0.503199	2.623462976	0.0388566	0.072822467	0.06152	0	110	99	118	86	117	160	119	75	94	79
ENSMUSG00000030314	chr6	Atg7	1.1E+08	1.1E+08	5273	0.41573272	3.794589157	0.0388793	0.072855245	0.04449	0	146	99	227	162	287	316	340	231	378	364
ENSMUSG00000020078	chr10	Vps26a	6.2E+07	6.2E+07	3252	-0.35074765	5.512077179	0.0388945	0.072869422	0.03316	0	759	560	922	802	813	951	921	693	756	809
ENSMUSG00000021774	chr14	Ube2e1	1.8E+07	1.8E+07	4457	-0.36332617	5.43275058	0.0388973	0.072869422	0.03567	0	736	581	832	716	770	830	998	599	776	701
ENSMUSG00000041303	chr1	Gtf3c3	5.4E+07	5.4E+07	4925	-0.41824804	3.474909381	0.0389181	0.072898695	0.04387	0	202	110	247	212	194	274	219	123	182	196
ENSMUSG00000028423	chr4	Nfx1	4.1E+07	4.1E+07	8564	-0.32402872	5.227701978	0.038925	0.072901879	0.02785	0	589	463	739	643	710	768	707	549	682	723
ENSMUSG00000019470	chr8	Xab2	3608421	3610219	4685	0.353206629	4.193960506	0.0389898	0.07301353	0.03181	0	205	163	306	223	331	475	395	323	467	451
ENSMUSG00000006299	chr1	Aamp	7.4E+07	7.4E+07	3458	0.395189908	7.072590418	0.0390106	0.073042695	0.04334	0	1598	1198	2020	1763	2294	3416	2871	2400	3711	3393
ENSMUSG00000026527	chr1	Rgs7	1.8E+08	1.8E+08	6019	-1.40195963	0.354605422	0.0390506	0.073107842	0.46868	0	31	9	4	4	90	31	8	12	9	8
ENSMUSG00000070343	chr3	Gm10288	1.5E+08	1.5E+08	537	0.418024462	3.802531985	0.0390727	0.073139363	0.04476	0	190	113	222	155	227	452	259	306	284	326
ENSMUSG00000020491	chr11	2810021J22Rik	5.9E+07	5.9E+07	3928	-0.64814833	1.504855609	0.0392079	0.073382767	0.09703	0	52	48	38	61	47	68	55	36	28	37
ENSMUSG00000020027	chr10	Socs2	9.5E+07	9.5E+07	9531	-0.70394936	4.222677056	0.0392339	0.073421617	0.13429	0	261	282	255	669	210	368	147	300	387	233

ENSMUSG00000087408	chr8	Cers1	7E+07	7E+07	3171	-0.41990863	4.568528919	0.0392467	0.073435808	0.04724	0	382	359	339	343	598	414	502	249	499	450
ENSMUSG00000057421	chrX	Las1l	9.6E+07	9.6E+07	8143	-0.35025495	5.466193912	0.0392712	0.073471824	0.03325	0	754	573	936	718	742	926	932	567	776	840
ENSMUSG00000057894	chr7	Zfp329	1.3E+07	1.3E+07	6732	-0.53476381	2.19861627	0.0393099	0.073534362	0.06699	0	88	61	100	92	57	94	89	45	78	80
ENSMUSG00000017421	chr11	Zfp207	8E+07	8E+07	6658	-0.35151099	5.694660504	0.0394255	0.073740847	0.0337	0	812	682	974	830	1078	1124	1061	739	882	904
ENSMUSG00000024772	chr19	Ehd1	6276725	6277378	3705	0.447030778	5.552874561	0.0395004	0.073863166	0.05506	0	441	374	665	493	1126	1394	912	860	1317	1115
ENSMUSG00000037820	chr2	Tgm2	1.6E+08	1.6E+08	4608	0.441558838	6.878214257	0.0395015	0.073863166	0.05443	0	1145	896	2325	1149	2346	3554	3014	2252	2700	2514
ENSMUSG00000027610	chr2	Gss	1.6E+08	1.6E+08	5915	0.468820773	3.331668096	0.039539	0.073923419	0.05661	0	115	65	143	108	221	286	199	210	245	247
ENSMUSG00000078648	chr15	Gm17546	9.6E+07	9.6E+07	732	-0.80430494	0.589484918	0.0396005	0.074028641	0.13596	0	24	24	43	31	13	17	35	11	16	29
ENSMUSG00000003423	chr7	Pih1d1	4.5E+07	4.5E+07	2024	0.373546166	5.809412252	0.0396234	0.074061481	0.03828	0	651	501	838	786	944	1456	1205	893	1653	1362
ENSMUSG00000026181	chr16	Ppm1f	1.7E+07	1.7E+07	4922	-0.33346299	4.720250078	0.0396434	0.074079269	0.02903	0	398	318	590	398	535	517	553	389	524	415
ENSMUSG00000056418	chr9	BC043934	9.6E+07	9.6E+07	2356	1.136366478	0.02115001	0.0396402	0.074079269	0.28205	0	3	7	4	1	28	41	13	21	24	27
ENSMUSG00000004383	chr8	Large	7.3E+07	7.3E+07	7883	-0.47744967	5.205012877	0.0396787	0.074135269	0.0625	0	476	353	1160	825	526	739	931	435	516	599
ENSMUSG00000031176	chrX	Dynlt3	9654267	9656063	2576	-0.37374704	5.845533876	0.0396973	0.074160118	0.03846	0	1118	658	1064	999	1048	1356	1159	763	992	948
ENSMUSG00000021916	chr14	Glt8d1	3.1E+07	3.1E+07	2521	0.412492285	4.124412163	0.0397102	0.074174415	0.04401	0	235	179	200	186	316	592	362	287	405	425
ENSMUSG00000025020	chr19	Slit1	4.2E+07	4.2E+07	5921	0.757942244	0.813174725	0.0397547	0.074247524	0.12776	0	19	4	32	22	18	34	65	40	35	35
ENSMUSG00000031314	chrX	Taf1	1E+08	1E+08	8428	-0.40094318	4.089899393	0.0397901	0.074293875	0.04214	0	300	216	373	268	301	454	372	208	223	280
ENSMUSG00000087635	chr2	Gm13414	3.5E+07	3.5E+07	727	-0.92419623	-0.10360981	0.039788	0.074293875	0.16252	0	20	13	19	20	10	19	25	4	6	8
ENSMUSG00000027895	chr3	Kcnc4	1.1E+08	1.1E+08	3013	0.44131314	7.042685854	0.0398658	0.074425327	0.05451	0	1971	1166	1671	1939	1593	2840	3232	2525	3716	3255
ENSMUSG00000036078	chr4	Sigmar1	4.2E+07	4.2E+07	3136	0.497665245	3.891604098	0.0399786	0.07462599	0.06638	0	135	104	199	140	384	433	294	311	371	363
ENSMUSG00000026864	chr2	Hspa5	3.5E+07	3.5E+07	4229	0.444176057	8.284703436	0.0400073	0.07466939	0.05561	0	3404	2718	4854	4465	4715	11919	6907	6302	5766	6536
ENSMUSG00000060477	chr6	Irak2	1.1E+08	1.1E+08	4194	0.60691379	3.796547445	0.0400125	0.07466939	0.09971	0	94	91	139	134	408	472	268	266	357	364
ENSMUSG00000031077	chr7	Fadd	1.4E+08	1.4E+08	3903	0.418991613	3.229160196	0.0400212	0.07467317	0.04348	0	91	80	180	108	154	271	211	177	234	203
ENSMUSG00000073437	chr17	D330041H03Rik	2.4E+07	2.4E+07	3749	-0.57028758	1.573603954	0.0400252	0.07467317	0.069	0	49	39	85	45	45	51	50	38	40	61
ENSMUSG00000078931	chr8	Pdf	1.1E+08	1.1E+08	1704	-0.34762586	5.650300196	0.0400517	0.074712835	0.03312	0	840	651	1017	843	873	1023	1044	704	910	889
ENSMUSG00000027905	chr3	Ddx20	1.1E+08	1.1E+08	4142	-0.38146906	3.581438302	0.0401686	0.074920882	0.03616	0	201	124	278	194	237	250	225	144	210	248
ENSMUSG00000051515	chr7	Fam181b	9.3E+07	9.3E+07	1836	0.648082467	1.43570548	0.040229	0.075023468	0.09944	0	29	9	52	21	49	79	53	53	68	72
ENSMUSG00000028016	chr3	Ints12	1.3E+08	1.3E+08	7257	-0.39257156	3.308517585	0.0402775	0.075104036	0.03785	0	162	119	215	156	197	200	218	131	156	177
ENSMUSG00000025421	chr18	Hdhd2	7.7E+07	7.7E+07	4822	-0.36654791	5.667039544	0.0402905	0.075118286	0.03697	0	864	564	1195	916	815	1045	1037	729	900	873
ENSMUSG00000029534	chr6	St7	1.8E+07	1.8E+07	9109	-0.3815998	3.65584856	0.0402994	0.075124939	0.03662	0	187	151	276	250	210	270	240	169	209	241
ENSMUSG00000063087	chr18	Gm10125	5491503	5492097	7466	0.961703548	-0.22469277	0.040327	0.07516633	0.16643	0	6	5	5	5	17	25	7	23	25	18
ENSMUSG00000026159	chr1	Agfg1	8.3E+07	8.3E+07	8384	-0.34193866	5.140152711	0.0403431	0.075186248	0.03168	0	583	465	657	668	564	757	704	487	612	660
ENSMUSG00000015536	chr13	Mocs2	1.1E+08	1.1E+08	9054	-0.34219982	5.209856737	0.0404095	0.075299992	0.03174	0	588	491	646	538	856	754	726	532	645	710
ENSMUSG00000050229	chr1	Pigm	1.7E+08	1.7E+08	7554	0.523928716	3.138773658	0.0405054	0.075468821	0.07097	0	110	63	91	83	203	235	196	191	181	247
ENSMUSG00000022856	chr16	Tmem41a	2.2E+07	2.2E+07	1359	0.583413104	2.549537217	0.0405297	0.075504014	0.08268	0	71	74	47	51	92	192	117	92	165	153
ENSMUSG00000040506	chr2	Ambra1	9.2E+07	9.2E+07	6122	-0.37427912	4.512880394	0.0405409	0.075514835	0.0373	0	286	262	555	451	418	447	546	261	405	414
ENSMUSG00000004568	chr8	Arhgef18	3393006	3393102	8395	-0.36960105	3.710015146	0.040558	0.075516686	0.03438	0	177	171	270	244	247	267	259	177	227	246
ENSMUSG00000018900	chr11	Slc22a5	5.4E+07	5.4E+07	3071	-0.40956268	3.861283144	0.0405557	0.075516686	0.04328	0	244	140	426	232	238	287	280	190	253	278
ENSMUSG00000030020	chr6	Prickle2	9.2E+07	9.2E+07	8637	0.557810786	1.838771577	0.0405496	0.075516686	0.06855	0	46	28	37	43	57	110	83	79	61	90
ENSMUSG00000033909	chr11	Usp36	1.2E+08	1.2E+08	7689	-0.35229438	4.433468258	0.040605	0.075594097	0.03249	0	277	229	505	410	443	437	401	269	435	426
ENSMUSG00000020523	chr11	Fam114a2	5.7E+07	5.7E+07	3075	-0.38601435	5.70349872	0.0406379	0.075645284	0.0414	0	951	713	1034	933	753	1189	959	743	910	876
ENSMUSG00000026279	chr1	Thap4	9.4E+07	9.4E+07	6519	-0.35506709	5.028171262	0.0406644	0.075684489	0.03418	0	449	417	724	666	502	648	663	435	645	571
ENSMUSG00000024587	chr18	Nars	6.4E+07	6.5E+07	2632	-0.39162081	7.024440514	0.0407019	0.075743653	0.04329	0	2188	1594	3039	2182	2209	2594	2875	1704	2277	2250
ENSMUSG00000033099	chr15	Nol12	7.9E+07	7.9E+07	4317	0.354411183	4.794433121	0.0407069	0.075743653	0.03337	0	368	298	355	336	459	702	592	486	754	671
ENSMUSG00000015291	chrX	Gdi1	7.4E+07	7.4E+07	4296	0.436352942	6.001704731	0.0407359	0.07578738	0.05324	0	771	621	679	678	1376	1869	1386	1070	1584	1757
ENSMUSG00000097944	chr8	A130014A01Rik	1.2E+08	1.2E+08	2323	-0.61880517	1.061788	0.0407893	0.075876683	0.07777	0	27	30	55	36	36	54	35	24	26	26
ENSMUSG00000022346	chr15	Myc	6.2E+07	6.2E+07	2767	0.669837365	2.299635097	0.0407963	0.075879797	0.10909	0	56	70	30	46	62	166	84	101	126	132
ENSMUSG00000022324	chr15	Matn2	3.4E+07	3.4E+07	3583	0.550108197	3.518931874	0.0408181	0.075910193	0.0802	0	132	110	100	95	261	420	239	244	267	225
ENSMUSG00000026110	chr1	Mgat4a	3.7E+07	3.7E+07	12881	0.455949593	2.92146292	0.0408513	0.07594171	0.05108	0	71	59	136	107	112	183	224	124	157	209
ENSMUSG00000031298	chrX	Gpr64	1.6E+08	1.6E+08	5278	-0.7773271	0.653153768	0.0408505	0.07594171	0.12819	0	31	14	28	15	58	30	29	15	13	27
ENSMUSG00000041440	chr9	Gk5	9.6E+07	9.6E+07	8493	-0.71294696	0.783974085	0.0408503	0.07594171	0.10667	0	33	32	38	17	31	27	37	25	21	17
ENSMUSG00000034401	chr4	Spata6	1.1E+08	1.1E+08	5616	0.54692314	2.425255708	0.0408814	0.075987663	0.07273	0	43	48	65	54	118	189	123	80	117	147
ENSMUSG00000029440	chr5	Psmd9	1.2E+08	1.2E+08	4562	0.37367416	4.224249717	0.0409374	0.07607157	0.03677	0	229	159	301	227	326	472	366	324	568	437
ENSMUSG00000050213	chr4	Snip1	1.3E+08	1.3E+08	2428	0.414415857	3.151316511	0.0409329	0.07607157	0.04196	0	118	73	139	98	147	270	205	164	214	186
ENSMUSG00000022510	chr16	Trp63	2.6E+07	2.6E+07	8391	0.548694509	3.46687708	0.040975	0.076121255	0.07839	0	110	134	117	194	87	264	279	189	299	314
ENSMUSG00000026158	chr1	Ogfrl1	2.3E+07	2.3E+07	8109	-0.41755563	3.187024999	0.0409749	0.076121255	0.04406	0	160	128	158	163	159	207	179	113	145	162
ENSMUSG00000043831	chr7	Lysmd4	6.7E+07	6.7E+07	3383	-0.39128185	3.623946151	0.0410921	0.076328696	0.03938	0	220	171	244	200	203	256	241	144	254	210
ENSMUSG00000026109	chr1	Tmeff2	5.1E+07	5.1E+07	6707	0.746258346	2.244060012	0.0411575	0.076440021	0.14325	0	45	41	32	27	118	232	96	82	101	100
ENSMUSG00000031530	chr8	Dusp4	3.5E+07	3.5E+07	2740	-1.27030568	1.309397954	0.0411902	0.076490583	0.41537	0	47	36	6	7	169	35	34	15	28	36
ENSMUSG00000019864	chr10	Rtn4ip1	4.4E+07	4.4E+07	3135	-0.45586349	5.256219942	0.0413181	0.076717985	0.05779	0	512	327	1245	824	556	696	786	485	649	721
ENSMUSG00000057440	chr18	Mpp7	7347962	7351144	4975	-0.63705709	1.852079261	0.0413313	0.076732426	0.09822	0	76	32	67	39	120	89	53	46	50	49
ENSMUSG00000031533	chr8	Mrps31	2.2E+07	2.2E+07	1536	-0.34398188	4.763591343	0.0413501	0.076751705	0.03158	0	454	281	612	501	468	530	535	433	454	498
ENSMUSG00000032217	chr9	Rnf111	7E+07	7E+07	5003	-0.4171795	3.55955868	0.0413527	0.076751705	0.04534	0	210	184	201	180	215	208	269	153	200	208
ENSMUSG00000029780	chr6	Nt5c3	5.7E+07	5.7E+07	4250	-0.36703281	5.530844094	0.0413684	0.076761021	0.03742	0	789	595	1020	811	694	965	878	683	743	894
ENSMUSG00000071654	chr19	Uqcc3	8880016	8880616	829	0.373119938	5.559227953	0.0413686	0.076761021	0.0387	0	493	447	762	635	795	1242	893	849	1352	1146
ENSMUSG00000004221	chrX	Ikbkg	7.4E+07	7.4E+07	8110	-0.33638858	4.863167796	0.0413825	0.076776596	0.03045	0	447	314	707	520	496	648	618	378	490	542
ENSMUSG00000042595	chrX	Fam199x	1.4E+08	1.4E+08	8299	-0.47768847	2.381108765	0.041455	0.076890761	0.05339	0	90	65	133	83	82	94	111	65	82	92
ENSMUSG00000043059	chr5	Zfp513	3.1E+07	3.1E+07	2476	0.422514486	3.325079091	0.0414547	0.076890761	0.04442	0	107	110	134	108	179	277	215	178	232	273

ENSMUSG00000025479	chr7	Cyp2e1	1.4E+08	1.4E+08	1827	1.467054581	5.658060125	0.0414804	0.076927752	0.57878	0	670	271	14	26	1041	2252	484	1223	1542	2166
ENSMUSG00000028909	chr4	Ptpru	1.3E+08	1.3E+08	7113	0.711643727	1.022291909	0.0414897	0.076934677	0.11136	0	16	10	20	18	49	63	57	37	32	57
ENSMUSG00000071151	chr10	Gm4799	8.3E+07	8.3E+07	657	0.648234157	0.967282072	0.0415821	0.077095959	0.08904	0	16	10	29	22	34	41	36	34	65	54
ENSMUSG00000055799	chr6	Tcf7l1	7.3E+07	7.3E+07	3924	0.601064373	3.100648489	0.0417673	0.077429021	0.09592	0	68	66	87	67	238	251	178	148	242	240
ENSMUSG00000003458	chr1	Ncstn	1.7E+08	1.7E+08	3975	0.34421992	5.277125136	0.0418066	0.077491568	0.03249	0	484	403	539	456	692	967	913	640	955	1014
ENSMUSG00000083621	chrX	Gm14586	5.3E+07	5.3E+07	408	0.501336562	3.669603383	0.0418433	0.077549382	0.06682	0	136	121	118	183	225	260	273	190	436	372
ENSMUSG00000022704	chr16	Qtrtd1	4.4E+07	4.4E+07	4629	-0.52094126	2.411041513	0.0418671	0.077583202	0.06557	0	80	76	99	67	147	85	95	79	74	107
ENSMUSG00000005566	chr7	Trim28	1.3E+07	1.3E+07	4044	0.378752416	5.959228612	0.0418754	0.077588376	0.04038	0	658	605	860	908	1063	1641	1295	1095	1695	1540
ENSMUSG00000039410	chr4	Prdm16	1.5E+08	1.5E+08	9321	-0.66690468	1.927130662	0.0419507	0.07770741	0.10978	0	70	28	59	52	150	82	73	39	49	58
ENSMUSG00000054612	chr7	Mgmt	1.4E+08	1.4E+08	818	0.609142156	2.122503285	0.0419498	0.07770741	0.09078	0	48	36	51	37	84	114	73	77	171	92
ENSMUSG00000021951	chr14	N6amt2	5.8E+07	5.8E+07	836	-0.43820747	3.990518456	0.0419944	0.07777802	0.05167	0	347	199	242	204	375	295	289	200	354	253
ENSMUSG00000032733	chr9	Snx33	5.7E+07	5.7E+07	4564	0.602584879	3.445165621	0.0420495	0.077859596	0.0975	0	105	112	83	76	273	356	218	194	296	288
ENSMUSG00000098140	chr5	Gm26938	1.4E+08	1.4E+08	744	0.473435987	2.505163604	0.0420467	0.077859596	0.05477	0	76	33	96	70	85	153	123	114	133	142
ENSMUSG00000042032	chr11	Mat2b	4.1E+07	4.1E+07	5001	-0.38642089	6.154690913	0.0420984	0.077939796	0.04234	0	1082	846	1848	1131	1283	1423	1630	885	1146	1351
ENSMUSG00000005506	chr2	Celf1	9.1E+07	9.1E+07	8446	-0.37800604	6.635710793	0.0421114	0.077953542	0.04077	0	1505	1344	2001	1684	1934	1923	2250	1225	1748	1861
ENSMUSG00000042688	chr9	Mapk6	7.5E+07	7.5E+07	6675	-0.33238115	5.090937466	0.0421882	0.078085394	0.03039	0	524	474	637	618	576	684	735	461	586	657
ENSMUSG00000041966	chr2	Dcaf17	7.1E+07	7.1E+07	9806	-0.48996423	2.599968716	0.0422761	0.078237896	0.05986	0	100	98	113	87	122	144	121	86	79	86
ENSMUSG00000014361	chr2	Mertk	1.3E+08	1.3E+08	4336	0.619925346	1.813202403	0.0424276	0.07850784	0.08876	0	43	35	42	22	59	104	120	41	93	76
ENSMUSG00000097750	chr7	Gm4673	3.1E+07	3.1E+07	3660	-0.69197344	0.162102219	0.042452	0.078542596	0.0822	0	18	8	27	22	23	22	19	9	13	19
ENSMUSG00000039929	chr16	Urb1	9.1E+07	9.1E+07	8190	-0.43485878	3.127034094	0.0425116	0.078642576	0.04761	0	132	105	148	137	238	171	149	123	154	162
ENSMUSG00000038291	chr8	Snx25	4.6E+07	4.6E+07	4440	-0.48844606	2.807669638	0.0425658	0.078732363	0.06083	0	101	114	138	137	108	146	153	98	98	101
ENSMUSG00000031200	chrX	Mtcp1	7.5E+07	7.5E+07	4478	-0.56866331	1.446035107	0.042592	0.078770559	0.07208	0	43	42	56	52	42	63	43	27	34	56
ENSMUSG00000004939	chr10	Nmrk2	8.1E+07	8.1E+07	1840	0.596906284	8.538352589	0.0426305	0.07882089	0.10274	0	2328	1942	8260	3224	8472	11713	11888	5499	8982	9119
ENSMUSG00000025745	chr5	Hadha	3E+07	3E+07	5341	-0.6248199	9.002119886	0.0426278	0.07882089	0.11245	0	6481	3064	20775	12128	7726	8611	10858	5714	7220	9638
ENSMUSG00000014177	chr11	Tvp23b	6.3E+07	6.3E+07	2235	0.404537184	3.535955001	0.042649	0.078844711	0.04213	0	148	92	159	134	226	379	265	199	255	268
ENSMUSG00000025794	chr9	Rpl14	1.2E+08	1.2E+08	935	0.399042975	7.578756584	0.0427058	0.07893937	0.04597	0	2250	1985	2838	2323	3038	5474	3747	3782	4489	4907
ENSMUSG00000002105	chr2	Slc39a13	9.1E+07	9.1E+07	4869	0.333555628	4.908186352	0.042753	0.079016119	0.03023	0	361	301	415	407	517	728	705	492	821	712
ENSMUSG00000038893	chr11	Fam117a	9.5E+07	9.5E+07	3029	0.56908077	2.571245985	0.0427621	0.0790213	0.08337	0	67	48	59	43	144	154	141	117	144	160
ENSMUSG00000046010	chr11	Zfp830	8.3E+07	8.3E+07	1591	-0.39631697	3.409317633	0.0427671	0.0790213	0.03968	0	170	136	236	178	186	210	196	170	176	181
ENSMUSG00000027957	chr3	Slc35a3	1.2E+08	1.2E+08	10173	-0.41491603	3.394386581	0.0427814	0.079026927	0.04442	0	177	129	189	164	246	200	257	126	170	179
ENSMUSG00000073680	chr4	Tmem88b	1.6E+08	1.6E+08	3471	0.778702959	0.251580455	0.04278	0.079026927	0.11865	0	9	6	12	7	27	39	18	20	29	34
ENSMUSG00000040841	chr7	Six5	1.9E+07	1.9E+07	3007	0.546397437	2.654757427	0.0427912	0.079032068	0.07485	0	79	67	59	57	112	230	120	94	176	151
ENSMUSG00000055771	chr18	Gm7936	3E+07	3E+07	375	0.839767825	0.070749991	0.0427954	0.079032068	0.12635	0	8	8	4	18	11	19	24	19	27	33
ENSMUSG00000047215	chr5	Rpl9	6.5E+07	6.5E+07	3080	0.417230821	7.995054991	0.0428553	0.079132249	0.05042	0	3086	2574	3638	2972	4233	7922	4550	5008	6117	6541
ENSMUSG00000025971	chr1	9430016H08Rik	5.7E+07	5.7E+07	7878	-0.33957373	4.235270589	0.0429109	0.079224505	0.03033	0	314	215	400	287	383	360	405	262	365	320
ENSMUSG00000013419	chr9	Zfp651	1.2E+08	1.2E+08	6353	-0.51969428	7.50926617	0.0429539	0.079293332	0.07812	0	2434	2107	4838	4487	2523	2752	4759	1769	3418	2987
ENSMUSG00000032386	chr9	Trip4	6.6E+07	6.6E+07	8394	-0.34382398	4.356615789	0.0429839	0.07933841	0.03179	0	338	286	421	302	366	451	448	271	352	350
ENSMUSG00000045930	chr12	Clec14a	5.8E+07	5.8E+07	4539	0.39077251	3.720425465	0.0430072	0.079360388	0.03989	0	166	121	211	126	242	381	304	240	338	273
ENSMUSG00000052331	chr1	Ankrd44	5.5E+07	5.5E+07	14175	-0.56693813	3.518429496	0.0430065	0.079360388	0.08842	0	224	207	126	127	313	253	198	136	140	232
ENSMUSG00000044317	chr7	Gpr4	1.9E+07	1.9E+07	2884	0.535033252	2.406283196	0.0430131	0.079361002	0.07288	0	41	27	98	69	100	125	139	95	148	126
ENSMUSG00000030094	chr6	Xpc	9.1E+07	9.1E+07	5490	-0.39702858	3.652175477	0.0430313	0.079384117	0.0413	0	218	136	327	196	213	292	252	137	233	219
ENSMUSG00000042487	chr9	Leo1	7.5E+07	7.5E+07	2192	-0.36413317	4.863011881	0.0431342	0.079563427	0.03692	0	519	409	476	532	481	594	663	367	540	479
ENSMUSG00000081485	chr11	Gm12338	7.6E+07	7.6E+07	192	0.357900794	5.846904433	0.0431814	0.079640081	0.03637	0	814	511	889	785	813	1554	1249	1119	1379	1346
ENSMUSG00000089889	chr5	0610040B10Rik	1.4E+08	1.4E+08	683	0.598283637	1.161436868	0.0432026	0.079668604	0.07698	0	25	12	34	24	35	65	45	51	39	61
ENSMUSG00000035443	chr9	Thyn1	2.7E+07	2.7E+07	959	0.367686529	4.098573431	0.0434538	0.080121371	0.03581	0	203	176	300	232	209	441	379	348	382	417
ENSMUSG00000046413	chr8	Irx3os	9.2E+07	9.2E+07	3687	-0.83543081	2.609028424	0.0434649	0.080131188	0.19062	0	32	48	290	123	138	70	174	48	85	75
ENSMUSG00000031960	chr8	Aars	1.1E+08	1.1E+08	9282	-0.4310899	6.922242383	0.043478	0.080134411	0.05386	0	1575	1225	3405	2532	2078	2113	2360	1668	2366	2136
ENSMUSG00000033701	chr1	Acbd6	1.6E+08	1.6E+08	6453	0.373681647	4.97395075	0.0434749	0.080134411	0.03918	0	361	239	572	446	492	750	577	564	963	786
ENSMUSG00000037426	chr5	Depdc5	3.3E+07	3.3E+07	11767	-0.4273159	3.473176726	0.0435639	0.080282051	0.04777	0	133	131	256	239	208	197	235	123	224	201
ENSMUSG00000027469	chr2	Tpx2	1.5E+08	1.5E+08	4677	-0.6958729	2.314631205	0.0436042	0.080345898	0.12704	0	157	37	88	44	140	99	79	73	69	63
ENSMUSG00000058706	chr6	0610030E20Rik	7.2E+07	7.2E+07	4632	-0.37401467	4.01557663	0.0436423	0.080405529	0.03765	0	300	228	262	258	301	354	331	219	256	296
ENSMUSG00000026065	chr1	Slc9a4	4.1E+07	4.1E+07	4562	1.219229985	0.051110515	0.0436753	0.080455677	0.35996	0	2	0	32	8	3	17	31	15	28	39
ENSMUSG00000037805	chr17	Rpl10a	2.8E+07	2.8E+07	2349	0.407370101	7.362550044	0.0437841	0.08064547	0.04834	0	1952	1730	2104	2169	2640	4470	3256	2911	4499	4283
ENSMUSG00000030546	chr7	Plin1	8E+07	8E+07	1916	-1.72709724	5.657410159	0.0438024	0.080668635	0.80047	0	1016	639	12	30	4532	874	189	426	497	444
ENSMUSG00000053198	chr7	Prx	2.7E+07	2.7E+07	5579	0.462979792	3.306848881	0.0438227	0.080695389	0.05583	0	92	86	179	150	121	306	220	119	267	286
ENSMUSG00000052833	chr7	Sae1	1.6E+07	1.6E+07	1884	0.359575447	5.934326252	0.0439187	0.080861691	0.03705	0	746	583	914	851	956	1689	1284	1216	1493	1377
ENSMUSG00000007805	chr1	Twist2	9.2E+07	9.2E+07	3174	0.901439529	0.827927414	0.043946	0.080894637	0.19711	0	16	11	11	12	38	73	12	36	63	38
ENSMUSG00000031990	chr9	Jam3	2.7E+07	2.7E+07	2539	0.459156895	3.380277654	0.0439482	0.080894637	0.057	0	104	63	206	106	208	288	226	217	239	255
ENSMUSG00000034936	chr11	Arl4d	1E+08	1E+08	1382	0.453351277	2.569633196	0.0439548	0.080896276	0.04989	0	61	48	94	76	98	171	113	99	153	163
ENSMUSG00000042354	chr14	Gnl3	3.1E+07	3.1E+07	1883	-0.37605944	4.581379891	0.0440352	0.081022835	0.03923	0	428	366	432	374	390	517	430	401	387	392
ENSMUSG00000081534	chr15	Slc48a1	9.8E+07	9.8E+07	2690	0.406956514	6.233709914	0.0440322	0.081022835	0.04806	0	811	534	1216	904	1598	1937	1882	1181	2007	1923
ENSMUSG00000027067	chr2	Ssrp1	8.5E+07	8.5E+07	3737	0.355989058	5.599192126	0.04407	0.081076338	0.03618	0	567	418	800	621	857	1400	926	901	1184	1205
ENSMUSG00000036864	chr7	Proser3	3.1E+07	3.1E+07	3512	-0.55478471	1.642048412	0.0440791	0.081082363	0.07173	0	59	42	59	64	45	42	66	39	51	55
ENSMUSG00000049439	chr1	Cyp20a1	6E+07	6E+07	2286	0.49509983	3.251813504	0.0440869	0.081086218	0.06476	0	92	114	113	85	181	349	215	183	203	196
ENSMUSG00000054099	chr5	Slc25a40	8422850	8423039	2777	-0.46323459	2.422554027	0.0441106	0.081119159	0.05165	0	82	67	113	91	112	115	122	71	71	82
ENSMUSG00000028889	chr4	Yrdc	1.2E+08	1.2E+08	1981	0.395033948	3.504201387	0.0441438	0.081169524	0.04064	0	111	104	201	137	193	321	240	223	238	294
ENSMUSG00000033106	chr8	Slc7a6os	1.1E+08	1.1E+08	1525	0.407086018	3.368036334	0.0441587	0.081175616	0.04294	0	121	79	158	132	186	295	207	205	218	275

ENSMUSG00000039834	chr2	Zfp335	1.6E+08	1.6E+08	4743	-0.3802754	3.757390537	0.0441531	0.081175616	0.03832	0	199	163	321	249	225	290	241	158	292	238
ENSMUSG00000096957	chr8	E230013L22Rik	1.1E+07	1.1E+07	1856	-0.80680821	0.538627343	0.0441663	0.081178979	0.14021	0	19	9	62	18	31	24	27	16	12	23
ENSMUSG00000025921	chr1	Rdh10	1.6E+07	1.6E+07	4160	0.52348865	2.252966384	0.044325	0.081459988	0.06792	0	55	40	67	36	95	115	115	107	104	118
ENSMUSG00000020315	chr11	Sptbn1	3E+07	3E+07	17492	-0.41861161	7.419791949	0.0443767	0.081544376	0.0514	0	2253	1972	3664	2631	4673	3865	3665	1979	2622	3255
ENSMUSG00000081049	chrX	Rps24-ps3	7.9E+07	7.9E+07	402	0.501575702	2.113785954	0.0443917	0.081561202	0.05675	0	54	45	50	47	64	133	94	82	109	92
ENSMUSG00000020325	chr10	Fstl3	8E+07	8E+07	2445	0.649065596	1.902492848	0.0445445	0.081831144	0.10314	0	37	45	25	29	72	106	73	80	88	106
ENSMUSG00000052593	chr12	Adam17	2.1E+07	2.1E+07	7154	0.350807503	5.470758513	0.0445643	0.081856765	0.03505	0	515	418	873	602	559	1261	1105	750	1005	1042
ENSMUSG00000019326	chr11	Aoc3	1E+08	1E+08	4621	-1.15374417	5.681165685	0.044604	0.081918989	0.37786	0	850	738	168	159	3668	1112	351	606	572	647
ENSMUSG00000073792	chr4	Alg6	1E+08	1E+08	8544	-0.47423075	2.814381429	0.0447191	0.082119605	0.05827	0	143	101	163	94	103	123	139	92	119	128
ENSMUSG00000044348	chrX	Slc25a53	1.4E+08	1.4E+08	7963	-0.59361734	0.936515498	0.0447281	0.082125391	0.07077	0	34	23	33	27	50	39	25	21	36	30
ENSMUSG00000004562	chr14	Arhgef40	5.2E+07	5.2E+07	10366	0.425877091	4.463734254	0.0448401	0.082320353	0.0512	0	190	191	349	219	514	662	455	352	528	633
ENSMUSG00000036534	chr8	Slc38a7	9.6E+07	9.6E+07	4144	0.389280091	3.415312163	0.0448629	0.082351325	0.03916	0	111	92	178	152	167	320	251	157	254	273
ENSMUSG00000026893	chr2	Gca	6.3E+07	6.3E+07	3409	-0.64020149	1.613461842	0.0448852	0.082381491	0.0991	0	57	23	101	55	47	44	75	36	44	41
ENSMUSG00000037216	chr1	Lipt1	3.8E+07	3.8E+07	2051	-0.4468068	2.714063156	0.0449444	0.08247942	0.04911	0	103	60	141	116	159	118	121	78	130	122
ENSMUSG00000029447	chr5	Cct6a	1.3E+08	1.3E+08	1599	-0.36505636	6.522076663	0.0449543	0.082486826	0.03897	0	1406	1199	1995	1469	1768	1856	1904	1348	1603	1578
ENSMUSG00000024208	chr17	Uqcc2	2.7E+07	2.7E+07	837	0.398218291	6.927643801	0.0449622	0.082490428	0.04655	0	1493	1267	1679	1707	1701	3020	2615	2150	3596	2906
ENSMUSG00000022840	chr16	Adcy5	3.5E+07	3.5E+07	7007	-0.96116282	3.147180908	0.0450456	0.082632614	0.26036	0	122	157	45	56	512	187	71	106	130	123
ENSMUSG00000062127	chr3	Cttnbp2nl	1.1E+08	1.1E+08	5000	0.419130041	3.380906603	0.045053	0.082635511	0.04694	0	94	79	203	131	181	306	306	165	228	229
ENSMUSG00000002546	chr2	Golga2	3.2E+07	3.2E+07	5500	-0.37328323	6.347176063	0.0451318	0.082769231	0.04079	0	1252	968	1725	1602	1413	1662	1591	946	1623	1585
ENSMUSG00000035172	chr11	Plekhh3	1E+08	1E+08	3582	-0.38263106	5.054499071	0.0452057	0.082893781	0.04172	0	353	378	778	697	688	581	661	400	728	619
ENSMUSG00000045128	chr8	Rpl18a	7.1E+07	7.1E+07	1291	0.392407079	8.344125209	0.0452127	0.082895926	0.04566	0	4063	3135	4400	4641	4904	8630	7143	5565	8325	8604
ENSMUSG00000041238	chr18	Rbbp8	1.2E+07	1.2E+07	3867	0.58571734	1.633418243	0.0452874	0.083021931	0.08309	0	38	20	52	27	47	119	47	63	70	72
ENSMUSG00000014769	chr17	Psmb1	1.5E+07	1.5E+07	1036	0.381789209	7.167298972	0.0453096	0.083030098	0.04303	0	1873	1342	2203	1715	2348	4069	2968	2725	3400	3630
ENSMUSG00000031851	chr8	Ntpcr	1.3E+08	1.3E+08	2673	0.370815095	3.682262666	0.0453079	0.083030098	0.03621	0	166	107	222	174	178	387	270	228	310	295
ENSMUSG00000075600	chr15	Zc3h3	7.6E+07	7.6E+07	3360	0.527867036	2.037408277	0.0452989	0.083030098	0.06652	0	61	29	60	38	61	107	107	53	122	104
ENSMUSG00000025499	chr7	Hras	1.4E+08	1.4E+08	3733	0.402744081	6.246549089	0.0453176	0.08303396	0.04743	0	1025	776	998	986	1093	1713	1857	1294	2392	1662
ENSMUSG00000026035	chr1	Ppil3	5.8E+07	5.8E+07	4291	0.438328259	3.122819028	0.0453248	0.08303621	0.0505	0	116	58	129	95	167	260	194	174	194	199
ENSMUSG00000081769	chr11	Gm12216	5.4E+07	5.4E+07	2647	0.774421602	0.860934923	0.0453794	0.083125433	0.13323	0	24	14	14	15	26	72	22	28	33	69
ENSMUSG00000032363	chr9	Adamts7	9E+07	9E+07	6282	0.682837255	1.119494465	0.0454338	0.083214141	0.11272	0	18	8	29	16	54	58	59	39	58	47
ENSMUSG00000066842	chr1	Hmcn1	1.5E+08	1.5E+08	21191	-0.5513689	1.993270726	0.0454887	0.083303947	0.07581	0	54	76	68	64	79	78	67	65	60	53
ENSMUSG00000021130	chr12	Galnt16	8.1E+07	8.1E+07	3920	0.478201501	3.65227187	0.0455014	0.083316281	0.06292	0	141	118	145	115	276	465	276	207	341	233
ENSMUSG00000064193	chr2	Gm4735	8.1E+07	8.1E+07	1302	0.575630857	3.519147041	0.0455701	0.083431116	0.09391	0	113	59	120	109	323	286	259	249	331	262
ENSMUSG00000005907	chr5	Pex1	3596066	3596517	7740	-0.44062486	2.862379764	0.0455817	0.083441519	0.04859	0	109	72	175	108	180	155	127	98	134	118
ENSMUSG00000096199	chr12	Ptrhd1	4234027	4234278	4013	0.414499154	3.224643951	0.0456841	0.083618033	0.04432	0	115	91	114	124	151	278	195	162	254	206
ENSMUSG00000028676	chr4	Srsf10	1.4E+08	1.4E+08	7003	-0.32938222	4.624742936	0.0457263	0.083684314	0.03001	0	352	289	585	380	497	567	550	341	393	418
ENSMUSG00000029229	chr5	Chic2	7.5E+07	7.5E+07	6712	0.420420766	3.300121675	0.0457503	0.083717303	0.04569	0	116	112	131	103	161	282	237	206	206	214
ENSMUSG00000075703	chr5	Ept1	3E+07	3E+07	10855	-0.33870639	3.984514653	0.0457956	0.083789273	0.03071	0	255	196	294	271	312	348	330	214	283	270
ENSMUSG00000021660	chr13	Btf3	9.8E+07	9.8E+07	1739	0.393480833	7.223012463	0.0458141	0.083812342	0.04594	0	1965	1469	2154	1808	2340	4386	2954	2984	3408	3744
ENSMUSG00000012114	chr16	Med15	1.8E+07	1.8E+07	3383	0.328647087	4.542484372	0.0458829	0.083927177	0.02995	0	251	201	368	315	449	582	557	393	549	597
ENSMUSG00000056220	chr1	Pla2g4a	1.5E+08	1.5E+08	6391	0.68401962	1.45067489	0.0459081	0.083962368	0.11027	0	27	27	23	34	37	109	100	36	37	60
ENSMUSG00000000078	chr13	Klf6	5861489	5861842	4217	0.344135353	5.193133371	0.045941	0.084011489	0.0338	0	406	379	524	431	703	978	925	648	713	968
ENSMUSG00000015092	chr2	Edf1	2.6E+07	2.6E+07	1317	0.374718481	6.673189872	0.0459628	0.084031357	0.04154	0	1121	951	1762	1305	1661	2637	2104	1836	2741	2574
ENSMUSG00000024065	chr17	Ehd3	7.4E+07	7.4E+07	3658	0.503964342	2.702608183	0.0459758	0.084031357	0.06638	0	65	60	82	53	146	169	160	129	170	143
ENSMUSG00000039016	chr9	Timm8b	5.1E+07	5.1E+07	527	-0.37210523	6.006940558	0.045972	0.084031357	0.04062	0	1147	794	1384	1127	1006	1300	1315	920	1226	1026
ENSMUSG00000073725	chr1	Lmbrd1	2.5E+07	2.5E+07	5960	-0.34413986	5.62771425	0.0459689	0.084031357	0.03438	0	790	589	1092	830	900	1057	1149	632	867	834
ENSMUSG00000018974	chr5	Sart3	1.1E+08	1.1E+08	3586	0.383524687	3.818322471	0.0459993	0.084042219	0.04037	0	151	97	249	176	277	389	340	228	366	328
ENSMUSG00000033029	chr15	1700088E04Rik	7.9E+07	7.9E+07	5292	0.774664333	0.636813482	0.0459997	0.084042219	0.12908	0	12	5	23	28	13	42	40	15	42	51
ENSMUSG00000045100	chr6	Slc25a26	9.5E+07	9.5E+07	1915	-0.33361495	4.465927538	0.0459981	0.084042219	0.03071	0	367	257	475	326	449	439	443	279	485	379
ENSMUSG00000020456	chr11	Ogdh	6291633	6291693	5456	-0.52108523	10.11580874	0.0460902	0.084189462	0.08115	0	14992	9327	35123	25807	17523	16288	26036	12420	19527	20488
ENSMUSG00000058546	chr11	Rpl23a	7.8E+07	7.8E+07	847	0.387194693	7.659961341	0.0460923	0.084189462	0.04472	0	2468	1838	3098	2686	3246	5827	3919	3678	4861	5451
ENSMUSG00000037916	chr19	Ndufv1	4007497	4007665	2521	-0.51536495	8.830878804	0.046103	0.084198088	0.07932	0	6077	3739	14914	10314	7204	7461	10775	5149	7950	7720
ENSMUSG00000020486	chr11	Sept4	8.8E+07	8.8E+07	3563	0.49634808	4.063003839	0.0461621	0.084295018	0.07081	0	137	100	277	169	417	553	314	275	407	483
ENSMUSG00000046707	chr8	Csnk2a2	9.5E+07	9.5E+07	3766	0.35861148	3.811209015	0.0461753	0.084308133	0.03385	0	172	143	197	190	216	386	312	247	364	311
ENSMUSG00000025413	chr4	Ttc4	1.1E+08	1.1E+08	3568	-0.33744695	5.602214623	0.0461882	0.084320723	0.0331	0	709	664	972	851	873	1003	971	650	916	909
ENSMUSG00000029617	chr5	Ccz1	1.4E+08	1.4E+08	1762	-0.33321159	5.248939634	0.0462475	0.084418006	0.03201	0	604	522	698	611	738	865	864	480	655	647
ENSMUSG00000038077	chr6	Kcna6	1.3E+08	1.3E+08	5945	0.878788143	0.259803454	0.0463213	0.0845416	0.15572	0	15	7	12	5	18	63	22	10	27	27
ENSMUSG00000067370	chr17	B3galt4	3.4E+07	3.4E+07	1569	0.681515141	1.134980718	0.0463499	0.084582769	0.10565	0	14	19	21	25	42	64	36	38	80	46
ENSMUSG00000030602	chr7	Pak4	2.8E+07	2.8E+07	7845	0.350562274	4.557337066	0.0463713	0.084610856	0.03469	0	247	188	349	330	479	574	568	429	608	531
ENSMUSG00000029135	chr5	Fosl2	3.2E+07	3.2E+07	5855	0.379340513	4.567287768	0.046451	0.084745199	0.04076	0	232	222	299	327	487	551	556	406	540	707
ENSMUSG00000101645	chr2	Gm28635	8.5E+07	8.5E+07	4734	-0.35110651	5.71643816	0.0464773	0.084782171	0.03609	0	743	681	1106	895	1041	1094	1221	663	961	874
ENSMUSG00000030759	chr7	Far1	1.1E+08	1.1E+08	8055	0.379972077	3.912184312	0.0465345	0.084875567	0.03877	0	175	181	224	150	242	435	385	255	309	375
ENSMUSG00000047123	chr17	Ticam1	5.6E+07	5.6E+07	2992	0.452335489	2.712296969	0.0465764	0.084940948	0.05319	0	68	43	112	78	123	197	134	108	171	165
ENSMUSG00000027765	chr3	P2ry1	6.1E+07	6.1E+07	4291	-0.5714124	3.780704397	0.0465964	0.084966422	0.09324	0	193	110	525	295	168	260	345	147	185	215
ENSMUSG00000052423	chr1	B4galt3	1.7E+08	1.7E+08	5467	0.387935527	3.595048908	0.0466042	0.084969561	0.03997	0	147	121	171	136	210	345	231	218	310	300
ENSMUSG00000015176	chr19	Nolc1	4.6E+07	4.6E+07	3634	-0.3419703	5.029634703	0.0466275	0.085000898	0.03334	0	412	380	787	637	574	659	642	505	554	598
ENSMUSG00000044813	chr4	Shb	4.5E+07	4.5E+07	3199	0.497738226	2.804632523	0.0466351	0.085003738	0.06565	0	76	62	87	82	126	178	110	167	181	179
ENSMUSG00000049929	chrX	Lpar4	1.1E+08	1.1E+08	4238	0.713175495	1.109602849	0.0466422	0.08500563	0.11429	0	26	24	19	17	27	104	38	38	43	43

ENSMUSG00000034949	chr10	Zfr2	8.1E+07	8.1E+07	7483	0.493496778	1.797802217	0.0466705	0.085046174	0.05355	0	36	35	53	35	52	92	78	58	83	96
ENSMUSG00000020680	chr11	Taf15	8.3E+07	8.3E+07	2919	0.330448796	5.017636381	0.0466818	0.085055711	0.03121	0	414	275	517	407	583	946	625	579	732	848
ENSMUSG00000002504	chr17	Slc9a3r2	2.5E+07	2.5E+07	2257	0.401673797	5.08971609	0.0467337	0.085139184	0.04731	0	308	222	796	422	576	825	830	549	929	881
ENSMUSG00000013275	chr1	Slc41a1	1.3E+08	1.3E+08	4912	-0.74278209	6.043719927	0.0467663	0.085181507	0.16343	0	826	362	3361	1487	699	973	1691	679	724	1081
ENSMUSG00000058192	chr9	Zfp846	2.1E+07	2.1E+07	2861	-0.55063925	1.442376021	0.0467691	0.085181507	0.06793	0	43	41	51	40	60	41	63	35	37	44
ENSMUSG00000047583	chr3	Tyw3	1.5E+08	1.5E+08	4499	-0.58874034	1.630028355	0.0468043	0.085234717	0.08542	0	32	59	72	48	59	66	57	24	56	51
ENSMUSG00000037926	chr11	Ssh2	7.7E+07	7.7E+07	18519	-0.43881808	6.101855392	0.0468413	0.085290953	0.05723	0	1018	702	2076	1295	1037	1250	1557	819	989	1459
ENSMUSG00000069833	chr19	Ahnak	8989284	8989429	18543	0.403488471	8.56755356	0.046861	0.085315749	0.04905	0	4458	3700	4897	4374	7393	11305	8902	6814	9128	8741
ENSMUSG00000059119	chr7	Nap1l4	1.4E+08	1.4E+08	2283	-0.39355009	7.875285875	0.0468887	0.085354458	0.04659	0	3733	2799	5376	4318	4046	4164	5211	3171	4523	3914
ENSMUSG00000073910	chr4	Mob3b	3.5E+07	3.5E+07	6200	0.715311523	1.410734356	0.0468944	0.085354458	0.12514	0	26	20	16	23	61	79	54	36	62	99
ENSMUSG00000027298	chr2	Tyro3	1.2E+08	1.2E+08	6198	0.701323784	0.664865422	0.0469545	0.085445866	0.10716	0	17	11	23	12	22	72	25	31	35	26
ENSMUSG00000068877	chr3	Selenbp2	9.5E+07	9.5E+07	2271	-0.7612349	0.237642326	0.0469568	0.085445866	0.11901	0	18	20	11	28	24	17	22	7	17	22
ENSMUSG00000032305	chr9	Fam219b	5.8E+07	5.8E+07	3055	0.359854586	4.04850543	0.0469929	0.085500443	0.0354	0	184	157	243	205	310	463	347	258	446	412
ENSMUSG00000001300	chr8	Efnb2	8617434	8620976	4324	-0.4539465	3.162271368	0.0470085	0.085506658	0.0543	0	137	90	259	133	180	154	198	128	123	168
ENSMUSG00000045664	chr19	Cdc42ep2	5917556	5918993	1491	0.404750043	5.230331717	0.0470049	0.085506658	0.04819	0	340	251	712	634	579	839	877	627	1112	955
ENSMUSG00000079049	chr13	Serpinb1c	3.3E+07	3.3E+07	1353	0.799876894	1.174777891	0.0470932	0.085638481	0.15803	0	49	10	22	17	18	54	86	52	47	38
ENSMUSG00000098399	chr7	Gm27995	1E+08	1E+08	100	0.750766653	0.295350111	0.0470884	0.085638481	0.10774	0	17	6	18	6	16	45	20	18	27	35
ENSMUSG00000079109	chr5	Pms2	1.4E+08	1.4E+08	8442	-0.49059694	2.468595044	0.0471389	0.085710507	0.06093	0	111	76	118	64	111	91	122	72	88	95
ENSMUSG00000079363	chr5	Gbp4	1.1E+08	1.1E+08	4538	0.875248582	3.465216254	0.0471675	0.085751329	0.22142	0	79	84	172	132	121	993	169	85	141	202
ENSMUSG00000026942	chr2	Traf2	2.6E+07	2.6E+07	5101	0.318594194	4.594908602	0.0471936	0.085765321	0.02807	0	265	259	380	336	376	693	559	424	561	534
ENSMUSG00000071054	chr17	Safb	5.7E+07	5.7E+07	7268	0.338323427	5.640707359	0.0471851	0.085765321	0.03357	0	567	454	867	615	878	1322	1093	834	1256	1268
ENSMUSG00000087381	chr4	Gm16008	1.6E+08	1.6E+08	1324	-0.65966277	1.250159046	0.0471904	0.085765321	0.10498	0	33	50	58	26	41	39	52	19	31	46
ENSMUSG00000042857	chr13	Gm9776	9.4E+07	9.4E+07	2980	0.701858714	0.203158372	0.0472384	0.085835774	0.08336	0	11	8	16	6	19	29	34	20	22	27
ENSMUSG00000032103	chr9	Pus3	3.6E+07	3.6E+07	2972	-0.3749477	3.954448645	0.0473482	0.086024145	0.03905	0	262	230	271	249	281	295	342	220	233	297
ENSMUSG00000020893	chr11	Per1	6.9E+07	6.9E+07	5631	-0.46268137	4.173107467	0.0473759	0.086063265	0.06133	0	172	229	502	387	311	263	300	227	401	364
ENSMUSG00000026922	chr2	Agpat2	2.7E+07	2.7E+07	2130	-1.14925854	5.621674136	0.047395	0.086086764	0.38451	0	917	265	311	139	3996	919	395	587	734	502
ENSMUSG00000026255	chr1	Efhd1	8.7E+07	8.7E+07	2125	0.595953689	3.45372791	0.0474088	0.086100663	0.10097	0	94	104	78	93	291	390	229	179	277	293
ENSMUSG00000019577	chr6	Pdk4	5483351	5485592	3511	-0.90669409	9.481867088	0.047431	0.086129972	0.24415	0	14919	1710	36981	14834	8155	11965	9031	9585	4835	15565
ENSMUSG00000066000	chr4	2610305D13Rik	1.5E+08	1.5E+08	4111	-0.55620557	2.036570982	0.047515	0.08627116	0.07755	0	62	28	117	89	79	85	70	39	72	75
ENSMUSG00000022561	chr15	Gpaa1	7.6E+07	7.6E+07	2846	0.345629966	5.176993634	0.0475507	0.086324977	0.03462	0	386	353	567	546	558	859	765	588	1060	909
ENSMUSG00000005609	chr7	Ctr9	1.1E+08	1.1E+08	6544	-0.3332649	4.772730784	0.0475664	0.086342306	0.03181	0	401	385	520	510	452	598	517	372	551	465
ENSMUSG00000031434	chrX	Morc4	1.4E+08	1.4E+08	6051	0.419328675	3.274010184	0.0475974	0.086387342	0.04671	0	131	93	120	102	171	274	225	200	225	200
ENSMUSG00000001285	chr15	Myg1	1E+08	1E+08	2823	0.42094014	3.782460056	0.0476202	0.086417428	0.04949	0	147	119	170	157	304	397	267	236	381	341
ENSMUSG00000039737	chr5	Prkrip1	1.4E+08	1.4E+08	3967	0.340457103	3.99703655	0.0477003	0.086551595	0.03174	0	182	138	271	199	287	432	349	288	393	371
ENSMUSG00000029385	chr5	Ccng2	9.3E+07	9.3E+07	5458	-0.35744241	4.490933796	0.0477235	0.086582571	0.03631	0	425	243	486	308	464	492	528	277	337	421
ENSMUSG00000022074	chr14	Tnfrsf10b	7E+07	7E+07	3171	0.644711949	1.536629463	0.0477391	0.086599689	0.10219	0	24	24	38	16	66	88	62	66	73	58
ENSMUSG00000000142	chr11	Axin2	1.1E+08	1.1E+08	5506	-0.50576381	2.864821009	0.0477576	0.086607781	0.06816	0	108	61	176	116	204	112	121	97	108	174
ENSMUSG00000029175	chr5	Slc35f6	3.1E+07	3.1E+07	3311	0.327391357	4.538870124	0.0477505	0.086607781	0.0304	0	268	179	461	302	385	621	537	387	548	584
ENSMUSG00000096458	chr12	Moap1	1E+08	1E+08	1328	-0.45450025	2.732053534	0.0477621	0.086607781	0.05263	0	102	69	188	96	134	138	121	100	105	106
ENSMUSG00000028551	chr4	Cdkn2c	1.1E+08	1.1E+08	2686	-0.80437996	3.872922685	0.0477771	0.086623826	0.1897	0	306	219	97	97	694	333	154	183	247	184
ENSMUSG00000033751	chr8	Gadd45gip1	8.5E+07	8.5E+07	2494	0.370930234	4.921888934	0.0478635	0.086769184	0.04016	0	284	246	590	487	428	712	627	550	793	827
ENSMUSG00000045411	chr7	2410002F23Rik	4.4E+07	4.4E+07	5233	0.503708163	3.076436051	0.0478896	0.086786195	0.06913	0	77	94	125	80	144	291	146	165	148	262
ENSMUSG00000054034	chrX	Tceal5	1.4E+08	1.4E+08	1263	0.39166841	5.134145478	0.0478842	0.086786195	0.04459	0	489	426	412	483	399	991	725	643	893	857
ENSMUSG00000098624	chr5	Mir7036	1.4E+08	1.4E+08	65	1.013075351	-0.27023001	0.0478914	0.086786195	0.20766	0	2	8	2	5	18	25	10	17	17	28
ENSMUSG00000030104	chr6	Edem1	1.1E+08	1.1E+08	5858	0.52601878	4.341666817	0.0479039	0.086797572	0.08102	0	235	173	169	160	534	709	442	390	466	468
ENSMUSG00000033576	chr15	Apol6	7.7E+07	7.7E+07	4499	-0.63501801	5.600374232	0.0479514	0.086852082	0.12066	0	453	254	1423	843	1890	825	1034	504	568	1039
ENSMUSG00000036992	chr2	Nxt1	1.5E+08	1.5E+08	1116	0.456973799	2.468319336	0.0479526	0.086852082	0.05212	0	66	49	82	63	87	184	107	107	134	117
ENSMUSG00000041920	chr11	Slc16a6	1.1E+08	1.1E+08	4883	-0.5415648	2.49996734	0.0479447	0.086852082	0.07624	0	86	53	158	132	80	86	113	90	83	90
ENSMUSG00000026890	chr2	Lhx6	3.6E+07	3.6E+07	4805	0.643494414	1.042684715	0.0479665	0.086866074	0.09406	0	13	15	35	14	41	54	67	32	50	43
ENSMUSG00000020121	chr10	Srgap1	1.2E+08	1.2E+08	9132	0.687643941	1.318422767	0.0480569	0.087018524	0.11163	0	23	26	21	13	54	67	55	52	70	56
ENSMUSG00000021540	chr13	Smad5	5.7E+07	5.7E+07	7420	-0.32829064	5.44105371	0.0480692	0.087029722	0.03164	0	713	526	813	773	819	950	873	613	819	732
ENSMUSG00000024493	chr18	Lars	4.2E+07	4.2E+07	3856	-0.35231037	5.784181434	0.0480847	0.08704359	0.03687	0	855	659	1315	957	913	1157	1173	794	925	956
ENSMUSG00000026427	chr1	Eif2d	1.3E+08	1.3E+08	7374	-0.3121418	5.072359617	0.0480893	0.08704359	0.02803	0	518	400	677	610	612	615	672	473	674	657
ENSMUSG00000071291	chr13	Zfp58	6.7E+07	6.7E+07	2435	-0.5296032	1.92648617	0.0481063	0.087063074	0.0701	0	68	65	59	61	70	77	72	44	47	77
ENSMUSG00000004105	chr2	Angptl2	3.3E+07	3.3E+07	6286	0.465040905	6.692661547	0.0481284	0.087091849	0.0653	0	1535	1096	839	1139	1802	2943	2263	2003	2574	2594
ENSMUSG00000022484	chr15	Hoxc10	1E+08	1E+08	1909	-0.37506286	6.469521952	0.0482104	0.087217713	0.04241	0	1425	1087	1854	1340	1918	1570	2091	1066	1638	1664
ENSMUSG00000024150	chr17	Mcfd2	8.7E+07	8.7E+07	2612	0.358279108	5.537656829	0.048205	0.087217713	0.03795	0	595	448	594	584	853	1337	1026	919	1102	983
ENSMUSG00000048087	chr16	Gm4737	4.6E+07	4.6E+07	2081	-0.66687308	0.689481808	0.0482247	0.087232264	0.09921	0	34	24	26	26	29	36	34	18	23	12
ENSMUSG00000025133	chr7	Ints4	9.7E+07	9.7E+07	3243	-0.31961399	4.426245802	0.0482604	0.087274385	0.02846	0	317	250	502	336	417	441	427	286	433	391
ENSMUSG00000032370	chr9	Lactb	6.7E+07	6.7E+07	2031	-0.32900937	4.291458858	0.0482567	0.087274385	0.03024	0	311	255	393	337	337	366	396	259	382	387
ENSMUSG00000017667	chr2	Zfp334	1.7E+08	1.7E+08	8205	-0.48813889	2.335270437	0.0482813	0.087300994	0.06184	0	96	78	102	86	66	105	85	62	89	88
ENSMUSG00000024414	chr11	Mrpl27	9.5E+07	9.5E+07	985	0.320940911	5.253564891	0.0483405	0.087374283	0.02994	0	524	365	570	486	615	1008	811	697	892	956
ENSMUSG00000027170	chr2	Eif3m	1E+08	1E+08	2590	-0.36732465	6.077616272	0.0483318	0.087374283	0.04049	0	1136	859	1524	1119	1103	1468	1445	965	1095	1136
ENSMUSG00000078184	chr1	B020018G12Rik	1.8E+08	1.8E+08	1338	0.742340671	0.169414486	0.0483376	0.087374283	0.09578	0	8	10	10	15	13	30	16	26	26	30
ENSMUSG00000037341	chrX	Slc9a7	2E+07	2E+07	3819	-0.76413727	1.078768778	0.0483554	0.087389873	0.14608	0	33	39	43	58	13	29	30	29	30	36
ENSMUSG00000024205	chr11	Rpl36-ps2	7.7E+07	7.7E+07	311	0.724789948	0.46907488	0.0483637	0.087393541	0.11053	0	14	5	12	18	24	28	31	18	47	39
ENSMUSG00000025050	chr19	Pcgf6	4.7E+07	4.7E+07	2098	-0.46628009	2.422330367	0.0483939	0.087422813	0.05415	0	74	75	115	74	128	108	102	69	106	74

ENSMUSG00000039842	chr8	Mcph1	1.9E+07	1.9E+07	7806	-0.47205096	2.483586874	0.0483872	0.087422813	0.0578	0	80	67	117	107	117	122	129	50	106	80
ENSMUSG00000047669	chr10	Msl3l2	5.6E+07	5.6E+07	2140	0.74034363	0.271280988	0.0483986	0.087422813	0.10702	0	14	9	9	9	20	47	19	18	34	24
ENSMUSG00000003604	chr2	Aven	1.1E+08	1.1E+08	5001	0.380610686	3.898236824	0.0484508	0.087505842	0.04002	0	198	132	169	219	251	367	334	256	394	380
ENSMUSG00000041199	chr17	Rpusd1	2.6E+07	2.6E+07	1703	0.419099146	2.620028172	0.048489	0.087563713	0.044	0	69	48	105	77	98	179	149	95	152	146
ENSMUSG00000031024	chr7	St5	1.1E+08	1.1E+08	4526	0.427582363	3.69064195	0.0485587	0.087678291	0.05107	0	101	139	209	159	223	434	249	254	267	317
ENSMUSG00000041926	chr1	Rnpep	1.4E+08	1.4E+08	6977	0.341513006	4.77680087	0.0485801	0.087705538	0.03372	0	304	243	394	360	548	738	575	491	741	611
ENSMUSG00000036513	chr3	Commd2	5.8E+07	5.8E+07	4757	0.412161934	3.520769965	0.0486817	0.08787768	0.04621	0	122	127	144	138	201	377	232	217	241	279
ENSMUSG00000016946	chr17	Kctd5	2.4E+07	2.4E+07	2751	0.388497376	3.556199285	0.0487166	0.087911295	0.04041	0	144	128	150	143	190	338	235	220	290	281
ENSMUSG00000036572	chrX	Upf3b	3.7E+07	3.7E+07	3999	-0.34279816	4.200637669	0.0487123	0.087911295	0.03309	0	302	250	370	308	303	363	401	244	347	319
ENSMUSG00000087249	chr11	Gm16062	6E+07	6E+07	771	-0.49831179	3.246605301	0.0487191	0.087911295	0.0708	0	165	158	156	204	119	206	185	82	178	174
ENSMUSG00000039209	chr16	Rpl39l	1E+07	1E+07	831	0.885107074	0.547677669	0.0488233	0.088087914	0.18755	0	13	13	7	3	35	44	28	28	32	47
ENSMUSG00000029761	chr6	Cald1	3.5E+07	3.5E+07	7687	0.357615355	5.501918169	0.0488915	0.088188333	0.03795	0	494	486	627	532	862	1401	1003	806	996	1076
ENSMUSG00000054280	chr5	Prr14l	3.3E+07	3.3E+07	11004	-0.39931136	3.030210556	0.0488873	0.088188333	0.04181	0	132	101	153	145	164	178	160	110	120	156
ENSMUSG00000022003	chr14	Slc25a30	7.6E+07	7.6E+07	1706	-0.86665812	1.028664904	0.0489475	0.088277897	0.19217	0	21	18	56	37	68	32	68	17	16	12
ENSMUSG00000030872	chr7	Gga2	1.2E+08	1.2E+08	9769	0.331932835	5.112747273	0.048983	0.088330684	0.03212	0	402	341	463	484	623	1081	768	604	810	739
ENSMUSG00000021911	chr14	Parg	3.2E+07	3.2E+07	5778	-0.33413445	4.5844505	0.0491099	0.088546567	0.03213	0	405	315	531	372	385	543	528	321	374	438
ENSMUSG00000035297	chr5	Cops4	1E+08	1E+08	5006	-0.36422767	6.242526044	0.0491154	0.088546567	0.04014	0	1161	869	1751	1402	1313	1471	1604	1065	1425	1274
ENSMUSG00000030521	chr7	Mphosph10	6.4E+07	6.4E+07	3651	-0.36726468	4.346144622	0.0491469	0.088591967	0.03888	0	404	263	380	301	360	518	412	280	296	340
ENSMUSG00000054509	chr14	Parp4	5.7E+07	5.7E+07	6534	-0.41331338	4.37173828	0.0493708	0.088984207	0.0499	0	264	233	619	396	308	433	468	225	310	422
ENSMUSG00000074807	chr2	Gm10762	1.3E+08	1.3E+08	1133	-0.41587205	2.921056129	0.0493964	0.089018925	0.04498	0	118	100	150	123	156	126	146	108	151	128
ENSMUSG00000022995	chr1	Enah	1.8E+08	1.8E+08	21452	0.494170074	5.673720551	0.049456	0.089103349	0.07422	0	502	324	1098	940	413	1223	1375	912	1231	1423
ENSMUSG00000051391	chr5	Ywhag	1.4E+08	1.4E+08	5500	-0.3808309	8.353189092	0.0494501	0.089103349	0.04471	0	4694	3642	6892	5520	7764	6443	6938	4234	6057	5851
ENSMUSG00000028396	chr4	2310002L09Rik	7.4E+07	7.4E+07	2158	-0.44446407	5.43301808	0.0496122	0.089373377	0.05972	0	828	389	1099	785	738	1093	1089	507	482	684
ENSMUSG00000035759	chr10	Bbs10	1.1E+08	1.1E+08	2753	-0.62983184	0.774811341	0.0496217	0.089379013	0.08753	0	34	25	28	27	33	29	36	16	16	36
ENSMUSG00000032249	chr9	Anp32a	6.2E+07	6.2E+07	3166	0.384617808	6.064231633	0.0497631	0.089622084	0.0451	0	805	522	1199	724	1261	2058	1339	1262	1460	1722
ENSMUSG00000040732	chr16	Erg	9.5E+07	9.5E+07	3466	-0.45861354	3.014320449	0.0498062	0.089688245	0.05664	0	136	64	207	117	204	158	165	97	149	132
ENSMUSG00000015289	chrX	Lage3	7.4E+07	7.4E+07	2021	0.385139162	4.449842053	0.0498498	0.089755234	0.04314	0	320	196	273	233	408	619	419	389	636	486
ENSMUSG00000020717	chr11	Pecam1	1.1E+08	1.1E+08	6228	0.407479078	6.488013017	0.0498832	0.089792355	0.05101	0	928	594	1816	1071	1685	2627	1913	1722	2116	2192
ENSMUSG00000057367	chr9	Birc2	7818227	7818943	4580	-0.31022695	4.801348516	0.049877	0.089792355	0.02784	0	446	335	601	412	551	621	570	365	452	580
ENSMUSG00000029463	chr5	Fam216a	1.2E+08	1.2E+08	1388	0.521534992	2.022042018	0.049897	0.089805638	0.06739	0	45	36	50	35	81	113	82	84	106	92
ENSMUSG00000042523	chr12	Dnal1	8.4E+07	8.4E+07	6938	-0.42276883	3.035853121	0.0499168	0.089829831	0.04769	0	145	77	194	150	149	163	182	102	127	148
ENSMUSG00000024997	chr19	Prdx3	6.1E+07	6.1E+07	1478	-0.38492687	7.63356185	0.0499344	0.089838336	0.04575	0	3279	2284	4669	3626	3264	3762	4344	2706	3395	3628
ENSMUSG00000043673	chr12	Kcns3	1.1E+07	1.1E+07	3059	-0.97026583	0.026940899	0.0499325	0.089838336	0.22609	0	24	17	4	8	39	20	10	8	18	10
ENSMUSG00000046269	chrX	Usp27x	7371276	7371869	4277	0.832619102	-0.22172425	0.0499885	0.089924224	0.11516	0	8	8	6	9	8	28	17	19	9	24
ENSMUSG00000024539	chr18	Ptpn2	6.8E+07	6.8E+07	3125	0.384464584	4.033338979	0.0500726	0.090063886	0.04212	0	214	162	253	196	239	478	314	390	345	347
ENSMUSG00000000282	chr11	Mnt	7.5E+07	7.5E+07	4627	0.352049263	3.835377797	0.0500845	0.090073793	0.03444	0	150	129	225	179	273	355	353	246	334	357
ENSMUSG00000048174	chr1	Tmem81	1.3E+08	1.3E+08	2018	0.60978253	1.457693594	0.0501177	0.090121869	0.08892	0	22	23	33	21	61	75	70	37	64	86
ENSMUSG00000031532	chr8	Saraf	3.4E+07	3.4E+07	1897	-0.39210461	7.490073607	0.0501492	0.090166906	0.04755	0	2987	2269	4033	3279	2824	3537	4102	2288	3259	2992
ENSMUSG00000042590	chr13	Ipo11	1.1E+08	1.1E+08	7878	-0.33428597	4.233703736	0.0501705	0.090193743	0.03172	0	299	237	406	311	327	372	437	251	337	323
ENSMUSG00000026585	chr1	Kifap3	1.6E+08	1.6E+08	4012	-0.32454156	4.784158717	0.0501888	0.090205815	0.03079	0	466	350	510	463	507	626	622	385	427	477
ENSMUSG00000030595	chr7	Nfkbib	2.9E+07	2.9E+07	2169	0.328219899	4.664538828	0.0501901	0.090205815	0.03095	0	326	250	358	379	370	609	559	427	697	615
ENSMUSG00000035597	chr12	Prpf39	6.5E+07	6.5E+07	4401	-0.36415318	3.858571719	0.0501969	0.090206421	0.03744	0	233	198	302	225	264	299	284	177	218	337
ENSMUSG00000025809	chr8	Itgb1	1.3E+08	1.3E+08	4081	0.379824278	8.318577697	0.050274	0.090321846	0.04478	0	4115	2981	5210	4171	4561	10019	7927	5926	6469	7186
ENSMUSG00000030035	chr6	Wbp1	8.3E+07	8.3E+07	2079	0.399523927	4.766723814	0.0502731	0.090321846	0.04803	0	283	146	608	377	444	695	720	455	650	686
ENSMUSG00000078695	chr11	Cisd3	9.8E+07	9.8E+07	833	0.365037557	5.517266531	0.0503185	0.090390343	0.04039	0	491	360	807	620	822	1033	954	813	1280	1219
ENSMUSG00000026641	chr1	Usf1	1.7E+08	1.7E+08	2806	0.310417543	4.718392002	0.0503287	0.090396993	0.02782	0	327	241	412	315	498	700	593	441	632	648
ENSMUSG00000046761	chr15	Fam83h	7.6E+07	7.6E+07	4627	0.821607413	0.403063625	0.050389	0.090493742	0.15799	0	12	7	8	7	33	44	22	29	40	22
ENSMUSG00000050240	chr16	Hic2	1.7E+07	1.7E+07	6354	-0.57543512	1.330719345	0.0503965	0.0904956	0.07765	0	41	37	39	60	38	55	36	29	41	42
ENSMUSG00000056596	chr4	Trnp1	1.3E+08	1.3E+08	1654	0.829420663	-0.0610593	0.0504349	0.090553054	0.13394	0	6	6	6	6	22	26	20	10	24	32
ENSMUSG00000032184	chr9	Lysmd2	7.6E+07	7.6E+07	1200	0.432506271	4.280638625	0.0504791	0.0906125	0.05459	0	298	206	190	195	331	684	383	364	430	449
ENSMUSG00000063362	chr8	Alg11	2.2E+07	2.2E+07	4960	-0.43294806	3.082330325	0.050481	0.0906125	0.05195	0	136	138	146	111	186	168	180	114	141	136
ENSMUSG00000006386	chr4	Tek	9.5E+07	9.5E+07	4712	-0.33501072	4.788282192	0.0504883	0.090614071	0.03279	0	418	292	618	421	626	585	653	374	408	516
ENSMUSG00000001930	chr6	Vwf	1.3E+08	1.3E+08	16064	0.420526482	4.426902731	0.0505257	0.090662576	0.05178	0	217	240	309	358	233	476	469	330	655	610
ENSMUSG00000080316	chr17	Spaca6	1.8E+07	1.8E+07	6897	0.805393669	2.165829515	0.0505283	0.090662576	0.18009	0	53	52	27	14	87	199	73	63	104	150
ENSMUSG00000009394	chr6	Syn2	1.2E+08	1.2E+08	5646	0.714689359	1.061116616	0.0505595	0.090697381	0.12769	0	18	8	18	18	55	48	55	35	49	65
ENSMUSG00000058806	chr10	Col13a1	6.2E+07	6.2E+07	4605	0.580352823	0.868010557	0.0505606	0.090697381	0.06596	0	18	13	23	22	28	58	36	36	42	39
ENSMUSG00000035151	chr8	Elmod2	8.3E+07	8.3E+07	11138	-0.42698898	3.285408025	0.0506388	0.090826038	0.0508	0	192	129	157	144	208	242	189	135	155	137
ENSMUSG00000001909	chr8	Trmt1	8.5E+07	8.5E+07	6306	-0.31540754	4.838379288	0.0506818	0.090864635	0.02916	0	396	375	591	506	522	551	555	365	559	610
ENSMUSG00000028419	chr4	Chmp5	4.1E+07	4.1E+07	1519	0.34294588	5.203809927	0.0506868	0.090864635	0.03509	0	498	350	495	407	713	1146	834	638	802	862
ENSMUSG00000030752	chr7	Kdm8	1.3E+08	1.3E+08	2385	-0.36041396	3.620439189	0.0506737	0.090864635	0.03572	0	174	154	250	235	226	248	245	172	236	205
ENSMUSG00000035984	chr18	Nme5	3.5E+07	3.5E+07	1154	0.828124944	-0.21892543	0.0506927	0.090864635	0.11634	0	10	5	10	7	8	12	25	14	14	32
ENSMUSG00000085586	chr11	Gm11613	9.8E+07	9.8E+07	1971	-0.47645328	3.018587764	0.0506766	0.090864635	0.06336	0	138	107	199	163	93	137	168	109	125	153
ENSMUSG00000053774	chr16	Ubxn7	3.2E+07	3.2E+07	10318	-0.36716534	4.30643687	0.0507906	0.091028429	0.03931	0	336	272	278	330	440	394	405	282	307	391
ENSMUSG00000028680	chr4	Plk3	1.2E+08	1.2E+08	2531	0.88856523	1.447002812	0.0508412	0.091091663	0.21711	0	9	14	13	34	73	53	50	48	83	112
ENSMUSG00000029017	chr5	Pmpcb	2.2E+07	2.2E+07	5141	-0.38408083	6.330624024	0.0508434	0.091091663	0.0454	0	1205	748	2092	1543	1490	1540	1700	1071	1515	1407
ENSMUSG00000031958	chr8	Ldhd	1.1E+08	1.1E+08	5328	-0.3516359	5.96635036	0.0508453	0.091091663	0.03778	0	1035	659	1449	1105	1119	1367	1357	843	1090	1053
ENSMUSG00000032667	chr6	Pon2	5264147	5265479	4655	0.360209705	6.29241139	0.0510215	0.091395561	0.04	0	1048	643	1416	902	1274	2315	1863	1406	1650	1910

ENSMUSG00000028974	chr4	Dffa	1.5E+08	1.5E+08	3540	-0.54433467	6.188938657	0.0510535	0.091441232	0.09168	0	1022	669	2150	2008	830	1197	1805	725	1048	1446
ENSMUSG00000049281	chr9	Scn3b	4E+07	4E+07	5546	0.665804353	0.913126345	0.051097	0.091507414	0.10617	0	29	5	25	21	25	66	43	36	47	32
ENSMUSG00000030754	chr7	Copb1	1.1E+08	1.1E+08	3315	-0.37985315	5.48587513	0.0511338	0.091561708	0.04407	0	791	583	875	690	872	1138	1071	576	707	586
ENSMUSG00000005575	chr7	Ube2m	1.3E+07	1.3E+07	2287	0.381118222	6.690858793	0.0512224	0.091708563	0.0451	0	1085	845	1819	1545	1618	2442	2308	1764	2920	2640
ENSMUSG00000038319	chr5	Kcnh2	2.4E+07	2.4E+07	4845	0.511089774	2.776074103	0.0512647	0.091772673	0.07363	0	77	36	115	69	141	143	163	113	215	183
ENSMUSG00000020752	chr11	Recql5	1.2E+08	1.2E+08	6986	-0.37749485	3.289721643	0.0512741	0.091777695	0.03868	0	138	133	227	150	183	198	194	137	172	171
ENSMUSG00000024982	chr19	Zdhhc6	5.5E+07	5.5E+07	2284	-0.3177463	4.702833137	0.0513241	0.091855523	0.02965	0	397	334	482	410	557	543	620	320	463	468
ENSMUSG00000028744	chr4	Pqlc2	1.4E+08	1.4E+08	3516	0.471777114	2.369413603	0.0513543	0.091897771	0.05706	0	58	46	59	67	90	138	110	86	158	116
ENSMUSG00000031231	chrX	Cox7b	1.1E+08	1.1E+08	1214	-0.42255132	8.445542191	0.0513998	0.091967556	0.05597	0	5950	3611	9043	7024	4948	6866	7490	4815	5831	5846
ENSMUSG00000019763	chr10	Rmnd1	4401915	4403501	5894	-0.41637315	5.012182762	0.0514139	0.091981055	0.05257	0	446	292	1033	629	483	688	723	362	501	621
ENSMUSG00000010047	chr9	Hyal2	1.1E+08	1.1E+08	3293	0.348673521	4.159394418	0.0514225	0.091984661	0.03498	0	183	165	292	243	314	468	396	333	492	362
ENSMUSG00000053317	chr4	Sec61b	4.7E+07	4.7E+07	1271	0.523525743	4.721938468	0.0514753	0.092067438	0.08293	0	360	325	186	329	354	858	382	576	793	571
ENSMUSG00000001986	chrX	Gria3	4.1E+07	4.1E+07	9859	0.672089594	1.084420662	0.0514996	0.09209917	0.10787	0	18	17	15	21	46	77	57	34	55	34
ENSMUSG00000025381	chr10	Cnpy2	1.3E+08	1.3E+08	1017	0.369644774	5.039492711	0.0515128	0.092099288	0.04094	0	422	357	388	386	588	1068	598	590	825	760
ENSMUSG00000038764	chr4	Ptpn3	5.7E+07	5.7E+07	7238	-0.9664727	6.583381029	0.0515112	0.092099288	0.28572	0	945	160	5741	2672	1137	1321	2166	931	1007	1337
ENSMUSG00000003190	chr7	Bcl2l12	4.5E+07	4.5E+07	1976	0.434536724	2.88054168	0.0515385	0.092133409	0.05097	0	99	59	92	95	123	207	147	118	187	208
ENSMUSG00000039671	chr2	Zmynd8	1.7E+08	1.7E+08	11031	0.339192532	4.32093095	0.0516037	0.092238261	0.0334	0	214	182	376	259	318	544	408	371	417	554
ENSMUSG00000102070	chr1	Gm28661	2.5E+07	2.5E+07	681	-0.41692381	4.213678104	0.0516886	0.092378223	0.05123	0	298	144	465	392	347	286	409	216	343	389
ENSMUSG00000020836	chr11	Coro6	7.7E+07	7.7E+07	3011	-0.594161	7.619130433	0.0516985	0.092384063	0.1103	0	2562	1675	7532	4711	2179	3163	4692	1953	2619	3996
ENSMUSG00000029861	chr6	Fam131b	4.2E+07	4.2E+07	4104	0.773896885	0.458353926	0.0517141	0.092388563	0.13037	0	6	15	17	6	26	37	30	21	28	48
ENSMUSG00000087644	chrX	Gm14703	7651106	7652711	1820	-0.92015815	0.572225533	0.0517083	0.092388563	0.20621	0	29	5	63	36	12	20	17	22	22	16
ENSMUSG00000057182	chr2	Scn3a	6.5E+07	6.5E+07	12459	1.03935327	-0.12242475	0.0517557	0.092448206	0.2288	0	3	8	8	17	2	14	22	24	12	36
ENSMUSG00000089945	chr4	Palm2Akap2	5.8E+07	5.8E+07	8456	-0.43177023	5.436656256	0.0517607	0.092448206	0.05719	0	600	319	1273	663	1120	847	968	528	643	854
ENSMUSG00000056836	chr7	Gm6851	4E+07	4E+07	390	0.807192417	0.193452667	0.0518694	0.092630554	0.13822	0	5	6	9	23	13	19	35	17	33	30
ENSMUSG00000064302	chr1	Clasp1	1.2E+08	1.2E+08	19275	-0.38104958	5.68540038	0.0518775	0.092633115	0.04472	0	724	610	1264	1043	787	901	1204	657	969	900
ENSMUSG00000047554	chr7	Tmem41b	1.1E+08	1.1E+08	5316	-0.34912027	4.198845793	0.0519078	0.092675458	0.03531	0	330	232	413	273	298	387	394	266	292	325
ENSMUSG00000083610	chr3	Oaz2-ps	1.4E+08	1.4E+08	537	-0.53774669	1.752554651	0.0519186	0.092682951	0.07205	0	73	40	63	63	52	53	71	43	65	44
ENSMUSG00000022449	chr15	Adamts20	9.4E+07	9.4E+07	8997	0.658141757	2.140152078	0.0519388	0.09270731	0.1175	0	76	47	40	52	23	121	103	98	119	96
ENSMUSG00000024513	chr18	Mbd2	7.1E+07	7.1E+07	3214	-0.32683604	5.267616914	0.0519831	0.09277454	0.03228	0	581	452	805	603	831	781	946	494	654	680
ENSMUSG00000048603	chr13	Gm9828	9.8E+07	9.8E+07	2557	-0.69645143	0.14868447	0.0519936	0.092781411	0.09475	0	16	17	26	16	20	13	21	6	23	18
ENSMUSG00000090262	chr5	Mpv17	3.1E+07	3.1E+07	3208	-0.34798625	4.681093101	0.0520061	0.092791974	0.03625	0	465	386	385	387	491	552	461	350	490	480
ENSMUSG00000001763	chr6	Tspan33	3E+07	3E+07	5195	0.605411042	1.945785671	0.0520223	0.092809129	0.09983	0	33	20	98	48	34	111	85	57	110	107
ENSMUSG00000002900	chr12	Lamb1	3.1E+07	3.1E+07	9917	0.431992128	5.489621685	0.0520302	0.092811353	0.05766	0	510	400	555	437	1036	1479	802	961	1008	1051
ENSMUSG00000027309	chr2	4930402H24Rik	1.3E+08	1.3E+08	10659	-0.5701248	3.660766533	0.0522045	0.093110425	0.09733	0	213	153	166	119	513	285	222	157	211	179
ENSMUSG00000048307	chr15	Ankrd46	3.6E+07	3.6E+07	2480	-0.30470027	4.901441398	0.0522906	0.093252119	0.02755	0	492	365	561	499	570	707	522	420	562	559
ENSMUSG00000022091	chr14	Sorbs3	7E+07	7E+07	2914	0.404962463	5.6529598	0.0523298	0.09329822	0.05096	0	636	335	943	500	984	1318	1099	735	1257	1574
ENSMUSG00000031922	chr9	Cep57	1.4E+07	1.4E+07	4180	-0.47408099	2.365150728	0.0523232	0.09329822	0.05876	0	93	60	122	79	95	114	115	69	60	83
ENSMUSG00000003435	chr7	Supt5	2.8E+07	2.8E+07	3509	-0.36647374	6.356283006	0.0524473	0.093495911	0.04195	0	1171	929	1957	1569	1433	1606	1702	971	1559	1626
ENSMUSG00000003934	chr11	Efnb3	7E+07	7E+07	3183	0.702877578	0.199436389	0.0524683	0.093521402	0.08416	0	14	7	18	12	8	35	29	15	30	24
ENSMUSG00000049396	chr11	Gemin4	7.6E+07	7.6E+07	3734	-0.44832363	2.810244261	0.052526	0.093612486	0.05498	0	107	88	124	154	128	155	100	79	136	142
ENSMUSG00000024759	chr19	Atl3	7494040	7494361	6698	-0.54784124	4.585134793	0.0525592	0.093659761	0.09245	0	442	361	247	239	852	540	503	299	357	331
ENSMUSG00000055546	chr11	Timd4	4.7E+07	4.7E+07	2173	-0.78739303	0.732735214	0.0526394	0.093790603	0.15414	0	25	32	16	23	52	47	25	18	19	13
ENSMUSG00000018707	chr12	Dync1h1	1.1E+08	1.1E+08	15658	-0.42788032	7.726476641	0.0526835	0.093857271	0.0579	0	2869	2133	5643	4889	3202	4378	4224	2649	3882	3677
ENSMUSG00000081810	chr4	Gm11878	2.3E+07	2.3E+07	400	0.587224042	1.201509726	0.0527025	0.09387932	0.07766	0	34	16	25	26	30	59	45	36	75	56
ENSMUSG00000032570	chr9	Atp2c1	1.1E+08	1.1E+08	9689	-0.35839062	4.912634313	0.0527164	0.093880155	0.03907	0	556	398	591	520	452	599	760	393	469	519
ENSMUSG00000038876	chr10	Rnf146	2.9E+07	2.9E+07	4454	-0.33169315	5.557578832	0.052712	0.093880155	0.03382	0	747	602	999	801	805	910	1024	648	827	904
ENSMUSG00000001333	chr4	Sync	1.3E+08	1.3E+08	2862	-0.44038275	5.091397657	0.0527285	0.093889835	0.06003	0	625	469	695	680	437	646	1004	398	523	450
ENSMUSG00000027506	chr3	Tpd52	8925593	8931174	7487	0.351802081	5.013134498	0.0527381	0.09389497	0.03711	0	472	374	381	403	454	905	729	594	765	739
ENSMUSG00000003418	chr2	St8sia6	1.4E+07	1.4E+07	7664	-0.6743553	0.439213237	0.0529258	0.094205279	0.09078	0	24	9	39	23	26	19	24	12	19	27
ENSMUSG00000098253	chr18	Mir7219	6.8E+07	6.8E+07	54	-0.58677477	2.51406861	0.0529241	0.094205279	0.09872	0	78	50	183	133	83	87	154	47	96	89
ENSMUSG00000028062	chr3	Lamtor2	8.9E+07	8.9E+07	1218	0.348964437	5.512472202	0.052944	0.094213754	0.03751	0	661	399	669	541	779	1259	912	797	1243	1075
ENSMUSG00000092356	chr2	Gm20532	2.7E+07	2.7E+07	780	0.436878886	4.056424251	0.0529434	0.094213754	0.05803	0	157	90	364	191	321	504	338	312	377	439
ENSMUSG00000023707	chr5	Ogfod2	1.2E+08	1.2E+08	2260	0.357510618	4.265527285	0.0529827	0.094235418	0.03753	0	259	173	292	240	310	472	373	327	595	452
ENSMUSG00000031988	chr9	Vps26b	2.7E+07	2.7E+07	6872	-0.32382967	5.543216986	0.0529831	0.094235418	0.0322	0	716	530	1006	780	925	952	1054	621	828	844
ENSMUSG00000034648	chr6	Lrrn1	1.1E+08	1.1E+08	3756	1.104846753	2.576074111	0.0529776	0.094235418	0.3675	0	17	8	174	95	12	107	180	199	104	197
ENSMUSG00000043458	chr18	Pcdhb12	3.7E+07	3.7E+07	3034	0.759034771	-0.2730684	0.0529827	0.094235418	0.08862	0	8	3	11	10	8	15	19	16	21	20
ENSMUSG00000039585	chr9	Myo9a	6E+07	6E+07	13034	-0.34791274	4.208491125	0.053001	0.094243323	0.0355	0	318	232	354	339	303	399	413	266	296	304
ENSMUSG00000055013	chr1	Agap1	8.9E+07	8.9E+07	17469	0.323433358	5.038335898	0.0529991	0.094243323	0.03138	0	397	339	578	433	454	751	915	489	780	859
ENSMUSG00000036285	chr5	Noa1	7.7E+07	7.7E+07	4029	-0.31391931	4.263366458	0.0530099	0.094247312	0.02821	0	284	227	416	311	379	390	365	282	351	372
ENSMUSG00000021716	chr13	Srek1ip1	1E+08	1E+08	3254	-0.34270746	4.144027167	0.0530268	0.094265452	0.03384	0	266	178	437	319	317	345	358	243	307	354
ENSMUSG00000061360	chr15	Phf5a	8.2E+07	8.2E+07	937	0.33348176	5.297602253	0.0532455	0.094642192	0.03397	0	492	381	537	566	644	1012	799	749	1031	908
ENSMUSG00000008604	chr3	Ubqln4	8.9E+07	8.9E+07	4147	-0.3739346	6.921035167	0.0532578	0.094652051	0.04422	0	1696	1306	2863	2354	2303	2346	2667	1510	2290	2172
ENSMUSG00000026123	chr1	Plekhb2	3.5E+07	3.5E+07	7987	-0.42308233	6.474042332	0.0533249	0.094759235	0.05651	0	1263	877	2534	1768	1463	1558	2169	973	1521	1719
ENSMUSG00000092260	chr8	Zfp963	7E+07	7E+07	2299	-0.56186321	1.475834286	0.0533587	0.094807346	0.07581	0	68	34	46	35	58	53	52	36	42	42
ENSMUSG00000060600	chr11	Eno3	7.1E+07	7.1E+07	1739	-0.4066855	12.54318289	0.0533754	0.094824951	0.0529	0	94589	78625	115825	117899	103564	105306	115423	77118	135951	97221
ENSMUSG00000054716	chr7	Zfp771	1.3E+08	1.3E+08	1371	0.397960272	3.465455786	0.0533861	0.094831947	0.04525	0	110	99	204	140	172	302	201	191	318	275
ENSMUSG00000022394	chr15	L3mbtl2	8.2E+07	8.2E+07	5945	-0.3368623	3.822971841	0.0534429	0.094886045	0.03186	0	213	153	299	247	291	288	271	199	281	247

ENSMUSG00000025246	chrX	Tbl1x	7.8E+07	7.8E+07	7052	-0.40735014	4.281332014	0.0534377	0.094886045	0.05025	0	277	313	302	261	497	458	436	251	316	278
ENSMUSG00000043207	chr4	Zmpste24	1.2E+08	1.2E+08	7145	-0.33575966	4.897350167	0.0534272	0.094886045	0.03437	0	490	438	530	506	494	660	676	394	489	519
ENSMUSG00000089810	chr9	Gm16536	4.6E+07	4.6E+07	1589	0.448037859	3.438755385	0.0534436	0.094886045	0.05906	0	116	66	139	190	189	284	212	220	295	259
ENSMUSG00000038371	chr7	Sbf2	1.1E+08	1.1E+08	12127	-0.34595031	3.896021797	0.053557	0.095066351	0.03454	0	198	183	334	239	315	338	303	162	267	300
ENSMUSG00000038467	chr2	Chmp4b	1.5E+08	1.5E+08	2027	0.357054221	7.24873915	0.0535587	0.095066351	0.0405	0	1840	1383	2539	2017	2399	3977	3485	2700	3737	3771
ENSMUSG00000057497	chr6	Fam136a	8.6E+07	8.6E+07	1605	-0.35065615	3.85616932	0.0535805	0.095093051	0.03526	0	228	181	303	236	275	283	347	204	238	238
ENSMUSG00000039086	chr2	Ss18l1	1.8E+08	1.8E+08	4343	-0.486152	1.924412054	0.0536583	0.095218985	0.05839	0	55	55	93	65	58	70	73	54	60	61
ENSMUSG00000040767	chr11	Snrnp25	3.2E+07	3.2E+07	1041	0.38474036	3.409196349	0.0536877	0.095259218	0.04159	0	146	91	154	124	179	283	244	177	304	227
ENSMUSG00000048924	chr13	Ccdc125	1E+08	1E+08	2705	-0.69682325	0.07446296	0.0537185	0.095301778	0.08096	0	18	13	16	16	27	14	13	13	19	16
ENSMUSG00000030428	chr7	Ttyh1	4119408	4119424	6345	0.752564586	-0.1039746	0.05373	0.095306522	0.10708	0	7	4	19	5	12	24	15	20	20	25
ENSMUSG00000040797	chr6	Iqsec3	1.2E+08	1.2E+08	13603	0.710066213	0.740814676	0.0537348	0.095306522	0.12752	0	15	6	34	11	27	67	25	31	31	46
ENSMUSG00000066595	chr1	Mfsd7b	1.9E+08	1.9E+08	5177	-0.51030423	3.349782883	0.0538514	0.095501323	0.07739	0	162	94	309	231	122	167	231	131	133	201
ENSMUSG00000038729	chr4	Akap2	5.8E+07	5.8E+07	8163	-0.42713878	5.431801572	0.0539195	0.095609924	0.05699	0	594	317	1269	662	1115	845	965	527	645	852
ENSMUSG00000011114	chr9	Tbrg1	3.8E+07	3.8E+07	3482	0.307613075	5.000520548	0.0539399	0.095622049	0.02835	0	404	339	459	400	548	938	729	515	754	746
ENSMUSG00000027395	chr2	Polr1b	1.3E+08	1.3E+08	5805	-0.36192497	3.859582309	0.0539348	0.095622049	0.03801	0	196	194	273	302	253	283	288	213	246	272
ENSMUSG00000056501	chr2	Cebpb	1.7E+08	1.7E+08	1504	0.470239339	4.479198399	0.0539625	0.095649993	0.06885	0	150	133	425	341	429	584	401	516	606	513
ENSMUSG00000028743	chr4	Akr7a5	1.4E+08	1.4E+08	1793	0.341126478	5.146124045	0.0539709	0.09565282	0.03582	0	397	304	592	496	605	868	690	586	1074	866
ENSMUSG00000030499	chr7	Kctd15	3.5E+07	3.5E+07	2991	-0.37931825	5.225876398	0.0540273	0.095740647	0.04488	0	601	616	561	583	744	673	717	466	862	647
ENSMUSG00000044211	chr6	Gm7887	4.9E+07	4.9E+07	734	-0.75166673	0.143083272	0.0541054	0.095866906	0.11282	0	21	17	28	19	10	11	22	15	15	14
ENSMUSG00000036270	chr8	Edc4	1.1E+08	1.1E+08	5497	-0.33406342	4.863548621	0.0541178	0.095876772	0.03395	0	377	359	650	575	499	549	558	362	627	572
ENSMUSG00000037813	chr2	D630003M21Rik	1.6E+08	1.6E+08	5104	0.486604453	2.045781006	0.0541754	0.095966765	0.05983	0	32	34	67	61	62	117	88	72	113	95
ENSMUSG00000020691	chr11	Mettl2	1.1E+08	1.1E+08	3399	-0.40641976	2.880607632	0.0541955	0.095990165	0.0447	0	111	89	173	121	139	142	152	109	112	130
ENSMUSG00000004070	chr16	Hmox2	4726361	4726471	2217	0.336887777	5.535422289	0.05426	0.096092255	0.03545	0	504	381	933	625	728	1255	1037	804	1155	1106
ENSMUSG00000039234	chr3	Sec24d	1.2E+08	1.2E+08	3856	0.451667106	3.327914034	0.0543779	0.096288992	0.0595	0	123	88	120	92	219	338	275	180	202	202
ENSMUSG00000020869	chr11	Lrrc59	9.5E+07	9.5E+07	3073	-0.33238377	5.38690098	0.0543958	0.096308474	0.03423	0	595	518	736	764	914	908	849	646	714	697
ENSMUSG00000042670	chr2	Immp1l	1.1E+08	1.1E+08	955	-0.35089951	5.558687395	0.0544414	0.096376994	0.03863	0	802	705	813	754	831	1068	877	683	878	777
ENSMUSG00000040631	chr8	Dok4	9.5E+07	9.5E+07	2604	0.424054146	3.446507457	0.0544684	0.096412634	0.05333	0	103	74	228	113	210	311	268	197	278	228
ENSMUSG00000024754	chr19	Tmem2	2.2E+07	2.2E+07	6667	-0.34377256	4.275866013	0.0544791	0.096419326	0.03528	0	311	273	388	328	311	461	385	285	292	340
ENSMUSG00000038398	chr8	Upf3a	1.4E+07	1.4E+07	1402	0.366125256	3.794719217	0.0545407	0.096516323	0.039	0	190	106	191	193	239	390	279	245	364	328
ENSMUSG00000024140	chr17	Epas1	8.7E+07	8.7E+07	5309	-0.46638906	7.125330845	0.0545648	0.096546648	0.06966	0	1622	1195	4888	2630	2560	2579	2492	1789	2446	2837
ENSMUSG00000009545	chr7	Kcnq1	1.4E+08	1.4E+08	4093	0.649655504	0.591247252	0.0546552	0.096694551	0.08436	0	12	11	20	18	21	36	47	17	47	30
ENSMUSG00000028309	chr4	Rnf20	5E+07	5E+07	7288	-0.33090864	4.898108126	0.0546665	0.096702255	0.03341	0	441	349	642	588	493	653	658	446	499	469
ENSMUSG00000025757	chr3	Hspa4l	4.1E+07	4.1E+07	11792	-0.47915724	3.472937898	0.0547816	0.096893684	0.06839	0	156	113	384	189	161	265	240	129	145	188
ENSMUSG00000021376	chr13	Tpmt	4.7E+07	4.7E+07	1914	-0.52465121	1.832129756	0.0548899	0.097054581	0.06941	0	54	34	91	42	100	66	67	44	59	59
ENSMUSG00000028910	chr4	Mecr	1.3E+08	1.3E+08	3041	-0.38907365	4.512233445	0.0548982	0.097054581	0.04611	0	326	230	427	307	725	460	439	321	383	434
ENSMUSG00000032563	chr9	Mrpl3	1.1E+08	1.1E+08	5961	-0.339639	5.437497138	0.0549019	0.097054581	0.03604	0	763	487	1016	704	711	957	964	595	725	731
ENSMUSG00000053289	chr9	Ddx10	5.3E+07	5.3E+07	3368	-0.37864231	3.6682759	0.0549053	0.097054581	0.0417	0	217	168	245	225	214	279	262	204	185	200
ENSMUSG00000056536	chr1	Pign	1.1E+08	1.1E+08	13595	-0.42523988	2.68295326	0.0549072	0.097054581	0.04948	0	100	88	140	104	116	166	124	81	90	105
ENSMUSG00000056413	chr5	Adap1	1.4E+08	1.4E+08	3232	1.042771629	2.251681447	0.0550379	0.097273448	0.32793	0	36	13	16	10	173	136	88	92	180	145
ENSMUSG00000024831	chr19	Ighmbp2	3260924	3261635	4101	-0.45919766	2.471385531	0.0550916	0.097355952	0.0571	0	89	79	84	112	106	91	103	75	108	96
ENSMUSG00000039050	chr2	Osbpl2	1.8E+08	1.8E+08	4187	-0.30123835	4.846212663	0.0551197	0.097393474	0.02757	0	464	356	615	449	515	653	629	359	516	530
ENSMUSG00000029559	chr5	2210016L21Rik	1.1E+08	1.1E+08	3303	0.330263169	4.17528451	0.0551419	0.0974204	0.03216	0	209	159	309	233	312	449	400	282	467	482
ENSMUSG00000057278	chr6	Snrpg	8.6E+07	8.6E+07	350	0.411194557	3.485148201	0.0551736	0.097449698	0.0485	0	143	128	139	106	195	324	229	196	277	286
ENSMUSG00000064326	chr12	Siva1	1.1E+08	1.1E+08	782	0.35305317	3.675831998	0.0551793	0.097449698	0.03551	0	137	132	208	151	218	320	289	223	322	315
ENSMUSG00000092595	chr17	Gm20427	3.4E+07	3.4E+07	3703	0.360476669	7.081239268	0.0551719	0.097449698	0.04179	0	1638	1191	2129	1911	2177	3748	2841	2411	3401	3360
ENSMUSG00000026021	chr1	Sumo1	6E+07	6E+07	2076	-0.33348416	5.41865949	0.05527	0.097585183	0.03481	0	699	558	882	695	751	941	938	649	685	693
ENSMUSG00000071655	chr19	Ubxn1	8871559	8871585	1068	0.373723473	7.3422511	0.05527	0.097585183	0.04507	0	1769	1418	2712	2186	2780	4010	3437	2812	4305	4371
ENSMUSG00000090946	chr12	Ccdc71l	3.2E+07	3.2E+07	4240	0.372463195	3.455126788	0.0552911	0.097610233	0.03983	0	125	97	209	117	181	273	275	198	279	240
ENSMUSG00000061603	chr12	Akap6	5.3E+07	5.3E+07	10263	-0.44426192	5.945427293	0.0553066	0.097625275	0.06312	0	1070	731	1445	1365	728	1063	1595	773	892	1098
ENSMUSG00000017404	chr11	Rpl19	9.8E+07	9.8E+07	1022	0.368625024	7.942197068	0.0554423	0.097852442	0.044	0	3163	2377	3540	3248	3885	7054	5047	4496	5974	6125
ENSMUSG00000042215	chr1	Bag2	3.4E+07	3.4E+07	3059	-0.39468973	4.431901373	0.0555378	0.098008738	0.0479	0	329	271	540	438	266	413	488	316	372	327
ENSMUSG00000049134	chr19	Nrap	5.6E+07	5.6E+07	5507	-0.55953039	10.2743044	0.0555737	0.098059675	0.10141	0	17612	10234	40219	34108	12761	21675	25509	14279	21202	21566
ENSMUSG00000018405	chr11	Mrm1	8.5E+07	8.5E+07	2868	0.418476996	3.751249091	0.0556097	0.09811092	0.05298	0	128	93	314	189	171	393	395	219	288	302
ENSMUSG00000002565	chr12	Scin	4E+07	4E+07	2999	0.754951343	0.441370911	0.0556682	0.098201845	0.13709	0	16	4	24	14	13	29	47	12	26	49
ENSMUSG00000031161	chrX	Hdac6	7930120	7930537	5817	0.418906959	3.037034222	0.0556908	0.098229248	0.04993	0	72	73	123	98	168	222	208	127	201	208
ENSMUSG00000021218	chr13	Gdi2	3538075	3538343	2681	0.364059268	6.973414681	0.0557142	0.098258255	0.04279	0	1568	1119	1995	1497	2236	4002	2907	2266	2610	2930
ENSMUSG00000103400	chr1	RP24-229G16.1	1.7E+08	1.7E+08	2041	0.693380257	-0.03149359	0.0557343	0.098281223	0.08397	0	9	7	14	5	15	32	24	13	20	22
ENSMUSG00000022610	chr15	Mapk12	8.9E+07	8.9E+07	1889	-0.36021474	7.28678209	0.0558471	0.098467764	0.04204	0	2542	1916	3155	2865	2774	3192	2892	2089	3084	2923
ENSMUSG00000031370	chrX	Zrsr2	1.6E+08	1.6E+08	7194	0.329024124	4.019717118	0.0559387	0.09861697	0.03165	0	180	158	260	197	296	398	394	284	376	403
ENSMUSG00000062329	chr5	Cytl1	3.8E+07	3.8E+07	974	0.601549065	2.653696803	0.0560422	0.098786942	0.10414	0	64	93	77	78	37	145	159	126	135	199
ENSMUSG00000095440	chr15	Fignl2	1E+08	1E+08	4206	0.8375415	1.487242487	0.0560713	0.098825888	0.1991	0	22	19	9	15	84	86	63	56	71	78
ENSMUSG00000039936	chr4	Pik3cd	1.5E+08	1.5E+08	6259	0.387719511	4.112860675	0.0561144	0.098889467	0.04588	0	273	109	291	188	293	557	449	249	393	405
ENSMUSG00000104195	chr5	RP24-497L12.1	1.3E+08	1.3E+08	1364	0.757715723	-0.24267202	0.0562194	0.099062004	0.09797	0	10	2	6	10	13	22	19	15	19	19
ENSMUSG00000021253	chr12	Tgfb3	8.6E+07	8.6E+07	3384	0.353956286	5.795641684	0.0562965	0.09918544	0.03993	0	681	512	946	887	653	1434	1320	932	1309	1464
ENSMUSG00000045374	chr11	Wdr81	7.5E+07	7.5E+07	7038	0.345156046	3.89409525	0.0563707	0.099303535	0.03469	0	198	140	199	187	260	395	322	240	384	375
ENSMUSG00000006676	chr9	Usp19	1.1E+08	1.1E+08	7048	-0.3732843	7.956982167	0.0565537	0.099607222	0.04556	0	3499	2977	5558	4769	4570	4527	5146	3174	5028	4582
ENSMUSG00000032131	chr9	Abcg4	4.4E+07	4.4E+07	5211	0.862970622	-0.2317081	0.0565629	0.099607222	0.14102	0	2	8	4	7	18	25	19	17	17	19

ENSMUSG00000060376	chr7	Bckdha	2.6E+07	2.6E+07	1773	-0.39176016	7.772907936	0.0565643	0.099607222	0.05012	0	3524	1922	5278	4312	4236	3898	4367	2913	4332	4050
ENSMUSG00000015702	chr3	Anxa9	9.5E+07	9.5E+07	2073	0.863077983	-0.2585508	0.0565756	0.099614453	0.15315	0	6	4	4	4	21	20	16	14	17	28
ENSMUSG00000021798	chr14	Ldb3	3.5E+07	3.5E+07	6016	-0.42036354	10.97609392	0.0565992	0.099643602	0.058	0	29994	24859	44910	45204	28928	34810	42940	24930	38979	37175
ENSMUSG00000032059	chr9	Alg9	5.1E+07	5.1E+07	3889	0.410393089	3.328519867	0.0566495	0.099719542	0.04918	0	97	95	128	132	198	282	214	162	294	227
ENSMUSG00000026626	chr1	Ppp2r5a	1.9E+08	1.9E+08	9607	-0.47871856	6.941405863	0.0566878	0.099774573	0.07464	0	2060	1274	1851	1500	4465	2422	2201	1519	2418	2108
ENSMUSG00000099632	chr2	2900093K20Rik	1.6E+08	1.6E+08	567	0.722022255	0.194662653	0.0566951	0.099774812	0.10695	0	8	5	13	9	25	40	20	17	27	29
ENSMUSG00000022270	chr15	Fam134b	2.6E+07	2.6E+07	3346	-0.54797071	7.100701485	0.0567054	0.099780432	0.09777	0	2426	1050	5105	2710	1555	2910	3010	1735	1624	2347
ENSMUSG00000047879	chr18	Usp14	9995432	9996248	5974	-0.33264	5.524683178	0.0567371	0.099823747	0.03515	0	772	556	949	825	764	967	988	677	829	745
ENSMUSG00000008575	chr4	Nfib	8.2E+07	8.2E+07	14957	-0.34865308	7.032864394	0.0567676	0.099864767	0.0396	0	2115	1632	2650	2145	2565	2924	2635	1725	2284	2431
ENSMUSG00000053965	chr3	Pde5a	1.2E+08	1.2E+08	6728	0.526702124	2.094691432	0.0567818	0.099877253	0.07364	0	39	49	60	55	50	117	68	80	105	135
ENSMUSG00000102828	chr18	RP23-407E2.30	3.8E+07	3.8E+07	1530	-0.46451131	3.426960349	0.0568085	0.099911663	0.06547	0	165	165	155	135	311	267	219	122	179	156
ENSMUSG00000074210	chr7	E130208F15Rik	3E+07	3E+07	1733	-0.64263025	1.017746273	0.0568663	0.099988249	0.1022	0	21	22	67	29	46	28	46	15	32	37
ENSMUSG00000085287	chr17	4833418N02Rik	8.7E+07	8.7E+07	2762	-0.59227075	1.488437991	0.0568633	0.099988249	0.0919	0	42	22	68	55	68	64	59	24	26	56
ENSMUSG00000025436	chr10	Xrcc6bp1	1.3E+08	1.3E+08	1362	0.543658147	1.100054744	0.0568779	0.0999961	0.06467	0	26	17	31	21	30	67	55	43	43	40
ENSMUSG00000033983	chr11	Coil	8.9E+07	8.9E+07	3520	-0.46780666	2.086960223	0.0569252	0.100066842	0.05702	0	74	58	92	62	78	66	68	63	75	85
ENSMUSG00000006462	chr2	A530013C23Rik	1.7E+08	1.7E+08	5964	-0.44880528	2.186780813	0.0569524	0.100077034	0.05311	0	60	65	103	76	86	82	86	50	83	92
ENSMUSG00000028800	chr4	Hdac1	1.3E+08	1.3E+08	3445	0.434204125	3.589516762	0.0569488	0.100077034	0.05689	0	121	122	179	100	256	421	245	205	284	278
ENSMUSG00000043924	chr4	Ncmap	1.4E+08	1.4E+08	2227	0.628804875	1.024661358	0.0569437	0.100077034	0.09638	0	21	15	45	20	14	60	41	35	42	63
ENSMUSG00000063808	chr7	Gpatch1	3.5E+07	3.5E+07	3295	-0.41909323	2.834067599	0.0569929	0.100135594	0.04867	0	134	73	172	120	117	157	128	95	118	128
ENSMUSG00000028433	chr4	Ubap2	4.1E+07	4.1E+07	4802	-0.38095464	6.299549456	0.0570113	0.100155341	0.04707	0	1177	850	1899	1582	1313	1285	1756	1001	1499	1540
ENSMUSG00000037996	chr4	Slc24a2	8.7E+07	8.7E+07	12217	-1.11463345	0.005851179	0.0571173	0.100329049	0.32101	0	9	4	58	22	8	10	29	4	8	9
ENSMUSG00000004947	chr5	Dtx2	1.4E+08	1.4E+08	7032	0.463381456	3.721990502	0.0571712	0.100393519	0.06614	0	147	111	134	122	334	392	281	246	335	316
ENSMUSG00000025228	chr19	Actr1a	4.6E+07	4.6E+07	2742	0.355265945	6.855696616	0.0571755	0.100393519	0.0412	0	1227	1019	2007	1593	1972	2855	2877	1944	2870	2928
ENSMUSG00000042642	chr3	Flad1	8.9E+07	8.9E+07	4087	-0.36287697	5.576135931	0.0571615	0.100393519	0.04216	0	625	491	1207	920	908	808	1064	586	913	957
ENSMUSG00000024273	chr18	2700062C07Rik	2.4E+07	2.4E+07	1040	0.579479482	2.000868276	0.0571964	0.100417716	0.0937	0	43	32	38	38	87	127	68	102	80	96
ENSMUSG00000021510	chr13	A530054K11Rik	6.8E+07	6.8E+07	5217	-0.44956743	2.591665171	0.0572116	0.100431838	0.0574	0	96	102	115	93	101	139	100	80	86	117
ENSMUSG00000032000	chr9	Birc3	7848699	7849456	5009	0.363493107	3.343291154	0.0572703	0.100514962	0.03701	0	124	96	159	131	156	312	258	159	212	241
ENSMUSG00000085385	chr2	9430008C03Rik	1.6E+08	1.6E+08	7052	0.627341641	1.65431378	0.0572733	0.100514962	0.10599	0	35	37	33	17	55	99	55	67	60	97
ENSMUSG00000042682	chr14	Selk	3E+07	3E+07	1240	0.340262204	6.157704655	0.0573491	0.100635406	0.03748	0	933	642	1132	879	1220	1974	1563	1317	1638	1746
ENSMUSG00000003123	chr7	Lipe	2.5E+07	2.5E+07	4518	-1.06461065	6.70449306	0.0573607	0.100643091	0.36146	0	1581	751	690	345	8298	2017	690	1097	1501	1693
ENSMUSG00000029591	chr5	Ung	1.1E+08	1.1E+08	2566	-0.66769125	3.98227941	0.0573735	0.100653046	0.14154	0	181	79	788	334	199	292	334	170	197	276
ENSMUSG00000037355	chr5	Uvssa	3.3E+07	3.3E+07	8666	-0.48780436	2.32088179	0.0573835	0.100658007	0.06721	0	87	71	111	76	86	137	72	47	71	106
ENSMUSG00000024287	chr18	Thoc1	9958180	9958246	3855	-0.36689608	3.50641826	0.0574191	0.100695211	0.03932	0	148	158	225	208	218	241	217	166	177	217
ENSMUSG00000026032	chr1	Ndufb3	5.9E+07	5.9E+07	763	0.387533363	7.181390664	0.0574156	0.100695211	0.04932	0	1730	997	2874	2036	2159	3987	3207	2707	3187	3915
ENSMUSG00000030930	chr7	Chst15	1.3E+08	1.3E+08	5388	0.423935181	3.824119976	0.0575529	0.100917306	0.05546	0	152	117	187	130	346	351	321	267	368	351
ENSMUSG00000018286	chr11	Psmb6	7.1E+07	7.1E+07	1872	0.377985054	7.477154217	0.057602	0.100990696	0.04698	0	2386	1776	2606	2139	2767	4540	3599	3473	4896	4169
ENSMUSG00000034259	chr15	Exosc4	7.6E+07	7.6E+07	1945	0.327216041	4.473070887	0.0576789	0.101112817	0.03283	0	276	196	361	324	336	517	445	409	562	596
ENSMUSG00000025227	chr19	Tmem180	4.6E+07	4.6E+07	2804	0.643548394	1.517386304	0.0576989	0.101135278	0.10884	0	21	30	26	39	43	51	108	34	86	70
ENSMUSG00000039043	chr7	2610034B18Rik	8E+07	8E+07	2277	0.43529242	2.929223292	0.0577444	0.101202375	0.056	0	86	47	137	84	146	259	179	121	168	178
ENSMUSG00000019809	chr10	Pex3	1.4E+07	1.4E+07	4740	-0.37486903	3.819152414	0.0577961	0.10128045	0.04181	0	215	137	310	223	345	302	311	217	224	207
ENSMUSG00000057229	chr7	Atp5sl	2.6E+07	2.6E+07	2916	-0.43612794	5.169250648	0.0578446	0.101352748	0.06117	0	446	286	1199	774	560	643	718	428	672	713
ENSMUSG00000036875	chr10	Dna2	6.3E+07	6.3E+07	5878	0.722441833	0.337525748	0.0578968	0.101431449	0.10579	0	11	9	13	14	18	53	19	16	23	39
ENSMUSG00000033910	chr3	Gucy1a3	8.2E+07	8.2E+07	6968	-0.38909897	3.308686259	0.0579286	0.101474583	0.04437	0	136	137	235	156	181	250	188	120	144	190
ENSMUSG00000025156	chr11	Gps1	1.2E+08	1.2E+08	2879	-0.34543263	5.686744364	0.0580449	0.101665566	0.03859	0	871	710	927	869	916	982	1105	743	1024	820
ENSMUSG00000013663	chr19	Pten	3.3E+07	3.3E+07	11507	-0.34743624	5.042276072	0.0581178	0.101763721	0.03834	0	475	384	656	476	842	639	858	412	520	589
ENSMUSG00000020530	chr11	Ggnbp2	8.5E+07	8.5E+07	4726	-0.33935989	5.405894201	0.0581227	0.101763721	0.03703	0	701	586	813	631	816	1005	931	600	605	748
ENSMUSG00000061882	chr5	Ccdc62	1.2E+08	1.2E+08	4306	0.416085277	2.563559657	0.0581132	0.101763721	0.04655	0	69	53	88	70	98	159	135	99	123	172
ENSMUSG00000029714	chr5	Gigyf1	1.4E+08	1.4E+08	5437	-0.32087851	5.023941647	0.0581666	0.101827918	0.03263	0	542	412	602	568	584	616	619	372	662	742
ENSMUSG00000102171	chr14	RP23-117H6.2	4.8E+07	4.8E+07	2556	-0.59571853	0.810371598	0.0582052	0.101882687	0.08217	0	30	30	34	24	31	39	23	20	20	36
ENSMUSG00000061613	chr17	U2af1	3.2E+07	3.2E+07	974	0.310797653	4.976141531	0.0582411	0.101932905	0.03036	0	394	291	545	383	530	835	595	601	773	771
ENSMUSG00000060860	chr7	Ube2s	4808155	4808484	858	0.316422994	5.017512168	0.0582485	0.101932988	0.03139	0	399	329	467	435	542	709	722	561	876	822
ENSMUSG00000013150	chr8	Gfod2	1.1E+08	1.1E+08	4608	-0.39941118	3.601149038	0.0582757	0.101967899	0.04862	0	221	174	180	221	217	212	249	141	261	217
ENSMUSG00000026162	chr1	Nhej1	7.5E+07	7.5E+07	1118	0.418016146	2.465769341	0.0583112	0.102004686	0.04637	0	71	45	87	61	90	154	122	91	136	140
ENSMUSG00000039953	chr4	Clstn1	1.5E+08	1.5E+08	4662	0.346462304	5.662130682	0.0583089	0.102004686	0.03897	0	524	385	1019	675	875	1440	1218	772	1226	1264
ENSMUSG00000016386	chr2	Mpped2	1.1E+08	1.1E+08	3425	-1.41740798	1.276720397	0.058356	0.102044875	0.60124	0	13	1	171	93	5	17	47	14	30	23
ENSMUSG00000037795	chr5	N4bp2	6.6E+07	6.6E+07	9871	-0.59521382	2.396718688	0.0583555	0.102044875	0.10541	0	90	73	117	138	44	89	128	63	71	78
ENSMUSG00000040521	chr10	Tsfm	1.3E+08	1.3E+08	2904	0.357678864	4.663386848	0.0583478	0.102044875	0.04074	0	260	167	548	350	416	631	551	434	693	625
ENSMUSG00000025290	chr14	Rps24	2.4E+07	2.4E+07	840	0.380815032	8.33589588	0.0583873	0.102086841	0.04815	0	4305	3245	4910	4089	4553	9969	6231	6221	7186	8207
ENSMUSG00000087658	chr6	Hotairm1	5.2E+07	5.2E+07	1025	0.906871658	0.328964478	0.0583951	0.102087673	0.21567	0	10	4	8	6	34	44	14	25	21	48
ENSMUSG00000020629	chr12	Adi1	2.9E+07	2.9E+07	1886	-0.35844937	6.384397951	0.0585306	0.102311862	0.04218	0	1308	998	1787	1279	1798	1464	1998	1110	1564	1441
ENSMUSG00000053117	chr19	E330013P04Rik	6E+07	6E+07	5106	0.714120445	0.62665899	0.0586008	0.102421796	0.11386	0	13	16	10	21	19	50	35	18	27	56
ENSMUSG00000016319	chrX	Slc25a5	3.7E+07	3.7E+07	1646	0.461428102	5.957773522	0.0587953	0.102748953	0.07027	0	655	403	972	531	1589	2022	1335	1315	1397	1345
ENSMUSG00000028184	chr3	Lphn2	1.5E+08	1.5E+08	8403	-0.39993679	3.665635235	0.0588047	0.102752464	0.04841	0	162	184	276	232	225	278	225	226	200	180
ENSMUSG00000026073	chr1	Il1r2	4E+07	4E+07	1908	0.924918855	0.012190555	0.0588801	0.102871571	0.20321	0	4	7	9	4	23	24	51	13	21	12
ENSMUSG00000025401	chr10	Myo1a	1.3E+08	1.3E+08	3386	0.886736957	0.327239332	0.0589238	0.102934975	0.18325	0	17	16	7	2	15	49	29	28	22	24
ENSMUSG00000032501	chr15	Trib1	6E+07	6E+07	5699	0.388066806	4.262965798	0.0589434	0.10295639	0.04798	0	173	126	432	238	342	473	476	375	413	490
ENSMUSG00000033902	chr2	Mapkbp1	1.2E+08	1.2E+08	7584	-0.339548	3.780736549	0.0589731	0.102995407	0.03449	0	217	183	240	251	251	285	264	188	260	252

ENSMUSG00000003099	chr7	Ppp5c	1.7E+07	1.7E+07	3136	-0.35624558	6.025190342	0.0590286	0.103079537	0.04157	0	924	688	1647	1167	1218	1179	1460	861	1255	1158
ENSMUSG00000025172	chr19	Ankrd2	4.2E+07	4.2E+07	1100	1.599094786	7.095934383	0.0590582	0.10311843	0.78973	0	240	2	2801	2483	80	4486	4451	2677	3171	6707
ENSMUSG00000030207	chr6	8430419L09Rik	1.4E+08	1.4E+08	5776	0.423754001	2.347085735	0.0592375	0.103418583	0.04769	0	51	49	84	62	77	130	120	87	111	142
ENSMUSG00000004031	chr1	Brinp2	1.6E+08	1.6E+08	8767	-0.62849064	0.342639842	0.0592585	0.103442346	0.0772	0	20	16	26	15	32	21	22	16	22	14
ENSMUSG00000014873	chr2	Surf2	2.7E+07	2.7E+07	3408	-0.35899813	3.519269938	0.0592684	0.103446877	0.03779	0	184	152	220	184	223	249	233	170	206	172
ENSMUSG00000100347	chr1	Gm7895	9.4E+07	9.4E+07	1173	-0.63206222	1.432576697	0.0593659	0.103604143	0.1082	0	46	24	81	58	36	51	72	29	29	33
ENSMUSG00000022206	chr15	Npr3	1.2E+07	1.2E+07	6927	-0.97856871	4.898742437	0.0593982	0.103647564	0.31043	0	308	419	127	164	2127	385	298	410	355	578
ENSMUSG00000020949	chr12	Fkbp3	6.5E+07	6.5E+07	947	-0.38391864	7.18119512	0.0594207	0.103673894	0.04912	0	2526	1738	3348	2647	2162	2833	3098	2198	2316	2519
ENSMUSG00000030598	chr7	Fbxo17	2.9E+07	2.9E+07	2497	0.506340012	2.30391024	0.0594298	0.10367687	0.07336	0	50	39	80	35	106	157	125	96	110	98
ENSMUSG00000039852	chr4	Rere	1.5E+08	1.5E+08	8525	-0.35063	6.718839261	0.0594861	0.103762303	0.04083	0	1750	1266	1986	1806	2127	2000	2398	1356	1906	1959
ENSMUSG00000036432	chr3	Siah2	5.9E+07	5.9E+07	2999	0.325753116	4.015600815	0.0594937	0.103762498	0.03203	0	208	144	278	215	242	429	368	321	381	338
ENSMUSG00000041037	chr7	Irgq	2.5E+07	2.5E+07	6123	-0.38815306	5.023534317	0.0595551	0.103856717	0.04869	0	443	336	937	666	460	540	748	427	630	562
ENSMUSG00000000738	chr8	Spg7	1.2E+08	1.2E+08	4188	-0.37695149	6.976177534	0.0596818	0.104064787	0.04737	0	1874	1437	2948	2377	2235	2086	2919	1709	2433	2159
ENSMUSG00000032593	chr9	Amigo3	1.1E+08	1.1E+08	2543	-0.8383431	1.696992002	0.0597023	0.104087547	0.20755	0	32	12	157	89	39	36	48	35	57	55
ENSMUSG00000047003	chr15	Zfp41	7.6E+07	7.6E+07	4068	-0.52800981	1.751586788	0.0597393	0.104139133	0.07641	0	67	49	56	60	55	63	82	31	61	45
ENSMUSG00000059689	chr6	Zfp637	1.2E+08	1.2E+08	2565	-0.30444467	4.80907634	0.0598089	0.104247574	0.02934	0	468	382	487	441	531	651	544	390	521	493
ENSMUSG00000021356	chr13	Irf4	3.1E+07	3.1E+07	4715	0.669794995	1.672289395	0.0598353	0.104267611	0.12172	0	28	44	21	30	48	142	58	48	79	71
ENSMUSG00000059895	chr15	Ptp4a3	7.4E+07	7.4E+07	4619	-0.42804217	9.749151877	0.0598349	0.104267611	0.06164	0	12632	8078	23713	17383	15031	13512	18286	9736	17099	17703
ENSMUSG00000042557	chr9	Sin3a	5.7E+07	5.7E+07	5385	-0.32657549	4.426443779	0.0598588	0.104295547	0.03331	0	350	244	519	365	339	496	466	263	366	399
ENSMUSG00000032002	chr9	Dcun1d5	7184566	7184882	1201	-0.3712101	5.620599056	0.0598717	0.104305184	0.04529	0	757	584	1051	1076	710	1075	1123	687	795	770
ENSMUSG00000074886	chr13	Grk6	5.5E+07	5.5E+07	3241	0.356324658	4.29122313	0.0598992	0.104340093	0.03937	0	206	206	252	247	382	644	424	296	433	499
ENSMUSG00000100594	chr1	2810414N06Rik	1.5E+08	1.5E+08	1381	-0.60315153	1.417539999	0.0600131	0.104525476	0.09696	0	69	32	38	31	64	44	46	35	53	33
ENSMUSG00000028495	chr4	Rps6	8.7E+07	8.7E+07	1586	0.373523551	7.483210967	0.0600626	0.104598681	0.04677	0	2208	1875	2483	2427	2684	5213	3453	3235	4418	4600
ENSMUSG00000039048	chr9	Foxred1	3.5E+07	3.5E+07	4064	-0.33571866	4.614214692	0.060094	0.104640348	0.03534	0	375	213	628	383	534	499	508	330	399	506
ENSMUSG00000024736	chr19	Tmem132a	1.1E+07	1.1E+07	4069	0.516423739	4.06384967	0.0601088	0.104653213	0.08608	0	100	129	335	339	148	447	439	285	493	366
ENSMUSG00000021967	chr14	Mrpl57	5.8E+07	5.8E+07	2321	0.318018939	4.627329121	0.0601182	0.104656498	0.03166	0	313	226	340	367	414	648	519	426	688	545
ENSMUSG00000028601	chr4	Echdc2	1.1E+08	1.1E+08	2287	-0.32526184	4.181862705	0.0602159	0.104813701	0.03243	0	283	208	365	261	423	408	324	240	375	321
ENSMUSG00000030801	chr7	Kat8	1.3E+08	1.3E+08	1573	-0.31802718	4.342310618	0.0602669	0.104889414	0.03152	0	302	274	403	361	342	391	426	258	397	396
ENSMUSG00000034211	chr5	Mrps17	1.3E+08	1.3E+08	2330	0.303715024	5.130033768	0.0604294	0.105146127	0.02973	0	455	284	648	468	552	932	747	652	807	843
ENSMUSG00000043131	chr6	Mob1a	8.3E+07	8.3E+07	4794	0.353834836	5.094508889	0.0604238	0.105146127	0.04046	0	393	367	396	400	700	1088	801	614	780	693
ENSMUSG00000030744	chr7	Rps3	9.9E+07	9.9E+07	4483	0.372020691	8.587112724	0.0604433	0.1051573	0.04674	0	4845	4044	5419	5025	5797	10955	7796	6773	9807	9672
ENSMUSG00000028793	chr4	Rnf19b	1.3E+08	1.3E+08	2872	0.291881796	4.979116211	0.0604787	0.105205736	0.02709	0	408	260	543	446	513	810	829	520	726	712
ENSMUSG00000028842	chr4	Ago3	1.3E+08	1.3E+08	16571	-0.36061677	3.604861201	0.0607012	0.105579782	0.0394	0	193	181	238	194	206	262	230	184	194	221
ENSMUSG00000062376	chr19	2010012O05Rik	4.7E+07	4.7E+07	2176	-0.3413997	3.70960804	0.0607288	0.105614712	0.03516	0	220	154	259	230	236	310	270	171	236	209
ENSMUSG00000002031	chr9	Ift46	4.5E+07	4.5E+07	5658	0.335235226	4.211087874	0.0607579	0.105652104	0.03445	0	236	188	253	231	321	575	425	264	422	473
ENSMUSG00000056214	chr18	Pard6g	8E+07	8E+07	3143	0.639519671	1.241758839	0.060767	0.105654929	0.10626	0	27	25	19	14	46	84	44	43	59	54
ENSMUSG00000066406	chr7	Akap13	7.5E+07	7.5E+07	15203	-0.37547936	6.411177548	0.0608868	0.105850142	0.0473	0	1432	1143	1654	1652	1277	1531	1835	1025	1523	1793
ENSMUSG00000027201	chr2	Myef2	1.3E+08	1.3E+08	5936	0.615753924	1.826105527	0.060921	0.105896345	0.11108	0	35	26	37	28	83	125	67	73	51	113
ENSMUSG00000047126	chr11	Cltc	8.7E+07	8.7E+07	8499	-0.37115306	7.543148624	0.0609816	0.105988661	0.04657	0	3051	2220	4214	3033	3514	4261	4383	2507	2904	2907
ENSMUSG00000041798	chr11	Gck	5900820	5901087	3033	-0.85286716	3.104661217	0.0611488	0.106265937	0.23574	0	35	39	373	174	298	122	246	57	100	117
ENSMUSG00000080242	chr6	Gm15487	3.8E+07	3.8E+07	465	0.331516562	4.760260774	0.0612161	0.106369734	0.03543	0	290	229	565	346	424	614	672	409	755	678
ENSMUSG00000036940	chr4	Kdm1a	1.4E+08	1.4E+08	5179	0.29331742	4.712014109	0.0612294	0.106379794	0.02696	0	307	273	475	339	386	705	602	481	595	587
ENSMUSG00000058833	chr8	2810428I15Rik	7.1E+07	7.1E+07	1822	0.373355542	6.17299211	0.0612462	0.106395803	0.04663	0	916	708	917	907	1293	1805	1472	1240	2194	1697
ENSMUSG00000048096	chr1	Lmod1	1.4E+08	1.4E+08	3948	-0.67875176	3.645113837	0.0612775	0.106436891	0.15012	0	363	151	88	127	417	329	138	139	169	231
ENSMUSG00000030214	chr6	Plbd1	1.4E+08	1.4E+08	2633	-0.45884717	4.242096618	0.0613911	0.106597289	0.068	0	265	131	630	307	415	475	287	245	247	404
ENSMUSG00000068141	chr17	Gm10232	3044014	3044733	720	0.59116419	0.981097035	0.0613833	0.106597289	0.08417	0	27	14	24	26	20	46	32	43	48	58
ENSMUSG00000079105	chr15	C7	4988762	4989006	2709	2.124601884	3.278281053	0.0613926	0.106597289	1.33495	0	2	4	110	14	184	24	1611	14	15	26
ENSMUSG00000019932	chr10	Kera	9.8E+07	9.8E+07	1950	0.754835969	4.669395129	0.0614651	0.106696704	0.18821	0	421	344	161	101	298	1612	474	441	382	513
ENSMUSG00000054051	chr14	Ercc6	3.3E+07	3.3E+07	8422	-0.43514337	2.862118901	0.0614583	0.106696704	0.05725	0	132	114	139	107	120	129	154	77	121	157
ENSMUSG00000029029	chr4	Wrap73	1.5E+08	1.5E+08	4335	0.34581788	3.786698449	0.0615053	0.106740038	0.03664	0	160	117	257	181	212	354	279	238	381	333
ENSMUSG00000040268	chr7	Plekha1	1.3E+08	1.3E+08	8527	-0.33001183	5.446727799	0.0614986	0.106740038	0.03593	0	682	558	872	817	715	955	941	617	666	826
ENSMUSG00000054619	chr15	Mettl7a1	1E+08	1E+08	1883	-0.41602246	5.203339052	0.0615802	0.106856856	0.0575	0	659	461	555	392	1145	869	629	441	627	733
ENSMUSG00000041645	chr12	Ddx24	1E+08	1E+08	3157	-0.35703849	6.178531822	0.0616761	0.107010096	0.04277	0	953	799	1815	1395	1296	1398	1498	934	1416	1344
ENSMUSG00000024683	chr19	Mrpl16	1.2E+07	1.2E+07	1122	-0.33055807	5.336759764	0.0617093	0.107054456	0.03586	0	623	444	1032	710	635	768	838	569	724	795
ENSMUSG00000051225	chr15	Fam83a	5.8E+07	5.8E+07	3171	-1.5905909	0.613888601	0.061719	0.107057982	0.74838	0	21	14	2	2	138	27	1	15	16	14
ENSMUSG00000063200	chr13	Nol7	4.3E+07	4.3E+07	1811	-0.33389588	5.736900987	0.0617725	0.107137593	0.03709	0	922	694	947	906	977	1139	1023	847	917	921
ENSMUSG00000025075	chr19	Habp2	5.6E+07	5.6E+07	3193	1.759295267	0.315218414	0.0617804	0.107138026	0.91487	0	0	0	36	5	2	4	21	3	68	80
ENSMUSG00000047485	chrX	Klhl34	1.6E+08	1.6E+08	1935	-1.38804866	3.707182141	0.0618781	0.107294162	0.61556	0	70	7	878	588	23	122	249	64	110	213
ENSMUSG00000056427	chr11	Slit3	3.5E+07	3.5E+07	6067	0.41988676	3.969707824	0.0619115	0.107338803	0.05631	0	157	149	205	149	364	494	477	241	363	295
ENSMUSG00000032179	chr9	Bmp5	7.6E+07	7.6E+07	4025	0.473064781	4.039563232	0.0619749	0.107435474	0.07186	0	289	173	155	172	211	632	330	343	296	370
ENSMUSG00000037958	chr11	Ccdc55	7.7E+07	7.7E+07	3628	-0.31403903	4.056304105	0.0620135	0.107489123	0.03023	0	265	197	336	253	346	352	354	227	310	289
ENSMUSG00000049878	chr4	Rlf	1.2E+08	1.2E+08	6990	-0.36250634	3.922740317	0.0620405	0.107522475	0.04139	0	251	236	277	243	247	317	330	226	256	233
ENSMUSG00000015165	chr7	Hnrnpl	2.9E+07	2.9E+07	5953	0.351560804	6.393368448	0.0620695	0.107559456	0.04173	0	1014	756	1391	970	1540	2283	1698	1442	2078	2265
ENSMUSG00000029469	chr5	Ift81	1.2E+08	1.2E+08	3453	0.54082908	2.369095265	0.0620856	0.107574197	0.08889	0	45	26	92	70	91	157	88	101	91	181
ENSMUSG00000028653	chr4	Trit1	1.2E+08	1.2E+08	2087	0.401104347	3.507599635	0.0621513	0.107674672	0.0499	0	122	111	142	128	236	329	220	232	250	287
ENSMUSG00000081453	chr16	Gm6767	5.1E+07	5.1E+07	1381	0.956666999	-0.28803375	0.0622092	0.107761633	0.22039	0	7	3	9	2	16	7	33	17	26	10
ENSMUSG00000048647	chr2	Exd1	1.2E+08	1.2E+08	6042	-0.53054911	1.711676235	0.0622203	0.107767533	0.07946	0	58	46	52	56	70	90	69	26	43	50

ENSMUSG00000098413	chr19	Mir6990	6914196	6914286	91	-0.75685893	0.545790368	0.0623249	0.107935488	0.14077	0	17	10	62	30	17	28	26	13	19	20
ENSMUSG00000019774	chr10	Mtrf1l	5811887	5813406	3261	-0.41254148	2.765961912	0.0623481	0.10796226	0.04948	0	97	99	163	97	124	155	113	92	110	128
ENSMUSG00000024165	chr17	Hn1l	2.5E+07	2.5E+07	2933	-0.44534279	3.087763883	0.0625744	0.108340743	0.06161	0	130	152	130	153	143	193	158	124	145	117
ENSMUSG00000032806	chrX	Slc10a3	7.4E+07	7.4E+07	2023	0.446578643	2.446010393	0.0626153	0.108393022	0.0574	0	55	48	80	66	96	172	97	85	156	132
ENSMUSG00000092417	chr17	Gpank1	3.5E+07	3.5E+07	1879	0.345183534	3.51558826	0.06262	0.108393022	0.03561	0	141	105	191	129	197	313	252	198	274	277
ENSMUSG00000035382	chr9	Pcsk7	4.6E+07	4.6E+07	3784	-0.32056936	3.952410245	0.0626564	0.10844256	0.03166	0	236	193	326	265	274	319	340	208	262	293
ENSMUSG00000005299	chr5	Letm1	3.4E+07	3.4E+07	9650	-0.41336668	6.52329471	0.0627227	0.108543911	0.05814	0	1216	781	2732	1861	1671	1685	2125	1159	1573	1653
ENSMUSG00000030790	chr7	Adm	1.1E+08	1.1E+08	1619	0.540571713	2.36343616	0.0627478	0.108573961	0.08735	0	50	53	67	36	106	165	85	121	109	129
ENSMUSG00000029047	chr4	Pex10	1.6E+08	1.6E+08	3298	-0.38078747	3.450952878	0.0627794	0.108615223	0.04401	0	145	108	277	200	223	205	249	141	181	203
ENSMUSG00000019433	chr8	Gipc1	8.4E+07	8.4E+07	1615	0.333711514	4.59533102	0.0627999	0.108623583	0.03621	0	240	189	512	348	369	636	590	377	647	547
ENSMUSG00000028962	chr5	Slc4a2	2.4E+07	2.4E+07	6195	0.303928026	4.587362534	0.0628074	0.108623583	0.02945	0	281	219	399	285	464	611	624	370	574	578
ENSMUSG00000035236	chr2	Scai	3.9E+07	3.9E+07	11668	-0.52501697	1.621691094	0.0628028	0.108623583	0.07574	0	60	45	67	36	57	70	52	36	34	64
ENSMUSG00000036106	chr15	Prr5	8.5E+07	8.5E+07	1917	0.647720554	2.397690993	0.0628726	0.108722863	0.13253	0	35	45	66	24	145	163	99	117	138	127
ENSMUSG00000039754	chr5	Alkbh4	1.4E+08	1.4E+08	2117	0.414904828	2.552562117	0.0629451	0.108834803	0.04863	0	65	51	89	81	89	153	121	91	167	151
ENSMUSG00000073542	chr18	Cep76	6.8E+07	6.8E+07	3979	-0.40561152	2.893885553	0.0630502	0.109003074	0.0488	0	130	102	139	107	151	145	155	111	107	133
ENSMUSG00000005950	chr11	P2rx5	7.3E+07	7.3E+07	2395	0.34798573	4.647189559	0.0631645	0.109187273	0.03993	0	279	157	526	374	386	742	575	425	630	538
ENSMUSG00000020211	chr10	Sf3a2	8.1E+07	8.1E+07	2658	0.339970405	4.885889853	0.0633149	0.10941294	0.03819	0	325	229	532	410	522	728	613	431	908	750
ENSMUSG00000028465	chr4	Tln1	4.4E+07	4.4E+07	9801	0.423494919	7.330797024	0.0633185	0.10941294	0.06172	0	1380	1102	3215	2762	2284	4227	3486	2706	4504	4212
ENSMUSG00000043015	chr1	Tmem194b	5.3E+07	5.3E+07	7078	0.784192018	0.772159651	0.063312	0.10941294	0.16387	0	9	21	13	7	37	64	31	34	30	49
ENSMUSG00000035868	chr17	3110052M02Rik	2.2E+07	2.2E+07	1383	-0.67156318	0.288651678	0.0634185	0.109572313	0.10404	0	13	24	21	14	32	28	19	13	15	16
ENSMUSG00000069678	chr6	Pcgf1	8.3E+07	8.3E+07	1471	0.430047392	2.886660313	0.0634413	0.109598254	0.05416	0	89	87	89	73	124	209	166	145	164	177
ENSMUSG00000038967	chr11	Pdk2	9.5E+07	9.5E+07	3163	-0.42318709	8.943433769	0.0634573	0.109612245	0.0619	0	6841	4744	12747	10336	9128	7235	10862	5612	10180	9790
ENSMUSG00000009640	chr4	Dmap1	1.2E+08	1.2E+08	2636	0.336483611	4.085986248	0.0635733	0.109799253	0.0359	0	217	130	265	242	292	413	364	272	451	454
ENSMUSG00000034190	chr14	Chmp7	7E+07	7E+07	2706	-0.32781305	5.932293596	0.0636191	0.109864726	0.03641	0	992	762	1199	1036	1136	1242	1357	806	1200	1017
ENSMUSG00000029729	chr5	Zkscan1	1.4E+08	1.4E+08	8541	-0.32571884	4.039431872	0.063684	0.109963301	0.0331	0	275	203	340	274	281	358	295	266	287	286
ENSMUSG00000041438	chr8	Cirh1a	1.1E+08	1.1E+08	2248	-0.29235815	4.520373977	0.0637181	0.110008662	0.02699	0	328	268	496	378	453	507	423	346	418	430
ENSMUSG00000092187	chr7	Gm20457	6.4E+07	6.4E+07	682	-0.64893445	0.774213439	0.0638119	0.110156974	0.10251	0	32	14	30	33	43	44	13	21	28	25
ENSMUSG00000019920	chr10	Lims1	5.8E+07	5.8E+07	4891	-0.44669071	5.50680086	0.0638608	0.11022788	0.06784	0	665	380	1413	1000	637	936	1154	555	611	762
ENSMUSG00000032199	chr9	Polr2m	7.1E+07	7.1E+07	2424	-0.37634718	7.686942601	0.0638955	0.110274264	0.04899	0	3150	2268	5082	3915	3417	3780	4771	2601	3865	3620
ENSMUSG00000025134	chr11	Alyref	1.2E+08	1.2E+08	3839	0.334701796	4.164870302	0.0640023	0.110444935	0.03585	0	200	157	305	241	308	501	327	360	415	441
ENSMUSG00000018509	chr11	Cenpv	6.3E+07	6.3E+07	1811	0.375179642	3.68285006	0.0640216	0.110464632	0.04378	0	162	125	172	197	174	344	237	263	320	309
ENSMUSG00000027340	chr2	Slc23a2	1.3E+08	1.3E+08	7951	-0.37165255	4.161173644	0.0641387	0.110639836	0.04459	0	226	188	500	354	286	387	359	231	271	370
ENSMUSG00000061759	chr10	1700052N19Rik	4432467	4432711	8243	-0.32414409	4.602461891	0.0641389	0.110639836	0.03448	0	463	328	392	401	412	515	506	309	469	440
ENSMUSG00000024800	chr19	Rpp30	3.6E+07	3.6E+07	1155	-0.37575287	3.281193165	0.0641625	0.110666943	0.04318	0	167	144	197	138	166	185	193	141	175	170
ENSMUSG00000025348	chr10	Itga7	1.3E+08	1.3E+08	4013	0.361868864	6.83069409	0.064244	0.110790288	0.04519	0	1067	996	2112	1675	1836	3195	2784	1882	2964	2498
ENSMUSG00000030588	chr7	Yif1b	2.9E+07	2.9E+07	1378	0.338474518	4.954498425	0.0642498	0.110790288	0.03829	0	315	235	618	433	529	751	647	481	871	836
ENSMUSG00000078923	chr2	Ube2v1	1.7E+08	1.7E+08	2721	-0.32962921	5.296974633	0.0642756	0.110821092	0.03641	0	551	446	857	742	744	702	994	499	702	718
ENSMUSG00000028803	chr4	Nipal3	1.4E+08	1.4E+08	7588	-0.43829977	4.200543117	0.0643088	0.110864692	0.06342	0	286	150	588	375	249	353	434	202	302	337
ENSMUSG00000061589	chr10	Dot1l	8.1E+07	8.1E+07	8705	-0.29869686	5.068381569	0.0643251	0.110865634	0.02936	0	471	362	748	612	641	672	645	422	638	748
ENSMUSG00000073481	chr1	Marc2	1.8E+08	1.8E+08	6629	0.37948968	6.008970043	0.0643237	0.110865634	0.0494	0	765	533	990	663	1384	1923	1188	1203	1615	1594
ENSMUSG00000024142	chr17	Mlst8	2.4E+07	2.4E+07	3366	-0.32410457	4.346103902	0.0644551	0.111075989	0.03403	0	295	276	345	385	384	404	443	256	413	355
ENSMUSG00000034064	chr16	Poglut1	3.9E+07	3.9E+07	4658	0.354985387	4.032210719	0.0646776	0.111445653	0.04015	0	220	165	222	172	299	498	350	335	336	360
ENSMUSG00000032850	chr5	Rnft2	1.2E+08	1.2E+08	5593	-0.57221664	1.389989878	0.0647994	0.111641888	0.0879	0	29	24	47	51	85	49	52	35	38	36
ENSMUSG00000031355	chrX	Arhgap6	1.7E+08	1.7E+08	12128	-0.49821987	2.309137108	0.0648329	0.111683269	0.07437	0	115	52	113	81	70	101	115	63	60	81
ENSMUSG00000060181	chr10	Slc35e3	1.2E+08	1.2E+08	3482	0.403071416	2.804272524	0.0648394	0.111683269	0.04787	0	87	59	109	76	122	207	144	127	145	188
ENSMUSG00000025722	chr7	Wdr73	8.1E+07	8.1E+07	3721	0.403453352	2.944409647	0.0648625	0.111709443	0.04905	0	90	61	102	91	158	213	170	133	182	198
ENSMUSG00000066800	chr1	Rnasel	1.5E+08	1.5E+08	6641	0.739709845	1.773539297	0.0649159	0.111787602	0.16601	0	38	45	15	15	66	139	84	63	70	76
ENSMUSG00000067279	chr19	Ppp1r3c	3.7E+07	3.7E+07	2719	-0.45972965	8.397048463	0.064946	0.111825764	0.07378	0	4327	5506	6756	7437	4755	5484	8432	3634	7012	5074
ENSMUSG00000070605	chr4	Gm13251	1.5E+08	1.5E+08	4550	-0.49154111	2.369100522	0.0649617	0.111838996	0.07344	0	106	63	96	88	93	132	95	46	114	60
ENSMUSG00000083879	chr2	Gm14038	1.3E+08	1.3E+08	807	-0.46500137	1.921276332	0.065092	0.112049668	0.05686	0	61	42	79	68	77	76	70	63	56	53
ENSMUSG00000006205	chr7	Htra1	1.3E+08	1.3E+08	2879	0.460157426	5.693229942	0.0651317	0.112104158	0.07269	0	440	695	482	626	953	1588	865	974	1479	1280
ENSMUSG00000039089	chr10	L3mbtl3	2.6E+07	2.6E+07	4651	-0.40067057	3.25545421	0.0651543	0.11212935	0.05053	0	137	146	195	174	150	194	233	107	160	160
ENSMUSG00000024299	chr17	Adamts10	3.4E+07	3.4E+07	5453	0.573860466	3.580975311	0.065202	0.112197724	0.1086	0	125	154	94	84	245	436	191	177	264	426
ENSMUSG00000021371	chr13	Mcur1	4.4E+07	4.4E+07	4350	-0.3523114	5.903797825	0.0652572	0.112278935	0.04255	0	901	557	1470	984	1321	1133	1372	774	959	1224
ENSMUSG00000010392	chr11	Gosr1	7.7E+07	7.7E+07	4289	-0.29591688	4.709458715	0.065478	0.112615041	0.02851	0	410	292	526	393	581	622	557	374	442	440
ENSMUSG00000040158	chr11	Tax1bp3	7.3E+07	7.3E+07	2989	0.452200731	2.791292079	0.0654811	0.112615041	0.06405	0	81	43	109	69	148	225	135	121	160	178
ENSMUSG00000047822	chr9	Gm6484	2.2E+07	2.2E+07	864	-1.64366616	0.548065184	0.0654798	0.112615041	0.81454	0	22	17	0	3	126	16	13	11	27	1
ENSMUSG00000059708	chrX	Akap17b	3.7E+07	3.7E+07	6003	-0.48338248	2.298187559	0.0654847	0.112615041	0.07012	0	73	58	129	95	75	96	117	44	100	67
ENSMUSG00000026918	chr2	Brd3	2.7E+07	2.7E+07	7336	-0.32009703	5.356479255	0.0655672	0.112743155	0.03476	0	588	545	809	806	655	834	886	563	751	738
ENSMUSG00000029426	chr5	Scarb2	9.2E+07	9.2E+07	2110	-0.37837623	6.402631378	0.0656387	0.112852192	0.04977	0	1346	1062	2115	1580	1121	1945	1654	1154	1294	1605
ENSMUSG00000070493	chr5	Chchd2	1.3E+08	1.3E+08	2269	0.351895958	8.522226316	0.0656987	0.112941615	0.04355	0	4384	3157	6319	4787	6201	9387	8421	6639	8616	9544
ENSMUSG00000021737	chr14	Psmd6	1.4E+07	1.4E+07	2326	-0.34040324	6.585450659	0.0657877	0.113080658	0.04033	0	1586	1239	1930	1683	1619	2026	1960	1355	1784	1650
ENSMUSG00000041570	chr1	Camsap2	1.4E+08	1.4E+08	9195	-0.33452392	3.701155418	0.0658039	0.113094651	0.03486	0	188	167	259	214	264	300	260	192	203	229
ENSMUSG00000014077	chr2	Chp1	1.2E+08	1.2E+08	3499	-0.34685642	6.026317506	0.0658842	0.113218861	0.04162	0	995	796	1166	939	1673	1413	1379	783	1215	1206
ENSMUSG00000033306	chr16	Lpp	2.4E+07	2.4E+07	15994	-0.37210805	4.724132844	0.065903	0.113237237	0.04683	0	492	403	382	456	445	667	510	411	390	400
ENSMUSG00000085227	chr5	6330418K02Rik	1.4E+08	1.4E+08	1339	0.620757203	0.507706182	0.0659114	0.113237796	0.08966	0	9	8	23	12	28	35	30	24	32	42
ENSMUSG00000039456	chr16	Morc3	9.4E+07	9.4E+07	4178	-0.35297687	4.066523023	0.0661784	0.113682573	0.04091	0	248	247	314	291	294	443	356	219	246	270

ENSMUSG00000018287	chr11	Spag7	7.1E+07	7.1E+07	1480	0.33838441	6.465096579	0.0662856	0.113852698	0.03992	0	1161	787	1492	1040	1491	2043	2174	1559	2277	2119
ENSMUSG00000054874	chr19	Pcnxl3	5664635	5665247	8757	-0.30859175	4.404338348	0.0664322	0.114090664	0.03098	0	303	280	393	356	428	431	448	316	408	341
ENSMUSG00000024639	chr19	Gnaq	1.6E+07	1.6E+07	6185	-0.36817025	4.236640698	0.0665091	0.11420864	0.04513	0	252	256	298	294	504	441	444	215	303	320
ENSMUSG00000038910	chr17	Plcl2	5.1E+07	5.1E+07	4050	-0.34546945	6.214466443	0.0665488	0.114262962	0.04159	0	1252	871	1578	1180	1438	1328	1781	908	1454	1330
ENSMUSG00000031954	chr8	Cfdp1	1.1E+08	1.1E+08	1215	0.323388315	4.665838849	0.0665752	0.114294286	0.03463	0	343	249	341	277	494	771	525	459	574	586
ENSMUSG00000026604	chr1	Ptpn14	1.9E+08	1.9E+08	13413	-0.32081518	4.432232414	0.066675	0.114451594	0.03369	0	286	235	477	426	407	395	458	281	385	465
ENSMUSG00000064371	chrMT	mt-Tt	15289	15355	67	-0.71483045	1.599443698	0.0667863	0.114628568	0.15676	0	28	18	112	56	82	35	78	21	39	60
ENSMUSG00000098462	chr19	Gm27694	5799000	5799085	86	-0.4805706	2.868796592	0.0668099	0.114655121	0.07444	0	127	110	122	81	193	162	171	79	87	135
ENSMUSG00000033460	chrX	Armcx1	1.3E+08	1.3E+08	3227	0.542377845	1.93962125	0.0668447	0.114700661	0.08685	0	46	32	38	30	85	129	91	81	75	79
ENSMUSG00000031808	chr8	Slc27a1	7.2E+07	7.2E+07	2795	-0.53143542	6.606667536	0.0668695	0.114729246	0.09925	0	1415	571	3797	1929	1568	1779	1823	990	1472	2287
ENSMUSG00000038880	chr17	Mrps34	2.5E+07	2.5E+07	2064	0.340144541	5.904580265	0.0669671	0.11488272	0.04033	0	658	471	1186	816	972	1571	1236	1092	1550	1450
ENSMUSG00000052429	chr7	Prmt1	4.5E+07	4.5E+07	2521	0.342218101	6.570913817	0.0669913	0.114896128	0.04104	0	1091	978	1529	1350	1374	2483	1977	1721	2419	2367
ENSMUSG00000066839	chr9	Ecsit	2.2E+07	2.2E+07	1684	-0.37175356	6.497247173	0.06699	0.114896128	0.0485	0	1275	893	2367	1794	1557	1605	1985	1158	1748	1667
ENSMUSG00000025732	chr17	Fam195a	2.6E+07	2.6E+07	816	-0.46560478	5.23486256	0.0670452	0.114974462	0.0752	0	471	238	1226	874	668	667	722	384	681	851
ENSMUSG00000053617	chr19	Sh3pxd2a	4.7E+07	4.7E+07	10464	-0.3553343	6.546869801	0.0671095	0.115070577	0.04438	0	1533	1098	1665	1329	2395	1954	2018	1177	1682	1719
ENSMUSG00000026470	chr1	Stx6	1.6E+08	1.6E+08	10637	0.401662115	3.961771229	0.0671457	0.115118674	0.0541	0	176	104	213	164	389	450	352	279	375	371
ENSMUSG00000003070	chr10	Efna2	8E+07	8E+07	2131	0.659946322	0.744564594	0.0671632	0.115134579	0.10362	0	22	20	13	13	20	50	33	41	39	31
ENSMUSG00000020181	chr10	Nav3	1.1E+08	1.1E+08	13806	-0.60152824	1.165429796	0.0671842	0.115142474	0.09618	0	50	26	40	40	39	45	45	38	20	27
ENSMUSG00000039483	chr2	Asb6	3.1E+07	3.1E+07	5439	0.346910772	3.609940116	0.0671806	0.115142474	0.03754	0	143	118	177	151	221	338	270	183	326	297
ENSMUSG00000039156	chr5	Stim2	5.4E+07	5.4E+07	5215	-0.32523587	5.198659535	0.0672052	0.115164297	0.03621	0	536	523	630	560	811	635	851	487	684	711
ENSMUSG00000029388	chr5	Eif2b1	1.2E+08	1.2E+08	2577	-0.29688786	5.247889236	0.0672339	0.115194627	0.02983	0	546	397	841	700	728	811	802	515	727	682
ENSMUSG00000040667	chr11	Nup88	7.1E+07	7.1E+07	8144	-0.3066336	5.237334363	0.0672393	0.115194627	0.03201	0	592	483	805	629	631	806	821	572	583	696
ENSMUSG00000024055	chr17	Cyp4f13	3.3E+07	3.3E+07	3330	0.606243744	2.463005481	0.0672887	0.115265256	0.11598	0	51	65	43	34	127	176	113	77	141	177
ENSMUSG00000021133	chr12	4933426M11Rik	8.1E+07	8.1E+07	5001	-0.36713003	6.360727656	0.0673135	0.115293563	0.04741	0	1548	1112	1618	1332	1283	1587	1918	1209	1304	1386
ENSMUSG00000034263	chr9	Vwa9	6.5E+07	6.5E+07	3208	-0.3210064	4.449232453	0.0674148	0.115438965	0.0341	0	288	306	418	394	409	438	477	338	379	360
ENSMUSG00000073198	chr12	Gm10480	1.8E+07	1.8E+07	1203	-0.68456051	0.164311843	0.0674122	0.115438965	0.11102	0	27	15	12	19	21	16	27	11	14	14
ENSMUSG00000024007	chr17	Ppil1	2.9E+07	2.9E+07	2163	0.385502872	3.386455696	0.0674366	0.115462131	0.0463	0	103	113	145	145	169	274	219	182	313	223
ENSMUSG00000041236	chr13	Vps41	1.9E+07	1.9E+07	3195	-0.33171561	5.945838583	0.0674509	0.11547249	0.03846	0	1061	831	1108	1057	1060	1280	1347	806	1141	1099
ENSMUSG00000001249	chr7	Hpn	3.1E+07	3.1E+07	4101	-0.4001483	3.610837063	0.067479	0.115506602	0.05235	0	192	145	277	237	196	182	316	129	232	232
ENSMUSG00000071847	chr18	Apcdd1	6.3E+07	6.3E+07	2799	-0.78766616	2.782187005	0.0675088	0.115543375	0.20951	0	143	133	40	51	269	172	54	80	109	107
ENSMUSG00000031969	chr9	Acad8	2.7E+07	2.7E+07	4143	-0.3090136	5.527664983	0.0675586	0.115614609	0.03279	0	714	511	1069	770	839	916	911	700	839	872
ENSMUSG00000000686	chr11	Abhd15	7.8E+07	7.8E+07	3035	-1.08647265	0.574650769	0.0676985	0.115839803	0.35006	0	24	15	10	3	100	23	18	15	16	20
ENSMUSG00000085088	chr11	4931413K12Rik	7.6E+07	7.6E+07	1282	-0.71408296	-0.1153996	0.0677133	0.115851094	0.11005	0	18	12	15	10	23	17	12	5	10	22
ENSMUSG00000034709	chr17	Ppp1r21	8.9E+07	8.9E+07	4255	0.37745293	3.402619584	0.067751	0.115892049	0.04449	0	138	110	154	106	179	348	247	189	226	221
ENSMUSG00000073125	chrX	Xlr3b	7.3E+07	7.3E+07	3780	-0.90333135	0.326367254	0.0677538	0.115892049	0.23991	0	26	34	21	15	12	16	17	2	19	34
ENSMUSG00000038518	chr13	Jarid2	4.5E+07	4.5E+07	9715	-0.30396933	4.431305829	0.0679666	0.11624181	0.03021	0	364	242	439	316	452	468	373	328	370	446
ENSMUSG00000037531	chr3	Mrpl47	3.3E+07	3.3E+07	4419	-0.31480726	4.900919181	0.0680393	0.116352077	0.03344	0	440	296	768	548	499	618	633	401	524	584
ENSMUSG00000027217	chr2	Tspan18	9.3E+07	9.3E+07	8175	-0.73224669	2.71772291	0.0680603	0.116373734	0.17851	0	98	48	66	69	371	124	128	69	89	99
ENSMUSG00000034848	chr2	Ttc21b	6.6E+07	6.6E+07	9282	-0.47591566	1.947175564	0.0680831	0.116398572	0.06357	0	53	44	97	66	77	78	86	57	57	47
ENSMUSG00000000581	chr11	C1d	1.7E+07	1.7E+07	3995	-0.31319664	4.863675201	0.0681999	0.11658395	0.03322	0	503	346	604	488	490	566	716	417	469	512
ENSMUSG00000045757	chr7	Zfp764	1.3E+08	1.3E+08	2508	-0.46616929	1.656231346	0.0682318	0.116624275	0.058	0	57	43	53	57	55	62	58	45	50	50
ENSMUSG00000016495	chr19	Plgrkt	2.9E+07	2.9E+07	3799	0.325492198	3.981962663	0.0683309	0.116779561	0.03399	0	213	152	243	179	271	485	329	258	357	392
ENSMUSG00000017210	chr11	Med24	9.9E+07	9.9E+07	6528	-0.34145177	5.768632112	0.0683519	0.116796188	0.04086	0	719	659	1205	1134	903	1000	1114	708	1059	1099
ENSMUSG00000040365	chr11	Trim41	4.9E+07	4.9E+07	3511	0.303163091	5.145673212	0.0683573	0.116796188	0.03145	0	394	295	606	543	594	900	836	526	904	903
ENSMUSG00000008683	chr7	Rps15a	1.2E+08	1.2E+08	6262	0.363312044	7.209585772	0.0683862	0.116831324	0.04704	0	1922	1535	2306	1794	2184	4505	2736	2791	3518	3676
ENSMUSG00000031465	chr8	Angpt2	1.9E+07	1.9E+07	3690	0.4799625	1.764524276	0.0683974	0.116836173	0.06221	0	40	30	57	30	52	99	72	55	101	70
ENSMUSG00000034681	chr17	Rnps1	2.4E+07	2.4E+07	1920	-0.32568127	4.168527998	0.0684073	0.11683885	0.03489	0	273	213	425	314	290	373	419	230	327	306
ENSMUSG00000104394	chr1	RP23-306B14.3	1.9E+08	1.9E+08	2262	-0.58121785	0.56433003	0.0684335	0.116869306	0.07916	0	26	20	26	24	29	37	27	17	20	15
ENSMUSG00000056071	chr3	S100a9	9.1E+07	9.1E+07	522	0.951962716	0.700559715	0.0684667	0.116911843	0.24904	0	7	30	15	9	9	99	41	19	25	30
ENSMUSG00000021271	chr12	Zfp839	1.1E+08	1.1E+08	3725	-0.35212839	3.562786076	0.0684886	0.116934985	0.0395	0	225	123	246	201	205	247	209	150	208	258
ENSMUSG00000018417	chr1	Myo1b	5.2E+07	5.2E+07	10792	-0.34181687	3.803023574	0.0684978	0.11693648	0.03752	0	198	162	329	198	308	316	305	196	210	245
ENSMUSG00000045237	chrX	1110012L19Rik	7E+07	7E+07	1094	-0.36326597	3.903140254	0.0685466	0.117005599	0.04376	0	297	202	264	179	313	355	293	195	229	286
ENSMUSG00000020963	chr12	Tshr	9.1E+07	9.1E+07	4873	-1.31438776	2.345146218	0.0685849	0.117056642	0.57572	0	101	87	7	5	354	112	25	59	46	55
ENSMUSG00000002265	chr7	Peg3	6703892	6711731	13314	0.784247498	5.162318591	0.0685991	0.117066676	0.21499	0	629	574	112	170	272	1518	603	669	882	1070
ENSMUSG00000038236	chr6	Hoxa7	5.2E+07	5.2E+07	3761	0.335614368	3.613605815	0.068683	0.117195565	0.03527	0	145	124	197	146	202	299	285	198	291	331
ENSMUSG00000084403	chr4	Rps15a-ps8	5.4E+07	5.4E+07	387	0.617441429	0.400377702	0.0688255	0.117424427	0.08748	0	17	5	19	12	20	36	24	23	39	28
ENSMUSG00000025982	chr1	Sf3b1	5.5E+07	5.5E+07	11370	-0.34737527	6.798638474	0.0688711	0.117487977	0.04306	0	1762	1300	2456	1853	2136	2827	2310	1483	1639	1990
ENSMUSG00000007656	chr9	Arpp19	7.5E+07	7.5E+07	4957	0.358356093	6.444489057	0.0689239	0.117563777	0.04574	0	1018	696	1832	1179	1178	2337	2448	1566	1745	2044
ENSMUSG00000026036	chr1	Nif3l1	5.8E+07	5.8E+07	7763	-0.33146204	3.791454646	0.0689385	0.117574332	0.03489	0	224	136	333	221	270	284	269	199	266	242
ENSMUSG00000002064	chr11	Sdf2	7.8E+07	7.8E+07	1515	0.339313696	5.851651973	0.0690288	0.117714117	0.04039	0	839	627	744	713	863	1591	1261	999	1526	1300
ENSMUSG00000078566	chr7	Bnip3	1.4E+08	1.4E+08	2265	-0.38247289	7.24280053	0.0692576	0.118089821	0.0525	0	2262	1449	4040	2575	3043	3004	3339	2061	2092	3149
ENSMUSG00000020014	chr10	Cfap54	9.3E+07	9.3E+07	14460	-0.6471143	0.245123781	0.0693232	0.118187308	0.0901	0	16	17	27	11	31	19	17	12	24	16
ENSMUSG00000034659	chr19	Tmem109	1.1E+07	1.1E+07	3798	-0.41295169	8.487874493	0.0694157	0.11833072	0.06157	0	6049	5551	5175	6475	6921	5672	6905	4266	8308	6760
ENSMUSG00000044433	chr8	Camsap3	3587450	3587959	4295	0.857323519	0.990443906	0.0694295	0.118339741	0.2299	0	19	6	7	12	61	49	33	46	62	53
ENSMUSG00000044986	chr15	Tst	7.8E+07	7.8E+07	1096	0.440304914	4.547757852	0.0695239	0.11848626	0.0675	0	324	182	231	284	485	600	342	411	799	612
ENSMUSG00000024797	chr19	Vps51	6067842	6068375	4748	0.322481636	4.233083256	0.0695524	0.118520477	0.03473	0	188	156	314	275	351	482	434	298	500	447
ENSMUSG00000037364	chr5	Srrt	1.4E+08	1.4E+08	3024	0.321577567	5.305475434	0.069624	0.118628085	0.03595	0	428	404	553	521	758	1067	791	681	939	1064

ENSMUSG00000024580	chr18	Grpel2	6.2E+07	6.2E+07	4030	-0.31283026	4.69453008	0.0696396	0.118629126	0.03313	0	381	291	628	492	389	516	531	375	466	491
ENSMUSG00000034007	chr9	Scaper	5.6E+07	5.6E+07	5158	-0.39095914	3.19600375	0.0696415	0.118629126	0.04926	0	148	135	192	148	146	150	213	111	156	185
ENSMUSG00000002588	chr6	Pon1	5168090	5168496	2898	1.11380442	1.810666496	0.069655	0.118637647	0.41176	0	47	15	2	7	94	168	46	78	74	114
ENSMUSG00000027381	chr2	Bcl2l11	1.3E+08	1.3E+08	8029	0.388707579	3.070880893	0.0696769	0.118660502	0.04759	0	95	65	132	132	125	211	184	154	173	248
ENSMUSG00000041040	chr1	Fam117b	6E+07	6E+07	7290	0.376044836	3.436009665	0.0696857	0.118661037	0.04546	0	101	102	170	144	197	320	262	168	204	312
ENSMUSG00000038072	chr5	Galnt11	2.5E+07	2.5E+07	2993	-0.30632815	4.241894925	0.0697397	0.118738716	0.03081	0	289	214	427	311	351	394	430	271	333	317
ENSMUSG00000039741	chr11	Bahcc1	1.2E+08	1.2E+08	11118	-0.36793852	3.386978013	0.0697533	0.118747443	0.04319	0	140	141	178	168	259	234	180	134	186	209
ENSMUSG00000009614	chr2	Sardh	2.7E+07	2.7E+07	5432	0.754516832	2.562403995	0.069771	0.118763174	0.19341	0	68	34	32	23	181	225	116	113	187	114
ENSMUSG00000037204	chr15	Atg101	1E+08	1E+08	1230	0.304755573	5.140006755	0.0698355	0.118858442	0.03213	0	441	322	581	427	640	849	781	595	1015	778
ENSMUSG00000038766	chr3	Gabpb2	9.5E+07	9.5E+07	15465	-0.30751942	4.30099883	0.0698618	0.11888888	0.03164	0	335	251	348	341	352	471	410	260	321	369
ENSMUSG00000036880	chr18	Acaa2	7.5E+07	7.5E+07	1515	-0.50957521	8.045896033	0.0698848	0.118913568	0.09373	0	3516	1440	9036	5517	5570	4926	5729	2945	3843	5365
ENSMUSG00000042616	chr4	Oscp1	1.3E+08	1.3E+08	5254	0.645178775	0.844791588	0.0698995	0.118924072	0.11304	0	19	12	11	14	44	49	46	33	40	43
ENSMUSG00000021388	chr13	Aspn	5E+07	5E+07	2346	0.446942835	5.001791646	0.0699299	0.11896134	0.07083	0	263	230	627	344	679	1056	1203	491	472	670
ENSMUSG00000022702	chr16	Hira	1.9E+07	1.9E+07	6132	-0.31227001	4.588290347	0.0699447	0.11897209	0.03301	0	336	304	462	400	514	419	580	321	484	410
ENSMUSG00000036026	chr17	Tmem63b	4.6E+07	4.6E+07	5098	-0.42469914	6.198558222	0.0699766	0.119012	0.06465	0	1037	743	2344	1405	1013	1281	1837	884	1327	1193
ENSMUSG00000067058	chr5	Rps15a-ps5	1.1E+08	1.1E+08	393	0.535231883	0.969374209	0.0699927	0.119024976	0.06806	0	27	17	23	24	21	43	48	38	45	49
ENSMUSG00000024993	chr19	Fam45a	6.1E+07	6.1E+07	6242	-0.34409997	3.534443911	0.0700129	0.119044912	0.0382	0	199	150	207	195	214	270	251	149	183	205
ENSMUSG00000005687	chr3	Bcas2	1E+08	1E+08	4390	0.294682676	5.364898972	0.0700288	0.119057426	0.03016	0	550	389	678	550	637	1005	959	771	918	1010
ENSMUSG00000018761	chr11	Mpdu1	7E+07	7E+07	2420	0.558213855	3.914800713	0.070121	0.119199723	0.10864	0	128	139	130	98	444	458	277	282	391	438
ENSMUSG00000024091	chr17	Vapa	6.6E+07	6.6E+07	1640	-0.35070535	6.882322214	0.0701376	0.119213527	0.04433	0	1937	1594	2114	1888	2387	2253	2691	1678	2180	1911
ENSMUSG00000048429	chr9	1810026J23Rik	2.2E+07	2.2E+07	3170	-0.33132555	6.608461293	0.0701777	0.119267176	0.03942	0	1505	1189	2100	1689	1763	1958	2165	1353	1688	1790
ENSMUSG00000029815	chr6	Malsu1	4.9E+07	4.9E+07	3079	-0.28688604	4.740805645	0.0702653	0.119397989	0.02767	0	429	302	602	431	470	521	518	400	531	504
ENSMUSG00000031217	chrX	Efnb1	9.9E+07	9.9E+07	3452	0.376984469	3.845243533	0.0702717	0.119397989	0.0482	0	168	94	222	166	322	396	293	250	357	375
ENSMUSG00000002308	chr17	Cd320	3.4E+07	3.4E+07	2592	0.372923006	3.957722712	0.070336	0.119492755	0.04629	0	202	158	206	214	226	370	263	282	474	400
ENSMUSG00000051695	chr6	Pcbp1	8.7E+07	8.7E+07	1830	0.346262078	6.829536407	0.070367	0.119531062	0.04328	0	1199	992	2079	1525	1933	2860	2425	2102	2969	2755
ENSMUSG00000036114	chr4	Rpp25l	4.2E+07	4.2E+07	856	0.315152401	4.807514582	0.0704489	0.119655703	0.03398	0	385	285	417	339	448	666	528	523	760	699
ENSMUSG00000066613	chr5	Zfp932	1.1E+08	1.1E+08	3272	-0.42712925	2.513363631	0.0705797	0.119863224	0.05694	0	100	82	95	86	119	151	93	68	83	108
ENSMUSG00000068523	chr3	Gng5	1.5E+08	1.5E+08	2738	-0.34343038	6.996369666	0.0707224	0.120091013	0.04271	0	2098	1491	2737	2359	2131	2502	2602	1642	2548	2396
ENSMUSG00000054435	chr6	Gimap4	4.9E+07	4.9E+07	1837	0.415770104	3.223179939	0.0707757	0.12016713	0.05695	0	82	69	206	134	125	310	199	145	213	239
ENSMUSG00000022378	chr15	Fam49b	6.4E+07	6.4E+07	3869	-0.32284728	5.353177266	0.0708302	0.120244991	0.03681	0	658	511	821	798	614	887	936	549	677	725
ENSMUSG00000018740	chr11	Slc25a35	6.9E+07	6.9E+07	3677	-0.50119479	3.454684927	0.0708774	0.120310564	0.08576	0	161	87	225	125	420	250	200	128	150	215
ENSMUSG00000090381	chr14	Gm6158	2.4E+07	2.4E+07	564	0.625831964	0.367048868	0.0708885	0.120314901	0.08642	0	12	8	18	17	15	24	37	31	24	28
ENSMUSG00000085419	chr11	Gm11734	1.2E+08	1.2E+08	728	0.701576017	1.079425833	0.0710571	0.120586355	0.1334	0	35	25	13	19	16	54	78	37	42	45
ENSMUSG00000032119	chr9	Hinfp	4.4E+07	4.4E+07	2100	-0.57878794	1.163599717	0.0712748	0.120939205	0.09708	0	40	32	34	49	36	49	55	17	25	37
ENSMUSG00000066551	chr5	Hmgb1	1.5E+08	1.5E+08	4944	-0.34910059	6.949721884	0.0712822	0.120939205	0.04431	0	2260	1613	2365	1943	2193	2708	2506	1832	1904	2296
ENSMUSG00000091994	chr10	E130317F20Rik	8E+07	8E+07	3265	-0.49144302	1.353859652	0.0713145	0.120979384	0.06394	0	40	32	68	36	44	48	53	33	43	35
ENSMUSG00000029642	chr5	Polr1d	1.5E+08	1.5E+08	1985	0.308118093	5.870553607	0.0713445	0.121015608	0.03388	0	743	562	963	700	1014	1513	1306	1057	1381	1419
ENSMUSG00000043467	chr1	Zbtb37	1.6E+08	1.6E+08	18814	-0.43277488	2.613635544	0.0714259	0.121138977	0.06001	0	103	106	99	81	122	142	115	72	101	107
ENSMUSG00000038793	chr1	Lefty1	1.8E+08	1.8E+08	1758	0.645428953	0.71532079	0.0714626	0.121186548	0.11587	0	9	9	20	15	40	52	29	33	43	34
ENSMUSG00000008999	chr2	Bmp7	1.7E+08	1.7E+08	4019	-0.88768548	0.146897432	0.0715446	0.121310954	0.22182	0	13	13	13	16	47	26	14	5	4	27
ENSMUSG00000028461	chr4	Ccdc107	4.3E+07	4.3E+07	1547	0.339702601	4.348858049	0.0715533	0.12131109	0.03905	0	268	219	262	251	340	535	366	349	552	540
ENSMUSG00000021904	chr14	Sema3g	3.1E+07	3.1E+07	4538	0.363099487	4.288693011	0.0715736	0.121330811	0.04599	0	178	136	361	241	426	586	433	341	405	511
ENSMUSG00000038280	chr10	Ostm1	4.3E+07	4.3E+07	7211	-0.33528359	5.329544788	0.0717654	0.121641202	0.04007	0	687	521	791	800	536	908	793	558	705	723
ENSMUSG00000022283	chr15	Pabpc1	3.7E+07	3.7E+07	5768	0.384640214	6.304926283	0.0718503	0.121770455	0.0537	0	990	773	950	783	1720	2070	2370	1265	1790	1837
ENSMUSG00000027244	chr2	Atg13	9.2E+07	9.2E+07	4368	-0.33283713	5.395338591	0.0719298	0.121890463	0.03946	0	647	444	1065	744	702	798	971	484	739	896
ENSMUSG00000040795	chr4	Iqcc	1.3E+08	1.3E+08	3188	0.346532294	3.58651535	0.0719779	0.121957315	0.03943	0	169	99	221	137	177	336	257	234	287	259
ENSMUSG00000083012	chr5	Fam220a	1.4E+08	1.4E+08	2734	-0.36013861	6.331358482	0.0719918	0.121966104	0.04709	0	1064	898	2132	1499	1380	1482	1887	1065	1407	1469
ENSMUSG00000032058	chr9	Ppp2r1b	5.1E+07	5.1E+07	6449	-0.67706987	3.565358766	0.0721184	0.122159399	0.16147	0	183	157	96	93	595	230	169	158	168	208
ENSMUSG00000071656	chr19	Lrrn4cl	8850785	8851112	2583	0.447533854	4.192327371	0.0721233	0.122159399	0.06976	0	179	212	141	220	394	532	389	284	426	560
ENSMUSG00000023015	chr15	Racgap1	1E+08	1E+08	7079	0.637482853	1.253804527	0.0721853	0.12224954	0.11513	0	18	28	24	15	48	74	63	49	64	34
ENSMUSG00000089781	chr6	Gm15756	9.1E+07	9.1E+07	682	-0.48506501	2.277347223	0.0722995	0.122428212	0.07513	0	91	73	92	74	83	100	127	49	87	54
ENSMUSG00000017897	chr2	Eya2	1.7E+08	1.7E+08	2963	0.528219645	1.754941857	0.0723153	0.12244023	0.08453	0	28	27	38	32	81	103	85	62	62	87
ENSMUSG00000028439	chr4	Fam219a	4.2E+07	4.2E+07	3724	-0.31715696	5.041853198	0.0723589	0.122497611	0.03538	0	556	345	743	497	662	595	846	401	644	563
ENSMUSG00000049409	chr6	Prokr1	8.8E+07	8.8E+07	4055	-0.68065773	0.298700922	0.0723667	0.122497611	0.11159	0	23	13	29	27	14	22	31	13	13	12
ENSMUSG00000018648	chr11	Dusp14	8.4E+07	8.4E+07	1945	0.535862386	3.122859051	0.0724788	0.122672564	0.09996	0	69	55	166	57	216	167	277	160	207	235
ENSMUSG00000103458	chr18	PCDHA4	3.7E+07	3.7E+07	2856	-0.45977227	2.970118133	0.0725757	0.122821735	0.07123	0	117	127	116	92	221	186	163	89	131	116
ENSMUSG00000039686	chr2	Zer1	3E+07	3E+07	9784	-0.30543417	5.404110159	0.0727091	0.123032603	0.03314	0	637	426	1017	703	830	847	907	545	813	822
ENSMUSG00000015759	chr14	Cnih1	4.7E+07	4.7E+07	1570	0.33057431	5.981185231	0.0728428	0.123244101	0.03959	0	829	623	838	788	1147	1658	1339	1199	1488	1555
ENSMUSG00000022987	chr15	Zfp641	9.8E+07	9.8E+07	4254	-0.33481863	4.647741337	0.0729189	0.123357993	0.03956	0	502	321	473	363	426	563	616	285	468	389
ENSMUSG00000035000	chr2	Dpp4	6.2E+07	6.2E+07	6319	-0.51402119	3.034995013	0.0729895	0.123462515	0.09049	0	112	109	95	126	286	229	127	88	129	133
ENSMUSG00000042377	chr11	Fam83g	6.2E+07	6.2E+07	6659	0.5287851	2.185250231	0.0730063	0.123475986	0.08793	0	58	44	50	27	96	109	98	85	125	121
ENSMUSG00000026816	chr2	Gtf3c5	2.9E+07	2.9E+07	4560	0.306538022	3.942847112	0.0733848	0.124101195	0.03078	0	188	153	238	197	260	424	341	245	371	377
ENSMUSG00000016481	chr1	Cr1l	2E+08	2E+08	10349	-0.31753333	5.492555857	0.0734633	0.12421897	0.03636	0	752	627	838	746	752	985	866	707	726	840
ENSMUSG00000036835	chr7	Psenen	3.1E+07	3.1E+07	648	0.315356127	5.111784736	0.0734821	0.124235761	0.03516	0	457	356	422	456	617	903	697	587	902	870
ENSMUSG00000020903	chr11	Stx8	6.8E+07	6.8E+07	7137	0.286545884	4.431502214	0.073526	0.124295006	0.02777	0	273	209	340	294	352	527	492	383	536	497
ENSMUSG00000001120	chr10	Pcbp3	7.7E+07	7.7E+07	2933	0.575530598	1.654047772	0.0735924	0.124380737	0.10324	0	36	17	29	30	77	96	56	67	70	83
ENSMUSG00000018411	chr11	Mapt	1E+08	1E+08	7531	-0.37590035	6.234919122	0.0735944	0.124380737	0.05193	0	1044	795	1893	1547	1262	1307	1764	792	1501	1494

ENSMUSG00000022094	chr14	Slc39a14	7E+07	7E+07	10550	0.408906488	3.937982297	0.073605	0.12438364	0.059	0	163	97	370	211	186	454	428	315	303	291
ENSMUSG00000051185	chr1	Fam174a	9.5E+07	9.5E+07	4814	-0.31151616	5.700509654	0.0736258	0.124403784	0.03511	0	854	586	1092	875	973	950	1161	673	967	1060
ENSMUSG00000031367	chrX	Ap1s2	1.6E+08	1.6E+08	4965	0.312878307	5.221960163	0.0736566	0.124440849	0.03497	0	519	314	669	493	545	1033	1123	630	791	719
ENSMUSG00000026333	chr1	Gin1	9.8E+07	9.8E+07	6048	-0.43800073	1.935051798	0.0737234	0.124538662	0.05555	0	65	54	68	59	76	85	73	55	57	58
ENSMUSG00000001833	chr9	Sept7	2.5E+07	2.5E+07	2538	-0.33143392	6.42918899	0.0737644	0.124592833	0.04039	0	1345	1014	1827	1581	1515	1848	1941	1200	1473	1458
ENSMUSG00000024665	chr19	Fads2	1E+07	1E+07	1508	0.494659911	1.689913668	0.0738428	0.124701489	0.06764	0	29	35	35	35	60	95	72	49	85	78
ENSMUSG00000096983	chr11	2010015M23Rik	8.8E+07	8.8E+07	1199	-0.67780215	0.235622034	0.0738465	0.124701489	0.11268	0	29	15	30	9	18	24	19	12	12	20
ENSMUSG00000055760	chr17	Gemin6	8E+07	8E+07	1428	-0.38978784	2.723340625	0.0738885	0.124757469	0.04726	0	88	92	154	94	134	141	125	95	116	106
ENSMUSG00000075010	chr19	AW112010	1.1E+07	1.1E+07	770	0.528058149	3.706018817	0.0739303	0.124812965	0.09887	0	165	90	134	143	284	685	203	193	251	303
ENSMUSG00000025171	chr19	Ubtd1	4.2E+07	4.2E+07	1527	0.301680246	4.276934573	0.0739432	0.124819728	0.0309	0	218	191	312	261	333	497	470	350	498	383
ENSMUSG00000029345	chr5	Tfip11	1.1E+08	1.1E+08	4086	-0.31744509	4.385563141	0.0740529	0.124989948	0.03466	0	325	199	486	387	384	425	478	282	406	334
ENSMUSG00000037022	chr8	Mmaa	7.9E+07	7.9E+07	2843	-0.32714981	4.127469429	0.0740674	0.124999332	0.03623	0	263	158	432	323	325	343	350	243	332	329
ENSMUSG00000065887	chr4	n-R5s185	5.4E+07	5.4E+07	119	-0.53508247	1.562351865	0.0740833	0.125011028	0.08756	0	34	50	66	45	60	66	75	24	37	46
ENSMUSG00000067719	chr5	Gm10221	2.5E+07	2.5E+07	422	0.329818521	4.873664537	0.0741423	0.125095617	0.03866	0	327	251	454	462	486	620	844	394	721	822
ENSMUSG00000056770	chr12	Setd3	1.1E+08	1.1E+08	6035	-0.33515207	7.132998381	0.0741625	0.125114669	0.04171	0	2293	1727	2805	2492	2497	2761	2995	1862	2578	2687
ENSMUSG00000003778	chr18	Brd8	3.5E+07	3.5E+07	10633	-0.3112965	4.430810513	0.0742957	0.125324231	0.03377	0	358	284	457	308	388	537	471	294	329	371
ENSMUSG00000038462	chr13	Uqcrfs1	3.1E+07	3.1E+07	1363	-0.42506784	8.976919874	0.0743179	0.125346604	0.06753	0	7308	4477	15407	10396	7555	8876	11669	6430	8796	8867
ENSMUSG00000063531	chr5	Sema3e	1.4E+07	1.4E+07	7581	-0.60249447	0.393103973	0.0744237	0.125509944	0.09069	0	25	13	26	15	34	34	22	11	19	16
ENSMUSG00000032215	chr9	Rsl24d1	7.3E+07	7.3E+07	1716	0.278610657	5.120346844	0.0745	0.125623507	0.02752	0	429	312	611	508	535	893	779	632	803	818
ENSMUSG00000024974	chr19	Smc3	5.4E+07	5.4E+07	5541	-0.2980823	4.863238139	0.0745539	0.125699429	0.03146	0	465	382	589	471	500	673	643	425	434	528
ENSMUSG00000048142	chr5	Nat8l	3.4E+07	3.4E+07	6529	-1.33758295	3.860924731	0.0746022	0.125758314	0.62868	0	298	109	16	17	1256	247	57	123	240	184
ENSMUSG00000083337	chr11	Gm11539	9.6E+07	9.6E+07	557	0.704853228	0.307696356	0.0746068	0.125758314	0.11705	0	12	12	11	13	15	23	16	20	44	39
ENSMUSG00000033610	chr19	Pank1	3.5E+07	3.5E+07	3692	-0.71832249	4.276333929	0.0747686	0.126015926	0.18779	0	263	59	1028	381	261	353	485	187	200	309
ENSMUSG00000024181	chr17	Mrpl28	2.6E+07	2.6E+07	1274	0.349351272	6.144375437	0.07479	0.126036911	0.04519	0	779	514	1330	1142	1051	1722	1609	1270	1839	1728
ENSMUSG00000021732	chr13	Fgf10	1.2E+08	1.2E+08	4601	-1.13447015	1.087149345	0.0748234	0.126062808	0.42808	0	22	44	8	5	137	42	13	18	33	28
ENSMUSG00000027257	chr2	Pacsin3	9.1E+07	9.1E+07	4327	0.361466568	8.279158525	0.0748208	0.126062808	0.04901	0	3272	2472	5410	4798	5053	7138	7582	5103	7930	8453
ENSMUSG00000027338	chr2	Prnd	1.3E+08	1.3E+08	3211	0.775167024	1.244497669	0.0748656	0.126118695	0.20018	0	13	15	22	15	66	29	41	65	83	63
ENSMUSG00000020818	chr11	Mfsd11	1.2E+08	1.2E+08	7076	0.277421668	4.989190973	0.0749007	0.12616278	0.02718	0	367	296	554	408	573	834	760	518	794	700
ENSMUSG00000032502	chr9	Stac	1.1E+08	1.1E+08	2644	0.778216498	0.053374041	0.0749305	0.126197778	0.16117	0	6	5	8	10	23	40	15	14	38	14
ENSMUSG00000031644	chr8	Nek1	6.1E+07	6.1E+07	7886	-0.48054434	2.880571995	0.0752192	0.126668761	0.07886	0	127	90	194	135	97	155	198	92	77	113
ENSMUSG00000029054	chr4	Gabrd	1.6E+08	1.6E+08	2875	0.710756998	2.275179197	0.0752396	0.126687913	0.16928	0	99	54	25	44	29	139	82	126	125	122
ENSMUSG00000027882	chr3	Stxbp3a	1.1E+08	1.1E+08	5340	-0.35498769	5.205047831	0.0753229	0.126812974	0.0462	0	688	590	590	451	725	831	806	476	542	718
ENSMUSG00000031523	chr8	Dlc1	3.7E+07	3.7E+07	14694	-0.46448687	5.155113437	0.07536	0.126860222	0.07931	0	505	332	581	392	1460	758	589	506	575	660
ENSMUSG00000030124	chr6	Lag3	1.2E+08	1.2E+08	2109	1.049724814	0.934074005	0.0754226	0.126920471	0.36502	0	25	12	5	1	45	75	16	36	67	55
ENSMUSG00000030281	chr6	Il17rc	1.1E+08	1.1E+08	2671	0.60376119	2.592916183	0.0754201	0.126920471	0.12644	0	58	41	42	44	182	204	142	111	138	147
ENSMUSG00000082241	chr16	Gm15776	2.2E+07	2.2E+07	205	-0.50487481	1.223010308	0.0754229	0.126920471	0.07087	0	41	29	61	34	35	45	34	25	38	51
ENSMUSG00000043923	chr9	Ccdc84	4.4E+07	4.4E+07	1158	0.501202753	1.428611857	0.0756337	0.127259935	0.06848	0	24	22	28	37	51	76	66	46	54	71
ENSMUSG00000050628	chr11	Ubald2	1.2E+08	1.2E+08	1532	-0.30313428	4.438266377	0.0756992	0.127354743	0.03221	0	340	280	394	333	454	445	378	269	492	427
ENSMUSG00000002221	chr5	Paxip1	2.8E+07	2.8E+07	5052	-0.394975	3.13339335	0.0758099	0.127522191	0.05209	0	131	98	229	135	168	181	226	105	123	150
ENSMUSG00000028920	chr4	Fbxo42	1.4E+08	1.4E+08	5934	-0.30367868	4.065671313	0.0758169	0.127522191	0.0314	0	258	188	367	294	296	336	353	211	330	322
ENSMUSG00000030103	chr6	Bhlhe40	1.1E+08	1.1E+08	3272	-0.38435472	7.06391689	0.0758302	0.12752927	0.05547	0	1806	1315	3247	2581	2824	2052	3291	1770	2130	2751
ENSMUSG00000025153	chr11	Fasn	1.2E+08	1.2E+08	9849	-1.38035396	8.231422995	0.0759403	0.127699157	0.67736	0	9094	2575	226	412	22296	3923	1320	3700	6434	1349
ENSMUSG00000022579	chr15	Gpihbp1	7.6E+07	7.6E+07	2554	0.410515593	5.009223443	0.0759922	0.127771107	0.06251	0	251	191	660	353	764	879	679	577	867	790
ENSMUSG00000025220	chr19	Mgea5	4.6E+07	4.6E+07	5024	-0.31386623	5.964951744	0.0760884	0.127917508	0.03654	0	1071	826	1215	964	1112	1274	1248	867	1115	1261
ENSMUSG00000005686	chr7	Ampd3	1.1E+08	1.1E+08	5605	0.356426577	4.40547414	0.0761391	0.127987375	0.04574	0	282	141	403	341	258	532	465	467	471	479
ENSMUSG00000028834	chr4	Trim63	1.3E+08	1.3E+08	2842	-0.36880077	7.93744742	0.0761612	0.128009262	0.05143	0	4720	3231	4775	4167	3682	4263	5173	3593	4484	4492
ENSMUSG00000029869	chr6	Ephb6	4.2E+07	4.2E+07	3773	0.544596006	0.841039735	0.0762027	0.128063615	0.07482	0	15	13	23	22	31	61	33	28	47	38
ENSMUSG00000003970	chr15	Rpl8	7.7E+07	7.7E+07	862	0.353058082	8.543484236	0.0762692	0.128159953	0.04724	0	4251	3661	5949	5110	5910	10081	7099	6631	10018	9460
ENSMUSG00000032477	chr9	Cdc25a	1.1E+08	1.1E+08	3625	-0.37343514	3.075234572	0.0763416	0.128250906	0.04577	0	112	120	189	143	146	174	147	99	180	157
ENSMUSG00000038213	chr6	Tapbpl	1.3E+08	1.3E+08	2352	0.49934162	2.955623952	0.0763381	0.128250906	0.08596	0	79	69	100	52	190	290	168	119	160	206
ENSMUSG00000057236	chr4	Rbbp4	1.3E+08	1.3E+08	8744	0.326355918	6.1924747	0.0763715	0.128285854	0.03968	0	954	742	1155	822	1242	2018	1520	1341	1718	1804
ENSMUSG00000022216	chr14	Psme1	5.6E+07	5.6E+07	2209	0.355139328	5.747315939	0.0764171	0.12834699	0.04703	0	563	389	1037	666	1041	1779	1044	852	1248	1386
ENSMUSG00000026135	chr1	Zfp142	7.5E+07	7.5E+07	11355	-0.43127061	3.576770225	0.0764526	0.12837983	0.06469	0	151	114	332	294	159	222	231	168	228	191
ENSMUSG00000068264	chr2	Ap5s1	1.3E+08	1.3E+08	1660	0.328351842	4.342026468	0.0764549	0.12837983	0.0386	0	209	145	437	271	341	530	443	343	497	517
ENSMUSG00000029438	chr5	Bcl7a	1.2E+08	1.2E+08	8580	-0.35764352	4.05531185	0.0766831	0.128747609	0.0448	0	291	147	432	286	283	276	376	205	312	336
ENSMUSG00000021913	chr14	Ogdhl	3.2E+07	3.2E+07	3449	-0.82740504	1.439880389	0.0767341	0.12881775	0.22894	0	23	18	156	48	29	42	52	23	21	59
ENSMUSG00000075701	chr7	Vimp	6.6E+07	6.6E+07	1198	0.354934589	5.033561175	0.0767461	0.128822554	0.04588	0	536	327	370	407	488	1058	598	635	792	707
ENSMUSG00000007655	chr6	Cav1	1.7E+07	1.7E+07	3444	-0.49792356	7.624897361	0.0768383	0.128961882	0.09387	0	2743	2060	3252	2125	8071	4546	3270	2889	3283	2925
ENSMUSG00000005442	chr7	Cic	2.5E+07	2.5E+07	10294	0.309729222	5.437883317	0.0768652	0.12899155	0.03516	0	447	439	761	610	686	1086	1112	612	1066	1133
ENSMUSG00000037552	chr7	Plekhg2	2.8E+07	2.8E+07	6797	0.450779403	2.976536073	0.0768789	0.128999149	0.07058	0	64	50	141	104	157	240	139	116	235	207
ENSMUSG00000042787	chr9	Exog	1.2E+08	1.2E+08	3887	0.44600081	2.022417278	0.0769077	0.129031975	0.0596	0	47	37	81	40	50	100	90	80	105	92
ENSMUSG00000042962	chr12	Gm5436	8.4E+07	8.4E+07	642	0.465832886	3.189508535	0.0770234	0.129210716	0.07676	0	79	45	187	154	132	202	188	163	276	246
ENSMUSG00000051504	chr7	Siglech	5.6E+07	5.6E+07	3383	0.774628235	1.653683416	0.0771447	0.129398631	0.19161	0	20	60	13	17	44	104	73	50	90	83
ENSMUSG00000061607	chr17	Mdc1	3.6E+07	3.6E+07	7421	-0.37073346	2.949768005	0.0773952	0.129803244	0.04475	0	121	107	162	116	143	190	133	106	121	143
ENSMUSG00000052656	chr6	Rnf103	7.1E+07	7.1E+07	4348	-0.28960058	4.644443403	0.0774929	0.129951579	0.02982	0	341	312	498	429	502	516	565	344	384	521
ENSMUSG00000098650	chr11	Gm28048	2.3E+07	2.3E+07	2746	0.306807668	5.664496936	0.0775309	0.129999858	0.03483	0	651	538	852	617	758	1496	1098	943	1083	1176
ENSMUSG00000022064	chr14	Pibf1	9.9E+07	9.9E+07	3271	-0.52149171	1.592069526	0.0775732	0.130025168	0.08089	0	29	43	91	41	62	60	57	42	40	49

ENSMUSG00000031636	chr8	Pdlim3	4.6E+07	4.6E+07	1578	0.466779572	9.123062604	0.0775738	0.130025168	0.08315	0	8749	7067	4821	6892	5957	17177	11053	10830	15091	12755
ENSMUSG00000034320	chr18	Slc26a2	6.1E+07	6.1E+07	12370	-0.35293529	3.572614525	0.0775637	0.130025168	0.04282	0	191	175	220	168	237	261	257	182	183	188
ENSMUSG00000043557	chr17	Mdga1	3E+07	3E+07	9395	-0.44707017	3.606846357	0.0776053	0.130062309	0.07106	0	251	131	164	216	292	252	235	163	287	123
ENSMUSG00000040710	chr1	St8sia4	9.6E+07	9.6E+07	20091	0.403581428	2.806695159	0.0776724	0.130159339	0.05301	0	79	51	130	98	99	195	210	92	154	174
ENSMUSG00000001280	chr15	Sp1	1E+08	1E+08	8325	0.282194318	5.096571541	0.0780405	0.130760455	0.02883	0	467	323	519	459	567	1027	742	613	683	822
ENSMUSG00000019929	chr10	Dcn	9.7E+07	9.7E+07	2084	0.421787006	9.301219585	0.0781233	0.130883629	0.06825	0	8471	7677	6634	5823	11230	21896	15434	10776	12588	15054
ENSMUSG00000039485	chr10	Tspyl4	3.4E+07	3.4E+07	3879	0.471323989	2.084443771	0.0781861	0.130973198	0.0702	0	34	35	88	47	64	153	111	59	86	97
ENSMUSG00000100410	chr13	2310020H05Rik	9.9E+07	9.9E+07	720	0.807041664	0.696145608	0.0782674	0.131093704	0.19867	0	8	7	30	30	9	53	19	33	25	66
ENSMUSG00000006335	chr7	Tfpt	3620324	3620474	1197	0.340794542	3.578721782	0.0783208	0.131151806	0.0394	0	129	116	180	175	192	322	225	219	291	308
ENSMUSG00000019715	chr2	Gle1	3E+07	3E+07	6087	-0.29441407	5.341952058	0.0783177	0.131151806	0.03209	0	604	527	708	754	752	890	768	540	821	762
ENSMUSG00000063415	chr6	Cyp26b1	8.5E+07	8.5E+07	4849	0.757889419	2.335320265	0.0783491	0.131183473	0.20368	0	81	42	68	53	24	263	82	80	39	196
ENSMUSG00000004994	chr8	Ccdc130	8.4E+07	8.4E+07	2694	0.350646791	3.311016222	0.0785286	0.131468415	0.04078	0	124	100	138	122	167	245	241	178	197	275
ENSMUSG00000029550	chr5	Sppl3	1.2E+08	1.2E+08	4240	0.287276578	5.110234067	0.0785772	0.131534095	0.03006	0	430	354	490	434	642	904	747	624	797	838
ENSMUSG00000025464	chr7	Paox	1.4E+08	1.4E+08	1765	0.458265523	2.508894759	0.0786654	0.131665915	0.06981	0	57	43	79	56	130	186	104	100	151	130
ENSMUSG00000015672	chr13	Mrpl32	1.5E+07	1.5E+07	768	-0.30120142	4.435775865	0.0787169	0.131720816	0.03203	0	333	243	512	330	407	465	450	353	348	371
ENSMUSG00000020610	chr11	Amz2	1.1E+08	1.1E+08	5584	-0.33007178	6.477545657	0.078715	0.131720816	0.04152	0	1383	1217	1734	1604	1479	1755	1929	1150	1690	1680
ENSMUSG00000019897	chr10	Ccdc59	1.1E+08	1.1E+08	4314	0.329525233	3.9017238	0.0787502	0.131760747	0.03796	0	186	141	243	160	276	445	298	291	306	366
ENSMUSG00000052926	chr8	Rnaseh2a	8.5E+07	8.5E+07	3509	0.322101625	3.918685337	0.0788108	0.131846459	0.03651	0	156	123	311	203	243	387	337	249	370	389
ENSMUSG00000034462	chr5	Pkd2	1E+08	1E+08	10169	0.309921919	4.610533661	0.0789401	0.132046017	0.03465	0	268	245	386	277	487	713	610	400	447	641
ENSMUSG00000058979	chr6	Cecr5	1.2E+08	1.2E+08	3355	-0.31012914	4.531426673	0.0789489	0.132046017	0.03452	0	352	238	589	413	370	449	436	300	444	507
ENSMUSG00000022914	chr16	Brwd1	9.6E+07	9.6E+07	20280	-0.31896786	5.313364248	0.0792062	0.132460516	0.03791	0	630	452	1052	644	594	829	805	570	642	811
ENSMUSG00000018565	chr11	Elp5	7E+07	7E+07	2294	0.297489907	4.982144274	0.0793744	0.13272601	0.03279	0	334	243	657	450	520	800	755	543	770	731
ENSMUSG00000098488	chr2	Pla2g4b	1.2E+08	1.2E+08	5831	-0.62264318	1.042567986	0.0793952	0.132744862	0.12248	0	44	42	38	27	22	37	51	17	28	31
ENSMUSG00000026254	chr1	Eif4e2	8.7E+07	8.7E+07	7497	-0.32978061	6.090311655	0.0794537	0.132813631	0.04147	0	1125	897	1444	1183	1036	1462	1497	847	1277	1216
ENSMUSG00000074576	chr2	Mocs3	1.7E+08	1.7E+08	1973	0.464753974	2.139321643	0.0794552	0.132813631	0.0703	0	43	33	76	44	84	123	86	75	144	87
ENSMUSG00000025216	chr19	Lbx1	4.5E+07	4.5E+07	2484	-0.3590326	5.525058969	0.0795129	0.132885843	0.04864	0	577	488	1070	886	975	659	975	603	1101	810
ENSMUSG00000056692	chr17	D17Wsu92e	2.8E+07	2.8E+07	4250	-0.37125269	8.830150746	0.0795174	0.132885843	0.05341	0	6780	4622	11508	8864	7833	8046	10721	5612	8598	8301
ENSMUSG00000022433	chr15	Csnk1e	7.9E+07	7.9E+07	6406	-0.31101598	5.496221798	0.0795891	0.132989858	0.03631	0	696	552	860	719	962	788	1067	609	763	938
ENSMUSG00000023460	chr17	Rab12	6.6E+07	6.6E+07	3021	-0.36906634	7.522510089	0.079663	0.133097436	0.05262	0	2490	2015	4856	2652	4140	3371	4443	2462	2860	3506
ENSMUSG00000026309	chr1	Ilkap	9.1E+07	9.1E+07	5556	0.293505333	5.457572429	0.0796932	0.133132057	0.03229	0	537	378	790	568	763	1176	952	809	1011	1039
ENSMUSG00000053626	chr8	Tll1	6.4E+07	6.4E+07	4928	0.833871576	-0.33391281	0.0797762	0.133254896	0.16266	0	7	3	4	5	18	23	29	10	19	9
ENSMUSG00000024026	chr17	Glo1	3.1E+07	3.1E+07	1935	-0.33691125	7.723071827	0.079852	0.133365603	0.04396	0	3756	2786	4036	3349	3736	4234	4251	2986	3955	3887
ENSMUSG00000007721	chr8	Ccdc124	7.1E+07	7.1E+07	911	0.32275432	5.810699044	0.0798691	0.133378285	0.03953	0	639	505	883	841	934	1296	1232	946	1654	1305
ENSMUSG00000051065	chr16	Mb21d2	2.9E+07	2.9E+07	3080	-0.34897592	3.799770085	0.0798796	0.133379909	0.04276	0	258	130	303	213	291	313	329	195	218	211
ENSMUSG00000022337	chr15	Emc2	4.3E+07	4.3E+07	1245	-0.3322953	6.230628795	0.0800849	0.133706846	0.04229	0	1257	866	1763	1227	1258	1767	1584	1094	1127	1327
ENSMUSG00000020263	chr10	Appl2	8.4E+07	8.4E+07	5949	-0.32930292	4.291003741	0.0801113	0.133719044	0.03963	0	311	242	433	315	346	546	400	201	289	398
ENSMUSG00000027984	chr3	Hadh	1.3E+08	1.3E+08	4977	-0.47664421	8.276612504	0.0801082	0.133719044	0.08807	0	3929	1862	10866	5413	7221	5362	6289	3783	4949	6547
ENSMUSG00000033454	chr12	Zbtb1	7.6E+07	7.6E+07	12190	-0.3528135	3.55926937	0.080165	0.133792785	0.04327	0	202	156	244	181	204	217	292	171	176	205
ENSMUSG00000053226	chr8	Dand5	8.5E+07	8.5E+07	1584	-0.34959774	3.270395277	0.080349	0.134083813	0.04148	0	154	111	235	162	155	207	174	116	188	192
ENSMUSG00000055531	chr10	Cpsf6	1.2E+08	1.2E+08	10510	-0.27691892	4.532039823	0.0805568	0.134414686	0.02761	0	379	298	440	379	400	487	475	323	422	454
ENSMUSG00000052485	chr13	Tmem171	9.9E+07	9.9E+07	1583	0.835367529	-0.17102083	0.0806628	0.13457334	0.18695	0	4	1	20	14	4	29	25	10	16	23
ENSMUSG00000062300	chr7	Pvrl2	2E+07	2E+07	3440	0.57820726	2.646712316	0.0806711	0.13457334	0.12021	0	61	38	61	40	190	164	179	101	179	142
ENSMUSG00000100493	chr4	Gm29294	1.3E+08	1.3E+08	1868	0.566427646	1.430684365	0.0807697	0.134721852	0.10166	0	27	15	35	25	60	66	48	37	72	97
ENSMUSG00000092085	chr1	Gm17224	1.7E+08	1.7E+08	500	1.672002911	2.440095414	0.0808264	0.134800448	0.9839	0	1	1	129	41	46	7	135	4	332	366
ENSMUSG00000026965	chr2	Anapc2	2.5E+07	2.5E+07	3445	0.292812053	5.618642028	0.0808382	0.134803982	0.0324	0	624	456	772	656	853	1424	1115	833	1185	1059
ENSMUSG00000003344	chr10	Btbd2	8.1E+07	8.1E+07	3586	-0.29808213	5.184669225	0.0809286	0.134922671	0.03323	0	564	373	820	685	624	722	749	434	791	700
ENSMUSG00000004054	chr19	Map3k11	5689131	5689266	3801	0.356555467	4.529086674	0.0809236	0.134922671	0.04761	0	224	148	439	357	415	532	648	308	651	563
ENSMUSG00000098743	chrX	Gm27927	1E+08	1E+08	126	-1.77998945	0.578198405	0.0809481	0.134939087	1.06562	0	58	60	0	29	0	15	0	14	20	19
ENSMUSG00000051107	chr13	Gm15440	5.2E+07	5.2E+07	1231	0.327689424	5.883945036	0.0809604	0.134943696	0.04105	0	674	624	839	766	1048	1285	1316	1021	1697	1442
ENSMUSG00000032714	chr10	Syde1	7.9E+07	7.9E+07	3288	0.500495319	3.682389217	0.080987	0.134971904	0.09322	0	119	101	112	113	377	397	264	227	311	351
ENSMUSG00000039956	chr16	Mrap	9.1E+07	9.1E+07	1464	-1.52783014	2.397133391	0.0811397	0.135200907	0.83205	0	93	44	1	3	492	64	27	61	83	32
ENSMUSG00000102752	chr1	Gm7694	1.7E+08	1.7E+08	3827	0.64528849	0.142702742	0.0811437	0.135200907	0.0956	0	7	8	16	8	20	39	17	18	24	27
ENSMUSG00000027500	chr3	Stmn2	8509360	8509630	5602	0.480932034	1.957568855	0.0812455	0.135354405	0.07196	0	28	38	69	61	42	102	89	65	85	114
ENSMUSG00000056899	chr12	Immp2l	4.1E+07	4.1E+07	1832	-0.39825945	2.589453609	0.0813289	0.135477396	0.05088	0	89	55	156	92	134	117	111	86	105	109
ENSMUSG00000063049	chr8	Ing2	4.8E+07	4.8E+07	3019	-0.31832582	3.852273283	0.0813574	0.135508745	0.03618	0	221	215	253	229	268	293	293	181	286	276
ENSMUSG00000059713	chr4	Rcan3	1.4E+08	1.4E+08	5111	0.364831436	3.307094737	0.0814135	0.135585972	0.04678	0	96	76	212	111	175	281	244	163	224	236
ENSMUSG00000021639	chr13	Gtf2h2	1E+08	1E+08	4372	-0.33039915	3.52102986	0.0814521	0.135634196	0.03792	0	175	146	247	186	207	280	226	166	200	176
ENSMUSG00000020375	chr11	Rufy1	5E+07	5E+07	2764	-0.28244141	4.804902293	0.081517	0.135717971	0.02937	0	412	337	612	474	489	534	628	353	518	584
ENSMUSG00000099966	chr14	2810402E24Rik	2.1E+07	2.1E+07	3040	-0.44296068	2.140749124	0.0815217	0.135717971	0.06123	0	64	39	117	64	106	90	87	58	63	82
ENSMUSG00000015149	chr7	Sirt2	2.9E+07	2.9E+07	3568	-0.32308427	6.568441227	0.0817026	0.13600285	0.04054	0	1449	1024	2135	1690	1785	1814	2065	1193	1843	1853
ENSMUSG00000024668	chr19	Sdhaf2	1.1E+07	1.1E+07	3096	-0.32676547	5.505403112	0.0817234	0.13602143	0.04072	0	681	477	1167	830	726	882	1077	622	827	764
ENSMUSG00000023064	chr14	Sncg	3.4E+07	3.4E+07	852	-1.16105024	6.154520368	0.0817561	0.136059719	0.50682	0	1004	1111	132	117	5415	1649	567	895	578	861
ENSMUSG00000062151	chr9	Unc13c	7.3E+07	7.3E+07	8796	-0.86423625	-0.15797924	0.0817785	0.136080765	0.20749	0	17	7	25	25	5	7	26	7	10	9
ENSMUSG00000047832	chr12	Cdca4	1.1E+08	1.1E+08	2417	0.479941534	2.269684454	0.0818496	0.136182927	0.07722	0	37	47	66	51	100	178	82	81	120	112
ENSMUSG00000031938	chr9	4931406C07Rik	1.5E+07	1.5E+07	2981	-0.73502886	4.309325118	0.0819333	0.136306081	0.20652	0	431	154	139	136	1103	433	249	258	317	276
ENSMUSG00000033933	chr6	Vhl	1.1E+08	1.1E+08	2997	0.381098093	3.480861104	0.0820574	0.136496416	0.05161	0	117	103	134	142	237	340	225	215	224	289
ENSMUSG00000006445	chr4	Epha2	1.4E+08	1.4E+08	4674	0.465336194	1.949065635	0.0820717	0.136503982	0.072	0	31	22	61	62	69	107	82	77	84	97

ENSMUSG00000040740	chr4	Slc25a34	1.4E+08	1.4E+08	2670	-0.90124542	4.994985257	0.0823096	0.136883403	0.31107	0	460	69	1825	887	178	618	475	258	203	795
ENSMUSG00000054381	chr7	Zfp747	1.3E+08	1.3E+08	2657	-0.50457486	1.654626399	0.0823258	0.136894091	0.08192	0	71	49	51	44	49	60	58	48	38	56
ENSMUSG00000046844	chr8	Vat1l	1.1E+08	1.1E+08	5462	-1.14903961	0.678459105	0.0824299	0.137050884	0.45227	0	19	5	9	9	130	39	15	9	11	25
ENSMUSG00000087578	chr6	Ccdc142os	8.3E+07	8.3E+07	1083	0.525782935	0.697100529	0.0824975	0.13714711	0.06415	0	16	12	27	18	21	48	38	28	32	38
ENSMUSG00000084215	chr4	Gm11814	1E+07	1E+07	929	0.595166165	0.824962289	0.0825289	0.137183041	0.10042	0	18	11	19	25	27	29	55	26	61	34
ENSMUSG00000039105	chr4	Atp6v1g1	6.4E+07	6.4E+07	1135	0.352165786	7.566127151	0.0826938	0.137440831	0.04884	0	2485	2171	2479	2348	2883	4603	4086	3251	4916	5118
ENSMUSG00000031672	chr8	Got2	9.6E+07	9.6E+07	2585	-0.5188787	8.809285398	0.0827554	0.13752699	0.10615	0	5786	3201	15990	11720	5077	8043	9573	5214	7541	8051
ENSMUSG00000000948	chr7	Snrpn	6E+07	6E+07	5216	-0.34206041	6.020446218	0.0828055	0.137593878	0.04553	0	1077	694	1512	1174	1084	1059	1565	795	1259	1262
ENSMUSG00000048826	chr17	Dact2	1.4E+07	1.4E+07	2808	-0.74091537	1.899058317	0.0829801	0.137867684	0.19773	0	36	34	38	45	212	72	77	43	42	49
ENSMUSG00000035121	chr14	Neil2	6.3E+07	6.3E+07	1932	0.818052025	0.038543712	0.0830449	0.137959068	0.179	0	11	6	7	2	24	39	20	10	21	32
ENSMUSG00000005899	chr16	Smpd4	1.8E+07	1.8E+07	8926	-0.30810282	3.79725823	0.0832085	0.138214445	0.03314	0	195	157	298	238	282	284	296	210	242	242
ENSMUSG00000029020	chr4	Mfn2	1.5E+08	1.5E+08	5194	-0.43851123	9.364100103	0.0832412	0.138236942	0.07629	0	8269	5614	19969	15230	10420	10733	15605	7967	11688	12140
ENSMUSG00000073147	chr5	5031425E22Rik	2.3E+07	2.3E+07	5142	-0.33102589	3.622768918	0.0832418	0.138236942	0.03873	0	164	156	259	172	293	270	239	155	207	259
ENSMUSG00000002661	chr17	Alkbh7	5.7E+07	5.7E+07	1029	0.354536433	4.088377636	0.0832686	0.138265064	0.04699	0	197	110	349	260	240	367	383	284	467	458
ENSMUSG00000090000	chr18	Ier3ip1	7.7E+07	7.7E+07	1894	0.294031904	5.604340498	0.0832893	0.138283057	0.03319	0	677	460	728	598	850	1321	1086	852	1122	1161
ENSMUSG00000050947	chr3	Amigo1	1.1E+08	1.1E+08	5540	-0.35472169	5.560879911	0.0833699	0.138400595	0.04908	0	811	805	760	782	683	959	1012	629	828	868
ENSMUSG00000070315	chr9	4930581F22Rik	3.5E+07	3.5E+07	3462	0.607416025	0.364426323	0.0834295	0.138483156	0.07936	0	15	13	13	10	18	36	28	17	29	37
ENSMUSG00000051238	chr9	Swsap1	2.2E+07	2.2E+07	1846	0.451224339	2.349479802	0.0834867	0.138561699	0.0691	0	58	47	65	41	111	146	109	83	143	117
ENSMUSG00000027933	chr3	Ints3	9E+07	9E+07	4460	-0.2929866	4.949495681	0.0836013	0.138735359	0.03235	0	394	387	696	529	581	637	722	419	614	485
ENSMUSG00000028093	chr3	Acp6	9.7E+07	9.7E+07	4592	-0.28409981	4.400414075	0.0838246	0.139089616	0.02944	0	336	233	388	383	414	444	389	285	397	454
ENSMUSG00000018765	chr11	Fxr2	7E+07	7E+07	3766	-0.33041063	6.809323544	0.0838365	0.139092901	0.04317	0	1729	1410	2315	2013	1962	2150	2369	1338	2424	2072
ENSMUSG00000024972	chr19	Lgals12	7596660	7598171	2773	-1.57954339	2.963278546	0.0839011	0.139183602	0.90491	0	152	73	3	1	715	202	28	56	49	79
ENSMUSG00000034931	chr11	Dhx8	1E+08	1E+08	5032	-0.29936154	4.145093309	0.0840244	0.139371627	0.0324	0	242	206	400	328	305	346	369	243	340	337
ENSMUSG00000044367	chr11	Slc16a13	7E+07	7E+07	2601	0.727469986	0.57947291	0.0841381	0.139543768	0.16753	0	6	10	17	9	39	49	18	26	35	49
ENSMUSG00000007564	chr17	Ppp2r1a	2.1E+07	2.1E+07	3375	0.337399493	7.094979104	0.0841626	0.139567842	0.04523	0	1562	1072	2417	1967	2327	3189	3144	2329	3633	3475
ENSMUSG00000026790	chr2	Odf2	3E+07	3E+07	9919	0.333077519	3.529019847	0.0841995	0.139612498	0.03983	0	136	86	208	152	202	294	249	220	246	304
ENSMUSG00000026939	chr2	Tmem141	2.6E+07	2.6E+07	1122	0.35226031	3.846037901	0.0843071	0.13977439	0.04456	0	217	160	178	151	226	453	295	239	352	329
ENSMUSG00000031448	chr8	Adprhl1	1.3E+07	1.3E+07	1820	0.61238725	5.392887406	0.0844243	0.139946093	0.14776	0	271	206	1119	814	217	886	1222	763	893	1468
ENSMUSG00000101013	chr5	A630072M18Rik	2.1E+07	2.1E+07	5410	0.484391123	1.648320064	0.0844306	0.139946093	0.0705	0	38	31	38	25	58	92	64	63	78	65
ENSMUSG00000015714	chr3	Cers2	9.5E+07	9.5E+07	3676	0.40496477	5.251909674	0.0845223	0.140064823	0.06419	0	396	338	401	381	1012	1240	768	710	829	951
ENSMUSG00000061897	chr2	Gm14292	1.8E+08	1.8E+08	456	-0.59110781	1.131761299	0.0845132	0.140064823	0.11091	0	19	37	57	39	39	33	62	22	28	30
ENSMUSG00000101316	chr11	Gm12663	1.7E+07	1.7E+07	958	-0.63739058	0.670470355	0.0845322	0.140064823	0.12073	0	32	29	22	30	20	23	39	18	27	15
ENSMUSG00000023026	chr15	Dip2b	1E+08	1E+08	9553	0.323402356	3.704965352	0.0846553	0.140252189	0.03734	0	153	119	239	154	217	422	270	216	305	288
ENSMUSG00000020806	chr11	Rhbdf2	1.2E+08	1.2E+08	5293	-0.30953861	4.149752208	0.0846755	0.140252589	0.03533	0	233	219	346	339	346	346	407	203	347	346
ENSMUSG00000047221	chr5	Fam185a	2.1E+07	2.1E+07	3894	-0.32658	4.026987605	0.0846741	0.140252589	0.03891	0	214	171	411	317	277	364	333	231	249	317
ENSMUSG00000028069	chr3	Gpatch4	8.8E+07	8.8E+07	2447	-0.2742103	4.916406777	0.0847046	0.140284182	0.02842	0	472	406	567	493	532	610	578	418	586	631
ENSMUSG00000004814	chr5	Ccl24	1.4E+08	1.4E+08	1289	0.885547467	2.514265932	0.0847581	0.140339639	0.29266	0	48	70	9	27	133	263	76	181	118	98
ENSMUSG00000039693	chr4	Msantd3	4.9E+07	4.9E+07	1973	0.308014233	3.919397105	0.0847509	0.140339639	0.03429	0	164	134	261	232	236	366	329	278	387	351
ENSMUSG00000059323	chr15	Tonsl	7.7E+07	7.7E+07	5815	0.299420835	5.874751445	0.0847681	0.140339669	0.03498	0	754	603	857	762	989	1474	1276	1040	1455	1431
ENSMUSG00000025646	chr9	Atrip	1.1E+08	1.1E+08	6725	0.281473761	5.046875294	0.084958	0.140637425	0.03014	0	405	305	574	462	526	906	642	595	879	714
ENSMUSG00000051671	chr8	Coa6	1.3E+08	1.3E+08	762	-0.31431254	3.743194259	0.0849708	0.140642084	0.03505	0	221	147	324	205	232	274	261	187	256	250
ENSMUSG00000027963	chr3	Extl2	1.2E+08	1.2E+08	3446	-0.30345367	3.901896336	0.0852026	0.141009033	0.03304	0	257	165	288	239	300	342	324	215	255	245
ENSMUSG00000032244	chr9	Fem1b	6.3E+07	6.3E+07	6488	-0.30641305	4.789772403	0.085335	0.141211552	0.03577	0	428	393	554	462	438	570	564	457	523	414
ENSMUSG00000007097	chr1	Atp1a2	1.7E+08	1.7E+08	7038	-0.42103316	10.60403711	0.085353	0.141215974	0.07139	0	23207	14071	46765	33505	21063	29549	30259	18630	25403	34893
ENSMUSG00000027242	chr2	Wdr76	1.2E+08	1.2E+08	6305	-0.48900898	1.30152816	0.0853578	0.141215974	0.07037	0	34	34	63	36	44	44	58	22	40	43
ENSMUSG00000021619	chr13	Atg10	9.1E+07	9.1E+07	1609	-0.34383663	3.418932296	0.0855576	0.141529831	0.04152	0	141	109	252	208	205	210	229	143	187	201
ENSMUSG00000079481	chrX	Nhsl2	1E+08	1E+08	16952	0.411059035	2.579387662	0.0855997	0.14158277	0.05717	0	75	60	71	59	115	178	120	102	140	155
ENSMUSG00000000296	chr10	Tpd52l1	3.1E+07	3.1E+07	1267	-0.33601244	4.383581569	0.0856158	0.141592717	0.04299	0	422	298	381	322	287	454	395	316	376	355
ENSMUSG00000026836	chr2	Acvr1	5.8E+07	5.8E+07	4829	-0.33510744	4.057088157	0.0856408	0.141617296	0.04164	0	231	181	335	323	344	340	438	229	254	261
ENSMUSG00000041241	chr4	Mul1	1.4E+08	1.4E+08	4000	-0.33375738	5.688538964	0.0856829	0.141670125	0.04381	0	701	515	1366	1012	850	987	1106	699	1039	889
ENSMUSG00000022114	chr14	Spry2	1.1E+08	1.1E+08	2085	0.293229327	4.061329021	0.0857009	0.141683295	0.03084	0	210	177	254	207	277	430	413	301	377	366
ENSMUSG00000095687	chr17	Rnaset2a	8128610	8128886	1259	0.336397843	3.877826472	0.0858255	0.141872464	0.04166	0	127	144	284	196	241	418	318	235	410	315
ENSMUSG00000005583	chr13	Mef2c	8.4E+07	8.4E+07	6760	-0.4396789	9.063891307	0.0858511	0.141898076	0.07799	0	8917	8506	11045	11133	5491	9116	12977	7169	8535	9200
ENSMUSG00000027536	chr3	Chmp4c	1E+07	1E+07	10087	-0.54962004	4.792412905	0.0860046	0.142135072	0.11896	0	292	139	1076	770	368	482	570	374	468	418
ENSMUSG00000009828	chr9	Ick	7.8E+07	7.8E+07	11524	0.390913245	3.312632734	0.0861617	0.142378028	0.05577	0	107	79	140	98	237	303	230	176	213	237
ENSMUSG00000066113	chr4	Adamtsl1	8.6E+07	8.6E+07	10870	-0.64129061	3.447808934	0.086296	0.142583134	0.16036	0	266	299	96	93	145	246	167	142	168	159
ENSMUSG00000079022	chr15	Col22a1	7.2E+07	7.2E+07	9203	0.381872762	5.203642295	0.0863594	0.142671055	0.05726	0	720	330	514	444	355	1108	759	717	849	862
ENSMUSG00000037005	chrX	Xpnpep2	4.8E+07	4.8E+07	4878	0.573966291	1.035232057	0.0865937	0.143041275	0.09758	0	23	16	14	24	40	60	32	42	52	51
ENSMUSG00000031939	chr9	Taf1d	1.5E+07	1.5E+07	1361	-0.4469058	2.528166122	0.0867015	0.143202513	0.07002	0	112	94	92	81	103	130	95	97	74	97
ENSMUSG00000056091	chr6	St3gal5	7.2E+07	7.2E+07	2618	-0.73487227	5.716855784	0.0867206	0.143217078	0.21504	0	454	175	3053	914	962	748	1396	449	578	978
ENSMUSG00000035578	chr16	Iqcg	3.3E+07	3.3E+07	3462	0.42294798	2.775106034	0.0867327	0.143220294	0.06378	0	77	52	135	102	75	167	131	111	208	181
ENSMUSG00000019179	chr5	Mdh2	1.4E+08	1.4E+08	2089	-0.42481951	9.986276076	0.0868052	0.143300514	0.07331	0	14015	8316	32813	20390	16195	17371	23767	12576	18242	17997
ENSMUSG00000030245	chr6	Golt1b	1.4E+08	1.4E+08	2818	0.315244569	4.485224381	0.086812	0.143300514	0.03736	0	283	255	287	248	417	654	501	388	561	462
ENSMUSG00000052563	chr11	D930048N14Rik	5.2E+07	5.2E+07	3429	0.752098474	0.603969728	0.0867939	0.143300514	0.19065	0	6	6	16	15	40	45	18	43	44	26
ENSMUSG00000038697	chr8	Taf5l	1.2E+08	1.2E+08	3033	-0.30023919	3.852244427	0.0869898	0.143577258	0.03258	0	209	178	281	257	274	322	295	215	260	239
ENSMUSG00000020235	chr10	Fzr1	8.1E+07	8.1E+07	4488	0.290153513	4.727225739	0.0871332	0.143763141	0.03214	0	272	238	487	420	404	684	591	406	708	634
ENSMUSG00000021958	chr14	Pinx1	6.4E+07	6.4E+07	1351	0.418109448	1.941878585	0.0871277	0.143763141	0.05286	0	42	36	54	45	65	101	79	75	96	87

ENSMUSG00000022751	chr16	Nit2	5.7E+07	5.7E+07	1280	-0.3221537	4.245345568	0.0871275	0.143763141	0.03953	0	328	269	272	309	378	396	360	251	413	321
ENSMUSG00000072949	chr12	Acot1	8.4E+07	8.4E+07	1559	-1.18379788	1.016532703	0.0872743	0.143979038	0.50752	0	22	4	171	25	5	39	17	10	15	43
ENSMUSG00000027737	chr3	Slc7a11	5E+07	5E+07	13922	1.087035804	0.249465431	0.0873342	0.144060787	0.42877	0	1	1	45	2	9	17	37	21	31	40
ENSMUSG00000052539	chr3	Magi3	1E+08	1E+08	6773	-0.50492285	2.02718022	0.0873866	0.144122592	0.08797	0	86	54	77	33	105	81	60	59	77	62
ENSMUSG00000061877	chr7	BC048679	8.1E+07	8.1E+07	640	-0.78360734	3.657098878	0.0873922	0.144122592	0.24078	0	114	40	693	358	104	251	154	130	154	272
ENSMUSG00000020648	chr12	Dus4l	3.2E+07	3.2E+07	1768	-0.47926961	1.83045579	0.0874354	0.144176872	0.07395	0	44	38	102	68	60	78	66	56	43	55
ENSMUSG00000024899	chr19	Papss2	3.3E+07	3.3E+07	3635	0.425400333	3.274141602	0.0874915	0.144235593	0.06804	0	89	66	146	107	234	309	265	116	224	248
ENSMUSG00000030718	chr7	Ppme1	1E+08	1E+08	2361	0.304372543	5.191069006	0.0874891	0.144235593	0.03636	0	363	305	660	633	546	925	849	580	936	896
ENSMUSG00000034108	chr19	Ccs	4825366	4825664	1057	0.35026865	3.825926044	0.0875644	0.144338778	0.04546	0	164	137	195	207	232	421	229	224	385	384
ENSMUSG00000027074	chr2	Slc43a3	8.5E+07	8.5E+07	4464	0.370976308	4.770051991	0.0876031	0.144385615	0.05441	0	273	203	557	244	601	860	675	386	530	781
ENSMUSG00000074643	chr2	Cpne1	1.6E+08	1.6E+08	4507	-0.3281374	4.042675486	0.0876348	0.144420767	0.04057	0	235	228	306	225	388	401	360	230	234	290
ENSMUSG00000030603	chr7	Psmc4	2.8E+07	2.8E+07	2169	0.307979917	6.684396261	0.0876503	0.144429473	0.03828	0	1280	991	1692	1442	1565	2675	2325	1853	2428	2469
ENSMUSG00000064360	chrMT	mt-Nd3	9459	9806	348	-0.83962354	1.370389249	0.0877788	0.14462412	0.25703	0	34	21	37	95	58	11	71	11	60	35
ENSMUSG00000041215	chr16	Yeats2	2E+07	2E+07	6116	-0.39322703	2.657677456	0.0877912	0.144627527	0.05377	0	102	84	136	83	131	162	98	87	88	125
ENSMUSG00000041696	chr9	Rasl12	6.5E+07	6.5E+07	3877	-0.9071444	3.679826985	0.087819	0.144656439	0.32298	0	143	87	104	51	996	277	135	160	182	160
ENSMUSG00000029703	chr5	Lrwd1	1.4E+08	1.4E+08	6650	0.378169833	2.832346313	0.0878883	0.144753487	0.04905	0	87	61	102	90	125	199	171	92	196	174
ENSMUSG00000026192	chr1	Atic	7.2E+07	7.2E+07	7985	0.30341108	5.238596463	0.087909	0.144770725	0.03607	0	489	398	528	494	625	1001	715	772	973	798
ENSMUSG00000021111	chr12	Papola	1.1E+08	1.1E+08	6595	-0.31256102	5.953302895	0.0879384	0.144802015	0.0392	0	980	803	1344	1008	1037	1449	1375	887	972	1058
ENSMUSG00000046691	chr8	Chtf8	1.1E+08	1.1E+08	3036	0.266143086	5.047793774	0.0879716	0.144839801	0.0273	0	398	301	532	455	608	927	754	528	804	740
ENSMUSG00000071454	chr12	Dtnb	3572381	3572647	9603	0.5678582	0.879775925	0.088008	0.144882701	0.09556	0	12	13	39	16	28	44	56	25	55	34
ENSMUSG00000024335	chr17	Brd2	3.4E+07	3.4E+07	7285	-0.31308403	6.926584276	0.0880346	0.144909379	0.03978	0	1778	1536	2564	1904	2464	2594	2327	1832	2164	2279
ENSMUSG00000030847	chr7	Bag3	1.3E+08	1.3E+08	2591	0.522382909	7.407756742	0.0880582	0.144914239	0.11116	0	1189	685	4657	2785	1979	4559	3807	3209	4259	4843
ENSMUSG00000037406	chr8	Htra4	2.5E+07	2.5E+07	1795	0.894381787	0.043631887	0.0880518	0.144914239	0.25581	0	4	6	20	1	19	20	51	7	22	24
ENSMUSG00000038151	chr10	Prdm1	4.4E+07	4.4E+07	5492	0.614532885	0.58606134	0.0881103	0.144983055	0.10809	0	9	7	23	27	18	39	29	20	36	50
ENSMUSG00000086329	chr2	Gm14233	1.3E+08	1.3E+08	439	0.46936605	1.751457883	0.0881926	0.145101396	0.06907	0	31	33	48	37	58	103	54	63	73	97
ENSMUSG00000025486	chr7	Sirt3	1.4E+08	1.4E+08	1570	-0.36839837	4.550568013	0.0882495	0.145177913	0.05286	0	348	184	708	436	394	460	594	292	355	426
ENSMUSG00000030512	chr7	Snrpa1	6.6E+07	6.6E+07	3082	0.303200804	4.368471734	0.0882851	0.145219586	0.03487	0	270	180	280	317	349	606	441	408	455	430
ENSMUSG00000030726	chr7	Pold3	1E+08	1E+08	4134	0.339824242	3.292053843	0.0885594	0.145653631	0.04176	0	123	78	149	129	177	285	189	181	227	237
ENSMUSG00000036062	chr4	N28178	4.3E+07	4.3E+07	7118	0.576404807	0.467253523	0.0886321	0.145756137	0.08036	0	17	8	14	16	22	41	29	23	24	40
ENSMUSG00000062981	chr10	Mrpl42	9.5E+07	9.5E+07	666	-0.32534273	7.657781222	0.0886704	0.145802075	0.04337	0	3319	2373	4359	3599	3368	3948	4187	2838	3845	3722
ENSMUSG00000006675	chr9	P4htm	1.1E+08	1.1E+08	3890	0.413788821	2.455368507	0.0886813	0.14580275	0.05975	0	75	45	75	52	105	138	113	114	118	145
ENSMUSG00000025650	chr9	Col7a1	1.1E+08	1.1E+08	10267	0.609334234	4.152774485	0.0887148	0.145823748	0.1476	0	176	197	110	83	493	614	286	296	435	603
ENSMUSG00000057378	chr2	Ryr3	1.1E+08	1.1E+08	17682	0.898393467	-0.26836695	0.0887058	0.145823748	0.2338	0	18	2	9	5	3	31	10	23	10	20
ENSMUSG00000003813	chr8	Rad23a	8.5E+07	8.5E+07	2577	-0.3194237	7.19756227	0.0888436	0.146004568	0.04173	0	2212	1754	3058	2561	2801	2799	2889	2066	3011	2721
ENSMUSG00000022906	chr16	Parp9	3.6E+07	3.6E+07	4872	0.39666673	3.165232523	0.0888484	0.146004568	0.05722	0	109	76	128	91	184	334	201	119	208	205
ENSMUSG00000029128	chr5	Rab28	4.2E+07	4.2E+07	1636	-0.32871511	6.332431526	0.0888561	0.146004568	0.04392	0	1415	985	1656	1315	1394	1619	2038	1025	1308	1456
ENSMUSG00000027661	chr2	Slc2a10	1.7E+08	1.7E+08	3570	0.504302713	1.597178197	0.0888824	0.146030683	0.07974	0	38	31	37	21	54	110	72	50	57	68
ENSMUSG00000081752	chrX	Gm14680	6.3E+07	6.3E+07	1101	-0.40802531	3.082780885	0.0890312	0.146258035	0.06235	0	158	138	126	119	162	170	200	100	164	118
ENSMUSG00000005897	chr10	Nr2c1	9.4E+07	9.4E+07	4607	-0.34619007	3.175940998	0.0891222	0.146390432	0.04268	0	164	97	172	146	183	210	155	133	139	179
ENSMUSG00000042579	chr3	4632404H12Rik	9E+07	9E+07	2791	-0.55297946	1.386776816	0.0891554	0.146427836	0.09912	0	38	25	96	38	38	47	57	24	49	37
ENSMUSG00000003308	chr9	Keap1	2.1E+07	2.1E+07	4664	-0.3137361	6.350182447	0.089209	0.146498778	0.03999	0	1274	853	1901	1412	1504	1630	1764	1068	1646	1446
ENSMUSG00000089838	chr1	Gm2962	1.7E+08	1.7E+08	336	-0.4605087	3.317140406	0.0892431	0.146537515	0.08003	0	163	88	365	161	121	198	176	158	163	157
ENSMUSG00000051675	chr4	Trim32	6.6E+07	6.6E+07	3229	-0.32414745	3.661274404	0.0893561	0.146705978	0.03895	0	196	156	212	226	264	298	279	169	187	231
ENSMUSG00000048930	chr6	Tada3	1.1E+08	1.1E+08	3883	0.306905493	4.046414891	0.0894834	0.146897769	0.03547	0	179	135	282	260	273	416	409	244	437	388
ENSMUSG00000025203	chr19	Scd2	4.4E+07	4.4E+07	5453	0.682137428	6.358336339	0.0895573	0.147001754	0.1896	0	522	615	541	422	2916	2631	3261	1303	2089	1350
ENSMUSG00000044534	chr9	Ackr2	1.2E+08	1.2E+08	2784	-0.7106516	1.059455344	0.0896928	0.147207052	0.17207	0	26	31	21	23	89	47	35	31	16	27
ENSMUSG00000028098	chr3	Rnf115	9.7E+07	9.7E+07	2265	-0.35118746	6.141000089	0.0897678	0.147312802	0.05029	0	1056	713	1726	1469	1104	1407	1696	983	1041	1301
ENSMUSG00000049807	chr11	Arhgap23	9.7E+07	9.7E+07	6637	0.387921913	4.046761933	0.0898002	0.147348829	0.05902	0	148	151	240	147	422	412	382	316	412	393
ENSMUSG00000000276	chr11	Dgke	8.9E+07	8.9E+07	8387	-0.40973391	3.003613958	0.0898412	0.147398827	0.06199	0	119	73	245	136	134	184	164	85	118	166
ENSMUSG00000047675	chr4	Rps8	1.2E+08	1.2E+08	1726	0.343031518	8.169395082	0.0898695	0.147428102	0.04865	0	3636	3165	4279	3593	4340	8252	5280	5523	6888	7263
ENSMUSG00000103283	chr13	RP23-206J9.6	6.8E+07	6.8E+07	1796	0.775802148	-0.01845579	0.0899086	0.147474983	0.17239	0	9	4	15	1	21	37	20	11	19	28
ENSMUSG00000012443	chr19	Kif11	3.7E+07	3.7E+07	4819	0.691924961	0.343203257	0.0899198	0.147476047	0.14135	0	11	5	13	23	15	44	24	35	26	15
ENSMUSG00000068749	chr3	Psma5	1.1E+08	1.1E+08	1321	0.304614478	6.000423637	0.0899544	0.147515613	0.03758	0	852	661	1001	779	1026	1773	1310	1207	1449	1551
ENSMUSG00000030313	chr6	Dennd5b	1.5E+08	1.5E+08	10621	-0.35134743	3.094413799	0.0900442	0.147633666	0.04449	0	141	100	188	157	131	192	163	119	130	167
ENSMUSG00000032840	chr5	2410131K14Rik	1.2E+08	1.2E+08	5649	-0.32625969	4.08002337	0.0900475	0.147633666	0.04055	0	239	171	423	308	305	335	430	205	281	309
ENSMUSG00000030157	chr6	Clec2d	1.3E+08	1.3E+08	1213	0.419640867	5.871586045	0.0900865	0.147680305	0.07185	0	840	672	694	412	1117	2166	1101	1031	1149	1558
ENSMUSG00000025169	chr11	Ogfod3	1.2E+08	1.2E+08	1308	0.314821042	3.796314482	0.0901065	0.147695838	0.03688	0	163	128	212	178	258	309	310	238	378	341
ENSMUSG00000039167	chr3	Eltd1	1.5E+08	1.5E+08	4343	-0.37609356	4.668286223	0.0901398	0.147715995	0.05597	0	283	186	757	497	560	572	567	343	390	426
ENSMUSG00000073802	chr4	Cdkn2b	8.9E+07	8.9E+07	1393	0.509329859	2.203907644	0.0901377	0.147715995	0.09219	0	41	53	48	39	98	112	82	103	138	101
ENSMUSG00000038422	chr4	Hdhd3	6.2E+07	6.3E+07	1366	0.530072005	2.86857307	0.0901681	0.147744989	0.10901	0	61	34	99	77	200	240	111	146	197	182
ENSMUSG00000053062	chr16	Jam2	8.5E+07	8.5E+07	5872	-0.3133221	5.288741034	0.0902061	0.147772737	0.0392	0	556	363	1060	654	743	869	907	514	632	709
ENSMUSG00000099492	chr1	Gm5525	2.9E+07	2.9E+07	1312	0.554098839	1.214470483	0.0901999	0.147772737	0.09699	0	17	19	43	33	24	48	54	28	59	84
ENSMUSG00000026670	chr1	Uap1	1.7E+08	1.7E+08	4011	-0.2933536	5.610525367	0.0903482	0.147988224	0.03467	0	748	546	965	801	1048	1136	1140	646	838	819
ENSMUSG00000005846	chr16	Rsl1d1	1.1E+07	1.1E+07	2258	-0.31140385	5.791930019	0.0904005	0.148056722	0.03937	0	901	708	1204	976	817	1172	1150	850	948	974
ENSMUSG00000024357	chr18	Sil1	3.5E+07	3.5E+07	1695	0.293996273	4.691937875	0.0904321	0.148091067	0.0335	0	340	263	361	325	458	661	491	429	716	639
ENSMUSG00000002395	chr8	Use1	7.1E+07	7.1E+07	2203	0.301841435	5.514377794	0.0904863	0.148162562	0.03675	0	528	381	877	697	661	1211	984	725	1093	1230
ENSMUSG00000022223	chr14	Sdr39u1	5.6E+07	5.6E+07	1226	-0.34603486	6.501029747	0.0905217	0.148194913	0.04926	0	1363	911	2189	1719	1629	1521	2218	1045	1749	1777

ENSMUSG00000050914	chr8	Ankrd37	4.6E+07	4.6E+07	1403	0.460587836	1.842888998	0.0905272	0.148194913	0.06727	0	45	41	48	49	32	96	85	68	81	84
ENSMUSG00000063801	chr7	Ap3s2	8E+07	8E+07	5797	-0.30191026	5.669493454	0.0905567	0.148226044	0.03695	0	914	648	980	833	827	1046	1095	714	1001	860
ENSMUSG00000029122	chr5	Evc	3.7E+07	3.7E+07	7701	-0.61336234	4.392966158	0.090598	0.148276199	0.15209	0	206	98	1052	470	256	397	454	202	307	379
ENSMUSG00000031502	chr8	Col4a1	1.1E+07	1.1E+07	6818	0.401997542	8.108914258	0.090695	0.148408597	0.0672	0	2230	2016	5062	3223	6336	7406	5939	5747	7147	5973
ENSMUSG00000085241	chr4	Snhg3	1.3E+08	1.3E+08	986	0.43508018	2.26376255	0.0907084	0.148408597	0.06546	0	55	45	70	50	83	154	81	111	102	103
ENSMUSG00000096544	chr3	Gm4617	1.2E+08	1.2E+08	489	0.72116765	-0.29241477	0.0907106	0.148408597	0.10172	0	5	9	6	8	11	24	22	13	20	11
ENSMUSG00000027993	chr3	Trim2	8.4E+07	8.4E+07	18113	0.473158712	2.374895248	0.0907292	0.148421786	0.07858	0	60	54	44	55	105	190	112	91	102	121
ENSMUSG00000034292	chr1	Traf3ip1	9.1E+07	9.1E+07	3712	-0.359729	2.652374751	0.0907749	0.148479148	0.04451	0	104	81	138	98	105	131	114	80	111	128
ENSMUSG00000066151	chr4	Fkbp15	6.2E+07	6.2E+07	7515	0.27794371	4.392495544	0.0907917	0.148489307	0.02953	0	259	172	377	312	332	576	483	331	482	516
ENSMUSG00000020589	chr12	Fam49a	1.2E+07	1.2E+07	4846	0.486954265	3.170120412	0.0908537	0.148573406	0.09131	0	117	80	75	70	222	288	179	169	178	262
ENSMUSG00000074971	chr2	Fibin	1.1E+08	1.1E+08	2267	0.401566322	4.630270477	0.0909048	0.148639672	0.06416	0	267	313	345	251	405	1153	562	356	423	506
ENSMUSG00000032673	chr11	Prorsd1	3E+07	3E+07	2128	-0.3001199	3.934058424	0.090969	0.148727268	0.03375	0	250	195	307	256	253	338	287	238	286	255
ENSMUSG00000042328	chr5	Hps4	1.1E+08	1.1E+08	3948	0.407545933	2.530741723	0.0909889	0.148742487	0.05704	0	52	57	83	66	114	144	140	81	156	153
ENSMUSG00000027108	chr2	Ola1	7.3E+07	7.3E+07	3561	-0.29351578	5.405609454	0.0910943	0.148897387	0.03462	0	688	509	864	710	755	900	920	682	756	654
ENSMUSG00000039191	chr5	Rbpj	5.4E+07	5.4E+07	5817	0.308595952	4.249238388	0.0911399	0.148954522	0.0364	0	246	191	295	205	348	623	392	295	403	481
ENSMUSG00000066632	chr12	Pgk1-rs7	1.1E+07	1.1E+07	1731	-0.53232105	1.800124199	0.091151	0.148955335	0.10046	0	54	50	94	52	54	33	60	35	90	68
ENSMUSG00000031714	chr8	Gab1	8.1E+07	8.1E+07	4859	-0.32137259	4.31046699	0.0912169	0.149028323	0.03995	0	265	194	579	333	341	431	400	253	350	398
ENSMUSG00000042626	chr3	Shc1	8.9E+07	8.9E+07	5645	0.314368943	5.092408769	0.0912145	0.149028323	0.03941	0	406	390	446	362	680	1042	673	620	762	813
ENSMUSG00000026694	chr1	Mettl13	1.6E+08	1.6E+08	9740	-0.31410053	3.771677428	0.0913177	0.149175617	0.03721	0	218	197	230	223	251	264	269	196	266	253
ENSMUSG00000102836	chr18	RP23-407E2.5	3.7E+07	3.7E+07	313	-0.5773916	1.53468905	0.0913977	0.149288946	0.11995	0	43	61	33	33	76	68	58	25	52	36
ENSMUSG00000069094	chr3	Pde7a	1.9E+07	1.9E+07	7748	-0.36082174	5.837978437	0.0914135	0.149297284	0.05362	0	954	797	1263	1029	745	1103	1555	704	910	951
ENSMUSG00000022948	chr16	Setd4	9.4E+07	9.4E+07	4702	0.594429358	0.862071539	0.0914581	0.149352849	0.11113	0	18	11	21	20	34	58	22	38	31	61
ENSMUSG00000003316	chr8	Glg1	1.1E+08	1.1E+08	7090	-0.31029399	6.011106182	0.0916046	0.149557177	0.03957	0	965	786	1346	1173	1131	1418	1547	851	1132	1051
ENSMUSG00000039873	chr2	Neurl2	1.6E+08	1.6E+08	1014	0.29012446	4.615718089	0.0916005	0.149557177	0.03285	0	278	228	406	365	399	558	535	376	716	601
ENSMUSG00000031823	chr8	Zdhhc7	1.2E+08	1.2E+08	3472	0.291914321	5.328023887	0.0916275	0.149577121	0.03438	0	425	369	776	570	631	913	1039	675	1056	879
ENSMUSG00000053110	chr9	Yap1	7931999	7934732	9257	0.32242908	6.332187894	0.0916881	0.149658728	0.04297	0	826	761	1330	1220	1327	2106	1754	1694	1748	1852
ENSMUSG00000071342	chr12	Lsmem1	4E+07	4E+07	1213	-0.42795299	5.565139951	0.0917413	0.149728176	0.07557	0	1281	714	679	538	723	869	931	693	921	731
ENSMUSG00000085881	chr13	Gm15912	7.4E+07	7.4E+07	578	0.589567572	0.700803468	0.0917755	0.149766457	0.10082	0	20	12	11	14	34	52	31	31	34	39
ENSMUSG00000057967	chr11	Fgf18	3.3E+07	3.3E+07	1187	0.62353791	0.403488346	0.0918165	0.149816053	0.09898	0	19	15	8	12	15	42	27	24	29	29
ENSMUSG00000026308	chr1	Klhl30	9.1E+07	9.1E+07	3089	0.344015525	7.430448066	0.0919542	0.150023144	0.04942	0	2425	1611	2814	2533	2053	4730	4039	2970	4760	3515
ENSMUSG00000019464	chr8	Ptger1	8.4E+07	8.4E+07	4959	0.688076123	-0.12274404	0.0919982	0.150042582	0.10308	0	11	5	12	11	7	19	23	8	27	26
ENSMUSG00000021139	chr12	Gm20498	8.1E+07	8.1E+07	3241	-0.30560272	5.65506093	0.091977	0.150042582	0.03821	0	916	693	969	758	806	1128	927	774	900	916
ENSMUSG00000038544	chr4	Inip	6E+07	6E+07	5995	0.36825111	2.602081519	0.0919969	0.150042582	0.04612	0	71	50	87	85	104	184	129	104	142	139
ENSMUSG00000024381	chr18	Bin1	3.2E+07	3.2E+07	2451	0.339338693	9.788627575	0.0920362	0.150087106	0.04843	0	10198	8482	14396	13356	12782	21428	21300	15264	25034	19148
ENSMUSG00000030629	chr7	Zfand6	8.5E+07	8.5E+07	1668	-0.3186516	6.477272207	0.0920507	0.150093423	0.0421	0	1543	1101	1626	1321	1880	1629	1983	1288	1532	1745
ENSMUSG00000053253	chr14	Ndfip2	1.1E+08	1.1E+08	11553	-0.29743512	3.908652498	0.0922163	0.150345875	0.03324	0	239	167	281	247	321	344	339	208	261	242
ENSMUSG00000023939	chr17	Mrpl14	4.6E+07	4.6E+07	949	0.411206692	5.852800932	0.0923388	0.150528196	0.07038	0	552	313	1534	828	729	1400	1420	946	1642	1426
ENSMUSG00000047719	chr4	Ubiad1	1.5E+08	1.5E+08	2992	-0.37393587	4.348192666	0.0924794	0.150739748	0.05551	0	229	167	610	450	346	415	420	282	344	370
ENSMUSG00000020630	chr12	Rnaseh1	2.9E+07	2.9E+07	1457	0.379691843	2.843759063	0.0925102	0.150772533	0.05281	0	90	47	100	106	130	229	163	114	156	174
ENSMUSG00000029769	chr6	Ccdc136	2.9E+07	2.9E+07	4298	0.321810361	3.555639274	0.0925951	0.150893379	0.03897	0	133	94	229	166	177	266	277	203	300	290
ENSMUSG00000006373	chrX	Pgrmc1	3.7E+07	3.7E+07	1857	0.442528887	4.509171665	0.0926578	0.150977921	0.08007	0	246	174	251	175	661	761	474	434	521	521
ENSMUSG00000028411	chr4	Aptx	4.1E+07	4.1E+07	5886	-0.27955907	4.549122592	0.0928086	0.15120605	0.0308	0	403	323	424	373	380	516	474	329	426	441
ENSMUSG00000051375	chr18	Pcdh1	3.8E+07	3.8E+07	8797	0.363360163	4.017716566	0.0928701	0.151288779	0.05293	0	157	108	324	165	364	436	344	282	414	400
ENSMUSG00000041124	chr9	Msantd4	4383535	4384142	2731	-0.30397416	5.515984426	0.0931535	0.151732724	0.03784	0	668	479	1141	805	796	1031	1007	607	700	921
ENSMUSG00000033060	chr14	Lmo7	1E+08	1E+08	11951	-0.384898	6.231442133	0.0932681	0.151901782	0.06197	0	1151	818	1937	1691	872	1507	1770	961	1288	1255
ENSMUSG00000025077	chr19	Dclre1a	5.7E+07	5.7E+07	6384	-0.40967348	2.320469103	0.0934898	0.152245274	0.0584	0	82	71	87	73	107	92	112	77	66	86
ENSMUSG00000021039	chr12	Snw1	8.7E+07	8.7E+07	2231	-0.29411622	5.983065222	0.0935303	0.152293543	0.03588	0	1010	828	1207	1059	1120	1322	1259	935	1148	1201
ENSMUSG00000093798	chr10	Gm8355	1.5E+07	1.5E+07	756	0.344021063	3.870141136	0.0935703	0.152340952	0.04652	0	158	115	329	208	181	412	282	284	342	353
ENSMUSG00000021120	chr12	Pigh	7.9E+07	7.9E+07	2349	0.517898208	2.123506226	0.0935858	0.152348425	0.093	0	66	51	42	43	52	177	73	66	107	103
ENSMUSG00000003992	chr13	Ssbp2	9.1E+07	9.1E+07	7961	-0.31303987	3.644275114	0.09368	0.152484133	0.03671	0	218	155	222	199	241	241	248	196	236	216
ENSMUSG00000019804	chr10	Snx3	4.3E+07	4.3E+07	1413	0.307091903	6.902120419	0.0936992	0.152497629	0.03963	0	1382	1174	1931	1575	2084	3100	2834	2043	2972	2756
ENSMUSG00000038738	chr7	Shank1	4.4E+07	4.4E+07	8293	0.770684773	-0.24969943	0.0937148	0.152505331	0.17573	0	3	1	8	10	20	30	21	16	11	16
ENSMUSG00000033075	chr15	Senp1	9.8E+07	9.8E+07	11873	-0.31401098	3.401918792	0.0938563	0.152700186	0.03625	0	159	136	223	174	186	233	206	139	193	201
ENSMUSG00000087260	chr3	Lamtor5	1.1E+08	1.1E+08	881	0.269255717	5.229312046	0.0938471	0.152700186	0.02928	0	479	366	594	497	643	977	787	717	837	890
ENSMUSG00000016833	chr5	Mrps18c	1E+08	1E+08	1076	0.27381859	4.618790525	0.0939203	0.152786537	0.02951	0	332	219	377	341	418	690	478	447	552	602
ENSMUSG00000004789	chr12	Dlst	8.5E+07	8.5E+07	2767	-0.43787236	8.580475325	0.0939844	0.152873197	0.08128	0	4819	2812	12809	8076	6541	6489	9197	4613	6684	6835
ENSMUSG00000024168	chr17	Tmem204	2.5E+07	2.5E+07	2022	0.359678535	4.219984904	0.0941027	0.153047853	0.05262	0	148	122	408	255	356	473	410	315	455	506
ENSMUSG00000103125	chr18	RP23-407E2.6	3.7E+07	3.7E+07	429	-0.57738638	1.53468905	0.0941307	0.15307568	0.11991	0	43	61	33	33	76	68	58	25	52	36
ENSMUSG00000020311	chr11	Erlec1	3.1E+07	3.1E+07	3260	-0.26592662	4.939027585	0.0943115	0.1532956	0.02838	0	537	365	584	503	527	735	610	430	540	576
ENSMUSG00000032470	chr9	Mras	9.9E+07	9.9E+07	5134	0.303887729	3.776155915	0.0943201	0.1532956	0.03466	0	166	140	233	184	197	309	332	239	357	311
ENSMUSG00000055067	chr1	Smyd3	1.8E+08	1.8E+08	9184	-0.39188053	2.726957854	0.0943169	0.1532956	0.05569	0	116	70	106	144	123	135	107	90	141	111
ENSMUSG00000056486	chr2	Chn1	7.4E+07	7.4E+07	5146	-0.56968799	1.802251319	0.0943206	0.1532956	0.11658	0	63	26	43	49	137	62	50	47	60	62
ENSMUSG00000063802	chr7	Hspbp1	4660521	4660845	1488	0.286953456	4.852202195	0.0943195	0.1532956	0.03323	0	310	247	528	441	471	652	655	467	812	688
ENSMUSG00000034614	chr11	Pik3ip1	3330401	3331004	4272	-0.33168393	5.464286979	0.0943559	0.153335185	0.04575	0	975	524	708	705	745	1023	994	565	722	777
ENSMUSG00000030737	chr7	Slco2b1	1E+08	1E+08	5612	0.432898261	4.516520824	0.0943746	0.153347801	0.07662	0	282	259	174	200	535	662	594	387	420	666
ENSMUSG00000028088	chr3	Fmo5	9.8E+07	9.8E+07	5675	-0.33655143	3.627549771	0.094461	0.153470323	0.04355	0	217	173	201	175	257	288	202	197	210	220
ENSMUSG00000042709	chr11	Atpaf2	6E+07	6E+07	2137	-0.33934941	4.873384671	0.0945188	0.153546568	0.04683	0	438	254	540	422	909	549	622	402	538	560

ENSMUSG00000079316	chrX	Rab9	1.7E+08	1.7E+08	1749	-0.31386187	4.08827306	0.0945836	0.153633952	0.03857	0	285	206	289	223	424	364	353	234	278	338
ENSMUSG00000036006	chr13	Fam65b	2.5E+07	2.5E+07	11662	-0.61027571	3.67715724	0.0947512	0.1538884	0.15342	0	223	390	124	154	142	242	201	172	261	164
ENSMUSG00000094114	chr13	Gm21967	1.2E+08	1.2E+08	1648	-0.44365682	1.971105193	0.0948147	0.153973709	0.06888	0	65	53	88	62	65	92	71	35	52	93
ENSMUSG00000015837	chr11	Sqstm1	5E+07	5E+07	3356	0.342997499	9.144127888	0.0949064	0.154069069	0.05032	0	5918	4237	10924	7866	10054	14280	13512	9355	14292	14261
ENSMUSG00000016756	chr13	Cmah	2.4E+07	2.4E+07	9972	0.561877426	1.65257873	0.0948883	0.154069069	0.11049	0	26	34	24	32	67	127	66	42	59	88
ENSMUSG00000030399	chr7	Ckm	1.9E+07	1.9E+07	1415	-0.36839013	14.19830068	0.094896	0.154069069	0.05811	0	302109	243124	348972	346934	351078	296259	374358	237424	476996	310564
ENSMUSG00000103515	chr8	Il17c	1.2E+08	1.2E+08	1990	0.622592284	0.534096685	0.0949436	0.154111688	0.12671	0	10	3	34	19	17	38	34	26	27	41
ENSMUSG00000029613	chr5	Eif2ak1	1.4E+08	1.4E+08	5675	-0.28991742	5.727582657	0.0950123	0.154205328	0.03499	0	880	624	951	950	985	1055	1097	700	1071	1021
ENSMUSG00000031910	chr8	Has3	1.1E+08	1.1E+08	6380	-0.55416106	1.170050381	0.0950856	0.154306511	0.09954	0	34	20	76	26	46	26	48	29	37	39
ENSMUSG00000038240	chr10	Pdss2	4.3E+07	4.3E+07	5963	-0.30896111	4.615211112	0.0952014	0.154463191	0.03823	0	367	233	657	428	411	450	555	341	502	408
ENSMUSG00000039771	chr5	Polr2j	1.4E+08	1.4E+08	1106	0.287649781	4.670905976	0.0952042	0.154463191	0.03284	0	353	280	398	329	348	625	493	483	640	622
ENSMUSG00000046675	chr12	Tmem251	1E+08	1E+08	3369	0.360063434	2.843203199	0.0952868	0.154579256	0.0456	0	86	73	103	98	105	197	159	147	154	158
ENSMUSG00000025979	chr1	Mob4	5.5E+07	5.5E+07	4855	-0.28474642	5.593590771	0.0953303	0.154631918	0.03371	0	789	632	968	770	818	1054	1050	668	871	874
ENSMUSG00000028961	chr4	Pgd	1.5E+08	1.5E+08	6447	0.543374787	5.517272905	0.0953849	0.1547027	0.12471	0	518	344	354	263	1436	1241	914	872	1464	1096
ENSMUSG00000073375	chr17	Lrrc30	6.8E+07	6.8E+07	1759	-0.4276199	6.793321475	0.095448	0.154787165	0.07793	0	1721	1751	2210	2272	1395	1959	3072	1146	2340	1403
ENSMUSG00000033955	chr2	Tnks1bp1	8.5E+07	8.5E+07	6184	0.362722391	5.510347313	0.0955149	0.154867643	0.05537	0	434	392	666	457	1161	1274	954	868	1121	1063
ENSMUSG00000055866	chr1	Per2	9.1E+07	9.1E+07	5856	-0.76205585	1.420435576	0.0955197	0.154867643	0.21631	0	40	9	83	17	120	54	37	33	28	45
ENSMUSG00000000876	chr2	Pxmp4	1.5E+08	1.5E+08	3114	-0.2812547	4.568079455	0.0956866	0.155102325	0.03132	0	399	257	574	327	434	512	457	360	463	411
ENSMUSG00000003849	chr8	Nqo1	1.1E+08	1.1E+08	1553	-0.30858166	4.166319556	0.095682	0.155102325	0.03793	0	346	232	323	268	308	356	423	232	340	309
ENSMUSG00000030583	chr7	Sipa1l3	2.9E+07	2.9E+07	16555	-0.36814222	2.782563451	0.0957112	0.155124273	0.04936	0	110	84	135	99	155	143	128	69	145	137
ENSMUSG00000001552	chr11	Jup	1E+08	1E+08	6436	0.337237555	6.705232347	0.0957316	0.155139344	0.04846	0	1067	806	1854	1717	1686	2249	2540	1884	2583	2722
ENSMUSG00000030213	chr6	Atf7ip	1.4E+08	1.4E+08	19678	-0.26459187	5.107910351	0.095752	0.15515456	0.02843	0	518	367	773	609	608	794	718	456	625	668
ENSMUSG00000026664	chr2	Phyh	4919019	4919144	1893	-0.44022983	8.139188749	0.0957712	0.155167722	0.08298	0	4080	2035	9969	4968	4878	4997	6997	3566	3936	5375
ENSMUSG00000034487	chr9	Kdelc2	5.3E+07	5.3E+07	3644	0.425022721	3.572157534	0.0958691	0.155308347	0.07132	0	171	132	113	100	233	422	223	225	259	275
ENSMUSG00000031398	chrX	Plxna3	7.4E+07	7.4E+07	7880	0.641976364	1.275481884	0.0959006	0.155323569	0.1369	0	25	32	14	22	37	109	37	41	48	60
ENSMUSG00000033931	chr8	Rbm34	1.3E+08	1.3E+08	3429	-0.39201555	2.827981806	0.0958903	0.155323569	0.05751	0	97	110	148	90	155	175	121	107	100	125
ENSMUSG00000026200	chr1	Glb1l	7.5E+07	7.5E+07	5905	0.657526295	1.521547802	0.0959189	0.155335201	0.15689	0	32	31	16	15	65	125	62	56	51	58
ENSMUSG00000057286	chr11	St6galnac2	1.2E+08	1.2E+08	7090	0.38640137	2.584806551	0.0959415	0.155353835	0.05338	0	59	66	100	56	107	157	137	111	131	152
ENSMUSG00000068706	chr15	Gm10250	5120602	5121172	571	0.38372345	5.134407107	0.0959528	0.155354306	0.06209	0	358	198	873	555	420	759	818	679	834	975
ENSMUSG00000010936	chr8	Vac14	1.1E+08	1.1E+08	3028	0.287813491	5.01606973	0.0960319	0.155446399	0.03404	0	360	284	615	431	553	645	878	517	821	808
ENSMUSG00000027955	chr3	Fam198b	8E+07	8E+07	9598	0.292307957	4.324068853	0.0960209	0.155446399	0.03374	0	234	215	350	205	361	505	449	352	514	446
ENSMUSG00000016940	chr11	Kctd2	1.2E+08	1.2E+08	3009	0.291580344	4.46050722	0.0961974	0.1556964	0.03438	0	254	172	383	280	443	575	457	386	510	568
ENSMUSG00000036983	chr17	Tfb1m	3519263	3519795	1327	-0.36877609	2.922025902	0.0962121	0.155702148	0.05136	0	124	116	139	127	119	166	136	118	129	124
ENSMUSG00000097820	chr9	E530011L22Rik	1.2E+08	1.2E+08	3304	0.632999316	0.715101129	0.0963447	0.155898743	0.13769	0	11	6	42	23	12	37	35	32	50	35
ENSMUSG00000021171	chr12	Esyt2	1.2E+08	1.2E+08	5539	0.28703683	5.53147345	0.0965299	0.156180417	0.0343	0	580	457	802	598	725	1442	1122	808	866	1049
ENSMUSG00000031349	chrX	Nsdhl	7.3E+07	7.3E+07	2853	-0.43971307	3.167966081	0.0965993	0.156274775	0.07594	0	154	111	123	100	296	190	139	130	171	149
ENSMUSG00000020253	chr9	Ppm1m	1.1E+08	1.1E+08	3485	0.61642916	3.432100686	0.0966193	0.156289057	0.15759	0	108	56	81	60	370	384	204	195	256	308
ENSMUSG00000101335	chr9	Gm28229	8.8E+07	8.8E+07	2153	0.51044477	1.154730956	0.0967258	0.156443336	0.08572	0	19	16	31	26	42	47	46	53	39	66
ENSMUSG00000023341	chr16	Mx2	9.8E+07	9.8E+07	3614	0.72245939	0.159144241	0.0967551	0.156472617	0.16353	0	6	5	15	6	27	43	23	10	36	19
ENSMUSG00000025451	chr13	Paip1	1.2E+08	1.2E+08	3456	-0.28929865	5.766071196	0.0967915	0.156513474	0.0352	0	877	675	1116	903	941	1187	1101	852	898	1007
ENSMUSG00000026568	chr1	Mpc2	1.7E+08	1.7E+08	7344	-0.34799969	7.506556276	0.0969382	0.156716735	0.05216	0	2505	1728	5001	3325	3327	3462	4115	2340	3423	3288
ENSMUSG00000034573	chr5	Ptpn13	1E+08	1E+08	8280	0.42519171	2.147141356	0.0969396	0.156716735	0.06264	0	58	39	47	59	74	131	129	81	82	90
ENSMUSG00000019813	chr10	Cep57l1	4.2E+07	4.2E+07	7526	-0.48159654	1.627357867	0.0970064	0.156770617	0.08174	0	68	41	50	54	46	80	49	38	36	59
ENSMUSG00000028060	chr3	2810403A07Rik	8.9E+07	8.9E+07	2999	-0.30176401	4.493123777	0.0969944	0.156770617	0.03692	0	368	302	347	393	437	473	449	362	330	453
ENSMUSG00000058600	chr15	Rpl30	3.4E+07	3.4E+07	3020	0.325403767	7.711218194	0.0970024	0.156770617	0.04566	0	2809	2101	3228	2644	3258	5945	3959	3848	5069	5273
ENSMUSG00000033429	chr7	Mcee	6.4E+07	6.4E+07	824	-0.29032815	4.963103665	0.097059	0.15683745	0.03452	0	507	321	813	506	486	695	611	469	509	612
ENSMUSG00000024900	chr19	Cpt1a	3323301	3323374	4300	0.338288009	4.077796311	0.0972586	0.157141921	0.04611	0	231	157	278	158	310	492	355	326	287	476
ENSMUSG00000022685	chr16	Parn	1.4E+07	1.4E+07	2902	0.327033448	3.657901625	0.097287	0.15716155	0.04163	0	131	122	184	158	254	343	252	232	328	282
ENSMUSG00000036138	chr9	Acaa1a	1.2E+08	1.2E+08	4414	0.302978242	4.987179061	0.0972932	0.15716155	0.03838	0	341	238	539	401	696	832	645	571	815	744
ENSMUSG00000031871	chr8	Cdh5	1E+08	1E+08	3986	-0.36156773	6.267150768	0.0973049	0.157162386	0.05585	0	943	608	2041	1310	1986	1443	1620	1082	1418	1396
ENSMUSG00000072893	chr11	4933439C10Rik	6E+07	6E+07	5616	0.643432461	1.44269296	0.0973339	0.157191096	0.14904	0	30	33	23	17	46	108	33	35	57	102
ENSMUSG00000038685	chr2	Rtel1	1.8E+08	1.8E+08	6616	-0.34307805	3.159540604	0.0974556	0.157369664	0.04525	0	129	126	162	146	180	218	139	111	186	160
ENSMUSG00000055900	chr4	Tmem69	1.2E+08	1.2E+08	2069	-0.30411232	4.209665205	0.0975263	0.157465598	0.03692	0	314	207	428	333	261	384	336	268	356	359
ENSMUSG00000084020	chr11	Wsb2-ps	6.3E+07	6.3E+07	1217	0.463021055	1.628514662	0.0975611	0.157503623	0.0742	0	28	21	49	37	59	70	105	42	77	66
ENSMUSG00000027811	chr3	4930579G24Rik	8E+07	8E+07	1970	-0.49412826	1.01053257	0.0975942	0.157538909	0.07583	0	28	33	26	36	44	40	37	23	35	31
ENSMUSG00000032735	chr18	Ablim3	6.2E+07	6.2E+07	4560	-0.35246684	4.463266419	0.0976679	0.157625891	0.05081	0	324	174	513	301	642	390	504	291	411	404
ENSMUSG00000042541	chr6	Shfm1	6557294	6558491	1472	0.316536014	6.427690108	0.0976705	0.157625891	0.04296	0	1118	828	1539	1049	1300	2524	1621	1712	1986	1980
ENSMUSG00000054091	chr3	1810037I17Rik	1.2E+08	1.2E+08	1131	0.365306008	5.320443416	0.0977948	0.157808382	0.05693	0	401	256	1021	560	518	1123	843	738	804	1137
ENSMUSG00000023456	chr6	Tpi1	1.2E+08	1.2E+08	2209	-0.33606107	11.2115695	0.0978657	0.157904513	0.04925	0	37117	28681	48920	40814	45406	42383	54163	29715	51254	40308
ENSMUSG00000042520	chr3	Ubap2l	9E+07	9E+07	5446	-0.30782653	6.109010886	0.0978976	0.157919679	0.04053	0	1025	830	1500	1315	1105	1370	1470	882	1373	1316
ENSMUSG00000082029	chr2	H3f3c	1.2E+08	1.2E+08	411	-0.74134817	-0.22637384	0.0978949	0.157919679	0.16705	0	24	15	7	12	11	11	22	6	10	11
ENSMUSG00000028128	chr3	F3	1.2E+08	1.2E+08	1876	0.576607299	3.343933046	0.0980028	0.15803494	0.13768	0	101	89	64	74	292	373	186	233	155	291
ENSMUSG00000042275	chr13	Pelo	1.2E+08	1.2E+08	1600	0.30654632	3.911414529	0.0979831	0.15803494	0.03728	0	163	137	271	179	280	376	291	277	388	369
ENSMUSG00000091561	chr18	Gm6665	3.2E+07	3.2E+07	258	0.708293499	0.134159817	0.097992	0.15803494	0.13192	0	15	11	3	11	14	31	16	20	28	30
ENSMUSG00000024050	chr17	Wiz	3.2E+07	3.2E+07	9204	-0.28025637	4.720754349	0.0980709	0.158126505	0.03225	0	384	377	418	447	522	514	556	367	527	492
ENSMUSG00000022568	chr15	Scrib	7.6E+07	7.6E+07	5736	-0.26961469	4.939310978	0.0981103	0.158171834	0.02986	0	445	337	631	598	535	664	590	391	656	590
ENSMUSG00000028779	chr4	Pef1	1.3E+08	1.3E+08	1915	0.310941903	5.424116656	0.0982054	0.158307002	0.04109	0	478	314	679	593	918	1002	1072	728	1126	979

ENSMUSG00000037197	chr2	Rbm17	1.2E+07	1.2E+07	2405	0.2727816	5.265458667	0.0982543	0.158367638	0.03097	0	479	386	647	457	680	1028	789	690	846	987
ENSMUSG00000024576	chr18	Csnk1a1	6.2E+07	6.2E+07	10502	-0.32057767	7.686705464	0.0982879	0.158403621	0.04467	0	3188	2573	4488	3142	4007	4382	4764	3020	3385	3423
ENSMUSG00000102615	chr8	RP23-81K14.2	1.5E+07	1.5E+07	4097	0.815692564	-0.25204162	0.0983083	0.15841826	0.17571	0	3	10	5	2	19	27	17	15	15	21
ENSMUSG00000002032	chr9	Tmem25	4.5E+07	4.5E+07	2902	-0.46306463	3.358254285	0.0983796	0.158514882	0.08671	0	116	85	369	177	193	165	282	102	158	189
ENSMUSG00000030470	chr7	Csrp3	4.9E+07	4.9E+07	973	1.28507864	6.79804213	0.098521	0.158699862	0.6803	0	512	4	2004	2559	120	4463	2407	1993	1742	6012
ENSMUSG00000064358	chrMT	mt-Co3	8607	9390	784	-0.65257022	4.593136081	0.0985283	0.158699862	0.18159	0	289	180	391	872	536	193	835	126	486	343
ENSMUSG00000083863	chr2	Gm13341	2.3E+07	2.3E+07	672	-0.65846857	1.460496062	0.0985281	0.158699862	0.16444	0	37	35	62	62	52	11	67	21	54	61
ENSMUSG00000028538	chr4	St3gal3	1.2E+08	1.2E+08	2768	-0.33470239	6.305704296	0.0986379	0.158858038	0.04829	0	1105	846	1987	1583	1248	1376	1704	1028	1633	1500
ENSMUSG00000021390	chr13	Ogn	5E+07	5E+07	2540	-0.4403152	6.131314607	0.0986595	0.158874614	0.08403	0	1092	1444	956	952	1346	1949	1679	731	1004	958
ENSMUSG00000028070	chr3	Apoa1bp	8.8E+07	8.8E+07	908	0.298695209	5.467822615	0.0986753	0.158881814	0.03784	0	499	395	725	606	819	1043	875	772	1246	1086
ENSMUSG00000020910	chr11	Adprm	6.7E+07	6.7E+07	1977	0.370570121	2.712329226	0.0988286	0.159110337	0.05206	0	86	48	121	78	100	193	144	140	128	141
ENSMUSG00000030795	chr7	Fus	1.3E+08	1.3E+08	5690	0.335345974	6.956316993	0.09886	0.159142625	0.04889	0	1392	1092	1977	1463	2559	3621	2337	2224	2921	3250
ENSMUSG00000027323	chr2	Rad51	1.2E+08	1.2E+08	6649	0.596534117	0.413302077	0.0989292	0.159217498	0.09712	0	18	8	10	13	24	43	25	20	38	26
ENSMUSG00000097368	chr5	Gm10390	1.2E+08	1.2E+08	8066	-0.82103785	0.910571259	0.098925	0.159217498	0.25355	0	32	7	85	32	28	12	45	8	23	47
ENSMUSG00000090175	chr1	Ugt1a9	8.8E+07	8.8E+07	2190	0.982381905	3.700201357	0.0989649	0.159256677	0.40398	0	138	82	21	8	430	450	325	255	411	335
ENSMUSG00000012126	chr4	Ubxn11	1.3E+08	1.3E+08	4742	0.696074568	0.492961874	0.0990382	0.159356446	0.15781	0	10	6	18	11	32	31	22	13	44	56
ENSMUSG00000047676	chr3	Rpsa-ps10	1.5E+08	1.5E+08	1031	0.331527011	7.216747135	0.0990514	0.159359317	0.04782	0	1763	1618	1964	2120	2389	3898	3040	2495	4087	3659
ENSMUSG00000036639	chr5	Nudt1	1.4E+08	1.4E+08	1390	0.405149413	2.702599542	0.099124	0.159457953	0.06084	0	72	69	72	81	119	194	124	96	194	153
ENSMUSG00000009566	chr2	Fpgs	3.3E+07	3.3E+07	3802	0.375012531	3.231929146	0.0991967	0.159556597	0.05492	0	96	93	115	114	197	251	173	180	256	218
ENSMUSG00000027835	chr3	Pdcd10	7.6E+07	7.6E+07	2939	-0.35655438	3.390542277	0.0994744	0.159984861	0.05062	0	166	153	190	143	224	261	238	148	159	144
ENSMUSG00000014668	chr5	Chfr	1.1E+08	1.1E+08	3169	-0.27943642	4.092294694	0.0995782	0.160115119	0.03084	0	250	214	369	272	306	378	347	258	294	308
ENSMUSG00000073627	chr1	C130036L24Rik	8.6E+07	8.6E+07	6437	0.568040001	0.578733882	0.0995731	0.160115119	0.09396	0	12	13	13	15	31	33	32	25	47	32
ENSMUSG00000083458	chr19	Gm5510	6152715	6153200	486	0.567383152	0.519007708	0.0996976	0.160288625	0.08462	0	9	16	16	19	19	31	32	26	41	31
ENSMUSG00000029767	chr6	Calu	2.9E+07	2.9E+07	4733	0.317469459	7.428858256	0.0997754	0.160395341	0.04413	0	2185	1579	2998	2255	2699	5563	4044	3099	3551	3648
ENSMUSG00000044937	chr10	BC030307	8.7E+07	8.7E+07	4646	-0.50278111	1.351962023	0.099796	0.160410113	0.08393	0	39	37	69	45	27	43	50	30	49	39
ENSMUSG00000062270	chr9	Morf4l1	9E+07	9E+07	9754	-0.32642023	6.992456757	0.0999121	0.160578373	0.04661	0	2389	1669	2361	1868	2313	2898	2759	1875	2121	2056
ENSMUSG00000000148	chr5	Brat1	1.4E+08	1.4E+08	6179	0.333053576	3.254676875	0.1000357	0.160740134	0.04251	0	94	87	157	139	162	270	191	182	216	226
ENSMUSG00000090165	chr1	Ugt1a10	8.8E+07	8.8E+07	2267	0.968542038	3.696364032	0.1000339	0.160740134	0.39495	0	138	83	21	9	430	447	321	252	411	335
ENSMUSG00000020682	chr11	Mmp28	8.3E+07	8.3E+07	3874	-0.65387373	1.716087482	0.1001046	0.16083244	0.16802	0	48	33	29	34	163	59	62	36	50	51
ENSMUSG00000034930	chr6	Rtkn	8.3E+07	8.3E+07	3943	0.309727897	4.216976305	0.1001193	0.160837591	0.03832	0	222	212	254	283	257	528	426	269	511	407
ENSMUSG00000030216	chr6	Wbp11	1.4E+08	1.4E+08	5029	-0.27846652	5.277164106	0.1001628	0.160889021	0.03264	0	562	410	959	620	723	734	849	535	743	761
ENSMUSG00000018372	chr11	Cep95	1.1E+08	1.1E+08	4199	-0.3905346	2.331812977	0.1004592	0.161346653	0.05569	0	93	62	106	79	83	111	107	64	65	99
ENSMUSG00000028099	chr3	Polr3c	9.7E+07	9.7E+07	3386	-0.25465864	4.680155895	0.1004911	0.161379405	0.0265	0	372	314	540	403	484	524	569	334	484	514
ENSMUSG00000037096	chr3	Gm9762	7.9E+07	7.9E+07	441	-0.49540194	1.190197536	0.1006908	0.161681631	0.08205	0	41	30	44	35	43	27	57	21	44	40
ENSMUSG00000030741	chr7	Spns1	1.3E+08	1.3E+08	3707	0.270526174	4.972761122	0.1007261	0.161719889	0.03055	0	385	290	479	444	567	799	650	503	872	728
ENSMUSG00000035186	chr17	Ubd	3.7E+07	3.7E+07	931	1.449459385	-0.04334723	0.100766	0.161765295	0.77733	0	6	4	0	1	23	80	1	9	7	36
ENSMUSG00000018381	chr11	Abi3	9.6E+07	9.6E+07	4153	0.608750887	2.171931784	0.100965	0.162066202	0.15249	0	26	15	119	37	89	109	76	75	141	145
ENSMUSG00000043372	chr11	Hexim2	1E+08	1E+08	2373	-0.41512414	1.834839523	0.1009833	0.162077103	0.05853	0	50	44	71	50	89	66	65	46	76	55
ENSMUSG00000036622	chr4	Atp13a2	1.4E+08	1.4E+08	6000	-0.28059508	5.01980513	0.1010083	0.16209868	0.03327	0	485	406	610	565	613	594	746	402	743	553
ENSMUSG00000021532	chr13	Fastkd3	6.9E+07	6.9E+07	2362	-0.327276	3.313678546	0.1011457	0.162300663	0.04154	0	163	107	192	198	171	204	216	144	167	173
ENSMUSG00000050064	chr3	Zfp697	9.8E+07	9.8E+07	5163	0.638317577	-0.08756499	0.101179	0.162335509	0.10472	0	5	8	10	7	19	31	19	16	14	24
ENSMUSG00000022679	chr16	Mpv17l	1.4E+07	1.4E+07	3760	0.51090808	1.131877862	0.1011932	0.162339674	0.08076	0	23	24	25	34	20	46	57	44	54	48
ENSMUSG00000030643	chr7	Rab30	9.3E+07	9.3E+07	2116	0.454729742	1.998012686	0.1012213	0.162366119	0.07316	0	29	47	43	52	74	116	94	66	101	89
ENSMUSG00000061028	chr7	Clasrp	2E+07	2E+07	2153	0.353839461	3.584101496	0.1012386	0.162375306	0.04953	0	150	145	150	133	197	286	222	223	311	327
ENSMUSG00000044134	chr5	Fam109a	1.2E+08	1.2E+08	2335	0.325697005	3.285061684	0.1014022	0.162619115	0.04096	0	118	78	166	130	166	250	205	176	265	210
ENSMUSG00000059316	chr2	Slc27a4	3E+07	3E+07	4412	0.301537522	4.215733197	0.1014861	0.162735064	0.03768	0	205	132	347	278	327	506	429	283	497	414
ENSMUSG00000026655	chr2	Fam107b	3613758	3613938	3762	0.610991508	2.906457009	0.1015778	0.162863464	0.15663	0	71	52	64	31	244	246	170	155	155	195
ENSMUSG00000027547	chr2	Sall4	1.7E+08	1.7E+08	5536	-0.54183541	1.122986627	0.101656	0.162970341	0.09687	0	27	20	54	43	48	19	47	26	36	46
ENSMUSG00000032086	chr9	Bace1	4.6E+07	4.6E+07	6348	-0.29380132	5.234427192	0.1016903	0.163006701	0.03702	0	534	537	798	459	805	837	868	509	673	628
ENSMUSG00000026305	chr1	Lrrfip1	9.1E+07	9.1E+07	6469	-0.31563635	6.807649965	0.1017181	0.163032502	0.04396	0	1840	1565	2106	1787	1970	2135	2327	1736	2140	1913
ENSMUSG00000019984	chr10	Med23	2.5E+07	2.5E+07	6692	-0.32985788	3.381750372	0.1017709	0.163098497	0.04318	0	157	120	214	203	179	210	248	118	207	175
ENSMUSG00000087590	chr18	2410004N09Rik	3.4E+07	3.4E+07	430	0.447185195	2.015401335	0.1018957	0.16327987	0.06973	0	48	41	55	43	63	127	59	70	96	118
ENSMUSG00000020111	chr10	Micu1	6E+07	6E+07	9234	0.315407525	6.424879126	0.1019327	0.163320571	0.04381	0	990	688	1754	1273	1210	2089	2144	1384	2114	2156
ENSMUSG00000026834	chr2	Acvr1c	5.8E+07	5.8E+07	9292	-1.37531841	2.043259703	0.1019628	0.163350174	0.76861	0	124	67	1	1	253	70	18	44	39	61
ENSMUSG00000028076	chr3	Cd1d1	8.7E+07	8.7E+07	2570	-1.1267585	3.322653828	0.1019868	0.163369885	0.53593	0	188	127	20	12	734	263	54	121	100	111
ENSMUSG00000031691	chr8	Tnpo2	8.5E+07	8.5E+07	4990	-0.25672911	5.170297042	0.1020285	0.163418016	0.02789	0	569	456	702	522	709	787	668	507	696	737
ENSMUSG00000061104	chr8	Gm10094	9.6E+07	9.6E+07	780	0.392733138	2.572471835	0.1020799	0.163481646	0.0589	0	71	38	79	88	113	144	124	110	136	168
ENSMUSG00000025141	chr11	Myadml2	1.2E+08	1.2E+08	992	-0.31195143	6.251361604	0.1021004	0.16349582	0.04272	0	1137	840	1783	1398	1291	1353	1582	1014	1635	1443
ENSMUSG00000025578	chr11	Cbx8	1.2E+08	1.2E+08	3675	0.411196472	2.26973898	0.1021614	0.163574864	0.06227	0	42	46	60	62	98	132	95	91	107	129
ENSMUSG00000029005	chr4	Draxin	1.5E+08	1.5E+08	5200	0.744657346	-0.06190091	0.102196	0.163603503	0.14451	0	7	12	3	14	9	26	29	15	26	13
ENSMUSG00000030935	chr7	Acsm3	1.2E+08	1.2E+08	4936	-1.67638687	1.889532641	0.1022026	0.163603503	1.119	0	91	5	0	3	362	56	3	20	47	54
ENSMUSG00000001227	chr17	Sema6b	5.6E+07	5.6E+07	3977	0.470883996	2.439593645	0.102243	0.163649392	0.08913	0	35	35	98	61	124	131	116	103	173	110
ENSMUSG00000025510	chr7	Cd151	1.4E+08	1.4E+08	2010	0.326526932	7.186068008	0.1023336	0.163775782	0.04735	0	1798	1337	2186	1604	2997	3762	3335	2402	3822	3495
ENSMUSG00000020848	chr11	Doc2b	7.6E+07	7.6E+07	4361	0.644437679	-0.2256774	0.1023806	0.163832369	0.08609	0	9	7	12	9	6	23	14	13	20	23
ENSMUSG00000031584	chr8	Gsr	3.4E+07	3.4E+07	2754	-0.25839604	5.208372585	0.1024065	0.163855021	0.02833	0	555	448	722	607	714	772	829	543	658	675
ENSMUSG00000043432	chr7	Leng9	4147915	4150374	2460	0.454017319	1.792979581	0.1025219	0.164021052	0.07628	0	39	17	59	49	56	82	72	48	96	105
ENSMUSG00000054693	chr9	Adam10	7.1E+07	7.1E+07	4913	-0.27535385	4.752735793	0.1026378	0.164187669	0.03203	0	427	381	529	388	478	665	562	382	492	430

ENSMUSG00000032114	chr9	Slc37a4	4.4E+07	4.4E+07	2083	-0.38243114	7.186149726	0.1026739	0.16422679	0.06513	0	2366	2123	2206	2204	3404	1960	2894	1911	3625	2596
ENSMUSG00000030268	chr6	Bcat1	1.4E+08	1.5E+08	9322	1.282490721	-0.03560286	0.1026971	0.164237912	0.6429	0	3	0	0	5	32	67	5	17	19	18
ENSMUSG00000089943	chr1	Ugt1a5	8.8E+07	8.8E+07	2203	0.971094331	3.692760926	0.1027089	0.164237912	0.40417	0	138	82	21	8	430	443	321	252	411	335
ENSMUSG00000090171	chr1	Ugt1a2	8.8E+07	8.8E+07	2211	0.971094366	3.692760926	0.102716	0.164237912	0.40418	0	138	82	21	8	430	443	321	252	411	335
ENSMUSG00000006471	chr2	Ndor1	2.5E+07	2.5E+07	5835	-0.31896729	3.261128681	0.1027739	0.164311665	0.03978	0	138	133	182	149	192	199	208	117	186	171
ENSMUSG00000029016	chr4	Clcn6	1.5E+08	1.5E+08	5933	0.337228286	3.617966964	0.1028134	0.164356162	0.04587	0	126	114	170	148	268	365	282	173	299	307
ENSMUSG00000007107	chr1	Atp1a4	1.7E+08	1.7E+08	3667	-0.73996652	0.519617943	0.1028384	0.164377297	0.18648	0	44	16	13	22	30	34	11	28	15	14
ENSMUSG00000006418	chr2	Rnf114	1.7E+08	1.7E+08	3356	-0.32512825	6.058666337	0.1029379	0.164517687	0.04658	0	967	680	1838	1164	1086	1386	1550	804	1205	1237
ENSMUSG00000071252	chr13	2210408I21Rik	7.7E+07	7.7E+07	4558	-0.43204073	1.282428958	0.1030693	0.164708839	0.05762	0	42	26	42	43	51	46	46	28	39	48
ENSMUSG00000050786	chr6	Ccdc126	4.9E+07	4.9E+07	2421	-0.40345032	1.752998508	0.103217	0.164926198	0.05469	0	56	43	71	54	58	74	67	42	46	65
ENSMUSG00000040264	chr3	Gbp5	1.4E+08	1.4E+08	5844	0.657463532	2.465173349	0.1033661	0.165145499	0.17996	0	60	38	57	62	103	382	91	44	73	140
ENSMUSG00000032349	chr9	Elovl5	7.8E+07	7.8E+07	3522	0.413038308	4.41521197	0.1033793	0.165147835	0.07402	0	255	174	254	154	582	681	428	418	494	487
ENSMUSG00000032182	chr9	Yipf2	2.2E+07	2.2E+07	2150	0.37081759	3.309967187	0.1034416	0.165228519	0.05525	0	131	83	115	105	221	304	210	171	246	219
ENSMUSG00000070044	chr8	Fam149a	4.5E+07	4.5E+07	5954	0.573348662	2.187450433	0.1034987	0.165300898	0.13225	0	46	29	37	34	133	180	87	78	89	122
ENSMUSG00000041378	chr16	Cldn5	1.9E+07	1.9E+07	1414	0.560437047	4.764552123	0.1035792	0.165410611	0.13883	0	221	121	259	197	986	713	572	511	746	786
ENSMUSG00000041734	chr3	Kirrel	8.7E+07	8.7E+07	7463	0.402669487	3.847308732	0.1037077	0.165596941	0.06836	0	154	149	139	140	353	503	305	262	312	313
ENSMUSG00000086725	chr11	A630052C17Rik	2.9E+07	2.9E+07	2203	-0.51854715	0.398868798	0.1037218	0.16560067	0.07408	0	26	18	22	18	24	27	25	13	18	22
ENSMUSG00000031256	chrX	Cstf2	1.3E+08	1.3E+08	9180	-0.32535809	3.168833223	0.1037497	0.165626443	0.04092	0	133	112	173	156	175	170	175	144	172	149
ENSMUSG00000091050	chr15	9330020H09Rik	9.9E+07	9.9E+07	2147	0.614734853	-0.00027111	0.1038723	0.165803184	0.09805	0	12	7	15	5	14	28	14	17	30	21
ENSMUSG00000028563	chr4	Tm2d1	9.8E+07	9.8E+07	1124	-0.26388453	4.567886572	0.1039361	0.16587627	0.0289	0	377	282	443	357	499	512	520	364	394	429
ENSMUSG00000093769	chr3	Hist2h3c1	9.6E+07	9.6E+07	1820	-0.39070934	1.874428996	0.1039417	0.16587627	0.05118	0	50	46	82	59	72	68	74	48	71	59
ENSMUSG00000042826	chr11	Fgf11	7E+07	7E+07	3044	0.405599129	3.377849761	0.1040565	0.166040612	0.06645	0	149	122	100	166	104	255	244	180	265	267
ENSMUSG00000012848	chr7	Rps5	1.3E+07	1.3E+07	1734	0.315725541	8.239363029	0.1040822	0.166043722	0.04491	0	3760	3039	4298	4340	4859	8093	6290	5300	7527	7486
ENSMUSG00000076128	chr14	Mir686	5.5E+07	5.5E+07	109	0.280634454	4.511664652	0.1040798	0.166043722	0.03302	0	309	217	415	271	351	612	457	435	600	459
ENSMUSG00000066191	chr4	Anks6	4.7E+07	4.7E+07	5237	0.531706041	1.237227523	0.1042314	0.166262848	0.10401	0	20	14	33	17	60	69	54	46	42	62
ENSMUSG00000060862	chr4	Zbtb40	1.4E+08	1.4E+08	10710	-0.3272569	3.593996767	0.104388	0.166493706	0.04408	0	167	174	224	244	183	265	241	149	237	217
ENSMUSG00000027936	chr3	Crtc2	9E+07	9E+07	4094	0.291830804	4.597119995	0.1044087	0.166507907	0.03623	0	255	217	392	301	510	634	502	363	593	675
ENSMUSG00000024901	chr19	Peli3	4930651	4932867	3786	-0.51583468	1.306775925	0.1044541	0.166544478	0.0975	0	47	35	42	35	51	51	57	16	56	28
ENSMUSG00000078921	chr11	Tgtp2	4.9E+07	4.9E+07	2938	0.832937127	2.101209177	0.1044554	0.166544478	0.29345	0	37	24	81	45	45	390	68	30	31	80
ENSMUSG00000031660	chr8	Brd7	8.8E+07	8.8E+07	5244	-0.30849328	6.132966219	0.1044717	0.166551434	0.04228	0	1064	799	1692	1257	1107	1364	1574	1021	1245	1268
ENSMUSG00000000915	chr5	Hip1r	1.2E+08	1.2E+08	5022	0.392458383	3.921200465	0.1045066	0.166588221	0.06672	0	113	101	364	175	286	292	418	286	383	371
ENSMUSG00000042203	chr17	Tbc1d22b	3E+07	3E+07	4139	-0.30185137	3.902823926	0.1045213	0.166592683	0.03688	0	233	139	358	264	275	290	319	198	314	261
ENSMUSG00000026019	chr1	Wdr12	6E+07	6E+07	11955	-0.26642747	4.606030835	0.1047089	0.16685385	0.02995	0	359	347	465	398	409	512	463	366	469	463
ENSMUSG00000040997	chr14	Abhd4	5.4E+07	5.4E+07	2749	0.281050334	5.424310661	0.1047035	0.16685385	0.03451	0	559	382	659	549	814	1153	896	710	946	1179
ENSMUSG00000032462	chr9	Pik3cb	9.9E+07	9.9E+07	7193	-0.32204581	3.402276599	0.1048358	0.167037103	0.04087	0	149	104	257	182	210	226	233	130	198	186
ENSMUSG00000029638	chr6	Glcci1	8509600	8510319	7756	-0.5135942	2.282634104	0.1048618	0.16705946	0.10528	0	64	61	72	49	190	98	98	58	64	92
ENSMUSG00000021234	chr12	Fam161b	8.4E+07	8.4E+07	4656	-0.66203051	0.587093904	0.1048948	0.167093046	0.14621	0	30	11	49	19	26	31	38	19	16	9
ENSMUSG00000000740	chr8	Rpl13	1.2E+08	1.2E+08	2352	0.330585851	8.168754435	0.1049285	0.167127692	0.04946	0	3341	3053	4284	4097	4394	7749	5170	5234	7776	7158
ENSMUSG00000089675	chr1	Ugt1a8	8.8E+07	8.8E+07	2227	0.965331185	3.696206134	0.1051642	0.167484108	0.40447	0	139	83	21	8	431	443	322	252	411	336
ENSMUSG00000009293	chr10	Ube2g2	7.8E+07	7.8E+07	2431	0.314910703	6.79302786	0.1052143	0.167506876	0.0446	0	1178	1097	2068	1695	1472	2672	3006	1868	2566	2627
ENSMUSG00000021707	chr13	Dhfr	9.2E+07	9.2E+07	5290	-0.38757852	2.307941487	0.1052039	0.167506876	0.05588	0	92	65	85	87	82	114	105	63	86	71
ENSMUSG00000031585	chr8	Gtf2e2	3.4E+07	3.4E+07	2348	0.334040851	3.463383304	0.1052048	0.167506876	0.04443	0	147	124	176	113	165	331	225	215	255	230
ENSMUSG00000018882	chr11	Mrpl45	9.7E+07	9.7E+07	2596	-0.34969396	6.194820449	0.1052417	0.16753154	0.05478	0	972	722	2103	1500	1062	1404	1581	946	1375	1380
ENSMUSG00000023075	chr4	Akirin1	1.2E+08	1.2E+08	3450	-0.28783475	5.130831269	0.105287	0.167576842	0.03606	0	541	476	579	493	804	755	763	552	615	560
ENSMUSG00000029307	chr5	Dmp1	1E+08	1E+08	2760	0.84826505	0.284708276	0.1052941	0.167576842	0.25022	0	18	9	4	8	18	83	20	15	16	18
ENSMUSG00000017550	chr11	Atad5	8E+07	8E+07	7532	-0.64910683	0.608908437	0.1054471	0.167801292	0.15249	0	27	28	40	18	17	31	30	13	8	36
ENSMUSG00000039782	chr5	Cpeb2	4.3E+07	4.3E+07	7122	-0.34586214	4.518424917	0.1055015	0.167830767	0.05218	0	418	317	349	323	501	419	677	257	377	377
ENSMUSG00000048402	chr1	Gli2	1.2E+08	1.2E+08	6869	0.553812613	0.853502036	0.1055014	0.167830767	0.09348	0	14	20	14	21	33	53	33	30	52	40
ENSMUSG00000086370	chrX	Ftx	1E+08	1E+08	7598	-0.60414475	0.925688808	0.105497	0.167830767	0.13575	0	40	32	36	31	21	53	24	12	20	45
ENSMUSG00000016194	chr1	Hsd11b1	1.9E+08	1.9E+08	4251	-0.65475611	3.398523121	0.1055578	0.167901227	0.18669	0	177	78	118	75	583	229	179	147	169	114
ENSMUSG00000026814	chr2	Eng	3.3E+07	3.3E+07	4048	0.318994065	5.651396824	0.1056873	0.168088265	0.04553	0	467	379	1133	624	922	1334	1155	890	1242	1144
ENSMUSG00000038732	chr13	Mboat1	3E+07	3E+07	3474	0.43601004	1.79208291	0.1058197	0.168279686	0.06547	0	49	35	42	45	40	100	69	69	68	90
ENSMUSG00000059511	chr13	Gm20563	6.2E+07	6.2E+07	276	0.450838874	1.335770733	0.1058422	0.168296433	0.06753	0	37	19	35	21	43	62	63	45	51	66
ENSMUSG00000018669	chr11	Cdk5rap3	9.7E+07	9.7E+07	3812	0.284133005	4.663734542	0.1059046	0.168376539	0.03433	0	335	248	358	367	409	669	442	434	667	655
ENSMUSG00000032786	chr9	Alas1	1.1E+08	1.1E+08	4310	-0.41900548	7.36031288	0.1060169	0.168535937	0.07968	0	1639	1291	5443	3162	3538	2819	3908	1935	2912	3068
ENSMUSG00000057110	chr2	Cntrl	3.5E+07	3.5E+07	10334	-0.37146347	3.283778159	0.1060438	0.168559659	0.05816	0	151	173	181	132	163	231	200	95	164	199
ENSMUSG00000051550	chr7	Zfp579	4983483	4983540	4159	0.35884538	3.292186433	0.1061382	0.168690596	0.05252	0	111	91	129	111	207	290	209	135	216	293
ENSMUSG00000005474	chr5	Myl10	1.4E+08	1.4E+08	822	1.209407403	1.844327001	0.1062962	0.16888424	0.61723	0	15	0	97	58	1	191	102	57	35	127
ENSMUSG00000024646	chr18	Cyb5a	8.5E+07	8.5E+07	2143	0.554107383	5.479090552	0.106289	0.16888424	0.13805	0	546	396	225	298	1294	1616	755	915	1158	1040
ENSMUSG00000041560	chr7	Gltscr2	1.6E+07	1.6E+07	1555	0.289778554	5.966788204	0.1062855	0.16888424	0.03762	0	755	513	1220	863	994	1592	1426	1001	1590	1532
ENSMUSG00000064030	chr10	Wibg	1.3E+08	1.3E+08	1285	0.294724312	3.697427711	0.1063637	0.168972347	0.03508	0	148	120	203	177	235	338	275	217	332	307
ENSMUSG00000040040	chr14	Ift88	5.7E+07	5.7E+07	4628	-0.41174277	2.014932368	0.1064404	0.16907507	0.06034	0	78	36	77	66	89	97	81	51	59	66
ENSMUSG00000042807	chr1	Hecw2	5.4E+07	5.4E+07	12947	-0.50441143	1.710494914	0.1067885	0.169573608	0.09512	0	52	41	110	48	35	64	67	42	40	60
ENSMUSG00000047821	chr11	Trim16	6.3E+07	6.3E+07	4568	-0.29618069	5.502245225	0.1067776	0.169573608	0.03889	0	627	484	1139	820	770	987	1020	679	714	805
ENSMUSG00000078676	chr11	Casc3	9.9E+07	9.9E+07	4303	0.251627671	5.093669972	0.1067905	0.169573608	0.02735	0	411	344	561	456	593	813	752	624	768	853
ENSMUSG00000057054	chr11	Inca1	7.1E+07	7.1E+07	1377	-0.43511097	1.904179256	0.1068162	0.169595266	0.0685	0	50	34	94	59	91	67	58	48	57	91
ENSMUSG00000028085	chr3	Gatb	8.6E+07	8.6E+07	4299	-0.29313637	4.280542088	0.1068888	0.169691334	0.03587	0	296	163	448	364	384	401	395	294	348	357

ENSMUSG00000029027	chr4	Dffb	1.5E+08	1.5E+08	2351	0.539630026	1.167144937	0.1069999	0.169839862	0.09464	0	20	26	21	23	39	63	46	32	42	80
ENSMUSG00000055184	chr1	Fam72a	1.3E+08	1.3E+08	2191	0.635364554	-0.05217636	0.1070066	0.169839862	0.10284	0	13	7	11	4	15	30	26	11	16	25
ENSMUSG00000049265	chr5	Kcnk3	3.1E+07	3.1E+07	3810	-1.14899279	2.765258792	0.1070307	0.169858834	0.56997	0	128	39	18	6	573	124	44	59	110	97
ENSMUSG00000049811	chr11	Fam161a	2.3E+07	2.3E+07	4396	0.501635232	1.393361262	0.1070699	0.169901834	0.084	0	26	34	30	21	43	69	70	37	51	80
ENSMUSG00000047238	chrX	Mageh1	1.5E+08	1.5E+08	1410	0.423524839	2.328646041	0.1072321	0.170140002	0.06912	0	62	42	73	39	107	155	98	97	114	117
ENSMUSG00000032092	chr9	Mpzl2	4.5E+07	4.5E+07	3107	-0.67377958	0.700722296	0.1075573	0.170636709	0.1601	0	27	17	14	17	71	33	20	20	24	25
ENSMUSG00000037514	chr2	Pank2	1.3E+08	1.3E+08	4912	-0.2568863	4.512096094	0.1076088	0.170699121	0.02807	0	342	294	404	367	458	538	449	308	413	450
ENSMUSG00000013465	chr2	Nelfb	2.5E+07	2.5E+07	3432	0.245139827	5.096860118	0.1076637	0.170766758	0.02598	0	407	334	569	472	601	944	821	558	778	752
ENSMUSG00000060675	chr19	Pla2g16	7557459	7557564	6396	-0.35480748	7.716855955	0.1077433	0.170873813	0.05781	0	2815	1880	6251	3376	4322	4078	4995	2577	3584	4028
ENSMUSG00000028256	chr3	Odf2l	1.5E+08	1.5E+08	2584	-0.42425435	2.441162215	0.1079746	0.171221151	0.07306	0	110	78	117	68	84	151	109	66	67	87
ENSMUSG00000062526	chr18	Mppe1	6.7E+07	6.7E+07	2007	0.392144273	2.695607183	0.1080471	0.171316884	0.0636	0	63	35	131	86	120	200	169	106	131	149
ENSMUSG00000031734	chr8	Irx3	9.2E+07	9.2E+07	2611	0.468318096	2.702256472	0.1081324	0.171432629	0.09371	0	51	29	180	76	97	161	174	112	166	155
ENSMUSG00000097080	chr18	1700086O06Rik	3.8E+07	3.8E+07	1931	0.595269157	0.44112277	0.1081858	0.171497934	0.11737	0	10	8	18	8	33	44	22	21	33	35
ENSMUSG00000037791	chr11	Phf12	7.8E+07	7.8E+07	4909	-0.28317054	4.106744723	0.1082606	0.17159709	0.03357	0	270	188	383	263	339	359	423	226	303	300
ENSMUSG00000004945	chr17	Tmem242	5410870	5411467	1837	-0.28934561	6.159125478	0.1082827	0.171612765	0.03795	0	1049	813	1649	1217	1278	1428	1514	1026	1347	1331
ENSMUSG00000020846	chr11	Fam101b	7.6E+07	7.6E+07	3512	0.296911982	4.861503754	0.1085388	0.171999228	0.03915	0	305	249	480	334	655	778	590	562	683	674
ENSMUSG00000097039	chr15	Pvt1	6.2E+07	6.2E+07	6996	0.623699477	1.036542642	0.1086294	0.172123372	0.13056	0	21	35	16	13	23	43	51	44	56	45
ENSMUSG00000033364	chr1	Usp37	7.4E+07	7.4E+07	11081	-0.3119302	3.358932891	0.1086769	0.172159675	0.03979	0	161	141	197	171	173	212	216	151	190	168
ENSMUSG00000043004	chr14	Gng2	2E+07	2E+07	4390	0.490231834	3.377064439	0.1086701	0.172159675	0.1023	0	85	147	78	183	118	336	180	160	264	317
ENSMUSG00000031503	chr8	Col4a2	1.1E+07	1.1E+07	6619	0.385127536	7.581657159	0.1087996	0.172334611	0.06859	0	1455	1312	3766	2516	4173	4773	4165	3968	5009	4278
ENSMUSG00000048349	chr14	Pou4f1	1E+08	1E+08	4672	-0.56413606	1.506982632	0.1088337	0.17236912	0.1229	0	32	45	81	53	37	22	66	33	49	58
ENSMUSG00000031012	chrX	Cask	1.4E+07	1.4E+07	9145	-0.31867652	3.539490062	0.1089113	0.172472536	0.04187	0	180	148	196	187	256	218	273	165	174	232
ENSMUSG00000089960	chr1	Ugt1a1	8.8E+07	8.8E+07	2224	0.956220286	3.699857127	0.1089832	0.172567001	0.40625	0	140	83	21	8	435	443	321	254	411	335
ENSMUSG00000024970	chr19	AI846148	7356464	7358487	3183	0.347909421	3.121022099	0.1090983	0.172729799	0.04999	0	95	67	146	130	144	231	157	146	207	256
ENSMUSG00000059824	chr7	Dbp	4.6E+07	4.6E+07	2945	-0.35203961	5.349463925	0.1091899	0.172855236	0.05592	0	729	413	835	488	1071	827	567	711	586	953
ENSMUSG00000025428	chr18	Atp5a1	7.8E+07	7.8E+07	3135	-0.41113501	11.45745133	0.1092027	0.172856037	0.07853	0	36284	22424	92131	59845	43001	48410	64386	36110	48812	52626
ENSMUSG00000027502	chr2	Rtfdc1	1.7E+08	1.7E+08	2644	0.291390967	5.80983109	0.1093343	0.173044744	0.03856	0	671	520	876	656	1149	1464	1209	921	1412	1394
ENSMUSG00000013584	chr9	Aldh1a2	7.1E+07	7.1E+07	2264	0.959497438	1.158997398	0.1094203	0.173152866	0.39351	0	3	7	71	5	35	36	121	53	26	45
ENSMUSG00000053684	chr10	BC048403	1.2E+08	1.2E+08	3136	-0.45105148	1.116282849	0.1094273	0.173152866	0.06672	0	40	25	32	35	49	50	34	24	37	38
ENSMUSG00000026047	chr1	Kdelc1	4.4E+07	4.4E+07	3199	0.384972513	2.539829923	0.1094503	0.173169684	0.05753	0	86	42	86	81	81	199	129	109	122	112
ENSMUSG00000032741	chr5	Tpcn1	1.2E+08	1.2E+08	4645	-0.30103607	6.132022067	0.1094859	0.173206513	0.04138	0	1022	704	1770	1197	1296	1346	1467	912	1349	1447
ENSMUSG00000063388	chr18	BC023105	6E+07	6E+07	1227	-0.55119405	4.556286631	0.10962	0.17339912	0.13829	0	493	454	289	223	563	469	799	292	243	190
ENSMUSG00000025035	chr19	Arl3	4.7E+07	4.7E+07	822	-0.34627267	5.589053321	0.1099675	0.173929228	0.05495	0	949	795	711	605	864	1030	802	710	1025	798
ENSMUSG00000056209	chr19	Npm3	4.6E+07	4.6E+07	1187	0.354007386	3.700379166	0.1100499	0.174039871	0.05265	0	187	161	167	149	167	387	235	272	285	305
ENSMUSG00000028821	chr4	Syf2	1.3E+08	1.3E+08	2043	0.272304426	5.487822024	0.110199	0.174256111	0.03337	0	609	447	715	522	789	1179	937	787	1046	1119
ENSMUSG00000038902	chr3	Pogz	9.5E+07	9.5E+07	9218	-0.27260916	4.291550642	0.11042	0.174585756	0.03185	0	290	264	393	327	327	449	366	313	345	347
ENSMUSG00000057572	chr4	Zbtb8os	1.3E+08	1.3E+08	4500	0.322056606	3.696419025	0.1104354	0.174590491	0.04347	0	183	131	181	131	238	411	271	238	279	283
ENSMUSG00000068391	chr15	Chrac1	7.3E+07	7.3E+07	2353	-0.27643005	5.488845225	0.1104607	0.174610769	0.03464	0	759	592	764	725	830	933	973	646	867	778
ENSMUSG00000026365	chr1	Cfh	1.4E+08	1.4E+08	8383	0.412317477	4.583997495	0.1105743	0.174770712	0.07616	0	218	334	271	252	435	811	888	296	392	520
ENSMUSG00000001729	chr12	Akt1	1.1E+08	1.1E+08	4098	0.313544355	6.181730335	0.1105961	0.1747855	0.04547	0	742	563	1617	985	1155	1976	1686	1290	1663	1710
ENSMUSG00000092310	chr9	Gm20509	7.3E+07	7.3E+07	1016	-0.33992342	2.857991746	0.1107804	0.175057022	0.04576	0	124	78	171	116	122	162	145	104	122	122
ENSMUSG00000054808	chr7	Actn4	2.9E+07	2.9E+07	5026	0.396158645	6.16776783	0.1109609	0.175322475	0.07297	0	598	560	1012	715	2018	1925	1587	1308	1784	1834
ENSMUSG00000033285	chr3	Wdr3	1E+08	1E+08	5218	-0.3055818	3.825608587	0.1110079	0.175375967	0.03977	0	221	199	260	239	243	312	293	231	204	257
ENSMUSG00000034308	chr8	Sdr42e1	1.2E+08	1.2E+08	2957	0.632223399	0.674104047	0.1110323	0.175375967	0.13684	0	12	11	11	13	42	61	32	20	36	40
ENSMUSG00000038502	chr7	Ptov1	4.5E+07	4.5E+07	4212	0.306094265	6.68071448	0.1110223	0.175375967	0.04351	0	1312	913	1523	1498	1735	2517	2138	1638	2865	2602
ENSMUSG00000046152	chr8	Fut10	3.1E+07	3.1E+07	5007	-0.4271713	1.770142115	0.1112491	0.17569872	0.06789	0	67	42	60	60	56	70	81	41	60	43
ENSMUSG00000035640	chr10	Dos	8E+07	8E+07	4996	0.523445993	1.01238748	0.1112931	0.175748325	0.09047	0	18	18	30	32	19	43	44	35	70	38
ENSMUSG00000034758	chr10	Tle6	8.2E+07	8.2E+07	3088	-0.37871889	2.177277622	0.1113298	0.175786494	0.05453	0	70	70	82	70	81	98	74	55	81	93
ENSMUSG00000031112	chrX	Stk26	5.1E+07	5.1E+07	5271	-0.54072445	0.596952351	0.1113717	0.175832866	0.09743	0	39	18	22	16	31	30	29	14	25	23
ENSMUSG00000097061	chr12	9330151L19Rik	6.9E+07	6.9E+07	2546	0.40938301	2.160928263	0.1113927	0.175846296	0.0618	0	50	56	50	56	64	128	96	87	93	108
ENSMUSG00000005823	chr17	Gpr108	5.7E+07	5.7E+07	2095	0.252277958	5.107315217	0.111431	0.175886889	0.0282	0	445	330	527	490	591	915	784	543	886	761
ENSMUSG00000029213	chr5	Commd8	7.2E+07	7.2E+07	3464	-0.29858646	4.406798849	0.1114699	0.175928597	0.03934	0	384	265	410	292	407	545	476	308	289	357
ENSMUSG00000020358	chr11	Hnrnpab	5.2E+07	5.2E+07	2782	0.310967385	7.007478841	0.1115322	0.176006974	0.04518	0	1491	1321	2001	1571	2347	3399	2502	2509	3164	3060
ENSMUSG00000025086	chr19	Trub1	5.7E+07	5.7E+07	6395	-0.33934803	2.819155884	0.1115601	0.176031218	0.04558	0	111	100	142	104	127	143	130	105	117	139
ENSMUSG00000045427	chrX	Hnrnph2	1.3E+08	1.3E+08	4369	-0.30372913	5.470681178	0.111666	0.176178557	0.04234	0	841	588	872	643	708	918	1113	611	723	753
ENSMUSG00000036403	chr5	Cep135	7.7E+07	7.7E+07	7188	-0.49235728	1.043093427	0.111723	0.176248581	0.08464	0	38	29	47	34	24	44	48	19	30	31
ENSMUSG00000031921	chr8	Terf2	1.1E+08	1.1E+08	4597	-0.27204352	4.131462276	0.1117559	0.176280658	0.03179	0	245	240	339	289	321	347	366	233	348	345
ENSMUSG00000040669	chr6	Phc1	1.2E+08	1.2E+08	5297	-0.30099467	3.842604575	0.1121628	0.176902647	0.03853	0	208	180	296	187	332	259	334	197	260	272
ENSMUSG00000027487	chr2	Cdk5rap1	1.5E+08	1.5E+08	3434	-0.3831907	3.497188534	0.1122639	0.177042264	0.06293	0	178	92	362	204	157	233	240	150	196	191
ENSMUSG00000058163	chr11	Gm5431	4.9E+07	4.9E+07	3800	0.701410331	0.006272092	0.1122828	0.177052168	0.12828	0	11	13	8	5	12	37	32	10	18	19
ENSMUSG00000001416	chr3	Cct3	8.8E+07	8.8E+07	6370	0.29668586	6.753270287	0.1123834	0.177170836	0.04122	0	1279	1024	2046	1505	1534	2939	2360	2052	2460	2444
ENSMUSG00000020732	chr11	Rab37	1.2E+08	1.2E+08	5330	0.758828694	-0.1161505	0.1123759	0.177170836	0.19841	0	10	3	8	6	19	37	13	16	6	33
ENSMUSG00000075588	chr11	Hoxb2	9.6E+07	9.6E+07	3488	0.911743607	-0.45944495	0.1124656	0.177280615	0.29514	0	5	1	4	3	20	36	5	9	22	11
ENSMUSG00000035206	chr10	Sppl2b	8.1E+07	8.1E+07	2866	-0.31377704	3.848817622	0.1125202	0.177346742	0.0425	0	172	178	339	275	246	288	320	183	311	226
ENSMUSG00000029687	chr6	Ezh2	4.8E+07	4.8E+07	6197	-0.35218454	2.663927796	0.1125378	0.177354591	0.04998	0	96	97	125	87	119	129	122	91	96	129
ENSMUSG00000033857	chr11	Engase	1.2E+08	1.2E+08	5184	0.440541374	3.009375358	0.1128459	0.17782006	0.08331	0	97	93	80	59	176	243	155	124	234	198
ENSMUSG00000056310	chr5	Tyw1	1.3E+08	1.3E+08	7388	-0.28604597	3.736874177	0.1128669	0.177833184	0.03427	0	187	153	242	239	287	295	269	188	258	228

ENSMUSG00000020544	chr11	Cox11	9.1E+07	9.1E+07	1423	-0.29666206	4.226642428	0.1129136	0.177886824	0.03813	0	246	193	490	314	350	364	425	293	305	335
ENSMUSG00000040479	chr2	Dgkz	9.2E+07	9.2E+07	6270	-0.31513644	5.934597132	0.1131534	0.178244507	0.04649	0	1010	1000	1005	867	1093	1211	1234	756	1184	1286
ENSMUSG00000057531	chr13	Dtnbp1	4.5E+07	4.5E+07	1334	-0.31493635	5.887942542	0.1132765	0.178418369	0.04609	0	758	489	1553	1115	1246	1172	1204	785	1114	1198
ENSMUSG00000043631	chr13	Ecm2	5E+07	5E+07	3596	0.293867818	4.953631068	0.1132993	0.178434275	0.03899	0	395	316	499	354	545	1047	840	459	498	746
ENSMUSG00000022960	chr16	Donson	9.2E+07	9.2E+07	2834	0.524068263	0.76215531	0.1134865	0.178709103	0.08609	0	22	11	25	14	27	46	46	17	35	52
ENSMUSG00000028028	chr3	Alpk1	1.3E+08	1.3E+08	6709	0.566439134	0.494685243	0.1135104	0.178726691	0.09574	0	19	13	15	8	23	48	31	17	28	38
ENSMUSG00000052534	chr1	Pbx1	1.7E+08	1.7E+08	13844	-0.28440349	4.840937591	0.1135947	0.178839248	0.03663	0	401	337	665	553	428	591	563	342	517	679
ENSMUSG00000013236	chr17	Ptprs	5.6E+07	5.6E+07	6970	0.271648312	5.405939347	0.1136297	0.178874315	0.03382	0	531	402	848	571	576	1059	1087	694	1041	923
ENSMUSG00000027076	chr2	Timm10	8.5E+07	8.5E+07	815	0.284347634	4.430188749	0.1138007	0.179123375	0.03605	0	242	185	478	298	292	605	454	370	486	531
ENSMUSG00000021835	chr14	Bmp4	4.6E+07	4.6E+07	2224	0.400137349	2.636933024	0.1138198	0.179133328	0.06446	0	93	64	64	67	104	147	129	104	146	192
ENSMUSG00000028394	chr4	Pole3	6.3E+07	6.3E+07	2040	0.253783159	4.59910868	0.1138645	0.17918366	0.02859	0	308	209	435	317	425	646	523	467	518	549
ENSMUSG00000025666	chrX	Tmem47	8.1E+07	8.1E+07	4025	-0.35871237	3.200684292	0.1139865	0.179355437	0.05583	0	163	141	161	166	120	192	201	127	162	145
ENSMUSG00000020536	chr11	Llgl1	6.1E+07	6.1E+07	4862	0.255825726	4.48579247	0.1140198	0.179387738	0.02857	0	251	221	408	325	345	597	494	374	528	526
ENSMUSG00000039117	chr2	Taf4a	1.8E+08	1.8E+08	4627	-0.31892897	3.347298297	0.1140933	0.179483199	0.04243	0	150	117	247	164	179	212	219	152	145	200
ENSMUSG00000018733	chr11	Pex12	8.3E+07	8.3E+07	3536	-0.31644994	3.587074386	0.1141594	0.179567109	0.04273	0	218	152	212	163	252	254	254	194	183	208
ENSMUSG00000028458	chr4	Tesk1	4.3E+07	4.3E+07	4434	-0.31532868	5.988884035	0.1142315	0.179640169	0.04671	0	879	721	1401	1147	1240	1104	1585	702	1436	1080
ENSMUSG00000054455	chr2	Vapb	1.7E+08	1.7E+08	7131	-0.30544731	7.479365846	0.1142309	0.179640169	0.04442	0	2915	2272	3574	3046	3026	3482	3806	2228	3667	3433
ENSMUSG00000001105	chr11	Ift20	7.9E+07	7.9E+07	1525	0.276017975	4.049540184	0.1143116	0.179746089	0.03237	0	215	180	248	210	266	469	368	297	389	342
ENSMUSG00000002679	chr12	Med6	8.2E+07	8.2E+07	1447	0.335972249	3.210075588	0.1143453	0.17977891	0.04628	0	138	90	115	104	161	250	206	176	222	197
ENSMUSG00000035293	chr12	G2e3	5.1E+07	5.1E+07	7886	-0.47945738	1.413871447	0.1144083	0.179857733	0.08745	0	54	36	60	29	47	51	52	34	26	60
ENSMUSG00000025198	chr19	Erlin1	4.4E+07	4.4E+07	4961	0.371769777	3.343867483	0.1145576	0.180072317	0.05907	0	127	106	103	147	169	329	186	219	206	224
ENSMUSG00000030255	chr6	Sspn	1.5E+08	1.5E+08	4996	-0.31360783	6.380114433	0.1146757	0.180237758	0.04648	0	1343	850	2146	1410	1356	1595	1998	1153	1404	1543
ENSMUSG00000032308	chr9	Ulk3	5.8E+07	5.8E+07	2826	0.367522413	2.587066602	0.1147433	0.18032379	0.05337	0	66	55	99	64	111	202	132	82	132	152
ENSMUSG00000038954	chr17	Supt3	4.5E+07	4.5E+07	4121	0.346902759	3.326694665	0.1147708	0.180346746	0.05262	0	129	67	162	107	217	275	209	192	252	217
ENSMUSG00000034189	chr8	Hsdl1	1.2E+08	1.2E+08	3168	-0.27498766	4.391629713	0.1149762	0.180649364	0.03369	0	352	257	401	341	374	468	498	282	408	314
ENSMUSG00000035051	chr17	Dhx57	8E+07	8E+07	5077	-0.28938775	3.508697697	0.1150251	0.180696839	0.03551	0	181	142	213	193	207	262	235	141	207	217
ENSMUSG00000097204	chr3	Gm17690	9.6E+07	9.6E+07	3467	-0.43233599	1.615592023	0.1150322	0.180696839	0.06812	0	43	26	68	57	71	69	57	37	37	64
ENSMUSG00000054469	chr17	Lclat1	7.3E+07	7.3E+07	4689	-0.26217849	4.409661962	0.1151408	0.180847108	0.03011	0	341	234	439	379	360	433	434	332	395	388
ENSMUSG00000021054	chr12	Sgpp1	7.6E+07	7.6E+07	3324	0.253227128	4.635430957	0.1152183	0.180925882	0.0287	0	309	217	446	351	410	638	588	485	483	575
ENSMUSG00000022724	chr16	Mina	5.9E+07	5.9E+07	5290	-0.27523489	4.174546016	0.1152258	0.180925882	0.03289	0	247	197	439	317	311	394	344	267	345	332
ENSMUSG00000024078	chr17	Ttc27	7.5E+07	7.5E+07	2820	-0.29246032	3.504449125	0.1152296	0.180925882	0.03616	0	164	155	231	181	202	259	211	160	202	218
ENSMUSG00000002881	chr1	Nab1	5.2E+07	5.2E+07	4100	-0.32554427	3.945460001	0.1155479	0.181399007	0.04708	0	231	174	306	267	323	328	433	210	245	200
ENSMUSG00000021361	chr13	Tmem14c	4.1E+07	4.1E+07	945	0.282243089	5.985263533	0.1155568	0.181399007	0.03762	0	769	542	1188	791	1125	1707	1339	1151	1546	1430
ENSMUSG00000004637	chr8	Wwox	1.1E+08	1.1E+08	10173	-0.32623624	2.952451447	0.1155918	0.181433523	0.04277	0	109	82	163	150	147	159	137	106	150	151
ENSMUSG00000028322	chr4	Exosc3	4.5E+07	4.5E+07	1324	0.304324591	3.52783887	0.11563	0.181473204	0.03878	0	153	112	165	166	174	355	237	210	239	268
ENSMUSG00000015224	chr4	Cyp2j9	9.7E+07	9.7E+07	3337	0.597100736	0.968324182	0.1159038	0.181882528	0.13126	0	16	20	20	10	45	72	33	24	55	49
ENSMUSG00000031767	chr8	Nudt7	1.1E+08	1.1E+08	5618	-0.37288777	4.465568576	0.1159286	0.181901096	0.06381	0	284	148	726	335	507	543	438	285	318	423
ENSMUSG00000030034	chr6	Ino80b	8.3E+07	8.3E+07	1503	0.345896054	3.395250067	0.1160679	0.182099399	0.05265	0	144	71	202	141	151	242	197	204	302	248
ENSMUSG00000022841	chr16	Ap2m1	2.1E+07	2.1E+07	4172	0.285929961	6.690240239	0.116091	0.182101523	0.03903	0	1300	911	1744	1507	1648	2896	2253	1786	2428	2404
ENSMUSG00000032064	chr9	Dixdc1	5.1E+07	5.1E+07	9971	-0.48758135	1.146598407	0.1161082	0.182101523	0.0869	0	43	34	34	23	51	49	43	31	29	31
ENSMUSG00000074088	chr4	Snrnp40	1.3E+08	1.3E+08	3987	0.271803117	3.938694682	0.1160995	0.182101523	0.03198	0	189	134	296	199	243	443	352	264	343	329
ENSMUSG00000087404	chr11	Gm11752	1.2E+08	1.2E+08	510	-0.95220313	0.371064207	0.116239	0.182286192	0.36434	0	31	42	8	22	6	13	5	22	28	16
ENSMUSG00000034349	chr3	Smc4	6.9E+07	6.9E+07	5210	0.350312315	3.054250694	0.1163102	0.182377556	0.05075	0	119	92	102	89	135	265	202	139	179	173
ENSMUSG00000027954	chr3	Efna1	8.9E+07	8.9E+07	1830	0.282877451	3.946441301	0.1164034	0.182503311	0.03515	0	192	128	275	202	267	434	295	276	333	402
ENSMUSG00000005161	chr8	Prdx2	8.5E+07	8.5E+07	3050	0.34768117	7.698200485	0.1164624	0.182575407	0.05836	0	2277	1391	4955	2997	2748	5444	4819	3683	4930	5197
ENSMUSG00000052658	chr9	5830454E08Rik	1.2E+08	1.2E+08	727	-0.5311264	0.259317059	0.116531	0.182662487	0.07708	0	17	16	23	15	28	22	27	11	17	17
ENSMUSG00000017664	chr2	Slc35c2	1.7E+08	1.7E+08	3914	0.269221618	4.762059446	0.1166329	0.182801817	0.03328	0	288	223	448	379	564	676	633	462	689	599
ENSMUSG00000053091	chr7	Lins	6.7E+07	6.7E+07	5886	-0.35105901	2.650295955	0.1166481	0.18280517	0.05155	0	90	73	109	124	130	145	140	63	112	113
ENSMUSG00000081094	chr8	Rpl19-ps11	1.9E+07	1.9E+07	718	0.286917711	4.247504745	0.1167234	0.182902665	0.03617	0	248	219	304	201	307	491	424	270	505	478
ENSMUSG00000066637	chr12	Ttc32	9029997	9030196	1000	-0.29135517	3.721703	0.116763	0.182923874	0.03666	0	211	162	285	229	201	256	263	188	264	246
ENSMUSG00000070461	chr2	9230112E08Rik	1.8E+08	1.8E+08	3352	-0.35522605	3.116781103	0.1167521	0.182923874	0.05525	0	127	127	196	158	111	168	198	104	159	156
ENSMUSG00000040998	chr3	Npnt	1.3E+08	1.3E+08	5026	0.57745949	3.759776111	0.1169206	0.183150411	0.1576	0	77	46	368	106	303	316	592	214	226	332
ENSMUSG00000041716	chr12	Gm20604	1E+08	1E+08	2795	-0.31797504	3.735473537	0.1169613	0.183193676	0.04392	0	198	128	359	212	244	270	307	198	240	202
ENSMUSG00000004099	chr9	Dnmt1	2.1E+07	2.1E+07	6304	0.307257257	3.751087438	0.1170219	0.183262029	0.04091	0	171	125	251	197	162	380	345	194	353	275
ENSMUSG00000021379	chr13	Id4	4.8E+07	4.8E+07	1660	0.703461011	0.932831238	0.1170311	0.183262029	0.18866	0	11	33	8	12	33	45	32	43	51	55
ENSMUSG00000028893	chr4	Sesn2	1.3E+08	1.3E+08	3475	-0.49843285	2.471915938	0.1171316	0.183367462	0.10814	0	65	60	81	65	231	101	98	75	110	82
ENSMUSG00000037287	chr9	Tbcel	4.2E+07	4.2E+07	5556	-0.30024757	4.202320823	0.1171249	0.183367462	0.04068	0	286	228	474	296	251	384	418	243	312	352
ENSMUSG00000061315	chr10	Naca	1.3E+08	1.3E+08	7034	-0.34212963	8.671573523	0.1171376	0.183367462	0.05681	0	5562	4063	9918	9256	6232	8107	7860	5489	7378	8463
ENSMUSG00000005312	chr13	Ubqln1	5.8E+07	5.8E+07	3686	-0.2800846	6.126916467	0.1173961	0.183731044	0.03735	0	974	795	1459	1188	1447	1424	1419	1070	1349	1236
ENSMUSG00000069255	chr13	Dusp22	3.1E+07	3.1E+07	1743	0.272890406	5.214503845	0.1173834	0.183731044	0.03489	0	453	297	785	538	521	1004	816	664	771	940
ENSMUSG00000002524	chr15	Puf60	7.6E+07	7.6E+07	1912	0.286844406	6.10730777	0.1174296	0.183742329	0.03931	0	757	618	1225	1001	1168	1742	1504	1167	1844	1578
ENSMUSG00000021420	chr13	Fars2	3.6E+07	3.6E+07	2125	-0.34112264	4.643935893	0.1174588	0.183742329	0.05388	0	323	195	819	454	416	488	537	308	448	510
ENSMUSG00000022967	chr16	Ifnar1	9.1E+07	9.1E+07	5879	0.286322609	4.271917595	0.1174435	0.183742329	0.03644	0	244	196	262	228	384	600	482	277	424	437
ENSMUSG00000024383	chr18	Map3k2	3.2E+07	3.2E+07	10791	-0.31505517	3.450472742	0.1174688	0.183742329	0.043	0	192	136	215	174	188	250	250	136	155	220
ENSMUSG00000035704	chr7	Alg8	9.7E+07	9.7E+07	2794	0.462135058	1.827323452	0.1174579	0.183742329	0.08379	0	43	30	34	39	73	127	74	72	59	80
ENSMUSG00000066150	chr4	Slc31a1	6.2E+07	6.2E+07	4280	-0.30328543	4.601123933	0.1175866	0.183906128	0.04217	0	316	245	675	465	367	589	499	351	418	394
ENSMUSG00000029629	chr6	Phf14	1.2E+07	1.2E+07	4547	-0.27155302	4.458024629	0.1176383	0.183966446	0.03307	0	303	220	529	361	443	475	500	283	359	454

ENSMUSG00000021417	chr13	Eci2	3.5E+07	3.5E+07	2615	-0.30741479	6.213327187	0.1176656	0.183988596	0.04525	0	1027	740	2077	1257	1278	1544	1484	1036	1318	1488
ENSMUSG00000015749	chr3	Anp32e	9.6E+07	9.6E+07	3566	-0.29040928	6.676185127	0.1178052	0.184186319	0.04067	0	1776	1251	2147	1554	1769	2062	2178	1412	1813	2072
ENSMUSG00000027603	chr2	Ggt7	1.6E+08	1.6E+08	3264	0.67319627	0.538182639	0.1178193	0.184187896	0.16645	0	8	14	20	10	26	57	13	15	36	52
ENSMUSG00000020264	chr11	Slc36a2	5.5E+07	5.5E+07	3255	-1.20409273	3.801962354	0.1179671	0.184398329	0.66552	0	266	80	13	17	1225	279	50	158	200	176
ENSMUSG00000008129	chr8	4930432K21Rik	8.4E+07	8.4E+07	2406	-0.64439278	0.223339733	0.1182022	0.184745201	0.14751	0	32	9	13	17	28	24	29	6	13	17
ENSMUSG00000024960	chr19	Plcb3	6953714	6954299	4201	0.343434194	4.251724775	0.1183911	0.185019848	0.05484	0	189	162	271	200	479	582	358	335	401	526
ENSMUSG00000059518	chr5	Znhit1	1.4E+08	1.4E+08	1860	0.262314347	4.988773721	0.1184945	0.185160903	0.03182	0	411	323	512	403	533	716	627	587	864	747
ENSMUSG00000026490	chr1	Cdc42bpa	1.8E+08	1.8E+08	21522	-0.26150622	5.025746858	0.1185264	0.185190025	0.03196	0	508	396	685	497	604	759	778	348	579	654
ENSMUSG00000022013	chr14	Dnajc15	7.8E+07	7.8E+07	648	-0.26412695	5.552616138	0.1185421	0.185194011	0.03289	0	731	510	963	699	1022	963	1031	674	903	838
ENSMUSG00000045569	chr18	Mc2r	6.8E+07	6.8E+07	1562	-1.24112297	0.088430294	0.1185661	0.185210824	0.64767	0	28	21	0	0	54	22	7	10	15	7
ENSMUSG00000052305	chr7	Hbb-bs	1E+08	1E+08	863	0.507134061	5.972333402	0.1188575	0.185645323	0.12472	0	200	468	1062	1034	1333	1804	1254	1376	1994	1099
ENSMUSG00000020708	chr11	Psmc5	1.1E+08	1.1E+08	1394	0.298872526	7.516534802	0.1189568	0.185779689	0.04359	0	2496	1867	2843	2405	2753	4607	3974	3419	4540	4253
ENSMUSG00000002058	chr11	Unc119	7.8E+07	7.8E+07	2448	0.46713242	2.885233684	0.1190091	0.185840683	0.09978	0	74	51	98	53	206	194	130	157	206	175
ENSMUSG00000022635	chr15	Zcrb1	9.3E+07	9.3E+07	3074	-0.28283123	6.202966203	0.119037	0.185863705	0.03857	0	1265	897	1391	1200	1333	1469	1563	1113	1297	1407
ENSMUSG00000026142	chr1	Rhbdd1	8.2E+07	8.2E+07	6966	-0.29810087	3.6248011	0.1191259	0.185977839	0.03906	0	204	156	206	209	239	220	281	160	226	252
ENSMUSG00000037366	chr4	Pafah2	1.3E+08	1.3E+08	3616	0.410764927	2.180292464	0.1191373	0.185977839	0.07087	0	56	36	77	32	93	127	94	86	109	104
ENSMUSG00000097413	chr18	A830052D11Rik	3.2E+07	3.2E+07	1130	-0.42180654	2.004486138	0.1191499	0.185977839	0.07163	0	82	48	59	57	92	76	62	63	85	57
ENSMUSG00000017491	chr14	Rarb	1.6E+07	1.6E+07	3034	-0.33641217	3.09283346	0.1192834	0.186165507	0.04873	0	143	106	140	145	175	160	203	108	124	181
ENSMUSG00000020553	chr11	Pctp	9E+07	9E+07	2723	-0.34622733	2.922642344	0.1194148	0.186334792	0.05182	0	110	112	145	114	148	155	187	78	136	137
ENSMUSG00000028914	chr4	Casp9	1.4E+08	1.4E+08	5197	0.368929944	2.668557185	0.1194185	0.186334792	0.05686	0	70	52	94	69	136	217	135	106	130	148
ENSMUSG00000033906	chrX	Zdhhc15	1E+08	1E+08	5509	0.755806239	-0.03410377	0.1194335	0.186337533	0.18191	0	5	15	5	7	14	36	14	21	29	11
ENSMUSG00000030685	chr7	Kctd13	1.3E+08	1.3E+08	2487	0.460093621	1.88964847	0.1195006	0.186421416	0.08725	0	47	25	41	36	84	95	59	70	98	105
ENSMUSG00000032267	chr9	Usp28	4.9E+07	4.9E+07	4220	-0.36254237	6.034296022	0.119672	0.18666816	0.06387	0	903	767	1505	1650	722	1360	1280	929	1102	1259
ENSMUSG00000036353	chr3	P2ry12	5.9E+07	5.9E+07	2379	0.597414107	0.424387429	0.1199583	0.187093934	0.11264	0	8	14	14	15	22	47	43	22	16	26
ENSMUSG00000027523	chr2	Gnas	1.7E+08	1.7E+08	11186	-0.30102883	10.03250296	0.1200562	0.187204937	0.0448	0	16468	11366	21626	17933	21100	20423	22723	14285	19903	19984
ENSMUSG00000032763	chr10	Ilvbl	7.9E+07	7.9E+07	2325	0.324583812	4.036418067	0.1200493	0.187204937	0.04914	0	158	108	352	213	314	476	339	259	353	466
ENSMUSG00000041697	chr5	Cox6a1	1.2E+08	1.2E+08	702	0.613918745	5.924692505	0.1200885	0.187234421	0.18343	0	664	285	437	286	2204	2015	1011	1151	1798	1635
ENSMUSG00000032399	chr9	Rpl4	6.4E+07	6.4E+07	1422	-0.30485508	9.301456933	0.1201308	0.187279531	0.04593	0	10216	8696	11736	10414	11013	13674	12320	8590	12001	12084
ENSMUSG00000028300	chr4	3110043O21Rik	3.5E+07	3.5E+07	4603	-0.27808005	4.469461706	0.1202559	0.187453783	0.03578	0	370	302	345	306	489	473	408	305	407	476
ENSMUSG00000042289	chr7	Hsd3b7	1.3E+08	1.3E+08	6154	0.267083881	5.143978375	0.1203235	0.187517427	0.03357	0	446	350	491	419	733	1014	799	589	758	849
ENSMUSG00000050382	chr7	Kif7	8E+07	8E+07	4581	0.54032679	1.192249714	0.1203235	0.187517427	0.11142	0	20	24	19	20	50	86	38	46	45	51
ENSMUSG00000023007	chr15	Prpf40b	9.9E+07	9.9E+07	4952	-0.25362231	4.423682224	0.1204549	0.187680635	0.02901	0	356	232	422	341	421	411	451	293	439	426
ENSMUSG00000054426	chr3	A930005H10Rik	1.2E+08	1.2E+08	2385	0.309353434	3.914034214	0.120453	0.187680635	0.04255	0	217	161	184	188	248	390	292	233	380	427
ENSMUSG00000042035	chr3	Igsf3	1E+08	1E+08	7389	0.367307142	3.009885264	0.1205444	0.18779909	0.05716	0	110	99	89	112	97	233	176	145	186	186
ENSMUSG00000060149	chr17	BC002059	1.7E+07	1.7E+07	1964	-0.45894285	1.555276321	0.1206397	0.187926805	0.08273	0	68	37	49	41	51	77	57	34	33	51
ENSMUSG00000022668	chr16	Gtpbp8	4.5E+07	4.5E+07	3527	-0.31215249	3.45703892	0.1206984	0.187997242	0.04251	0	164	125	272	186	175	242	236	161	166	202
ENSMUSG00000024935	chr19	Slc1a1	2.9E+07	2.9E+07	6170	0.454303802	2.13751517	0.1207838	0.188109463	0.08691	0	42	32	71	83	47	138	64	78	124	109
ENSMUSG00000021265	chr12	Slc25a29	1.1E+08	1.1E+08	2606	0.361483559	3.689015614	0.1208636	0.188191972	0.05963	0	127	115	250	225	135	357	253	176	337	384
ENSMUSG00000026511	chr1	Srp9	1.8E+08	1.8E+08	5541	0.252628043	4.887926873	0.1208602	0.188191972	0.02976	0	341	279	497	427	515	709	598	520	758	723
ENSMUSG00000051396	chr2	Hspa14	3488850	3489069	8083	0.28633395	4.03155899	0.1211077	0.188551127	0.03736	0	196	139	264	188	345	481	340	285	382	366
ENSMUSG00000038936	chr1	Sccpdh	1.8E+08	1.8E+08	7562	-0.27823333	5.847493305	0.1211494	0.1885951	0.03755	0	1010	768	1106	792	1051	1270	1074	867	1139	1019
ENSMUSG00000101225	chr7	1700008J07Rik	1.3E+08	1.3E+08	2432	-0.3926773	1.758400486	0.1211982	0.188650146	0.05782	0	49	45	57	56	75	59	73	38	58	68
ENSMUSG00000039356	chr2	Exosc2	3.2E+07	3.2E+07	2888	0.303970524	3.508923906	0.1212618	0.188728204	0.04038	0	151	116	179	121	198	276	257	231	262	249
ENSMUSG00000081111	chr8	Gm5913	9.7E+07	9.7E+07	1399	-0.5596678	0.248535634	0.1214419	0.188987396	0.0898	0	23	12	28	19	17	17	19	18	24	12
ENSMUSG00000026429	chr1	Ube2t	1.3E+08	1.3E+08	4832	-0.58190439	1.086139147	0.1215187	0.189086026	0.12786	0	30	17	84	34	27	26	49	29	34	28
ENSMUSG00000005621	chr7	Zfp592	8.1E+07	8.1E+07	7412	-0.27358488	4.321423342	0.1217211	0.189379913	0.03401	0	303	205	472	350	343	380	454	301	385	338
ENSMUSG00000037656	chr8	Slc20a2	2.2E+07	2.2E+07	3649	-0.35559197	6.563368892	0.1217707	0.189436047	0.06239	0	1467	921	2821	1792	1210	1877	2260	1180	1503	1831
ENSMUSG00000041773	chr13	Enc1	9.7E+07	9.7E+07	4742	0.659885253	2.913342384	0.1218536	0.189544031	0.20785	0	56	47	46	29	283	202	195	160	172	202
ENSMUSG00000037373	chr5	Ctbp1	3.3E+07	3.3E+07	2288	-0.29918769	7.417670555	0.1220871	0.189865191	0.04444	0	2606	2025	3421	3116	3126	3218	3864	2279	3505	3030
ENSMUSG00000038417	chr10	Fig4	4.1E+07	4.1E+07	3263	-0.30642126	3.496088302	0.1220864	0.189865191	0.04179	0	148	137	217	192	250	245	279	134	202	188
ENSMUSG00000062743	chr17	Zfp677	2.1E+07	2.1E+07	2917	-0.6483495	0.063286261	0.1221512	0.18994369	0.14067	0	17	15	20	10	26	17	33	7	8	13
ENSMUSG00000052296	chr7	Ppp6r1	4631501	4632244	3787	-0.30049054	6.376946498	0.1222351	0.19005319	0.0445	0	1154	937	1897	1644	1360	1713	1963	1017	1512	1573
ENSMUSG00000026917	chr2	Wdr5	2.8E+07	2.8E+07	3596	-0.24908291	5.055901206	0.1223353	0.190187823	0.02939	0	532	413	680	570	516	755	695	480	633	583
ENSMUSG00000020911	chr11	Krt19	1E+08	1E+08	1855	0.581654543	0.365892032	0.1224103	0.190283387	0.10533	0	7	11	23	18	12	40	36	12	34	26
ENSMUSG00000020357	chr11	Flt4	5E+07	5E+07	8232	0.380964663	3.151849922	0.1226907	0.190676922	0.06651	0	55	68	181	134	160	227	230	142	196	238
ENSMUSG00000029066	chr4	Mrpl20	1.6E+08	1.6E+08	1664	0.252552079	5.233859692	0.1226778	0.190676922	0.03064	0	464	310	683	493	702	1036	835	684	807	860
ENSMUSG00000006218	chr4	Fam131c	1.4E+08	1.4E+08	1433	-1.20759243	0.66266524	0.1228621	0.190922168	0.64815	0	7	0	137	26	8	14	20	5	11	43
ENSMUSG00000008333	chr2	Snrpb2	1.4E+08	1.4E+08	2857	0.314049734	3.994049961	0.1228964	0.19095436	0.04487	0	208	196	211	184	247	483	296	331	333	359
ENSMUSG00000018040	chr15	Rrp7a	8.3E+07	8.3E+07	5411	0.256159046	5.201670039	0.1229567	0.191026913	0.03111	0	447	401	500	555	605	918	880	639	859	835
ENSMUSG00000032782	chr11	Cntrob	6.9E+07	6.9E+07	6660	0.455225442	1.816415679	0.1230117	0.191091092	0.08878	0	49	17	56	31	72	81	66	79	87	87
ENSMUSG00000003746	chr10	Man1a	5.4E+07	5.4E+07	9058	0.34445341	4.352351433	0.1231128	0.191226999	0.05597	0	236	246	210	213	433	627	595	355	385	409
ENSMUSG00000027714	chr3	Exosc9	3.7E+07	3.7E+07	4711	0.266815346	4.268153928	0.1231403	0.191227343	0.03295	0	242	167	384	234	315	529	455	356	364	461
ENSMUSG00000037339	chr5	Fam53a	3.4E+07	3.4E+07	9110	-0.26784277	5.895210888	0.1231315	0.191227343	0.03508	0	795	682	1299	1035	1162	1241	1218	788	1269	1091
ENSMUSG00000005667	chr6	Mthfd2	8.3E+07	8.3E+07	2722	0.510882525	4.251276544	0.1231835	0.191273335	0.1281	0	130	117	494	86	454	397	430	394	588	458
ENSMUSG00000037999	chr5	Arap2	6.3E+07	6.3E+07	8716	-0.41974431	1.935408329	0.1233491	0.191509293	0.0729	0	71	43	67	49	96	105	76	45	47	63
ENSMUSG00000090035	chr10	Galnt4	9.9E+07	9.9E+07	5089	0.398804377	2.339247135	0.12341	0.191582628	0.06992	0	54	28	84	80	86	177	94	93	113	108
ENSMUSG00000031729	chr8	Ist1	1.1E+08	1.1E+08	2341	0.265208979	5.536799305	0.1235427	0.191767351	0.03427	0	540	410	830	601	868	1229	984	772	1046	1220

ENSMUSG00000011254	chr11	Thg1l	4.6E+07	4.6E+07	3015	0.363085114	3.049013902	0.1235656	0.191781737	0.05787	0	109	82	97	91	160	243	142	168	190	201
ENSMUSG00000024044	chr17	Epb4.1l3	6.9E+07	6.9E+07	4109	0.426255849	1.409081166	0.1236762	0.191932091	0.0652	0	25	25	32	35	47	87	61	39	52	66
ENSMUSG00000031432	chrX	Prps1	1.4E+08	1.4E+08	1993	-0.25952108	5.41962744	0.1237099	0.191939108	0.0327	0	719	563	761	665	776	928	901	628	760	810
ENSMUSG00000089911	chr3	Hiat1	1.2E+08	1.2E+08	4087	-0.27547631	3.910889177	0.1237168	0.191939108	0.03427	0	227	186	309	219	304	321	361	212	238	273
ENSMUSG00000090258	chr12	Churc1	7.7E+07	7.7E+07	5693	0.247972286	5.201578166	0.1237218	0.191939108	0.02949	0	479	336	729	468	563	996	802	650	835	842
ENSMUSG00000064373	chr15	Sepp1	3268547	3268768	2845	0.356967451	8.246462997	0.1238951	0.192186696	0.06404	0	4308	3354	3630	2879	5769	10765	8236	4717	6109	6147
ENSMUSG00000002228	chr3	Ppm1j	1E+08	1E+08	1721	-0.26017438	5.448523945	0.1240198	0.192358895	0.03285	0	656	511	881	666	911	844	907	571	959	837
ENSMUSG00000044349	chr2	Snhg11	1.6E+08	1.6E+08	8521	-1.12591333	0.958997867	0.1242455	0.192687698	0.58432	0	34	29	1	6	128	59	14	16	9	27
ENSMUSG00000029610	chr5	Aimp2	1.4E+08	1.4E+08	1654	-0.36119751	6.966782345	0.1243006	0.192735559	0.06548	0	2391	1796	1850	1737	2658	1758	2882	1537	2946	2192
ENSMUSG00000044285	chr14	Gm1821	4.6E+07	4.6E+07	690	-0.38376859	3.289133757	0.1243039	0.192735559	0.0678	0	134	123	334	108	152	209	168	139	185	168
ENSMUSG00000023909	chr17	Paqr4	2.4E+07	2.4E+07	2507	0.499886304	3.190011095	0.1243234	0.192744547	0.12019	0	87	44	102	68	300	252	224	171	239	204
ENSMUSG00000045482	chr5	Trrap	1.4E+08	1.4E+08	15185	-0.25110726	4.834801634	0.1243737	0.192801221	0.02994	0	450	318	606	502	474	611	582	345	629	547
ENSMUSG00000029199	chr5	Lias	6.5E+07	6.5E+07	4570	-0.26332745	5.557458814	0.1243956	0.192813941	0.03375	0	688	473	1081	806	910	974	1032	654	853	923
ENSMUSG00000092607	chr3	Scnm1	9.5E+07	9.5E+07	1885	0.251377471	4.369074581	0.1244514	0.192879059	0.02898	0	249	202	372	294	312	503	458	337	493	525
ENSMUSG00000024425	chr18	Ndfip1	3.8E+07	3.8E+07	930	-0.2684948	5.289693766	0.1244948	0.192925011	0.03509	0	624	487	824	553	749	947	947	524	667	617
ENSMUSG00000061723	chr7	Tnnt3	1.4E+08	1.4E+08	1391	-0.30763612	14.09766149	0.1245928	0.193055587	0.04799	0	287165	222375	340911	278103	335086	317077	381753	234046	372241	317883
ENSMUSG00000029279	chr5	Brdt	1.1E+08	1.1E+08	5115	0.525858495	1.243567306	0.1247196	0.19323058	0.10131	0	29	32	16	21	36	66	45	40	57	67
ENSMUSG00000103766	chr3	RHBG	8.8E+07	8.8E+07	1524	0.593990745	0.946139779	0.1248024	0.193337506	0.13673	0	23	17	15	26	26	43	20	46	38	73
ENSMUSG00000059291	chr4	Rpl11	1.4E+08	1.4E+08	2697	0.30019709	7.162272467	0.1248442	0.193380939	0.04528	0	1920	1560	2144	1672	2351	4181	2869	2620	3392	3295
ENSMUSG00000030691	chr7	Fchsd2	1E+08	1E+08	9199	0.335718494	3.145423356	0.1248614	0.193386248	0.04977	0	125	78	123	88	176	277	196	141	191	214
ENSMUSG00000006526	chr14	Tmem110	3.1E+07	3.1E+07	4058	-0.32059518	3.851814403	0.1249193	0.193454575	0.04762	0	258	171	233	170	382	286	259	223	265	279
ENSMUSG00000000031	chr7	H19	1.4E+08	1.4E+08	2372	0.736860233	10.52565229	0.1250333	0.193609669	0.27049	0	8971	4856	26914	41999	2966	41652	35931	30533	38665	43260
ENSMUSG00000002820	chr9	Atg4d	2.1E+07	2.1E+07	2541	-0.31165914	5.803099066	0.1250935	0.193673451	0.04825	0	712	559	1374	1137	993	1029	1305	607	1217	1051
ENSMUSG00000055254	chr13	Ntrk2	5.9E+07	5.9E+07	13806	-0.7691597	4.152041863	0.1251021	0.193673451	0.29058	0	280	342	59	74	926	410	194	241	258	251
ENSMUSG00000026172	chr1	Bcs1l	7.5E+07	7.5E+07	2192	-0.27342385	4.407236745	0.1253108	0.19396012	0.03512	0	356	200	446	415	351	438	461	268	432	395
ENSMUSG00000028343	chr4	Erp44	4.8E+07	4.8E+07	3418	0.264238907	5.232638851	0.1253149	0.19396012	0.03384	0	504	391	551	464	664	1094	757	746	828	788
ENSMUSG00000024130	chr17	Abca3	2.4E+07	2.4E+07	8797	0.247789982	4.653329092	0.1253334	0.193967376	0.02911	0	285	212	468	332	480	675	583	393	566	620
ENSMUSG00000055675	chr8	Kbtbd11	1.5E+07	1.5E+07	7137	0.655098549	2.856426713	0.1254066	0.1940593	0.20608	0	79	63	21	37	223	264	180	100	180	197
ENSMUSG00000063765	chr15	Chadl	8.2E+07	8.2E+07	4965	0.513911036	0.951564678	0.1257356	0.194546935	0.09701	0	20	16	21	18	39	48	25	40	55	50
ENSMUSG00000032221	chr9	Mns1	7.2E+07	7.2E+07	2537	0.623710898	-0.17244085	0.1257873	0.194605357	0.11553	0	6	4	22	8	7	22	18	11	21	25
ENSMUSG00000040852	chr17	Plekhh2	8.5E+07	8.5E+07	6886	-0.40329251	2.739283935	0.1260078	0.194924976	0.074	0	136	88	138	114	82	126	105	95	89	170
ENSMUSG00000090952	chr17	Gm17251	3.4E+07	3.4E+07	925	0.405461145	2.553600511	0.1260716	0.195002235	0.07411	0	68	45	106	76	86	165	75	128	127	175
ENSMUSG00000053411	chr15	Cbx7	8E+07	8E+07	6487	-0.27167038	4.560540964	0.126125	0.195063276	0.03551	0	434	306	379	330	476	496	496	278	436	522
ENSMUSG00000036632	chr3	Alg5	5.5E+07	5.5E+07	3537	0.284534437	3.724888187	0.1261697	0.195067957	0.03632	0	169	141	194	154	235	369	277	245	299	297
ENSMUSG00000042015	chr13	Wdr41	9.5E+07	9.5E+07	5029	-0.23855967	4.820577658	0.1261588	0.195067957	0.02713	0	456	358	521	455	501	620	583	401	551	526
ENSMUSG00000073062	chrX	Zxdb	9.5E+07	9.5E+07	5619	-0.51435058	0.556476031	0.1261623	0.195067957	0.07858	0	23	13	29	21	39	23	29	22	19	23
ENSMUSG00000100755	chr3	Rps23-ps	3.8E+07	3.8E+07	425	0.279529618	4.252323114	0.1262662	0.19519558	0.03631	0	264	206	316	243	255	557	346	351	423	471
ENSMUSG00000022434	chr15	Fam118a	8.5E+07	8.5E+07	2543	-0.29187402	3.440764833	0.1267109	0.195861414	0.03795	0	176	143	211	151	213	237	202	166	190	204
ENSMUSG00000028998	chr5	Tomm7	2.4E+07	2.4E+07	1125	0.284611858	6.090428743	0.1268262	0.19599034	0.04065	0	971	658	1053	767	1215	1864	1389	1257	1568	1640
ENSMUSG00000029486	chr5	Mrpl1	9.6E+07	9.6E+07	4295	-0.26389997	5.087234589	0.1268285	0.19599034	0.03382	0	522	338	836	599	553	732	797	493	572	603
ENSMUSG00000039183	chr17	Nubp2	2.5E+07	2.5E+07	1430	0.288416168	3.882324175	0.1268362	0.19599034	0.039	0	170	114	241	208	287	408	303	264	391	299
ENSMUSG00000048170	chr7	Mcmbp	1.3E+08	1.3E+08	5107	-0.26915965	4.370385231	0.1270274	0.196264129	0.03439	0	301	277	386	380	340	463	441	327	358	338
ENSMUSG00000021243	chr12	Fcf1	8.5E+07	8.5E+07	1117	0.288660903	3.832767505	0.1270997	0.19635432	0.03845	0	162	137	201	193	277	403	272	266	337	327
ENSMUSG00000027947	chr3	Il6ra	9E+07	9E+07	3343	-0.50772366	2.108126086	0.1271222	0.196367436	0.11706	0	47	64	87	37	148	78	116	39	65	69
ENSMUSG00000039515	chr2	Ppp2r4	3E+07	3E+07	5188	0.298361664	6.878009752	0.1272016	0.196468457	0.04526	0	1353	1044	1730	1645	2321	2952	2519	1968	3197	2794
ENSMUSG00000079641	chrX	Rpl39	3.7E+07	3.7E+07	1434	0.315699928	6.562352507	0.1272881	0.196580371	0.05048	0	1370	1029	1481	1142	1260	3174	1724	1804	2136	2021
ENSMUSG00000031565	chr8	Fgfr1	2.6E+07	2.6E+07	8120	0.310835496	6.386569273	0.127435	0.196785532	0.0489	0	1033	890	1011	948	1759	2332	1883	1349	1924	2157
ENSMUSG00000036435	chr5	Exoc1	7.7E+07	7.7E+07	9158	0.255954684	4.032988026	0.1275806	0.196988753	0.03012	0	215	140	293	228	260	458	394	275	349	365
ENSMUSG00000102252	chr7	Snrpn	6E+07	6E+07	2159	-0.30610815	6.59800144	0.1276004	0.196997619	0.04762	0	1561	1019	2270	1717	1632	1638	2391	1199	1865	1907
ENSMUSG00000020184	chr10	Mdm2	1.2E+08	1.2E+08	5070	-0.27762939	5.707821478	0.1276285	0.197007598	0.03864	0	786	710	1082	847	869	983	1257	725	931	992
ENSMUSG00000049832	chr17	Gm9840	3.6E+07	3.6E+07	327	0.522025315	0.944647036	0.127635	0.197007598	0.10386	0	12	16	30	37	17	38	53	41	42	43
ENSMUSG00000022855	chr16	Senp2	2.2E+07	2.2E+07	4499	-0.27030816	5.352066527	0.1277675	0.197190471	0.03638	0	706	577	742	579	714	861	955	568	760	693
ENSMUSG00000069631	chr11	Strada	1.1E+08	1.1E+08	5569	-0.26166991	4.985936931	0.1278655	0.197319938	0.0337	0	566	428	577	511	478	720	702	428	592	552
ENSMUSG00000018931	chr11	Natd1	6.1E+07	6.1E+07	4247	-0.27269055	3.980658637	0.1278811	0.197322337	0.03473	0	256	187	301	259	297	334	394	199	296	261
ENSMUSG00000067367	chr5	Lyar	3.8E+07	3.8E+07	2401	-0.25961817	4.255315308	0.1279377	0.197387968	0.0316	0	296	239	382	331	311	414	359	306	329	373
ENSMUSG00000047875	chr4	Gpr157	1.5E+08	1.5E+08	4900	-0.28283005	5.483312648	0.1280194	0.197492313	0.03983	0	591	456	1208	734	823	855	1011	568	860	899
ENSMUSG00000037971	chr9	1110032A03Rik	5.1E+07	5.1E+07	5293	-0.33496427	3.325855286	0.1280504	0.197518415	0.05105	0	171	102	176	125	282	211	200	134	177	191
ENSMUSG00000022673	chr16	Mcm4	1.6E+07	1.6E+07	3589	0.360784394	3.048360577	0.1281718	0.197683957	0.06031	0	113	72	118	73	172	244	187	166	202	146
ENSMUSG00000070283	chr9	Ndufaf3	1.1E+08	1.1E+08	1815	0.258340849	4.289652793	0.1282178	0.197711408	0.03181	0	233	153	340	290	353	484	426	350	456	471
ENSMUSG00000087993	chr10	Mir1982	8.1E+07	8.1E+07	74	0.418369784	1.716930577	0.1282124	0.197711408	0.06967	0	32	35	39	35	64	78	63	56	91	86
ENSMUSG00000039826	chr2	Trub2	3E+07	3E+07	6316	-0.27833523	4.987136439	0.1283112	0.197812205	0.03787	0	444	302	871	559	518	618	694	461	624	557
ENSMUSG00000047187	chr4	Rab2a	8535644	8535908	2133	-0.29373787	7.433199568	0.1283114	0.197812205	0.0443	0	3050	2272	3149	2675	3090	3599	3605	2505	3040	3320
ENSMUSG00000047260	chr11	Emc6	7.3E+07	7.3E+07	1415	0.281099598	6.122172339	0.1283526	0.197853995	0.04006	0	864	638	1321	882	1118	1711	1390	1282	1789	1682
ENSMUSG00000037375	chr1	Hhat	1.9E+08	1.9E+08	9150	0.496157217	0.962833189	0.1286411	0.198276858	0.09219	0	21	17	30	15	33	66	40	40	50	25
ENSMUSG00000015126	chr17	Tsr3	2.5E+07	2.5E+07	1192	0.257352769	4.33073976	0.1286982	0.198282396	0.03129	0	256	187	329	270	350	511	393	334	537	482
ENSMUSG00000022757	chr16	Tfg	5.7E+07	5.7E+07	2292	-0.2558802	5.639387604	0.1287012	0.198282396	0.03272	0	730	572	933	886	996	1025	1065	710	1000	898
ENSMUSG00000025140	chr11	Pycr1	1.2E+08	1.2E+08	3935	0.436685368	2.956266664	0.1286981	0.198282396	0.08754	0	104	112	83	55	118	231	145	120	238	183

ENSMUSG00000062822	chr13	4833420G17Rik	1.2E+08	1.2E+08	2574	0.451515126	1.977173246	0.1286682	0.198282396	0.08462	0	44	42	52	42	62	156	88	43	66	118
ENSMUSG00000085793	chr12	Lin52	8.4E+07	8.4E+07	2144	-0.31821609	3.542506256	0.1287506	0.198336714	0.04783	0	210	153	168	226	193	278	216	163	181	232
ENSMUSG00000029752	chr6	Asns	7675169	7675524	2735	0.671492698	3.074487564	0.1287996	0.198390448	0.2228	0	87	68	31	29	283	251	176	198	233	183
ENSMUSG00000069379	chr18	Gm4950	5.2E+07	5.2E+07	618	0.49259998	0.571282349	0.1288433	0.198435869	0.07342	0	18	12	20	15	21	40	24	30	38	32
ENSMUSG00000028837	chr4	Psmb2	1.3E+08	1.3E+08	1204	0.278541377	6.211585473	0.1288886	0.198483852	0.03949	0	894	638	1322	1014	1286	1968	1473	1287	1797	1875
ENSMUSG00000019320	chr17	Noxo1	2.5E+07	2.5E+07	3013	0.523634766	0.569759761	0.1289399	0.198530298	0.08568	0	14	16	17	13	24	38	35	15	38	43
ENSMUSG00000019818	chr10	Cd164	4.2E+07	4.2E+07	4449	-0.30278369	7.342033056	0.128947	0.198530298	0.04719	0	2689	2075	2804	2275	3699	3459	3607	2383	2914	2671
ENSMUSG00000025869	chr13	Nop16	5.5E+07	5.5E+07	1845	0.25788208	4.455945245	0.1289701	0.198544022	0.0314	0	276	242	326	284	369	614	440	395	532	478
ENSMUSG00000030346	chr6	Rad51ap1	1.3E+08	1.3E+08	3969	0.511306678	0.472060463	0.128997	0.198563599	0.08971	0	18	6	20	20	16	35	26	32	26	33
ENSMUSG00000032067	chr9	Pts	5.1E+07	5.1E+07	1035	-0.34498102	3.789002444	0.1290338	0.198598537	0.05744	0	244	181	178	173	383	348	249	185	226	255
ENSMUSG00000054452	chr10	Aes	8.2E+07	8.2E+07	1411	-0.31983092	9.398245425	0.1290813	0.198649802	0.053	0	10529	7046	15425	12935	11441	11987	13988	8062	15464	12950
ENSMUSG00000039031	chr10	Arhgap18	2.7E+07	2.7E+07	3884	0.319920928	3.832603949	0.1291592	0.198747888	0.04883	0	181	129	201	143	312	475	299	262	272	325
ENSMUSG00000061780	chr10	Cfd	8E+07	8E+07	923	1.18438191	8.66333771	0.1291813	0.198760057	0.68824	0	4085	2717	63	283	12044	17392	2283	10207	15281	12773
ENSMUSG00000083443	chr6	Gm15519	1.1E+08	1.1E+08	1566	-0.59379886	0.658551637	0.129404	0.199080886	0.13268	0	21	16	46	30	25	18	36	20	37	10
ENSMUSG00000027660	chr3	Skil	3.1E+07	3.1E+07	9694	-0.33724117	3.8387054	0.1294433	0.199119545	0.05412	0	193	132	363	219	338	268	381	200	180	274
ENSMUSG00000062580	chr1	Timm17a	1.4E+08	1.4E+08	7893	-0.31293098	6.924197419	0.1295112	0.199202178	0.05037	0	1739	1151	3472	2097	2029	2523	2412	1726	2115	2438
ENSMUSG00000076060	chr6	Mir704	4.8E+07	4.8E+07	77	0.627309148	0.762916244	0.1295447	0.199231798	0.15927	0	10	18	12	15	38	85	37	22	31	29
ENSMUSG00000068798	chr3	Rap1a	1.1E+08	1.1E+08	2401	-0.27532633	5.780743464	0.1296841	0.199424273	0.03846	0	906	658	1148	883	957	1151	1384	694	889	1073
ENSMUSG00000048078	chr7	Tenm4	9.6E+07	9.6E+07	21030	-0.9670794	3.020880083	0.1297802	0.199550253	0.46225	0	162	153	13	22	454	158	32	119	127	117
ENSMUSG00000027893	chr3	Ahcyl1	1.1E+08	1.1E+08	6690	-0.28995765	5.568077708	0.1298774	0.199677738	0.04242	0	787	471	892	626	1259	1064	1000	694	771	891
ENSMUSG00000003134	chr1	Tbc1d8	3.9E+07	3.9E+07	5239	-0.29517715	3.927030311	0.1299606	0.199783813	0.0419	0	260	221	275	260	215	364	280	221	245	299
ENSMUSG00000001964	chrX	Emd	7.4E+07	7.4E+07	2517	0.236272079	4.981869582	0.1299981	0.199819473	0.0274	0	368	274	580	450	559	803	715	522	749	746
ENSMUSG00000030019	chr6	Fbxl14	1.2E+08	1.2E+08	2963	0.286441089	3.904109195	0.1300428	0.19986629	0.03908	0	144	131	249	196	318	403	372	254	355	312
ENSMUSG00000026435	chr1	Slc45a3	1.3E+08	1.3E+08	3563	0.454071168	2.143067359	0.1300787	0.199899697	0.09298	0	50	24	76	87	41	122	96	57	129	117
ENSMUSG00000045302	chr5	Preb	3.1E+07	3.1E+07	7176	0.268855104	5.942609172	0.1301251	0.199949088	0.03678	0	710	553	980	916	1109	1488	1508	971	1547	1460
ENSMUSG00000030161	chr6	Gabarapl1	1.3E+08	1.3E+08	1765	0.282467518	6.021258577	0.1301522	0.199968798	0.04083	0	876	481	1154	872	1154	1834	1522	1042	1317	1714
ENSMUSG00000028393	chr4	Alad	6.3E+07	6.3E+07	1871	-0.35711382	6.388965273	0.1303819	0.200299727	0.06567	0	1015	595	2635	1475	1817	1729	1399	1086	1680	1732
ENSMUSG00000045092	chr3	S1pr1	1.2E+08	1.2E+08	3029	-0.27825069	4.654310345	0.1304718	0.200415853	0.03787	0	329	269	694	376	470	587	563	348	365	502
ENSMUSG00000048856	chr12	Slc25a47	1.1E+08	1.1E+08	1579	-0.52903527	0.371227776	0.1305799	0.200560047	0.0848	0	14	13	37	18	28	21	18	20	22	19
ENSMUSG00000023990	chr17	Tfeb	4.8E+07	4.8E+07	5669	-0.29024835	6.343094642	0.1307761	0.20083927	0.04342	0	1262	1013	1413	1518	1497	1481	1583	1079	1865	1544
ENSMUSG00000062647	chr2	Rpl7a	2.7E+07	2.7E+07	1781	0.296971105	8.336283415	0.1308921	0.200980109	0.04602	0	4008	3445	4560	4482	5302	8381	6716	5436	8381	8021
ENSMUSG00000086765	chr4	Gm11827	1.1E+07	1.1E+07	1368	0.632038781	-0.07491656	0.1308964	0.200980109	0.10569	0	5	12	6	11	14	24	24	13	18	26
ENSMUSG00000078427	chr10	Sarnp	1.3E+08	1.3E+08	1062	0.239790683	4.675387363	0.1309335	0.201014949	0.02772	0	367	246	441	323	395	713	560	472	536	567
ENSMUSG00000028948	chr4	Nol9	1.5E+08	1.5E+08	4956	-0.2668711	3.973413409	0.1310333	0.201146239	0.03344	0	241	183	309	294	262	337	335	237	286	270
ENSMUSG00000022512	chr16	Cldn1	2.6E+07	2.6E+07	3247	0.492148231	2.204124115	0.1313364	0.201589379	0.11236	0	60	26	84	86	28	171	105	84	83	105
ENSMUSG00000093071	chr4	Gm25951	1.4E+08	1.4E+08	64	0.495436452	0.56953771	0.1313796	0.201633643	0.07494	0	20	16	17	15	16	33	38	28	34	31
ENSMUSG00000061533	chr12	Cep128	9.1E+07	9.1E+07	11591	0.515550853	0.68312422	0.1315599	0.201888253	0.0874	0	16	16	28	17	15	59	39	18	37	32
ENSMUSG00000003198	chr17	Zfp959	5.6E+07	5.6E+07	2028	-0.39471628	1.572652967	0.1316177	0.201954849	0.06083	0	55	40	59	46	45	70	52	35	46	57
ENSMUSG00000029346	chr5	Srrd	1.1E+08	1.1E+08	1638	0.347639546	2.291257054	0.1316932	0.202039315	0.04968	0	65	40	66	59	91	121	120	80	120	114
ENSMUSG00000043445	chr17	Pgp	2.4E+07	2.4E+07	1027	-0.32954766	5.15287168	0.1317015	0.202039315	0.05513	0	443	307	1113	711	530	639	770	456	750	648
ENSMUSG00000000088	chr9	Cox5a	5.8E+07	5.8E+07	690	0.345818998	9.12126148	0.1318027	0.202172499	0.06281	0	5654	3496	12256	9019	8207	13264	12875	10171	13207	14743
ENSMUSG00000020802	chr11	Ube2o	1.2E+08	1.2E+08	5288	-0.28649501	5.048519258	0.1318638	0.202243967	0.04121	0	426	325	842	667	545	603	741	439	733	566
ENSMUSG00000022016	chr14	Akap11	7.8E+07	7.8E+07	9419	-0.29139757	5.247895185	0.1319905	0.202416182	0.04324	0	621	514	840	523	646	660	1056	496	702	627
ENSMUSG00000023915	chr17	Tnfrsf21	4.3E+07	4.3E+07	3626	0.268366209	4.647971403	0.1324457	0.203092035	0.03555	0	302	270	356	299	488	565	561	508	506	648
ENSMUSG00000024454	chr18	Hdac3	3.8E+07	3.8E+07	4026	-0.27368761	6.078470711	0.1324648	0.203099177	0.03877	0	1152	893	1214	1046	1223	1391	1348	935	1391	1270
ENSMUSG00000024937	chr19	Ehbp1l1	5707376	5708425	6440	-0.30670565	9.156752902	0.1325092	0.203145118	0.0496	0	8766	6218	13167	10618	9467	11062	12420	7662	12121	9658
ENSMUSG00000048039	chr3	Isg20l2	8.8E+07	8.8E+07	2893	0.295289987	3.624531683	0.1325709	0.203217371	0.04102	0	147	113	185	202	184	332	263	260	265	259
ENSMUSG00000022131	chr14	Gpr180	1.2E+08	1.2E+08	2877	-0.25723838	4.898511485	0.1326175	0.203244377	0.03315	0	519	389	480	483	544	599	612	417	658	518
ENSMUSG00000024732	chr19	Ccdc86	1.1E+07	1.1E+07	5774	-0.26296728	4.351244944	0.1326077	0.203244377	0.03381	0	294	291	352	328	391	387	440	293	427	360
ENSMUSG00000033216	chr6	Eefsec	8.8E+07	8.8E+07	2679	0.346014897	2.735792098	0.1327923	0.203445571	0.05474	0	80	44	131	79	116	176	144	111	189	140
ENSMUSG00000066621	chr5	Tecpr1	1.4E+08	1.4E+08	9665	-0.26947212	5.333283368	0.1327862	0.203445571	0.03688	0	531	459	790	605	1003	749	829	508	806	901
ENSMUSG00000102349	chr19	RP24-458F14.4	5801941	5802393	453	1.487401938	0.287125391	0.132786	0.203445571	1.01861	0	0	1	35	6	6	0	30	1	23	112
ENSMUSG00000048731	chr17	Ggnbp1	2.7E+07	2.7E+07	6943	-0.24140765	4.590082984	0.1329008	0.203589629	0.02817	0	338	277	546	373	457	503	444	365	443	515
ENSMUSG00000017264	chr4	Exosc10	1.5E+08	1.5E+08	3594	-0.23998927	4.514977186	0.1330291	0.203741652	0.02794	0	334	264	460	419	393	496	455	315	445	458
ENSMUSG00000086938	chr19	4930481A15Rik	5406740	5407083	2240	-0.60336747	0.179848484	0.1330219	0.203741652	0.12976	0	10	22	19	13	30	12	28	13	13	19
ENSMUSG00000028233	chr4	Tgs1	3574875	3575129	5314	-0.31236993	3.445286394	0.1330734	0.203765031	0.04599	0	153	154	239	164	192	241	265	158	159	177
ENSMUSG00000032475	chr9	Nck1	1E+08	1E+08	4792	-0.24262402	4.572000651	0.1330651	0.203765031	0.02874	0	397	286	473	349	439	592	479	352	401	432
ENSMUSG00000059401	chrX	Mamld1	7.1E+07	7.1E+07	4796	0.375176997	1.880181776	0.1331172	0.203809768	0.0569	0	37	32	64	45	60	88	95	72	65	94
ENSMUSG00000062729	chr1	Ppox	1.7E+08	1.7E+08	4515	0.318944989	3.483138575	0.1332159	0.203938628	0.04747	0	132	118	140	141	212	309	201	182	293	291
ENSMUSG00000025868	chr13	Higd2a	5.5E+07	5.5E+07	648	0.279838758	6.721337981	0.1332587	0.203966772	0.04102	0	1250	967	1962	1438	1693	2510	2243	1926	2573	2651
ENSMUSG00000100017	chr14	2410022M11Rik	5.7E+07	5.7E+07	3645	0.512096831	1.056319321	0.1332633	0.203966772	0.11445	0	16	6	37	24	46	62	38	34	56	49
ENSMUSG00000032715	chr2	Trib3	1.5E+08	1.5E+08	2125	0.479668275	1.762478382	0.1333801	0.204123201	0.10579	0	30	16	54	43	73	67	58	61	122	82
ENSMUSG00000025218	chr19	Poll	4.6E+07	4.6E+07	2324	-0.27062443	4.174153825	0.1335966	0.204432283	0.03579	0	275	219	351	319	320	334	389	210	419	345
ENSMUSG00000027099	chr2	Mtx2	7.5E+07	7.5E+07	3675	-0.34215884	4.817893091	0.1336953	0.204560905	0.05955	0	361	208	902	545	478	622	642	403	386	523
ENSMUSG00000016554	chr15	Eif3d	7.8E+07	7.8E+07	1910	0.26089683	6.008510056	0.1338708	0.204807101	0.03531	0	759	625	1149	879	1057	1674	1427	1149	1549	1443
ENSMUSG00000033554	chr3	Dph5	1.2E+08	1.2E+08	4086	-0.32133711	2.7691293	0.1339145	0.204847136	0.04521	0	96	85	150	104	134	135	120	108	116	135
ENSMUSG00000097184	chr16	4632428C04Rik	3E+07	3E+07	2430	-0.71505795	2.30361252	0.1339262	0.204847136	0.24902	0	60	13	287	57	90	92	135	53	46	56

ENSMUSG00000031667	chr8	Aktip	9.1E+07	9.1E+07	2992	-0.26403201	5.977646805	0.133947	0.204856748	0.0362	0	1052	750	1273	994	1129	1282	1438	884	1143	1185
ENSMUSG00000025795	chr10	Rassf3	1.2E+08	1.2E+08	3425	0.363612257	6.380197982	0.1340455	0.204969502	0.06973	0	1060	404	1978	1294	1021	2165	2170	1394	1895	2110
ENSMUSG00000060803	chr19	Gstp1	4035407	4035661	757	0.298567075	6.429612672	0.13405	0.204969502	0.04665	0	1187	967	1082	1081	1439	2215	1710	1542	2286	2050
ENSMUSG00000066877	chr1	Nck2	4.3E+07	4.3E+07	4321	-0.28767468	3.831856719	0.1341117	0.205041514	0.04019	0	235	196	280	195	262	288	291	173	338	237
ENSMUSG00000044716	chr5	Dok7	3.5E+07	3.5E+07	4228	0.288566397	4.162757117	0.1342076	0.205165717	0.04117	0	218	149	409	246	215	437	438	298	400	457
ENSMUSG00000045886	chr10	Gm9803	4.4E+07	4.4E+07	516	0.395401319	2.141584927	0.1343751	0.205377119	0.06895	0	54	40	53	54	80	103	72	98	103	120
ENSMUSG00000049922	chr2	Slc35c1	9.2E+07	9.2E+07	3275	0.296710568	3.515793148	0.1343751	0.205377119	0.04179	0	133	103	178	139	228	348	225	177	285	270
ENSMUSG00000032602	chr9	Slc25a20	1.1E+08	1.1E+08	4844	-0.36950391	6.435383941	0.134407	0.205403478	0.07187	0	1132	596	2852	1586	1631	1616	1745	1084	1379	2024
ENSMUSG00000083097	chr2	Gm14494	1.5E+08	1.5E+08	435	-0.40835346	1.443998523	0.1345483	0.205596894	0.06851	0	43	35	64	42	43	53	66	25	51	42
ENSMUSG00000039556	chrX	Ppp1r3f	7557296	7560886	5153	-0.38417379	2.200791855	0.1346073	0.205664756	0.06394	0	70	49	93	95	81	61	98	57	95	92
ENSMUSG00000024387	chr17	Csnk2b	3.5E+07	3.5E+07	2067	0.283014127	6.526908692	0.13466	0.20570755	0.04216	0	1115	846	1512	1301	1581	2106	1939	1512	2453	2451
ENSMUSG00000041278	chr11	Ttc1	4.4E+07	4.4E+07	2032	-0.25077983	5.629377667	0.1346647	0.20570755	0.03248	0	828	610	953	792	860	1045	1005	697	943	990
ENSMUSG00000099034	chr15	2810039B14Rik	7.6E+07	7.6E+07	6418	0.597275049	-0.0463159	0.1348428	0.205957157	0.09183	0	11	11	8	7	13	25	23	10	25	24
ENSMUSG00000031379	chrX	Pir	1.6E+08	1.6E+08	5553	0.364141764	2.422002643	0.1348833	0.20599659	0.05821	0	82	49	70	50	96	160	119	80	133	125
ENSMUSG00000031527	chr8	Eri1	3.5E+07	3.5E+07	5067	0.31770555	3.030744499	0.134905	0.20600729	0.04484	0	112	88	122	97	119	254	209	124	167	183
ENSMUSG00000028341	chr4	Nr4a3	4.8E+07	4.8E+07	5987	0.656586116	2.142493013	0.1349367	0.206010938	0.21245	0	21	29	78	106	20	97	66	123	159	79
ENSMUSG00000055681	chr8	Cope	7E+07	7E+07	3353	0.2731879	6.252582215	0.1349362	0.206010938	0.03909	0	1013	764	1108	1023	1305	2005	1636	1290	1973	1734
ENSMUSG00000025161	chr11	Slc16a3	1.2E+08	1.2E+08	5318	-0.35647706	7.8491013	0.1350796	0.206206586	0.06766	0	2368	2362	5486	5183	4693	3613	5286	2648	5292	4185
ENSMUSG00000014245	chr11	Pigl	6.2E+07	6.2E+07	2268	-0.375569	1.788408844	0.1352617	0.206455091	0.05838	0	60	38	61	58	71	77	80	44	48	56
ENSMUSG00000056763	chr1	Cspp1	1E+07	1E+07	17553	-0.39655809	1.929481169	0.1352718	0.206455091	0.06902	0	72	53	79	48	65	98	62	36	62	81
ENSMUSG00000020519	chr11	Sap30l	5.8E+07	5.8E+07	1151	0.247259491	4.686419702	0.135322	0.206509284	0.03069	0	277	227	471	395	435	611	564	476	635	577
ENSMUSG00000028035	chr3	Dnajb4	1.5E+08	1.5E+08	4318	-0.36688747	5.920969053	0.1353774	0.20656288	0.07086	0	754	511	1951	1303	837	1242	1367	912	849	1089
ENSMUSG00000039361	chr7	Picalm	9E+07	9E+07	4174	-0.29102215	6.384559673	0.1353866	0.20656288	0.04465	0	1306	952	1878	1082	1855	1955	1842	1273	1314	1397
ENSMUSG00000010538	chr3	Tsacc	8.8E+07	8.8E+07	1112	0.497321963	1.379231688	0.1354434	0.206627114	0.10365	0	33	17	26	40	40	59	35	62	56	82
ENSMUSG00000033769	chr6	Exoc6b	8.5E+07	8.5E+07	11187	-0.24291975	4.390231529	0.1355293	0.206735667	0.02892	0	310	269	392	355	377	462	415	309	418	375
ENSMUSG00000074102	chr9	Rbm15b	1.1E+08	1.1E+08	6511	0.289086749	3.567146172	0.1356008	0.20682217	0.03979	0	125	110	181	152	244	301	264	199	300	274
ENSMUSG00000035960	chr14	Apex1	5.1E+07	5.1E+07	1422	0.251653884	4.994235366	0.1357098	0.206965911	0.03208	0	410	335	525	379	551	872	583	620	754	721
ENSMUSG00000036686	chr8	Cc2d1a	8.4E+07	8.4E+07	3710	-0.24829639	4.381587462	0.1357645	0.207026908	0.02993	0	293	211	484	351	400	427	421	293	428	397
ENSMUSG00000032788	chr10	Pdxk	7.8E+07	7.8E+07	5124	0.316755654	4.121952272	0.1358469	0.20712995	0.05056	0	211	147	228	182	424	539	415	307	398	338
ENSMUSG00000086629	chrX	2810403D21Rik	1.1E+08	1.1E+08	7094	-0.5499369	0.187707674	0.1359573	0.207275796	0.10456	0	24	14	26	10	20	26	18	14	9	21
ENSMUSG00000025917	chr1	Cops5	1E+07	1E+07	3766	-0.28389864	6.926578361	0.1361032	0.207453172	0.04294	0	2035	1618	2209	2033	2074	2583	2631	1762	2251	2131
ENSMUSG00000039616	chr18	Mocos	2.5E+07	2.5E+07	2884	0.323145251	2.715424381	0.1360891	0.207453172	0.04818	0	78	45	118	83	122	180	160	103	158	147
ENSMUSG00000030127	chr6	Cops7a	1.2E+08	1.2E+08	2711	-0.29117335	7.038089891	0.1363056	0.207739101	0.04528	0	2064	1705	2386	2297	2395	2455	2770	1596	2925	2555
ENSMUSG00000024160	chr17	Spsb3	2.5E+07	2.5E+07	2719	-0.24576335	5.078478215	0.1365587	0.208102199	0.03081	0	463	388	736	647	546	687	722	470	692	626
ENSMUSG00000021113	chr12	Snapc1	7.4E+07	7.4E+07	2125	0.299430177	3.355422722	0.1366643	0.208240468	0.04311	0	112	80	199	161	148	247	270	178	215	246
ENSMUSG00000086914	chr9	Gm16124	5.4E+07	5.4E+07	516	-0.32978046	2.649948306	0.1368981	0.208574046	0.04849	0	101	65	133	119	107	132	124	76	137	102
ENSMUSG00000022571	chr15	Pycrl	7.6E+07	7.6E+07	1353	0.303669304	3.325500838	0.1369295	0.208599168	0.04351	0	108	99	164	129	177	298	185	180	260	211
ENSMUSG00000002108	chr2	Nr1h3	9.1E+07	9.1E+07	2515	-0.24184213	4.876754475	0.136959	0.20862147	0.02945	0	407	311	536	496	688	643	583	410	600	551
ENSMUSG00000051319	chr2	1500011K16Rik	1.3E+08	1.3E+08	800	-0.26262952	5.930858222	0.1369974	0.208634631	0.03629	0	953	707	1157	970	1269	1213	1176	899	1337	1089
ENSMUSG00000097383	chr10	1500026H17Rik	9E+07	9E+07	3027	-0.62498812	0.264330366	0.1369901	0.208634631	0.13958	0	17	5	47	17	21	22	20	12	12	24
ENSMUSG00000027274	chr2	Mkks	1.4E+08	1.4E+08	3227	-0.2597892	5.760729061	0.1371055	0.20877661	0.03545	0	876	663	1137	908	867	1252	1037	816	1007	989
ENSMUSG00000027775	chr3	Mfsd1	6.8E+07	6.8E+07	3042	0.265175202	5.081636005	0.1374843	0.20931066	0.03594	0	512	383	468	348	583	1011	832	534	742	734
ENSMUSG00000031016	chr7	Wee1	1.1E+08	1.1E+08	1941	-0.50100522	0.734520653	0.137486	0.20931066	0.09283	0	23	20	44	24	30	31	39	23	28	13
ENSMUSG00000098992	chr11	Gm27597	9.8E+07	9.8E+07	80	0.282488368	7.084501567	0.1377018	0.209616323	0.04282	0	1860	1391	1917	1853	2181	3869	2870	2348	3107	3264
ENSMUSG00000020334	chr11	Slc22a4	5.4E+07	5.4E+07	2553	0.356971047	3.329510555	0.1378636	0.209839855	0.06387	0	88	69	231	157	138	326	268	161	173	243
ENSMUSG00000001855	chr2	Nup214	3.2E+07	3.2E+07	9659	-0.26535957	4.115671754	0.1379715	0.209935842	0.0345	0	242	184	390	324	302	323	349	242	365	340
ENSMUSG00000021411	chr13	Pxdc1	3.5E+07	3.5E+07	2103	0.499612535	2.54590548	0.1379683	0.209935842	0.12573	0	41	33	67	49	190	165	130	92	141	170
ENSMUSG00000030663	chr7	1110004F10Rik	1.2E+08	1.2E+08	1495	-0.24799303	5.46117746	0.1379491	0.209935842	0.03212	0	660	575	861	671	834	988	944	657	792	783
ENSMUSG00000014606	chr11	Slc25a11	7.1E+07	7.1E+07	2120	-0.35582921	8.797139047	0.1380854	0.210086359	0.06859	0	6233	4177	12557	9726	5976	7674	10228	5517	8586	8541
ENSMUSG00000060090	chrX	Rp2h	2E+07	2E+07	5141	-0.36658153	2.444723076	0.1382944	0.210381465	0.06208	0	88	63	128	74	109	139	131	67	67	87
ENSMUSG00000069520	chr10	Tmem19	1.2E+08	1.2E+08	3010	0.230557263	4.726451915	0.1383525	0.210447034	0.02688	0	327	236	495	360	448	677	618	477	542	628
ENSMUSG00000039662	chr4	Icmt	1.5E+08	1.5E+08	5287	-0.25008382	5.471277214	0.1384072	0.210507452	0.03274	0	646	515	936	730	841	925	1049	594	869	772
ENSMUSG00000058571	chr14	Gpc6	1.2E+08	1.2E+08	9428	0.435852754	2.89422888	0.138727	0.210970982	0.0919	0	95	82	72	67	149	326	126	126	150	159
ENSMUSG00000031065	chrX	Cdk16	2.1E+07	2.1E+07	4378	-0.298359	7.534844806	0.1387655	0.211006596	0.04825	0	2606	2016	4346	3562	3139	3497	3969	2257	4005	3592
ENSMUSG00000031980	chr8	Agt	1.2E+08	1.2E+08	1891	0.28840193	4.229709067	0.1389527	0.21126835	0.04212	0	234	156	275	324	288	394	459	306	559	400
ENSMUSG00000044405	chr2	Adig	1.6E+08	1.6E+08	810	-0.64454933	4.006082875	0.1389737	0.211277387	0.21873	0	221	136	332	89	808	372	73	261	325	237
ENSMUSG00000029641	chr5	Rasl11a	1.5E+08	1.5E+08	1126	0.504319877	0.767546931	0.1390731	0.211400833	0.09064	0	12	18	21	17	31	53	30	20	47	45
ENSMUSG00000043257	chr4	Pigv	1.3E+08	1.3E+08	4180	-0.26165507	3.873405164	0.139085	0.211400833	0.03348	0	252	177	263	244	258	305	318	202	293	256
ENSMUSG00000000295	chr10	Hddc2	3.1E+07	3.1E+07	3509	0.30642355	3.22825073	0.139583	0.21213466	0.04424	0	103	111	150	116	141	246	197	192	201	213
ENSMUSG00000027429	chr2	Sec23b	1.4E+08	1.4E+08	6302	0.285367257	3.8315358	0.1396112	0.212154626	0.04031	0	174	141	215	163	278	415	275	288	310	308
ENSMUSG00000021890	chr14	Eaf1	3.1E+07	3.1E+07	4238	0.236554042	4.864453575	0.1397221	0.212254038	0.02872	0	352	284	544	380	479	698	746	552	620	614
ENSMUSG00000025144	chr11	Stra13	1.2E+08	1.2E+08	1077	0.287730486	4.088053555	0.1396929	0.212254038	0.0411	0	228	186	202	241	277	378	365	291	468	412
ENSMUSG00000029467	chr5	Atp2a2	1.2E+08	1.2E+08	5293	-1.05117201	8.529211615	0.1397161	0.212254038	0.57852	0	743	482	25632	14011	1367	4396	4834	3528	2401	9758
ENSMUSG00000074415	chr9	2610203C20Rik	4.1E+07	4.1E+07	12655	0.459649077	2.987609738	0.1397782	0.212316274	0.10515	0	129	102	78	52	118	264	125	159	143	245
ENSMUSG00000038065	chr6	Mturn	5.5E+07	5.5E+07	5695	-0.44582432	4.320089223	0.1399479	0.212551063	0.10536	0	254	256	207	215	844	429	354	237	299	441
ENSMUSG00000045996	chr15	Polr2k	3.6E+07	3.6E+07	624	-0.27391315	3.852522208	0.1399656	0.212554995	0.03741	0	241	199	238	242	248	297	320	200	281	249
ENSMUSG00000034566	chr11	Atp5h	1.2E+08	1.2E+08	1465	0.351091746	8.633377525	0.1399817	0.212556439	0.06745	0	3947	2644	9353	6540	4915	9187	9096	7314	9609	10624

ENSMUSG00000030431	chr7	Tmem238	4784595	4785279	1337	0.457017784	1.246795107	0.1401111	0.21272991	0.08531	0	17	20	36	30	43	71	44	38	77	41
ENSMUSG00000049488	chr4	Tmem67	1.2E+07	1.2E+07	7744	0.457224898	0.882178229	0.1403535	0.213074809	0.06945	0	23	19	24	17	26	61	47	27	36	38
ENSMUSG00000026946	chr2	Nmi	5.2E+07	5.2E+07	2001	0.387672815	2.683645651	0.1403688	0.21307497	0.0716	0	78	63	90	49	138	237	137	101	129	148
ENSMUSG00000023051	chr15	Tarbp2	1E+08	1E+08	4549	0.241485578	4.705293492	0.1404244	0.213136291	0.02992	0	323	228	505	397	372	591	649	458	605	601
ENSMUSG00000069808	chr11	Fam57a	7.6E+07	7.6E+07	6615	0.40323561	1.316264996	0.1406021	0.21338293	0.06276	0	27	24	39	27	38	82	51	47	53	47
ENSMUSG00000087497	chr11	2810001G20Rik	6.4E+07	6.4E+07	1057	0.428466448	1.260445749	0.1406814	0.213480164	0.06895	0	34	19	35	34	24	68	49	37	52	66
ENSMUSG00000097239	chr11	Gm27029	1E+08	1E+08	2079	0.269985477	6.635274149	0.1408356	0.213691003	0.03961	0	1296	932	1746	1369	1519	2488	2178	1858	2464	2188
ENSMUSG00000027454	chr2	Gins1	1.5E+08	1.5E+08	1516	0.514884885	0.832836372	0.1409938	0.213907967	0.10272	0	32	14	16	15	25	67	34	31	39	33
ENSMUSG00000019873	chr10	Reep3	6.7E+07	6.7E+07	5473	0.263534615	4.680240122	0.1411072	0.214056911	0.03599	0	261	260	417	287	562	727	602	403	543	634
ENSMUSG00000024240	chr18	Epc1	6435951	6437307	4475	-0.24768405	4.279555597	0.1411811	0.214145817	0.03093	0	292	239	411	335	308	456	351	268	381	382
ENSMUSG00000034121	chr11	Mks1	8.8E+07	8.8E+07	4044	-0.43855268	1.46013368	0.1412896	0.214287179	0.08114	0	44	41	47	28	71	65	44	39	36	50
ENSMUSG00000048581	chr3	E130311K13Rik	6.4E+07	6.4E+07	2398	-0.33705363	2.426401847	0.1415297	0.21462815	0.05141	0	95	70	103	85	89	120	91	87	87	95
ENSMUSG00000020380	chr11	Rad50	5.4E+07	5.4E+07	5375	-0.31516869	2.81044764	0.1416453	0.214780267	0.04615	0	113	90	145	105	127	173	148	96	112	114
ENSMUSG00000033900	chr3	Map9	8.2E+07	8.2E+07	6671	-0.42878981	1.792155008	0.1418711	0.215099419	0.08231	0	56	51	52	36	97	67	79	42	59	52
ENSMUSG00000029145	chr5	Eif2b4	3.1E+07	3.1E+07	2594	0.281004581	5.940778172	0.141899	0.215114764	0.04286	0	659	510	1183	1016	900	1449	1371	1014	1633	1498
ENSMUSG00000030849	chr7	Fgfr2	1.3E+08	1.3E+08	7240	-0.45548983	0.738696462	0.1419119	0.215114764	0.07359	0	29	19	33	19	39	35	32	20	20	31
ENSMUSG00000020462	chr11	Cfap36	2.9E+07	2.9E+07	2744	0.315084103	3.740488283	0.141959	0.215162905	0.04943	0	191	165	201	122	199	379	328	270	280	255
ENSMUSG00000038074	chr6	Fkbp14	5.5E+07	5.5E+07	4185	0.334762794	3.428352376	0.1419838	0.215177218	0.05463	0	147	125	135	130	162	395	212	175	260	204
ENSMUSG00000035295	chr2	Wdr38	3.9E+07	3.9E+07	2871	0.941621718	0.254048189	0.1420709	0.215285856	0.42337	0	3	3	37	7	10	5	17	11	59	51
ENSMUSG00000022257	chr15	Laptm4b	3.4E+07	3.4E+07	1897	-0.28092094	5.183341409	0.142089	0.215290125	0.04225	0	579	522	497	491	881	752	696	510	747	684
ENSMUSG00000019432	chr17	Ddx39b	3.5E+07	3.5E+07	3783	0.279723973	6.628957951	0.1423182	0.215614145	0.04283	0	1178	1023	1457	1406	1688	2422	1947	1814	2424	2556
ENSMUSG00000090145	chr1	Ugt1a6b	8.8E+07	8.8E+07	2382	0.868377607	3.760695673	0.1424223	0.215748488	0.40083	0	144	92	22	10	479	454	334	260	417	338
ENSMUSG00000101104	chr1	Gm29247	4.4E+07	4.4E+07	676	0.405794967	1.777369732	0.1424466	0.215761985	0.06935	0	45	25	45	52	49	125	70	63	71	64
ENSMUSG00000025885	chr18	Myo5b	7.4E+07	7.4E+07	9766	-0.70922109	0.648004318	0.1426537	0.216028974	0.22568	0	9	5	58	53	21	34	21	12	24	26
ENSMUSG00000037852	chr8	Cpe	6.5E+07	6.5E+07	2087	0.298176383	8.340722032	0.1426485	0.216028974	0.04927	0	4552	3271	5410	4105	4597	6859	9338	6021	7737	6795
ENSMUSG00000024098	chr17	Twsg1	6.6E+07	6.6E+07	4046	-0.27964519	5.567650133	0.1426943	0.216067207	0.04242	0	800	603	876	843	761	1041	1247	588	743	862
ENSMUSG00000032883	chr1	Acsl3	7.9E+07	7.9E+07	4357	0.371019405	4.468903385	0.1427634	0.216148495	0.07433	0	290	132	384	159	565	605	675	408	424	465
ENSMUSG00000084013	chr2	Gm14270	1.7E+08	1.7E+08	846	0.369421767	1.715776989	0.1431276	0.21667648	0.05408	0	46	31	48	39	44	88	78	63	66	73
ENSMUSG00000029291	chr5	Rufy3	8.9E+07	8.9E+07	3986	-0.43157224	2.377545718	0.1431728	0.216721469	0.09084	0	94	79	113	94	53	109	123	83	59	74
ENSMUSG00000031143	chrX	Ccdc22	7593809	7594167	3427	0.26120238	4.210561215	0.1431901	0.216724341	0.03469	0	210	173	291	298	302	482	359	314	483	439
ENSMUSG00000000197	chr14	Nalcn	1.2E+08	1.2E+08	7115	0.558759418	0.032478737	0.1432775	0.216833181	0.09489	0	10	5	14	12	15	38	28	15	18	14
ENSMUSG00000030232	chr6	Aebp2	1.4E+08	1.4E+08	8111	-0.24963617	5.291577118	0.1435504	0.217222822	0.03328	0	590	444	912	669	621	790	896	551	703	763
ENSMUSG00000038816	chr4	Ctnnal1	5.7E+07	5.7E+07	7661	-0.3135177	3.221938134	0.1436684	0.217377821	0.04825	0	136	80	234	174	172	226	190	106	170	174
ENSMUSG00000055725	chr5	Paqr3	9.7E+07	9.7E+07	7566	-0.43173237	0.951882615	0.1437601	0.21749323	0.07011	0	26	24	50	32	29	43	39	20	27	35
ENSMUSG00000097566	chr17	A930024N18Rik	1.5E+07	1.5E+07	3955	-0.6741826	0.295124458	0.1437846	0.217506848	0.19397	0	36	17	21	5	25	23	29	7	10	24
ENSMUSG00000074247	chr8	Dda1	7.1E+07	7.1E+07	2846	0.247627393	5.195112327	0.1439049	0.217665349	0.03274	0	386	358	580	506	731	877	832	606	943	848
ENSMUSG00000056050	chr1	Mia3	1.8E+08	1.8E+08	4431	-0.27890378	6.466030157	0.143965	0.217732629	0.04286	0	1217	935	2047	1509	1766	1688	2173	1154	1639	1648
ENSMUSG00000041132	chr5	N4bp2l1	1.5E+08	1.5E+08	1906	0.446805099	2.092830079	0.1440093	0.217776193	0.09464	0	56	27	45	40	104	135	79	60	97	131
ENSMUSG00000029576	chr5	Radil	1.4E+08	1.4E+08	4803	0.532703412	1.563159767	0.1441307	0.217924552	0.13598	0	27	26	32	16	78	78	53	35	97	88
ENSMUSG00000041372	chr6	B4galnt3	1.2E+08	1.2E+08	3779	-0.64997919	-0.06837769	0.1441385	0.217924552	0.15107	0	14	6	26	23	12	10	26	13	12	7
ENSMUSG00000038481	chr10	Cdk19	4E+07	4E+07	5807	-0.39207158	4.676306148	0.1442651	0.218092445	0.08324	0	275	253	715	253	821	547	729	293	359	389
ENSMUSG00000029625	chr5	Cpsf4	1.5E+08	1.5E+08	3598	0.260480351	3.762693106	0.1442884	0.218104155	0.03321	0	160	137	210	187	236	361	289	221	326	327
ENSMUSG00000035258	chr16	Abi3bp	5.6E+07	5.6E+07	4735	0.335552915	4.965180924	0.1443196	0.21812795	0.06056	0	481	383	417	257	500	1225	761	524	527	623
ENSMUSG00000028359	chr4	Orm3	6.3E+07	6.3E+07	773	-1.26290363	0.444088121	0.1443914	0.218212847	0.76992	0	28	15	0	0	99	32	7	9	18	13
ENSMUSG00000026499	chr1	Acbd3	1.8E+08	1.8E+08	6780	-0.24952198	4.080508923	0.1445125	0.2183723	0.03121	0	253	184	353	284	323	398	361	251	278	308
ENSMUSG00000073940	chr7	Hbb-bt	1E+08	1E+08	703	0.541971248	2.574119636	0.1445694	0.218434768	0.15497	0	17	30	122	103	109	152	109	103	221	128
ENSMUSG00000009647	chr10	Mcu	5.9E+07	5.9E+07	6936	0.269410311	5.485465414	0.1446846	0.218585382	0.03945	0	514	414	947	680	549	1094	1175	739	1020	1043
ENSMUSG00000062038	chr5	Gm10108	1.3E+07	1.3E+07	318	-0.47344935	1.386042467	0.144717	0.218610742	0.10339	0	52	34	35	48	49	63	58	33	19	48
ENSMUSG00000031770	chr8	Herpud1	9.4E+07	9.4E+07	2333	-0.2724105	6.851408485	0.1447883	0.218694939	0.0412	0	1790	1283	2654	1740	2224	2218	2497	1637	2289	2171
ENSMUSG00000062116	chr7	Zfp954	7114690	7116200	1999	0.337980078	2.58087167	0.1449213	0.218872267	0.05235	0	73	62	96	68	93	203	113	109	129	127
ENSMUSG00000034379	chr16	Wdr5b	3.6E+07	3.6E+07	1784	-0.39261245	2.090937459	0.1450904	0.219103924	0.07022	0	46	59	101	63	93	120	76	57	66	58
ENSMUSG00000035125	chr6	Gcfc2	8.2E+07	8.2E+07	7571	-0.42196435	1.274611526	0.1452132	0.219255971	0.07237	0	31	29	43	36	65	46	55	28	31	47
ENSMUSG00000082675	chrX	Gm6382	1.4E+08	1.4E+08	942	0.615306116	-0.15677176	0.1452223	0.219255971	0.10917	0	7	9	14	10	6	17	12	18	25	24
ENSMUSG00000097588	chr4	Gm17388	1.4E+08	1.4E+08	3515	0.721175899	-0.10483085	0.145261	0.219290794	0.18077	0	9	12	1	9	13	19	17	16	16	36
ENSMUSG00000035696	chr4	Rnf38	4.4E+07	4.4E+07	8336	-0.27089467	3.48068571	0.1453817	0.219449437	0.03657	0	188	134	204	183	204	254	228	136	214	217
ENSMUSG00000041688	chrX	Amot	1.5E+08	1.5E+08	8402	-0.33558735	6.767863646	0.1454336	0.219480505	0.06293	0	1826	1414	2379	2296	1126	2203	2125	1567	1828	2234
ENSMUSG00000046556	chr8	Zfp319	9.5E+07	9.5E+07	4106	-0.29535322	3.032674381	0.1454286	0.219480505	0.04191	0	134	101	150	125	164	179	186	100	146	148
ENSMUSG00000070720	chr4	Tmem200b	1.3E+08	1.3E+08	1370	0.543516654	0.925602981	0.1454815	0.219529161	0.14212	0	8	6	44	20	39	63	45	26	43	44
ENSMUSG00000041459	chr4	Tardbp	1.5E+08	1.5E+08	7796	-0.27468995	6.651698125	0.1456396	0.219744041	0.04208	0	1721	1357	1949	1432	1782	2369	2006	1464	1690	1915
ENSMUSG00000020790	chr11	Ankfy1	7.3E+07	7.3E+07	11332	0.244027934	4.609072349	0.1457416	0.219874365	0.03101	0	267	258	417	329	422	762	575	420	523	465
ENSMUSG00000024805	chr19	Pcgf5	3.6E+07	3.6E+07	1659	-0.28518868	4.068743174	0.1458642	0.220035634	0.04224	0	259	195	430	285	227	323	389	235	305	306
ENSMUSG00000043424	chr18	Eif3j2	4.3E+07	4.3E+07	2379	-0.28077416	5.634191871	0.1459977	0.22021335	0.04348	0	950	682	853	700	853	1265	904	786	820	859
ENSMUSG00000002846	chr16	Timmdc1	3.8E+07	3.8E+07	1784	-0.24616203	5.105228535	0.1461649	0.220441834	0.03257	0	486	408	813	602	525	696	746	480	700	634
ENSMUSG00000098332	chr9	5031420N21Rik	7.3E+07	7.3E+07	2999	0.355225787	2.655386395	0.1462434	0.220536558	0.06019	0	98	63	74	73	97	173	109	128	146	156
ENSMUSG00000021069	chr12	Pygl	7E+07	7E+07	3828	-0.94584349	4.930599582	0.146382	0.220674357	0.48617	0	855	206	52	57	2033	654	236	415	463	364
ENSMUSG00000040964	chr4	Arhgef10l	1.4E+08	1.4E+08	5693	-0.29849937	6.334101847	0.146372	0.220674357	0.04968	0	1039	798	2164	1466	1451	1473	1917	1002	1642	1490
ENSMUSG00000055932	chr8	Fto	9.1E+07	9.1E+07	13026	-0.26244466	6.394993692	0.1463702	0.220674357	0.03833	0	1299	931	1681	1441	1642	1633	1777	1155	1758	1598

ENSMUSG00000020331	chr10	Hcn2	8E+07	8E+07	3195	0.461866998	1.120765266	0.1466267	0.221019527	0.09302	0	18	14	38	22	43	44	61	24	67	53
ENSMUSG00000029390	chr5	Tmed2	1.2E+08	1.2E+08	2199	-0.26670836	6.186186061	0.1466747	0.221067497	0.03965	0	1140	976	1352	1125	1370	1722	1606	1011	1189	1355
ENSMUSG00000060568	chr1	Fam78b	1.7E+08	1.7E+08	6325	-0.39196039	1.573908919	0.1466901	0.221067497	0.06437	0	39	42	53	47	66	49	68	45	46	48
ENSMUSG00000021244	chr12	Ylpm1	8.5E+07	8.5E+07	9914	-0.24352921	4.198310774	0.146847	0.221272917	0.03027	0	288	198	395	294	339	413	402	263	305	355
ENSMUSG00000047193	chr9	Dync2h1	6928503	6929623	16161	-0.38464531	1.700522728	0.1468686	0.221272917	0.0653	0	47	46	66	64	44	62	73	42	51	56
ENSMUSG00000101089	chr19	2610016A17Rik	2.6E+07	2.6E+07	1097	-0.97339892	0.641427865	0.1468737	0.221272917	0.46725	0	41	31	5	2	66	33	4	20	23	23
ENSMUSG00000041870	chr5	Ankrd13a	1.1E+08	1.1E+08	4098	0.247465687	4.753567575	0.1469161	0.221289237	0.0328	0	292	236	453	354	568	769	668	460	591	546
ENSMUSG00000074884	chr2	Serf2	1.2E+08	1.2E+08	5455	0.274017581	8.176833351	0.1469069	0.221289237	0.04249	0	3916	2678	5134	3911	4321	7600	6374	5161	6659	6961
ENSMUSG00000102692	chr3	Dchs2	8.3E+07	8.3E+07	10783	-0.70385404	-0.12203593	0.1470429	0.221456423	0.20207	0	23	8	16	23	6	23	22	5	12	5
ENSMUSG00000025092	chr19	Hspa12a	5.9E+07	5.9E+07	5733	-0.47188452	3.246511666	0.1471032	0.221475839	0.11914	0	129	115	103	91	412	219	149	119	162	172
ENSMUSG00000033149	chr16	Phldb2	4.6E+07	4.6E+07	7577	-0.33214453	3.428417917	0.1470947	0.221475839	0.05669	0	191	129	220	130	237	265	250	168	132	165
ENSMUSG00000079243	chr9	Xirp1	1.2E+08	1.2E+08	5839	0.505251393	7.76958149	0.1470971	0.221475839	0.14384	0	1477	1039	4961	5231	1451	5899	4199	4655	5897	5559
ENSMUSG00000038268	chr11	Ovca2	7.5E+07	7.5E+07	2670	0.311526309	3.100924543	0.147274	0.221709317	0.04807	0	80	80	136	114	171	261	182	153	170	208
ENSMUSG00000061313	chr8	Ddhd2	2.6E+07	2.6E+07	4267	-0.31551741	4.360687966	0.1474169	0.221900489	0.05341	0	363	205	292	262	627	482	375	300	365	368
ENSMUSG00000049295	chr14	Zfp219	5.2E+07	5.2E+07	3262	0.26403937	4.600724099	0.1476167	0.222177494	0.03761	0	262	200	422	307	518	524	564	376	640	629
ENSMUSG00000026799	chr2	Med27	2.9E+07	2.9E+07	3310	0.273104406	3.713242547	0.1481203	0.222911535	0.03788	0	174	110	198	214	199	332	269	228	315	327
ENSMUSG00000090124	chr1	Ugt1a7c	8.8E+07	8.8E+07	4219	0.834570057	3.868116264	0.1482287	0.223050782	0.38255	0	159	109	27	11	506	485	374	275	435	361
ENSMUSG00000084846	chr3	A730011C13Rik	9.5E+07	9.5E+07	2234	-0.54200625	0.292109105	0.1482895	0.223118242	0.12069	0	20	18	20	12	31	30	22	6	13	27
ENSMUSG00000024533	chr18	Spire1	6.7E+07	6.7E+07	5178	0.280893482	3.611430782	0.1483648	0.223207684	0.03995	0	162	108	204	188	168	316	342	225	251	239
ENSMUSG00000030247	chr6	Kcnj8	1.4E+08	1.4E+08	2188	-0.29613432	4.32248094	0.1488198	0.223868198	0.04669	0	246	173	596	349	365	477	391	283	310	400
ENSMUSG00000040752	chr14	Myh6	5.5E+07	5.5E+07	6407	-1.79353612	6.221166603	0.1489226	0.223998689	1.61453	0	19	0	5314	4336	5	410	105	553	160	2166
ENSMUSG00000026483	chr1	Fam129a	1.5E+08	1.5E+08	7380	0.24613847	4.396611848	0.1491335	0.224291965	0.03175	0	213	215	366	301	370	629	492	318	448	495
ENSMUSG00000031904	chr8	Slc7a6	1.1E+08	1.1E+08	3730	-0.33280333	3.25057709	0.1492274	0.224409126	0.05661	0	156	115	152	111	269	205	187	143	150	177
ENSMUSG00000030559	chr7	Rab38	8.8E+07	8.8E+07	1471	0.85745269	-0.21996529	0.1493373	0.224550306	0.30352	0	3	9	4	0	24	27	14	20	23	13
ENSMUSG00000044148	chrX	1810030O07Rik	1.3E+07	1.3E+07	2699	0.248535019	4.355010917	0.1494415	0.224682861	0.03239	0	290	210	343	245	319	575	417	391	477	418
ENSMUSG00000032329	chr9	Hmg20a	5.6E+07	5.6E+07	3691	-0.25726555	4.293280265	0.1497493	0.225121533	0.03536	0	322	270	355	260	387	431	471	268	319	362
ENSMUSG00000053119	chr6	Chmp3	7.2E+07	7.2E+07	3250	0.260737529	6.16311598	0.1500048	0.225481441	0.03834	0	918	748	1198	881	1193	2118	1562	1273	1467	1680
ENSMUSG00000030353	chr6	Tead4	1.3E+08	1.3E+08	3596	0.331719018	3.142458478	0.1500418	0.225512886	0.05551	0	76	108	166	104	129	188	251	163	187	210
ENSMUSG00000002379	chr17	Ndufa11	5.7E+07	5.7E+07	2661	0.32209393	7.377772167	0.1500785	0.225543951	0.05953	0	1720	1214	3600	2678	2314	3575	3748	2643	4644	4514
ENSMUSG00000027291	chr2	Vps39	1.2E+08	1.2E+08	8605	-0.23838768	5.066627257	0.1502705	0.225808228	0.03133	0	515	421	592	635	545	764	739	414	675	617
ENSMUSG00000024421	chr18	Lama3	1.2E+07	1.2E+07	10745	-0.50275481	1.228554076	0.1504467	0.226048747	0.1203	0	23	33	53	61	28	69	43	18	35	34
ENSMUSG00000026707	chr2	Nsun6	1.5E+07	1.5E+07	5006	-0.42058013	1.231315517	0.150591	0.226225836	0.07322	0	32	34	53	27	50	47	31	31	51	39
ENSMUSG00000027860	chr3	Vangl1	1E+08	1E+08	4038	0.473892667	1.76333399	0.1505968	0.226225836	0.11039	0	27	37	47	22	77	93	51	63	109	76
ENSMUSG00000020485	chr11	Supt4a	8.8E+07	8.8E+07	942	0.237013272	4.507377885	0.1506372	0.22626229	0.02974	0	326	219	351	317	358	578	483	423	553	484
ENSMUSG00000041453	chr5	Rpl21	1.5E+08	1.5E+08	3400	0.280205509	7.303079067	0.1508143	0.226504061	0.04507	0	2227	1655	2491	2089	2238	4746	3266	2894	3471	3567
ENSMUSG00000078772	chr4	Gm12353	2E+07	2E+07	554	-0.38268132	2.932654174	0.1511212	0.22694065	0.07526	0	97	61	219	156	137	136	180	124	94	137
ENSMUSG00000004936	chr9	Map2k1	6.4E+07	6.4E+07	3391	-0.26452404	6.357035886	0.1513137	0.227205418	0.03999	0	1320	1069	1486	1278	1561	1785	1894	1099	1567	1405
ENSMUSG00000078963	chr18	Hsbp1l1	8E+07	8E+07	1251	-0.59043416	1.03293739	0.1515898	0.227595654	0.16109	0	40	14	77	38	14	37	22	23	40	39
ENSMUSG00000000085	chr4	Scmh1	1.2E+08	1.2E+08	7731	-0.24131693	5.180188177	0.1517894	0.227870906	0.03217	0	541	374	812	659	616	690	799	483	772	696
ENSMUSG00000031093	chrX	Dock11	3.6E+07	3.6E+07	9240	0.436738148	3.052291627	0.151833	0.22791199	0.10133	0	105	92	59	73	190	323	216	109	155	198
ENSMUSG00000054408	chr8	Spcs3	5.5E+07	5.5E+07	3466	0.256418288	5.641019944	0.1519263	0.228003262	0.03703	0	707	486	850	628	773	1614	1134	896	1017	982
ENSMUSG00000063275	chr2	Ptpla	1.4E+07	1.4E+07	2118	0.324923584	5.617889947	0.1519226	0.228003262	0.05981	0	699	635	583	667	578	1167	883	1065	1379	1044
ENSMUSG00000014867	chr2	Surf4	2.7E+07	2.7E+07	3281	0.269008184	7.274860401	0.1519576	0.228025867	0.04176	0	1953	1574	2386	2243	2447	4123	3535	2600	3900	3401
ENSMUSG00000050428	chr7	Fbxo46	1.9E+07	1.9E+07	3025	0.366637388	1.854493105	0.1521489	0.22828771	0.05888	0	44	34	50	34	71	91	86	55	85	93
ENSMUSG00000075419	chr2	Dolk	3E+07	3E+07	2104	-0.25371964	4.791518623	0.1521647	0.22828771	0.03513	0	395	282	475	441	723	571	527	392	600	517
ENSMUSG00000092558	chr17	Med20	4.8E+07	4.8E+07	7324	-0.24266649	4.468693456	0.1521862	0.228295639	0.03185	0	376	285	419	354	355	518	441	325	365	447
ENSMUSG00000001707	chr13	Eef1e1	3.9E+07	3.9E+07	1032	-0.28248001	3.509568618	0.1522338	0.228342503	0.04106	0	163	162	210	194	197	203	231	177	208	227
ENSMUSG00000039005	chr4	Tlr4	6.7E+07	6.7E+07	5556	0.359081275	2.430408502	0.152299	0.228391477	0.06241	0	50	55	66	87	90	175	134	88	93	130
ENSMUSG00000080875	chr5	Gm7332	9260945	9261388	444	0.419310023	2.078311299	0.1522969	0.228391477	0.08868	0	22	35	87	54	77	119	94	92	97	79
ENSMUSG00000028884	chr4	Rpa2	1.3E+08	1.3E+08	2993	0.239579132	4.643946135	0.1524074	0.228529657	0.03095	0	376	245	363	322	417	630	513	463	623	545
ENSMUSG00000061411	chr2	Nol4l	1.5E+08	1.5E+08	9083	0.482787483	1.299755228	0.152516	0.228668019	0.1114	0	26	11	36	18	64	63	54	49	66	48
ENSMUSG00000033249	chr8	Hsf4	1.1E+08	1.1E+08	1753	0.289951156	3.61061666	0.1525457	0.228688109	0.04355	0	148	124	191	156	207	311	224	184	370	295
ENSMUSG00000019977	chr10	Hbs1l	2.1E+07	2.1E+07	4893	-0.25715963	6.305063449	0.1526248	0.228782214	0.03793	0	1221	892	1597	1397	1431	1621	1733	1041	1575	1518
ENSMUSG00000022665	chr16	Ccdc80	4.5E+07	4.5E+07	4140	0.621356728	6.073160362	0.1529639	0.229262612	0.22184	0	513	675	363	200	2373	2665	1593	1425	1430	1365
ENSMUSG00000040195	chr10	Tmem194	1.3E+08	1.3E+08	7822	0.376461097	2.136802462	0.1529943	0.229262612	0.06738	0	68	29	67	49	73	159	103	67	81	99
ENSMUSG00000094910	chr12	D430019H16Rik	1.1E+08	1.1E+08	5786	0.558465355	0.223118027	0.1529854	0.229262612	0.12741	0	13	4	10	10	29	21	24	20	29	34
ENSMUSG00000094936	chr19	Rbm4	4784293	4785567	4940	0.29696214	3.453315263	0.1530113	0.229263624	0.04655	0	105	80	195	175	202	284	256	164	278	265
ENSMUSG00000053838	chr11	Nudcd3	6105691	6108355	6496	-0.26836114	6.369453057	0.1531471	0.229442555	0.0415	0	1165	991	1797	1530	1365	1610	1857	1125	1664	1517
ENSMUSG00000028691	chr4	Prdx1	1.2E+08	1.2E+08	3043	0.274999874	8.203153473	0.1532429	0.229561619	0.04414	0	3902	3057	4735	3337	5206	7948	6626	5251	6486	7096
ENSMUSG00000023010	chr15	Tmbim6	9.9E+07	9.9E+07	3806	0.278215108	8.202752465	0.1534563	0.229834777	0.04525	0	3701	2576	4572	3881	5737	7376	6772	4908	7661	6756
ENSMUSG00000026556	chr1	Vangl2	1.7E+08	1.7E+08	6990	0.473700423	0.717830777	0.1534581	0.229834777	0.0913	0	20	6	29	15	30	48	38	21	35	44
ENSMUSG00000078768	chr7	Zfp566	3E+07	3E+07	1728	-0.41841377	1.1476178	0.153513	0.229892565	0.07411	0	39	26	44	26	50	43	47	22	29	49
ENSMUSG00000025532	chr5	Crcp	1.3E+08	1.3E+08	1579	-0.26276015	4.267750921	0.1535461	0.229917567	0.03788	0	336	265	292	292	370	467	383	247	403	321
ENSMUSG00000030400	chr7	Ercc2	1.9E+07	1.9E+07	4170	-0.24657856	4.19862888	0.1538954	0.230416026	0.03259	0	294	231	323	302	340	360	339	258	407	363
ENSMUSG00000031171	chrX	Ftsj1	8238668	8240830	4760	-0.24759892	3.866421923	0.153938	0.230455228	0.03176	0	238	155	285	237	285	309	329	203	278	257
ENSMUSG00000038259	chr2	Gdf5	1.6E+08	1.6E+08	2320	1.034407637	0.890756543	0.154086	0.230652115	0.58115	0	2	1	6	6	82	21	28	55	51	72
ENSMUSG00000042662	chr2	Dusp15	1.5E+08	1.5E+08	4391	0.634787384	0.019883487	0.1544608	0.23118845	0.14279	0	16	6	12	12	6	28	19	6	33	29

ENSMUSG00000024474	chr18	Ik	3.7E+07	3.7E+07	1996	0.252286121	6.109322207	0.1544986	0.231220429	0.03673	0	858	625	1244	994	1098	1746	1579	1263	1505	1640
ENSMUSG00000030407	chr7	Qpctl	1.9E+07	1.9E+07	2100	0.389648364	1.998024957	0.154539	0.231231444	0.07448	0	45	23	57	43	95	115	84	70	96	91
ENSMUSG00000050010	chr5	Shisa3	6.8E+07	6.8E+07	4753	-0.44946802	1.41531997	0.154523	0.231231444	0.08853	0	32	21	80	57	42	57	50	34	33	52
ENSMUSG00000022109	chr14	Med4	7.4E+07	7.4E+07	1304	0.244872069	4.267861305	0.154702	0.231450689	0.03215	0	299	176	315	228	315	493	426	325	479	429
ENSMUSG00000074405	chr7	Zfp865	5020376	5020655	3873	-0.25752422	3.613793576	0.1547586	0.231510626	0.03402	0	188	134	250	196	243	257	272	166	242	213
ENSMUSG00000025574	chr11	Tk1	1.2E+08	1.2E+08	5198	-0.40478102	2.014427569	0.1548569	0.23163304	0.08131	0	91	47	56	69	72	110	66	60	65	52
ENSMUSG00000029283	chr5	Cdc7	1.1E+08	1.1E+08	4128	0.633354677	0.271543078	0.154909	0.231686255	0.17972	0	8	7	11	6	35	32	21	30	15	36
ENSMUSG00000044072	chr11	Eml6	3E+07	3E+07	9279	-0.41766305	1.266165649	0.1551306	0.2319929	0.07809	0	41	32	38	47	39	47	51	29	26	53
ENSMUSG00000035778	chr2	Ggta1	3.5E+07	3.5E+07	4709	0.282810934	3.77282723	0.1552294	0.232115908	0.04339	0	183	103	232	168	261	410	330	268	235	296
ENSMUSG00000021250	chr12	Fos	8.5E+07	8.5E+07	2352	0.652227589	3.456996424	0.1553086	0.232209617	0.24279	0	48	98	54	84	378	110	240	274	289	411
ENSMUSG00000029131	chr5	Dnajb6	3E+07	3E+07	5721	-0.2592544	5.935781831	0.155363	0.232266235	0.03883	0	1026	663	1353	1012	1023	1318	1429	855	990	1195
ENSMUSG00000061374	chr7	Fiz1	5007057	5009205	2834	-0.2296628	4.421725195	0.1554619	0.232389299	0.02827	0	295	239	463	345	424	429	447	299	434	427
ENSMUSG00000040236	chr8	Trappc5	3676299	3676603	2546	-0.23529922	5.324233112	0.1555811	0.232542719	0.0313	0	620	451	935	606	694	827	875	562	794	751
ENSMUSG00000001052	chr3	Sec24b	1.3E+08	1.3E+08	6020	-0.22752882	4.649814111	0.1556725	0.232604979	0.02816	0	358	277	455	390	587	550	500	367	465	506
ENSMUSG00000028755	chr4	Cda	1.4E+08	1.4E+08	1035	0.684719673	1.781451398	0.1556565	0.232604979	0.25882	0	32	4	106	51	13	101	71	59	68	124
ENSMUSG00000031347	chrX	Cetn2	7.3E+07	7.3E+07	1646	0.243712667	4.655309781	0.155654	0.232604979	0.03253	0	404	263	375	289	393	675	557	473	537	563
ENSMUSG00000050846	chr15	Zfp623	7.6E+07	7.6E+07	2463	-0.30078863	2.6683616	0.1557952	0.232763514	0.04291	0	96	77	124	105	122	120	136	87	107	131
ENSMUSG00000029462	chr5	Vps29	1.2E+08	1.2E+08	3089	0.223727233	4.542117066	0.1558503	0.232820983	0.02704	0	280	232	380	328	409	659	534	401	516	484
ENSMUSG00000025986	chr1	Slc39a10	4.7E+07	4.7E+07	6095	-0.296536	3.092261312	0.1561347	0.233220969	0.04476	0	124	103	160	152	165	194	175	140	123	148
ENSMUSG00000039983	chr2	Ccdc32	1.2E+08	1.2E+08	2214	0.290251844	3.25325119	0.1562095	0.233307875	0.04313	0	107	94	162	104	183	274	243	163	213	185
ENSMUSG00000020260	chr10	Pofut2	7.7E+07	7.7E+07	2219	0.22680931	4.788475869	0.1562436	0.23333404	0.02841	0	345	265	475	356	501	808	625	448	664	550
ENSMUSG00000043162	chr6	Pyurf	5.8E+07	5.8E+07	3573	-0.236039	5.365820727	0.1565601	0.233781798	0.03164	0	594	459	942	657	760	786	887	600	837	793
ENSMUSG00000001507	chr11	Itga3	9.5E+07	9.5E+07	5710	0.330602552	2.873401395	0.1566235	0.233851449	0.05606	0	74	71	120	124	94	203	142	126	207	154
ENSMUSG00000023952	chr17	Gtpbp2	4.6E+07	4.6E+07	5305	-0.24337557	5.699088461	0.1566411	0.233852853	0.03419	0	736	629	1152	854	906	1060	1155	704	980	1037
ENSMUSG00000035842	chr17	Ddx11	6.6E+07	6.6E+07	4149	0.47570294	0.217757558	0.1569623	0.234307545	0.07014	0	10	10	15	16	15	30	25	18	30	23
ENSMUSG00000030653	chr7	Pde2a	1E+08	1E+08	4220	-0.23983385	5.005347339	0.1570464	0.234408066	0.0324	0	440	329	770	485	667	672	734	372	653	647
ENSMUSG00000035139	chr13	Secisbp2	5.2E+07	5.2E+07	4626	-0.25792627	3.696126263	0.1572451	0.234679694	0.03508	0	172	168	243	216	261	267	264	187	266	228
ENSMUSG00000038346	chr6	Zfp384	1.3E+08	1.3E+08	6421	-0.21999191	4.727572302	0.1572828	0.234711033	0.02647	0	385	292	575	407	519	542	577	398	498	506
ENSMUSG00000026107	chr1	Nabp1	5.1E+07	5.1E+07	8498	-0.29079641	4.452757854	0.1573606	0.23480209	0.04771	0	395	287	321	266	536	469	396	350	467	334
ENSMUSG00000021143	chr12	Pacs2	1.1E+08	1.1E+08	5480	-0.25907124	6.059800793	0.157447	0.23490608	0.0393	0	1024	754	1402	1227	1104	1398	1536	875	1295	1215
ENSMUSG00000002409	chr7	Dyrk1b	2.8E+07	2.8E+07	2695	-0.2719606	5.71943381	0.1575105	0.234950747	0.04309	0	761	581	1155	971	928	876	1008	664	1280	1107
ENSMUSG00000049960	chr14	Mrps16	2E+07	2E+07	566	0.238007256	5.630376514	0.1575075	0.234950747	0.03276	0	625	463	839	660	886	1291	1034	909	1106	1179
ENSMUSG00000047370	chr7	Gm7367	6E+07	6E+07	633	-0.51745191	0.373617366	0.1576144	0.235080821	0.10152	0	20	17	28	19	23	12	31	12	30	17
ENSMUSG00000032290	chr9	Ptpn9	5.7E+07	5.7E+07	4054	0.297720776	3.601167297	0.1577364	0.235237755	0.04742	0	130	133	155	150	248	377	294	224	247	234
ENSMUSG00000028483	chr4	Snapc3	8.3E+07	8.3E+07	6760	0.275995652	3.484366444	0.1577927	0.235271635	0.03944	0	157	118	166	144	167	292	239	222	232	261
ENSMUSG00000079415	chr19	Cntf	1.3E+07	1.3E+07	1073	0.430455796	1.347671052	0.1577925	0.235271635	0.08359	0	26	20	36	46	28	81	59	34	43	76
ENSMUSG00000020271	chr11	Fbxw11	3.3E+07	3.3E+07	4327	-0.26278215	6.049370085	0.1578612	0.235348746	0.04055	0	1047	858	1185	1004	1340	1194	1556	904	1253	1322
ENSMUSG00000044556	chr4	Tex38	1.2E+08	1.2E+08	802	0.482813114	0.705614569	0.1578791	0.235350503	0.0888	0	19	15	22	17	22	30	28	23	51	50
ENSMUSG00000016200	chr1	Syt14	1.9E+08	1.9E+08	10540	-0.5658	0.430126227	0.1579912	0.235455994	0.12549	0	9	14	47	24	23	20	28	16	14	26
ENSMUSG00000016327	chrX	Atp1b4	3.8E+07	3.8E+07	4201	0.453577125	3.860675985	0.1580082	0.235455994	0.11762	0	280	104	214	239	63	473	267	275	368	344
ENSMUSG00000026439	chr1	Rbbp5	1.3E+08	1.3E+08	3930	-0.22534604	4.803592019	0.157984	0.235455994	0.02857	0	418	364	522	453	498	624	651	372	518	511
ENSMUSG00000056121	chr17	Fez2	7.8E+07	7.8E+07	2020	-0.27866938	6.320577695	0.1580171	0.235455994	0.04588	0	1435	1018	1407	1022	1718	1700	1872	1115	1507	1301
ENSMUSG00000030727	chr7	Rabep2	1.3E+08	1.3E+08	5322	1.177147676	6.211655309	0.1580728	0.235489046	0.78178	0	56	48	2471	763	615	203	1822	108	4146	4601
ENSMUSG00000045466	chr6	Zfp956	4.8E+07	4.8E+07	2968	-0.32521073	2.6767248	0.1580583	0.235489046	0.05361	0	126	83	119	85	112	118	118	81	116	147
ENSMUSG00000086527	chr6	Gm15856	1.2E+08	1.2E+08	1162	1.286572463	-0.18445917	0.1583325	0.23585091	0.87296	0	0	0	30	4	3	2	15	2	58	32
ENSMUSG00000055371	chr2	Stam2	5.3E+07	5.3E+07	6007	-0.25652065	3.78971045	0.1584275	0.23596728	0.03538	0	206	177	262	214	271	325	322	193	219	245
ENSMUSG00000024197	chr17	Plin3	5.6E+07	5.6E+07	2159	-0.42661438	5.305025822	0.1586103	0.236214431	0.1071	0	412	200	1572	858	641	793	915	436	631	755
ENSMUSG00000029513	chr5	Prkab1	1.2E+08	1.2E+08	3066	0.252649077	3.985890712	0.1586421	0.236236793	0.03479	0	168	152	272	229	278	386	327	314	371	355
ENSMUSG00000034538	chr7	Zfp418	7171330	7171558	2725	-0.4800987	0.276169786	0.1587095	0.23631211	0.0849	0	23	17	21	17	19	25	21	13	12	26
ENSMUSG00000025278	chr14	Flnb	7817957	7818443	9100	-0.24042132	4.397749136	0.1587885	0.236404589	0.03203	0	282	226	421	371	445	551	434	250	377	414
ENSMUSG00000004843	chr16	Chmp2b	6.6E+07	6.6E+07	1838	-0.22338213	5.080507126	0.1588285	0.236439077	0.02828	0	529	391	751	496	605	756	777	488	581	633
ENSMUSG00000038296	chr7	Galnt18	1.1E+08	1.1E+08	2575	0.347836842	2.586430671	0.1589138	0.236540913	0.06447	0	64	34	115	85	109	159	143	131	125	117
ENSMUSG00000100550	chr10	2310039L15Rik	9.5E+07	9.5E+07	642	-0.63892961	0.416713604	0.1589785	0.236612063	0.19894	0	21	19	8	46	16	31	14	14	29	14
ENSMUSG00000074476	chr9	Spc24	2.2E+07	2.2E+07	1349	0.467493012	0.961327716	0.1591322	0.236815662	0.08627	0	26	23	19	27	17	56	43	29	52	41
ENSMUSG00000028618	chr4	Tmem59	1.1E+08	1.1E+08	2056	0.28586288	6.859610504	0.1592519	0.236968764	0.04872	0	1665	1256	1487	1261	2188	3391	2557	2057	2504	2728
ENSMUSG00000031232	chrX	Magt1	1.1E+08	1.1E+08	4672	-0.24254818	5.214825586	0.1593379	0.23707153	0.03406	0	653	462	637	641	605	935	703	557	669	660
ENSMUSG00000052914	chr4	Cyp2j6	9.7E+07	9.7E+07	3605	0.338622481	2.771321365	0.1593646	0.237086168	0.06136	0	76	45	113	87	142	240	134	113	144	154
ENSMUSG00000026456	chr1	Cyb5r1	1.3E+08	1.3E+08	4437	0.256737277	6.808107179	0.1594773	0.237228553	0.03932	0	1490	1027	2004	1473	1812	2732	2730	1841	2748	2593
ENSMUSG00000002968	chr7	Med25	4.5E+07	4.5E+07	2297	-0.2710494	5.518947329	0.1597294	0.237578387	0.04309	0	636	474	1016	869	852	801	1054	529	1099	841
ENSMUSG00000037235	chr5	Mxd4	3.4E+07	3.4E+07	3882	0.275563165	5.930944564	0.1600924	0.238093171	0.04507	0	657	558	953	716	1383	1603	1616	927	1520	1300
ENSMUSG00000102781	chr2	Pla2r1	6E+07	6E+07	4464	-0.43052712	1.383927457	0.1601626	0.238172275	0.08839	0	35	40	42	32	69	60	65	29	32	39
ENSMUSG00000097769	chr18	Snhg4	3.6E+07	3.6E+07	4666	0.338023433	2.165951164	0.1602529	0.238281232	0.0556	0	45	38	80	54	81	137	88	73	92	119
ENSMUSG00000075033	chr16	Nxpe3	5.6E+07	5.6E+07	6430	0.521883599	0.635625688	0.1605	0.238623374	0.11711	0	28	9	26	15	11	35	25	27	37	50
ENSMUSG00000083626	chr7	Gm4459	1.4E+08	1.4E+08	468	0.345782369	2.274897348	0.1605584	0.238684838	0.06075	0	56	32	87	76	70	93	126	91	110	122
ENSMUSG00000024999	chr19	Noc3l	3.9E+07	3.9E+07	3977	-0.29145802	2.900241259	0.1606054	0.238729422	0.04244	0	109	91	145	125	145	158	144	116	140	125
ENSMUSG00000056938	chr11	Acbd4	1E+08	1E+08	2937	-0.41068743	5.165263173	0.1607924	0.238982174	0.10029	0	652	383	426	300	1415	800	557	437	630	785
ENSMUSG00000023330	chr2	Dtwd1	1.3E+08	1.3E+08	1350	-0.32011972	2.910259024	0.1609661	0.239201798	0.055	0	129	107	149	90	144	170	109	106	136	163

ENSMUSG00000030539	chr7	Sema4b	8E+07	8E+07	5434	0.45505283	2.496671082	0.1609743	0.239201798	0.11469	0	58	38	50	46	174	149	114	106	150	139
ENSMUSG00000024603	chr18	Dctn4	6.1E+07	6.1E+07	3714	-0.23208304	5.390875191	0.1609998	0.239214266	0.03126	0	587	448	844	764	818	958	839	634	795	761
ENSMUSG00000075389	chr11	2810410L24Rik	1.2E+08	1.2E+08	3028	-0.35752157	1.775831996	0.1610324	0.239237418	0.05879	0	50	43	54	57	79	82	55	40	68	60
ENSMUSG00000042997	chr3	Nhlrc3	5.3E+07	5.3E+07	5601	0.28289552	3.267269748	0.1613714	0.23971569	0.04225	0	111	77	150	142	181	268	232	143	199	251
ENSMUSG00000026575	chr1	Nme7	1.6E+08	1.6E+08	5876	0.363044221	2.009359728	0.1615936	0.240020268	0.06445	0	37	39	68	40	79	103	112	57	79	109
ENSMUSG00000026782	chr1	Abi2	6E+07	6E+07	8543	0.387581555	3.210657169	0.1616198	0.240033808	0.08631	0	89	70	242	60	170	259	269	180	174	189
ENSMUSG00000036693	chr5	Nop14	3.5E+07	3.5E+07	2734	-0.23109318	4.547353838	0.1617341	0.240178189	0.02975	0	350	226	544	413	404	521	465	342	430	464
ENSMUSG00000035021	chr12	Baz1a	5.5E+07	5.5E+07	7159	-0.38831525	1.773206069	0.1617809	0.240222194	0.07312	0	40	42	82	51	75	76	90	42	45	48
ENSMUSG00000022159	chr14	Rab2b	5.2E+07	5.2E+07	4163	0.41234723	2.432222883	0.1618176	0.240251327	0.09234	0	51	47	62	42	150	159	113	94	117	143
ENSMUSG00000053093	chr14	Myh7	5.5E+07	5.5E+07	8586	-1.9049639	8.53677222	0.1618669	0.240298953	1.90099	0	22	3	26796	22178	9	1790	157	2552	619	10801
ENSMUSG00000030683	chr7	Sez6l2	1.3E+08	1.3E+08	4210	0.538307326	0.332567757	0.1619385	0.240379913	0.13745	0	7	5	31	13	18	26	19	31	35	25
ENSMUSG00000089797	chr8	Gm16118	1.1E+08	1.1E+08	680	-0.58065143	0.129387788	0.1619878	0.240427621	0.14111	0	18	9	16	17	32	33	21	8	6	17
ENSMUSG00000033961	chr7	Zfp446	1.3E+07	1.3E+07	5801	-0.36453963	1.889204026	0.1620805	0.240539689	0.06436	0	67	55	73	54	53	83	76	53	61	54
ENSMUSG00000027569	chr2	Mrgbp	1.8E+08	1.8E+08	3499	0.306066785	2.740758663	0.1622413	0.240752858	0.04709	0	65	61	110	87	129	175	156	102	158	166
ENSMUSG00000039157	chr2	Fam102a	3.3E+07	3.3E+07	6066	0.396372101	3.409094093	0.1622708	0.240771274	0.09047	0	74	79	171	94	305	301	221	159	263	304
ENSMUSG00000031399	chrX	Fam3a	7.4E+07	7.4E+07	2485	0.227576941	4.319372133	0.1627168	0.241407493	0.02869	0	272	185	317	255	368	506	465	316	463	477
ENSMUSG00000032252	chr9	Glce	6.2E+07	6.2E+07	6828	-0.28171993	3.619335385	0.1628738	0.241614838	0.04411	0	222	165	211	158	247	293	248	172	179	254
ENSMUSG00000028838	chr4	Extl1	1.3E+08	1.3E+08	4333	-0.39220997	6.210742356	0.1629253	0.241665628	0.09317	0	832	590	2642	1534	1080	1023	2021	951	1273	1347
ENSMUSG00000085786	chr6	Gm15987	1.3E+08	1.3E+08	2231	0.734701053	-0.0590811	0.1630269	0.241790828	0.22301	0	8	12	0	6	20	32	19	22	15	20
ENSMUSG00000044751	chr11	Gm12231	5.5E+07	5.5E+07	695	-0.31057005	4.107324096	0.1634913	0.24245383	0.05526	0	237	163	552	301	228	378	347	251	280	330
ENSMUSG00000057778	chr11	Cyb5d2	7.3E+07	7.3E+07	5143	-0.22083812	4.831362082	0.1635121	0.242459071	0.02811	0	454	335	503	504	505	627	638	385	539	540
ENSMUSG00000028455	chr4	Stoml2	4.3E+07	4.3E+07	3022	-0.24863019	5.922314236	0.1635561	0.242498728	0.03706	0	880	645	1409	1059	1054	1335	1158	830	1287	1142
ENSMUSG00000037085	chr15	Trmt12	5.9E+07	5.9E+07	4133	0.282441971	3.074196676	0.1636585	0.242624855	0.04157	0	109	82	127	100	152	218	210	134	213	173
ENSMUSG00000028427	chr4	Aqp7	4.1E+07	4.1E+07	2828	-0.51975326	4.044188345	0.1637573	0.242745687	0.16078	0	251	150	180	116	846	409	211	206	243	339
ENSMUSG00000021427	chr13	Ssr1	3.8E+07	3.8E+07	9306	0.26785349	5.880603008	0.1639048	0.242938721	0.04303	0	881	676	766	679	969	1767	1245	1081	1258	1308
ENSMUSG00000044231	chr13	Nhlrc1	4.7E+07	4.7E+07	2293	-0.23828665	3.885146249	0.1639982	0.243051427	0.03095	0	203	180	310	242	273	310	318	205	291	274
ENSMUSG00000038526	chr3	Car14	9.6E+07	9.6E+07	2543	-0.32585275	5.353795229	0.1642314	0.243371269	0.06405	0	502	441	979	973	572	743	620	430	945	1046
ENSMUSG00000031634	chr8	Ufsp2	4.6E+07	4.6E+07	2566	-0.24083893	5.107859653	0.1642492	0.243372055	0.03427	0	612	469	579	502	610	782	718	540	644	572
ENSMUSG00000034810	chr2	Scn7a	6.7E+07	6.7E+07	7338	0.397959885	4.019444604	0.1644616	0.243660921	0.09318	0	201	181	133	109	426	530	412	294	320	352
ENSMUSG00000078765	chr7	U2af1l4	3.1E+07	3.1E+07	3804	0.218433203	4.999081612	0.1645622	0.243784319	0.0276	0	414	308	515	452	554	807	660	515	799	776
ENSMUSG00000021385	chr13	Ippk	4.9E+07	4.9E+07	2776	-0.30482708	3.089764234	0.1646128	0.243826952	0.04994	0	123	100	183	165	134	196	173	143	133	130
ENSMUSG00000025474	chr7	Tubgcp2	1.4E+08	1.4E+08	3085	-0.24080555	4.502774818	0.1646258	0.243826952	0.03316	0	318	242	542	409	364	458	470	289	472	466
ENSMUSG00000001138	chr1	Cnnm3	3.7E+07	3.7E+07	6420	-0.23663563	4.17111711	0.1647975	0.244034248	0.0317	0	258	218	325	310	357	413	382	210	345	376
ENSMUSG00000002845	chr16	Tmem39a	3.9E+07	3.9E+07	4094	0.30137209	3.241312663	0.1648005	0.244034248	0.0486	0	124	93	110	117	189	282	228	141	229	200
ENSMUSG00000031753	chr8	Cog4	1.1E+08	1.1E+08	4053	-0.26191665	6.368152484	0.1648271	0.244047758	0.04182	0	1237	966	1843	1492	1292	1695	1848	1131	1662	1457
ENSMUSG00000026245	chr1	Farsb	7.8E+07	7.8E+07	2620	-0.23967615	5.668788259	0.1649654	0.244226819	0.03445	0	760	626	966	878	920	955	1025	777	1023	1012
ENSMUSG00000032212	chr9	Sltm	7.1E+07	7.1E+07	3646	-0.21919982	5.02401018	0.1650043	0.244232823	0.02815	0	554	403	583	510	570	724	703	455	600	635
ENSMUSG00000040842	chr4	Szrd1	1.4E+08	1.4E+08	3327	-0.2757467	7.133231397	0.1649911	0.244232823	0.04675	0	2165	1592	3010	2566	2346	2640	3196	1833	3110	2401
ENSMUSG00000027006	chr2	Dnajc10	8E+07	8E+07	5004	-0.25207149	5.783142093	0.1650335	0.244250219	0.03848	0	916	706	983	894	980	1285	1338	721	915	991
ENSMUSG00000008373	chr7	Prpf31	3629985	3630056	5439	0.22051506	4.593046946	0.165112	0.244340671	0.02782	0	299	221	440	326	418	570	535	394	612	567
ENSMUSG00000051730	chr2	Mettl5	7E+07	7E+07	2437	-0.29594924	2.884935869	0.1651294	0.244340671	0.04699	0	123	102	146	108	123	138	152	95	143	151
ENSMUSG00000025995	chr1	Wdr75	4.6E+07	4.6E+07	4900	-0.24889877	4.095923628	0.1651726	0.244354792	0.03488	0	248	221	365	273	288	408	346	277	268	306
ENSMUSG00000039382	chrX	Wdr45	7721973	7722230	2717	0.230978475	4.981246529	0.1651738	0.244354792	0.0314	0	404	263	579	378	623	913	676	473	735	761
ENSMUSG00000070425	chr7	Trpc2	1E+08	1E+08	5673	-0.34965263	2.401790077	0.1651933	0.244357902	0.06682	0	97	71	112	88	66	130	93	51	93	115
ENSMUSG00000029699	chr5	Ssc4d	1.4E+08	1.4E+08	2976	-0.34516393	1.83007035	0.165327	0.244503989	0.05542	0	57	41	58	68	68	70	58	52	67	67
ENSMUSG00000035678	chr17	Tnfsf9	5.7E+07	5.7E+07	1230	0.538662832	-0.10313044	0.1653135	0.244503989	0.09136	0	7	6	11	7	20	28	18	15	21	18
ENSMUSG00000020262	chr10	Adarb1	7.7E+07	7.7E+07	11272	-0.32501148	3.422505563	0.1655622	0.244813445	0.05866	0	136	95	286	134	286	233	246	125	189	196
ENSMUSG00000038150	chr11	Ormdl3	9.9E+07	9.9E+07	2184	-0.42237665	6.007730997	0.1656179	0.244813445	0.10938	0	938	637	766	636	2829	1459	1047	866	1202	1131
ENSMUSG00000050668	chr17	Gpatch11	7.9E+07	7.9E+07	4198	-0.2484866	4.050714152	0.1656235	0.244813445	0.03485	0	241	221	326	261	298	405	326	261	250	317
ENSMUSG00000061477	chr12	Rps7	2.9E+07	2.9E+07	961	0.267694889	7.160011134	0.1656196	0.244813445	0.0441	0	1836	1616	2225	1972	2050	4131	2990	2569	3255	3236
ENSMUSG00000099309	chr9	Mir7085	4.4E+07	4.4E+07	66	-0.66702884	0.338201723	0.1655882	0.244813445	0.21116	0	24	25	6	22	27	17	34	12	25	7
ENSMUSG00000001999	chr2	Blvra	1.3E+08	1.3E+08	2446	0.249957303	3.956412731	0.1657095	0.244873343	0.03435	0	207	175	233	179	265	427	330	273	366	337
ENSMUSG00000032740	chr11	Ccdc88a	2.9E+07	2.9E+07	10891	0.379897907	2.189024997	0.165692	0.244873343	0.07322	0	72	43	61	40	75	132	106	86	68	128
ENSMUSG00000061286	chr7	Exosc5	2.6E+07	2.6E+07	1030	0.264972776	4.224566094	0.1657164	0.244873343	0.04012	0	252	198	235	225	362	470	350	355	448	461
ENSMUSG00000030876	chr7	Mettl9	1.2E+08	1.2E+08	1822	-0.23206948	4.593546385	0.1658523	0.245024967	0.03073	0	365	234	507	371	532	562	547	357	410	422
ENSMUSG00000044320	chr2	1700001O22Rik	3.1E+07	3.1E+07	2788	-0.87110971	2.128708085	0.1658539	0.245024967	0.44148	0	39	28	147	8	243	61	170	17	51	25
ENSMUSG00000000440	chr6	Pparg	1.2E+08	1.2E+08	1984	-0.75462812	3.609692812	0.1658749	0.245030142	0.34096	0	193	146	71	23	777	278	133	177	180	159
ENSMUSG00000026113	chr1	Inpp4a	3.7E+07	3.7E+07	10387	-0.28640102	4.170693883	0.1659544	0.245121763	0.0478	0	295	192	399	382	221	404	420	234	297	331
ENSMUSG00000070808	chr7	Gltscr1	1.6E+07	1.6E+07	5360	-0.28999735	3.209053454	0.1660218	0.245195558	0.04521	0	124	101	214	148	189	158	206	110	177	206
ENSMUSG00000020261	chr11	Slc36a1	5.5E+07	5.5E+07	5626	0.290185414	3.187206778	0.1661574	0.24536996	0.04553	0	109	94	139	99	175	263	210	149	235	173
ENSMUSG00000029627	chr5	Zkscan14	1.5E+08	1.5E+08	1967	-0.25448457	3.530490438	0.166193	0.245396687	0.03487	0	172	125	237	190	230	227	228	153	226	251
ENSMUSG00000015790	chr2	Surf1	2.7E+07	2.7E+07	1753	0.219092137	4.997351873	0.166247	0.24545057	0.02814	0	388	302	523	433	608	899	671	560	683	738
ENSMUSG00000028882	chr4	Ppp1r8	1.3E+08	1.3E+08	2924	0.232792381	4.406320771	0.1663476	0.245573257	0.03126	0	253	198	405	253	386	493	474	380	522	479
ENSMUSG00000049502	chr16	Dtx3l	3.6E+07	3.6E+07	5724	-0.26235253	3.899595248	0.1663992	0.24562354	0.03917	0	232	172	328	214	291	419	335	174	241	256
ENSMUSG00000032577	chr9	Mapkapk3	1.1E+08	1.1E+08	5542	-0.2279387	5.434075851	0.1664602	0.245687803	0.03101	0	667	468	908	683	836	980	929	637	827	749
ENSMUSG00000022797	chr16	Tfrc	3.3E+07	3.3E+07	6185	-0.36848138	7.182282019	0.1665489	0.245792854	0.08417	0	1220	1716	4392	3242	2095	2452	3599	1807	2519	2794
ENSMUSG00000027890	chr3	Gstm4	1.1E+08	1.1E+08	1707	0.245823175	4.067833237	0.1666631	0.245935523	0.03397	0	241	162	248	196	311	390	398	283	386	412

ENSMUSG00000002014	chrX	Ssr4	7.4E+07	7.4E+07	3096	0.256660195	5.517934541	0.1669037	0.246264576	0.03963	0	608	541	594	573	789	1330	909	807	1085	1029
ENSMUSG00000022551	chr15	Cyc1	7.6E+07	7.6E+07	1194	-0.34346856	8.982607597	0.1670354	0.246432996	0.07362	0	6502	3943	15788	10294	8188	9017	12144	6388	9719	9077
ENSMUSG00000027611	chr2	Procr	1.6E+08	1.6E+08	2031	0.435981383	3.37861299	0.1670632	0.246448069	0.11304	0	85	76	116	73	345	307	249	157	245	280
ENSMUSG00000100621	chr19	Gm28374	6076945	6077478	728	0.316424472	2.584566423	0.1672349	0.246675396	0.05011	0	66	58	79	82	113	180	143	84	132	146
ENSMUSG00000063882	chr4	Uqcrh	1.2E+08	1.2E+08	1237	0.275742846	8.83727632	0.1674287	0.246935311	0.04761	0	5948	3760	9188	6519	6473	11805	10094	7934	10442	11598
ENSMUSG00000027671	chr3	Actl6a	3.3E+07	3.3E+07	3886	-0.24957385	4.013345658	0.1675397	0.247073069	0.03529	0	225	212	319	282	274	360	332	268	280	269
ENSMUSG00000028467	chr4	Gba2	4.4E+07	4.4E+07	4481	-0.27057787	3.655876285	0.1676294	0.247179394	0.04062	0	154	128	309	194	281	306	250	164	213	253
ENSMUSG00000058966	chr7	Fam57b	1.3E+08	1.3E+08	2804	-0.32672283	6.010489197	0.1677273	0.247297765	0.06599	0	893	582	1322	1600	1102	1031	1327	702	1724	1164
ENSMUSG00000037533	chr11	Rapgef6	5.5E+07	5.5E+07	12911	-0.28968792	3.453174732	0.1677671	0.247330456	0.04847	0	176	160	216	176	160	250	250	112	209	209
ENSMUSG00000010607	chr9	Pigyl	2.2E+07	2.2E+07	777	0.242958081	4.060707437	0.1679718	0.247606132	0.0332	0	194	173	261	217	310	484	349	274	406	357
ENSMUSG00000031722	chr8	Hp	1.1E+08	1.1E+08	1343	1.146465268	6.548112972	0.1682586	0.248002779	0.77944	0	567	303	17	35	3930	4904	1009	2649	3020	1679
ENSMUSG00000039201	chrX	Tbc1d25	8154472	8156066	2794	0.375953878	2.144713919	0.1683112	0.248054376	0.07423	0	29	37	64	77	81	99	115	77	97	114
ENSMUSG00000029528	chr5	Pxn	1.2E+08	1.2E+08	8195	-0.2501089	6.557985487	0.1683831	0.248115607	0.03883	0	1432	1132	2000	1517	1685	1924	1921	1246	1986	1862
ENSMUSG00000033499	chr13	Larp4b	9093881	9094180	8464	-0.2700087	6.664553003	0.1683882	0.248115607	0.04537	0	1433	1128	2345	1972	1575	1978	2226	1332	1908	2110
ENSMUSG00000005268	chr15	Prlr	1E+07	1E+07	15339	0.771180161	0.20289702	0.1684438	0.248169179	0.30467	0	11	1	32	15	1	52	21	17	21	25
ENSMUSG00000028161	chr3	Ppp3ca	1.4E+08	1.4E+08	5512	-0.32876158	8.023630809	0.168494	0.248169179	0.06788	0	5174	4112	3283	4395	3991	4873	4602	3595	5054	5709
ENSMUSG00000041268	chr9	Dmxl2	5.4E+07	5.4E+07	13419	0.313464082	2.549149897	0.1684637	0.248169179	0.05108	0	65	52	111	79	85	151	146	96	103	165
ENSMUSG00000054545	chr1	Ugt1a6a	8.8E+07	8.8E+07	4312	0.83669496	3.784474493	0.1684953	0.248169179	0.42299	0	154	100	21	8	483	461	340	262	416	341
ENSMUSG00000034022	chr15	Cpsf1	7.7E+07	7.7E+07	4515	-0.22376752	5.000581785	0.1685654	0.248244772	0.02964	0	400	357	729	570	583	670	693	431	631	638
ENSMUSG00000072825	chr12	Cep170b	1.1E+08	1.1E+08	6642	0.230091773	4.276067923	0.168582	0.248244772	0.03029	0	246	183	377	261	289	495	464	328	476	392
ENSMUSG00000050555	chr9	Hyls1	3.6E+07	3.6E+07	5970	0.436689375	0.609143851	0.1686317	0.248291874	0.072	0	13	15	28	15	20	40	43	21	31	34
ENSMUSG00000018379	chr11	Srsf1	8.8E+07	8.8E+07	5710	-0.2461935	5.959310319	0.1687621	0.248457783	0.03725	0	798	716	1347	1075	1230	1451	1146	963	1069	1250
ENSMUSG00000001774	chr9	Chordc1	1.8E+07	1.8E+07	2205	-0.2459899	5.390655609	0.1689298	0.24866521	0.03668	0	612	450	1098	679	657	897	832	621	774	839
ENSMUSG00000046897	chr15	Zfp740	1E+08	1E+08	4822	-0.2283147	5.46229368	0.1689385	0.24866521	0.03165	0	716	515	770	688	906	995	874	612	835	898
ENSMUSG00000043065	chr16	Spice1	4.4E+07	4.4E+07	5416	-0.38935441	2.266245516	0.1690845	0.24885408	0.08267	0	99	44	121	70	77	111	128	47	56	90
ENSMUSG00000059741	chr9	Myl3	1.1E+08	1.1E+08	1306	-1.68288364	7.701802457	0.1692954	0.249138319	1.58092	0	103	0	17141	9807	9	1033	1271	1377	671	5810
ENSMUSG00000040124	chr1	Gorab	1.6E+08	1.6E+08	2855	-0.36625876	1.667318792	0.1693157	0.249142028	0.06596	0	55	39	46	53	68	85	59	39	54	45
ENSMUSG00000097350	chr17	4732491K20Rik	1.2E+07	1.2E+07	3142	-0.49339472	1.178041861	0.1693478	0.24916313	0.12288	0	18	23	74	40	44	43	53	13	35	47
ENSMUSG00000086477	chr7	Gm15506	9.9E+07	9.9E+07	1133	0.517042582	0.239103579	0.1695331	0.249409591	0.0941	0	13	12	18	14	8	32	32	14	19	34
ENSMUSG00000049536	chrX	Tceal1	1.4E+08	1.4E+08	2803	-0.3451862	2.31559999	0.1696118	0.249499175	0.06265	0	108	60	104	62	77	118	95	66	91	78
ENSMUSG00000034235	chr14	Usp54	2.1E+07	2.1E+07	8921	-0.32479577	2.3158861	0.1696398	0.249514203	0.05406	0	61	66	113	69	106	108	105	76	76	83
ENSMUSG00000055980	chr1	Irs1	8.2E+07	8.2E+07	9144	-0.36450544	6.386228315	0.1696874	0.249558123	0.08346	0	1726	1520	1008	1458	949	1737	1510	1098	1772	1470
ENSMUSG00000034255	chr11	Arhgap27	1E+08	1E+08	6415	0.403025907	2.759854401	0.1699176	0.249870484	0.09743	0	51	30	173	72	140	165	165	121	176	155
ENSMUSG00000001569	chr5	Nom1	2.9E+07	2.9E+07	4895	-0.23310999	4.321543301	0.169993	0.249928909	0.03128	0	316	226	426	315	354	436	443	320	313	376
ENSMUSG00000051232	chr11	Tmem199	7.9E+07	7.9E+07	1902	-0.2568365	3.776035921	0.169978	0.249928909	0.03772	0	243	171	237	186	279	294	287	179	290	240
ENSMUSG00000029822	chr6	Osbpl3	5E+07	5E+07	9023	0.479436602	4.008926419	0.1700683	0.250013422	0.1385	0	289	274	92	137	118	483	395	270	364	432
ENSMUSG00000041828	chr11	Abca8a	1.1E+08	1.1E+08	6272	0.284156117	6.384257279	0.1702051	0.250188271	0.05041	0	1102	957	1107	995	1467	2735	2368	1175	1545	1864
ENSMUSG00000020525	chr11	Ppm1d	8.5E+07	8.5E+07	3173	-0.29711251	2.734232236	0.1702339	0.250204368	0.04767	0	81	81	146	123	120	157	138	88	105	126
ENSMUSG00000004263	chr6	Atn1	1.2E+08	1.2E+08	5085	0.267626841	6.877690519	0.1703543	0.250355136	0.0451	0	1363	1017	1979	1617	2256	2773	2587	1820	3265	2886
ENSMUSG00000039367	chr14	Sec24c	2.1E+07	2.1E+07	4446	-0.25319757	6.532774219	0.1705599	0.250631023	0.04024	0	1316	1169	1794	1671	1635	1992	2084	1229	1812	1676
ENSMUSG00000045639	chr7	Zfp629	1.3E+08	1.3E+08	6723	-0.32432821	4.142327751	0.1706884	0.250793599	0.06276	0	224	135	597	318	276	372	409	230	289	326
ENSMUSG00000019689	chr6	1110001J03Rik	3.9E+07	3.9E+07	689	-0.23596969	5.257120513	0.1708284	0.250947883	0.03399	0	569	459	812	688	591	808	687	523	876	740
ENSMUSG00000028633	chr4	Ctps	1.2E+08	1.2E+08	3316	-0.27238099	4.394625335	0.1708292	0.250947883	0.04464	0	308	350	376	325	323	483	360	364	377	360
ENSMUSG00000049800	chr11	Sertad2	2.1E+07	2.1E+07	6352	-0.23869923	4.122806787	0.1708677	0.250978212	0.03282	0	222	211	366	309	319	383	366	250	287	364
ENSMUSG00000019437	chr11	Tlcd1	7.8E+07	7.8E+07	5009	0.629401701	3.023643391	0.1709174	0.251024883	0.24219	0	44	29	122	64	260	131	160	54	288	393
ENSMUSG00000063760	chr10	Rnf217	3.1E+07	3.2E+07	11013	-0.25814246	4.511183314	0.1709459	0.251040406	0.03989	0	385	261	476	450	287	447	471	328	442	450
ENSMUSG00000028959	chr5	Fastk	2.4E+07	2.4E+07	4372	-0.28912829	7.659731585	0.1711488	0.251312123	0.05307	0	2752	2178	4914	4022	3180	3696	4654	2448	4328	3831
ENSMUSG00000028443	chr4	Nudt2	4.1E+07	4.1E+07	845	-0.23978037	4.132074443	0.1712799	0.251451887	0.03344	0	290	230	340	270	285	373	344	264	365	305
ENSMUSG00000032109	chr9	Nlrx1	4.4E+07	4.4E+07	3980	-0.25048466	4.605011128	0.1712798	0.251451887	0.03717	0	314	220	539	464	510	446	448	329	553	515
ENSMUSG00000002249	chr17	Tead3	2.8E+07	2.8E+07	4398	0.319613802	2.964846818	0.1713519	0.251531327	0.05805	0	67	67	174	105	119	210	164	145	210	152
ENSMUSG00000036775	chr17	Decr2	2.6E+07	2.6E+07	2288	0.344290514	2.92875187	0.1717968	0.252152024	0.06713	0	93	68	96	77	173	231	144	122	227	150
ENSMUSG00000066643	chr12	Wdr35	8973892	8974179	7273	-0.28075494	3.486807226	0.1718107	0.252152024	0.04548	0	195	148	206	195	164	220	245	162	173	238
ENSMUSG00000095123	chr10	Gm21781	4391587	4396424	4838	0.510263763	1.040915765	0.1720431	0.252466668	0.1221	0	18	27	21	13	40	68	33	32	37	68
ENSMUSG00000021013	chr12	Ttc8	9.9E+07	9.9E+07	2749	-0.35457808	1.857033313	0.1721021	0.252526893	0.0654	0	66	51	58	41	81	84	63	48	60	67
ENSMUSG00000027555	chr3	Car13	1.5E+07	1.5E+07	2299	0.583022311	1.450851212	0.1722212	0.252649173	0.18797	0	36	25	12	12	73	107	57	47	67	50
ENSMUSG00000049680	chr11	Urgcp	5713417	5718263	5871	-0.26580797	6.036224025	0.1722215	0.252649173	0.04439	0	899	654	1594	1289	1079	1387	1390	814	1416	1206
ENSMUSG00000021719	chr13	Rgs7bp	1E+08	1E+08	5828	-0.52626327	0.279618728	0.1723542	0.25280274	0.1296	0	17	29	17	18	14	18	27	16	14	20
ENSMUSG00000022552	chr15	Sharpin	7.6E+07	7.6E+07	3765	0.222464043	4.740196951	0.1723622	0.25280274	0.02957	0	330	241	465	405	439	601	605	416	716	634
ENSMUSG00000020527	chr11	Myo19	8.5E+07	8.5E+07	7113	-0.3859101	1.941503534	0.1724782	0.252946348	0.07577	0	41	46	122	53	68	66	82	53	69	65
ENSMUSG00000025145	chr11	Lrrc45	1.2E+08	1.2E+08	3293	0.39642557	2.679360635	0.1726778	0.253191626	0.08698	0	84	81	71	57	108	208	95	89	147	212
ENSMUSG00000026463	chr1	Atp2b4	1.3E+08	1.3E+08	12248	-0.29015106	4.379355578	0.1726815	0.253191626	0.05117	0	298	245	289	280	636	507	396	262	365	422
ENSMUSG00000043366	chr7	Olfr78	1E+08	1E+08	3496	-0.57796246	0.233738317	0.1727731	0.25329942	0.15279	0	7	21	21	31	16	30	23	14	10	14
ENSMUSG00000076435	chr11	Acsf2	9.5E+07	9.5E+07	3432	-0.43375707	2.947340724	0.1728579	0.253397227	0.11079	0	116	70	119	75	312	187	101	88	137	166
ENSMUSG00000003199	chr17	Mpnd	5.6E+07	5.6E+07	2305	0.262919329	5.592933236	0.172884	0.253409051	0.04333	0	585	415	725	587	1074	1143	1253	739	1326	1004
ENSMUSG00000026203	chr1	Dnajb2	7.5E+07	7.5E+07	4249	-0.25254056	6.536678214	0.1729248	0.253442402	0.04043	0	1440	1034	2201	1525	1507	2077	1858	1289	1790	1787
ENSMUSG00000036104	chr1	Rab3gap1	1.3E+08	1.3E+08	11718	-0.23621906	5.346258144	0.1731451	0.253738672	0.03433	0	549	411	1009	706	720	880	910	586	745	747
ENSMUSG00000100783	chr5	2310047D07Rik	1.5E+08	1.5E+08	823	-0.33319013	2.64580317	0.1731958	0.253786456	0.06212	0	132	67	111	110	96	114	109	70	143	132

ENSMUSG00000050737	chr2	Ptges	3.1E+07	3.1E+07	3931	0.530233792	3.586566355	0.1732531	0.253843971	0.17411	0	141	114	60	68	361	343	150	244	420	284
ENSMUSG00000100863	chr4	Gm12669	9.2E+07	9.2E+07	1009	-0.28313997	3.107581088	0.1733012	0.253887885	0.04433	0	148	98	187	132	146	171	174	110	144	201
ENSMUSG00000097318	chr16	1700007L15Rik	3.3E+07	3.3E+07	737	0.588537999	0.019095094	0.1733308	0.253904669	0.16712	0	11	0	21	9	16	28	24	21	14	23
ENSMUSG00000010911	chr2	Apip	1E+08	1E+08	1000	-0.22809922	4.49032033	0.1735292	0.254168862	0.0307	0	372	241	477	367	382	469	499	355	392	411
ENSMUSG00000030619	chr7	Eed	9E+07	9E+07	2218	-0.22100894	4.321432059	0.1736209	0.254276638	0.0287	0	311	251	377	315	360	446	443	289	369	360
ENSMUSG00000046191	chr18	Pcdhb20	3.8E+07	3.8E+07	3559	0.581864725	0.547089472	0.1737257	0.254403475	0.14813	0	14	21	10	10	23	53	19	16	39	43
ENSMUSG00000024830	chr19	Rps6kb2	4156713	4157199	2445	0.242174746	4.377651017	0.1738195	0.254514344	0.03424	0	238	246	309	293	333	515	493	287	491	557
ENSMUSG00000093577	chr3	Gm20632	9.6E+07	9.6E+07	2427	0.535655327	-0.05958963	0.1742296	0.255088132	0.11775	0	7	4	18	5	20	27	20	12	17	28
ENSMUSG00000017734	chr2	Dbndd2	1.6E+08	1.6E+08	4389	0.243140866	5.311442335	0.1742894	0.255149083	0.03678	0	538	338	669	615	610	1170	745	629	1079	853
ENSMUSG00000039063	chr2	Echdc3	6188465	6189651	2685	-0.30270641	3.562882037	0.1744435	0.255347961	0.05339	0	206	115	199	162	316	215	199	171	286	209
ENSMUSG00000028479	chr4	Gne	4.4E+07	4.4E+07	6358	-0.28255207	3.447855922	0.1745199	0.255406478	0.04606	0	130	143	206	162	265	279	212	154	202	170
ENSMUSG00000036398	chr17	Ppp1r11	3.7E+07	3.7E+07	1975	0.226460892	5.520182413	0.1745066	0.255406478	0.03199	0	579	412	794	671	777	1166	1037	728	1155	1046
ENSMUSG00000024853	chr19	Sf3b2	5273923	5274527	3231	0.255611891	6.863967499	0.1745842	0.255459239	0.04195	0	1329	979	2265	1754	1874	2987	2762	1994	2640	2746
ENSMUSG00000025236	chr9	Adpgk	5.9E+07	5.9E+07	2470	0.303577826	3.085328265	0.1746084	0.255459239	0.05311	0	118	66	136	93	165	203	175	190	175	198
ENSMUSG00000038210	chr6	Hoxa11	5.2E+07	5.2E+07	2287	-0.83262347	0.139911061	0.1746106	0.255459239	0.37453	0	6	27	32	24	6	3	40	9	16	8
ENSMUSG00000029655	chr5	N4bp2l2	1.5E+08	1.5E+08	12262	-0.24634605	3.990151687	0.1746638	0.255510405	0.03585	0	280	207	271	245	277	367	334	240	254	302
ENSMUSG00000034974	chr10	Dapk3	8.1E+07	8.1E+07	1766	0.260605938	4.383136042	0.174818	0.255682692	0.04145	0	221	170	375	361	327	489	403	359	606	476
ENSMUSG00000101166	chr7	Gm28496	4.4E+07	4.4E+07	2991	-0.49530461	0.3393409	0.1748058	0.255682692	0.11164	0	14	26	27	10	25	27	19	15	16	24
ENSMUSG00000035376	chr16	Ptplb	3.5E+07	3.5E+07	3603	-0.7598382	2.932018191	0.1749347	0.255826775	0.35592	0	127	55	29	26	534	154	113	91	113	109
ENSMUSG00000043866	chr7	Taf10	1.1E+08	1.1E+08	4584	0.223746488	5.220614164	0.1750211	0.255914174	0.03077	0	481	385	576	551	596	959	752	617	956	867
ENSMUSG00000068735	chr2	Trp53i11	9.3E+07	9.3E+07	3690	0.336017263	4.080157723	0.175031	0.255914174	0.07082	0	138	83	295	275	396	430	426	320	335	423
ENSMUSG00000029456	chr5	Acad10	1.2E+08	1.2E+08	6068	-0.39298523	2.282143519	0.1751245	0.256004006	0.08669	0	85	41	67	66	162	100	76	58	101	94
ENSMUSG00000101188	chr1	Eif4a-ps4	6.1E+07	6.1E+07	1218	0.278331041	3.625250611	0.1751289	0.256004006	0.04511	0	118	136	216	174	194	363	279	259	241	235
ENSMUSG00000052105	chr17	Mtcl1	6.6E+07	6.6E+07	9268	-0.41102875	2.329983424	0.175213	0.256100189	0.09451	0	47	45	177	103	72	110	103	67	80	80
ENSMUSG00000002012	chrX	Pnck	7.4E+07	7.4E+07	1971	0.356164291	3.721873026	0.1752446	0.256119686	0.07628	0	199	180	163	96	202	295	256	275	402	267
ENSMUSG00000061731	chr15	Ext1	5.3E+07	5.3E+07	8077	0.265249318	4.171982041	0.175516	0.256489661	0.04215	0	191	199	256	257	325	551	401	376	349	335
ENSMUSG00000022817	chr16	Itgb5	3.4E+07	3.4E+07	3362	-0.26567425	7.118769559	0.1756021	0.256588781	0.04555	0	1871	1352	3383	2250	2967	3075	3133	1811	2473	2679
ENSMUSG00000009406	chrX	Elk1	2.1E+07	2.1E+07	5381	0.263105963	3.605416812	0.1757706	0.256771285	0.03936	0	157	135	159	153	219	298	273	221	297	266
ENSMUSG00000028607	chr4	Cpt2	1.1E+08	1.1E+08	2391	-0.35771729	6.858750809	0.1757619	0.256771285	0.08263	0	1436	659	3684	2397	2301	2363	2529	1398	1899	2438
ENSMUSG00000058351	chr14	Smim4	3.1E+07	3.1E+07	592	0.409280224	2.994206049	0.175782	0.256771285	0.1034	0	55	34	223	95	143	182	196	143	187	215
ENSMUSG00000024137	chr17	E4f1	2.4E+07	2.4E+07	2561	-0.24451133	3.728943618	0.1759677	0.257015785	0.03467	0	202	152	272	234	223	282	266	162	266	282
ENSMUSG00000049115	chr13	Agtr1a	3E+07	3E+07	2467	-0.37013011	2.145231555	0.1760562	0.257118259	0.07492	0	78	55	55	65	115	120	72	61	72	69
ENSMUSG00000037108	chr5	Zcwpw1	1.4E+08	1.4E+08	2541	0.563391796	-0.16729308	0.1761472	0.257224379	0.12981	0	7	6	8	5	22	24	14	16	14	27
ENSMUSG00000023868	chr17	Pde10a	8525372	8525815	12598	-0.50565772	2.062231951	0.1767906	0.258137126	0.15283	0	46	34	101	149	36	92	85	37	56	87
ENSMUSG00000015016	chr8	Acsf3	1.2E+08	1.2E+08	2206	-0.27490447	4.387338591	0.1768135	0.258143589	0.04578	0	276	167	503	320	538	422	377	312	473	360
ENSMUSG00000001403	chr2	Ube2c	1.6E+08	1.6E+08	2600	1.12549069	6.906150642	0.1769345	0.258293397	0.78298	0	142	74	4145	1059	1180	207	3038	198	6784	7181
ENSMUSG00000032374	chr9	Plod2	9.3E+07	9.3E+07	5392	0.531102455	2.958032125	0.1771374	0.258562704	0.16983	0	96	142	58	97	32	267	155	174	151	186
ENSMUSG00000039917	chr5	Rhbdd2	1.4E+08	1.4E+08	7478	0.289434616	3.685048602	0.1772114	0.258643843	0.05056	0	135	113	171	166	300	329	244	248	310	310
ENSMUSG00000056204	chr8	Pgpep1	7.1E+07	7.1E+07	4882	0.237410426	4.452329446	0.1774085	0.258904523	0.03459	0	256	169	421	357	343	551	472	345	549	533
ENSMUSG00000027455	chr2	Nsfl1c	1.5E+08	1.5E+08	3967	0.241684331	6.310153452	0.1774909	0.258997844	0.03768	0	1072	731	1355	1085	1300	2092	1655	1411	1855	1864
ENSMUSG00000029701	chr6	Rbm28	2.9E+07	2.9E+07	5666	-0.22668219	5.104546333	0.1775289	0.259026331	0.03216	0	508	476	573	480	741	784	676	530	601	679
ENSMUSG00000024841	chr19	Eif1ad	5366813	5367210	2469	-0.21949767	4.778713515	0.1777526	0.259325729	0.02935	0	418	295	651	383	519	595	613	395	500	521
ENSMUSG00000030447	chr7	Cyfip1	5.6E+07	5.6E+07	8925	0.228466788	5.140725119	0.1778002	0.259368253	0.03283	0	402	302	709	473	628	990	977	536	749	722
ENSMUSG00000033405	chr14	Nudt15	7.4E+07	7.4E+07	2592	-0.47573496	1.207721676	0.1778607	0.259429496	0.1149	0	51	31	42	40	27	31	60	38	36	24
ENSMUSG00000024182	chr17	Axin1	2.6E+07	2.6E+07	3828	-0.20901012	4.642018377	0.1779481	0.259530065	0.02637	0	343	293	535	403	460	555	540	351	498	454
ENSMUSG00000004056	chr7	Akt2	2.8E+07	2.8E+07	7131	-0.25603949	7.994871682	0.1780329	0.25957486	0.04301	0	3923	3034	4944	3897	5325	4883	5551	3597	4974	5052
ENSMUSG00000050103	chr12	Agmo	3.7E+07	3.7E+07	6285	-0.48426123	2.04775538	0.1780253	0.25957486	0.1359	0	59	45	49	39	176	102	60	44	62	86
ENSMUSG00000086119	chr9	Gm2415	1.2E+08	1.2E+08	3735	0.533452643	1.549382039	0.1780344	0.25957486	0.1676	0	31	12	29	19	92	79	43	50	97	73
ENSMUSG00000030879	chr7	Mrpl17	1.1E+08	1.1E+08	4153	0.229998923	5.704981247	0.1782467	0.259857363	0.03381	0	641	496	898	679	960	1271	1150	863	1310	1227
ENSMUSG00000041231	chr11	Ublcp1	4.4E+07	4.4E+07	2542	-0.23929679	4.198557549	0.1783385	0.259964182	0.03469	0	254	223	409	331	282	441	371	239	376	323
ENSMUSG00000042429	chr1	Adora1	1.3E+08	1.3E+08	5785	-0.89638534	2.900547321	0.178364	0.259974352	0.50332	0	138	64	13	20	539	98	41	71	197	123
ENSMUSG00000032381	chr9	Fam96a	6.6E+07	6.6E+07	1240	-0.23553219	5.662191138	0.1785329	0.260179742	0.03549	0	773	569	1167	845	815	1156	1123	701	947	908
ENSMUSG00000033628	chr18	Pik3c3	3E+07	3E+07	4466	-0.21142946	4.557871339	0.178542	0.260179742	0.02697	0	401	256	468	363	426	547	465	337	457	453
ENSMUSG00000047420	chr6	Fam180a	3.5E+07	3.5E+07	1528	0.478361684	0.614105878	0.178583	0.260185494	0.10309	0	17	14	16	16	26	48	24	37	20	39
ENSMUSG00000051906	chr8	Cd209f	4102787	4103249	1528	0.629807498	3.574407875	0.1785673	0.260185494	0.25142	0	120	148	29	57	333	490	168	338	262	199
ENSMUSG00000024146	chr17	Cript	8.7E+07	8.7E+07	1712	-0.22461563	5.231741464	0.1788755	0.260584571	0.03199	0	652	487	635	595	644	833	798	544	657	755
ENSMUSG00000034274	chr11	Thoc5	4895320	4895378	2861	0.23100762	4.093256499	0.1789564	0.260653827	0.03188	0	213	151	294	260	275	427	350	297	416	402
ENSMUSG00000099583	chr13	Hist1h3d	2.4E+07	2.4E+07	560	-0.53719401	-0.0170501	0.1789602	0.260653827	0.12828	0	16	14	17	16	16	11	13	9	32	10
ENSMUSG00000022710	chr16	Usp7	8689595	8690886	7766	-0.24128358	6.424095169	0.1791592	0.260916454	0.03795	0	1282	1104	1652	1429	1529	1862	1778	1241	1585	1686
ENSMUSG00000085666	chr10	Gm9855	4.2E+07	4.2E+07	1194	-0.32115032	1.93811326	0.1793099	0.261108914	0.05225	0	53	50	80	62	69	66	73	58	73	71
ENSMUSG00000007833	chr7	Aldh16a1	4.5E+07	4.5E+07	5501	0.242636705	4.458989053	0.1795613	0.261420674	0.03665	0	231	175	396	352	400	561	457	341	595	513
ENSMUSG00000020393	chr11	Kremen1	5191552	5195121	7722	-0.45620786	6.278421831	0.1795491	0.261420674	0.13629	0	748	511	3006	2048	863	1045	2139	949	1241	1397
ENSMUSG00000000223	chrX	Drp2	1.3E+08	1.3E+08	8553	0.37126079	2.698040285	0.1795877	0.261431992	0.07715	0	86	79	92	99	50	202	138	104	125	182
ENSMUSG00000049751	chr12	Rpl36al	6.9E+07	6.9E+07	1353	0.290927361	6.35495289	0.1796705	0.261525425	0.05527	0	1228	933	925	1052	1299	2378	1396	1523	2118	1875
ENSMUSG00000024033	chr17	Rsph1	3.1E+07	3.1E+07	1164	-0.54412953	1.691166858	0.1797721	0.261646042	0.17677	0	55	55	27	98	31	70	28	41	54	73
ENSMUSG00000038290	chr11	Smg6	7.5E+07	7.5E+07	8453	-0.20807774	4.80779202	0.1802092	0.262255011	0.02673	0	426	311	562	482	494	639	614	387	503	555
ENSMUSG00000022323	chr15	Hrsp12	3.4E+07	3.4E+07	3192	-0.27988391	3.265505687	0.1802704	0.26230499	0.04611	0	155	123	154	142	213	227	165	146	201	150

ENSMUSG00000029863	chr6	Casp2	4.2E+07	4.2E+07	6986	0.310423042	2.844661566	0.1802809	0.26230499	0.05338	0	93	86	102	77	113	219	147	140	140	162
ENSMUSG00000023055	chr15	Calcoco1	1E+08	1E+08	3963	-0.25475827	6.69289706	0.1806108	0.262757714	0.04275	0	1775	1137	2117	1820	1673	2058	2186	1350	1944	2269
ENSMUSG00000039128	chr2	Cdc123	5794294	5794880	3463	-0.22022503	5.310502197	0.1807013	0.26286204	0.03085	0	675	460	742	557	799	919	735	599	757	777
ENSMUSG00000041740	chr5	Rnf10	1.2E+08	1.2E+08	4447	-0.27291281	8.273524346	0.1808517	0.263053639	0.04956	0	4395	3249	7319	5791	5255	5836	7193	3850	6338	5972
ENSMUSG00000037353	chr15	Letmd1	1E+08	1E+08	2579	-0.48301679	3.895189944	0.1810204	0.263271677	0.1497	0	313	101	148	128	677	268	207	190	321	287
ENSMUSG00000033157	chr16	Abhd10	4.6E+07	4.6E+07	3710	-0.25327651	3.405405783	0.181088	0.263342693	0.03703	0	153	131	199	172	210	207	229	139	206	214
ENSMUSG00000002617	chr17	Zfp40	2.3E+07	2.3E+07	4482	-0.42068437	0.745814514	0.1813438	0.263687299	0.08773	0	30	24	24	31	25	33	37	15	21	36
ENSMUSG00000074506	chr3	Gm10705	8.7E+07	8.7E+07	461	-0.50147981	-0.04342542	0.1813912	0.263728891	0.08623	0	14	13	18	16	16	17	14	15	8	20
ENSMUSG00000002847	chr16	Pla1a	3.8E+07	3.8E+07	1972	0.405399454	3.80523132	0.1814412	0.263774321	0.10546	0	113	112	120	135	457	428	351	260	322	278
ENSMUSG00000000384	chr11	Tbrg4	6615598	6615766	3696	-0.28982228	5.822011047	0.1814833	0.263808088	0.05495	0	701	455	1506	1254	947	1092	1289	793	1016	1075
ENSMUSG00000031783	chr8	Polr2c	9.5E+07	9.5E+07	1580	-0.22908756	5.742958471	0.181745	0.264161117	0.03411	0	844	666	1118	824	907	1149	1098	813	1020	1007
ENSMUSG00000029009	chr4	Mthfr	1.5E+08	1.5E+08	7315	-0.27412132	3.522864063	0.1818451	0.264279222	0.04539	0	129	148	220	181	276	289	235	128	218	217
ENSMUSG00000018583	chr11	G3bp1	5.5E+07	5.5E+07	7064	-0.26894363	7.304567729	0.1818676	0.264284665	0.04819	0	2440	2174	3085	2866	2290	3279	3203	2452	2875	2963
ENSMUSG00000058325	chr7	Dock1	1.3E+08	1.3E+08	6807	0.266907753	3.740456387	0.1819797	0.264420128	0.04367	0	153	117	218	143	302	376	315	242	274	293
ENSMUSG00000080904	chr11	Gm11966	5818497	5818583	87	0.432003463	2.118177962	0.1820381	0.264477582	0.1069	0	55	33	34	70	79	72	105	54	143	130
ENSMUSG00000024845	chr19	Tmem134	4125934	4126200	4601	0.250714839	6.317039837	0.1821177	0.264565845	0.04148	0	959	743	1226	1089	1554	1939	1737	1231	2089	1999
ENSMUSG00000028631	chr4	Kcnq4	1.2E+08	1.2E+08	4024	0.289802457	5.191821882	0.1822482	0.264727897	0.05513	0	382	268	1024	462	455	837	893	645	816	947
ENSMUSG00000042116	chr4	Vwa1	1.6E+08	1.6E+08	3623	0.239484339	4.225687837	0.1822999	0.264775607	0.03538	0	223	185	330	193	382	523	432	313	427	399
ENSMUSG00000026313	chr1	Hdac4	9.2E+07	9.2E+07	15375	-0.27506288	5.543840759	0.1826101	0.26519874	0.04965	0	813	573	861	937	612	784	853	690	1075	923
ENSMUSG00000026767	chr2	Fam188a	1.2E+07	1.2E+07	6294	-0.29896257	2.872672233	0.1827149	0.265323419	0.05087	0	127	78	135	102	168	167	170	104	112	121
ENSMUSG00000024944	chr19	Arl2	6134374	6134801	2891	0.244533452	5.659654499	0.1828703	0.265521677	0.03913	0	619	462	880	750	821	1138	1015	795	1470	1246
ENSMUSG00000089774	chr16	Slc5a3	9.2E+07	9.2E+07	10913	-0.36932944	3.674110606	0.1832176	0.265998406	0.08687	0	242	146	188	106	417	357	210	155	202	240
ENSMUSG00000032905	chr18	Atg12	4.7E+07	4.7E+07	2492	-0.23066127	5.169387077	0.1833099	0.26610475	0.03453	0	623	502	591	528	633	790	805	502	721	614
ENSMUSG00000034445	chr19	Cyb561a3	1.1E+07	1.1E+07	1474	-0.32895803	2.580812018	0.1834645	0.266301631	0.0634	0	99	73	92	124	102	108	158	65	110	105
ENSMUSG00000002052	chr11	Supt6	7.8E+07	7.8E+07	7095	-0.23631838	5.990768343	0.183614	0.266484738	0.03679	0	934	656	1398	1102	1188	1267	1401	860	1278	1250
ENSMUSG00000074698	chr2	Csnk2a1	1.5E+08	1.5E+08	7089	-0.24693891	7.035018975	0.1836286	0.266484738	0.04081	0	2067	1556	2798	2051	2333	2791	2780	2002	2336	2476
ENSMUSG00000028868	chr4	Wasf2	1.3E+08	1.3E+08	6258	0.236177032	5.321885848	0.1837903	0.266691813	0.03637	0	401	371	667	529	868	1050	932	633	931	947
ENSMUSG00000058447	chr7	Gm26920	3E+07	3E+07	2374	-0.38319399	1.439706329	0.1839188	0.266850632	0.07604	0	47	36	50	32	59	72	61	31	34	41
ENSMUSG00000098954	chr4	Mir7658	1.6E+08	1.6E+08	57	0.494050148	0.4234914	0.1840107	0.266956329	0.11307	0	12	12	11	14	28	24	32	30	39	20
ENSMUSG00000064105	chr19	Cnnm2	4.7E+07	4.7E+07	3558	-0.46395935	2.090095492	0.1841033	0.267063027	0.12917	0	56	49	58	38	176	97	80	42	90	59
ENSMUSG00000047414	chr12	Flrt2	9.6E+07	9.6E+07	7721	0.252892976	3.587382152	0.1841283	0.267071693	0.03898	0	149	98	221	154	218	292	298	240	245	254
ENSMUSG00000042364	chr13	Snx18	1.1E+08	1.1E+08	4446	0.216563073	4.474048347	0.1844219	0.2674699	0.02911	0	286	207	365	304	402	632	501	377	431	531
ENSMUSG00000020376	chr11	Rnf130	5E+07	5E+07	1558	0.236821191	5.539276313	0.1845727	0.267661017	0.03664	0	701	469	635	582	823	1362	1049	784	1044	985
ENSMUSG00000087128	chr4	Gm12655	9.4E+07	9.4E+07	961	-0.35829573	1.396809328	0.1849555	0.268188296	0.06219	0	40	34	64	39	39	57	52	38	42	41
ENSMUSG00000016510	chr5	Mtif3	1.5E+08	1.5E+08	5127	-0.24962408	4.238432194	0.1850077	0.268236315	0.03871	0	266	183	520	289	330	378	434	258	371	341
ENSMUSG00000027193	chr2	Api5	9.4E+07	9.4E+07	4545	-0.21286594	5.145678849	0.1850541	0.268250036	0.02925	0	579	436	681	529	634	863	741	535	613	643
ENSMUSG00000072407	chr10	Gm6419	7.5E+07	7.5E+07	432	-0.44910527	0.44640749	0.1850554	0.268250036	0.08307	0	17	17	32	24	21	15	26	16	27	26
ENSMUSG00000008668	chr17	Rps18	3.4E+07	3.4E+07	2491	0.25767126	6.985942742	0.1851709	0.268389703	0.04467	0	1644	1442	1734	1736	2062	3670	2601	2176	2811	3076
ENSMUSG00000047222	chr14	Rnase2a	5.1E+07	5.1E+07	686	0.728645266	2.658169744	0.1852222	0.268436354	0.34106	0	49	91	11	36	149	359	44	109	92	219
ENSMUSG00000021072	chr12	Tmx1	7E+07	7E+07	3299	-0.21186059	4.579513993	0.1852742	0.268483978	0.02801	0	369	276	462	373	462	457	551	348	443	483
ENSMUSG00000025280	chr14	Polr3a	2.4E+07	2.4E+07	4683	-0.27549068	3.193975293	0.1853033	0.268498319	0.0442	0	144	82	182	176	178	183	182	148	164	165
ENSMUSG00000021494	chr13	Ddx41	5.6E+07	5.6E+07	2205	0.237790273	3.745908301	0.1853312	0.268511107	0.03374	0	181	130	227	165	227	396	293	229	297	282
ENSMUSG00000041135	chr4	Ripk2	1.6E+07	1.6E+07	2816	0.342717629	2.043855316	0.1856956	0.269011212	0.06577	0	53	26	58	49	88	108	117	65	80	97
ENSMUSG00000097346	chr13	Gm26619	9.8E+07	9.8E+07	1073	0.853592965	0.084559059	0.1858377	0.269189231	0.4391	0	4	1	31	12	6	8	19	3	49	46
ENSMUSG00000027133	chr2	Nop10	1.1E+08	1.1E+08	1109	0.229874886	5.28761777	0.1858705	0.26920896	0.0344	0	568	398	557	567	601	1005	771	733	846	973
ENSMUSG00000019487	chr17	Trip10	5.7E+07	5.7E+07	2290	-0.25031195	7.0938166	0.1859728	0.269329299	0.04242	0	1915	1572	3238	2230	2407	2881	2795	1796	2787	2722
ENSMUSG00000054309	chr12	Cpsf3	2.1E+07	2.1E+07	2560	0.217564073	4.440810044	0.1860069	0.269350824	0.02972	0	249	207	391	310	374	565	436	391	522	484
ENSMUSG00000045827	chr13	Serpinb9	3.3E+07	3.3E+07	3494	0.283551681	3.274750686	0.1862133	0.269621887	0.04826	0	140	88	130	118	179	333	230	148	205	188
ENSMUSG00000038369	chr2	Ncoa6	1.6E+08	1.6E+08	9744	-0.22832527	4.304596454	0.1862477	0.269643921	0.03208	0	298	193	418	349	372	420	385	329	329	399
ENSMUSG00000027679	chr3	Dnajc19	3.4E+07	3.4E+07	1015	-0.22781145	5.449333206	0.1863009	0.269693077	0.03424	0	714	548	789	759	711	995	833	680	823	818
ENSMUSG00000064366	chrMT	mt-Tl2	11671	11741	71	-0.78213931	0.283560507	0.1863794	0.269778951	0.35381	0	18	17	28	26	18	5	28	2	5	48
ENSMUSG00000038705	chr2	Gmeb2	1.8E+08	1.8E+08	4988	-0.25293443	3.276594417	0.1867637	0.270307209	0.03749	0	157	117	165	152	197	209	193	130	186	192
ENSMUSG00000086596	chr9	Susd5	1.1E+08	1.1E+08	3874	0.514453236	0.672388212	0.1868287	0.270373421	0.11924	0	20	21	17	18	12	64	32	27	22	37
ENSMUSG00000001440	chr11	Kpnb1	9.7E+07	9.7E+07	6590	-0.2490235	6.878693434	0.1870219	0.270577596	0.04213	0	1693	1445	2351	2120	2043	2759	2573	1744	1988	2095
ENSMUSG00000004865	chr17	Srpk1	2.9E+07	2.9E+07	9647	-0.21050495	4.446095036	0.1870134	0.270577596	0.02779	0	345	253	399	356	409	511	412	303	442	425
ENSMUSG00000074063	chr8	Osgin1	1.2E+08	1.2E+08	2674	0.316246087	3.503188281	0.1870276	0.270577596	0.06449	0	131	84	207	89	278	276	261	214	274	256
ENSMUSG00000042462	chr7	Dctpp1	1.3E+08	1.3E+08	676	0.243065106	3.976757247	0.187087	0.270635501	0.0365	0	232	142	281	221	211	379	324	255	416	381
ENSMUSG00000103988	chr3	Dnajc19	3.4E+07	3.4E+07	333	-0.22685743	5.431371369	0.1875318	0.271251053	0.03414	0	713	546	771	742	700	988	823	676	811	800
ENSMUSG00000029153	chr5	Ociad2	7.3E+07	7.3E+07	2509	-0.36271432	5.815658856	0.1875596	0.271263311	0.08942	0	1213	1064	506	751	947	1037	1022	822	1164	1018
ENSMUSG00000027488	chr2	Snta1	1.5E+08	1.5E+08	3094	0.314677486	7.59075555	0.1876156	0.271316194	0.06785	0	1722	1391	4160	3427	2727	3921	5083	2833	5389	4975
ENSMUSG00000020431	chr11	Adcy1	7063489	7064235	12522	-0.55038322	0.330872395	0.1877949	0.271481473	0.13613	0	20	7	37	23	21	8	24	14	28	22
ENSMUSG00000029521	chr5	Chek2	1.1E+08	1.1E+08	2247	-0.39521597	1.406772501	0.1878073	0.271481473	0.07876	0	32	26	55	32	82	52	51	37	43	45
ENSMUSG00000030695	chr7	Aldoa	1.3E+08	1.3E+08	2754	-0.28111937	14.16454215	0.1877803	0.271481473	0.05447	0	255136	216642	322862	365885	365063	318994	378516	228442	434739	360340
ENSMUSG00000061143	chr3	Maml3	5.2E+07	5.2E+07	10486	0.321137301	2.257045444	0.1878065	0.271481473	0.0596	0	52	32	107	55	79	112	123	79	110	113
ENSMUSG00000026563	chr1	Tada1	1.7E+08	1.7E+08	4110	0.298410298	2.578782027	0.1879738	0.271694156	0.04953	0	58	58	94	86	105	169	149	79	138	144
ENSMUSG00000062352	chr12	Itgb1bp1	2.1E+07	2.1E+07	3321	0.214140356	4.89327223	0.1881724	0.271953157	0.02961	0	317	303	474	426	574	753	661	491	705	688
ENSMUSG00000030062	chr6	Rpn1	8.8E+07	8.8E+07	3642	0.258428683	6.572188164	0.1882565	0.272046755	0.0456	0	1052	798	1984	1178	1745	2842	2407	1580	2098	1879

ENSMUSG00000029003	chr4	Mad2l2	1.5E+08	1.5E+08	2622	0.35533494	3.500023664	0.1885437	0.272433744	0.08343	0	96	64	215	109	308	250	333	188	267	264
ENSMUSG00000023806	chr17	Rsph3b	6904716	6905120	1614	-0.33266451	2.645494619	0.1886772	0.272542385	0.06516	0	92	52	179	112	101	136	154	72	99	111
ENSMUSG00000057388	chr17	Mrpl18	1.3E+07	1.3E+07	1398	-0.27781941	6.57183248	0.1886505	0.272542385	0.05267	0	1393	874	2754	1641	1459	2041	2105	1358	1615	1798
ENSMUSG00000059772	chr7	Slx1b	1.3E+08	1.3E+08	3521	0.290646309	2.774983673	0.1886652	0.272542385	0.04852	0	96	66	101	71	126	190	147	124	146	159
ENSMUSG00000027808	chr3	Serp1	5.9E+07	5.9E+07	2440	0.32007719	4.849485338	0.188709	0.272560252	0.06828	0	355	326	248	286	707	976	677	521	557	595
ENSMUSG00000037692	chr4	Ahdc1	1.3E+08	1.3E+08	8444	-0.25981192	5.416966102	0.1887463	0.272586041	0.0452	0	516	441	1053	836	743	743	1021	531	945	794
ENSMUSG00000024403	chr17	Atp6v1g2	3.5E+07	3.5E+07	2510	0.383730992	1.274819379	0.1888687	0.272734681	0.06779	0	27	29	31	33	28	64	46	39	60	61
ENSMUSG00000002343	chr8	Armc6	7E+07	7E+07	3262	0.259303116	3.786089514	0.188902	0.272754765	0.04173	0	181	141	189	205	220	334	267	277	367	279
ENSMUSG00000028811	chr4	Yars	1.3E+08	1.3E+08	5943	-0.22653626	5.792464843	0.1890104	0.272883219	0.03442	0	772	636	1251	858	1056	1172	1070	840	1153	1030
ENSMUSG00000024952	chr19	Rps6ka4	6829085	6829738	3119	0.218462138	4.436894044	0.1891505	0.273057249	0.03057	0	235	189	415	313	389	549	558	343	477	486
ENSMUSG00000089739	chr2	Gm20431	1.7E+08	1.7E+08	2367	-0.23727429	5.564652323	0.1893544	0.273323528	0.03782	0	659	533	991	844	874	883	1222	612	894	902
ENSMUSG00000029507	chr5	Pus1	1.1E+08	1.1E+08	2180	0.246305469	4.021658554	0.1894492	0.273432242	0.0385	0	177	143	276	255	282	411	293	262	423	426
ENSMUSG00000009681	chr10	Bcr	7.5E+07	7.5E+07	6537	0.306940964	3.227179207	0.1896567	0.273675439	0.0579	0	97	94	116	109	216	297	177	158	209	225
ENSMUSG00000085779	chr10	Atcayos	8.1E+07	8.1E+07	4375	-0.32024019	5.873538776	0.1896437	0.273675439	0.06999	0	1055	618	1878	843	615	1132	980	944	1086	1191
ENSMUSG00000003665	chr17	Has1	1.8E+07	1.8E+07	2090	0.77378971	0.011871111	0.189752	0.273700214	0.35278	0	6	3	0	7	36	16	17	20	31	29
ENSMUSG00000021645	chr13	Smn1	1E+08	1E+08	2592	0.255268396	3.243458217	0.1897491	0.273700214	0.03818	0	110	98	160	119	162	220	232	156	230	216
ENSMUSG00000025162	chr11	Csnk1d	1.2E+08	1.2E+08	5022	0.237559237	6.259233587	0.1897205	0.273700214	0.03849	0	961	705	1283	1051	1380	1994	1600	1266	1968	1759
ENSMUSG00000070942	chr1	Il1rl2	4E+07	4E+07	6812	0.577969719	2.42000805	0.1897388	0.273700214	0.21289	0	54	72	13	28	141	191	130	84	130	124
ENSMUSG00000074922	chr19	Fam122a	2.4E+07	2.4E+07	855	-0.26719105	3.128734517	0.1897964	0.273736159	0.04185	0	128	86	192	138	186	165	182	117	182	168
ENSMUSG00000046747	chr12	Gm9812	5.6E+07	5.6E+07	968	0.512315528	-0.16382213	0.1900734	0.27410753	0.1108	0	8	3	14	6	19	23	15	15	25	16
ENSMUSG00000052533	chr2	Nup188	3E+07	3E+07	6241	-0.24794497	3.528295535	0.1901047	0.274124428	0.03694	0	155	132	230	204	226	231	202	183	233	226
ENSMUSG00000060073	chr12	Psma3	7.1E+07	7.1E+07	3894	-0.24533329	6.957085366	0.1901354	0.274140507	0.04151	0	2002	1634	2259	1921	2285	2902	2393	1869	2325	2283
ENSMUSG00000039601	chr17	Rcan2	4.4E+07	4.4E+07	3744	-0.4793967	6.363360437	0.1902211	0.274235928	0.15797	0	832	407	3705	1829	1066	1398	2467	789	1063	1527
ENSMUSG00000056412	chr4	Gm12396	4.1E+07	4.1E+07	306	0.321791768	2.396906592	0.1905361	0.27466174	0.05781	0	70	61	64	55	92	155	105	96	120	116
ENSMUSG00000035158	chr6	Mitf	9.8E+07	9.8E+07	6215	-0.27676579	4.176290577	0.1905927	0.274686889	0.04975	0	237	181	525	328	257	347	432	228	310	378
ENSMUSG00000038517	chr11	Tbkbp1	9.7E+07	9.7E+07	3975	0.338402345	2.798230939	0.1905927	0.274686889	0.07299	0	61	46	137	77	158	197	155	100	205	142
ENSMUSG00000021983	chr14	Atp8a2	6E+07	6E+07	6419	0.445030985	1.359667018	0.19082	0.274986244	0.10615	0	45	26	24	24	34	62	47	61	74	42
ENSMUSG00000001786	chr10	Fbxo7	8.6E+07	8.6E+07	6180	0.23871227	3.742663302	0.1909155	0.275067431	0.03492	0	177	129	245	173	204	354	282	200	350	312
ENSMUSG00000043323	chr5	Fbrsl1	1.1E+08	1.1E+08	4947	-0.25229201	4.11291246	0.1909155	0.275067431	0.04043	0	206	172	447	304	326	315	376	233	338	366
ENSMUSG00000031781	chr8	Ciapin1	9.5E+07	9.5E+07	5691	0.284059297	5.138536907	0.1911903	0.27543507	0.05529	0	348	203	910	485	588	864	853	559	781	954
ENSMUSG00000049891	chr8	Gm7984	7.5E+07	7.5E+07	534	-0.4898719	0.298986728	0.1912188	0.275447784	0.10431	0	16	9	32	29	16	31	18	15	20	14
ENSMUSG00000022887	chr16	Masp1	2.3E+07	2.3E+07	2752	-0.57986846	1.648723915	0.1912583	0.275448047	0.20912	0	33	14	114	106	21	54	66	38	43	51
ENSMUSG00000024869	chr19	Nudt8	4000580	4000847	4298	0.344371585	4.421617929	0.191253	0.275448047	0.08073	0	196	110	586	367	238	460	590	370	462	582
ENSMUSG00000029439	chr5	Sfswap	1.3E+08	1.3E+08	3302	-0.24153077	4.127221937	0.1913606	0.275560574	0.03757	0	219	213	423	286	299	377	366	195	363	370
ENSMUSG00000031562	chr8	Dctd	4.8E+07	4.8E+07	3409	0.550479203	0.052369541	0.1913757	0.275560574	0.1269	0	6	12	8	17	12	27	21	21	31	12
ENSMUSG00000044475	chr10	Ascc1	6E+07	6E+07	1578	0.227527209	4.157241471	0.1914029	0.275571515	0.03258	0	218	198	315	202	307	438	377	305	420	437
ENSMUSG00000103171	chr3	DNAJC19	3.4E+07	3.4E+07	393	-0.22585701	5.393258807	0.1914581	0.27562267	0.03442	0	693	540	754	713	677	968	807	668	773	774
ENSMUSG00000057637	chr4	Prdm2	1.4E+08	1.4E+08	7420	-0.23348568	5.148525009	0.1914895	0.275639574	0.03659	0	469	422	854	657	506	799	695	456	672	773
ENSMUSG00000024862	chr19	Klc2	5107746	5108688	4134	-0.26831168	6.388623362	0.1915369	0.275679466	0.04973	0	1184	877	1824	1731	1371	1425	1963	1047	1846	1606
ENSMUSG00000035845	chr15	Alg12	8.9E+07	8.9E+07	2356	0.302523746	2.410215794	0.1920132	0.276308357	0.05169	0	61	54	88	51	102	135	138	88	119	116
ENSMUSG00000042828	chr7	Trim72	1.3E+08	1.3E+08	2553	0.312465268	7.965857502	0.1920022	0.276308357	0.06832	0	2627	1675	6015	4318	2822	6037	6364	4369	6110	5757
ENSMUSG00000041939	chr5	Mvk	1.1E+08	1.1E+08	2674	0.267273077	3.587610291	0.1920368	0.276313886	0.04526	0	115	113	207	153	247	310	229	191	316	305
ENSMUSG00000057841	chr6	Rpl32	1.2E+08	1.2E+08	517	0.255106544	7.38241537	0.1920797	0.276347334	0.04534	0	2102	1867	2726	2301	2414	4771	3239	2968	3944	3876
ENSMUSG00000040339	chr3	Fam102b	1.1E+08	1.1E+08	5702	0.283452385	4.051303129	0.1921233	0.276381719	0.05198	0	175	204	206	164	371	497	416	264	347	366
ENSMUSG00000066640	chr5	Fbxl18	1.4E+08	1.4E+08	12563	-0.22785014	4.074084344	0.192161	0.27640752	0.03277	0	229	196	359	293	299	342	327	237	377	314
ENSMUSG00000027593	chr2	Raly	1.5E+08	1.5E+08	3292	0.232943081	6.053458485	0.1922842	0.276556447	0.03723	0	843	659	1078	971	1074	1762	1371	1127	1675	1490
ENSMUSG00000098274	chr16	Rpl24	5.6E+07	5.6E+07	1030	0.253365469	7.860114297	0.1923096	0.276564646	0.04492	0	2943	2361	3618	3170	3971	6123	4369	4212	5604	5759
ENSMUSG00000001739	chr5	Cldn15	1.4E+08	1.4E+08	2124	0.477647722	2.386463449	0.1923824	0.276640884	0.14877	0	55	32	51	31	170	166	92	121	93	136
ENSMUSG00000032384	chr9	Csnk1g1	6.6E+07	6.6E+07	11973	-0.27886126	3.171137035	0.1925696	0.276881681	0.04887	0	124	146	160	145	147	178	195	125	159	177
ENSMUSG00000041313	chr5	Slc7a1	1.5E+08	1.5E+08	7527	0.329218117	2.78539487	0.1927401	0.277098421	0.06914	0	70	47	168	67	124	189	140	139	146	162
ENSMUSG00000018209	chr2	Stk4	1.6E+08	1.6E+08	5860	0.221263595	4.258623463	0.1927775	0.277123767	0.03076	0	257	212	284	269	295	501	445	336	380	458
ENSMUSG00000024697	chr19	Gna14	1.6E+07	1.6E+07	3383	0.510943487	-0.00022217	0.1928067	0.277137419	0.1171	0	4	8	21	11	12	29	31	15	21	12
ENSMUSG00000041096	chrX	Tspyl2	1.5E+08	1.5E+08	2820	0.27076669	3.711938545	0.1929575	0.277325777	0.04651	0	121	153	219	160	241	366	268	230	241	368
ENSMUSG00000037465	chr15	Klf10	3.8E+07	3.8E+07	3045	-0.34449178	4.818622594	0.1929787	0.277327729	0.08139	0	432	393	212	655	619	509	575	459	444	550
ENSMUSG00000001632	chr6	Brpf1	1.1E+08	1.1E+08	6714	-0.2397336	3.930699549	0.1932419	0.277677517	0.03653	0	200	179	264	253	356	305	352	204	311	272
ENSMUSG00000038299	chr18	Wdr36	3.3E+07	3.3E+07	3281	-0.20712288	4.607226913	0.1933904	0.277862505	0.02805	0	410	304	457	363	422	578	491	356	471	444
ENSMUSG00000034789	chr13	Rab24	5.5E+07	5.5E+07	1865	0.222030903	5.361735338	0.1937328	0.278325895	0.03325	0	561	439	659	519	681	1182	783	670	1005	955
ENSMUSG00000003464	chr1	Pex19	1.7E+08	1.7E+08	3815	-0.25859048	7.100734511	0.1937742	0.27835698	0.04687	0	1834	1274	3390	2414	2741	2678	2910	1855	2700	2819
ENSMUSG00000020828	chr11	Pld2	7.1E+07	7.1E+07	6252	0.298316356	3.538214707	0.1942013	0.278941846	0.05603	0	167	146	128	115	207	315	260	180	322	244
ENSMUSG00000045555	chr10	Mettl24	4.1E+07	4.1E+07	1529	0.532228805	0.024565437	0.1942484	0.27898092	0.11072	0	11	9	12	12	11	38	23	22	10	17
ENSMUSG00000022438	chr15	Parvb	8.4E+07	8.4E+07	4416	0.301124538	6.495998932	0.1942903	0.278993439	0.06376	0	923	615	2293	1438	1086	2074	2446	1525	2135	2126
ENSMUSG00000060279	chr7	Ap2a1	4.5E+07	4.5E+07	4301	0.246912509	6.442593279	0.1942969	0.278993439	0.04266	0	1017	745	1643	1296	1428	1877	2163	1392	2273	2058
ENSMUSG00000024440	chr18	Pcdh12	3.8E+07	3.8E+07	6055	-0.33978248	3.126162713	0.1943768	0.279079676	0.07252	0	98	59	226	171	213	148	203	133	152	147
ENSMUSG00000022177	chr14	Haus4	5.5E+07	5.5E+07	1587	0.277795328	3.110895141	0.194693	0.279505026	0.04787	0	87	75	175	108	153	234	205	114	220	208
ENSMUSG00000034509	chr17	Mad2l1bp	4.6E+07	4.6E+07	1269	0.263109778	4.330397082	0.1947597	0.279572227	0.04685	0	189	145	491	306	300	496	461	325	497	487
ENSMUSG00000036339	chr14	Tmem260	4.8E+07	4.8E+07	8165	0.306017315	2.155084446	0.1954095	0.280476209	0.05141	0	63	43	60	51	76	129	97	76	96	100
ENSMUSG00000029253	chr5	Cenpc1	8.6E+07	8.6E+07	3173	-0.40197546	2.083334691	0.1956209	0.28073792	0.1028	0	74	53	124	52	57	84	132	37	56	69

ENSMUSG00000031311	chrX	Nono	1E+08	1E+08	4375	0.226391348	5.930663851	0.1956519	0.28073792	0.03556	0	820	623	971	808	1029	1719	1473	1091	1219	1306
ENSMUSG00000050796	chr4	B3galt6	1.6E+08	1.6E+08	3184	0.350401924	1.618884916	0.1956469	0.28073792	0.06674	0	31	25	52	31	62	75	69	53	87	58
ENSMUSG00000039828	chr15	Wdr70	7873055	7873253	2151	-0.26470475	3.779948101	0.1959603	0.281140361	0.04597	0	210	212	284	189	212	263	301	202	297	215
ENSMUSG00000049489	chr11	Fam58b	7.9E+07	7.9E+07	1224	0.23836241	3.8968832	0.1959724	0.281140361	0.03584	0	187	172	215	184	261	375	297	261	346	373
ENSMUSG00000021066	chr12	Atl1	7E+07	7E+07	2818	-0.45830847	0.419241559	0.1959995	0.281150497	0.09378	0	9	19	29	20	33	26	20	17	19	26
ENSMUSG00000049950	chr2	Rpp38	3328949	3329873	1042	-0.3359957	2.29101612	0.1961627	0.281355736	0.0681	0	90	72	87	71	77	99	60	77	101	98
ENSMUSG00000034429	chr15	Zfp707	7.6E+07	7.6E+07	3094	0.332299631	2.005499704	0.1961984	0.281378201	0.0614	0	45	38	61	60	57	85	73	69	106	114
ENSMUSG00000050106	chr11	Tmc8	1.2E+08	1.2E+08	3056	0.507387221	0.456203267	0.1962524	0.281426839	0.13843	0	5	7	32	15	23	33	28	18	25	49
ENSMUSG00000030410	chr7	Dmwd	1.9E+07	1.9E+07	2534	0.211361758	4.937369945	0.1963366	0.281518763	0.03008	0	361	287	587	435	503	682	730	455	793	746
ENSMUSG00000044709	chr7	Gemin7	2E+07	2E+07	1519	0.244583633	5.49567482	0.1964146	0.281601879	0.04125	0	583	520	580	665	718	1073	930	814	1252	953
ENSMUSG00000031668	chr6	Eif2ak3	7.1E+07	7.1E+07	5428	0.277852026	3.042586095	0.196444	0.281615272	0.04693	0	101	80	129	105	144	273	213	134	153	160
ENSMUSG00000039849	chr2	Pcif1	1.6E+08	1.6E+08	6544	-0.20984692	4.933837713	0.1965321	0.281712814	0.02947	0	384	323	617	546	644	633	631	411	616	647
ENSMUSG00000024302	chr18	Dtna	2.3E+07	2.3E+07	6587	-0.2836014	6.361654338	0.1966072	0.281791536	0.05696	0	1272	1115	1594	1665	1048	1454	2109	1222	1428	1428
ENSMUSG00000079557	chr17	March2	3.4E+07	3.4E+07	5997	0.234292839	6.61604246	0.1966664	0.281847694	0.03878	0	1244	939	1714	1307	1681	2356	2394	1530	2481	2250
ENSMUSG00000023170	chr11	Gps2	7E+07	7E+07	1604	-0.21284776	4.703326786	0.1967992	0.281986655	0.02987	0	390	253	546	430	529	472	547	370	534	562
ENSMUSG00000031068	chr7	Glrx3	1.4E+08	1.4E+08	1651	-0.2351588	6.924441403	0.1968036	0.281986655	0.03925	0	1832	1464	2267	2040	2328	2709	2513	1746	2193	2416
ENSMUSG00000073676	chr1	Hspe1	5.5E+07	5.5E+07	1474	0.244199447	6.19905485	0.1969539	0.282173245	0.04213	0	840	639	1535	1027	1158	1927	1451	1340	1709	1782
ENSMUSG00000034424	chr8	Gcsh	1.2E+08	1.2E+08	1579	-0.22325171	5.796654656	0.1970317	0.282255874	0.03464	0	872	590	1137	850	1134	1317	1037	891	1009	1034
ENSMUSG00000068079	chr2	Tcf15	1.5E+08	1.5E+08	980	0.416605008	3.06488461	0.1971159	0.28234766	0.11985	0	51	32	225	103	169	234	155	172	171	236
ENSMUSG00000063888	chr17	Rpl7l1	4.7E+07	4.7E+07	2606	0.213243034	5.429957118	0.197686	0.283135339	0.03133	0	560	449	690	580	738	1056	934	802	988	970
ENSMUSG00000050188	chr4	Lsm10	1.3E+08	1.3E+08	943	0.291153822	2.95237163	0.1977087	0.283138834	0.05235	0	101	72	104	93	152	218	147	153	193	152
ENSMUSG00000028672	chr4	Hmgcl	1.4E+08	1.4E+08	2434	0.21944869	5.657524603	0.1979284	0.283424595	0.03352	0	697	506	877	622	838	1218	1158	847	1293	1091
ENSMUSG00000091586	chr17	Cyp4f17	3.3E+07	3.3E+07	1693	0.419430822	1.142104323	0.1980475	0.283566224	0.09551	0	25	15	28	35	33	48	36	27	60	78
ENSMUSG00000031728	chr8	Zfp821	1.1E+08	1.1E+08	2127	0.273370256	2.827465868	0.1981618	0.283700836	0.04522	0	72	65	125	103	120	190	151	126	149	175
ENSMUSG00000003072	chr10	Atp5d	8E+07	8E+07	1928	0.3060441	8.81476087	0.1981955	0.283720084	0.06749	0	4509	2918	10608	7133	6632	9637	10576	7151	12664	11519
ENSMUSG00000037434	chr1	Slc30a1	1.9E+08	1.9E+08	5244	0.263059236	3.836583787	0.1982552	0.283775514	0.04659	0	140	116	328	156	274	396	334	261	294	316
ENSMUSG00000055401	chr4	Fbxo6	1.5E+08	1.5E+08	2207	0.230870345	5.016566124	0.1982826	0.283775514	0.03712	0	365	241	658	393	679	833	835	530	666	760
ENSMUSG00000056966	chr5	Gjc3	1.4E+08	1.4E+08	3515	-0.42612308	0.455243599	0.1982949	0.283775514	0.08181	0	25	14	28	21	23	36	27	10	22	20
ENSMUSG00000078922	chr11	Tgtp1	4.9E+07	4.9E+07	3205	0.750712842	1.296904175	0.1986241	0.28421763	0.36185	0	22	13	31	40	25	233	28	12	23	34
ENSMUSG00000003662	chr2	Ciao1	1.3E+08	1.3E+08	3197	-0.21376967	5.228074458	0.1986804	0.284269208	0.03149	0	623	475	764	521	643	782	696	595	734	756
ENSMUSG00000066319	chr9	Rtp3	1.1E+08	1.1E+08	1425	0.453617783	0.235504236	0.1988638	0.284502608	0.09665	0	10	6	24	9	21	38	22	21	26	20
ENSMUSG00000020069	chr10	Hnrnph3	6.3E+07	6.3E+07	3151	0.209466004	4.69755638	0.1989211	0.284555512	0.02947	0	361	249	510	286	432	658	624	406	558	639
ENSMUSG00000032192	chr9	Gnb5	7.5E+07	7.5E+07	1188	-0.27070585	3.511644458	0.1990447	0.284674271	0.04692	0	150	97	306	207	207	254	245	148	202	221
ENSMUSG00000098371	chr16	Gm28037	5.6E+07	5.6E+07	611	0.249484532	7.861453134	0.1990306	0.284674271	0.04488	0	2947	2369	3632	3182	3970	6121	4372	4209	5602	5756
ENSMUSG00000022428	chr15	Cby1	8E+07	8E+07	1119	-0.23992428	3.531729546	0.1990855	0.284674549	0.03622	0	159	122	254	204	214	265	251	153	228	200
ENSMUSG00000078773	chr4	Rad54b	1.2E+07	1.2E+07	5782	-0.72401084	-0.14914816	0.1990652	0.284674549	0.30874	0	20	25	4	11	10	29	4	8	18	7
ENSMUSG00000059923	chr11	Grb2	1.2E+08	1.2E+08	2916	0.234332758	6.341569261	0.1991843	0.284786876	0.03899	0	1085	902	1276	1107	1210	2055	1827	1370	2006	1811
ENSMUSG00000043122	chr12	A530016L24Rik	1.1E+08	1.1E+08	2636	-0.63594986	3.058682992	0.1992309	0.284824372	0.27795	0	145	88	51	36	473	194	65	118	167	120
ENSMUSG00000042606	chr7	Hirip3	1.3E+08	1.3E+08	3023	-0.27843433	2.749935976	0.199257	0.284832738	0.04703	0	102	78	145	111	117	152	164	80	113	119
ENSMUSG00000009378	chr19	Slc16a12	3.5E+07	3.5E+07	4051	-0.48881906	0.32212041	0.1992978	0.284862042	0.10465	0	12	16	31	14	31	27	21	22	14	14
ENSMUSG00000034432	chr1	Cops8	9.1E+07	9.1E+07	4448	-0.23758992	6.623052757	0.1993617	0.284924362	0.04044	0	1553	1242	1852	1605	1768	1910	2240	1373	1978	1866
ENSMUSG00000026249	chr1	Serpine2	8E+07	8E+07	8287	-0.26643235	6.694047615	0.1995283	0.28513343	0.05094	0	1493	1028	2282	1791	2139	1741	2877	1374	1928	1825
ENSMUSG00000035649	chr4	Zcchc7	4.5E+07	4.5E+07	9612	-0.25518798	3.805240257	0.1995768	0.285173671	0.04361	0	226	211	230	201	251	324	252	192	221	328
ENSMUSG00000029920	chr6	Smarcad1	6.5E+07	6.5E+07	5099	-0.26488416	3.007135514	0.1996838	0.285297506	0.04363	0	138	100	167	117	132	163	169	110	164	142
ENSMUSG00000035781	chr10	R3hdm4	8E+07	8E+07	1897	0.250793518	7.201999127	0.1997875	0.2853745	0.04538	0	1930	1345	2309	1973	2722	3231	3208	2507	3882	3662
ENSMUSG00000050164	chr15	Mchr1	8.1E+07	8.1E+07	2188	-1.08746126	2.473257121	0.1997988	0.2853745	0.79618	0	9	7	486	47	109	16	273	18	42	21
ENSMUSG00000067870	chr15	Rpl31-ps8	9.1E+07	9.1E+07	378	0.224562308	4.850833336	0.1997841	0.2853745	0.03396	0	438	331	419	387	394	867	598	466	639	661
ENSMUSG00000059278	chr11	Naa38	6.9E+07	6.9E+07	890	0.212018638	4.686423733	0.2000655	0.285726325	0.03024	0	353	249	394	381	422	621	526	426	695	578
ENSMUSG00000040283	chr11	Btnl9	4.9E+07	4.9E+07	6054	-0.4282584	3.422149459	0.2004422	0.286176932	0.12604	0	165	69	181	95	474	179	197	146	169	242
ENSMUSG00000044533	chr17	Rps2	2.5E+07	2.5E+07	1830	0.250154494	7.959039674	0.2004121	0.286176932	0.04541	0	3006	2577	4451	3689	3473	6503	4963	4355	6014	6116
ENSMUSG00000086324	chr16	Gm15564	3.6E+07	3.6E+07	821	0.389078625	3.161971545	0.2004298	0.286176932	0.10419	0	124	33	171	157	115	208	186	247	204	156
ENSMUSG00000025648	chr9	Pfkfb4	1.1E+08	1.1E+08	3333	-0.25686966	5.315474666	0.2006072	0.286376452	0.04642	0	655	443	852	442	943	691	964	611	828	627
ENSMUSG00000051113	chr7	Fam71e1	4.4E+07	4.4E+07	849	0.357827135	1.472614788	0.2006228	0.286376452	0.0701	0	28	25	55	36	34	72	44	49	73	70
ENSMUSG00000004896	chr3	Rrnad1	8.8E+07	8.8E+07	6342	0.290496388	2.925155838	0.2006647	0.28640713	0.05252	0	89	80	123	76	145	204	155	116	160	223
ENSMUSG00000029309	chr5	Sparcl1	1E+08	1E+08	3114	0.247707019	8.117988142	0.2009938	0.286847617	0.04467	0	3689	2785	4423	4130	4140	7889	5813	4913	5795	6860
ENSMUSG00000009376	chr6	Met	1.7E+07	1.7E+07	7679	-0.25072117	4.027393682	0.2011455	0.287035027	0.04182	0	293	173	405	229	247	341	354	263	257	310
ENSMUSG00000046862	chr4	Pramef8	1.4E+08	1.4E+08	4176	-0.23871342	3.607194938	0.2015719	0.287614134	0.03696	0	161	156	243	203	228	262	252	164	200	276
ENSMUSG00000059743	chr3	Fdps	8.9E+07	8.9E+07	1241	0.216832622	4.860864367	0.2017139	0.287787538	0.03258	0	356	261	420	407	611	764	669	533	645	602
ENSMUSG00000021595	chr13	Nsun2	7E+07	7E+07	5737	-0.22021228	5.681550624	0.201848	0.287949567	0.0344	0	694	607	1061	919	908	1149	1031	809	950	947
ENSMUSG00000037049	chr7	Smpd1	1.1E+08	1.1E+08	2411	-0.24249391	6.397698134	0.2020667	0.288232169	0.04247	0	1126	873	1979	1499	1567	1663	1921	1078	1747	1627
ENSMUSG00000028066	chr3	Pmf1	8.8E+07	8.8E+07	1351	0.255658098	3.706686669	0.2021667	0.288345612	0.04359	0	160	104	205	207	230	277	288	211	383	296
ENSMUSG00000024866	chr19	Acy3	3986661	3987305	1505	0.489814835	2.09341559	0.2022079	0.28837494	0.16216	0	40	25	44	24	142	146	62	70	103	124
ENSMUSG00000014837	chr8	4931428F04Rik	1.1E+08	1.1E+08	3552	0.392409632	1.113848192	0.2024288	0.288660713	0.08355	0	19	14	49	33	22	52	51	34	46	58
ENSMUSG00000051341	chr17	Zfp52	2.2E+07	2.2E+07	2175	-0.5255182	1.169375748	0.2025575	0.288814795	0.1651	0	21	21	82	44	32	48	52	34	11	37
ENSMUSG00000001127	chrX	Araf	2.1E+07	2.1E+07	6541	-0.23130542	6.387668191	0.2028388	0.289079231	0.03877	0	1429	982	1726	1267	1434	1761	1800	1209	1597	1607
ENSMUSG00000001783	chr10	Rtcb	8.6E+07	8.6E+07	2615	0.228640156	6.114809573	0.2027834	0.289079231	0.03767	0	990	653	1114	906	1186	1897	1441	1207	1532	1661
ENSMUSG00000025332	chrX	Kdm5c	1.5E+08	1.5E+08	7110	-0.26241494	5.355943018	0.202846	0.289079231	0.0494	0	692	531	627	871	568	967	632	644	849	740

ENSMUSG00000039678	chr2	Tbc1d13	3E+07	3E+07	4719	0.232930391	4.688169902	0.2027943	0.289079231	0.03787	0	270	240	401	323	591	695	515	450	638	573
ENSMUSG00000070423	chr7	Olfr558	1E+08	1E+08	2915	0.322754895	1.770189066	0.2028353	0.289079231	0.05867	0	43	25	60	38	60	107	77	60	64	73
ENSMUSG00000085829	chr14	Gm4285	7.6E+07	7.6E+07	902	0.453815095	0.055420293	0.2028811	0.28909989	0.07529	0	10	5	18	12	15	30	24	16	18	23
ENSMUSG00000033918	chr16	Parl	2E+07	2E+07	3892	0.214780335	5.26981737	0.2029297	0.289132552	0.03275	0	434	325	764	566	672	919	835	684	887	938
ENSMUSG00000048616	chr11	Nog	8.9E+07	8.9E+07	1695	0.313285374	3.246918424	0.2029452	0.289132552	0.06557	0	77	89	122	155	197	201	203	217	211	220
ENSMUSG00000047146	chr10	Tet1	6.3E+07	6.3E+07	14710	-0.39846814	1.360489502	0.2029744	0.289144686	0.09573	0	55	33	48	48	24	60	49	35	32	46
ENSMUSG00000023908	chr17	Pkmyt1	2.4E+07	2.4E+07	2039	0.738582686	0.212648693	0.2030946	0.289284942	0.33446	0	7	5	4	3	43	45	10	24	31	23
ENSMUSG00000024070	chr17	Prkd3	7.9E+07	7.9E+07	11017	-0.22986587	4.119067459	0.2031141	0.289284942	0.03582	0	275	223	296	264	345	459	355	249	265	332
ENSMUSG00000032413	chr9	Rasa2	9.7E+07	9.7E+07	15856	-0.41355161	2.375984958	0.2031719	0.289308503	0.11388	0	107	95	61	42	120	116	90	77	61	109
ENSMUSG00000034135	chr9	Sik3	4.6E+07	4.6E+07	7102	-0.2343229	5.213436462	0.20317	0.289308503	0.0387	0	472	371	896	747	596	690	761	543	749	766
ENSMUSG00000035095	chr14	Fam167a	6.3E+07	6.3E+07	4274	-0.45880863	1.082134117	0.2032314	0.289363876	0.11675	0	22	21	22	46	69	39	42	28	27	40
ENSMUSG00000022849	chr16	Hspbap1	3.6E+07	3.6E+07	4590	0.342769826	2.01994345	0.2033445	0.289495526	0.07086	0	38	43	58	41	85	106	68	77	97	105
ENSMUSG00000029158	chr5	Yipf7	7E+07	7E+07	1214	-0.26281196	6.235433795	0.2034661	0.289639237	0.05025	0	1303	781	1678	1469	995	1578	1630	1069	1204	1619
ENSMUSG00000031447	chr8	Lamp1	1.3E+07	1.3E+07	2255	0.244195986	9.448686345	0.2037532	0.290018504	0.0441	0	9599	6876	12325	9386	10360	18375	17222	11508	15958	15719
ENSMUSG00000075327	chr10	Zbtb2	4367074	4369851	3338	-0.28478457	2.670970545	0.2037967	0.290050954	0.04879	0	75	63	152	109	136	134	130	94	115	112
ENSMUSG00000015971	chr14	Actr8	3E+07	3E+07	2121	-0.19959047	4.917271622	0.2039695	0.290247337	0.02745	0	444	313	663	494	559	679	684	406	555	601
ENSMUSG00000024135	chr17	Srbd1	8.6E+07	8.6E+07	3530	-0.32453373	2.331062742	0.203976	0.290247337	0.06382	0	87	47	142	64	86	124	94	71	78	89
ENSMUSG00000086741	chr8	Gm15816	2.3E+07	2.3E+07	1688	0.583011664	1.921147608	0.2040411	0.290310446	0.23493	0	19	18	126	34	43	30	81	61	156	118
ENSMUSG00000053929	chr15	Cyhr1	7.7E+07	7.7E+07	6210	-0.24641863	6.703669206	0.2042376	0.290560631	0.0445	0	1530	1154	2320	1754	1892	1982	2598	1280	2191	1888
ENSMUSG00000027016	chr2	Zfp385b	7.7E+07	7.7E+07	8223	0.371789068	2.483832304	0.2042943	0.290611694	0.087	0	109	48	64	79	52	171	129	73	117	161
ENSMUSG00000029726	chr5	Mepce	1.4E+08	1.4E+08	3292	0.209307494	4.895023446	0.2046334	0.29103512	0.03063	0	316	291	536	442	523	736	591	514	728	715
ENSMUSG00000039304	chr3	Tnfsf10	2.7E+07	2.7E+07	5266	-0.33564369	3.056804525	0.2046252	0.29103512	0.07595	0	157	91	162	97	196	234	212	94	88	143
ENSMUSG00000000805	chr11	Car4	8.5E+07	8.5E+07	1966	0.305689748	3.481741487	0.2047651	0.291192904	0.0647	0	124	79	213	112	252	299	238	223	176	322
ENSMUSG00000045867	chr10	Cradd	9.5E+07	9.5E+07	1650	-0.36086161	3.06709868	0.2050182	0.291523229	0.08986	0	162	140	104	168	95	170	121	130	190	134
ENSMUSG00000024188	chr17	Luc7l	2.6E+07	2.6E+07	7509	0.230394546	4.043207379	0.205068	0.291564548	0.03569	0	219	167	273	192	296	483	315	307	331	392
ENSMUSG00000022837	chr16	Iqcb1	3.7E+07	3.7E+07	5387	-0.33015178	2.118957739	0.2051769	0.29168978	0.06633	0	95	49	75	58	79	107	81	55	88	62
ENSMUSG00000002963	chr7	Pnkp	4.5E+07	4.5E+07	3133	-0.20411673	4.719995797	0.2052815	0.291808921	0.02847	0	432	262	537	421	502	539	518	403	572	485
ENSMUSG00000012429	chr13	Mplkip	1.8E+07	1.8E+07	2672	0.33830235	2.110444169	0.2053597	0.291860852	0.06975	0	36	44	78	48	79	148	86	83	76	94
ENSMUSG00000039607	chr9	Rbms3	1.2E+08	1.2E+08	10413	0.298282561	3.080465182	0.2053509	0.291860852	0.05803	0	129	81	99	108	145	289	144	147	192	187
ENSMUSG00000071359	chr10	Tbpl1	2.3E+07	2.3E+07	3271	0.221857706	4.009825367	0.2054864	0.29201131	0.03241	0	202	179	269	186	283	459	353	261	341	380
ENSMUSG00000006699	chr4	Cdc42	1.4E+08	1.4E+08	2966	0.245403987	8.085178851	0.2055541	0.292077951	0.04472	0	3739	2909	3903	3479	4662	7609	5974	4794	5884	6277
ENSMUSG00000039239	chr1	Tgfb2	1.9E+08	1.9E+08	5791	0.241939456	4.882509585	0.2056321	0.292129608	0.04117	0	398	327	439	509	322	685	675	555	683	672
ENSMUSG00000053801	chr7	Grwd1	4.6E+07	4.6E+07	2053	0.228012034	4.2587891	0.2056229	0.292129608	0.03589	0	210	174	323	310	325	420	393	366	489	434
ENSMUSG00000046721	chr7	Rpl14-ps1	4.5E+07	4.5E+07	710	0.218537873	5.352595499	0.2057338	0.292244554	0.03398	0	548	470	630	495	686	1031	807	731	1014	936
ENSMUSG00000019518	chr5	Ap4m1	1.4E+08	1.4E+08	3640	-0.29384513	2.26450656	0.2057691	0.292265027	0.05134	0	65	63	98	74	93	99	110	72	84	72
ENSMUSG00000036777	chr9	Anln	2.2E+07	2.2E+07	5421	-0.41357554	1.064039404	0.2063546	0.293066986	0.10028	0	35	38	26	28	40	56	42	24	35	23
ENSMUSG00000031489	chr8	Adrb3	2.7E+07	2.7E+07	2893	-1.06773321	3.380315873	0.2064153	0.29312358	0.79763	0	264	114	2	6	716	278	36	85	129	182
ENSMUSG00000018651	chr11	Tada2a	8.4E+07	8.4E+07	2974	-0.24601204	3.857805971	0.2068474	0.293707378	0.04136	0	254	189	248	173	313	271	318	197	291	288
ENSMUSG00000000690	chr11	Hoxb6	9.6E+07	9.6E+07	1964	0.526218061	-0.22396991	0.2070361	0.293945604	0.12551	0	13	2	7	11	13	27	18	7	21	19
ENSMUSG00000093904	chr8	Tomm20	1.3E+08	1.3E+08	4986	-0.23392216	5.899171216	0.2071261	0.29404358	0.04003	0	877	595	1474	968	1067	1318	1427	833	996	1128
ENSMUSG00000029207	chr5	Apbb2	6.6E+07	6.6E+07	10551	-0.22088126	5.107349786	0.2071668	0.294071641	0.03464	0	569	331	728	444	796	678	777	498	689	644
ENSMUSG00000022471	chr15	Xrcc6	8.2E+07	8.2E+07	4476	-0.20062663	4.737713831	0.2073096	0.294244596	0.02813	0	401	316	575	447	414	619	527	371	529	528
ENSMUSG00000042500	chr4	Ago4	1.3E+08	1.3E+08	6947	-0.2546034	3.884992629	0.2075136	0.294504346	0.04473	0	219	170	366	273	185	302	307	185	298	303
ENSMUSG00000085493	chr5	Gm15469	3.1E+07	3.1E+07	961	1.228937405	0.439136784	0.2075592	0.294539159	1.00348	0	0	0	46	12	4	3	25	1	86	62
ENSMUSG00000031134	chrX	Rbmx	5.7E+07	5.7E+07	4330	-0.21705949	4.139602294	0.2076017	0.29456967	0.03227	0	261	204	323	303	338	393	372	221	302	407
ENSMUSG00000004356	chr10	Utp20	8.9E+07	8.9E+07	8831	-0.23035004	4.422047581	0.2078808	0.29477555	0.03722	0	300	283	387	416	335	487	423	361	395	353
ENSMUSG00000018678	chr11	Sp2	9.7E+07	9.7E+07	3415	-0.23760624	3.699023071	0.2078435	0.29477555	0.03759	0	187	150	228	205	293	240	253	182	254	294
ENSMUSG00000020475	chr11	Pgam2	5801640	5801839	840	0.264594164	11.06479656	0.2078818	0.29477555	0.05277	0	26957	20015	35380	31816	34036	44552	47207	35178	65378	48864
ENSMUSG00000029127	chr5	Zbtb49	3.8E+07	3.8E+07	7715	-0.36330584	1.116222186	0.2078412	0.29477555	0.06613	0	25	29	48	29	47	49	46	26	34	34
ENSMUSG00000045176	chr11	2310047M10Rik	6.9E+07	6.9E+07	1862	0.209627392	5.120779136	0.207798	0.29477555	0.03134	0	384	364	612	497	594	763	778	562	933	810
ENSMUSG00000049401	chr2	Ogfr	1.8E+08	1.8E+08	2580	0.213361368	4.775575389	0.2078194	0.29477555	0.03249	0	297	227	584	380	481	725	613	438	668	604
ENSMUSG00000085741	chr2	5430405H02Rik	1.6E+08	1.6E+08	3851	0.305006705	2.206394263	0.2078939	0.29477555	0.05404	0	69	39	61	59	77	141	103	71	92	113
ENSMUSG00000022364	chr15	Tbc1d31	5.8E+07	5.8E+07	6366	-0.36391772	1.799748276	0.2080832	0.295014113	0.08164	0	71	51	63	30	70	87	67	43	54	59
ENSMUSG00000054555	chr7	Adam12	1.3E+08	1.3E+08	8273	0.903833006	1.768220371	0.2083484	0.295360254	0.57917	0	54	2	6	3	120	205	56	77	64	45
ENSMUSG00000055044	chr19	Pdlim1	4E+07	4E+07	5260	0.628755251	5.355328717	0.2084907	0.295532151	0.29248	0	146	49	1271	922	267	963	857	761	929	1602
ENSMUSG00000016382	chrX	Pls3	7.6E+07	7.6E+07	4238	0.228377422	4.933403122	0.2085324	0.295561341	0.03759	0	363	279	536	380	606	986	779	551	534	573
ENSMUSG00000053012	chr6	Krcc1	7.1E+07	7.1E+07	1748	-0.21994091	4.720530136	0.2088772	0.296020108	0.03403	0	375	274	557	360	623	532	661	379	447	499
ENSMUSG00000041119	chr17	Pde9a	3.1E+07	3.1E+07	2834	0.3886472	1.21966648	0.2091514	0.296378861	0.08404	0	30	20	30	34	30	79	36	44	37	64
ENSMUSG00000008450	chr8	Nutf2	1.1E+08	1.1E+08	1966	-0.20636907	5.345162918	0.2091886	0.296401585	0.03088	0	650	491	762	626	753	821	895	580	868	736
ENSMUSG00000030888	chr7	Rrp8	1.1E+08	1.1E+08	3072	-0.23133764	4.044722553	0.2093383	0.296583751	0.03639	0	254	180	360	283	273	340	322	287	261	336
ENSMUSG00000013523	chr2	Bcas1	1.7E+08	1.7E+08	3775	0.52750974	0.097797387	0.2093754	0.296606355	0.13424	0	14	6	15	13	11	38	10	12	37	21
ENSMUSG00000053656	chr5	Dancr	7.4E+07	7.4E+07	2346	0.486933823	0.047269839	0.2094872	0.296734809	0.10401	0	11	7	17	12	11	31	11	16	19	34
ENSMUSG00000031310	chrX	Zmym3	1E+08	1E+08	8021	-0.2101794	4.128960625	0.2098147	0.297168698	0.0302	0	266	213	308	273	351	361	360	251	329	370
ENSMUSG00000073415	chr17	Gm10501	3.5E+07	3.5E+07	2200	-0.40312622	1.417353208	0.2102011	0.297685893	0.09514	0	41	33	71	43	35	40	75	39	43	31
ENSMUSG00000026678	chr1	Rgs5	1.7E+08	1.7E+08	4546	-0.26638168	8.19227013	0.2102351	0.297703874	0.05382	0	3688	2687	7872	4569	6326	7245	5768	4421	4731	5400
ENSMUSG00000061458	chr12	Nol10	1.7E+07	1.7E+07	3020	0.228828718	3.62344491	0.2102679	0.297720326	0.03476	0	152	124	193	168	217	310	261	231	284	270
ENSMUSG00000025651	chr9	Uqcrc1	1.1E+08	1.1E+08	4135	-0.32142849	9.783759935	0.2102946	0.297728137	0.07851	0	10890	6530	27751	18059	14440	14873	20677	11272	17817	16640

ENSMUSG00000018830	chr16	Myh11	1.4E+07	1.4E+07	6632	-0.22366103	5.312428512	0.2104322	0.297892772	0.03691	0	510	564	810	695	616	972	883	509	719	749
ENSMUSG00000022451	chr15	Twf1	9.5E+07	9.5E+07	3054	0.308142316	3.848061104	0.2105023	0.297962042	0.06809	0	178	127	167	140	373	482	354	278	249	279
ENSMUSG00000024758	chr19	Rtn3	7425901	7427875	5030	0.269272823	6.240183404	0.2105379	0.297982257	0.05452	0	935	694	974	807	1868	2201	1692	1313	1683	1686
ENSMUSG00000032175	chr9	Tyk2	2.1E+07	2.1E+07	4619	0.237180312	4.066633806	0.2106035	0.298045132	0.03806	0	199	198	239	266	235	486	393	236	393	381
ENSMUSG00000022722	chr16	Arl6	6E+07	6E+07	2098	0.382276036	1.646548398	0.2108304	0.298336079	0.09042	0	30	32	37	32	68	110	73	57	73	42
ENSMUSG00000032186	chr9	Tmod2	7.6E+07	7.6E+07	10391	0.280566524	3.000316995	0.2110034	0.298550727	0.05028	0	100	91	116	122	101	258	168	128	179	171
ENSMUSG00000020591	chr12	Ntsr2	1.7E+07	1.7E+07	1547	-0.37897835	1.540413024	0.211106	0.298635683	0.08775	0	43	48	40	53	50	40	55	30	70	59
ENSMUSG00000032737	chr7	Inppl1	1E+08	1E+08	4981	-0.27671446	7.110674861	0.2110994	0.298635683	0.05805	0	1967	1303	3960	2541	1988	2817	3267	1827	2729	2360
ENSMUSG00000014232	chr16	Cluap1	3908801	3908864	2279	0.237827528	3.387287438	0.2111896	0.298723821	0.03654	0	127	102	161	139	195	276	257	170	215	247
ENSMUSG00000006021	chr7	Kptn	1.6E+07	1.6E+07	3341	-0.22560501	3.677219252	0.2112432	0.298769494	0.03429	0	176	164	233	212	248	280	240	185	263	244
ENSMUSG00000049538	chr13	Adamts16	7.1E+07	7.1E+07	6836	-0.70806519	0.071835893	0.2117467	0.299451453	0.30327	0	13	20	2	9	45	22	20	16	9	8
ENSMUSG00000004929	chr10	Thop1	8.1E+07	8.1E+07	5059	-0.21592112	4.816216274	0.2118654	0.299528711	0.03339	0	391	278	669	520	466	572	542	387	630	563
ENSMUSG00000020955	chr12	Ap4s1	5.2E+07	5.2E+07	1113	-0.20910081	5.651576556	0.2118481	0.299528711	0.03235	0	790	555	967	877	894	1195	964	759	947	960
ENSMUSG00000038550	chr3	Ciart	9.6E+07	9.6E+07	2261	-0.52004253	0.550705649	0.2118578	0.299528711	0.1492	0	27	14	26	12	46	17	22	19	14	43
ENSMUSG00000004393	chr11	Ddx56	6258919	6259258	2533	0.261548029	4.750217517	0.2121942	0.299963303	0.05084	0	272	177	645	462	359	728	573	501	557	659
ENSMUSG00000070709	chr7	1700049G17Rik	2.8E+07	2.8E+07	7518	-0.33324449	1.572061981	0.212219	0.299968135	0.06308	0	54	26	53	53	59	67	66	39	50	43
ENSMUSG00000002059	chr11	Rab34	7.8E+07	7.8E+07	2385	0.524872242	3.45047059	0.2124231	0.300226399	0.2034	0	120	104	48	45	366	370	161	215	284	290
ENSMUSG00000029798	chr6	Herc6	5.8E+07	5.8E+07	5279	0.404651895	1.452150725	0.2124837	0.300281685	0.09259	0	25	32	38	24	51	104	72	33	43	65
ENSMUSG00000021830	chr14	Txndc16	4.5E+07	4.5E+07	10360	-0.21686865	4.330309679	0.2126864	0.300537906	0.03347	0	381	232	385	293	330	467	452	267	371	376
ENSMUSG00000033768	chr19	Nrxn2	6418731	6418972	13812	0.457945663	0.301352355	0.2127454	0.300560709	0.11346	0	5	6	24	14	25	36	25	15	28	31
ENSMUSG00000090110	chrX	Mtcp1	7.5E+07	7.5E+07	1310	0.301925641	2.00463964	0.212739	0.300560709	0.05311	0	52	42	65	42	63	111	79	65	89	103
ENSMUSG00000005983	chr16	1700037C18Rik	3895179	3895414	3227	0.389366038	1.441948692	0.2128204	0.30060617	0.09895	0	29	8	49	35	58	73	66	44	65	58
ENSMUSG00000036712	chr8	Cyld	8.9E+07	8.9E+07	8035	-0.21380463	5.313345619	0.2128043	0.30060617	0.03382	0	592	475	922	653	591	938	849	526	717	808
ENSMUSG00000067931	chr17	Zfp948	2.2E+07	2.2E+07	2612	-0.3699442	1.125539755	0.2128544	0.300623861	0.07121	0	31	27	34	36	50	55	37	31	26	40
ENSMUSG00000046792	chr7	Zfp787	6131489	6133171	1899	-0.22484767	4.527068629	0.2128932	0.300648456	0.03615	0	301	228	591	405	392	482	481	273	489	490
ENSMUSG00000027282	chr2	Mtch2	9.1E+07	9.1E+07	8490	-0.23288592	7.105117561	0.212933	0.300674395	0.04135	0	2043	1383	3060	2218	2776	3024	2779	2091	2574	2614
ENSMUSG00000020176	chr11	Grb10	1.2E+07	1.2E+07	9089	0.34884405	6.13818299	0.2134389	0.301358405	0.09246	0	1102	939	733	1064	574	2271	1038	1330	1652	1869
ENSMUSG00000006127	chr11	Inpp5k	7.6E+07	7.6E+07	5728	-0.20581284	5.512946659	0.2137264	0.301699506	0.03153	0	683	533	884	780	818	1051	903	627	843	984
ENSMUSG00000046598	chr16	Bdh1	3.1E+07	3.1E+07	3800	-1.21268413	5.72235518	0.213745	0.301699506	1.05302	0	101	2	5012	1306	64	378	1766	227	183	840
ENSMUSG00000058975	chr7	Kcnc1	4.6E+07	4.6E+07	9128	-0.31712223	6.945099025	0.2137186	0.301699506	0.07708	0	1800	896	3381	2935	1647	2078	2863	1547	2380	2518
ENSMUSG00000002769	chr17	Gnmt	4.7E+07	4.7E+07	1206	-0.55981917	0.180720103	0.2138405	0.301803823	0.17424	0	16	8	32	31	8	20	10	19	11	25
ENSMUSG00000032135	chr9	Mcam	4.4E+07	4.4E+07	3350	-0.41494269	5.498472646	0.2140401	0.302055208	0.13102	0	571	611	531	325	1968	1079	599	732	840	723
ENSMUSG00000063430	chr5	Wscd2	1.1E+08	1.1E+08	12253	-0.87939933	0.418924863	0.2141517	0.302182295	0.50025	0	14	13	7	1	95	33	7	19	15	15
ENSMUSG00000037007	chr5	Zfp113	1.4E+08	1.4E+08	6754	-0.28119912	2.333640597	0.2142611	0.302306201	0.04966	0	71	59	90	94	97	124	95	59	87	103
ENSMUSG00000038349	chr1	Plcl1	5.5E+07	5.5E+07	6687	-0.31570501	3.005995231	0.2143162	0.302353494	0.06767	0	114	66	238	118	158	150	220	97	143	128
ENSMUSG00000066270	chr9	Gm10157	1.2E+08	1.2E+08	343	-0.29846708	2.260458219	0.214421	0.302470939	0.05584	0	95	60	83	71	78	99	89	67	78	103
ENSMUSG00000028608	chr4	0610037L13Rik	1.1E+08	1.1E+08	5633	0.214217097	5.199893165	0.2145591	0.302635375	0.03363	0	476	432	502	513	609	1007	724	657	835	846
ENSMUSG00000040950	chr11	Mgl2	7E+07	7E+07	2094	0.638416208	3.021025518	0.2146784	0.302742788	0.29793	0	54	155	13	63	146	362	84	124	168	296
ENSMUSG00000046573	chr13	Lyrm4	3.6E+07	3.6E+07	1515	0.274577054	2.898268694	0.2146738	0.302742788	0.04877	0	91	78	110	113	107	214	140	139	154	183
ENSMUSG00000035686	chr7	Thrsp	9.7E+07	9.7E+07	1277	-0.972288	6.443579738	0.2147611	0.3028289	0.69864	0	2441	544	87	75	6128	1157	373	1514	2169	565
ENSMUSG00000035637	chr4	Grhpr	4.5E+07	4.5E+07	1603	0.214847869	4.959960473	0.2149021	0.302966843	0.03397	0	452	290	498	393	555	677	682	528	898	648
ENSMUSG00000040472	chr14	Rabggta	5.6E+07	5.6E+07	2630	0.23390737	3.92241527	0.2148896	0.302966843	0.03825	0	174	146	245	215	277	354	315	210	423	394
ENSMUSG00000021756	chr13	Il6st	1.1E+08	1.1E+08	11099	-0.26518072	7.609070439	0.2150647	0.303165633	0.05446	0	2733	2921	3660	3798	2604	4339	4049	2651	3492	3927
ENSMUSG00000057982	chr9	Zfp809	2.2E+07	2.2E+07	1325	-0.36856722	1.841724746	0.2150899	0.303170633	0.08691	0	70	59	63	45	52	67	46	54	58	88
ENSMUSG00000086191	chr11	Zfp652os	9.6E+07	9.6E+07	537	0.417095775	0.694555766	0.2152629	0.303383972	0.09035	0	16	14	24	25	18	31	33	28	55	29
ENSMUSG00000004035	chr3	Gstm7	1.1E+08	1.1E+08	1601	0.394428376	2.069807104	0.2153246	0.303440484	0.10656	0	58	22	80	74	37	95	70	71	94	148
ENSMUSG00000004952	chr5	Rasa4	1.4E+08	1.4E+08	6191	0.223610195	5.644324164	0.2157917	0.304068094	0.03753	0	705	547	683	716	790	1325	1076	732	1295	1187
ENSMUSG00000022529	chr16	Zfp263	3744093	3744767	4521	-0.24291101	3.482834284	0.2160357	0.304381443	0.04102	0	177	130	197	172	236	296	215	152	167	232
ENSMUSG00000000563	chr3	Atp5f1	1.1E+08	1.1E+08	4105	-0.26387555	9.440629141	0.2161846	0.304560603	0.05436	0	10713	6845	16836	13410	10415	14123	16155	9389	11886	14127
ENSMUSG00000005625	chr3	Psmd4	9.5E+07	9.5E+07	2808	0.232913889	7.31843329	0.2163919	0.304791418	0.04211	0	2015	1478	2683	2326	2706	4172	3284	2765	3932	3683
ENSMUSG00000071650	chr19	Ganab	8898090	8898159	3862	0.21952035	5.475770346	0.2163712	0.304791418	0.03636	0	518	430	701	602	893	1387	913	748	970	962
ENSMUSG00000005354	chr15	Txn2	7.8E+07	7.8E+07	4208	0.252203137	7.988636097	0.2164299	0.304814335	0.0496	0	3055	2010	5583	3639	3737	5977	5803	4289	6333	6147
ENSMUSG00000025645	chr9	Ccdc51	1.1E+08	1.1E+08	1526	-0.24860767	2.979427299	0.2164778	0.304851189	0.04102	0	114	97	164	119	149	188	167	95	148	148
ENSMUSG00000098794	chr2	Gm28038	3E+07	3E+07	378	0.551962156	2.399376236	0.2166235	0.305025689	0.22892	0	20	9	171	86	61	121	190	81	97	148
ENSMUSG00000098811	chr10	Mir6913	8.1E+07	8.1E+07	66	-0.50017294	-0.03064337	0.2167735	0.305206266	0.13733	0	17	18	16	11	14	14	16	4	27	16
ENSMUSG00000037262	chr2	Kin	1E+07	1E+07	1705	0.277410494	2.606458909	0.2169613	0.305439983	0.04908	0	73	56	100	83	100	200	113	99	131	141
ENSMUSG00000046056	chr7	Sbsn	3.1E+07	3.1E+07	3802	0.496461893	0.629804526	0.2174355	0.306076919	0.14762	0	14	10	10	11	47	50	32	25	31	36
ENSMUSG00000027333	chr2	Smox	1.3E+08	1.3E+08	3894	-0.74410019	7.057747799	0.2175238	0.306163619	0.423	0	769	633	6218	619	6185	864	6361	745	1443	1184
ENSMUSG00000031842	chr8	Pde4c	7.1E+07	7.1E+07	5545	-0.42186711	1.704856814	0.2175408	0.306163619	0.11405	0	29	27	90	64	76	50	75	30	39	89
ENSMUSG00000050973	chr7	Gdpgp1	8E+07	8E+07	3132	-0.40862388	0.670555514	0.2176438	0.306277968	0.09513	0	22	22	35	22	28	34	45	11	25	21
ENSMUSG00000016344	chr2	Ppdpf	1.8E+08	1.8E+08	1336	0.241830914	3.763512381	0.2178288	0.30648248	0.04154	0	187	117	200	181	259	371	265	228	380	269
ENSMUSG00000026586	chr1	Prrx1	1.6E+08	1.6E+08	11066	-0.24647198	6.224114205	0.2178329	0.30648248	0.04711	0	1272	890	1456	1362	1101	2046	1470	1071	1123	1430
ENSMUSG00000030652	chr7	Coq7	1.2E+08	1.2E+08	4003	0.242390436	5.409457977	0.2180082	0.306698465	0.04526	0	495	289	991	648	625	994	958	757	1006	1022
ENSMUSG00000022889	chr16	Mrpl39	8.5E+07	8.5E+07	2533	-0.20511559	4.825395475	0.2182439	0.3069992	0.03072	0	391	263	675	463	561	682	590	403	499	561
ENSMUSG00000020152	chr11	Actr2	2E+07	2E+07	5204	0.213040855	5.873018661	0.2183089	0.307059815	0.03478	0	787	567	1011	801	961	1688	1395	1045	1109	1282
ENSMUSG00000066149	chr4	Cdc26	6.2E+07	6.2E+07	7180	0.212888388	4.045451409	0.2184932	0.307288307	0.03212	0	207	157	297	213	290	468	330	274	403	355
ENSMUSG00000003154	chr6	Foxj2	1.2E+08	1.2E+08	5283	-0.19834091	5.242569662	0.2187099	0.307561198	0.02966	0	591	474	780	595	600	832	782	529	768	743

ENSMUSG00000017176	chr11	Nt5c3b	1E+08	1E+08	3420	0.252968943	3.303467645	0.2187531	0.307561198	0.04441	0	129	76	200	141	141	291	196	181	214	217
ENSMUSG00000039715	chr2	Wdr34	3E+07	3E+07	2359	0.27266556	2.770463591	0.2187493	0.307561198	0.04837	0	85	67	84	97	126	171	169	119	157	143
ENSMUSG00000050856	chr5	Atp5k	1.1E+08	1.1E+08	616	0.279892842	8.183099778	0.218843	0.307656855	0.06177	0	3456	2031	6855	4595	3562	6927	6106	5364	7379	7003
ENSMUSG00000068328	chr6	Aup1	8.3E+07	8.3E+07	1509	0.216987229	6.06199923	0.2193439	0.308330137	0.0364	0	846	664	1056	915	1216	1686	1489	1097	1612	1555
ENSMUSG00000021973	chr14	Micu2	5.8E+07	5.8E+07	2310	0.236988659	6.367421988	0.2194204	0.308406658	0.04376	0	1112	789	1525	1308	995	2233	2073	1423	1727	1806
ENSMUSG00000071644	chr19	Eef1g	8967041	8967225	2600	0.238949678	9.012252776	0.2194565	0.308426556	0.04521	0	6368	4848	9857	7540	7609	13012	11188	9008	12115	12471
ENSMUSG00000028318	chr4	Polr1e	4.5E+07	4.5E+07	3897	0.326354108	2.030589529	0.2195047	0.308432515	0.06931	0	33	39	84	54	61	125	81	84	72	93
ENSMUSG00000056851	chr15	Pcbp2	1E+08	1E+08	2868	-0.23144593	7.385838737	0.2194982	0.308432515	0.04219	0	2540	1997	2999	2898	3209	3613	3635	2168	3236	3392
ENSMUSG00000025495	chr7	Ptdss2	1.4E+08	1.4E+08	4875	-0.2122402	4.203022484	0.2198387	0.308870853	0.03253	0	265	206	386	341	296	388	403	246	378	351
ENSMUSG00000027189	chr2	Trim44	1E+08	1E+08	5645	-0.21233052	4.93567784	0.2200606	0.30915164	0.0338	0	487	336	520	422	740	733	665	447	490	606
ENSMUSG00000062110	chr5	Scfd2	7.4E+07	7.4E+07	8127	0.246462341	3.202797637	0.2201526	0.309249871	0.04149	0	118	78	144	136	160	251	186	175	213	192
ENSMUSG00000005774	chr3	Rfx5	9.5E+07	9.5E+07	5497	-0.25682179	3.341453888	0.2202892	0.309348801	0.04684	0	175	133	180	133	201	234	255	117	184	171
ENSMUSG00000022370	chr15	Mrpl13	5.6E+07	5.6E+07	7936	0.206042606	5.686692995	0.2202827	0.309348801	0.03267	0	679	480	853	700	940	1330	1133	872	1152	1220
ENSMUSG00000040843	chr1	Tiprl	1.7E+08	1.7E+08	5473	0.193729576	4.986501168	0.2202676	0.309348801	0.02801	0	406	325	597	391	531	829	709	589	633	717
ENSMUSG00000002475	chr18	Abhd3	1.1E+07	1.1E+07	1962	0.424588514	0.185184936	0.220833	0.310081481	0.08521	0	14	8	10	13	21	33	20	20	20	28
ENSMUSG00000092232	chr14	Gm20521	5.5E+07	5.5E+07	1245	0.212404847	5.285100346	0.221103	0.310429453	0.03437	0	474	412	646	525	678	1039	696	644	900	1051
ENSMUSG00000029578	chr5	Wipi2	1.4E+08	1.4E+08	8041	-0.20268751	5.550277824	0.2214349	0.31086431	0.03166	0	742	546	880	731	894	1003	1052	631	936	905
ENSMUSG00000027739	chr3	Rab33b	5.1E+07	5.1E+07	3538	-0.22758495	3.511878656	0.2215956	0.310976874	0.03618	0	178	128	239	176	209	242	269	143	216	218
ENSMUSG00000029344	chr5	Tpst2	1.1E+08	1.1E+08	2789	0.219590374	4.385749762	0.2215793	0.310976874	0.03617	0	231	178	385	273	426	517	401	358	542	494
ENSMUSG00000035834	chr13	Polr3g	8.2E+07	8.2E+07	3936	-0.33961952	2.018164119	0.2216037	0.310976874	0.07744	0	57	63	51	61	97	114	76	50	61	66
ENSMUSG00000036826	chr7	Igflr1	3.1E+07	3.1E+07	1270	0.397821726	1.717027599	0.2215774	0.310976874	0.10127	0	36	33	38	28	73	109	49	44	68	109
ENSMUSG00000030254	chr6	Rad18	1.1E+08	1.1E+08	5796	-0.45000418	0.172917654	0.2217215	0.311111075	0.09551	0	18	15	15	11	31	23	22	15	14	16
ENSMUSG00000025579	chr11	Gaa	1.2E+08	1.2E+08	4783	-0.24017215	7.810872386	0.2218792	0.311301124	0.04601	0	3689	2749	4131	3416	4372	4539	4735	2977	5294	3837
ENSMUSG00000001157	chr6	Gmcl1	8.7E+07	8.7E+07	3823	0.284704984	2.406671181	0.2219655	0.311363971	0.05191	0	65	48	76	66	102	149	111	103	123	101
ENSMUSG00000025867	chr13	Cplx2	5.4E+07	5.4E+07	4928	0.357621919	1.048746482	0.2219684	0.311363971	0.07155	0	26	16	29	21	39	57	36	43	41	48
ENSMUSG00000031021	chr7	Tmem9b	1.1E+08	1.1E+08	2002	0.205563116	5.510699137	0.2220055	0.311371618	0.03262	0	569	444	772	580	872	1078	1141	769	1049	1005
ENSMUSG00000032480	chr9	Dhx30	1.1E+08	1.1E+08	3726	-0.19178014	5.026620766	0.2220182	0.311371618	0.02759	0	431	369	673	583	586	698	672	471	669	635
ENSMUSG00000028330	chr4	Ncbp1	4.6E+07	4.6E+07	3386	0.190496859	4.829372231	0.2221867	0.311576784	0.02702	0	371	284	475	388	495	727	643	530	571	640
ENSMUSG00000062515	chr3	Fabp4	1E+07	1E+07	4489	-0.63445693	9.35097399	0.222212	0.311581011	0.31675	0	12098	5435	4027	2086	40312	17792	5843	9340	9831	10282
ENSMUSG00000028577	chr4	Plaa	9.5E+07	9.5E+07	6441	-0.21715994	5.672441192	0.2223715	0.311773487	0.03665	0	790	560	1152	862	808	1163	1134	783	850	947
ENSMUSG00000038602	chr10	Slc35f1	5.3E+07	5.3E+07	4941	-0.46682555	0.036427227	0.2228106	0.312358018	0.08776	0	16	8	22	23	13	20	15	15	13	17
ENSMUSG00000025403	chr10	Shmt2	1.3E+08	1.3E+08	2305	0.23352007	5.36463959	0.2230425	0.312620526	0.04267	0	502	308	897	663	562	918	967	643	1073	1005
ENSMUSG00000027624	chr2	Epb4.1l1	1.6E+08	1.6E+08	11528	0.402162501	4.281624091	0.2230204	0.312620526	0.12675	0	197	144	177	110	695	540	428	353	472	485
ENSMUSG00000009575	chr15	Cbx5	1E+08	1E+08	9006	-0.21226895	5.856621014	0.2232638	0.312899498	0.03537	0	944	687	1165	937	957	1300	1327	816	1006	1129
ENSMUSG00000028719	chr4	Cmpk1	1.1E+08	1.1E+08	3420	0.204828025	5.114353917	0.2234197	0.31308674	0.03221	0	430	342	574	414	700	963	806	648	720	683
ENSMUSG00000032609	chr9	Klhdc8b	1.1E+08	1.1E+08	8419	0.412603972	2.575331446	0.223487	0.313149686	0.12435	0	70	58	42	46	166	208	97	87	160	149
ENSMUSG00000040694	chr17	Apobec2	4.8E+07	4.8E+07	1218	0.246295792	9.042727159	0.2240682	0.313932689	0.04899	0	7114	4610	9416	8403	7221	16081	12208	9208	10974	11093
ENSMUSG00000064141	chr4	Zfp69	1.2E+08	1.2E+08	2782	0.475072913	0.016126515	0.2241335	0.313992865	0.11019	0	11	5	15	6	21	30	22	11	30	16
ENSMUSG00000025175	chr11	Fn3k	1.2E+08	1.2E+08	4399	-0.22830123	4.004347507	0.2242047	0.314029888	0.03786	0	236	160	293	299	329	276	314	235	368	319
ENSMUSG00000033752	chr3	Mnd1	8.4E+07	8.4E+07	875	0.503360247	0.734774997	0.2242003	0.314029888	0.1563	0	29	15	18	7	27	54	26	45	21	38
ENSMUSG00000025758	chr3	Plk4	4.1E+07	4.1E+07	5863	0.454720921	0.061313095	0.2242541	0.314067677	0.08577	0	13	9	12	8	17	32	27	14	24	15
ENSMUSG00000079659	chr5	Tmem243	9100737	9100859	988	-0.28973246	2.625021212	0.224317	0.314124451	0.05803	0	92	87	106	75	144	118	141	80	94	135
ENSMUSG00000046822	chr10	Slc39a3	8.1E+07	8.1E+07	4016	-0.22108314	4.851321916	0.2245021	0.314352218	0.03776	0	469	362	535	546	398	592	665	397	624	480
ENSMUSG00000058709	chr7	Egln2	2.7E+07	2.7E+07	2800	-0.23393006	6.89554713	0.2248191	0.314764675	0.04399	0	1815	1547	2147	1945	2203	2244	2645	1535	2667	2273
ENSMUSG00000052951	chr2	C130021I20Rik	3.4E+07	3.4E+07	4140	0.663643843	0.267273304	0.2248525	0.31478	0.24719	0	12	20	2	12	12	61	13	16	26	26
ENSMUSG00000029136	chr5	Rbks	3.2E+07	3.2E+07	1489	0.434875402	0.471963585	0.2249996	0.314954561	0.09751	0	18	9	12	16	27	39	41	18	20	35
ENSMUSG00000041577	chr1	Prelp	1.3E+08	1.3E+08	3615	0.377405958	6.646349236	0.2256758	0.315837973	0.11494	0	851	869	909	859	3353	3309	2305	1557	1934	2784
ENSMUSG00000043061	chr12	Tmem18	3.1E+07	3.1E+07	2952	-0.24214514	3.318575384	0.2256739	0.315837973	0.04212	0	141	135	164	161	203	235	227	131	187	165
ENSMUSG00000002345	chr8	2310045N01Rik	7E+07	7E+07	2743	0.232297477	3.748593479	0.2257769	0.315883328	0.0398	0	164	119	211	168	282	337	276	244	345	282
ENSMUSG00000034518	chr8	Hmgxb4	7.5E+07	7.5E+07	5227	-0.24212642	3.180765949	0.225789	0.315883328	0.04113	0	134	108	193	154	148	206	187	117	194	153
ENSMUSG00000035505	chr5	Cox18	9E+07	9E+07	2009	-0.23120678	3.72844837	0.2257761	0.315883328	0.03848	0	181	133	271	254	251	244	292	180	288	250
ENSMUSG00000057530	chr4	Ece1	1.4E+08	1.4E+08	5300	0.227626869	6.618095271	0.2257982	0.315883328	0.04174	0	1106	801	1816	1496	1794	2583	2263	1715	2143	2260
ENSMUSG00000025893	chr9	Kbtbd3	4309743	4309934	2310	-0.25826846	3.064009655	0.2259589	0.316076498	0.04652	0	137	88	170	152	137	198	130	131	168	150
ENSMUSG00000018449	chr11	Rpain	7.1E+07	7.1E+07	2842	0.304743773	2.739994576	0.2260132	0.316091407	0.06312	0	71	91	85	71	118	202	147	88	166	160
ENSMUSG00000098597	chr5	Mir6418	1.4E+08	1.4E+08	115	0.211151467	4.108586492	0.2260146	0.316091407	0.0328	0	201	160	297	237	326	509	396	259	344	419
ENSMUSG00000056665	chr15	Them6	7.5E+07	7.5E+07	1784	-0.23485525	3.558405331	0.2262027	0.31632291	0.03978	0	173	130	257	176	233	224	274	134	263	227
ENSMUSG00000022426	chr15	Josd1	8E+07	8E+07	3394	-0.19534824	5.003728766	0.2263388	0.316481717	0.0293	0	474	351	746	524	516	697	694	425	648	644
ENSMUSG00000027552	chr3	E2f5	1.5E+07	1.5E+07	1782	0.331437147	1.303900176	0.2266344	0.316863444	0.06077	0	27	24	30	36	40	60	54	38	53	67
ENSMUSG00000024833	chr19	Pola2	5940543	5941017	2872	0.210958758	3.872650966	0.2266698	0.31688134	0.03257	0	196	126	274	190	251	391	311	252	350	312
ENSMUSG00000083854	chr7	Dnajc19-ps	1E+08	1E+08	351	-0.34020178	1.097232425	0.2267595	0.316975184	0.06283	0	28	27	35	41	41	38	41	25	40	43
ENSMUSG00000032959	chr5	Pebp1	1.2E+08	1.2E+08	1771	0.225436778	7.824608938	0.2268696	0.317097447	0.04139	0	2945	2180	4236	3036	3570	5561	5513	3947	5181	5057
ENSMUSG00000030590	chr7	Fam98c	2.9E+07	2.9E+07	2712	0.230559036	4.093914107	0.2269977	0.317244846	0.04019	0	162	159	346	242	299	402	362	256	469	415
ENSMUSG00000042340	chr7	Ctf1	1.3E+08	1.3E+08	1345	0.249463465	3.279939753	0.2270388	0.317270756	0.04428	0	129	91	182	141	123	243	183	165	236	251
ENSMUSG00000042502	chr7	Cd2bp2	1.3E+08	1.3E+08	3379	0.199526328	5.514902967	0.2272561	0.317542689	0.03138	0	584	448	819	606	789	1137	1016	801	970	1116
ENSMUSG00000079168	chr8	Cd209g	4134733	4134787	1088	0.650800858	2.103087778	0.2273779	0.317681273	0.3176	0	43	50	8	13	129	213	72	94	86	68
ENSMUSG00000038252	chr6	Ncapd2	1.3E+08	1.3E+08	6267	-0.26545439	3.152413868	0.2275955	0.317953657	0.04967	0	109	84	247	135	177	188	174	121	160	187
ENSMUSG00000028713	chr4	Cyp4b1	1.2E+08	1.2E+08	2256	0.404704754	2.931572653	0.2276345	0.31797646	0.12603	0	75	60	66	56	250	215	163	122	237	153

ENSMUSG00000027075	chr2	Slc43a1	8.5E+07	8.5E+07	5716	-0.34923504	3.168555653	0.2278901	0.318301805	0.09357	0	201	155	102	110	150	180	126	136	135	229
ENSMUSG00000035772	chr2	Mrps2	2.8E+07	2.8E+07	2919	-0.23602545	4.590359324	0.2280414	0.318481331	0.04255	0	293	193	645	390	533	583	422	360	460	461
ENSMUSG00000045316	chr17	Fahd1	2.5E+07	2.5E+07	1407	-0.22389209	5.68906863	0.228157	0.318611051	0.03998	0	756	499	1295	914	820	1046	1094	722	978	1088
ENSMUSG00000039633	chr8	Lonrf1	3.6E+07	3.6E+07	3930	-0.2375567	3.61751007	0.2285166	0.319081565	0.04159	0	176	168	210	184	252	273	264	194	242	180
ENSMUSG00000019792	chr10	Trmt11	3.1E+07	3.1E+07	2359	-0.30497173	2.217975785	0.2285605	0.319084468	0.06254	0	58	58	103	77	88	128	106	60	60	74
ENSMUSG00000061032	chr10	Rrp1	7.8E+07	7.8E+07	2008	0.224844952	6.276299841	0.2285642	0.319084468	0.04103	0	907	660	1594	1131	1233	1842	1802	1229	1866	1922
ENSMUSG00000045288	chr11	Ush1g	1.2E+08	1.2E+08	3306	-0.89012863	0.185250229	0.2288639	0.319439308	0.54759	0	4	0	66	34	8	5	23	11	7	27
ENSMUSG00000089917	chr2	Uckl1	1.8E+08	1.8E+08	4629	-0.2118902	4.310492497	0.2288601	0.319439308	0.03367	0	349	195	407	257	423	440	440	288	350	382
ENSMUSG00000043243	chr8	Fam129c	7.2E+07	7.2E+07	3560	0.464727851	0.349962241	0.2290897	0.319722647	0.10209	0	12	16	9	12	23	37	25	18	23	37
ENSMUSG00000022335	chr15	Zfat	6.8E+07	6.8E+07	7321	-0.3106199	1.816301789	0.2292636	0.319933453	0.0624	0	43	48	78	64	53	63	78	52	57	65
ENSMUSG00000033021	chr1	Gmppa	7.5E+07	7.5E+07	2395	0.199714175	5.167747115	0.2293967	0.32003864	0.03103	0	502	373	512	532	590	958	748	543	901	844
ENSMUSG00000053644	chr18	Aldh7a1	5.7E+07	5.7E+07	5181	-0.20197511	4.707309252	0.2294054	0.32003864	0.03153	0	444	310	445	429	464	587	431	397	579	506
ENSMUSG00000055963	chr4	Triqk	1.3E+07	1.3E+07	3568	0.458520331	0.439562475	0.2294074	0.32003864	0.11572	0	16	9	12	11	32	49	21	24	30	25
ENSMUSG00000020776	chr11	Fbf1	1.2E+08	1.2E+08	7751	-0.23556688	3.564207924	0.2295107	0.320150878	0.04094	0	177	137	251	209	188	245	296	150	237	196
ENSMUSG00000063235	chr2	Ptpmt1	9.1E+07	9.1E+07	3684	-0.18983613	4.891074893	0.2295855	0.320223371	0.02777	0	428	347	634	417	583	607	643	414	621	582
ENSMUSG00000023336	chr8	Wfdc1	1.2E+08	1.2E+08	1213	-0.23286847	6.117800712	0.229673	0.320313559	0.04414	0	985	853	1252	1251	1316	1274	1615	882	1637	1220
ENSMUSG00000040254	chr5	Sema3d	1.2E+07	1.2E+07	6521	-0.43805076	0.956062551	0.2298021	0.320461718	0.12261	0	20	31	25	40	42	50	48	26	17	23
ENSMUSG00000024319	chr17	Vps52	3.4E+07	3.4E+07	3876	-0.2156537	5.705527503	0.2299117	0.320582766	0.03741	0	716	541	1117	970	950	1025	1114	654	1136	1093
ENSMUSG00000002814	chr11	Top3a	6.1E+07	6.1E+07	4599	-0.26265978	2.675073292	0.2299735	0.320617808	0.04948	0	85	84	138	94	120	136	142	66	118	139
ENSMUSG00000030145	chr6	Zfp248	1.2E+08	1.2E+08	5039	-0.39760828	0.978048817	0.2299826	0.320617808	0.10044	0	42	32	27	19	37	44	42	24	23	36
ENSMUSG00000038683	chr13	Pak1ip1	4.1E+07	4.1E+07	4049	0.201219624	5.410804096	0.2300246	0.32064445	0.03234	0	553	390	697	581	805	1034	935	800	916	982
ENSMUSG00000029417	chr5	Cxcl9	9.2E+07	9.2E+07	2905	0.94348273	1.257922212	0.23036	0.321080137	0.67637	0	20	5	5	1	95	175	25	19	15	91
ENSMUSG00000038692	chr11	Hoxb4	9.6E+07	9.6E+07	2566	0.623500153	-0.24095754	0.2305301	0.321285263	0.19573	0	5	9	7	3	19	36	10	6	20	22
ENSMUSG00000005699	chr8	Pard6a	1.1E+08	1.1E+08	1430	0.257781592	2.776445543	0.2307586	0.321528692	0.04558	0	92	57	117	97	106	181	135	122	169	151
ENSMUSG00000023830	chr17	Igf2r	1.3E+07	1.3E+07	9438	-0.24559585	6.70264649	0.2307646	0.321528692	0.04967	0	1461	1219	2496	1995	1401	2150	2396	1386	1941	2041
ENSMUSG00000039959	chr5	Hip1	1.4E+08	1.4E+08	7850	0.20033818	4.955739906	0.2307735	0.321528692	0.03161	0	393	305	546	345	623	854	713	569	649	634
ENSMUSG00000054405	chr4	Dnajc8	1.3E+08	1.3E+08	2555	0.196590043	5.526222193	0.2309042	0.321614857	0.03095	0	600	437	826	612	807	1221	1083	792	960	1036
ENSMUSG00000068015	chr14	Lrch1	7.5E+07	7.5E+07	4706	0.295140894	2.376104837	0.2308696	0.321614857	0.05682	0	67	66	79	54	73	154	105	94	108	118
ENSMUSG00000097195	chr9	Snhg5	8.9E+07	8.9E+07	1730	0.236851378	3.525173446	0.2309015	0.321614857	0.04065	0	137	128	169	158	196	332	232	222	221	265
ENSMUSG00000025509	chr7	Pnpla2	1.4E+08	1.4E+08	3020	-0.36579103	8.485148515	0.2309765	0.321683725	0.11086	0	3912	1972	9905	5019	12299	6545	6738	4188	5596	9590
ENSMUSG00000026632	chr1	Tatdn3	1.9E+08	1.9E+08	2786	-0.23938084	3.187063831	0.2311252	0.32182686	0.04257	0	156	125	162	130	155	197	188	119	179	177
ENSMUSG00000074001	chr9	Klhl40	1.2E+08	1.2E+08	2455	0.264870982	7.441049903	0.2311195	0.32182686	0.05814	0	2223	1487	3404	2997	1915	5426	4154	2976	4029	3182
ENSMUSG00000020849	chr11	Ywhae	7.6E+07	7.6E+07	2568	-0.2329462	8.692844174	0.2311555	0.321837147	0.04516	0	6295	5210	7717	6726	7757	7740	9192	6054	8108	8186
ENSMUSG00000028436	chr4	Dcaf12	4.1E+07	4.1E+07	3442	-0.20541846	5.67222046	0.2314011	0.322147051	0.03403	0	790	536	1094	827	927	1092	1214	706	914	994
ENSMUSG00000033208	chr10	S100b	7.6E+07	7.6E+07	1484	-0.64732087	2.62092348	0.2315078	0.322263654	0.33087	0	97	30	30	35	414	167	67	68	91	102
ENSMUSG00000047787	chr19	Flrt1	7092014	7097229	5859	-0.61152119	-0.19810889	0.2315532	0.322264436	0.22805	0	24	12	14	8	11	18	18	1	23	6
ENSMUSG00000061118	chr5	Dnajc30	1.4E+08	1.4E+08	1661	0.23051414	4.700338915	0.2315543	0.322264436	0.04261	0	297	173	566	433	395	643	520	423	657	655
ENSMUSG00000062353	chr5	Gm15772	3236431	3236868	438	0.289429793	2.849018556	0.2316024	0.322299393	0.06058	0	86	73	103	95	126	135	161	96	220	198
ENSMUSG00000042050	chr12	Wdr60	1.2E+08	1.2E+08	3725	0.215453591	3.88434251	0.231733	0.322449168	0.03415	0	196	147	270	208	208	430	384	235	293	303
ENSMUSG00000025821	chr6	Zfp282	4.8E+07	4.8E+07	7663	-0.23136291	3.334802341	0.2318867	0.322598999	0.03856	0	154	116	180	164	205	213	214	148	212	164
ENSMUSG00000085965	chr1	2310016D23Rik	6.1E+07	6.1E+07	388	-0.42961218	0.952021789	0.231886	0.322598999	0.1184	0	36	19	41	44	19	23	33	23	52	30
ENSMUSG00000042992	chr6	Loh12cr1	1.3E+08	1.3E+08	1822	-0.18667241	4.553534366	0.23198	0.322696751	0.02651	0	347	270	469	378	428	472	483	346	484	476
ENSMUSG00000093574	chr5	Gm20671	3.3E+07	3.3E+07	1731	-0.21637523	4.098736138	0.232133	0.322877526	0.03571	0	232	205	385	245	335	408	426	223	298	295
ENSMUSG00000072115	chr14	Ang	5.1E+07	5.1E+07	1273	0.389629197	2.360459965	0.2322315	0.322982498	0.10858	0	47	72	44	48	110	199	134	86	85	95
ENSMUSG00000030272	chr6	Camk1	1.1E+08	1.1E+08	6067	0.207981318	5.268910323	0.2324124	0.323170022	0.03446	0	521	424	555	468	724	1133	841	632	928	759
ENSMUSG00000036833	chr2	Pnpla7	2.5E+07	2.5E+07	7496	-0.22523303	5.446007978	0.2324004	0.323170022	0.0412	0	671	479	954	833	619	854	865	556	861	1038
ENSMUSG00000039568	chr16	Ubald1	4874778	4875869	5538	0.235152971	5.535265089	0.2324575	0.323200687	0.04501	0	568	448	611	621	996	1027	1005	670	1293	1208
ENSMUSG00000042594	chr5	Sh2b3	1.2E+08	1.2E+08	4734	0.210751653	4.436616121	0.2326489	0.323434829	0.03484	0	220	195	383	283	470	554	503	350	512	483
ENSMUSG00000040557	chr5	Wbscr27	1.3E+08	1.3E+08	3342	0.37522628	1.781553738	0.2326911	0.323461405	0.0935	0	31	42	43	24	79	105	69	54	90	73
ENSMUSG00000018999	chr6	Slc35b4	3.4E+07	3.4E+07	9177	0.273211528	3.660059304	0.2328442	0.323545935	0.05702	0	175	134	142	117	291	372	290	207	284	276
ENSMUSG00000027404	chr2	Snrpb	1.3E+08	1.3E+08	1976	0.230145878	7.042447291	0.2328408	0.323545935	0.04406	0	1687	1319	2117	1736	2369	2913	2892	2274	3594	2978
ENSMUSG00000036377	chr5	C530008M17Rik	7.7E+07	7.7E+07	12305	-0.54485775	-0.12179359	0.232775	0.323545935	0.1688	0	10	8	28	11	19	22	28	4	6	11
ENSMUSG00000042901	chr1	Aida	1.8E+08	1.8E+08	6175	0.194604639	4.761674569	0.2327993	0.323545935	0.02944	0	331	274	460	390	463	852	594	460	537	564
ENSMUSG00000070576	chr5	Mn1	1.1E+08	1.1E+08	6940	-0.22771876	5.27184056	0.2329536	0.323665825	0.0418	0	654	348	989	678	535	850	762	575	726	763
ENSMUSG00000054843	chr19	Atrnl1	5.8E+07	5.8E+07	6581	-0.22073496	3.735238183	0.2329936	0.323689465	0.03654	0	208	152	236	188	301	313	301	166	239	260
ENSMUSG00000020289	chr11	Nprl3	3.2E+07	3.2E+07	7572	-0.2026639	4.205862721	0.2334717	0.324321425	0.03119	0	269	210	359	312	343	350	386	261	410	358
ENSMUSG00000023452	chr5	Pisd	3.3E+07	3.3E+07	3814	0.190913918	4.877236833	0.2335211	0.324357941	0.02868	0	347	288	572	374	522	830	699	453	679	600
ENSMUSG00000032500	chr9	Dclk3	1.1E+08	1.1E+08	3495	-0.48933407	-0.06030434	0.233714	0.324593825	0.12978	0	11	10	14	24	17	25	13	14	17	5
ENSMUSG00000015747	chr3	Vps45	9.6E+07	9.6E+07	3991	0.233480507	3.447035284	0.2339812	0.324932639	0.03917	0	131	114	149	171	182	310	246	172	240	248
ENSMUSG00000040152	chr2	Thbs1	1.2E+08	1.2E+08	6073	-0.27835732	4.572444417	0.2340835	0.325042603	0.06314	0	306	371	489	296	490	777	523	314	253	400
ENSMUSG00000025902	chr1	Sox17	4490931	4492668	4772	0.331836962	2.419936711	0.2342782	0.325280788	0.0841	0	43	40	129	43	114	145	113	93	135	118
ENSMUSG00000040822	chr14	1700123O20Rik	5.5E+07	5.5E+07	1889	0.24490939	3.351660563	0.2343809	0.325391147	0.04524	0	125	90	173	122	202	303	197	204	214	210
ENSMUSG00000032558	chr9	Nphp3	1E+08	1E+08	6639	-0.35327769	1.407087749	0.2344347	0.325433556	0.08534	0	44	38	42	33	58	82	48	23	46	40
ENSMUSG00000067608	chr19	Pcna-ps2	9283238	9284494	1257	0.380573272	0.501063746	0.2345244	0.325525864	0.07976	0	17	9	25	13	23	35	30	27	37	22
ENSMUSG00000020305	chr11	Asb3	3.1E+07	3.1E+07	5275	-0.25055007	2.926402177	0.2346018	0.325601136	0.0458	0	106	111	137	120	135	169	135	108	156	142
ENSMUSG00000016664	chr15	Pacsin2	8.3E+07	8.3E+07	3885	-0.24254864	6.163635588	0.2348386	0.325894763	0.04891	0	959	708	1945	1226	1191	1515	1816	974	1256	1271
ENSMUSG00000019917	chr10	Sept10	5.9E+07	5.9E+07	2539	-0.24123227	3.164116598	0.2348693	0.325894763	0.04256	0	142	117	159	129	176	222	180	132	168	142

ENSMUSG00000089824	chr2	Rbm12	1.6E+08	1.6E+08	6689	-0.23971625	3.287409758	0.2348831	0.325894763	0.04271	0	126	135	161	148	219	217	191	131	193	190
ENSMUSG00000053390	chr17	Zfp952	3.3E+07	3.3E+07	4368	-0.27710335	2.734243965	0.2350913	0.326151401	0.05531	0	108	75	145	120	96	154	146	104	117	92
ENSMUSG00000059058	chr1	Tma7-ps	1.7E+08	1.7E+08	195	-0.23514092	3.761429154	0.235259	0.326323331	0.04266	0	238	178	242	230	194	269	272	209	291	232
ENSMUSG00000082456	chr11	Gm11598	1E+08	1E+08	357	0.460094702	0.301929902	0.2352618	0.326323331	0.10473	0	13	12	19	10	17	18	28	17	45	25
ENSMUSG00000026889	chr2	Rbm18	3.6E+07	3.6E+07	5740	-0.20351028	5.527857764	0.2355506	0.326627096	0.03386	0	732	525	987	725	777	982	1066	709	834	834
ENSMUSG00000043969	chr19	Emx2	5.9E+07	5.9E+07	3002	0.371974115	1.419213683	0.2355068	0.326627096	0.08411	0	26	38	45	27	29	66	51	59	60	58
ENSMUSG00000058743	chr7	Kcnj14	4.6E+07	4.6E+07	2654	-0.93378588	0.648296089	0.2355324	0.326627096	0.63717	0	26	13	3	2	113	26	9	41	12	8
ENSMUSG00000001661	chr15	Hoxc6	1E+08	1E+08	2408	0.263427405	3.448630233	0.2357799	0.326848041	0.05426	0	146	78	173	119	250	312	231	149	252	294
ENSMUSG00000023232	chr4	Serinc2	1.3E+08	1.3E+08	2319	0.227411449	6.590420154	0.2357732	0.326848041	0.04338	0	1353	906	1601	1130	1797	2257	2528	1426	2511	2097
ENSMUSG00000037017	chr5	Zscan21	1.4E+08	1.4E+08	3198	-0.19947271	3.946433698	0.2357435	0.326848041	0.02974	0	233	167	310	238	304	358	323	218	276	309
ENSMUSG00000026811	chr2	St6galnac6	3.3E+07	3.3E+07	4815	0.203090853	5.682942939	0.2358346	0.32689156	0.03381	0	683	553	796	688	877	1259	1105	879	1243	1185
ENSMUSG00000021476	chr13	Habp4	6.4E+07	6.4E+07	2566	-0.19928801	5.473937937	0.2360533	0.327130101	0.03257	0	703	518	847	776	732	1007	841	627	873	942
ENSMUSG00000027091	chr2	Zc3h15	8.4E+07	8.4E+07	2789	-0.20623139	5.887233419	0.2360328	0.327130101	0.03522	0	919	711	1155	956	1044	1338	1289	951	1005	1083
ENSMUSG00000059195	chr4	Gm12715	1E+08	1E+08	1128	0.29868185	2.001572546	0.2361764	0.327268377	0.0607	0	41	35	67	46	80	102	115	61	97	72
ENSMUSG00000028437	chr4	Ubap1	4.1E+07	4.1E+07	3583	-0.20004947	5.684886184	0.2363742	0.327510037	0.03302	0	782	603	954	758	1079	1167	1130	713	958	1009
ENSMUSG00000035765	chr18	Dym	7.5E+07	7.5E+07	2471	-0.21626582	6.47888728	0.2364204	0.327541681	0.03925	0	1239	1003	1901	1501	1680	1848	2078	1174	1782	1706
ENSMUSG00000023052	chr15	Npff	1E+08	1E+08	1002	0.592212701	0.109432391	0.2364911	0.327607335	0.20325	0	14	8	4	10	21	39	11	11	16	45
ENSMUSG00000006705	chr17	Pknox1	3.2E+07	3.2E+07	6892	-0.2338117	3.550474418	0.2366782	0.327801705	0.04126	0	164	126	280	186	210	245	300	143	226	203
ENSMUSG00000028251	chr4	Tstd3	2.2E+07	2.2E+07	1588	-0.22649069	4.176782206	0.236668	0.327801705	0.04017	0	243	205	471	307	260	423	387	275	301	333
ENSMUSG00000027305	chr2	Ndufaf1	1.2E+08	1.2E+08	1501	-0.21288208	5.432885569	0.2367791	0.327909148	0.03726	0	673	446	969	808	632	942	883	633	769	912
ENSMUSG00000014470	chr8	Rnf166	1.2E+08	1.2E+08	1985	-0.20807445	5.143783124	0.2368194	0.327932537	0.03514	0	520	355	755	681	579	679	806	505	780	615
ENSMUSG00000021044	chr12	Adck1	8.8E+07	8.8E+07	2330	-0.23656975	5.049236997	0.2376905	0.329106382	0.04569	0	401	275	963	620	550	703	720	480	644	595
ENSMUSG00000020883	chr11	Fbxl20	9.8E+07	9.8E+07	12106	-0.18726006	4.712284213	0.2378892	0.329217665	0.0279	0	357	316	536	395	515	587	545	344	465	608
ENSMUSG00000026721	chr1	Rabgap1l	1.6E+08	1.6E+08	23232	-0.24113942	3.888542372	0.2378371	0.329217665	0.04652	0	265	196	209	222	295	397	312	183	217	310
ENSMUSG00000026923	chr2	Notch1	2.6E+07	2.6E+07	14232	-0.21522126	4.227084942	0.2378596	0.329217665	0.03594	0	225	201	405	267	456	393	363	272	396	361
ENSMUSG00000031936	chr9	Hephl1	1.5E+07	1.5E+07	5261	0.526361405	-0.11966896	0.2379118	0.329217665	0.13768	0	9	7	7	8	19	31	19	23	9	15
ENSMUSG00000038712	chr3	Fam63a	9.5E+07	9.5E+07	6458	0.197667502	5.329862781	0.2378815	0.329217665	0.03183	0	517	431	652	575	646	959	848	618	961	1066
ENSMUSG00000042292	chr15	Mkl1	8.1E+07	8.1E+07	6114	-0.22852439	5.046664216	0.2378545	0.329217665	0.04307	0	427	394	554	628	692	554	713	379	858	656
ENSMUSG00000042225	chrX	Ammecr1	1.4E+08	1.4E+08	5437	0.283190247	2.512824229	0.2380483	0.329374155	0.05583	0	77	64	76	76	83	120	124	108	115	162
ENSMUSG00000040414	chr19	Slc25a28	4.4E+07	4.4E+07	1514	-0.20094712	4.574689913	0.2381987	0.329549755	0.0319	0	322	237	575	363	473	495	499	294	504	514
ENSMUSG00000024560	chr18	Cxxc1	7.4E+07	7.4E+07	2618	-0.20371261	4.256816301	0.2382791	0.329628439	0.03264	0	261	232	362	330	357	353	416	245	396	427
ENSMUSG00000041592	chr11	Sdk2	1.1E+08	1.1E+08	15469	0.425311676	-0.07435611	0.2386732	0.330141094	0.08078	0	8	9	13	8	16	21	19	13	27	19
ENSMUSG00000030822	chr7	Prr14	1.3E+08	1.3E+08	3456	0.192418991	4.346598212	0.2387221	0.330176155	0.02897	0	232	195	365	301	354	532	441	335	434	499
ENSMUSG00000063787	chr14	Chchd1	2.1E+07	2.1E+07	587	-0.23310298	5.995379874	0.2392794	0.330914368	0.04602	0	1076	814	1391	1060	813	1465	1171	1001	1259	1150
ENSMUSG00000028960	chr4	Ube4b	1.5E+08	1.5E+08	7078	-0.17942408	5.058665464	0.2393811	0.331022333	0.02595	0	472	362	683	517	672	720	686	446	694	699
ENSMUSG00000078490	chr4	C030017K20Rik	1.6E+08	1.6E+08	9951	-0.39834652	1.127207713	0.2394252	0.331050684	0.10848	0	45	33	24	23	51	37	41	23	32	55
ENSMUSG00000037196	chr17	Pacrg	1E+07	1E+07	1572	0.373697612	0.564909652	0.2394949	0.331114418	0.08081	0	18	7	31	18	18	34	37	25	28	35
ENSMUSG00000026659	chr1	Dusp12	1.7E+08	1.7E+08	2743	0.264534014	2.719244283	0.239673	0.33132801	0.04966	0	80	75	104	81	102	187	132	128	157	123
ENSMUSG00000050705	chr17	2310061I04Rik	3.6E+07	3.6E+07	2414	0.251950418	6.146786574	0.2397019	0.331335264	0.05428	0	748	469	1608	1066	1211	1506	1852	1107	1654	1860
ENSMUSG00000054312	chr3	Mrps21	9.6E+07	9.6E+07	1282	0.223554937	6.1737736	0.2397458	0.331363344	0.04233	0	966	739	1185	1076	1050	1717	1368	1212	1876	1850
ENSMUSG00000029864	chr6	Gstk1	4.2E+07	4.2E+07	930	-0.20599355	5.042903376	0.2398197	0.331432743	0.03517	0	569	416	533	566	538	781	565	460	597	773
ENSMUSG00000001156	chr6	Mxd1	8.7E+07	8.7E+07	4662	0.317789471	2.458828984	0.2399288	0.331550931	0.07241	0	90	53	48	63	104	164	119	84	126	131
ENSMUSG00000056367	chr5	Actr3b	2.6E+07	2.6E+07	1741	-0.58253219	3.419270496	0.2400077	0.33160422	0.28126	0	50	63	472	131	353	120	471	72	140	97
ENSMUSG00000082100	chr11	Glns-ps1	2E+07	2E+07	1118	-0.32015757	1.982186599	0.2400147	0.33160422	0.07237	0	79	46	48	65	82	71	68	56	89	69
ENSMUSG00000033065	chr15	Pfkm	9.8E+07	9.8E+07	2957	-0.24313694	11.78152416	0.2401436	0.331749592	0.05125	0	49655	34298	80394	69130	60429	67353	74557	48559	74281	69259
ENSMUSG00000029093	chr5	Sorcs2	3.6E+07	3.6E+07	8803	0.316514661	2.044548606	0.2402145	0.331814879	0.07107	0	50	32	86	42	67	144	93	47	102	86
ENSMUSG00000007950	chr8	Abhd8	7.1E+07	7.1E+07	1985	-0.20764767	4.945312667	0.240299	0.331876596	0.03559	0	496	375	580	480	552	583	604	382	815	579
ENSMUSG00000031917	chr8	Nip7	1.1E+08	1.1E+08	3031	0.22014716	3.853221347	0.2403065	0.331876596	0.03755	0	209	149	242	182	218	382	291	301	303	302
ENSMUSG00000042870	chr8	Tom1	7.5E+07	7.5E+07	2358	-0.20985695	5.241606895	0.2403827	0.331949232	0.03663	0	551	424	835	711	552	714	900	507	768	745
ENSMUSG00000007036	chr17	Abhd16a	3.5E+07	3.5E+07	3220	-0.20731381	5.968227603	0.2404135	0.33195901	0.03637	0	935	659	1204	1076	1249	1367	1421	781	1298	1201
ENSMUSG00000027861	chr3	Casq2	1E+08	1E+08	2736	0.716128307	6.674664066	0.2405529	0.33211887	0.43282	0	400	69	3376	2344	218	2683	2163	2196	2138	3843
ENSMUSG00000039254	chr2	Pomt1	3.2E+07	3.2E+07	6442	-0.21957007	3.907956153	0.2405919	0.332139935	0.03796	0	202	181	237	280	312	334	273	200	347	279
ENSMUSG00000020564	chr12	Atxn7l1	3.3E+07	3.3E+07	12523	-0.20481369	3.973609049	0.2407081	0.332267629	0.03248	0	245	184	286	222	334	350	349	232	299	274
ENSMUSG00000042659	chr7	Arrdc4	6.9E+07	6.9E+07	3989	0.235336749	3.166275862	0.2407678	0.332317337	0.04143	0	100	85	136	125	177	247	206	145	183	217
ENSMUSG00000038347	chr17	Tcte2	1.3E+07	1.3E+07	8560	-0.41117694	0.34553138	0.2409626	0.332553554	0.09587	0	28	19	17	14	21	20	19	15	26	24
ENSMUSG00000093290	chr7	Mir3572	3655962	3656047	86	0.423136444	0.313836658	0.2409872	0.332554687	0.09646	0	12	7	11	15	29	29	28	17	33	27
ENSMUSG00000004018	chr11	Fancl	2.6E+07	2.6E+07	3372	0.308689918	2.139269832	0.2410746	0.332642696	0.06308	0	58	53	69	40	67	128	87	63	118	100
ENSMUSG00000103235	chr9	DHX30	1.1E+08	1.1E+08	3585	-0.18405214	5.01826251	0.2411953	0.332776392	0.02758	0	426	368	662	578	585	696	667	471	669	632
ENSMUSG00000045519	chr9	Zfp560	2E+07	2E+07	4981	0.249853846	2.982218335	0.2416303	0.333343817	0.04539	0	118	78	119	90	133	185	166	145	183	191
ENSMUSG00000032637	chr7	Atxn2l	1.3E+08	1.3E+08	4782	0.228809469	5.47121049	0.2417551	0.333453269	0.04412	0	492	492	633	568	906	1018	950	607	1135	1275
ENSMUSG00000103183	chr4	RP23-118E21.11	1.6E+08	1.6E+08	4105	0.40749237	0.902092554	0.2417572	0.333453269	0.10429	0	19	17	23	17	39	43	24	38	37	62
ENSMUSG00000028649	chr4	Macf1	1.2E+08	1.2E+08	26689	0.224344637	6.638153098	0.2420566	0.333833487	0.04343	0	1199	854	2075	1534	1414	2627	2530	1542	2147	2344
ENSMUSG00000026229	chr1	Psmd1	8.6E+07	8.6E+07	7265	-0.22275627	7.627715288	0.2421213	0.333889793	0.04311	0	3166	2324	3832	3408	3344	4152	4419	2902	3853	3569
ENSMUSG00000039163	chr9	Cmc1	1.2E+08	1.2E+08	1181	0.210167207	3.865111342	0.2421555	0.333904186	0.03459	0	193	129	243	191	273	415	276	252	322	344
ENSMUSG00000045216	chr1	Hs6st1	3.6E+07	3.6E+07	5542	-0.19412737	5.265461622	0.2423119	0.334086924	0.0314	0	550	437	797	707	615	817	803	563	800	723
ENSMUSG00000097375	chr13	6720427I07Rik	4.9E+07	4.9E+07	2300	0.437141703	1.183120431	0.2424015	0.334177719	0.12884	0	16	25	35	36	25	45	32	41	41	95
ENSMUSG00000056919	chr9	Cep162	8.7E+07	8.7E+07	11607	-0.27228975	2.322845576	0.2425666	0.334372334	0.05367	0	75	60	114	73	87	121	108	50	84	106

ENSMUSG00000031901	chr8	Dus2	1.1E+08	1.1E+08	3367	-0.21364785	3.734657902	0.2425909	0.334372987	0.03515	0	214	151	234	204	274	285	240	199	293	247
ENSMUSG00000020231	chr10	Dip2a	7.6E+07	7.6E+07	8215	-0.26077698	3.31232523	0.2429063	0.334774895	0.05297	0	109	106	204	141	276	238	197	128	163	210
ENSMUSG00000031916	chr8	Cog8	1.1E+08	1.1E+08	4637	-0.20634506	6.118003806	0.2429884	0.334855076	0.03654	0	1050	833	1348	1169	1216	1451	1478	1006	1386	1351
ENSMUSG00000022560	chr15	Slc52a2	7.7E+07	7.7E+07	2700	0.285076746	2.676617466	0.2431549	0.335051614	0.06188	0	76	52	88	70	152	178	122	98	151	170
ENSMUSG00000029442	chr5	Wdr66	1.2E+08	1.2E+08	7583	0.350459083	1.967172347	0.243228	0.335119465	0.08615	0	48	40	44	57	60	92	64	45	119	125
ENSMUSG00000054237	chr19	Fra10ac1	3.8E+07	3.8E+07	1402	-0.20511288	3.920747245	0.243564	0.335549381	0.03304	0	234	174	311	225	283	395	306	213	240	306
ENSMUSG00000086228	chr9	Ubap1l	6.5E+07	6.5E+07	1381	-0.49834827	0.111933057	0.2435923	0.335555483	0.12715	0	18	4	33	21	14	22	22	14	13	13
ENSMUSG00000001305	chr1	Rrp15	1.9E+08	1.9E+08	3239	0.255387636	3.393792538	0.243768	0.33576449	0.04985	0	142	130	136	144	148	289	215	217	203	236
ENSMUSG00000070319	chr9	Eif3g	2.1E+07	2.1E+07	1075	0.210266086	5.915777518	0.2438509	0.335845697	0.03789	0	765	614	1038	823	1010	1465	1157	975	1593	1506
ENSMUSG00000047712	chr10	Ust	8204753	8207670	4284	0.367449194	1.787169732	0.244022	0.336048318	0.09821	0	41	37	31	28	83	112	64	53	73	91
ENSMUSG00000032594	chr9	Ip6k1	1.1E+08	1.1E+08	6487	0.192019465	5.499170385	0.2440556	0.336061685	0.03111	0	547	459	808	632	767	1124	1026	697	1054	1106
ENSMUSG00000096403	chr6	Gm9825	7981829	7983430	1602	0.193723068	4.557917988	0.2442098	0.336240907	0.03027	0	256	248	397	388	368	576	516	383	547	571
ENSMUSG00000097062	chr11	Gm17586	1.2E+08	1.2E+08	908	0.281631351	2.317619993	0.2442719	0.336293435	0.05834	0	53	41	78	55	114	118	126	88	107	113
ENSMUSG00000034442	chr12	Trmt5	7.3E+07	7.3E+07	1669	-0.24547888	2.909068529	0.2445614	0.336651659	0.04545	0	110	94	161	123	120	156	167	111	122	146
ENSMUSG00000050627	chr9	Gpd1l	1.1E+08	1.1E+08	5077	-0.19426632	5.4467186	0.2445801	0.336651659	0.03189	0	652	476	935	743	735	938	907	657	813	885
ENSMUSG00000026104	chr1	Stat1	5.2E+07	5.2E+07	7105	0.305534623	5.058176716	0.2448201	0.33691588	0.08032	0	400	281	597	416	602	1759	624	366	530	713
ENSMUSG00000034928	chr13	Rnf44	5.5E+07	5.5E+07	5202	-0.1953246	5.068231663	0.2448092	0.33691588	0.03177	0	422	333	735	572	705	701	807	422	672	657
ENSMUSG00000027203	chr2	Dut	1.3E+08	1.3E+08	2410	0.243097391	3.064841937	0.2448819	0.336967847	0.04399	0	121	85	129	110	124	221	190	163	187	159
ENSMUSG00000030309	chr6	Caprin2	1.5E+08	1.5E+08	7656	-0.33375775	1.609204206	0.2449498	0.33702831	0.08043	0	58	43	51	30	65	83	48	44	50	47
ENSMUSG00000030411	chr7	Nova2	1.9E+07	1.9E+07	8372	0.383157671	1.718099254	0.2452513	0.337410001	0.11798	0	22	18	49	35	96	76	61	68	85	76
ENSMUSG00000021097	chr12	Clmn	1E+08	1E+08	11962	-0.33003464	2.771249006	0.2454558	0.337658138	0.08743	0	92	98	96	76	207	141	106	115	91	158
ENSMUSG00000104213	chr12	Ighd	1.1E+08	1.1E+08	1900	0.475173825	0.113374812	0.2455671	0.337778179	0.13251	0	11	8	13	5	25	30	18	9	31	30
ENSMUSG00000100725	chr1	Gm28062	1.8E+08	1.8E+08	3030	-0.21910116	6.896162436	0.2457223	0.337958532	0.04211	0	1546	1398	2567	2041	2227	2811	2497	1811	1944	2346
ENSMUSG00000086688	chr11	Gm11560	1E+08	1E+08	948	-0.45406225	0.310598988	0.2460588	0.338388185	0.13211	0	10	17	26	18	30	21	36	6	24	15
ENSMUSG00000019969	chr12	Psen1	8.4E+07	8.4E+07	3114	0.180218347	5.181243404	0.2461154	0.338432786	0.0271	0	466	370	609	506	628	871	891	568	853	810
ENSMUSG00000059796	chr11	Eif4a1	7E+07	7E+07	4334	0.22345146	6.52230864	0.2461922	0.338505228	0.04382	0	971	917	1628	1254	1737	2536	2056	1838	1872	1868
ENSMUSG00000062257	chr9	Opcml	2.8E+07	2.8E+07	13120	-0.35292712	1.376824157	0.2462623	0.338568367	0.08346	0	36	19	51	37	77	56	51	27	39	57
ENSMUSG00000026698	chr1	Pigc	1.6E+08	1.6E+08	4250	0.213346887	4.246797314	0.2464163	0.338746979	0.03682	0	255	217	307	201	340	515	359	327	406	492
ENSMUSG00000009621	chr2	Vav2	2.7E+07	2.7E+07	6915	0.288822093	2.935622239	0.2465135	0.33884739	0.06708	0	75	52	155	78	178	219	163	145	174	155
ENSMUSG00000026620	chr1	Mark1	1.8E+08	1.8E+08	4356	0.341913135	1.954551259	0.2466023	0.338936176	0.09296	0	35	19	103	46	62	122	79	73	83	78
ENSMUSG00000103715	chr9	RP23-58N8.6	8.6E+07	8.6E+07	1352	-0.3158958	1.151743862	0.24672	0.33906469	0.05977	0	29	32	43	35	38	47	40	30	37	42
ENSMUSG00000027901	chr3	Dennd2d	1.1E+08	1.1E+08	6868	0.630494839	0.10091873	0.2467451	0.339066033	0.28023	0	11	5	2	4	36	38	22	11	17	34
ENSMUSG00000025870	chr13	Arl10	5.5E+07	5.5E+07	1729	-0.37946907	0.949894002	0.2471514	0.339591032	0.09689	0	26	31	18	31	48	35	42	26	32	30
ENSMUSG00000032324	chr9	Tspan3	5.6E+07	5.6E+07	1728	-0.21368019	6.943480848	0.2471836	0.339602016	0.0403	0	1910	1317	2587	2010	2276	2663	2813	1759	2243	2352
ENSMUSG00000046727	chr18	Cystm1	3.6E+07	3.6E+07	2840	-0.21467461	6.879116043	0.2474612	0.339950132	0.04075	0	1781	1456	2222	1919	2157	2321	2521	1642	2510	2289
ENSMUSG00000020149	chr11	Rab1	2E+07	2E+07	3799	-0.21730496	6.979494609	0.2475526	0.340009032	0.04178	0	1941	1406	2641	2064	2284	2761	3035	1816	2250	2255
ENSMUSG00000037894	chr3	H2afz	1.4E+08	1.4E+08	1776	-0.19487638	5.369428472	0.2475313	0.340009032	0.03261	0	634	524	751	645	758	948	899	620	851	668
ENSMUSG00000024014	chr17	Pim1	2.9E+07	2.9E+07	2638	0.292817315	3.877786317	0.2477453	0.340240475	0.07027	0	208	223	141	139	236	389	276	237	359	407
ENSMUSG00000020178	chr10	Adora2a	7.5E+07	7.5E+07	2534	0.380468201	1.865502166	0.2478958	0.340413744	0.11716	0	36	19	57	26	107	118	70	62	74	91
ENSMUSG00000064208	chr10	Gm10145	2.8E+07	2.8E+07	465	-0.47165834	0.116944418	0.2479856	0.340503817	0.12691	0	21	11	8	21	25	18	22	15	21	9
ENSMUSG00000073678	chr1	Pgap1	5.4E+07	5.4E+07	16611	-0.32239165	2.186605179	0.2480585	0.340570527	0.08055	0	95	61	73	78	58	91	114	64	56	86
ENSMUSG00000034024	chr10	Cct2	1.2E+08	1.2E+08	1962	-0.2131146	6.790406295	0.2481607	0.340677477	0.04024	0	1682	1363	2245	1828	1845	2591	2268	1682	2020	2056
ENSMUSG00000017801	chr11	Mlx	1E+08	1E+08	1999	0.215110198	3.961095271	0.2485511	0.341180116	0.03736	0	198	147	220	234	289	446	297	255	403	326
ENSMUSG00000002803	chr12	Btbd6	1.1E+08	1.1E+08	2088	-0.21840089	4.531343417	0.2487918	0.341382128	0.03992	0	289	219	568	466	373	483	537	308	486	402
ENSMUSG00000025269	chrX	Apex2	1.5E+08	1.5E+08	8744	-0.26313487	2.369385586	0.2487758	0.341382128	0.04853	0	69	52	119	89	97	122	102	73	97	85
ENSMUSG00000036898	chr5	Zfp157	1.4E+08	1.4E+08	8782	-0.30423021	1.676440217	0.248732	0.341382128	0.06214	0	35	43	69	54	59	73	48	39	61	68
ENSMUSG00000060950	chr12	Trmt61a	1.1E+08	1.1E+08	2433	0.287476014	2.816038046	0.2487957	0.341382128	0.06519	0	77	68	91	129	104	185	128	161	160	140
ENSMUSG00000072082	chr17	Ccnf	2.4E+07	2.4E+07	3099	0.39678753	0.393829798	0.2491046	0.341772566	0.08538	0	16	11	15	16	20	31	29	28	34	17
ENSMUSG00000056880	chr9	Gadl1	1.2E+08	1.2E+08	3966	-0.52492741	2.929325849	0.2493325	0.342051785	0.2334	0	70	35	309	57	276	93	274	96	80	93
ENSMUSG00000070934	chr4	Rraga	8.7E+07	8.7E+07	1618	-0.1951989	5.48039711	0.2496728	0.342485102	0.03293	0	684	487	861	786	795	915	949	732	813	862
ENSMUSG00000026201	chr1	Stk16	7.5E+07	7.5E+07	4518	0.196609182	4.368706439	0.2497962	0.342587422	0.03131	0	254	244	314	269	358	525	448	326	518	462
ENSMUSG00000032946	chr19	Rasgrp2	6399340	6399517	12384	-0.31604151	3.257671292	0.2497846	0.342587422	0.08318	0	126	128	157	80	318	214	164	119	190	193
ENSMUSG00000020876	chr11	Snx11	9.7E+07	9.7E+07	4232	0.218583627	4.030539332	0.2498375	0.34261054	0.03875	0	226	175	208	220	298	442	303	282	411	368
ENSMUSG00000032403	chr9	2300009A05Rik	6.3E+07	6.3E+07	2000	0.259420291	3.029768459	0.2500105	0.342814245	0.05427	0	87	60	152	128	142	176	156	146	196	228
ENSMUSG00000020346	chr11	Mgat1	4.9E+07	4.9E+07	4733	0.207804347	6.07350065	0.2501178	0.342927902	0.03822	0	767	624	1301	967	1148	1632	1631	1059	1682	1485
ENSMUSG00000028207	chr4	Asph	9448069	9448275	16102	-0.23701203	8.031605499	0.250157	0.342948081	0.05063	0	4618	3549	4291	4359	4127	5002	5374	3658	5630	5185
ENSMUSG00000033644	chr14	Piwil2	7E+07	7E+07	4913	-0.39142284	0.429509824	0.2505207	0.343413158	0.09043	0	24	14	29	17	24	35	22	11	15	31
ENSMUSG00000021905	chr14	Dph3	3.2E+07	3.2E+07	3555	-0.19912202	5.756229026	0.2508832	0.343842818	0.03493	0	823	668	1108	869	884	1210	1170	794	1085	951
ENSMUSG00000079057	chr8	Cyp4v3	4.5E+07	4.5E+07	6246	0.5377848	3.487574026	0.2508692	0.343842818	0.25278	0	110	85	35	39	446	317	291	186	255	320
ENSMUSG00000032380	chr9	Dapk2	6.6E+07	6.6E+07	3512	0.228080221	4.324606161	0.2509663	0.343883004	0.04341	0	321	210	314	304	215	541	416	367	393	503
ENSMUSG00000042451	chr1	Mybph	1.3E+08	1.3E+08	2329	0.689735896	7.991372243	0.2509667	0.343883004	0.42018	0	3691	4484	244	3661	552	6295	3219	5887	11107	5326
ENSMUSG00000059734	chr19	Ndufs8	3908870	3909074	963	-0.25585007	7.321450271	0.250986	0.343883004	0.05897	0	2294	1400	4213	3321	2256	3169	3564	2121	3139	3156
ENSMUSG00000045672	chr4	Col27a1	6.3E+07	6.3E+07	13022	0.535617749	2.597471332	0.2510985	0.344003423	0.24405	0	62	42	24	21	234	200	120	107	141	162
ENSMUSG00000046814	chr2	Gchfr	1.2E+08	1.2E+08	645	0.712247745	0.093719012	0.2511897	0.344094848	0.38873	0	21	3	1	2	28	33	19	19	40	10
ENSMUSG00000047084	chr7	Ngrn	8E+07	8E+07	1714	0.183188679	5.206543548	0.2513729	0.34431211	0.02886	0	487	375	614	516	626	953	757	688	826	807
ENSMUSG00000039740	chr4	Alg2	4.7E+07	4.7E+07	3450	-0.24175636	4.622321474	0.2515423	0.34451055	0.051	0	438	353	279	417	463	552	381	373	554	460
ENSMUSG00000029918	chr6	Mrps33	4E+07	4E+07	1236	-0.219904	4.063342194	0.2518327	0.344874632	0.04004	0	265	196	412	251	236	380	316	280	289	315

ENSMUSG00000031683	chr8	Lsm6	7.9E+07	7.9E+07	4076	-0.25750721	5.484099798	0.2521305	0.345215001	0.0593	0	928	684	625	678	610	938	686	678	902	989
ENSMUSG00000060373	chr14	Hnrnpc	5.2E+07	5.2E+07	2869	0.211018413	6.52394594	0.2521155	0.345215001	0.03996	0	1118	934	1782	1284	1379	2542	1961	1657	1929	2117
ENSMUSG00000025170	chr11	Rab40b	1.2E+08	1.2E+08	2008	-0.2476579	4.559874803	0.2522571	0.345354638	0.05371	0	418	353	342	313	456	451	686	328	427	338
ENSMUSG00000062202	chr17	Btbd9	3E+07	3E+07	6857	-0.20187852	4.339629985	0.2523117	0.345395661	0.03409	0	304	204	474	336	339	467	484	256	406	349
ENSMUSG00000000552	chr15	Zfp385a	1E+08	1E+08	2291	0.280847104	4.07980747	0.2523689	0.345440247	0.06832	0	149	151	197	224	455	431	334	242	508	407
ENSMUSG00000028470	chr4	Hint2	4.4E+07	4.4E+07	1540	0.214615405	4.563471852	0.2524932	0.345576606	0.04023	0	248	165	492	348	462	566	501	376	560	621
ENSMUSG00000004561	chr14	Mettl17	5.2E+07	5.2E+07	3970	0.238379197	3.826675717	0.2525954	0.345682769	0.04698	0	153	138	233	240	217	345	267	186	392	403
ENSMUSG00000097787	chr19	2700046G09Rik	3.2E+07	3.2E+07	1641	-0.34552805	1.013242123	0.2528872	0.346048411	0.07448	0	36	19	38	32	39	55	41	26	23	32
ENSMUSG00000031906	chr8	Smpd3	1.1E+08	1.1E+08	5148	0.483479191	1.423257216	0.2529594	0.346062909	0.18619	0	30	21	24	14	77	84	29	65	41	85
ENSMUSG00000033669	chr15	Zfp7	7.7E+07	7.7E+07	2769	0.476283323	0.055607844	0.2529353	0.346062909	0.12084	0	9	11	9	9	20	25	16	21	13	35
ENSMUSG00000066829	chr9	Zfp810	2.2E+07	2.2E+07	3238	0.401371099	0.764964172	0.2529718	0.346062909	0.09334	0	15	18	16	17	37	52	31	25	33	47
ENSMUSG00000030269	chr6	Mtmr14	1.1E+08	1.1E+08	2874	-0.20028972	4.313731781	0.2530243	0.346100897	0.03393	0	367	238	350	301	330	430	432	278	426	346
ENSMUSG00000074166	chr7	AW146154	4.1E+07	4.1E+07	3405	-0.2878742	2.027801409	0.2532908	0.346401629	0.06101	0	67	51	82	69	60	106	72	49	59	90
ENSMUSG00000074466	chr3	Gm15417	8.9E+07	8.9E+07	1669	0.222111749	4.255574433	0.2532935	0.346401629	0.04125	0	250	221	262	251	328	455	335	298	537	493
ENSMUSG00000034187	chr11	Nsf	1E+08	1E+08	8346	-0.20102785	4.22467987	0.2536172	0.346810423	0.0339	0	241	216	428	290	351	441	458	229	348	340
ENSMUSG00000033542	chr6	Arhgef5	4.3E+07	4.3E+07	9977	0.235340357	3.199122544	0.2537354	0.346938299	0.04272	0	107	109	154	103	156	241	231	129	215	210
ENSMUSG00000020611	chr11	Gna13	1.1E+08	1.1E+08	6421	-0.19054908	5.248327399	0.2538821	0.347091614	0.03162	0	542	402	847	604	711	835	927	566	638	709
ENSMUSG00000022023	chr14	Wbp4	7.9E+07	7.9E+07	3452	-0.17946477	4.993728157	0.253897	0.347091614	0.02777	0	500	379	659	494	520	671	705	461	588	664
ENSMUSG00000035062	chrX	Zc4h2	9.6E+07	9.6E+07	2257	0.387270866	1.155106531	0.2541107	0.34734989	0.09723	0	19	28	29	15	47	65	56	33	38	58
ENSMUSG00000006215	chr4	Zbtb17	1.4E+08	1.4E+08	3877	-0.21408038	5.062639645	0.25417	0.347397057	0.04006	0	417	322	867	631	538	606	709	444	738	702
ENSMUSG00000069911	chr11	Fam196b	3.4E+07	3.4E+07	5371	-0.67663512	-0.01082652	0.2546227	0.347981888	0.35987	0	22	32	7	12	2	26	5	13	16	14
ENSMUSG00000031949	chr8	Adat1	1.1E+08	1.1E+08	4399	-0.32339296	1.548847349	0.254667	0.348008537	0.07471	0	53	48	50	41	39	55	60	43	55	46
ENSMUSG00000051147	chr8	Nat2	6.7E+07	6.7E+07	1509	0.43023839	0.750351343	0.2547531	0.348092188	0.11999	0	25	15	11	14	35	62	32	31	28	34
ENSMUSG00000030541	chr7	Idh2	8E+07	8E+07	2588	-0.46777121	8.135422144	0.2549362	0.348308564	0.1996	0	2844	974	12747	7364	2836	4265	6442	3653	3516	6517
ENSMUSG00000039069	chr2	Mtg2	1.8E+08	1.8E+08	5949	-0.19688657	4.190010638	0.2553212	0.348732586	0.03259	0	302	203	405	271	295	408	396	235	377	350
ENSMUSG00000040818	chr14	Dennd6a	2.7E+07	2.7E+07	5710	-0.22585169	3.377125614	0.2553148	0.348732586	0.04117	0	179	119	198	135	213	244	235	135	168	210
ENSMUSG00000066233	chr9	Tmem42	1.2E+08	1.2E+08	1044	-0.24023808	3.192171571	0.2553012	0.348732586	0.04745	0	162	112	142	170	143	216	176	140	162	164
ENSMUSG00000021178	chr12	Psmc1	1E+08	1E+08	1518	0.211447959	7.198590956	0.255367	0.348761187	0.04095	0	1996	1458	2535	1986	2364	3687	3285	2668	3323	3283
ENSMUSG00000062070	chrX	Pgk1	1.1E+08	1.1E+08	2244	-0.22670275	9.454032199	0.2554629	0.34885821	0.04749	0	10850	8502	13605	11102	13190	13226	16155	9354	15485	12865
ENSMUSG00000006638	chr5	Abhd1	3.1E+07	3.1E+07	1758	0.455776372	0.349437625	0.2555937	0.348968925	0.13309	0	8	10	21	8	29	37	16	23	21	41
ENSMUSG00000032547	chr9	Ryk	1E+08	1E+08	4534	-0.20741686	6.054590581	0.2555909	0.348968925	0.03897	0	1091	811	1118	982	1363	1348	1448	936	1383	1272
ENSMUSG00000022774	chr16	Ncbp2	3.2E+07	3.2E+07	2305	0.205744673	4.481680776	0.2557397	0.349100267	0.03628	0	307	227	323	286	422	696	454	425	453	436
ENSMUSG00000048218	chr15	Amigo2	9.7E+07	9.7E+07	2871	0.309377485	1.351210409	0.2557306	0.349100267	0.05886	0	27	30	41	26	40	69	61	41	52	57
ENSMUSG00000035104	chr6	Eva1a	8.2E+07	8.2E+07	2805	0.422200129	0.532182013	0.2558747	0.349250569	0.12484	0	10	9	24	13	33	53	17	26	26	36
ENSMUSG00000020801	chr11	Med31	7.2E+07	7.2E+07	1730	0.267277581	2.666672842	0.2562161	0.349682471	0.05584	0	101	55	86	81	105	147	136	137	120	154
ENSMUSG00000075229	chr16	Ccdc58	3.6E+07	3.6E+07	1225	0.221885299	3.77604532	0.2564427	0.349957646	0.04152	0	167	122	289	196	190	384	251	259	287	328
ENSMUSG00000020718	chr11	Polg2	1.1E+08	1.1E+08	4356	0.282672181	2.089010498	0.2565806	0.350077713	0.05646	0	43	45	60	63	71	122	78	73	93	105
ENSMUSG00000052632	chr12	Asap2	2.1E+07	2.1E+07	5687	0.251442861	3.531690935	0.2565757	0.350077713	0.05466	0	171	73	209	139	224	317	270	247	197	245
ENSMUSG00000030688	chr7	Stard10	1E+08	1E+08	2383	-0.20177532	5.718463667	0.2567616	0.35029067	0.03675	0	849	562	1062	933	865	1183	1044	702	1194	969
ENSMUSG00000024926	chr19	Kat5	5603017	5603552	2008	0.185978984	4.341364356	0.2568346	0.350320034	0.02935	0	245	182	388	302	333	518	436	325	481	469
ENSMUSG00000041915	chr18	Ammecr1l	3.2E+07	3.2E+07	4769	-0.22020293	3.698798021	0.2568405	0.350320034	0.04008	0	194	132	226	211	301	247	299	164	239	291
ENSMUSG00000043487	chr12	Acot6	8.4E+07	8.4E+07	3388	0.260569836	3.128352144	0.256883	0.350320034	0.05731	0	115	62	185	144	99	204	191	163	207	202
ENSMUSG00000075569	chr5	Rsph10b	1.4E+08	1.4E+08	3101	-0.52381492	-0.0664147	0.2568635	0.350320034	0.18607	0	20	17	6	9	22	9	25	6	13	21
ENSMUSG00000025858	chr5	Get4	1.4E+08	1.4E+08	2431	0.186266586	5.216483405	0.2572094	0.350730936	0.03067	0	483	383	657	478	640	954	696	647	866	914
ENSMUSG00000058665	chr1	En1	1.2E+08	1.2E+08	2624	0.329939485	2.961042535	0.2574994	0.351092312	0.09554	0	58	32	184	126	148	199	173	161	161	181
ENSMUSG00000036955	chr10	2510003E04Rik	6.3E+07	6.3E+07	6547	-0.1858899	5.050303211	0.2575522	0.351130194	0.03047	0	469	360	669	588	596	712	848	427	629	614
ENSMUSG00000026478	chr1	Lamc1	1.5E+08	1.5E+08	8272	0.221079478	7.027952048	0.2578641	0.351521256	0.04525	0	1334	1221	2137	1960	2625	3489	3266	2194	2849	2788
ENSMUSG00000000579	chr17	Dynlt1c	6601671	6601836	3777	0.373277176	1.25352952	0.2580225	0.351687232	0.08821	0	28	31	21	30	35	77	43	44	58	43
ENSMUSG00000019773	chr10	Fbxo5	5799160	5799822	2003	0.545873102	-0.35971415	0.2580386	0.351687232	0.17065	0	5	7	4	3	22	24	14	10	20	14
ENSMUSG00000028636	chr4	Ppcs	1.2E+08	1.2E+08	1605	0.262430164	3.265917592	0.258083	0.351687232	0.05936	0	109	55	226	117	180	280	218	145	223	219
ENSMUSG00000045822	chr2	Zswim3	1.6E+08	1.6E+08	2708	-0.32298753	1.247208722	0.2580862	0.351687232	0.07494	0	44	31	38	29	48	61	54	25	34	39
ENSMUSG00000027015	chr2	Cybrd1	7.1E+07	7.1E+07	5339	0.589905419	0.248708836	0.2581899	0.351794414	0.21879	0	21	17	7	6	9	61	19	18	14	25
ENSMUSG00000027823	chr3	Gmps	6.4E+07	6.4E+07	8105	-0.18964034	5.328012586	0.2585211	0.352144058	0.032	0	572	431	875	688	701	905	829	663	682	780
ENSMUSG00000035851	chr5	Ythdc1	8.7E+07	8.7E+07	10352	-0.17610035	5.039859645	0.2585218	0.352144058	0.02722	0	522	383	622	517	588	761	660	518	575	671
ENSMUSG00000074826	chr13	Gm10767	6.7E+07	6.7E+07	2274	-0.5709474	-0.18721397	0.2584723	0.352144058	0.19877	0	7	7	26	15	18	4	16	3	21	21
ENSMUSG00000003062	chr13	Stard3nl	1.9E+07	1.9E+07	1283	0.256324311	2.626763703	0.2589803	0.352714215	0.04942	0	82	71	99	68	95	173	118	114	139	137
ENSMUSG00000020232	chr10	Hmg20b	8.1E+07	8.1E+07	3149	0.23644777	3.947879739	0.2589907	0.352714215	0.04939	0	136	111	346	214	306	444	353	225	366	349
ENSMUSG00000044876	chr7	Zfp444	6172226	6172399	3421	0.257122534	2.686687703	0.2590181	0.352717273	0.05118	0	85	63	100	76	114	157	144	89	193	135
ENSMUSG00000018387	chr11	Shroom1	5.3E+07	5.3E+07	4600	0.438478539	-0.02329511	0.2593726	0.35313616	0.10089	0	10	4	11	10	22	32	19	15	22	16
ENSMUSG00000024446	chr17	Rpp21	3.6E+07	3.6E+07	1218	-0.20840823	3.703329485	0.2593761	0.35313616	0.03609	0	182	147	259	223	245	268	247	166	306	261
ENSMUSG00000071657	chr19	Bscl2	8837467	8837864	5897	0.365514858	4.919305287	0.259462	0.353218891	0.12318	0	359	233	268	191	1023	767	502	517	977	743
ENSMUSG00000025176	chr19	Hoga1	4.2E+07	4.2E+07	2259	0.44900022	0.824188864	0.2596937	0.353499941	0.13892	0	21	20	11	15	37	63	22	37	31	44
ENSMUSG00000038611	chr7	Phrf1	1.4E+08	1.4E+08	6765	-0.19273612	4.297019153	0.2601811	0.354129138	0.03135	0	275	200	401	353	370	383	413	325	378	375
ENSMUSG00000035877	chr2	Zhx3	1.6E+08	1.6E+08	13259	0.180201816	4.688435751	0.260329	0.354261598	0.02862	0	336	229	454	360	471	593	542	465	618	588
ENSMUSG00000038429	chr6	Usp5	1.2E+08	1.2E+08	4621	0.208772356	6.417483799	0.260304	0.354261598	0.04052	0	995	747	1588	1347	1422	2073	1902	1446	2133	1914
ENSMUSG00000002550	chr2	Uck1	3.2E+07	3.2E+07	2751	-0.37941733	4.583492488	0.2604419	0.354380816	0.13202	0	361	211	268	183	1126	557	349	335	461	450
ENSMUSG00000030823	chr7	9130019O22Rik	1.3E+08	1.3E+08	3878	-0.29810481	1.535167857	0.260802	0.354770922	0.0623	0	47	35	45	58	46	56	50	38	58	58

ENSMUSG00000098132	chr7	Rassf10	1.1E+08	1.1E+08	3496	0.39916884	0.154506556	0.2608044	0.354770922	0.08087	0	11	9	22	8	16	25	21	18	29	24
ENSMUSG00000104204	chr6	RP23-291E6.6	5.8E+07	5.8E+07	2842	-0.38845293	0.786230469	0.2607718	0.354770922	0.09279	0	27	10	43	23	42	26	36	26	32	24
ENSMUSG00000026843	chr2	Fubp3	3.2E+07	3.2E+07	5914	-0.21695831	3.350537588	0.2608635	0.354782756	0.03779	0	149	113	222	145	204	203	207	144	188	226
ENSMUSG00000034300	chr18	Fam53c	3.5E+07	3.5E+07	4517	-0.17846914	5.124698973	0.2608775	0.354782756	0.0283	0	537	366	699	566	655	690	809	497	704	683
ENSMUSG00000070733	chr5	Fryl	7.3E+07	7.3E+07	14668	-0.20622704	4.262279499	0.260889	0.354782756	0.0373	0	348	240	281	299	357	447	364	300	326	396
ENSMUSG00000060708	chr5	Bloc1s4	3.7E+07	3.7E+07	1306	0.245638829	3.107359459	0.261077	0.355003963	0.05085	0	86	78	151	121	164	243	143	145	217	209
ENSMUSG00000099597	chr12	Gm28933	9.9E+07	9.9E+07	1407	0.995413923	-0.2573096	0.2611431	0.355059482	0.79361	0	0	0	21	10	8	1	25	1	27	44
ENSMUSG00000020863	chr11	Luc7l3	9.4E+07	9.4E+07	7278	-0.21538612	5.618125545	0.2614318	0.355389784	0.04294	0	706	660	819	975	751	1124	1018	715	770	1086
ENSMUSG00000035674	chr7	Ndufa3	3617373	3617407	858	0.238578522	7.49708791	0.2614367	0.355389784	0.05372	0	2180	1334	3890	2879	2609	4258	3676	3119	4722	4392
ENSMUSG00000024947	chr19	Men1	6334979	6335070	3458	0.235466952	3.346198988	0.2617028	0.355717022	0.04743	0	121	84	167	118	227	247	201	177	238	260
ENSMUSG00000002608	chr7	Ccdc97	2.6E+07	2.6E+07	3939	0.206174348	5.839400648	0.2617531	0.355750821	0.03945	0	694	469	1086	917	931	1248	1327	909	1481	1374
ENSMUSG00000070780	chr5	Rbm47	6.6E+07	6.6E+07	6859	0.694872185	1.501237937	0.2618907	0.355903331	0.42082	0	35	13	6	2	109	87	48	71	64	69
ENSMUSG00000051390	chr17	Zbtb22	3.4E+07	3.4E+07	2672	-0.18282951	4.589230493	0.2624371	0.356611382	0.02918	0	295	273	546	393	450	517	509	327	504	479
ENSMUSG00000035407	chr4	Kank4	9.9E+07	9.9E+07	4795	-0.34473445	0.798458901	0.2625495	0.356729599	0.0712	0	27	17	35	31	30	45	38	18	25	26
ENSMUSG00000003228	chr19	Grk5	6.1E+07	6.1E+07	3165	0.343104014	3.081306761	0.2625829	0.356740417	0.10517	0	81	55	103	77	269	286	163	166	159	193
ENSMUSG00000030733	chr7	Sh2b1	1.3E+08	1.3E+08	3422	-0.20871139	6.419932198	0.2626139	0.356747934	0.0409	0	1322	1073	1675	1342	1502	1841	1994	1129	1847	1460
ENSMUSG00000026211	chr1	Obsl1	7.5E+07	7.5E+07	8467	0.294815276	6.654647454	0.2626683	0.356787285	0.08185	0	1369	1255	1210	1857	845	2196	2286	1807	3073	2035
ENSMUSG00000024350	chr18	Dnajc18	3.6E+07	3.6E+07	5169	-0.18816239	5.075771964	0.2627134	0.356813961	0.03216	0	539	427	636	589	485	692	756	498	644	663
ENSMUSG00000049422	chr10	Chchd10	7.6E+07	7.6E+07	939	0.285521303	9.212410507	0.2627788	0.356868199	0.07758	0	5500	3495	14226	9028	10474	11368	15179	9321	16978	14527
ENSMUSG00000042625	chr17	Safb2	5.7E+07	5.7E+07	8165	0.188434578	4.681223538	0.2628084	0.356873972	0.03152	0	328	248	417	331	504	643	481	411	602	686
ENSMUSG00000041346	chr11	Wrap53	7E+07	7E+07	2062	0.259529814	2.280720908	0.2629241	0.356994249	0.05128	0	54	39	90	69	81	138	93	82	101	123
ENSMUSG00000078502	chr4	Gm13212	1.5E+08	1.5E+08	3595	0.294866836	1.356447569	0.2629479	0.356994249	0.05724	0	37	21	41	30	38	62	61	46	48	61
ENSMUSG00000050244	chr13	Heatr1	1.2E+07	1.2E+07	6537	-0.2333205	3.751820038	0.2631461	0.357228781	0.04709	0	153	171	279	269	221	340	225	230	239	232
ENSMUSG00000024136	chr17	Dnase1l2	2.4E+07	2.4E+07	2328	0.527097444	-0.01545986	0.2633377	0.357454191	0.16597	0	9	12	12	7	13	21	14	13	11	48
ENSMUSG00000039244	chr5	E130309D02Rik	1.4E+08	1.4E+08	4639	0.213969702	3.656189333	0.2634889	0.357624897	0.03931	0	140	104	224	189	238	301	293	187	336	280
ENSMUSG00000055762	chr15	Eef1d	7.6E+07	7.6E+07	5897	0.220913963	7.230732241	0.2635288	0.357644458	0.04633	0	1805	1379	2918	2269	2262	3614	2921	2603	3775	3759
ENSMUSG00000024583	chr18	Txnl1	6.4E+07	6.4E+07	2558	-0.2052673	6.11093869	0.2637153	0.357828299	0.03948	0	1113	795	1533	1042	1138	1644	1488	1049	1150	1323
ENSMUSG00000082935	chr1	Gm7658	2.2E+07	2.2E+07	1124	0.233550459	2.817346773	0.2637128	0.357828299	0.04177	0	95	69	107	99	112	183	172	119	150	153
ENSMUSG00000059939	chr4	9430015G10Rik	1.6E+08	1.6E+08	3695	0.316353478	2.02740719	0.2638222	0.35793873	0.07429	0	60	46	40	39	78	122	87	61	100	89
ENSMUSG00000088609	chr13	Gm24187	9834469	9834525	57	-0.33264997	2.58309573	0.2640267	0.358181482	0.09189	0	123	37	156	108	87	142	109	101	115	69
ENSMUSG00000042099	chr17	Kank3	3.4E+07	3.4E+07	3118	0.243880356	4.342049084	0.2640662	0.35820041	0.05453	0	190	166	369	230	499	548	393	319	400	619
ENSMUSG00000097658	chr11	Gm16755	1.2E+08	1.2E+08	933	0.887515537	-0.17274179	0.2640929	0.358201982	0.65149	0	2	0	29	10	3	3	16	2	45	36
ENSMUSG00000006932	chr9	Ctnnb1	1.2E+08	1.2E+08	5099	-0.2129073	8.078246526	0.2641593	0.358257375	0.04332	0	4248	3385	4954	4313	4929	6000	6120	3890	4955	5036
ENSMUSG00000029650	chr5	Slc46a3	1.5E+08	1.5E+08	2458	0.261014919	2.715585249	0.2641854	0.358258119	0.05666	0	84	44	123	82	125	181	179	80	158	144
ENSMUSG00000056014	chr5	A430033K04Rik	1.4E+08	1.4E+08	3900	-0.34842711	1.368168719	0.2643247	0.358412428	0.08791	0	35	20	59	63	37	46	59	35	35	51
ENSMUSG00000004661	chr9	Arid3b	5.8E+07	5.8E+07	7976	-0.28790325	2.000081218	0.2643571	0.35842166	0.06499	0	73	57	57	65	65	86	86	47	83	65
ENSMUSG00000039481	chr17	Nrtn	5.7E+07	5.7E+07	1023	0.401571219	1.488404253	0.2644146	0.358464977	0.13255	0	24	19	73	45	19	59	61	59	87	45
ENSMUSG00000022553	chr15	Maf1	7.6E+07	7.6E+07	2412	-0.20646779	6.564705769	0.2644403	0.358465164	0.04036	0	1478	1109	1823	1500	1771	1873	2108	1233	2107	1814
ENSMUSG00000025026	chr19	Add3	5.3E+07	5.3E+07	4938	-0.18378247	5.32191288	0.2645883	0.358631214	0.03103	0	522	499	738	644	815	975	860	580	700	775
ENSMUSG00000016528	chr1	Mapkapk2	1.3E+08	1.3E+08	3041	-0.25815905	8.252130557	0.2649501	0.359086864	0.06388	0	3737	2570	8978	5904	4918	5907	6826	3867	6057	6254
ENSMUSG00000033577	chr9	Myo6	8E+07	8E+07	12078	-0.21321707	3.825276281	0.2650568	0.359196782	0.03886	0	238	137	257	199	332	318	276	207	235	317
ENSMUSG00000022035	chr14	Ccdc25	6.6E+07	6.6E+07	2227	-0.18539664	4.974566437	0.2650839	0.359198867	0.03129	0	564	377	560	494	503	704	677	495	597	557
ENSMUSG00000033082	chr6	Clec1a	1.3E+08	1.3E+08	3268	-0.29731191	1.602381694	0.2657179	0.360023052	0.06645	0	55	36	55	46	52	67	65	42	35	65
ENSMUSG00000025374	chr10	Nabp2	1.3E+08	1.3E+08	2507	0.188972962	5.392277709	0.2658559	0.360175353	0.03303	0	525	431	703	548	778	1005	852	686	1083	993
ENSMUSG00000031591	chr8	Asah1	4.1E+07	4.1E+07	3390	0.198095781	4.70268275	0.265884	0.360178616	0.03512	0	365	265	383	375	434	844	687	411	462	504
ENSMUSG00000049940	chr3	Pgrmc2	4.1E+07	4.1E+07	3242	0.220085861	5.486292784	0.2661604	0.360518142	0.04534	0	611	482	523	547	952	1231	897	853	989	988
ENSMUSG00000028405	chr4	Aco1	4E+07	4E+07	4496	-0.27151209	5.159914499	0.2665506	0.361011838	0.06913	0	512	308	589	403	1271	864	559	561	718	634
ENSMUSG00000031295	chrX	Phka2	1.6E+08	1.6E+08	6068	-0.3649577	3.348037146	0.2666823	0.361155394	0.12045	0	158	108	112	83	426	234	169	128	177	212
ENSMUSG00000003847	chr8	Nfat5	1.1E+08	1.1E+08	18378	-0.19344724	4.805365413	0.2669037	0.361350445	0.03436	0	436	386	535	386	482	649	508	424	449	663
ENSMUSG00000039108	chr2	Lsm14b	1.8E+08	1.8E+08	2892	-0.18782284	5.548489568	0.2668918	0.361350445	0.03295	0	714	557	889	782	814	965	939	721	1007	871
ENSMUSG00000053483	chr1	Usp21	1.7E+08	1.7E+08	4756	0.19066328	4.519180718	0.2668816	0.361350445	0.03262	0	246	231	390	339	424	539	490	370	627	492
ENSMUSG00000024871	chr19	Doc2g	4003321	4003401	3027	0.439029239	0.900340624	0.2669517	0.361380637	0.15437	0	18	4	51	23	23	42	55	30	25	56
ENSMUSG00000027544	chr2	Nfatc2	1.7E+08	1.7E+08	10578	0.194606841	4.383507161	0.2670305	0.361452436	0.03316	0	316	229	317	297	286	471	487	352	468	510
ENSMUSG00000071113	chr8	Mboat4	3.4E+07	3.4E+07	1839	0.425234583	0.074378872	0.2672316	0.361689717	0.09901	0	17	6	13	16	8	23	20	20	27	20
ENSMUSG00000032437	chr9	Stt3b	1.2E+08	1.2E+08	4195	-0.20785987	6.595804212	0.2674058	0.361890542	0.04139	0	1397	1067	1952	1424	2115	2189	2342	1336	1790	1691
ENSMUSG00000037134	chr8	Prmt10	7.8E+07	7.8E+07	5679	-0.21374007	3.350075994	0.2674959	0.361977531	0.03766	0	152	99	230	169	185	227	204	140	190	212
ENSMUSG00000044139	chr7	Prss53	1.3E+08	1.3E+08	2134	-0.33509176	1.355974673	0.2675668	0.362038565	0.08249	0	43	28	31	48	57	67	35	33	54	38
ENSMUSG00000037904	chr12	Ankrd9	1.1E+08	1.1E+08	3160	-0.24215452	6.178231133	0.268044	0.362649232	0.05634	0	925	931	1400	1374	1280	1009	1735	895	1750	1470
ENSMUSG00000021782	chr14	Dlg5	2.4E+07	2.4E+07	8491	-0.232868	2.924911016	0.2683172	0.362983856	0.04468	0	128	91	133	113	146	151	152	124	128	153
ENSMUSG00000041633	chrX	Kctd12b	1.5E+08	1.5E+08	4906	-0.2544949	2.802139002	0.2684319	0.363104047	0.05275	0	106	77	143	84	166	162	142	103	101	143
ENSMUSG00000039115	chr9	Itga9	1.2E+08	1.2E+08	7691	0.299148548	4.044790793	0.2684891	0.363116795	0.08133	0	178	257	154	288	168	368	360	304	359	468
ENSMUSG00000041444	chr9	Arhgap32	3.2E+07	3.2E+07	17179	-0.26947018	2.389038147	0.2684931	0.363116795	0.06023	0	81	65	88	61	133	125	110	68	79	105
ENSMUSG00000028331	chr4	5830415F09Rik	4.6E+07	4.6E+07	2271	0.309009359	1.199314677	0.2685606	0.363173027	0.06306	0	29	20	28	34	36	58	47	44	54	45
ENSMUSG00000025409	chr10	Mbd6	1.3E+08	1.3E+08	4455	0.224330874	4.355860268	0.2686106	0.363205629	0.04612	0	211	209	327	229	472	455	463	286	484	600
ENSMUSG00000049728	chr7	Zfp668	1.3E+08	1.3E+08	4655	0.287582175	2.267386169	0.2686571	0.36323345	0.07123	0	43	29	98	85	76	118	100	91	121	101
ENSMUSG00000000538	chr11	Tom1l2	6E+07	6E+07	8764	-0.24837341	7.18623915	0.2686942	0.363248073	0.05983	0	1849	1356	3871	3023	2159	2832	3520	1836	2922	2760
ENSMUSG00000041079	chr16	Rwdd2b	8.7E+07	8.7E+07	2009	0.27867719	1.899021464	0.2687197	0.363248073	0.0577	0	34	35	71	55	55	98	86	72	79	73

ENSMUSG00000020102	chr10	Slc16a7	1.3E+08	1.3E+08	3890	-0.62035768	1.23171134	0.2687504	0.363254585	0.34256	0	40	22	10	7	137	53	48	24	33	28
ENSMUSG00000080727	chr3	C920021L13Rik	9.6E+07	9.6E+07	2553	0.42758198	-0.10099753	0.2688941	0.363413761	0.10873	0	6	6	12	7	23	17	24	12	22	22
ENSMUSG00000093672	chr10	Gm20655	1.8E+07	1.8E+07	3118	-0.51795215	0.184774011	0.26906	0.363603021	0.20963	0	42	15	6	13	12	26	17	13	15	19
ENSMUSG00000054079	chr11	Utp18	9.4E+07	9.4E+07	3597	0.238088248	3.103127251	0.2691531	0.363670569	0.0476	0	96	105	145	98	142	237	193	157	153	209
ENSMUSG00000062075	chr10	Lmnb2	8.1E+07	8.1E+07	4286	0.253379158	2.729476113	0.2691619	0.363670569	0.05283	0	66	67	135	90	97	178	144	133	152	121
ENSMUSG00000085653	chr1	Gm15179	7.5E+07	7.5E+07	867	-0.26769229	3.975835023	0.2692951	0.363815508	0.06713	0	312	211	183	223	336	483	245	163	274	344
ENSMUSG00000048368	chr13	Omd	5E+07	5E+07	1556	-0.35776305	0.671982832	0.2694327	0.363966457	0.08506	0	18	25	31	17	36	28	36	23	24	24
ENSMUSG00000034656	chr8	Cacna1a	8.4E+07	8.4E+07	11418	0.302774034	2.855662963	0.2695347	0.364064294	0.07998	0	79	60	159	109	84	219	169	80	121	246
ENSMUSG00000039910	chr10	Cited2	1.8E+07	1.8E+07	1968	-0.23008037	5.121691755	0.269583	0.364064294	0.04994	0	482	359	928	603	520	617	1015	494	640	544
ENSMUSG00000071567	chr14	A830039N20Rik	2.3E+07	2.3E+07	1353	-0.29302922	2.823644494	0.269563	0.364064294	0.075	0	109	79	188	111	102	151	172	87	74	173
ENSMUSG00000029381	chr5	Shroom3	9.3E+07	9.3E+07	7755	0.42242243	0.539275246	0.2696132	0.364069914	0.13475	0	10	4	36	12	30	33	31	22	31	41
ENSMUSG00000027803	chr3	Wwtr1	5.7E+07	5.7E+07	4779	0.189340315	5.077275522	0.2698286	0.364318692	0.03379	0	390	305	668	385	699	912	771	617	677	730
ENSMUSG00000058135	chr3	Gstm1	1.1E+08	1.1E+08	1394	0.28688401	7.232010689	0.2698493	0.364318692	0.08019	0	2213	1736	1236	1880	2937	3390	2687	2417	4070	4517
ENSMUSG00000033430	chr8	Terf2ip	1.1E+08	1.1E+08	3599	-0.18035303	4.522354166	0.270032	0.364530204	0.02953	0	343	275	447	391	379	581	504	335	402	413
ENSMUSG00000040990	chrX	Sh3kbp1	1.6E+08	1.6E+08	10100	0.168985044	5.076331579	0.2701308	0.364628425	0.02626	0	491	321	565	445	591	874	767	547	758	752
ENSMUSG00000044387	chr19	2410080I02Rik	2.3E+07	2.3E+07	414	-0.46206685	-0.23296485	0.2701686	0.364644408	0.11563	0	15	13	10	8	19	14	10	6	17	19
ENSMUSG00000104300	chr9	DHX30	1.1E+08	1.1E+08	3672	-0.17335301	5.00419546	0.2702961	0.364781456	0.02762	0	423	360	652	574	576	692	659	467	668	631
ENSMUSG00000082431	chr1	Tdpx-ps1	1E+08	1E+08	597	0.41976507	0.122931505	0.2709385	0.365613185	0.11986	0	8	5	15	21	15	14	21	21	30	27
ENSMUSG00000059005	chr2	Hnrnpa3	7.6E+07	7.6E+07	5396	0.202787328	6.598384278	0.2711585	0.365858056	0.03995	0	1267	1056	1686	1287	1503	2741	2229	1758	1906	2094
ENSMUSG00000070643	chr1	Sox13	1.3E+08	1.3E+08	4312	0.291616082	3.365665542	0.2711721	0.365858056	0.07948	0	77	72	270	94	225	279	262	168	223	236
ENSMUSG00000057766	chr18	Ankrd29	1.2E+07	1.2E+07	3295	-0.41895842	0.538194069	0.2713707	0.366090765	0.12816	0	18	23	25	14	37	45	25	14	11	28
ENSMUSG00000021235	chr12	Coq6	8.4E+07	8.4E+07	3142	-0.20502983	4.706019552	0.2713986	0.36609316	0.03853	0	360	198	661	456	514	537	575	366	516	514
ENSMUSG00000033356	chr15	Pus7l	9.5E+07	9.5E+07	3291	0.324152346	1.34771267	0.2714642	0.366124612	0.07726	0	25	26	42	30	41	72	60	59	36	49
ENSMUSG00000048007	chrX	Timm8a1	1.3E+08	1.3E+08	1421	-0.30093931	2.166946591	0.2714741	0.366124612	0.07255	0	61	39	134	78	66	101	105	60	76	68
ENSMUSG00000040370	chr6	Lyrm5	1.5E+08	1.5E+08	2682	-0.19887749	5.487677351	0.2718651	0.366616666	0.03756	0	638	388	1052	794	851	924	951	637	829	984
ENSMUSG00000016921	chr2	Srsf6	1.6E+08	1.6E+08	4810	0.213070867	6.134471741	0.2721255	0.366932592	0.04408	0	829	801	1070	909	1297	1897	1285	1303	1462	1820
ENSMUSG00000018932	chr11	Map2k3	6.1E+07	6.1E+07	3314	0.206957077	7.425256268	0.2723446	0.367192693	0.0422	0	2160	1625	3128	2398	2908	4219	4656	2756	3848	3661
ENSMUSG00000041012	chr9	Cmtm8	1.1E+08	1.1E+08	1064	0.344342023	1.29635796	0.2725322	0.367410232	0.09981	0	24	10	41	33	55	52	45	53	52	64
ENSMUSG00000049670	chr19	Morn4	4.2E+07	4.2E+07	1816	0.314608544	2.647643876	0.2727749	0.367702169	0.08691	0	81	72	90	43	129	117	206	125	133	116
ENSMUSG00000022332	chr15	Khdrbs3	6.9E+07	6.9E+07	1887	-0.44397838	3.86194554	0.2729231	0.367866614	0.18818	0	138	34	651	336	222	255	347	187	195	284
ENSMUSG00000027361	chr2	Gabpb1	1.3E+08	1.3E+08	7752	0.227509277	3.058350786	0.2729757	0.367866759	0.04252	0	119	83	116	111	142	207	195	152	164	196
ENSMUSG00000099210	chr7	Mir7051	4.3E+07	4.3E+07	73	0.27523854	2.349200828	0.2729617	0.367866759	0.06596	0	53	32	102	74	92	111	109	99	98	142
ENSMUSG00000019794	chr10	Katna1	7726000	7726123	2195	0.18127803	4.264183877	0.2730029	0.367868016	0.02926	0	244	199	310	263	344	539	427	326	385	432
ENSMUSG00000040034	chr10	Nup43	7667503	7667681	2560	-0.2588965	2.460621589	0.2730488	0.367894615	0.05667	0	80	72	129	91	72	119	119	76	108	89
ENSMUSG00000079037	chr2	Prnp	1.3E+08	1.3E+08	2343	0.214981013	7.397056912	0.273468	0.36842394	0.04568	0	2401	1911	2276	2233	2821	4459	3679	2868	3933	3823
ENSMUSG00000038332	chr10	Sesn1	4.2E+07	4.2E+07	3327	-0.31087404	5.040899422	0.2735478	0.368496084	0.09461	0	829	482	398	593	294	898	462	482	603	605
ENSMUSG00000024422	chr17	Dhx16	3.6E+07	3.6E+07	4094	0.1755913	4.419919168	0.2736414	0.368551344	0.02772	0	267	209	365	323	360	554	496	320	506	480
ENSMUSG00000047635	chr5	2810006K23Rik	1.2E+08	1.2E+08	2873	-0.22006264	3.135519966	0.2736385	0.368551344	0.0412	0	116	95	195	157	153	204	175	111	168	181
ENSMUSG00000051256	chr6	Jagn1	1.1E+08	1.1E+08	1201	0.187470769	4.729983082	0.273696	0.368589568	0.03251	0	346	288	357	361	512	641	541	457	672	593
ENSMUSG00000009733	chr15	Tfcp2	1E+08	1E+08	3250	-0.20455675	3.391129423	0.2738282	0.368679858	0.03587	0	160	108	219	175	189	225	221	156	189	209
ENSMUSG00000038827	chr4	Fam206a	5.7E+07	5.7E+07	5574	0.328313086	1.881790116	0.273837	0.368679858	0.08885	0	41	35	41	36	89	119	55	66	90	82
ENSMUSG00000039703	chr11	Nploc4	1.2E+08	1.2E+08	4776	-0.21510403	6.770060103	0.2738419	0.368679858	0.04563	0	1466	1098	2602	1958	1922	2132	2650	1462	2165	2085
ENSMUSG00000037224	chr5	Zfyve28	3.4E+07	3.4E+07	5775	0.362030228	0.993337728	0.2739967	0.368852778	0.10022	0	23	17	21	14	51	52	46	35	35	50
ENSMUSG00000034247	chr11	Plekhm1	1E+08	1E+08	5968	0.175171352	4.977432609	0.2742871	0.369208297	0.02863	0	388	322	497	449	588	724	737	468	779	755
ENSMUSG00000029722	chr5	Agfg2	1.4E+08	1.4E+08	3802	0.303361496	3.106063403	0.2744691	0.369417801	0.08445	0	63	82	119	95	233	267	166	110	230	216
ENSMUSG00000071646	chr19	Mta2	8941875	8942382	4093	0.190306399	5.575916979	0.2745892	0.369544098	0.03493	0	558	537	796	593	891	1211	986	828	1061	1158
ENSMUSG00000078570	chr4	1110065P20Rik	1.2E+08	1.2E+08	2069	0.203955876	3.881869581	0.2747147	0.369677504	0.03822	0	158	122	330	207	242	400	322	246	343	316
ENSMUSG00000032860	chr7	P2ry2	1E+08	1E+08	3000	-0.26867076	5.459807084	0.2750094	0.370038514	0.07056	0	503	323	1448	893	644	803	1051	600	826	849
ENSMUSG00000030322	chr6	Mbd4	1.2E+08	1.2E+08	5059	0.335763602	1.258345294	0.2751747	0.37022541	0.08137	0	33	30	32	23	31	71	40	46	42	63
ENSMUSG00000074024	chr7	4632427E13Rik	9.3E+07	9.3E+07	7303	-0.37516968	0.650628174	0.2753797	0.370465666	0.09152	0	25	21	26	15	39	31	23	23	19	36
ENSMUSG00000062169	chr1	Cnih4	1.8E+08	1.8E+08	3783	-0.19098109	5.200813258	0.275421	0.370485716	0.03533	0	639	501	560	555	643	779	775	530	779	686
ENSMUSG00000035919	chr9	Bbs9	2.2E+07	2.2E+07	6243	-0.22757144	2.979761081	0.2756735	0.370789837	0.04358	0	123	95	161	117	141	179	179	116	119	152
ENSMUSG00000019889	chr10	Ptprk	2.8E+07	2.8E+07	6177	-0.27218378	3.401232748	0.2757365	0.370803414	0.06715	0	94	94	272	200	243	230	239	171	146	192
ENSMUSG00000033557	chr1	Fam20b	1.6E+08	1.6E+08	8770	-0.20047676	6.107300753	0.2757324	0.370803414	0.03952	0	994	719	1690	1061	1216	1562	1515	996	1219	1367
ENSMUSG00000022111	chr14	Uchl3	1E+08	1E+08	929	-0.18220535	4.272727243	0.276081	0.37123108	0.0306	0	315	225	382	295	330	453	457	255	359	359
ENSMUSG00000024082	chr17	Ndufaf7	7.9E+07	7.9E+07	2303	-0.19154918	4.326109704	0.2761074	0.37123108	0.03339	0	297	195	464	292	400	418	494	297	358	365
ENSMUSG00000047417	chr10	Rexo1	8.1E+07	8.1E+07	7155	-0.19899577	4.075448736	0.2761621	0.371269016	0.03653	0	233	192	350	279	313	351	369	184	401	332
ENSMUSG00000020946	chr11	Gosr2	1E+08	1E+08	3266	-0.19645587	6.04570768	0.2764232	0.371561616	0.03816	0	946	830	1238	1089	1211	1470	1601	912	1194	1229
ENSMUSG00000022160	chr14	Mettl3	5.2E+07	5.2E+07	3987	0.201848536	3.569332441	0.2764327	0.371561616	0.03568	0	154	109	217	185	168	309	263	194	269	271
ENSMUSG00000078786	chr7	BC024978	2.7E+07	2.7E+07	2756	-0.22613455	2.947336307	0.2765048	0.371622827	0.04392	0	118	96	152	103	154	151	143	105	159	169
ENSMUSG00000000317	chr11	Bcl6b	7E+07	7E+07	3719	0.292026683	3.786056278	0.276542	0.371637197	0.0825	0	97	79	200	276	318	302	337	228	304	387
ENSMUSG00000022404	chr15	Slc25a17	8.1E+07	8.1E+07	1667	-0.25919859	3.414666462	0.27664	0.371733403	0.0611	0	189	110	199	102	290	267	198	162	184	187
ENSMUSG00000061898	chr5	Rbak	1.4E+08	1.4E+08	3623	-0.31499755	2.039610274	0.2768805	0.372020861	0.0847	0	66	69	88	41	67	81	90	70	49	77
ENSMUSG00000029446	chr5	Psph	1.3E+08	1.3E+08	4010	-0.23001107	3.489011628	0.2769645	0.372097476	0.04772	0	217	119	174	148	254	238	229	152	248	197
ENSMUSG00000037933	chr13	Bicd2	4.9E+07	4.9E+07	6351	-0.18681792	5.526726414	0.2769906	0.372097476	0.03393	0	610	543	1011	695	889	921	1074	692	843	919
ENSMUSG00000022773	chr16	Ypel1	1.7E+07	1.7E+07	4635	0.489828097	0.691582364	0.2770535	0.372110758	0.17523	0	23	25	11	12	18	40	14	37	50	37
ENSMUSG00000034321	chr19	Exosc1	4.2E+07	4.2E+07	1622	-0.21352354	3.458409643	0.277037	0.372110758	0.0417	0	179	149	167	168	209	244	210	152	201	241

ENSMUSG00000020705	chr11	Ddx42	1.1E+08	1.1E+08	4228	-0.17778914	5.46431359	0.2771006	0.37213833	0.03064	0	664	495	859	696	847	1008	832	632	867	955
ENSMUSG00000020956	chr12	Dtd2	5.2E+07	5.2E+07	3108	0.260190819	2.483551827	0.2771961	0.372230907	0.05601	0	72	54	91	58	106	152	104	92	111	161
ENSMUSG00000032902	chr3	Slc16a1	1E+08	1E+08	4426	-0.33737162	6.159973885	0.2772817	0.372300589	0.11364	0	751	292	2521	1485	1478	1424	1573	1060	1052	1409
ENSMUSG00000040612	chr1	Ildr2	1.7E+08	1.7E+08	8251	-0.36348131	2.001179217	0.277301	0.372300589	0.11365	0	40	43	59	79	118	135	61	60	43	59
ENSMUSG00000026851	chr2	BC005624	3.1E+07	3.1E+07	3280	0.183605844	5.258683111	0.2773932	0.372388671	0.03236	0	574	394	538	534	649	976	781	642	859	947
ENSMUSG00000010064	chr9	Slc38a3	1.1E+08	1.1E+08	5277	-0.49387651	4.989086172	0.2778505	0.372966842	0.24189	0	291	50	1272	1019	407	453	633	325	506	823
ENSMUSG00000036461	chr14	Elf1	7.9E+07	7.9E+07	4314	0.239884337	3.1816478	0.2779017	0.372999864	0.051	0	124	97	144	86	173	261	237	160	158	192
ENSMUSG00000094518	chr13	Gm6421	1.2E+08	1.2E+08	411	-0.4485204	0.296267235	0.2782167	0.37338695	0.1433	0	20	20	11	21	24	12	33	13	28	13
ENSMUSG00000038085	chr2	Cnbd2	1.6E+08	1.6E+08	3879	0.298358104	1.356702163	0.2783722	0.373524175	0.06627	0	25	27	45	28	42	47	61	44	68	57
ENSMUSG00000073530	chr1	Pappa2	1.6E+08	1.6E+08	10294	-0.48754561	0.713617491	0.2783712	0.373524175	0.18784	0	7	27	55	29	20	22	39	30	15	24
ENSMUSG00000008136	chr1	Fhl2	4.3E+07	4.3E+07	1897	0.72803545	1.967255529	0.2786043	0.373775473	0.50854	0	5	2	175	53	9	101	107	71	71	135
ENSMUSG00000041115	chrX	Iqsec2	1.5E+08	1.5E+08	6980	0.267923389	4.563020135	0.2786128	0.373775473	0.07095	0	236	135	628	428	261	637	596	315	593	560
ENSMUSG00000068457	chrY	Uty	1096861	1098573	9791	-1.65338267	1.686657064	0.2786618	0.37380551	2.35289	0	1	0	292	0	133	0	159	1	0	1
ENSMUSG00000027656	chr2	Wisp2	1.6E+08	1.6E+08	1924	0.451045307	2.836557339	0.2788176	0.373978689	0.19354	0	39	90	46	39	240	262	167	134	161	122
ENSMUSG00000034471	chr11	Caskin2	1.2E+08	1.2E+08	5177	-0.21492235	4.569306929	0.2790904	0.374308835	0.04387	0	265	202	676	395	469	513	507	315	497	448
ENSMUSG00000023277	chr9	Twf2	1.1E+08	1.1E+08	2129	0.280355385	7.289336482	0.2792064	0.374428653	0.07987	0	1786	930	4215	2497	1742	4240	3017	2824	3313	4338
ENSMUSG00000033323	chr18	Ctdp1	8E+07	8E+07	3910	0.209839115	3.393493877	0.2793076	0.374528579	0.03869	0	136	96	209	145	152	247	247	177	254	228
ENSMUSG00000025159	chr19	Mms19	4.2E+07	4.2E+07	10415	0.187312338	4.576786138	0.2794182	0.374631718	0.03265	0	284	301	346	301	430	592	520	400	521	585
ENSMUSG00000054414	chr3	Slc30a7	1.2E+08	1.2E+08	9020	0.227627805	3.384852766	0.279438	0.374631718	0.04558	0	131	101	136	164	188	337	229	169	191	240
ENSMUSG00000021255	chr12	Esrrb	8.6E+07	8.6E+07	6047	-0.67952872	3.441663598	0.2795776	0.374783134	0.45138	0	72	7	624	353	53	189	225	80	105	277
ENSMUSG00000022895	chr16	Ets2	9.6E+07	9.6E+07	4710	-0.20531265	5.834535864	0.2799119	0.375143436	0.0418	0	782	524	1407	829	1235	1167	1077	934	1021	1239
ENSMUSG00000043421	chr6	Hilpda	2.9E+07	2.9E+07	1103	0.312796638	2.589444198	0.2799267	0.375143436	0.09109	0	54	48	90	50	173	166	121	110	116	163
ENSMUSG00000074479	chr3	Gm10704	8.9E+07	8.9E+07	730	-0.22013076	3.635632553	0.2798862	0.375143436	0.04489	0	221	174	221	158	214	301	220	209	215	228
ENSMUSG00000031652	chr8	N4bp1	8.7E+07	8.7E+07	6469	-0.17761971	5.16159593	0.2800083	0.375181978	0.0307	0	461	390	776	633	643	856	754	439	755	709
ENSMUSG00000041571	chr7	Sepw1	1.6E+07	1.6E+07	736	0.244289126	10.1633944	0.2800089	0.375181978	0.06109	0	17571	13634	13893	14260	18208	28066	20721	19279	32155	28304
ENSMUSG00000038822	chr10	Hace1	4.6E+07	4.6E+07	12851	-0.273475	2.102379845	0.2800896	0.375254216	0.06216	0	77	47	93	62	70	99	108	59	58	72
ENSMUSG00000001334	chr4	Fndc5	1.3E+08	1.3E+08	2763	-0.45113221	6.831684362	0.2803601	0.375580793	0.20606	0	1159	382	5175	2963	1107	1654	3066	1096	1743	2530
ENSMUSG00000056267	chr9	Cep70	9.9E+07	9.9E+07	4806	-0.30652357	1.536755274	0.2804635	0.375683392	0.06936	0	57	24	57	42	58	76	62	35	42	48
ENSMUSG00000043773	chr9	1700048O20Rik	1.2E+08	1.2E+08	1642	0.543686023	-0.3612654	0.2805538	0.375768511	0.16585	0	10	10	3	7	9	22	8	15	10	26
ENSMUSG00000033712	chr14	Ccar2	7E+07	7E+07	3716	-0.17314769	4.592725681	0.2806619	0.375841507	0.02838	0	319	276	513	384	456	531	539	297	484	513
ENSMUSG00000074207	chr3	Adh1	1.4E+08	1.4E+08	2233	0.237583089	4.421642605	0.2806612	0.375841507	0.05597	0	216	164	384	229	554	447	540	399	560	420
ENSMUSG00000004788	chr12	Eif2b2	8.5E+07	8.5E+07	1885	-0.17455494	5.244966389	0.2806982	0.375854179	0.02986	0	533	475	682	631	702	771	809	530	832	743
ENSMUSG00000097445	chr9	Gm26631	5.8E+07	5.8E+07	2505	1.178454639	1.851141913	0.2808162	0.375976278	1.28607	0	0	0	119	35	30	0	126	2	152	225
ENSMUSG00000030678	chr7	Maz	1.3E+08	1.3E+08	2365	0.19949846	6.434151515	0.2810854	0.37630089	0.0402	0	1037	940	1402	1217	1490	2054	2105	1332	2259	1846
ENSMUSG00000022827	chr16	Rabl3	3.8E+07	3.8E+07	6369	0.232377647	2.95637659	0.2811335	0.376329305	0.04856	0	92	53	149	114	140	184	201	119	170	186
ENSMUSG00000008734	chr7	Gprc5b	1.2E+08	1.2E+08	4525	0.263030645	5.83993667	0.2811665	0.37633757	0.07029	0	641	493	907	454	1592	1167	1479	1001	1414	1360
ENSMUSG00000079033	chr8	Mef2b	7E+07	7E+07	1342	0.369011816	0.376101826	0.2813105	0.376494351	0.09958	0	9	8	26	10	28	36	22	21	28	31
ENSMUSG00000038628	chr2	Polr3k	1.8E+08	1.8E+08	3124	-0.18642775	4.494056415	0.2813425	0.376501225	0.03314	0	357	279	373	369	414	429	509	357	474	389
ENSMUSG00000000001	chr3	Gnai3	1.1E+08	1.1E+08	3262	0.222353035	4.568223996	0.2814494	0.376572423	0.04814	0	262	276	322	242	555	694	561	452	445	477
ENSMUSG00000034842	chr5	Art3	9.2E+07	9.2E+07	3932	-0.20896637	7.278843079	0.2814351	0.376572423	0.04463	0	2445	1714	3077	2373	3096	3540	3422	2442	2326	3169
ENSMUSG00000024847	chr19	Aip	4114446	4114796	1937	0.20923178	6.124732426	0.2815956	0.376732133	0.04412	0	982	791	913	900	1249	1601	1573	1169	1853	1522
ENSMUSG00000052369	chr15	Tmem106c	9.8E+07	9.8E+07	1635	0.240601932	3.831732782	0.2817923	0.376959374	0.05478	0	201	147	156	153	323	404	286	243	371	283
ENSMUSG00000087598	chr7	Zfp111	2.4E+07	2.4E+07	10160	-0.27915507	1.702512928	0.2821144	0.377354264	0.06161	0	55	46	54	40	64	67	55	52	61	58
ENSMUSG00000022272	chr15	Myo10	2.6E+07	2.6E+07	10122	-0.20379671	6.452879275	0.2824072	0.377709893	0.0423	0	1334	1047	1882	1254	1613	1592	2153	1272	1626	1765
ENSMUSG00000026770	chr2	Il2ra	1.2E+07	1.2E+07	5711	0.416335726	0.575330816	0.2824387	0.377715956	0.14263	0	11	8	29	15	30	31	21	41	19	45
ENSMUSG00000027479	chr2	Mapre1	1.5E+08	1.5E+08	7811	0.191486915	5.956655732	0.2824935	0.377753254	0.03697	0	797	650	970	798	1185	1660	1379	1132	1249	1410
ENSMUSG00000020349	chr11	Ppp2ca	5.2E+07	5.2E+07	7490	-0.22488018	7.362810957	0.2825486	0.377790891	0.05197	0	2152	1540	4244	3148	2680	3636	3646	2410	2802	3250
ENSMUSG00000028086	chr3	Fbxw7	8.5E+07	8.5E+07	7046	-0.1837285	4.852413967	0.2828758	0.378192379	0.03272	0	392	310	632	534	471	552	684	429	515	607
ENSMUSG00000040385	chr19	Ppp1ca	4192158	4192271	1379	0.202862479	7.620403489	0.2829229	0.378219322	0.04239	0	2470	2065	3325	2888	3091	4668	4674	3128	4988	4383
ENSMUSG00000025008	chr19	Tctn3	4.1E+07	4.1E+07	3273	0.283271118	1.96497844	0.2829631	0.378236971	0.06579	0	42	30	86	51	56	105	106	51	71	104
ENSMUSG00000027286	chr2	Lrrc57	1.2E+08	1.2E+08	2227	-0.18913839	4.020413562	0.2830251	0.378283817	0.03348	0	263	187	342	262	246	393	347	235	301	292
ENSMUSG00000029147	chr5	Ppm1g	3.1E+07	3.1E+07	2165	-0.18023419	5.50584445	0.2830724	0.378311016	0.03231	0	611	469	981	780	865	1045	1006	621	881	880
ENSMUSG00000031431	chrX	Tsc22d3	1.4E+08	1.4E+08	4341	0.207582877	7.292025102	0.2831019	0.378314367	0.04438	0	2149	1577	2532	1879	2937	3801	3701	2871	3758	3156
ENSMUSG00000037935	chr11	Smarce1	9.9E+07	9.9E+07	6650	0.171807247	5.211311356	0.2831407	0.378330188	0.02873	0	495	407	631	533	550	939	883	615	747	876
ENSMUSG00000027405	chr2	Nop56	1.3E+08	1.3E+08	4099	-0.17282216	4.840929762	0.2833191	0.378496373	0.02876	0	395	339	600	483	480	620	532	471	566	573
ENSMUSG00000069089	chr13	Cdk7	1E+08	1E+08	7595	-0.20327348	4.083073984	0.2833183	0.378496373	0.0399	0	291	242	282	250	269	423	343	263	280	315
ENSMUSG00000029189	chr5	Sel1l3	5.3E+07	5.3E+07	4511	-0.22555571	5.719265994	0.2835468	0.378764567	0.05156	0	827	488	1154	1161	694	1055	1026	858	1100	937
ENSMUSG00000038930	chr7	Rccd1	8E+07	8E+07	3630	0.236270846	2.687302644	0.2840166	0.379355954	0.04721	0	84	63	89	88	116	163	126	103	144	174
ENSMUSG00000034254	chr17	Agpat1	3.5E+07	3.5E+07	3001	-0.21296843	6.483819998	0.2842516	0.379633705	0.04665	0	1275	999	1626	1590	1819	1587	1987	1114	2235	1684
ENSMUSG00000003518	chr11	Dusp3	1E+08	1E+08	4682	-0.21301262	7.443285698	0.2843119	0.379678101	0.04705	0	2613	2260	3305	2615	3280	3521	4528	2367	3361	2988
ENSMUSG00000097392	chr5	D930016D06Rik	1E+08	1E+08	4509	-0.30815303	1.925472683	0.2846049	0.3800331	0.08626	0	66	61	51	60	62	85	85	51	39	85
ENSMUSG00000024962	chr19	Vegfb	6982473	6982867	1605	-0.2856916	6.946817867	0.2849475	0.380454468	0.08461	0	1409	838	3765	2722	2029	2030	3072	1403	2533	2556
ENSMUSG00000030880	chr7	Polr3e	1.2E+08	1.2E+08	4234	-0.211572	3.719733547	0.2849946	0.380481021	0.04127	0	220	122	258	173	313	316	232	196	269	244
ENSMUSG00000041765	chr14	Ubac2	1.2E+08	1.2E+08	2153	-0.17558098	5.163500709	0.2853154	0.380873166	0.03043	0	477	371	805	557	719	755	864	486	698	693
ENSMUSG00000010476	chr7	Ebf3	1.4E+08	1.4E+08	5021	-0.26996573	3.511960797	0.2853727	0.380877066	0.06983	0	153	133	166	129	374	287	213	169	175	222
ENSMUSG00000040848	chr1	Sft2d2	1.7E+08	1.7E+08	5702	0.210435512	4.550556915	0.2853998	0.380877066	0.04328	0	307	250	277	272	533	694	548	335	482	569
ENSMUSG00000043510	chr5	Hscb	1.1E+08	1.1E+08	905	-0.23812542	2.916405463	0.2853972	0.380877066	0.05034	0	114	80	151	111	163	159	119	90	172	173

ENSMUSG00000025503	chr7	Taldo1	1.4E+08	1.4E+08	1998	0.259357084	6.812364101	0.2857021	0.381222934	0.07001	0	1499	959	1245	1192	3005	2862	2235	1927	2978	2653
ENSMUSG00000037892	chr3	Pcdh18	5E+07	5E+07	5366	0.308978942	2.385515054	0.2857134	0.381222934	0.08342	0	61	64	49	47	121	151	140	87	104	107
ENSMUSG00000008348	chr5	Ubc	1.3E+08	1.3E+08	2893	-0.21643322	8.698952653	0.2859656	0.381523223	0.04911	0	6313	5629	6931	7349	6993	8439	7980	6443	8945	7774
ENSMUSG00000026791	chr2	Slc2a8	3.3E+07	3.3E+07	3209	0.203007864	3.827141394	0.2861439	0.38172481	0.03929	0	189	121	241	165	296	338	362	213	363	293
ENSMUSG00000096393	chr9	Gm590	1.1E+08	1.1E+08	499	0.688336071	-0.12665118	0.2862089	0.381775237	0.40827	0	8	0	24	16	0	29	31	14	8	20
ENSMUSG00000026197	chr1	Zfand2b	7.5E+07	7.5E+07	1772	0.196687655	3.614818887	0.2865111	0.382141934	0.03597	0	164	105	199	160	242	305	304	200	274	263
ENSMUSG00000032497	chr9	Lrrfip2	1.1E+08	1.1E+08	3260	0.183528531	5.921392032	0.2868281	0.382528412	0.03452	0	865	577	1102	809	968	1525	1468	1014	1275	1391
ENSMUSG00000036552	chr17	Ermard	1.5E+07	1.5E+07	6352	0.230333867	3.150135454	0.2869259	0.382622364	0.04823	0	121	91	126	94	181	263	180	141	189	214
ENSMUSG00000020585	chr12	Laptm4a	8921664	8922294	1773	0.205739756	8.557423538	0.2870691	0.382776997	0.04453	0	5476	4021	5977	4731	6158	10174	8197	6616	8420	8372
ENSMUSG00000022125	chr14	Cln5	1E+08	1E+08	2396	-0.18864674	4.185904914	0.2871881	0.382899243	0.03393	0	272	181	400	286	346	451	437	254	299	327
ENSMUSG00000019863	chr10	Qrsl1	4.4E+07	4.4E+07	3442	-0.24632995	4.538166065	0.2875535	0.383350044	0.06074	0	242	201	751	439	349	411	536	313	463	470
ENSMUSG00000033361	chrX	Prrg3	7.2E+07	7.2E+07	6087	0.262451335	3.048365524	0.2879008	0.383776464	0.06631	0	74	75	116	93	219	227	186	149	170	189
ENSMUSG00000037845	chr9	Fdxacb1	5.1E+07	5.1E+07	3256	0.232825541	2.521981765	0.2881149	0.384025448	0.04523	0	68	58	99	85	82	145	132	102	133	116
ENSMUSG00000049657	chr4	Zbtb5	4.5E+07	4.5E+07	5606	-0.23433675	2.595439567	0.2883113	0.384250651	0.04689	0	91	72	104	93	127	140	116	97	95	116
ENSMUSG00000090083	chr17	Rnf8	3E+07	3E+07	3178	-0.17121409	4.404799026	0.288342	0.384255086	0.02813	0	289	231	425	343	422	453	469	283	418	443
ENSMUSG00000036613	chr12	Tssc1	2.9E+07	2.9E+07	1692	0.234103289	2.69163394	0.2884761	0.384397269	0.04788	0	73	67	115	89	99	151	124	105	178	151
ENSMUSG00000020173	chr11	Cobl	1.2E+07	1.2E+07	8142	0.218576458	5.749223599	0.2887883	0.384776748	0.04925	0	687	672	740	875	678	1056	1289	898	1395	1309
ENSMUSG00000038845	chr11	Phb	9.6E+07	9.6E+07	2805	-0.21534892	6.96335811	0.2888312	0.38477812	0.04873	0	1756	1121	3162	2190	2201	2424	2655	1839	2698	2300
ENSMUSG00000084284	chrX	Tpt1-ps6	1E+08	1E+08	523	0.541107538	-0.11379435	0.2888442	0.38477812	0.16304	0	9	13	3	12	10	19	26	6	23	27
ENSMUSG00000023089	chr6	Ndufa5	2.5E+07	2.5E+07	1032	0.21946865	7.65189977	0.2893979	0.385479104	0.05109	0	2508	1563	4319	3182	2829	4779	4193	3461	4707	5197
ENSMUSG00000028451	chr4	1700022I11Rik	4.3E+07	4.3E+07	4542	1.118569782	-0.19689613	0.2895194	0.385604308	1.14008	0	0	0	34	4	2	1	20	0	34	50
ENSMUSG00000059013	chr2	Sh2d3c	3.3E+07	3.3E+07	5233	0.248812971	3.209322363	0.2895865	0.385657053	0.06123	0	82	56	200	136	189	229	214	144	216	229
ENSMUSG00000049241	chr5	Hcar1	1.2E+08	1.2E+08	3285	-0.84820986	2.300230456	0.2896618	0.385720694	0.71524	0	98	36	2	4	363	137	27	65	47	82
ENSMUSG00000002007	chrX	Srpk3	7.4E+07	7.4E+07	2784	0.181925789	5.344979046	0.2898155	0.385888695	0.03369	0	492	423	674	594	702	927	872	596	1113	971
ENSMUSG00000036093	chr2	Arl5a	5.2E+07	5.2E+07	5409	-0.18102367	4.946453659	0.2898456	0.385892259	0.03332	0	482	376	554	528	513	829	721	428	491	549
ENSMUSG00000004508	chr7	Gab2	9.7E+07	9.7E+07	5997	0.212867141	3.725691088	0.290184	0.386306072	0.04491	0	137	96	301	177	246	347	320	208	275	318
ENSMUSG00000025190	chr19	Got1	4.3E+07	4.4E+07	2539	-0.35957899	8.715065484	0.2902988	0.386422276	0.13739	0	4531	2524	14850	11677	3941	6810	10055	5174	7270	8929
ENSMUSG00000101892	chr15	9130401M01Rik	5.8E+07	5.8E+07	2666	0.19124499	4.042030803	0.2903574	0.386463596	0.03492	0	215	186	257	190	307	446	328	292	384	353
ENSMUSG00000001348	chr9	Acp5	2.2E+07	2.2E+07	1612	0.774824341	4.83285666	0.2909147	0.387168572	0.61714	0	291	160	14	9	1212	742	556	580	963	837
ENSMUSG00000052752	chr17	Traf7	2.5E+07	2.5E+07	5872	0.165527876	4.864625134	0.2910274	0.387281858	0.02727	0	362	287	482	404	557	753	634	453	660	694
ENSMUSG00000059554	chr10	Ccdc28a	1.8E+07	1.8E+07	2964	0.234299952	2.826434895	0.2911083	0.387352784	0.0482	0	97	74	127	92	94	201	157	123	126	176
ENSMUSG00000015839	chr2	Nfe2l2	7.6E+07	7.6E+07	3796	-0.1749371	5.131726124	0.2913694	0.387663339	0.03086	0	492	349	728	535	762	743	837	520	604	702
ENSMUSG00000038497	chr8	Tmco3	1.3E+07	1.3E+07	4533	-0.19887126	3.832839954	0.2914628	0.387750859	0.03798	0	197	168	318	203	271	276	336	191	325	240
ENSMUSG00000031583	chr8	Wrn	3.3E+07	3.3E+07	6372	-0.29033045	2.009192835	0.291634	0.387941861	0.07358	0	55	52	87	55	80	89	100	46	43	93
ENSMUSG00000038212	chr13	Hiatl1	6.5E+07	6.5E+07	3925	-0.22116241	3.628793341	0.2920273	0.388428177	0.04782	0	196	153	194	166	291	324	273	179	170	237
ENSMUSG00000017309	chr11	Cd300lg	1E+08	1E+08	2737	-0.23301321	5.221521641	0.2924511	0.388918141	0.05647	0	460	300	905	442	1107	864	826	462	643	792
ENSMUSG00000039989	chr11	Cbx4	1.2E+08	1.2E+08	5210	0.353512516	3.114856142	0.2924236	0.388918141	0.12712	0	72	63	91	73	297	272	129	157	215	220
ENSMUSG00000001419	chr3	Mef2d	8.8E+07	8.8E+07	5985	-0.20759166	7.777812891	0.292679	0.389184321	0.04629	0	3150	2262	4987	3705	3991	4029	5102	2880	4503	4639
ENSMUSG00000034285	chr11	Nipsnap1	4873951	4874103	2649	0.411270634	1.05024072	0.2928706	0.389402133	0.14992	0	27	15	13	14	60	68	34	34	48	48
ENSMUSG00000033191	chr4	Tie1	1.2E+08	1.2E+08	4917	0.22559264	5.453965216	0.2929829	0.389514566	0.05404	0	372	324	924	637	935	1086	836	693	1066	1213
ENSMUSG00000026988	chr2	Wdsub1	6E+07	6E+07	3598	-0.22590572	3.556635675	0.2931861	0.389747758	0.05058	0	165	176	184	135	284	271	261	154	213	224
ENSMUSG00000019777	chr10	Hdac2	3.7E+07	3.7E+07	4474	-0.19276193	5.991210369	0.293338	0.38991273	0.03929	0	1119	740	1114	980	1148	1424	1241	1070	1086	1276
ENSMUSG00000002768	chr17	Mea1	4.7E+07	4.7E+07	840	0.168477863	4.907118059	0.2934531	0.390028724	0.02875	0	422	277	471	409	572	767	647	479	738	655
ENSMUSG00000059461	chrX	Gm7331	1.6E+08	1.6E+08	387	0.505029964	-0.30734254	0.2937182	0.39034405	0.1654	0	7	8	4	6	18	15	7	14	24	23
ENSMUSG00000002885	chr8	Cd97	8.4E+07	8.4E+07	3757	0.179945973	5.30756936	0.2938022	0.390418692	0.03377	0	401	361	741	609	753	1066	954	624	851	879
ENSMUSG00000049076	chr16	Acap2	3.1E+07	3.1E+07	6493	0.204157839	3.818468793	0.2939272	0.390547817	0.04068	0	186	132	210	169	300	419	369	222	265	293
ENSMUSG00000001065	chr8	Zfp276	1.2E+08	1.2E+08	5530	-0.23529092	3.129417378	0.2939728	0.390568131	0.05334	0	117	104	201	164	124	214	181	94	197	151
ENSMUSG00000023186	chr9	Vwa5a	3.9E+07	3.9E+07	4899	0.222831104	5.529647328	0.2939982	0.390568131	0.05202	0	758	570	606	609	572	1463	1203	796	850	869
ENSMUSG00000020706	chr11	Ftsj3	1.1E+08	1.1E+08	4358	-0.17356965	5.197710526	0.2940761	0.390634651	0.03104	0	538	457	687	601	639	843	678	637	685	689
ENSMUSG00000069114	chr3	Zbtb10	9250602	9252080	7414	-0.22673031	2.903477877	0.2941428	0.390686246	0.04562	0	97	77	150	137	150	159	159	107	121	160
ENSMUSG00000024896	chr19	Minpp1	3.2E+07	3.2E+07	2619	0.179500586	4.252571205	0.2941916	0.390714129	0.03128	0	281	201	277	253	326	509	432	327	433	384
ENSMUSG00000005813	chr3	Metap1	1.4E+08	1.4E+08	2549	-0.19061674	6.185751956	0.2942365	0.390736649	0.03872	0	1164	837	1331	1217	1307	1547	1718	1067	1401	1307
ENSMUSG00000079484	chr2	Phyhd1	3E+07	3E+07	2657	0.475700535	4.115859157	0.294326	0.390818603	0.24097	0	55	36	667	245	218	416	649	236	311	492
ENSMUSG00000030613	chr7	Ccdc90b	9.3E+07	9.3E+07	1801	-0.17966288	4.398679464	0.2947684	0.391368957	0.03221	0	349	225	447	334	342	504	496	311	364	373
ENSMUSG00000021033	chr12	Gstz1	8.7E+07	8.7E+07	1665	-0.26004438	6.350949362	0.294892	0.391495935	0.07281	0	1265	959	1044	892	2663	1865	1397	1217	1633	1566
ENSMUSG00000025208	chr19	Mrpl43	4.5E+07	4.5E+07	1213	0.184955297	5.588724001	0.2950703	0.39169558	0.03617	0	562	457	1055	670	719	1263	1033	813	1114	1073
ENSMUSG00000027204	chr2	Fbn1	1.3E+08	1.3E+08	12128	0.235812402	7.111460715	0.2952616	0.391912471	0.06027	0	1263	1266	1974	2205	3085	4535	3371	2348	2868	2502
ENSMUSG00000030291	chr6	Med21	1.5E+08	1.5E+08	2102	-0.18568561	4.459959547	0.2953043	0.391932057	0.03537	0	368	303	345	333	381	502	510	327	394	394
ENSMUSG00000073096	chr6	Lrrc61	4.9E+07	4.9E+07	2913	-0.17171319	4.674201626	0.2956877	0.392403823	0.03	0	424	293	476	371	477	495	528	327	561	577
ENSMUSG00000022369	chr15	Mtbp	5.6E+07	5.6E+07	5481	0.36700796	0.796961353	0.296149	0.392978751	0.11488	0	17	8	26	13	48	53	42	24	37	35
ENSMUSG00000020368	chr11	Canx	5E+07	5E+07	4693	0.206085946	6.981964201	0.2963622	0.393195761	0.04612	0	1496	1193	2284	2161	1798	3760	2813	2256	2541	2678
ENSMUSG00000034793	chr11	G6pc3	1E+08	1E+08	2226	0.188952303	5.817012015	0.2963686	0.393195761	0.03797	0	745	576	852	842	961	1288	1223	876	1557	1270
ENSMUSG00000000126	chr11	Wnt9a	5.9E+07	5.9E+07	3329	-0.20581908	4.131716613	0.2966506	0.39353274	0.04233	0	208	177	432	288	346	338	452	249	275	366
ENSMUSG00000031391	chrX	L1cam	7.4E+07	7.4E+07	7347	0.258784271	2.350346917	0.2968909	0.39378328	0.05991	0	58	42	95	92	59	139	109	78	112	128
ENSMUSG00000092241	chr17	Gm20522	3.5E+07	3.5E+07	784	-0.32593236	1.537133139	0.2968956	0.39378328	0.09167	0	45	23	95	42	39	58	60	28	52	63
ENSMUSG00000052085	chr19	Dock8	2.5E+07	2.5E+07	7810	0.342437005	2.791135649	0.2970221	0.393913709	0.12119	0	56	47	130	42	208	229	180	82	150	166
ENSMUSG00000021661	chr13	Ankra2	9.8E+07	9.8E+07	3510	-0.19768476	3.931678068	0.2971626	0.394025591	0.03946	0	239	214	316	207	236	348	368	221	257	274

ENSMUSG00000061751	chr16	Kalrn	3.4E+07	3.4E+07	18660	-0.21216085	4.107863782	0.297148	0.394025591	0.04559	0	246	160	421	335	256	327	432	215	313	370
ENSMUSG00000010755	chr7	Cars	1.4E+08	1.4E+08	4639	-0.18309537	5.57014958	0.2974408	0.394357166	0.03557	0	642	521	1077	855	757	1003	965	713	952	959
ENSMUSG00000022469	chr15	Rapgef3	9.8E+07	9.8E+07	6336	-0.22899703	3.395391458	0.2975441	0.394456791	0.05032	0	132	100	241	142	266	234	175	158	234	191
ENSMUSG00000039531	chr10	Zufsp	3.4E+07	3.4E+07	2364	-0.2414923	2.402743048	0.2977956	0.394752896	0.05194	0	93	56	111	72	97	139	100	77	97	82
ENSMUSG00000075289	chr19	Carns1	4164324	4166564	3968	0.194971692	5.234302398	0.298003	0.394990623	0.0398	0	544	433	521	625	463	977	860	629	929	758
ENSMUSG00000010051	chr9	Hyal1	1.1E+08	1.1E+08	3777	-0.2368821	2.761346087	0.2981959	0.395208863	0.0512	0	110	74	103	102	161	130	136	90	145	135
ENSMUSG00000040247	chr19	Tbc1d10c	4184358	4185073	1758	0.264295479	2.365055539	0.2983257	0.395343503	0.06083	0	82	50	78	74	58	102	126	84	121	134
ENSMUSG00000020792	chr11	Exoc7	1.2E+08	1.2E+08	4367	-0.21237622	6.362727602	0.2986317	0.395711706	0.04929	0	1293	1150	1357	1073	1731	1838	1828	1170	1858	1215
ENSMUSG00000028031	chr3	Dkk2	1.3E+08	1.3E+08	3694	0.344128385	4.094932458	0.2986765	0.3957336	0.12654	0	114	211	309	91	434	722	247	316	370	334
ENSMUSG00000028521	chr4	Slc35d1	1E+08	1E+08	8528	-0.21282351	3.299783972	0.2989008	0.395993461	0.04464	0	173	128	142	160	175	225	207	149	175	179
ENSMUSG00000097333	chr13	Zfp87	6.8E+07	6.8E+07	2865	0.255909215	2.037688495	0.2993523	0.396554101	0.05412	0	47	38	57	58	77	123	89	66	78	97
ENSMUSG00000003068	chr10	Stk11	8E+07	8E+07	4580	-0.19510462	6.914696802	0.2994807	0.396684275	0.04181	0	1732	1272	2546	2058	2258	2415	2833	1587	2457	2412
ENSMUSG00000048706	chr4	Lurap1l	8.1E+07	8.1E+07	3066	-0.30640093	2.003476888	0.2995071	0.396684275	0.08298	0	47	35	68	59	130	79	79	68	64	68
ENSMUSG00000002102	chr2	Psmc3	9.1E+07	9.1E+07	2607	0.196198206	7.763254703	0.3002199	0.397590775	0.04266	0	2949	2117	3859	3191	3262	5233	4738	3824	5330	4795
ENSMUSG00000024542	chr18	Cep192	6.8E+07	6.8E+07	8091	0.264748195	1.634995079	0.3003232	0.397690028	0.05593	0	40	28	43	43	52	92	73	51	54	70
ENSMUSG00000036585	chr18	Fgf1	3.9E+07	3.9E+07	4648	-0.32088418	5.115860071	0.3004746	0.397852956	0.11198	0	433	156	1351	744	426	751	714	464	526	746
ENSMUSG00000036615	chr3	Rfxap	5.5E+07	5.5E+07	2242	-0.17626288	3.972238	0.3006302	0.398021478	0.03055	0	234	178	290	255	299	316	322	239	325	309
ENSMUSG00000000826	chr2	Dnajc5	1.8E+08	1.8E+08	6953	-0.18172838	5.956004937	0.3010804	0.398504625	0.0359	0	838	692	1342	1026	1145	1305	1417	935	1199	1154
ENSMUSG00000024393	chr17	Prrc2a	3.5E+07	3.5E+07	7631	-0.20840218	7.511952805	0.301061	0.398504625	0.04826	0	2355	2051	3818	3432	3273	3446	4062	2368	4218	3497
ENSMUSG00000029038	chr4	Ssu72	1.6E+08	1.6E+08	2689	0.163320072	5.22155702	0.3010279	0.398504625	0.0281	0	520	371	631	529	614	1029	808	623	811	812
ENSMUSG00000084235	chr5	Gm15421	2.3E+07	2.3E+07	399	0.353602884	0.5533757	0.3014284	0.398927572	0.08856	0	12	11	24	21	23	30	39	17	46	26
ENSMUSG00000034902	chr10	Pip5k1c	8.1E+07	8.1E+07	5730	0.180881726	5.267975757	0.3014991	0.398945912	0.03491	0	421	415	686	553	668	830	940	533	1002	950
ENSMUSG00000051323	chrX	Pcdh19	1.3E+08	1.3E+08	10464	0.240676497	2.931374454	0.3014707	0.398945912	0.05667	0	115	67	121	86	137	250	135	141	136	183
ENSMUSG00000027550	chr3	Lrrcc1	1.5E+07	1.5E+07	7475	0.296897648	1.711828848	0.301655	0.399114457	0.07806	0	34	31	44	37	71	120	54	49	72	71
ENSMUSG00000037720	chr5	Tmem33	6.7E+07	6.7E+07	7098	-0.17185855	4.632380425	0.301691	0.399124444	0.03069	0	340	311	422	364	546	589	552	385	436	446
ENSMUSG00000040043	chr10	Rbms2	1.3E+08	1.3E+08	5609	-0.19225181	6.153723305	0.3017937	0.399222705	0.0405	0	959	659	1574	1262	1429	1551	1598	972	1344	1447
ENSMUSG00000026034	chr1	Clk1	5.8E+07	5.8E+07	8132	-0.19651815	5.061898962	0.3018739	0.399291093	0.04168	0	463	408	598	575	645	904	558	447	462	883
ENSMUSG00000033594	chr8	Spata2l	1.2E+08	1.2E+08	2683	0.31753197	1.136687727	0.3020298	0.399459637	0.08033	0	18	16	44	29	37	62	50	22	53	57
ENSMUSG00000025207	chr19	Sema4g	4.5E+07	4.5E+07	4872	0.430831789	-0.08014178	0.3021775	0.399617413	0.13043	0	11	6	8	7	22	27	18	10	13	32
ENSMUSG00000098178	chr17	Yam1	4E+07	4E+07	1831	-0.25066926	11.35487359	0.3022639	0.399693948	0.07055	0	58850	21980	57856	36954	42692	61149	52175	42630	55302	35223
ENSMUSG00000024158	chr17	Hagh	2.5E+07	2.5E+07	1908	-0.17625944	5.678440054	0.3024071	0.399845575	0.03361	0	784	528	1167	749	946	1151	1009	780	985	1043
ENSMUSG00000078816	chr7	Prkcg	3303532	3303959	3112	0.429753535	0.627879791	0.3025203	0.399957504	0.16919	0	12	8	14	13	49	26	31	25	29	57
ENSMUSG00000036860	chr11	Mrpl55	5.9E+07	5.9E+07	1027	0.196410703	4.63759912	0.3027213	0.400185627	0.04171	0	244	184	591	375	425	597	556	399	552	643
ENSMUSG00000018189	chr1	Uchl5	1.4E+08	1.4E+08	2921	-0.17695085	4.484812776	0.3030209	0.400506122	0.03258	0	376	262	406	342	398	567	467	366	397	368
ENSMUSG00000028494	chr4	Plin2	8.7E+07	8.7E+07	3512	0.377422151	6.683131066	0.3030066	0.400506122	0.15908	0	1190	510	984	616	3943	2618	2111	1668	2407	3252
ENSMUSG00000031671	chr8	Setd6	9.6E+07	9.6E+07	1869	0.198175383	3.506213133	0.3031169	0.400595325	0.03769	0	158	129	178	135	188	281	239	186	262	277
ENSMUSG00000027804	chr3	Ppid	8E+07	8E+07	4638	-0.19549744	5.727316546	0.303196	0.400662101	0.04214	0	998	709	894	739	846	1220	1012	814	1083	970
ENSMUSG00000022663	chr16	Atg3	4.5E+07	4.5E+07	3154	-0.1634626	4.610682973	0.3034863	0.40090187	0.02772	0	358	294	449	357	492	555	565	367	456	438
ENSMUSG00000030002	chr6	Dusp11	8.6E+07	8.6E+07	7639	-0.17397903	4.93954667	0.3034469	0.40090187	0.03259	0	483	439	541	427	521	741	631	462	523	627
ENSMUSG00000040356	chr17	Skiv2l	3.5E+07	3.5E+07	4977	0.167441165	5.210098271	0.3034334	0.40090187	0.03002	0	435	359	586	594	678	914	839	605	886	804
ENSMUSG00000078517	chr4	Emc1	1.4E+08	1.4E+08	6683	0.175937484	5.675218098	0.3034918	0.40090187	0.03366	0	692	513	788	809	814	1234	1149	839	1183	1199
ENSMUSG00000070565	chr1	Rasal2	1.6E+08	1.6E+08	13740	-0.23118305	3.235728005	0.3035976	0.401003821	0.05292	0	142	116	224	156	123	231	187	159	163	144
ENSMUSG00000035969	chr4	Rusc2	4.3E+07	4.3E+07	7923	-0.19570129	5.624602548	0.3041916	0.401750551	0.0419	0	724	418	1187	930	820	978	1038	705	1058	973
ENSMUSG00000030894	chr7	Tpp1	1.1E+08	1.1E+08	3494	-0.1890742	6.122406676	0.3043587	0.401933425	0.03977	0	1103	807	1293	1188	1205	1457	1711	883	1387	1354
ENSMUSG00000052137	chr4	Rbm12b2	1.2E+07	1.2E+07	3468	0.266048442	1.957511101	0.304533	0.402125762	0.06304	0	58	29	47	58	68	95	90	78	80	79
ENSMUSG00000007570	chr17	Fance	2.8E+07	2.8E+07	3183	0.212715602	3.117181728	0.3047169	0.402324146	0.04433	0	107	82	167	106	147	231	156	145	198	223
ENSMUSG00000052180	chr13	Serpinb6c	3.4E+07	3.4E+07	1391	0.489095618	0.304532256	0.3047406	0.402324146	0.19989	0	13	14	22	7	14	56	11	33	12	22
ENSMUSG00000031105	chrX	Slc25a14	4.9E+07	4.9E+07	2364	0.327980775	1.399146963	0.3048851	0.402477014	0.09415	0	30	29	26	23	61	71	59	58	50	49
ENSMUSG00000010122	chr11	Slc47a1	6.1E+07	6.1E+07	3383	-0.31048631	5.068253775	0.304925	0.402491794	0.10714	0	312	298	1025	953	285	666	758	354	649	711
ENSMUSG00000003865	chr7	Gys1	4.5E+07	4.5E+07	4789	-0.27723274	9.10115258	0.3050117	0.402568368	0.08708	0	6331	4096	16355	13163	7373	9656	12954	7401	10960	10459
ENSMUSG00000048489	chr6	8430408G22Rik	1.2E+08	1.2E+08	1317	0.409536595	2.603273098	0.3050748	0.402613817	0.18338	0	56	14	207	61	86	107	124	97	129	242
ENSMUSG00000041476	chrX	Smpx	1.6E+08	1.6E+08	2275	0.201426478	8.215084985	0.3052047	0.402747311	0.04597	0	4193	3127	5461	3824	4300	8236	7560	5064	5462	6729
ENSMUSG00000021114	chr12	Atp6v1d	7.9E+07	7.9E+07	1403	0.187486716	6.388181371	0.3054935	0.403052538	0.03927	0	1193	834	1511	1183	1207	2079	2056	1374	1677	2063
ENSMUSG00000059363	chr19	Fxn	2.4E+07	2.4E+07	2053	0.195145204	3.775965042	0.3054772	0.403052538	0.03864	0	177	131	226	192	240	300	270	207	373	353
ENSMUSG00000025229	chr19	Pitx3	4.6E+07	4.6E+07	1526	0.338534635	2.568002174	0.3055451	0.403062117	0.11557	0	54	60	84	124	61	120	67	115	193	166
ENSMUSG00000032537	chr9	Ephb1	1E+08	1E+08	6487	0.314540506	1.069607189	0.3055582	0.403062117	0.09216	0	24	9	48	20	39	49	51	39	48	39
ENSMUSG00000020709	chr11	Adap2	8E+07	8E+07	1785	-0.37529695	0.935094114	0.3057121	0.403227141	0.12887	0	18	29	45	17	48	49	52	19	18	29
ENSMUSG00000035105	chr12	Egln3	5.4E+07	5.4E+07	2662	0.49716759	5.748405731	0.3057625	0.40325572	0.2769	0	375	103	1902	1108	165	1324	1591	799	1125	1731
ENSMUSG00000053641	chr9	Dennd4a	6.5E+07	6.5E+07	8645	0.277365301	2.74231452	0.3059339	0.403443817	0.07847	0	77	62	79	60	181	163	161	126	128	164
ENSMUSG00000021338	chr13	Lrrc16a	2.4E+07	2.4E+07	8977	0.356216113	0.476407321	0.3060928	0.403615515	0.08306	0	14	16	19	14	21	46	23	27	27	25
ENSMUSG00000040705	chr7	A930016O22Rik	1.9E+07	1.9E+07	1214	0.974608027	5.808651365	0.3061308	0.403627631	1.01603	0	28	28	2367	512	400	42	1194	64	3944	2580
ENSMUSG00000030042	chr6	Pole4	8.3E+07	8.3E+07	2509	-0.17083936	4.75785341	0.3065812	0.404183505	0.03133	0	418	336	437	381	583	600	552	374	609	501
ENSMUSG00000097210	chr7	Fam160a2	1.1E+08	1.1E+08	2508	-0.28115898	1.410670755	0.3066637	0.404254272	0.06585	0	50	36	39	37	47	56	45	41	49	47
ENSMUSG00000025047	chr19	Pdcd11	4.7E+07	4.7E+07	6041	-0.18671662	4.1606826	0.3068603	0.404475366	0.03583	0	257	172	387	341	295	408	356	297	337	316
ENSMUSG00000029012	chr5	Orc5	2.2E+07	2.2E+07	2825	-0.1875805	3.751353695	0.3069027	0.404493281	0.0356	0	209	148	217	208	301	298	275	190	279	256
ENSMUSG00000022750	chr16	Klhl22	1.8E+07	1.8E+07	5745	-0.16502531	5.068103274	0.3069654	0.404499933	0.02948	0	538	361	561	588	628	808	612	470	740	652
ENSMUSG00000030513	chr7	Pcsk6	6.6E+07	6.6E+07	5144	-0.22599038	4.915848176	0.3069399	0.404499933	0.05597	0	396	233	541	458	936	763	748	389	481	532

ENSMUSG00000040606	chr4	Kazn	1.4E+08	1.4E+08	10721	0.268682865	1.868039786	0.3072346	0.404816588	0.06807	0	46	26	52	50	73	73	73	80	82	84
ENSMUSG00000029840	chr6	Mtpn	3.6E+07	3.6E+07	3960	0.180087663	5.418423724	0.3073615	0.404945687	0.03553	0	570	489	598	568	778	1168	1037	747	927	818
ENSMUSG00000040213	chr3	Ccbl2	1.4E+08	1.4E+08	2619	-0.21356067	3.711814584	0.3074181	0.404982319	0.04744	0	233	123	255	251	199	299	260	179	195	322
ENSMUSG00000024118	chr17	1600002H07Rik	2.4E+07	2.4E+07	2551	0.284910352	1.716698869	0.3075233	0.405082847	0.07291	0	54	24	61	34	46	99	58	61	81	61
ENSMUSG00000021024	chr12	Psma6	5.5E+07	5.5E+07	1234	0.186606894	7.030263167	0.3077692	0.405368668	0.0396	0	1699	1325	2231	1765	2283	3310	2879	2287	2919	2978
ENSMUSG00000045064	chr12	Zc2hc1c	8.5E+07	8.5E+07	4482	-0.38981157	0.930717791	0.3082584	0.405974818	0.13434	0	17	15	51	17	64	35	43	15	37	34
ENSMUSG00000100599	chr15	1700120C14Rik	9.9E+07	9.9E+07	1731	0.182161511	4.524106215	0.3083242	0.406023442	0.0352	0	339	239	316	348	366	561	438	426	587	488
ENSMUSG00000008682	chrX	Rpl10	7.4E+07	7.4E+07	2053	0.209186549	8.314693123	0.3084548	0.406157285	0.05025	0	4380	3757	4688	4582	4531	9261	6007	5869	6976	7182
ENSMUSG00000057594	chr11	Arl16	1.2E+08	1.2E+08	2742	0.304721144	1.944778835	0.3085962	0.406305238	0.09272	0	56	23	49	32	101	112	97	59	83	80
ENSMUSG00000079654	chr6	Prrt4	2.9E+07	2.9E+07	3411	-0.56932138	0.406013788	0.3087541	0.406474998	0.28553	0	10	3	19	11	78	21	19	16	27	17
ENSMUSG00000056749	chr13	Nfil3	5.3E+07	5.3E+07	2026	-0.2238596	4.545933722	0.3087843	0.406476656	0.0559	0	252	399	390	441	353	466	591	282	520	383
ENSMUSG00000083649	chr7	Rasl2-9	5124938	5125950	1013	-0.3735274	0.883204922	0.3092033	0.406989966	0.11913	0	24	13	67	30	21	30	44	23	33	27
ENSMUSG00000102717	chr1	RP23-211F21.1	1.4E+08	1.4E+08	3246	0.961524459	1.07261451	0.3092634	0.407030921	0.98063	0	3	0	86	13	14	0	35	6	130	97
ENSMUSG00000079477	chr6	Rab7	8.8E+07	8.8E+07	2610	-0.19996449	7.95501233	0.3098577	0.407774842	0.04618	0	3138	3021	4997	4617	4325	5153	5680	3303	4614	5301
ENSMUSG00000045730	chr18	Adrb2	6.2E+07	6.2E+07	2143	0.18083493	3.757893503	0.3104805	0.408556073	0.03366	0	184	125	226	183	243	328	301	247	271	322
ENSMUSG00000024925	chr19	Rnaseh2c	5601873	5602080	1455	0.219526913	3.759973661	0.3106298	0.408714275	0.05039	0	195	140	165	209	219	363	211	221	361	342
ENSMUSG00000032285	chr9	Dnaja4	5.5E+07	5.5E+07	3589	0.311392923	6.843862895	0.3109302	0.409071077	0.11217	0	1106	519	3321	2196	1050	2848	2997	1751	2465	3202
ENSMUSG00000017718	chr11	Afmid	1.2E+08	1.2E+08	3539	0.240513778	2.77750885	0.3110154	0.409144823	0.05592	0	106	66	89	102	100	173	158	90	195	148
ENSMUSG00000084514	chr18	Mir1893	6490564	6490646	83	-0.32443645	0.832312871	0.3110807	0.409192304	0.08213	0	28	16	38	39	21	44	30	21	28	33
ENSMUSG00000032553	chr9	Srprb	1E+08	1E+08	4287	-0.17324525	5.273883444	0.311319	0.409467374	0.03364	0	571	486	631	664	716	795	825	534	897	713
ENSMUSG00000037572	chr14	Wdhd1	4.7E+07	4.7E+07	7192	0.366316311	0.175308553	0.3115279	0.409703792	0.09436	0	9	7	22	9	22	26	26	14	20	33
ENSMUSG00000021431	chr13	Snrnp48	3.8E+07	3.8E+07	1799	-0.22731298	2.944651189	0.3115728	0.409724378	0.05211	0	134	104	133	128	109	180	145	120	122	157
ENSMUSG00000024392	chr17	Bag6	3.5E+07	3.5E+07	6215	-0.20572467	7.255000755	0.3118347	0.410030264	0.04907	0	1982	1562	3438	2991	2591	2816	3262	2099	3311	3194
ENSMUSG00000022678	chr16	Nde1	1.4E+07	1.4E+07	3205	-0.15604357	5.106387658	0.3124666	0.410822702	0.02685	0	527	390	693	530	612	826	750	488	679	642
ENSMUSG00000032952	chr3	Ap4b1	1E+08	1E+08	2907	-0.19081169	4.095713947	0.3125832	0.410937435	0.0386	0	249	175	446	260	268	354	407	244	312	331
ENSMUSG00000028527	chr4	Ak4	1E+08	1E+08	4646	-0.30648531	4.843475302	0.3127306	0.411092688	0.10787	0	533	394	504	710	155	543	573	415	644	464
ENSMUSG00000029455	chr5	Aldh2	1.2E+08	1.2E+08	4704	0.212083243	7.917008307	0.3129198	0.411302888	0.05264	0	3237	1928	3839	3405	4898	5835	4245	4174	6116	6380
ENSMUSG00000004937	chr10	Sgta	8.1E+07	8.1E+07	1969	-0.18790068	6.886066616	0.3130691	0.411460617	0.04098	0	1695	1204	2355	2020	2396	2468	2444	1597	2593	2385
ENSMUSG00000076258	chr16	Gm23935	1.1E+07	1.1E+07	57	0.379569364	7.184510558	0.3132627	0.411676462	0.16798	0	1904	599	4208	2166	1221	3646	1977	4901	3478	2057
ENSMUSG00000097287	chr5	D130017N08Rik	1.4E+08	1.4E+08	4122	-0.22554335	2.595578583	0.313394	0.41181046	0.04871	0	93	62	135	85	118	115	139	75	108	134
ENSMUSG00000012296	chr17	Tjap1	4.6E+07	4.6E+07	2595	0.167620626	4.99580924	0.3134872	0.411894314	0.03105	0	366	321	589	509	498	703	757	462	795	783
ENSMUSG00000009079	chr11	Ewsr1	5069689	5070103	5907	0.191067789	6.263603702	0.3136047	0.412010088	0.04223	0	944	767	1208	961	1609	2037	1582	1281	1613	1977
ENSMUSG00000018263	chr5	Tbx5	1.2E+08	1.2E+08	3941	0.35996915	1.14658571	0.3136837	0.412075253	0.11437	0	19	22	18	23	58	52	41	35	47	69
ENSMUSG00000038806	chr1	Sde2	1.8E+08	1.8E+08	3471	-0.18278802	3.664142262	0.3139158	0.412341537	0.0346	0	194	145	229	197	250	279	304	177	220	246
ENSMUSG00000085479	chr11	9430073C21Rik	6.7E+07	6.7E+07	2173	0.702175062	3.670535801	0.3139875	0.412397166	0.55721	0	53	6	575	148	45	160	283	65	261	886
ENSMUSG00000055319	chr7	Sec23ip	1.3E+08	1.3E+08	4578	-0.15969837	4.691329148	0.3141364	0.412554019	0.02756	0	343	279	561	425	475	583	600	376	480	488
ENSMUSG00000031575	chr8	Ash2l	2.6E+07	2.6E+07	5236	0.16092921	4.932802164	0.3142235	0.412629832	0.02875	0	388	293	602	446	470	773	702	565	597	675
ENSMUSG00000017288	chr11	Vps53	7.6E+07	7.6E+07	5203	0.164904299	4.439530402	0.314571	0.413047505	0.02947	0	260	213	415	328	339	488	507	386	477	492
ENSMUSG00000091421	chr3	Gm4202	9.3E+07	9.3E+07	733	0.431986248	0.405490355	0.3147318	0.41321991	0.13799	0	18	15	13	18	11	28	58	14	24	22
ENSMUSG00000042644	chr17	Itpr3	2.7E+07	2.7E+07	8990	0.236075693	2.761412818	0.3149293	0.413440531	0.05568	0	64	66	123	114	100	206	161	92	128	172
ENSMUSG00000002635	chr7	Pdcd2l	3.4E+07	3.4E+07	1315	-0.17446236	3.805261766	0.3150072	0.413504007	0.03201	0	209	173	253	218	257	340	290	200	269	258
ENSMUSG00000021731	chr13	Mrps30	1.2E+08	1.2E+08	1590	0.169900907	5.047422936	0.3153884	0.413963262	0.03292	0	384	263	705	480	588	787	699	552	753	820
ENSMUSG00000098381	chr3	Mir7225	9.8E+07	9.8E+07	54	-0.21430467	8.241620553	0.315416	0.413963262	0.05433	0	4312	3308	5472	6353	5152	5414	6886	3816	5672	7366
ENSMUSG00000035828	chr15	Pim3	8.9E+07	8.9E+07	2419	-0.22029472	4.854787046	0.3157147	0.4143165	0.05469	0	427	224	568	359	878	619	451	448	607	620
ENSMUSG00000074579	chr3	Lekr1	6.6E+07	6.6E+07	7113	0.463411596	-0.07318151	0.3160837	0.414761893	0.18441	0	5	5	19	2	25	25	12	17	21	24
ENSMUSG00000004043	chr11	Stat5a	1E+08	1E+08	7133	-0.17243966	4.533876984	0.3161281	0.414781365	0.03215	0	273	243	550	370	457	488	435	358	457	501
ENSMUSG00000001445	chr11	Mrpl10	9.7E+07	9.7E+07	1708	-0.16585766	5.546314049	0.3161697	0.414797153	0.03134	0	671	502	1018	724	867	1011	989	693	922	939
ENSMUSG00000021990	chr14	Spata13	6.1E+07	6.1E+07	9102	0.24218437	2.669133431	0.3166122	0.415338871	0.05985	0	54	67	126	69	126	197	132	96	129	155
ENSMUSG00000026817	chr2	Ak1	3.3E+07	3.3E+07	2593	-0.20556199	10.74336622	0.3168689	0.415625555	0.05045	0	26709	20402	34148	27579	30118	29724	37046	24176	40976	32414
ENSMUSG00000055912	chr6	Tmem150a	7.2E+07	7.2E+07	1546	-0.16919804	4.949295756	0.31689	0.415625555	0.03229	0	366	396	597	482	636	627	603	412	640	731
ENSMUSG00000064346	chrMT	mt-Tw	4950	5016	67	0.306530882	6.762458754	0.3171882	0.415977684	0.11134	0	1204	764	1096	2149	2229	1588	3541	1061	3070	3356
ENSMUSG00000033335	chr9	Dnm2	2.1E+07	2.1E+07	5330	0.177921662	5.704850168	0.3172718	0.416048395	0.03686	0	570	465	1053	744	958	1323	1159	796	1294	1182
ENSMUSG00000059430	chr6	Actg2	8.4E+07	8.4E+07	1562	0.483817276	-0.28977391	0.3173972	0.416173939	0.15423	0	6	10	11	12	4	24	6	12	23	20
ENSMUSG00000060126	chr14	Tpt1	7.6E+07	7.6E+07	2380	-0.19981198	10.58653494	0.3174537	0.416209214	0.04779	0	25469	19229	31409	23871	23527	36274	30920	22784	27393	31256
ENSMUSG00000031353	chrX	Rbbp7	1.6E+08	1.6E+08	2909	-0.18666597	6.718915523	0.3176038	0.416366981	0.04118	0	1634	1273	2183	1634	1749	2372	2331	1692	1854	1917
ENSMUSG00000001576	chr17	Ergic1	2.7E+07	2.7E+07	6456	0.199596015	5.574125269	0.3178171	0.416607772	0.04652	0	545	447	606	647	1157	1194	1039	794	1172	1065
ENSMUSG00000093157	chr6	Mir3098	1.3E+08	1.3E+08	87	-0.35166302	0.489061429	0.3179252	0.416710424	0.08943	0	20	8	33	24	29	27	25	11	29	28
ENSMUSG00000025407	chr10	Gli1	1.3E+08	1.3E+08	3665	0.286801926	1.205425067	0.3180844	0.416880242	0.0671	0	25	24	43	32	25	70	47	32	52	51
ENSMUSG00000004996	chr8	Mri1	8.4E+07	8.4E+07	3273	0.182984607	3.803557642	0.3181763	0.416944315	0.03546	0	171	139	205	208	263	312	313	224	342	333
ENSMUSG00000041741	chr6	Pde3a	1.4E+08	1.4E+08	10794	-0.25007957	2.786894883	0.3181928	0.416944315	0.06655	0	107	116	100	106	111	171	103	107	116	146
ENSMUSG00000056131	chr9	Pgm3	8.7E+07	8.7E+07	4487	0.26910179	1.777193426	0.3182263	0.416949291	0.0632	0	43	42	42	39	58	103	88	50	71	67
ENSMUSG00000022847	chr16	Thpo	2.1E+07	2.1E+07	1837	0.226398127	2.675210911	0.3182573	0.416950941	0.05238	0	59	59	135	89	105	176	136	98	165	130
ENSMUSG00000075307	chr2	Klhl41	7E+07	7E+07	2529	-0.21232621	9.748659393	0.318462	0.417180194	0.05414	0	13769	9769	19250	15717	11300	18958	19034	12981	14353	17248
ENSMUSG00000032295	chr9	Man2c1	5.7E+07	5.7E+07	7052	0.162725793	4.739855512	0.3187256	0.417486429	0.02983	0	317	240	471	389	519	631	551	420	633	681
ENSMUSG00000043488	chr19	Frmd8os	5845623	5845750	612	-0.3617181	0.390777701	0.3187981	0.417542398	0.10538	0	17	12	17	26	32	29	19	17	12	33
ENSMUSG00000041164	chr11	Zmiz2	6389074	6389140	4655	-0.1994209	5.831115644	0.3193874	0.418275188	0.04681	0	670	600	1302	1013	1109	970	1430	692	1303	1114
ENSMUSG00000079434	chr1	Neu2	8.8E+07	8.8E+07	2590	0.47633219	3.590347714	0.3194519	0.41832061	0.26228	0	231	157	26	110	181	324	110	404	357	168

ENSMUSG00000020087	chr10	Tysnd1	6.2E+07	6.2E+07	2286	0.178492079	4.221618651	0.3195832	0.418453511	0.03571	0	231	150	324	264	380	446	372	293	464	468
ENSMUSG00000022217	chr14	Emc9	5.6E+07	5.6E+07	2465	0.174329526	4.574996052	0.3196982	0.418565014	0.03444	0	313	196	479	325	414	624	444	344	613	601
ENSMUSG00000019878	chr10	Hsf2	5.7E+07	5.7E+07	2613	-0.1641569	4.48423981	0.320102	0.419015443	0.02962	0	316	243	477	367	397	450	530	332	437	426
ENSMUSG00000021884	chr14	Hacl1	3.2E+07	3.2E+07	5123	-0.22598187	3.108762563	0.3200745	0.419015443	0.05339	0	110	98	144	116	240	188	195	115	156	165
ENSMUSG00000068479	chr2	Mfap1a	1.2E+08	1.2E+08	4198	-0.19059719	3.964811865	0.3201651	0.419058994	0.03927	0	251	136	342	258	291	385	355	235	229	304
ENSMUSG00000022878	chr16	Adipoq	2.3E+07	2.3E+07	1381	-0.86126562	6.570223524	0.3203528	0.419172405	0.85152	0	1816	1159	12	47	6659	2407	408	1455	1416	1215
ENSMUSG00000030722	chr7	Nfatc2ip	1.3E+08	1.3E+08	3388	-0.26840269	2.086016236	0.3203709	0.419172405	0.0674	0	45	48	103	67	87	74	97	75	64	74
ENSMUSG00000035885	chr19	Cox8a	7215158	7215484	545	0.34957281	6.187599925	0.3203713	0.419172405	0.1466	0	812	355	786	487	2762	2228	1270	1349	1866	1730
ENSMUSG00000091086	chr10	Gm5428	1.1E+08	1.1E+08	888	0.202499884	4.080138417	0.3203352	0.419172405	0.04595	0	222	182	342	194	248	499	311	368	302	360
ENSMUSG00000051223	chr1	Bzw1	5.8E+07	5.8E+07	4033	-0.19517303	6.469975601	0.3204365	0.41921863	0.04562	0	1404	1282	1383	1398	1515	2091	1899	1375	1531	1658
ENSMUSG00000084384	chr11	Gm12251	5.8E+07	5.8E+07	792	0.212307788	3.578527428	0.3205066	0.41927112	0.05005	0	142	83	212	222	188	258	255	187	311	304
ENSMUSG00000031787	chr8	Katnb1	9.5E+07	9.5E+07	3425	-0.21705278	3.353002859	0.3207031	0.419489076	0.05069	0	141	94	249	173	187	202	274	121	214	168
ENSMUSG00000037570	chr15	Mcrs1	9.9E+07	9.9E+07	1915	0.158630195	4.825732374	0.3209593	0.419785017	0.02849	0	313	282	487	426	537	690	629	469	667	631
ENSMUSG00000003166	chr16	Dgcr2	1.8E+07	1.8E+07	6638	-0.16290415	5.469468871	0.3214331	0.420365569	0.03105	0	646	536	783	737	821	1005	915	626	900	891
ENSMUSG00000032578	chr9	Cish	1.1E+08	1.1E+08	6419	0.551950295	4.078592943	0.3215797	0.420518138	0.36157	0	27	23	423	142	564	266	871	246	404	289
ENSMUSG00000047539	chr1	Fbxo28	1.8E+08	1.8E+08	5318	-0.15750277	4.864968486	0.3218557	0.420839702	0.02835	0	450	341	548	500	469	649	663	410	560	574
ENSMUSG00000069045	chrY	Ddx3y	1260771	1263367	5199	-1.61268726	4.229331943	0.3219254	0.420891608	2.66349	0	5	0	1624	1	942	4	1000	1	1	1
ENSMUSG00000022126	chr14	Irg1	1E+08	1E+08	2623	0.546978597	0.093972486	0.3222129	0.421228277	0.31191	0	2	1	13	23	22	15	39	5	29	30
ENSMUSG00000037458	chr15	Azin1	3.8E+07	3.8E+07	6231	0.18062299	5.61429053	0.3225648	0.421609654	0.03865	0	642	502	913	688	736	1303	1208	992	946	882
ENSMUSG00000070738	chr1	Dgkd	8.8E+07	8.8E+07	6850	-0.16962563	5.831921784	0.3225567	0.421609654	0.03397	0	769	582	1178	929	1183	1261	1197	853	1059	1177
ENSMUSG00000000346	chr15	Dazap2	1E+08	1E+08	1826	0.189664448	6.662641413	0.3227065	0.421755661	0.04352	0	1306	809	2148	1390	1705	2728	2426	1604	2005	2483
ENSMUSG00000015711	chr3	Prune	9.5E+07	9.5E+07	3618	-0.18891843	6.850667843	0.3230501	0.422165311	0.0432	0	1825	1275	2470	2011	1739	2385	2507	1739	2227	2284
ENSMUSG00000097756	chr7	A730056A06Rik	7.3E+07	7.3E+07	2663	0.37912027	-0.0595023	0.3232003	0.422322323	0.10128	0	10	6	20	14	6	25	18	19	20	16
ENSMUSG00000024590	chr18	Lmnb1	5.7E+07	5.7E+07	2962	-0.21433122	2.786541798	0.3233141	0.42243159	0.04639	0	117	83	111	97	143	153	137	98	139	126
ENSMUSG00000038671	chr2	Arfrp1	1.8E+08	1.8E+08	4320	0.165453714	5.377013913	0.3236197	0.422791572	0.03229	0	542	371	815	565	720	1126	849	659	888	1041
ENSMUSG00000014791	chr8	Elmo3	1.1E+08	1.1E+08	3060	-0.26906561	1.660657361	0.3238177	0.423010801	0.06399	0	46	33	57	44	77	67	43	45	64	68
ENSMUSG00000036160	chr2	Surf6	2.7E+07	2.7E+07	4071	-0.1991212	3.296803702	0.3240503	0.423275187	0.0402	0	145	102	204	144	204	205	194	172	185	172
ENSMUSG00000025915	chr1	Sgk3	9798107	9798246	14311	-0.21943224	3.216017324	0.3240905	0.42328835	0.05291	0	125	121	212	145	146	259	228	111	137	162
ENSMUSG00000025066	chr19	Sfr1	4.8E+07	4.8E+07	1583	0.179071943	6.060994241	0.3241935	0.423383447	0.03842	0	920	742	1006	890	1144	1797	1469	1200	1336	1518
ENSMUSG00000052488	chr8	Cherp	7.2E+07	7.2E+07	3794	-0.16136512	4.502694545	0.3245314	0.423785305	0.02932	0	312	234	456	396	428	491	516	288	473	458
ENSMUSG00000041143	chr4	Tmco4	1.4E+08	1.4E+08	3596	0.195330674	3.558453	0.3246278	0.42384896	0.04179	0	139	108	243	176	169	277	321	188	289	218
ENSMUSG00000042293	chr9	Gm5617	4.8E+07	4.8E+07	620	0.25533932	2.561926983	0.3246406	0.42384896	0.07346	0	67	31	128	69	125	166	107	105	136	138
ENSMUSG00000037408	chr1	Cnnm4	3.6E+07	3.6E+07	4829	-0.24895098	3.526356328	0.3247846	0.423997494	0.06973	0	176	85	310	257	134	237	238	161	200	247
ENSMUSG00000009281	chr6	Rarres2	4.9E+07	4.9E+07	708	0.459211071	6.126456094	0.3248588	0.424054921	0.25595	0	631	608	270	283	2843	2667	876	1318	1764	1789
ENSMUSG00000052135	chr4	Foxo6	1.2E+08	1.2E+08	2615	0.236013959	3.006558204	0.3250663	0.424286188	0.06367	0	113	51	179	95	132	148	184	163	184	193
ENSMUSG00000037846	chr10	Rtkn2	6.8E+07	6.8E+07	5547	0.423135251	0.62010486	0.3253525	0.42454121	0.16554	0	14	17	10	8	43	38	45	27	38	20
ENSMUSG00000098188	chr10	Sowahc	5.9E+07	5.9E+07	4482	-0.4838561	2.143841492	0.3253355	0.42454121	0.26785	0	103	53	24	13	193	104	75	63	59	73
ENSMUSG00000103578	chr10	Septin10	5.9E+07	5.9E+07	4477	-0.4838561	2.143841492	0.3253375	0.42454121	0.26785	0	103	53	24	13	193	104	75	63	59	73
ENSMUSG00000045180	chrX	Shroom2	1.5E+08	1.5E+08	8375	-0.43021992	0.397366032	0.3254289	0.424601496	0.1739	0	21	10	40	31	5	32	25	13	16	23
ENSMUSG00000051413	chr2	Plagl2	1.5E+08	1.5E+08	5735	-0.20843238	2.846041733	0.3255529	0.424684295	0.04636	0	96	100	138	111	126	144	168	101	129	140
ENSMUSG00000073758	chr4	Sh3d21	1.3E+08	1.3E+08	2717	0.36227507	0.653494624	0.3255393	0.424684295	0.12596	0	16	9	24	11	40	55	20	24	31	41
ENSMUSG00000020962	chr12	Gtf2a1	9.2E+07	9.2E+07	5587	-0.17821424	4.281381899	0.3256614	0.424778976	0.03591	0	302	229	334	256	441	399	465	311	333	364
ENSMUSG00000045294	chr5	Insig1	2.8E+07	2.8E+07	2697	-0.30817353	4.707513002	0.3256861	0.424778976	0.1142	0	396	226	279	235	1144	640	543	361	419	463
ENSMUSG00000029050	chr4	Ski	1.6E+08	1.6E+08	5562	0.175617414	6.197104088	0.3257432	0.424813916	0.03732	0	935	760	1139	1078	1303	1803	1769	1238	1665	1572
ENSMUSG00000029198	chr5	Grpel1	3.6E+07	3.6E+07	3528	-0.1800955	6.455573934	0.3258561	0.424921701	0.03942	0	1257	851	1929	1498	1651	1858	1911	1287	1679	1784
ENSMUSG00000024187	chr17	Itfg3	2.6E+07	2.6E+07	3981	0.212487677	6.567892621	0.3263899	0.425578156	0.05556	0	1035	675	2263	1570	1342	2311	2315	1383	2232	2378
ENSMUSG00000037070	chr8	Rbmxl1	7.9E+07	7.9E+07	1723	0.212866725	2.792185662	0.3265053	0.425689133	0.04543	0	93	75	106	91	110	189	140	130	144	151
ENSMUSG00000041506	chr9	Rrp9	1.1E+08	1.1E+08	2788	0.173806517	4.057033109	0.3266184	0.425796932	0.03434	0	195	151	316	239	296	412	325	299	416	354
ENSMUSG00000040048	chr17	Ndufb10	2.5E+07	2.5E+07	1217	0.229446224	8.248710375	0.3268698	0.426085136	0.06534	0	3035	2084	7528	5191	4218	7179	6933	5006	7099	7784
ENSMUSG00000029165	chr5	Agbl5	3.1E+07	3.1E+07	7053	-0.27850185	1.830085058	0.3269893	0.426201302	0.08214	0	48	59	71	51	52	69	90	30	61	80
ENSMUSG00000027858	chr3	Tspan2	1E+08	1E+08	4585	-0.19802223	3.233012171	0.3271598	0.426383829	0.04135	0	148	93	187	128	210	230	174	134	169	195
ENSMUSG00000046667	chr4	Rbm12b1	1.2E+07	1.2E+07	3122	0.30220661	1.218424995	0.3272149	0.426416041	0.07947	0	37	23	21	32	34	52	60	43	54	42
ENSMUSG00000046404	chr1	Yod1	1.3E+08	1.3E+08	6128	-0.25765333	2.175332915	0.3275084	0.426758895	0.0656	0	88	38	82	56	107	113	87	61	70	89
ENSMUSG00000038239	chr7	Hrc	4.5E+07	4.5E+07	2410	-0.20316666	10.13250466	0.3275482	0.426771178	0.05149	0	17356	12281	24465	19619	17703	19509	25169	15827	24763	22520
ENSMUSG00000032827	chr6	Ppp1r9a	4902917	4903031	14531	0.322477705	1.737504102	0.3275866	0.426781445	0.1043	0	39	39	28	28	81	110	63	62	70	66
ENSMUSG00000028792	chr4	Ak2	1.3E+08	1.3E+08	2140	0.282558823	5.372190328	0.3276292	0.426797302	0.09812	0	548	321	431	341	1276	1123	596	850	1072	997
ENSMUSG00000020654	chr12	Adcy3	4133103	4133778	6246	0.365285853	2.994794874	0.3276943	0.426802869	0.15816	0	104	59	55	43	277	241	156	152	158	207
ENSMUSG00000027551	chr2	Zfp64	1.7E+08	1.7E+08	5918	-0.21197297	2.806374371	0.3276938	0.426802869	0.0472	0	108	83	139	99	133	128	120	109	150	149
ENSMUSG00000027655	chr2	Dhx35	1.6E+08	1.6E+08	5170	-0.20623113	3.867332369	0.3279674	0.427118871	0.0484	0	167	149	428	237	229	342	323	177	278	292
ENSMUSG00000051346	chr10	Spryd4	1.3E+08	1.3E+08	1570	-0.18250526	5.206420336	0.328015	0.427141279	0.03966	0	461	361	978	663	572	743	840	543	711	734
ENSMUSG00000017670	chr2	Elmo2	1.7E+08	1.7E+08	6652	-0.16414124	4.692052857	0.3282138	0.427360498	0.03155	0	373	325	436	342	587	656	533	358	499	490
ENSMUSG00000022554	chr15	Hgh1	7.6E+07	7.6E+07	1959	0.243847032	2.128660701	0.3283391	0.427483898	0.06381	0	40	32	85	59	89	109	82	76	99	111
ENSMUSG00000036882	chr7	Arhgap33	3.1E+07	3.1E+07	4280	0.484267068	0.109513085	0.3287208	0.427941109	0.19412	0	16	7	5	4	29	36	18	12	19	33
ENSMUSG00000025104	chr7	Hdgfrp3	8.2E+07	8.2E+07	9575	0.232943395	2.258912772	0.3289786	0.428186928	0.05403	0	56	45	77	64	86	152	99	85	81	108
ENSMUSG00000030889	chr7	Vwa3a	1.2E+08	1.2E+08	5821	0.329446881	0.838025307	0.3290183	0.428186928	0.09253	0	17	15	23	17	42	49	48	20	30	49
ENSMUSG00000044600	chr8	Smim7	7.3E+07	7.3E+07	3266	0.171758999	5.942992149	0.3290317	0.428186928	0.036	0	859	655	1078	766	1020	1630	1311	1099	1406	1276
ENSMUSG00000056673	chrY	Kdm5d	897788	898115	15164	-1.52077155	1.756778422	0.3290013	0.428186928	2.44724	0	0	0	277	2	158	0	181	0	1	0

ENSMUSG00000046032	chrX	Snx12	1E+08	1E+08	2953	-0.17792204	4.919787272	0.3296434	0.428943108	0.03748	0	389	322	796	432	545	661	760	443	584	492
ENSMUSG00000042814	chr2	Mcts2	1.5E+08	1.5E+08	917	0.222000675	2.689631784	0.3299991	0.42936617	0.05278	0	74	58	135	71	115	152	125	125	133	165
ENSMUSG00000055491	chr19	Pprc1	4.6E+07	4.6E+07	7516	-0.16421554	4.424900034	0.3300794	0.429430028	0.03087	0	284	255	458	344	379	487	374	350	448	418
ENSMUSG00000087165	chr11	2010001A14Rik	5.8E+07	5.8E+07	714	0.355799342	0.775018236	0.3301094	0.429430028	0.12069	0	18	10	13	23	44	48	36	35	24	41
ENSMUSG00000098789	chr2	Jmjd7	1.2E+08	1.2E+08	1960	0.282539712	1.53723135	0.3302057	0.429515427	0.08191	0	30	15	64	33	57	70	75	45	51	77
ENSMUSG00000021891	chr14	Mettl6	3.1E+07	3.1E+07	2436	0.20075278	3.145835788	0.3310869	0.430621757	0.04319	0	133	84	132	131	133	234	183	168	184	193
ENSMUSG00000078902	chr2	Gm14443	1.8E+08	1.8E+08	4859	-0.40127719	-0.05248422	0.331173	0.430693771	0.11949	0	26	9	17	9	13	12	13	14	18	19
ENSMUSG00000029535	chr5	Triap1	1.2E+08	1.2E+08	1088	0.177591909	4.416007566	0.3316711	0.431266581	0.03677	0	320	231	318	236	400	609	446	388	482	406
ENSMUSG00000046605	chr11	B3gntl1	1.2E+08	1.2E+08	3518	-0.25575023	1.525377528	0.3316749	0.431266581	0.06248	0	39	38	49	52	49	80	50	34	48	54
ENSMUSG00000046962	chr16	Zbtb21	9.8E+07	9.8E+07	6010	-0.21962594	2.639837092	0.3318509	0.43145545	0.0497	0	90	56	128	110	125	126	141	85	98	139
ENSMUSG00000028221	chr4	Tmem55a	1.5E+07	1.5E+07	2339	-0.15769807	4.765821513	0.3319066	0.431466944	0.02905	0	410	257	575	467	489	666	595	404	496	505
ENSMUSG00000034889	chr10	Cactin	8.1E+07	8.1E+07	2724	0.176280956	4.190204482	0.3319213	0.431466944	0.03605	0	188	195	350	270	297	378	412	305	458	431
ENSMUSG00000018906	chr11	P4ha2	5.4E+07	5.4E+07	6239	0.171649528	5.125351344	0.332046	0.431589028	0.03552	0	370	350	673	613	487	974	803	511	817	753
ENSMUSG00000021483	chr13	Cdk20	6.4E+07	6.4E+07	1826	0.257649277	2.224311708	0.332167	0.431706248	0.06659	0	65	56	48	57	82	139	95	88	90	101
ENSMUSG00000097842	chr7	9330104G04Rik	1.7E+07	1.7E+07	2235	0.308621485	0.752229636	0.3322628	0.431790734	0.07389	0	20	15	19	22	30	48	35	20	45	34
ENSMUSG00000021215	chr13	Net1	3882565	3884473	3734	0.201852516	5.981505516	0.3323231	0.431829082	0.051	0	928	600	1061	605	1315	1636	1334	1343	1156	1425
ENSMUSG00000026155	chr1	Smap1	2.4E+07	2.4E+07	3575	0.170476834	4.138023857	0.3324941	0.431971266	0.03399	0	217	142	293	261	361	474	399	280	371	406
ENSMUSG00000027111	chr2	Itga6	7.2E+07	7.2E+07	9025	-0.206083	4.785137852	0.3324679	0.431971266	0.05086	0	321	209	770	415	632	704	574	445	445	476
ENSMUSG00000053646	chr9	Plxnb1	1.1E+08	1.1E+08	9545	0.272977905	1.210514155	0.3328107	0.432342593	0.06173	0	29	23	41	26	32	56	67	36	47	44
ENSMUSG00000031029	chr7	Eif3f	1.1E+08	1.1E+08	2891	0.190718394	7.322629433	0.3331276	0.432714243	0.04612	0	1797	1428	2808	2645	2812	3807	3377	2526	3882	4102
ENSMUSG00000020218	chr10	Wif1	1.2E+08	1.2E+08	2427	-0.37330374	2.546433416	0.3333467	0.432958676	0.16397	0	56	36	186	173	59	164	115	66	51	133
ENSMUSG00000097978	chr5	Gm5864	3.2E+07	3.2E+07	970	0.653000747	0.718286978	0.3335372	0.433165956	0.48154	0	5	1	47	41	1	25	42	23	36	65
ENSMUSG00000053841	chr4	Txlna	1.3E+08	1.3E+08	5348	0.157562548	4.903586352	0.3336796	0.433310749	0.02933	0	357	325	531	452	471	851	640	428	720	655
ENSMUSG00000051355	chr11	Commd1	2.3E+07	2.3E+07	5936	0.171599601	5.875965395	0.3337602	0.433375414	0.03657	0	760	661	1074	779	890	1535	1153	1093	1317	1296
ENSMUSG00000056076	chr5	Eif3b	1.4E+08	1.4E+08	2966	0.186421628	6.855304471	0.3341352	0.433822072	0.04416	0	1356	958	2276	1873	1911	2703	2586	1988	2751	2686
ENSMUSG00000000743	chr8	Chmp1a	1.2E+08	1.2E+08	3260	0.17318947	6.311692178	0.3343073	0.434005389	0.03777	0	999	740	1483	1160	1340	1942	1851	1221	1954	1778
ENSMUSG00000031385	chrX	Plxnb3	7.4E+07	7.4E+07	6493	-0.40048194	1.154556622	0.3345518	0.434282611	0.16997	0	23	12	92	47	19	45	44	20	40	43
ENSMUSG00000087138	chr7	Gm15545	4.5E+07	4.5E+07	1976	0.287156009	1.012911774	0.3348961	0.434689262	0.06925	0	21	16	31	30	33	52	44	33	31	57
ENSMUSG00000048970	chrX	C1galt1c1	3.9E+07	3.9E+07	1449	-0.20605267	3.451612474	0.3349295	0.434692446	0.04989	0	209	145	177	138	196	288	235	161	186	179
ENSMUSG00000030417	chr7	Pdcd5	3.6E+07	3.6E+07	2486	-0.16472449	5.823506945	0.3351594	0.43495058	0.0339	0	869	641	1085	981	944	1229	1169	841	1138	1144
ENSMUSG00000026878	chr2	Rab14	3.5E+07	3.5E+07	5431	-0.1744089	6.614279686	0.3352333	0.435006213	0.03855	0	1405	1041	2037	1653	1808	2260	2136	1456	1747	1950
ENSMUSG00000066900	chr5	Suds3	1.2E+08	1.2E+08	2418	-0.18092153	6.459382519	0.3356651	0.435526198	0.04152	0	1267	886	2015	1523	1491	1870	1991	1195	1872	1646
ENSMUSG00000048878	chr11	Hexim1	1E+08	1E+08	3495	0.178383829	5.26307796	0.3357861	0.435642924	0.03964	0	449	381	564	478	888	948	753	710	864	907
ENSMUSG00000026342	chr1	Slc35f5	1.3E+08	1.3E+08	2956	-0.19068998	4.998047009	0.3358563	0.435693773	0.04457	0	436	269	884	529	544	688	858	433	537	589
ENSMUSG00000044894	chr11	Uqcrq	5.3E+07	5.3E+07	1831	0.209408337	8.526616307	0.3359182	0.435733765	0.05653	0	4566	2608	8012	6195	5264	8451	8510	5786	9529	8740
ENSMUSG00000043572	chr4	Pars2	1.1E+08	1.1E+08	3094	-0.24347884	2.174185832	0.3360525	0.435827328	0.06147	0	44	47	101	84	94	94	98	60	95	73
ENSMUSG00000068921	chr3	Dap3	8.9E+07	8.9E+07	6483	-0.1581101	5.258915982	0.3360226	0.435827328	0.03063	0	585	383	830	665	619	882	803	540	760	772
ENSMUSG00000025235	chr9	Bbs4	5.9E+07	5.9E+07	2542	-0.23490875	3.002031861	0.3360951	0.435842298	0.06344	0	113	109	163	106	156	240	194	98	97	140
ENSMUSG00000023110	chr14	Prmt5	5.5E+07	5.5E+07	3958	-0.16431093	5.471014653	0.3361513	0.43587481	0.03357	0	627	527	757	798	818	972	940	690	912	798
ENSMUSG00000016933	chr2	Plcg1	1.6E+08	1.6E+08	7857	0.171926657	5.151978047	0.3364934	0.436278035	0.03703	0	423	289	728	413	761	871	819	565	743	905
ENSMUSG00000017802	chr11	Fam134c	1E+08	1E+08	3589	-0.16572003	5.940471479	0.336552	0.436299986	0.0346	0	866	720	1245	1004	1089	1314	1371	908	1209	1187
ENSMUSG00000026914	chr2	Psmd14	6.2E+07	6.2E+07	2820	-0.17089593	5.755340102	0.3366347	0.436299986	0.03674	0	812	644	1046	871	945	1317	1240	864	917	917
ENSMUSG00000039850	chr11	Endov	1.2E+08	1.2E+08	6138	-0.20818458	2.942802933	0.3366115	0.436299986	0.04789	0	124	84	166	105	143	205	153	111	111	155
ENSMUSG00000052798	chr10	Nup107	1.2E+08	1.2E+08	3111	-0.19892296	3.037222917	0.3365904	0.436299986	0.0446	0	131	103	152	131	134	203	167	106	132	182
ENSMUSG00000072647	chr5	Adam1a	1.2E+08	1.2E+08	3120	0.366945884	0.458894569	0.3368188	0.436498248	0.10706	0	15	12	11	16	29	45	33	14	21	37
ENSMUSG00000044854	chr1	1700056E22Rik	1.8E+08	1.8E+08	1272	0.427855758	0.020793685	0.3371319	0.436863664	0.17701	0	5	4	19	6	27	43	17	10	21	18
ENSMUSG00000034520	chr11	Gjc1	1E+08	1E+08	5003	0.275192509	2.315554666	0.3371681	0.436870173	0.08901	0	44	40	85	48	129	157	106	103	74	109
ENSMUSG00000039470	chr8	Zdhhc2	4E+07	4E+07	5528	-0.32005354	1.629168955	0.3372464	0.43693125	0.10533	0	48	29	49	31	102	72	57	55	36	53
ENSMUSG00000045333	chr8	Zfp423	8.8E+07	8.8E+07	5608	-0.19544224	3.692946076	0.3373052	0.436967074	0.04358	0	152	117	254	217	329	272	271	183	245	271
ENSMUSG00000063800	chr4	Prpf38a	1.1E+08	1.1E+08	5298	0.178767188	3.627141164	0.3374889	0.437164709	0.03677	0	144	123	224	173	214	323	247	241	249	276
ENSMUSG00000070699	chr7	Sars2	2.9E+07	2.9E+07	1910	-0.18438066	3.982917038	0.3376205	0.437294716	0.03956	0	239	133	363	271	291	336	346	205	370	276
ENSMUSG00000040253	chr3	Gbp7	1.4E+08	1.4E+08	5552	-0.33015758	3.170313891	0.3376706	0.437319318	0.13533	0	153	112	187	145	151	383	199	61	62	162
ENSMUSG00000041625	chr14	Ggact	1.2E+08	1.2E+08	1988	-0.19839197	3.188384427	0.3377286	0.437353958	0.04368	0	137	92	179	147	184	200	234	104	167	177
ENSMUSG00000078974	chr11	Sec61g	1.7E+07	1.7E+07	2464	0.167902741	5.191181162	0.3379205	0.437562168	0.03455	0	529	439	530	481	575	1026	705	638	862	759
ENSMUSG00000031174	chrX	Rpgr	1E+07	1E+07	7247	0.255934953	1.583593879	0.338099	0.437752896	0.06291	0	32	28	42	49	48	73	87	51	53	61
ENSMUSG00000020807	chr11	4933427D14Rik	7.2E+07	7.2E+07	5697	0.271699068	1.623748629	0.3381958	0.437837806	0.07332	0	45	28	38	32	61	83	52	65	67	65
ENSMUSG00000052291	chr10	5330438D12Rik	1.2E+08	1.2E+08	2229	0.425085345	-0.14701022	0.3382306	0.43784243	0.13411	0	9	9	9	4	20	29	11	18	14	21
ENSMUSG00000070867	chr4	Trabd2b	1.1E+08	1.1E+08	6617	0.390308386	3.084921556	0.3385059	0.43815832	0.18567	0	81	140	62	32	215	307	111	178	193	192
ENSMUSG00000038175	chr13	Mylip	4.5E+07	4.5E+07	3062	-0.23867649	4.179722835	0.3386784	0.438341128	0.07121	0	330	249	189	223	461	414	469	262	239	338
ENSMUSG00000089671	chr15	Gm16537	1E+08	1E+08	702	0.501052037	0.445099783	0.3388694	0.43854794	0.30063	0	6	1	42	14	22	16	19	14	49	51
ENSMUSG00000016308	chrX	Ube2a	3.7E+07	3.7E+07	1662	-0.1456442	4.854346145	0.3390635	0.438720279	0.02578	0	440	344	547	440	519	685	603	427	572	556
ENSMUSG00000051669	chr16	AU021092	5211828	5212212	1363	0.312268819	0.615568776	0.3390652	0.438720279	0.08931	0	10	11	28	29	19	32	37	25	31	37
ENSMUSG00000097047	chr17	1110020A21Rik	8.5E+07	8.5E+07	853	0.292005434	0.886977846	0.3391128	0.438741497	0.07424	0	31	13	30	17	28	48	41	34	32	42
ENSMUSG00000030199	chr6	Etv6	1.3E+08	1.3E+08	5983	0.211996991	3.522878222	0.3393345	0.438987814	0.05497	0	114	82	264	183	184	302	263	232	200	258
ENSMUSG00000029911	chr6	Ssbp1	4E+07	4E+07	3319	0.15451706	4.755111941	0.3397217	0.439413506	0.02931	0	363	247	475	387	478	755	576	509	540	544
ENSMUSG00000047044	chr19	D030056L22Rik	1.9E+07	1.9E+07	1677	0.21275077	2.642506859	0.3397262	0.439413506	0.04707	0	78	71	116	69	96	177	136	91	140	144
ENSMUSG00000000171	chr9	Sdhd	5.1E+07	5.1E+07	1287	-0.20297422	8.459923467	0.3398506	0.439533843	0.0539	0	4894	3194	9362	6231	5638	7420	7815	5565	6238	6729

ENSMUSG00000045160	chr6	Bola3	8.3E+07	8.3E+07	3211	-0.18425307	6.470294983	0.3400247	0.439718507	0.04385	0	1274	846	2092	1583	1475	1759	1996	1217	1760	1879
ENSMUSG00000048109	chr3	Rbm15	1.1E+08	1.1E+08	3270	-0.19157253	3.356454357	0.3400847	0.439728831	0.04205	0	170	116	179	179	170	217	171	165	198	223
ENSMUSG00000091780	chr15	Sco2	8.9E+07	8.9E+07	1143	0.219643539	3.751897755	0.3400954	0.439728831	0.05984	0	134	96	361	200	182	308	281	211	346	344
ENSMUSG00000022472	chr15	Desi1	8.2E+07	8.2E+07	3635	0.16094934	4.17409375	0.3401828	0.43980127	0.03063	0	248	160	325	263	302	466	402	266	445	397
ENSMUSG00000046756	chr11	Mrps7	1.2E+08	1.2E+08	2072	-0.17562345	6.215098029	0.3402236	0.439813474	0.0397	0	1017	775	1573	1314	1357	1507	1567	1011	1680	1471
ENSMUSG00000030881	chr7	Arfip2	1.1E+08	1.1E+08	4902	0.212065344	3.389609736	0.3408484	0.440580529	0.05265	0	128	117	133	115	235	296	209	193	207	245
ENSMUSG00000003476	chr6	Crhr2	5.5E+07	5.5E+07	5112	-0.20380363	5.228122288	0.3408864	0.440589138	0.05262	0	520	326	1027	758	471	730	724	628	714	764
ENSMUSG00000032127	chr9	Vps11	4.4E+07	4.4E+07	3179	-0.15196279	5.022573846	0.3409867	0.440674868	0.02846	0	473	320	715	524	595	727	703	416	657	706
ENSMUSG00000034724	chr5	Cnot6l	9.6E+07	9.6E+07	10313	-0.16411438	4.439063892	0.3410156	0.440674868	0.03258	0	315	220	462	351	405	505	516	283	341	487
ENSMUSG00000019088	chrX	Dnase1l1	7.4E+07	7.4E+07	2121	-0.20579493	6.665658022	0.3411917	0.440861759	0.05545	0	2020	1433	1373	1385	1763	2140	2014	1401	2226	1998
ENSMUSG00000021622	chr13	Ckmt2	9.2E+07	9.2E+07	1486	-0.37305256	10.7096575	0.341707	0.441413161	0.18267	0	17574	6305	79384	35056	17746	29868	45110	19428	25778	32431
ENSMUSG00000029500	chr5	Pgam5	1.1E+08	1.1E+08	2373	-0.15340891	5.197935956	0.3417128	0.441413161	0.02949	0	508	449	738	607	612	769	723	574	726	783
ENSMUSG00000083477	chr5	Gm5555	5E+07	5E+07	1014	0.371417132	0.190772994	0.3416722	0.441413161	0.11111	0	14	5	8	21	20	23	25	19	30	22
ENSMUSG00000029033	chr4	Acap3	1.6E+08	1.6E+08	5367	0.17300394	3.795140282	0.3418077	0.441495019	0.03548	0	145	140	260	183	268	333	313	242	313	306
ENSMUSG00000084093	chr1	Gm16418	1.7E+08	1.7E+08	171	0.257094566	2.057625396	0.341903	0.441577431	0.07053	0	52	28	64	79	59	94	78	68	116	99
ENSMUSG00000046636	chr18	Gm7729	2.8E+07	2.8E+07	801	0.27937536	0.785350385	0.341942	0.441587174	0.06601	0	17	17	34	18	25	40	39	30	33	40
ENSMUSG00000021819	chr14	Zswim8	2.1E+07	2.1E+07	6072	-0.15187375	5.101605009	0.3422957	0.4420033	0.0288	0	432	383	687	631	614	742	760	481	678	711
ENSMUSG00000060450	chr18	Rnf14	3.8E+07	3.8E+07	3515	-0.17599832	6.715546855	0.3424514	0.442163553	0.04061	0	1670	1305	1993	1584	1835	2331	2441	1545	2045	1871
ENSMUSG00000036944	chr15	Tmem71	6.7E+07	6.7E+07	2931	0.316120855	1.322793587	0.3426533	0.442383578	0.09854	0	29	34	30	26	38	76	43	50	32	72
ENSMUSG00000035203	chr7	Epn1	5080235	5080477	2807	-0.21046367	7.406612545	0.342789	0.442518033	0.05845	0	2068	1541	4377	3129	3097	3094	4180	2022	3900	3212
ENSMUSG00000028862	chr4	Map3k6	1.3E+08	1.3E+08	4604	0.301525325	1.955014729	0.3429588	0.442666112	0.10383	0	36	28	54	31	117	105	108	60	76	84
ENSMUSG00000045795	chr7	Whamm	8.2E+07	8.2E+07	3069	-0.18829589	3.320477612	0.3429668	0.442666112	0.04076	0	146	105	170	162	222	236	167	146	206	204
ENSMUSG00000080772	chr4	Gm12543	6E+07	6E+07	543	0.323752168	0.408814185	0.3434949	0.443306845	0.08394	0	17	7	18	15	26	39	27	26	24	23
ENSMUSG00000042978	chr7	Sbk1	1.3E+08	1.3E+08	4092	-0.17888269	5.474957489	0.3436681	0.443489596	0.04093	0	609	381	889	687	1121	904	1013	625	935	843
ENSMUSG00000049904	chr11	Tmem17	2.3E+07	2.3E+07	1568	-0.23832077	1.846869871	0.3437352	0.443535404	0.05788	0	63	47	55	51	67	80	70	57	59	65
ENSMUSG00000062198	chr12	2700097O09Rik	5.5E+07	5.5E+07	4939	-0.22636276	2.670391823	0.3438088	0.443589547	0.05944	0	105	93	123	74	110	167	118	73	102	148
ENSMUSG00000031639	chr8	Tlr3	4.5E+07	4.5E+07	4396	0.264491097	1.898770376	0.3438966	0.443662092	0.07494	0	40	32	69	35	79	130	81	45	72	90
ENSMUSG00000037031	chr10	Tspan15	6.2E+07	6.2E+07	3605	0.234212945	3.544492058	0.3439641	0.443708365	0.06876	0	162	75	168	112	319	335	288	171	258	257
ENSMUSG00000016087	chr9	Fli1	3.2E+07	3.2E+07	3486	0.204595672	3.13611698	0.3440902	0.4438301	0.05085	0	89	70	181	124	165	218	192	182	176	183
ENSMUSG00000020783	chr11	1200014J11Rik	7.3E+07	7.3E+07	8140	0.195939102	3.434978062	0.3443566	0.444132902	0.04516	0	170	102	200	141	143	316	199	192	225	252
ENSMUSG00000024761	chr19	Gm16437	7668287	7668793	507	-0.3218751	0.944580427	0.3447901	0.444612458	0.10271	0	36	26	45	24	21	24	51	26	36	30
ENSMUSG00000095588	chr4	Gm12350	3.4E+07	3.4E+07	462	0.172401024	3.684489511	0.3447918	0.444612458	0.03499	0	169	116	248	188	197	356	313	211	256	270
ENSMUSG00000028218	chr4	Fam92a	1.2E+07	1.2E+07	4683	0.226881802	2.817185951	0.3449353	0.444727469	0.05733	0	101	80	119	82	97	201	169	145	112	142
ENSMUSG00000039307	chr11	Hexdc	1.2E+08	1.2E+08	4723	-0.19721378	3.095924556	0.3449444	0.444727469	0.04544	0	139	114	157	100	170	201	182	114	169	155
ENSMUSG00000030037	chr6	Mrpl53	8.3E+07	8.3E+07	735	0.164173687	5.835467576	0.3450679	0.444845844	0.03506	0	778	558	1024	895	823	1348	1279	962	1340	1297
ENSMUSG00000019647	chr18	Sema6a	4.7E+07	4.7E+07	8778	0.175311081	3.567326519	0.3451025	0.444849464	0.03657	0	167	100	210	162	208	277	268	215	239	284
ENSMUSG00000044807	chr11	Zfp354c	5.1E+07	5.1E+07	5596	-0.28643203	2.255396246	0.3452172	0.444956494	0.09973	0	104	82	60	55	70	143	86	67	77	69
ENSMUSG00000026927	chr2	Sdccag3	2.6E+07	2.6E+07	3587	0.157670126	4.802085874	0.3454848	0.445206024	0.03121	0	316	286	430	400	575	750	616	481	543	648
ENSMUSG00000073131	chrX	Vma21	7.2E+07	7.2E+07	7303	-0.1552946	4.987794962	0.3455378	0.445206024	0.03067	0	562	371	545	475	551	648	748	459	631	616
ENSMUSG00000090330	chr7	9130221H12Rik	2.5E+07	2.5E+07	1577	0.205742631	2.834300177	0.3454555	0.445206024	0.04806	0	87	64	125	98	126	143	153	118	166	195
ENSMUSG00000100691	chr8	2010320M18Rik	7.1E+07	7.1E+07	1009	0.177223196	3.767691179	0.3455063	0.445206024	0.03783	0	173	132	243	175	248	360	234	245	317	323
ENSMUSG00000029060	chr4	Mib2	1.6E+08	1.6E+08	4724	-0.15700137	4.742816179	0.3457094	0.445386254	0.0312	0	365	341	468	464	475	539	562	352	625	544
ENSMUSG00000089665	chr8	Fcor	3671188	3671396	366	-0.73963638	1.309146778	0.3457594	0.445409715	0.68046	0	30	26	2	5	176	73	7	31	58	16
ENSMUSG00000099143	chr7	Gm27483	1.4E+08	1.4E+08	71	0.863659707	0.470908017	0.3458867	0.445532848	0.88655	0	0	0	46	24	4	4	27	3	66	68
ENSMUSG00000025016	chr19	Tm9sf3	4.1E+07	4.1E+07	6144	-0.17713926	6.850285387	0.3461193	0.445791476	0.04182	0	1981	1337	2093	1658	2180	2696	2634	1682	2025	2220
ENSMUSG00000014301	chr16	Pam16	4616464	4616633	857	0.147360113	4.85412158	0.3464072	0.446090685	0.02735	0	379	282	540	376	519	686	602	493	684	662
ENSMUSG00000030763	chr7	Lcmt1	1.2E+08	1.2E+08	1369	-0.1526055	4.809543055	0.3464152	0.446090685	0.02934	0	455	337	475	444	499	606	554	439	615	516
ENSMUSG00000020888	chr11	Dvl2	7E+07	7E+07	6298	0.24186361	3.289838144	0.3469932	0.446793978	0.07138	0	88	100	252	121	124	217	203	125	237	313
ENSMUSG00000027845	chr3	Dclre1b	1E+08	1E+08	8152	-0.24525408	1.749357202	0.3470694	0.446851107	0.05933	0	39	38	70	57	67	67	76	42	50	76
ENSMUSG00000005510	chr2	Ndufs3	9.1E+07	9.1E+07	2178	-0.18689153	8.251592929	0.3471513	0.446915425	0.04709	0	4470	3149	7318	5124	4862	6125	6677	4430	6161	6106
ENSMUSG00000056019	chr8	Zfp709	7.2E+07	7.2E+07	4234	-0.29238115	0.776380725	0.34732	0.447091637	0.07678	0	28	19	29	22	37	40	36	14	25	38
ENSMUSG00000014243	chr11	Zswim7	6.2E+07	6.2E+07	732	-0.15527824	4.523590054	0.3477178	0.447562622	0.02971	0	331	237	484	332	475	475	530	314	505	429
ENSMUSG00000040836	chr1	Gpr161	1.7E+08	1.7E+08	6962	0.283878783	1.188676652	0.3478021	0.447629986	0.06989	0	22	25	31	32	37	71	52	39	49	36
ENSMUSG00000023068	chr10	Nus1	5.2E+07	5.2E+07	4876	-0.15759295	5.41839223	0.3478513	0.447652274	0.03217	0	611	471	901	660	799	971	1016	660	740	794
ENSMUSG00000027438	chr2	Napb	1.5E+08	1.5E+08	7051	-0.23260296	3.244769117	0.3479845	0.447741534	0.06819	0	154	164	128	135	155	243	199	139	121	197
ENSMUSG00000103735	chr3	RP23-187F18.1	1.3E+07	1.3E+07	343	0.338412033	0.046675062	0.3479703	0.447741534	0.07972	0	10	9	17	8	18	21	24	15	28	18
ENSMUSG00000080896	chrX	Gm14567	3.9E+07	3.9E+07	174	0.399650435	0.345805887	0.3482706	0.448068612	0.13705	0	20	13	5	9	27	29	30	24	28	24
ENSMUSG00000057177	chr7	Gsk3a	2.5E+07	2.5E+07	2260	-0.17807606	6.777176764	0.3484437	0.448250109	0.04257	0	1600	1126	2207	1936	2037	2025	2325	1534	2325	2433
ENSMUSG00000009927	chr9	Rps25	4.4E+07	4.4E+07	683	0.184250787	7.998736899	0.3487286	0.448534382	0.04601	0	3625	2826	4042	3465	4016	6696	4798	4573	5894	6112
ENSMUSG00000026260	chr1	Ndufa10	9.2E+07	9.2E+07	3331	-0.22819128	8.41991981	0.3487155	0.448534382	0.07066	0	4439	2531	10155	6774	5258	6320	8125	4823	6511	6872
ENSMUSG00000020716	chr11	Nf1	7.9E+07	7.9E+07	15820	-0.14796075	4.551172866	0.3488181	0.448608349	0.02723	0	329	269	469	394	402	484	523	335	471	484
ENSMUSG00000017713	chr11	Tha1	1.2E+08	1.2E+08	2910	-0.18855826	3.084231974	0.3495677	0.449489911	0.04116	0	135	89	139	144	171	187	165	114	170	179
ENSMUSG00000021917	chr14	Spcs1	3.1E+07	3.1E+07	1546	0.176084468	6.260863385	0.3495533	0.449489911	0.04149	0	1169	831	1198	953	1256	2058	1620	1425	1733	1540
ENSMUSG00000056698	chr6	Elmod3	7.3E+07	7.3E+07	3560	-0.19638017	3.493182046	0.3500941	0.450125593	0.0461	0	142	102	296	181	210	227	260	143	213	242
ENSMUSG00000001844	chr5	Zdhhc4	1.4E+08	1.4E+08	2864	0.164785122	4.456972459	0.3503232	0.450337568	0.03483	0	276	179	366	313	462	493	508	323	528	551
ENSMUSG00000081669	chr6	Npm3-ps1	8.5E+07	8.5E+07	528	0.379953115	0.016831121	0.3503054	0.450337568	0.10236	0	14	11	13	9	11	25	16	19	31	13
ENSMUSG00000014980	chr1	Tsen15	1.5E+08	1.5E+08	4195	0.186872114	3.646099276	0.3503819	0.450371728	0.04177	0	185	148	191	157	184	323	249	251	268	262

ENSMUSG00000030946	chr7	Lhpp	1.3E+08	1.3E+08	2085	-0.18398381	4.459187228	0.3509998	0.451124611	0.04387	0	329	288	331	363	430	374	373	313	566	484
ENSMUSG00000051243	chr9	Islr2	5.8E+07	5.8E+07	4933	0.347317836	1.813022889	0.3511461	0.451271372	0.15365	0	19	16	47	38	122	99	79	49	88	82
ENSMUSG00000041439	chr1	Mfsd6	5.3E+07	5.3E+07	8231	0.202087486	3.418452057	0.3512203	0.451325365	0.05122	0	157	69	205	168	163	327	246	156	199	261
ENSMUSG00000093315	chr19	Mir5114	4.4E+07	4.4E+07	61	-0.47323327	1.132681066	0.3514097	0.451527342	0.27458	0	23	22	30	21	96	45	87	21	23	9
ENSMUSG00000019817	chr10	Plagl1	1.3E+07	1.3E+07	7819	-0.42199897	1.513846107	0.3514619	0.451553038	0.21499	0	58	28	18	19	121	80	32	34	55	46
ENSMUSG00000022892	chr16	App	8.5E+07	8.5E+07	3128	0.189503942	7.536840435	0.3515531	0.451628882	0.04918	0	2832	1706	2879	2186	3658	5311	5085	2875	3641	3794
ENSMUSG00000000184	chr6	Ccnd2	1.3E+08	1.3E+08	5701	0.20540977	4.079118932	0.3518867	0.451965546	0.05333	0	218	228	203	186	320	491	305	343	335	373
ENSMUSG00000020677	chr11	Ddx52	8.4E+07	8.4E+07	3332	-0.16010443	4.282235819	0.3519119	0.451965546	0.03149	0	287	203	410	290	378	449	400	340	335	356
ENSMUSG00000098547	chr11	Mir6921	6E+07	6E+07	80	0.457601541	0.347779521	0.3518918	0.451965546	0.24766	0	3	6	17	5	48	27	32	16	34	29
ENSMUSG00000027894	chr3	Slc6a17	1.1E+08	1.1E+08	10283	-0.39387307	1.363408883	0.3524371	0.452598633	0.17973	0	32	21	95	49	23	49	88	15	35	41
ENSMUSG00000022043	chr14	Trim35	6.6E+07	6.6E+07	4045	-0.19172238	7.466885295	0.3525374	0.452685996	0.05054	0	2539	1979	3960	3189	2681	3286	4524	2444	3576	3294
ENSMUSG00000025880	chr18	Smad7	7.5E+07	7.5E+07	4521	-0.23690006	2.855370724	0.3525895	0.452711454	0.06614	0	77	62	175	124	169	144	173	114	98	147
ENSMUSG00000068699	chr6	Flnc	2.9E+07	2.9E+07	9543	-0.30985959	9.747590322	0.3529343	0.453112664	0.13242	0	9124	5753	25306	26823	7300	19311	16855	12706	16769	13819
ENSMUSG00000019080	chr15	Mfsd3	7.7E+07	7.7E+07	2169	0.182782734	3.456121162	0.3531049	0.453217727	0.04004	0	146	112	179	153	181	293	223	173	299	212
ENSMUSG00000019710	chr3	Mrpl24	8.8E+07	8.8E+07	2255	0.156052811	5.544037348	0.353113	0.453217727	0.0326	0	650	418	853	625	839	1216	1004	774	962	1136
ENSMUSG00000044060	chr5	A830010M20Rik	1.1E+08	1.1E+08	9127	-0.20973532	3.188874742	0.3530833	0.453217727	0.05508	0	195	116	140	125	140	195	200	128	183	162
ENSMUSG00000024534	chr18	Sncaip	5.3E+07	5.3E+07	4522	-0.25599397	1.573982525	0.3532536	0.453356654	0.06887	0	41	36	64	34	65	71	75	32	44	54
ENSMUSG00000017740	chr2	Slc12a5	1.6E+08	1.6E+08	7177	-0.32929919	0.734182066	0.3533174	0.453397086	0.10344	0	24	20	16	23	49	32	23	23	28	37
ENSMUSG00000036188	chr12	Ankmy2	3.6E+07	3.6E+07	2446	0.1833331	3.318135736	0.353415	0.453421379	0.0404	0	131	100	167	114	194	273	213	142	235	234
ENSMUSG00000051978	chr8	Erich1	1.4E+07	1.4E+07	1579	-0.29897779	0.950044777	0.3534333	0.453421379	0.09217	0	36	28	34	19	34	41	52	26	24	28
ENSMUSG00000090996	chr2	Gm20458	1.6E+08	1.6E+08	1369	0.167705791	5.504761299	0.3534141	0.453421379	0.03772	0	616	400	778	707	764	1248	872	680	1249	950
ENSMUSG00000030509	chr7	Asb7	6.7E+07	6.7E+07	6226	-0.19243502	3.126084318	0.3536999	0.453597352	0.04429	0	120	93	199	149	144	190	212	107	161	173
ENSMUSG00000046679	chr6	C87436	8.6E+07	8.6E+07	4092	-0.19297154	3.207026945	0.3536979	0.453597352	0.04482	0	146	117	176	138	156	214	194	138	204	133
ENSMUSG00000067586	chr13	S1pr3	5.1E+07	5.1E+07	4484	0.203279942	3.327124279	0.3536592	0.453597352	0.05244	0	113	80	226	130	171	263	197	217	219	188
ENSMUSG00000101556	chr17	Gm28869	1.5E+07	1.5E+07	811	0.321397345	0.85053128	0.3536597	0.453597352	0.10278	0	16	19	23	18	38	55	36	23	24	59
ENSMUSG00000040350	chr11	Trim7	4.9E+07	4.9E+07	7149	0.198516059	5.652345301	0.353811	0.453698459	0.0535	0	483	540	965	926	622	1017	982	890	1277	1336
ENSMUSG00000024940	chr19	Ltbp3	5740904	5740985	5190	0.207790263	6.4500119	0.3538724	0.453735587	0.05941	0	971	837	1206	954	2311	2577	1732	1449	2009	1978
ENSMUSG00000005873	chr18	Reep5	3.4E+07	3.4E+07	2894	0.183524813	7.453537608	0.3541462	0.454019705	0.04663	0	2347	1700	3208	1862	3523	4260	4273	2891	4025	3866
ENSMUSG00000023353	chr5	Agap3	2.4E+07	2.4E+07	3207	0.156901316	5.476883041	0.3541587	0.454019705	0.0329	0	567	429	785	704	717	1000	1078	691	1095	995
ENSMUSG00000074064	chr8	Mlycd	1.2E+08	1.2E+08	2968	-0.22434242	5.875232585	0.3545633	0.45449685	0.06892	0	732	537	1888	948	862	1265	1059	733	893	1699
ENSMUSG00000032724	chr2	Abtb2	1E+08	1E+08	6032	-0.28635413	3.708769434	0.3548008	0.454759792	0.10723	0	130	76	451	311	172	235	324	202	194	248
ENSMUSG00000047248	chr7	C2cd3	1E+08	1E+08	11706	-0.18534001	3.040710858	0.3549395	0.454895938	0.03971	0	116	96	168	129	149	169	185	110	160	167
ENSMUSG00000050550	chr4	Gm11868	1.9E+07	1.9E+07	1478	-0.23609874	2.30752998	0.3549975	0.454902902	0.06317	0	71	53	104	83	90	117	136	69	61	82
ENSMUSG00000081895	chr7	Rpl17-ps10	7.3E+07	7.3E+07	555	0.241374424	2.465680671	0.3550098	0.454902902	0.06653	0	76	72	86	51	84	171	96	103	124	112
ENSMUSG00000035245	chr6	Eogt	9.7E+07	9.7E+07	4900	-0.21989322	2.781330727	0.3553238	0.455222058	0.05905	0	98	77	153	88	145	167	183	81	93	135
ENSMUSG00000083240	chr2	Gm13453	4E+07	4E+07	357	0.212248702	3.308534367	0.35532	0.455222058	0.05625	0	121	101	178	130	161	172	208	145	324	236
ENSMUSG00000012405	chr14	Rpl15	1.8E+07	1.8E+07	2397	-0.18081948	7.069601166	0.3554858	0.455388074	0.04547	0	2177	1873	2198	2060	2264	3113	2704	2051	2620	2544
ENSMUSG00000005470	chr8	Asf1b	8.4E+07	8.4E+07	2338	0.388523823	0.055115377	0.3555597	0.455441109	0.13495	0	11	12	10	6	21	40	19	19	20	11
ENSMUSG00000020477	chr11	Mrps24	5703983	5704732	1466	0.161704204	5.599448453	0.3558222	0.455735714	0.03558	0	525	453	1006	716	830	1206	1095	761	1176	1071
ENSMUSG00000019842	chr10	Traf3ip2	4E+07	4E+07	3687	0.225608664	2.008124098	0.3563315	0.456346424	0.05592	0	45	39	73	42	78	88	94	67	100	86
ENSMUSG00000057666	chr6	Gapdh	1.3E+08	1.3E+08	4133	-0.19704551	12.12472999	0.3565106	0.456534131	0.05465	0	59935	49806	90704	88770	73209	80848	94366	61105	109875	84348
ENSMUSG00000044330	chr3	Gm9790	8.6E+07	8.6E+07	288	0.208027307	2.779456077	0.3566766	0.456704973	0.05373	0	77	50	142	107	111	164	139	128	169	144
ENSMUSG00000066553	chr12	Gm6969	2.5E+07	2.5E+07	342	-0.16437963	5.43072763	0.3574274	0.457624483	0.03669	0	642	431	986	727	707	1000	1020	575	702	947
ENSMUSG00000024218	chr17	Taf11	2.8E+07	2.8E+07	2290	0.159207814	3.971872922	0.3574709	0.457638481	0.03209	0	197	150	302	209	272	435	334	275	348	311
ENSMUSG00000036139	chr15	Hoxc9	1E+08	1E+08	2430	0.179552131	3.401404016	0.3576871	0.457873467	0.0411	0	144	87	192	145	187	253	204	198	229	257
ENSMUSG00000057193	chr9	Slc44a2	2.1E+07	2.1E+07	3456	0.18235706	8.277501092	0.3577225	0.457877021	0.04682	0	4781	3437	4633	4343	4477	7443	7696	5264	7020	6703
ENSMUSG00000041679	chr8	Lrrc29	1.1E+08	1.1E+08	1922	-0.35586712	0.17895599	0.3578847	0.458042817	0.10533	0	9	18	19	11	31	23	20	13	22	16
ENSMUSG00000027566	chr2	Psma7	1.8E+08	1.8E+08	3072	0.170509506	6.742902147	0.3579569	0.458063389	0.04056	0	1475	1139	1962	1348	1716	2918	2129	1823	2470	2407
ENSMUSG00000083327	chrX	Vcp-rs	1E+08	1E+08	2406	-0.14896817	5.151923878	0.3579661	0.458063389	0.02958	0	572	376	721	547	626	735	835	529	739	643
ENSMUSG00000048439	chr5	Nupl2	2.4E+07	2.4E+07	3768	-0.19452757	2.830302326	0.358081	0.45816857	0.04471	0	108	71	149	124	120	155	155	99	120	151
ENSMUSG00000019837	chr10	Gtf3c6	4E+07	4E+07	1020	-0.16728109	4.172466754	0.3582074	0.458288524	0.03654	0	309	231	340	275	261	442	347	291	332	334
ENSMUSG00000008393	chr16	Carhsp1	8658587	8661103	2849	0.334587497	5.155462638	0.3582418	0.458290762	0.15621	0	352	236	260	228	1446	1140	670	616	846	855
ENSMUSG00000025873	chr13	Faf2	5.5E+07	5.5E+07	5084	0.160341594	4.227904539	0.3584526	0.458518637	0.03292	0	225	203	301	225	388	470	431	298	439	404
ENSMUSG00000003575	chr8	Crtc1	7E+07	7E+07	11182	-0.16840802	3.880020003	0.358585	0.458520679	0.03668	0	238	188	273	243	214	335	288	204	327	277
ENSMUSG00000017692	chr11	Rhbdl3	8E+07	8E+07	4734	0.308429616	2.484498762	0.3585765	0.458520679	0.12713	0	48	27	136	44	144	112	176	93	156	88
ENSMUSG00000026798	chr2	Coq4	3E+07	3E+07	3399	0.206572082	3.231331849	0.3585384	0.458520679	0.05637	0	106	57	197	144	174	206	205	178	234	196
ENSMUSG00000062421	chr11	Arf2	1E+08	1E+08	2998	-0.14556379	4.908205428	0.3585308	0.458520679	0.02815	0	441	355	570	487	524	718	674	445	608	508
ENSMUSG00000021957	chr14	Tkt	3.1E+07	3.1E+07	6533	-0.55081111	6.628595302	0.3587243	0.458656935	0.4202	0	2498	658	255	244	5703	2119	849	1667	2317	1189
ENSMUSG00000053553	chr5	3110082I17Rik	1.4E+08	1.4E+08	1429	0.199223889	2.787532162	0.3587625	0.458664028	0.04804	0	97	53	114	104	117	176	147	132	137	155
ENSMUSG00000039041	chr2	Adrm1	1.8E+08	1.8E+08	4457	0.175639486	6.430373934	0.3589176	0.458820433	0.04319	0	972	829	1583	1182	1671	1939	1961	1286	2340	1967
ENSMUSG00000026434	chr1	Nucks1	1.3E+08	1.3E+08	6779	-0.17673121	6.510481238	0.3592455	0.459197759	0.04383	0	1602	1162	1622	1171	1694	2072	1869	1502	1625	1745
ENSMUSG00000036537	chrX	Rnf113a1	3.7E+07	3.7E+07	1223	-0.2545617	1.129535011	0.3593363	0.459230106	0.06403	0	31	28	38	36	38	50	51	22	35	42
ENSMUSG00000042842	chr13	Serpinb6b	3.3E+07	3.3E+07	2200	0.322205533	1.797818384	0.3593216	0.459230106	0.12828	0	61	24	45	17	84	81	119	52	71	66
ENSMUSG00000036197	chr15	Gxylt1	9.3E+07	9.3E+07	6704	0.161214123	3.802339083	0.3594552	0.459340194	0.0323	0	195	132	230	193	246	370	352	224	283	292
ENSMUSG00000022297	chr15	Fzd6	3.9E+07	3.9E+07	4134	0.256830086	2.761837343	0.3599055	0.459873764	0.08642	0	50	43	177	105	108	162	196	96	123	182
ENSMUSG00000062713	chr16	Sim2	9.4E+07	9.4E+07	3670	-0.47561192	3.932479964	0.360198	0.460205624	0.31203	0	38	117	612	487	160	62	418	207	329	270
ENSMUSG00000020131	chr10	Pcsk4	8E+07	8E+07	2958	-0.37534995	0.61011253	0.3604782	0.460521642	0.13573	0	15	10	28	31	42	23	23	10	28	46

ENSMUSG00000039253	chr11	Fn3krp	1.2E+08	1.2E+08	2520	-0.20556536	2.632893306	0.3605495	0.460570799	0.05279	0	96	86	102	81	125	168	113	80	105	128
ENSMUSG00000024002	chr17	Brd4	3.2E+07	3.2E+07	8402	-0.15289311	5.165847581	0.3607895	0.460835355	0.03145	0	481	336	698	618	782	736	804	501	749	731
ENSMUSG00000050270	chr11	Tmem220	6.7E+07	6.7E+07	1669	0.292787663	1.479348502	0.3608815	0.460910881	0.09935	0	43	26	33	17	64	86	52	47	56	65
ENSMUSG00000006542	chr1	Prkag3	7.5E+07	7.5E+07	3682	-0.2541018	6.892878363	0.3611224	0.46117667	0.092	0	2295	2062	1308	1324	2334	1907	3058	1692	2783	1724
ENSMUSG00000020882	chr11	Cacnb1	9.8E+07	9.8E+07	4529	0.191592589	7.732525781	0.3611875	0.461217748	0.05232	0	3127	2393	3149	3119	2989	4440	4874	3347	6149	4625
ENSMUSG00000038836	chr6	Agbl3	3.5E+07	3.5E+07	11075	-0.29348428	0.542838851	0.3612525	0.461258765	0.0715	0	24	15	26	17	32	32	28	21	25	20
ENSMUSG00000022514	chr16	Il1rap	2.7E+07	2.7E+07	11360	-0.30079101	1.344557932	0.3612967	0.461273166	0.09868	0	60	21	56	28	41	58	63	37	31	38
ENSMUSG00000099312	chrX	Gm27733	1E+08	1E+08	68	0.994810521	2.007241148	0.3614132	0.461379998	1.28332	0	74	63	0	29	0	206	0	120	98	110
ENSMUSG00000032625	chr6	Thsd7a	1.2E+07	1.2E+07	13737	-0.33020212	1.707288944	0.3614643	0.461403245	0.13372	0	42	20	63	49	106	62	110	25	55	45
ENSMUSG00000054792	chr9	Klhl18	1.1E+08	1.1E+08	4526	-0.18068441	3.779174003	0.3616069	0.461543166	0.04255	0	211	136	280	260	217	325	338	160	290	230
ENSMUSG00000093752	chr2	Gm20716	1.7E+08	1.7E+08	5288	-0.16413923	6.419850718	0.3616696	0.461581227	0.03805	0	1322	1011	1720	1222	1588	2022	1851	1307	1553	1634
ENSMUSG00000068917	chr3	Clk2	8.9E+07	8.9E+07	5299	0.164990664	4.012527948	0.3617476	0.461638788	0.03501	0	198	162	253	214	328	466	328	248	328	400
ENSMUSG00000014195	chr11	Dnajc7	1E+08	1E+08	4863	0.176185604	6.747388027	0.3618374	0.461711375	0.0442	0	1320	999	2439	1352	1693	2704	2406	1913	2206	2533
ENSMUSG00000031461	chr8	Myom2	1.5E+07	1.5E+07	8853	-0.2039853	10.70239745	0.3623996	0.46238674	0.05998	0	22599	18397	35099	36670	22171	32013	39406	22977	32782	33509
ENSMUSG00000050953	chr10	Gja1	5.6E+07	5.6E+07	3105	0.245368509	4.544827884	0.3624974	0.46242731	0.08394	0	324	226	215	196	669	719	453	479	500	442
ENSMUSG00000061650	chr11	Med9	6E+07	6E+07	1920	0.150218525	4.680890374	0.3624816	0.46242731	0.03054	0	388	213	493	315	460	668	601	428	583	508
ENSMUSG00000005370	chr17	Msh6	8.8E+07	8.8E+07	4254	0.207962475	3.067654944	0.3626483	0.462507993	0.05523	0	112	76	132	98	171	271	196	158	160	135
ENSMUSG00000027630	chr3	Tbl1xr1	2.2E+07	2.2E+07	8362	0.16020761	5.442962201	0.3626596	0.462507993	0.03541	0	689	471	648	540	729	1035	1012	778	890	1006
ENSMUSG00000027716	chr3	Trpc3	3.7E+07	3.7E+07	5419	-0.26778604	2.222534007	0.3626513	0.462507993	0.08586	0	55	35	139	80	85	94	104	65	54	113
ENSMUSG00000040435	chr7	Ppp1r15a	4.6E+07	4.6E+07	2937	0.167612043	4.941321956	0.3628915	0.46276172	0.03819	0	376	335	473	518	464	612	692	482	651	912
ENSMUSG00000062590	chr1	Armc9	8.6E+07	8.6E+07	13006	0.237686212	1.648211801	0.3629951	0.46285173	0.05723	0	38	25	49	41	60	90	73	41	75	64
ENSMUSG00000057554	chr13	Lgals8	1.2E+07	1.2E+07	3688	-0.14698134	4.958846249	0.3631822	0.463048179	0.02947	0	489	371	631	440	536	790	716	447	521	597
ENSMUSG00000029022	chr4	Miip	1.5E+08	1.5E+08	3354	0.206767685	2.832246698	0.3633997	0.463241311	0.05129	0	83	71	115	109	116	188	156	93	139	212
ENSMUSG00000031661	chr8	Nkd1	8.9E+07	8.9E+07	4459	0.30221397	1.322132682	0.3633808	0.463241311	0.09765	0	20	32	28	24	57	68	43	45	48	68
ENSMUSG00000028772	chr4	Zcchc17	1.3E+08	1.3E+08	4560	-0.15688013	5.612350852	0.3634428	0.463254103	0.03454	0	757	595	884	812	820	970	1067	683	1060	1007
ENSMUSG00000040269	chr3	Mrps28	8802146	8802414	783	0.164364752	5.786171892	0.3636211	0.463439298	0.03807	0	782	542	999	773	853	1433	1015	1022	1365	1154
ENSMUSG00000047264	chr8	Zfp358	3493138	3493309	1999	-0.17374958	5.132017848	0.3636638	0.46345163	0.04183	0	385	360	728	647	746	638	784	411	847	749
ENSMUSG00000006378	chr15	Gcat	7.9E+07	7.9E+07	3851	-0.18456071	3.197506369	0.3640717	0.46392927	0.04177	0	148	104	152	144	182	183	161	143	195	192
ENSMUSG00000019868	chr10	Vta1	1.5E+07	1.5E+07	2263	0.147130118	4.399624834	0.3641527	0.463990347	0.02799	0	285	224	361	294	345	509	523	309	476	483
ENSMUSG00000026820	chr2	Ptges2	3.2E+07	3.2E+07	5058	-0.21044	5.681088855	0.3644717	0.464354618	0.06264	0	576	346	1498	1023	930	997	1106	752	1060	991
ENSMUSG00000019699	chr1	Akt3	1.8E+08	1.8E+08	4980	-0.1902074	3.227917125	0.3646878	0.464587766	0.04677	0	162	97	165	162	162	216	241	106	164	184
ENSMUSG00000022711	chr16	Pmm2	8637674	8637828	4519	0.155747443	4.392589529	0.3647885	0.464673832	0.03209	0	233	212	387	305	378	600	460	279	466	511
ENSMUSG00000033196	chr11	Myh2	6.7E+07	6.7E+07	7137	-0.59267332	11.46853193	0.3654857	0.465519659	0.49901	0	20500	1494	151551	100136	10279	43387	58701	29228	31951	72896
ENSMUSG00000071001	chr4	Hrct1	4.4E+07	4.4E+07	1452	0.343481126	2.002223457	0.3656762	0.465720005	0.15943	0	38	22	42	26	147	117	69	69	96	99
ENSMUSG00000022362	chr15	9130401M01Rik	5.8E+07	5.8E+07	1732	-0.15886008	4.239032155	0.3657332	0.465750357	0.03421	0	304	247	301	273	357	506	363	273	355	354
ENSMUSG00000007029	chr17	Vars	3.5E+07	3.5E+07	5608	0.159678108	5.381361261	0.3658855	0.465859658	0.03595	0	470	398	800	668	676	908	935	686	1110	890
ENSMUSG00000009995	chrX	Taz	7.4E+07	7.4E+07	5364	-0.15270036	5.742285104	0.3658681	0.465859658	0.03311	0	775	651	1014	826	990	1238	1087	723	1057	1173
ENSMUSG00000081603	chrX	Gm14681	6.7E+07	6.7E+07	411	0.252779428	1.164385209	0.3659446	0.465892604	0.06318	0	26	18	45	29	31	65	42	38	45	50
ENSMUSG00000026489	chr1	Adck3	1.8E+08	1.8E+08	5293	-0.36948271	9.723270445	0.3659781	0.465893023	0.19801	0	9906	2460	35842	22007	7605	14252	20024	11761	14514	15602
ENSMUSG00000042229	chr1	Rabif	1.3E+08	1.3E+08	2861	-0.16873701	3.691637315	0.3661171	0.466027615	0.03693	0	181	153	286	196	217	349	263	187	231	230
ENSMUSG00000002835	chr17	Chaf1a	5.6E+07	5.6E+07	3308	0.268748244	1.334011718	0.3662881	0.466203038	0.07599	0	26	21	53	33	35	78	50	26	66	58
ENSMUSG00000038866	chr1	Zcchc2	1.1E+08	1.1E+08	6774	-0.18350882	3.348500348	0.3663697	0.466257689	0.04274	0	135	120	193	156	214	228	258	134	156	211
ENSMUSG00000085148	chr11	Mir22hg	7.5E+07	7.5E+07	1924	-0.17126956	4.438808715	0.3663976	0.466257689	0.04008	0	302	286	385	286	470	508	355	353	346	533
ENSMUSG00000038225	chr8	Primpol	4.7E+07	4.7E+07	6309	0.290688417	1.595665344	0.366447	0.46627827	0.09347	0	43	37	32	29	53	113	52	57	51	60
ENSMUSG00000002205	chr7	Vrk3	4.5E+07	4.5E+07	3098	0.144074053	4.645082295	0.3665948	0.4663817	0.02751	0	368	266	373	341	436	647	571	398	568	534
ENSMUSG00000097404	chr19	Gm10814	6012620	6012684	1933	-0.38435126	0.296274963	0.3665736	0.4663817	0.14827	0	11	15	26	11	36	21	38	13	9	21
ENSMUSG00000002279	chr17	Lmf1	2.6E+07	2.6E+07	13471	0.18514863	4.141394894	0.3667864	0.466555066	0.04763	0	212	116	390	285	283	429	372	245	492	410
ENSMUSG00000075296	chr19	Aldh3b2	3972328	3972613	2141	0.649577516	1.198156848	0.3667976	0.466555066	0.56282	0	21	16	1	3	92	74	15	40	100	44
ENSMUSG00000038619	chr3	Ensa	9.6E+07	9.6E+07	2947	-0.17763075	7.613050305	0.3668984	0.466640976	0.04612	0	3072	2435	3677	3287	3107	3890	4806	2678	3831	3885
ENSMUSG00000032478	chr9	Nme6	1.1E+08	1.1E+08	1014	-0.1644616	4.372185442	0.3673565	0.46713892	0.03756	0	340	260	362	344	321	452	413	236	506	429
ENSMUSG00000053329	chr10	D10Jhu81e	7.8E+07	7.8E+07	1363	-0.18624716	7.887007808	0.3673362	0.46713892	0.05079	0	3544	2235	5936	4026	3731	4402	5349	3394	4875	4873
ENSMUSG00000008845	chr6	Cd163	1.2E+08	1.2E+08	4492	-0.2938774	3.469355135	0.3678065	0.467659599	0.12248	0	118	207	98	122	348	351	176	130	171	218
ENSMUSG00000041671	chr6	Pyroxd1	1.4E+08	1.4E+08	4933	-0.17068954	3.560721428	0.3678326	0.467659599	0.0386	0	197	153	212	182	181	290	252	165	227	213
ENSMUSG00000083774	chr7	Gm7180	8.1E+07	8.1E+07	513	-0.34060842	0.634944059	0.367909	0.467714272	0.11139	0	15	17	52	15	28	41	26	22	24	20
ENSMUSG00000025410	chr10	Dctn2	1.3E+08	1.3E+08	1918	0.16791301	6.973942975	0.3679905	0.467733121	0.04112	0	1730	1275	1999	1806	2154	3130	2648	2067	3172	2751
ENSMUSG00000037326	chr17	Capn15	2.6E+07	2.6E+07	3520	-0.21295538	2.303729475	0.3679636	0.467733121	0.05656	0	81	59	96	75	81	102	132	55	80	101
ENSMUSG00000027573	chr2	Gid8	1.8E+08	1.8E+08	2464	-0.14214906	5.08083939	0.3682145	0.467975417	0.02801	0	476	372	749	555	551	784	766	484	661	644
ENSMUSG00000073591	chr18	Pcdhb22	3.8E+07	3.8E+07	6609	0.294595756	1.146992302	0.3682627	0.467994256	0.10506	0	28	15	30	16	58	60	41	45	52	39
ENSMUSG00000024072	chr17	Yipf4	7.4E+07	7.4E+07	2133	-0.15131195	4.582643069	0.368637	0.468427424	0.03081	0	383	244	479	313	512	558	497	388	412	482
ENSMUSG00000001248	chr7	Gramd1a	3.1E+07	3.1E+07	5103	0.170696978	5.42848689	0.3688598	0.468554142	0.04209	0	483	358	1014	552	761	956	1067	653	901	1153
ENSMUSG00000028990	chr4	Lzic	1.5E+08	1.5E+08	1866	0.191104509	3.424295762	0.3688391	0.468554142	0.04864	0	150	112	165	130	194	284	183	230	243	215
ENSMUSG00000031520	chr8	Vegfc	5.4E+07	5.4E+07	1881	0.220704009	1.806865633	0.3688499	0.468554142	0.05128	0	46	37	56	43	54	91	70	62	80	73
ENSMUSG00000068267	chr2	Cenpb	1.3E+08	1.3E+08	4886	-0.18280083	7.665657452	0.3688703	0.468554142	0.04918	0	2771	1763	4536	3429	4348	4165	4633	2511	4397	4154
ENSMUSG00000024975	chr19	Pdcd4	5.4E+07	5.4E+07	2556	0.181038647	4.293641767	0.369072	0.468767841	0.04414	0	288	257	223	252	324	470	422	372	400	463
ENSMUSG00000024589	chr18	Nedd4l	6.5E+07	6.5E+07	8626	0.161701906	4.928501808	0.369159	0.46879354	0.0366	0	432	316	393	372	659	823	644	540	656	651
ENSMUSG00000064364	chrMT	mt-Th	11546	11612	67	0.483271974	0.071175814	0.3691559	0.46879354	0.26783	0	4	1	23	18	16	27	19	3	32	34
ENSMUSG00000007338	chr19	Mrpl49	6053630	6054982	1722	-0.14348653	4.99504466	0.3693656	0.469013364	0.02851	0	460	360	687	510	523	736	707	512	594	574

ENSMUSG00000101628	chr1	Gm28177	5.2E+07	5.2E+07	3532	-0.24933932	4.117079814	0.3700077	0.469786208	0.08928	0	267	191	399	261	319	753	335	146	200	286
ENSMUSG00000006599	chr7	Gtf2h1	4.7E+07	4.7E+07	2984	-0.15340659	4.355874062	0.3701988	0.469986309	0.03198	0	333	234	351	311	393	489	453	334	331	388
ENSMUSG00000029782	chr6	Tmem209	3E+07	3E+07	8130	-0.16608194	3.76833982	0.3704717	0.470290166	0.03677	0	224	173	222	187	268	314	264	214	274	251
ENSMUSG00000028936	chr4	Rpl22	1.5E+08	1.5E+08	2911	0.174965516	7.049182174	0.3705498	0.4703468	0.04514	0	1890	1518	1954	1772	2166	3583	2533	2379	2943	3060
ENSMUSG00000024664	chr19	Fads3	1E+07	1E+07	3269	-0.4382963	4.093299755	0.3708092	0.470633451	0.27831	0	228	230	84	61	921	466	176	272	288	286
ENSMUSG00000022706	chr16	Mrpl40	1.9E+07	1.9E+07	1214	0.147232173	4.480572031	0.3708559	0.470650101	0.0297	0	307	220	397	268	422	607	475	384	474	480
ENSMUSG00000022244	chr15	Amacr	1.1E+07	1.1E+07	2575	-0.15337384	4.624094171	0.3715783	0.471438917	0.03226	0	354	245	559	444	380	501	531	395	464	505
ENSMUSG00000045075	chr11	Gm9796	9.6E+07	9.6E+07	2250	-0.35417478	0.000152155	0.3715695	0.471438917	0.10076	0	14	12	10	16	24	13	24	9	20	16
ENSMUSG00000070730	chr2	Rmdn3	1.2E+08	1.2E+08	3537	-0.22600365	3.900307581	0.3715133	0.471438917	0.07089	0	234	110	207	205	501	367	261	217	272	304
ENSMUSG00000037722	chr14	Gnpnat1	4.5E+07	4.5E+07	2629	-0.19728011	2.959306305	0.3716649	0.471505984	0.05116	0	112	103	122	145	129	169	171	122	116	161
ENSMUSG00000059820	chr9	AU019823	5.1E+07	5.1E+07	5321	-0.17345416	3.44839098	0.3716984	0.471505984	0.03931	0	161	138	211	158	198	301	200	160	198	201
ENSMUSG00000033295	chr4	Ptprf	1.2E+08	1.2E+08	9130	0.210960136	2.394565496	0.3720877	0.471957152	0.05406	0	46	58	98	72	90	147	119	90	98	119
ENSMUSG00000026102	chr1	Inpp1	5.3E+07	5.3E+07	6460	-0.22083182	2.783855123	0.3723256	0.472216212	0.06376	0	116	60	111	111	164	174	125	84	99	176
ENSMUSG00000028293	chr4	Slc35a1	3.5E+07	3.5E+07	2293	-0.15014105	4.555841948	0.3724668	0.472352604	0.0312	0	396	269	400	318	483	576	478	381	442	419
ENSMUSG00000025505	chr7	Tmem80	1.4E+08	1.4E+08	3178	-0.15743958	4.074778164	0.3729436	0.472871734	0.03371	0	267	189	283	233	372	363	366	226	344	350
ENSMUSG00000104435	chr1	RP24-288J3.2	1.9E+08	1.9E+08	4718	0.786115571	0.00405911	0.3729347	0.472871734	0.83425	0	0	1	41	9	3	3	20	1	30	61
ENSMUSG00000014551	chr6	Mrps25	9.2E+07	9.2E+07	6576	0.138236276	4.923864894	0.3731401	0.473078073	0.02692	0	388	303	574	441	492	716	663	544	657	684
ENSMUSG00000031221	chrX	Igbp1	1E+08	1E+08	5717	-0.14210387	5.204373663	0.3731862	0.47309381	0.0289	0	529	435	759	582	621	872	809	536	639	782
ENSMUSG00000045095	chr6	Magi1	9.4E+07	9.4E+07	7701	0.190807995	2.750391476	0.3732356	0.473113621	0.04558	0	99	61	125	82	105	184	144	98	144	167
ENSMUSG00000027433	chr2	Xrn2	1.5E+08	1.5E+08	3981	-0.1573879	4.17403636	0.3733428	0.473206782	0.03344	0	262	199	388	241	363	410	401	287	288	370
ENSMUSG00000038615	chr11	Nfe2l1	9.7E+07	9.7E+07	5441	-0.20669468	9.773520418	0.3734679	0.473322603	0.06444	0	12018	7755	23285	17447	12249	17551	22560	11681	16518	16316
ENSMUSG00000040624	chr10	Plekhg1	3740364	3740540	8739	0.229005049	2.483548908	0.3735349	0.473364692	0.06661	0	73	61	78	57	113	192	100	90	99	138
ENSMUSG00000023072	chr7	Cep89	3.5E+07	3.5E+07	5087	0.203848308	2.652278962	0.3735918	0.473393974	0.05315	0	66	47	130	88	117	145	171	97	145	129
ENSMUSG00000071369	chr10	Map3k5	2E+07	2E+07	6262	-0.15583445	4.257427979	0.3736471	0.473421295	0.03293	0	261	216	343	326	378	413	377	337	392	325
ENSMUSG00000024480	chr18	Ap3s1	4.7E+07	4.7E+07	1479	-0.21876759	3.869390275	0.3739591	0.473731003	0.06724	0	233	144	189	167	476	345	310	216	274	248
ENSMUSG00000061518	chr1	Cox5b	3.7E+07	3.7E+07	1552	0.199860932	8.557937167	0.3739547	0.473731003	0.06032	0	4346	2701	8463	6489	5387	8224	8831	5520	9730	9586
ENSMUSG00000033819	chr15	Ppp1r16a	7.7E+07	7.7E+07	4119	0.150425902	5.082215647	0.3740272	0.473774556	0.03256	0	406	303	570	546	634	726	870	499	870	727
ENSMUSG00000026860	chr2	Sh3glb2	3E+07	3E+07	3990	0.196932422	5.150541346	0.3741987	0.473906123	0.05665	0	463	378	369	437	851	952	668	519	1058	748
ENSMUSG00000053192	chr3	Mllt11	9.5E+07	9.5E+07	1923	0.168900617	6.830705661	0.3741847	0.473906123	0.0426	0	1491	1335	1850	1445	1932	2662	2958	1979	2533	2300
ENSMUSG00000063902	chr7	Gm7964	8.4E+07	8.4E+07	1392	-0.18061819	3.65699663	0.3742671	0.473950012	0.04354	0	179	143	260	171	266	281	311	217	189	210
ENSMUSG00000091905	chr12	Gm6395	6.5E+07	6.5E+07	1491	-0.3349762	0.249659769	0.3743639	0.474029819	0.102	0	21	10	19	23	19	26	26	20	9	18
ENSMUSG00000020743	chr11	Mif4gd	1.2E+08	1.2E+08	2010	-0.16067073	5.280085477	0.374933	0.474664653	0.03767	0	539	438	596	609	937	858	719	509	862	866
ENSMUSG00000051335	chr13	Gfod1	4.3E+07	4.3E+07	6654	-0.24281455	2.985938269	0.37493	0.474664653	0.07929	0	95	56	198	188	125	164	179	129	104	162
ENSMUSG00000029326	chr5	Enoph1	1E+08	1E+08	1826	-0.18509705	3.003758133	0.3750135	0.474723826	0.04283	0	107	82	147	140	170	179	167	110	172	143
ENSMUSG00000022677	chr16	Fopnl	1.4E+07	1.4E+07	1465	-0.16090274	5.777439493	0.3751898	0.474844834	0.0383	0	974	664	969	824	897	1158	1084	921	1087	1059
ENSMUSG00000024913	chr19	Lrp5	3584828	3585291	9738	-0.18185266	5.063869509	0.3752107	0.474844834	0.0479	0	351	265	871	698	602	736	686	436	700	702
ENSMUSG00000026509	chr1	Capn2	1.8E+08	1.8E+08	6345	0.173850462	6.452617924	0.3752021	0.474844834	0.04538	0	1065	789	1624	1040	1868	2688	2051	1430	1746	1776
ENSMUSG00000021892	chr14	Sh3bp5	3.1E+07	3.1E+07	3194	-0.14954831	5.423545406	0.3758434	0.475602584	0.03268	0	584	452	953	724	742	1011	970	555	834	880
ENSMUSG00000095690	chr19	Rab11b-ps2	7398421	7399077	657	-0.20400129	2.521409848	0.3758831	0.475610001	0.05398	0	69	68	134	103	86	118	116	69	118	126
ENSMUSG00000022911	chr16	Arl13b	6.3E+07	6.3E+07	5087	-0.28098928	1.712586864	0.3759637	0.475669019	0.10262	0	58	39	70	31	68	90	94	38	47	34
ENSMUSG00000040666	chr16	Sh3bgr	9.6E+07	9.6E+07	1542	-0.18740535	9.274521817	0.3767617	0.476612324	0.05372	0	11484	7995	10640	8657	10330	12506	15015	9070	12858	10509
ENSMUSG00000058793	chr2	Cds2	1.3E+08	1.3E+08	9125	0.170927647	5.816917505	0.3767772	0.476612324	0.04392	0	562	461	1273	838	1016	1362	1444	847	1237	1322
ENSMUSG00000024436	chr17	Mrps18b	3.6E+07	3.6E+07	2089	-0.15366167	4.781887226	0.3776169	0.477631437	0.03382	0	327	296	618	515	457	560	588	385	611	548
ENSMUSG00000024222	chr17	Fkbp5	2.8E+07	2.8E+07	6363	-0.27961647	4.944045897	0.3777748	0.477753026	0.11801	0	211	442	611	875	365	604	1021	278	448	593
ENSMUSG00000030785	chr7	Cox6a2	1.3E+08	1.3E+08	658	0.198239725	9.748545329	0.3777812	0.477753026	0.06038	0	10815	7000	16880	15245	11625	16869	19069	13074	21780	24350
ENSMUSG00000024317	chr18	Rnf138	2.1E+07	2.1E+07	3110	-0.19834768	2.593451899	0.3778168	0.477755002	0.0487	0	98	67	92	95	128	130	129	94	100	118
ENSMUSG00000031097	chr7	Tnni2	1.4E+08	1.4E+08	1497	-0.17807744	12.94454439	0.3778835	0.477796294	0.04883	0	126717	97707	136998	118917	149145	151699	175927	107958	179722	151877
ENSMUSG00000021910	chr14	Nisch	3.1E+07	3.1E+07	13198	0.168058901	6.446077899	0.3780637	0.477894855	0.04289	0	945	751	1612	1381	1668	2253	1878	1310	2003	2166
ENSMUSG00000040648	chr1	Ppip5k2	9.8E+07	9.8E+07	14381	-0.20293712	2.34557236	0.3780476	0.477894855	0.05147	0	77	73	84	70	94	106	102	68	95	110
ENSMUSG00000090394	chr1	4930523C07Rik	1.6E+08	1.6E+08	10195	-0.20570516	2.951297854	0.3780336	0.477894855	0.05483	0	85	77	175	110	192	186	152	102	126	175
ENSMUSG00000027316	chr2	Gfra4	1.3E+08	1.3E+08	2165	0.421865029	0.993152015	0.3781021	0.477900305	0.24926	0	17	9	13	8	82	55	43	40	50	31
ENSMUSG00000022546	chr15	Gpt	7.7E+07	7.7E+07	1749	-0.20402444	5.137082348	0.378289	0.478093498	0.06138	0	398	212	975	588	852	712	631	508	715	807
ENSMUSG00000086610	chr5	Gm15408	1.5E+08	1.5E+08	1379	-0.22667732	1.824757181	0.3783539	0.47813242	0.06188	0	49	48	72	62	47	71	81	48	70	59
ENSMUSG00000026174	chr1	Rqcd1	7.5E+07	7.5E+07	3826	-0.14248701	4.460011989	0.3784979	0.478271314	0.02842	0	320	256	455	328	389	536	451	344	432	395
ENSMUSG00000054115	chr15	Skp2	9111985	9116968	7875	0.325994695	0.075041826	0.3786098	0.478369574	0.09274	0	9	8	10	19	17	26	17	21	23	20
ENSMUSG00000020514	chr11	Mrpl22	5.8E+07	5.8E+07	981	0.148908953	4.294246859	0.3787668	0.478438688	0.03102	0	263	195	317	296	333	513	394	362	459	385
ENSMUSG00000079428	chrX	Tceal7	1.4E+08	1.4E+08	1217	0.270736051	4.779257075	0.3787445	0.478438688	0.10936	0	590	307	258	446	168	707	541	585	682	537
ENSMUSG00000100254	chr7	TRPC2	1E+08	1E+08	2874	-0.30320178	0.511029797	0.3787156	0.478438688	0.09586	0	26	20	30	19	14	36	18	16	27	27
ENSMUSG00000042046	chr1	Dstyk	1.3E+08	1.3E+08	9345	-0.15171412	4.446848847	0.3788306	0.478476141	0.03272	0	335	243	458	363	334	551	491	334	385	377
ENSMUSG00000065460	chr2	Mir133a-2	1.8E+08	1.8E+08	104	0.315108532	1.452085965	0.3788998	0.478520439	0.12579	0	25	22	53	51	27	87	28	34	77	79
ENSMUSG00000005102	chr2	Eif2ak4	1.2E+08	1.2E+08	7457	-0.18999533	2.688005391	0.3789556	0.47854786	0.04382	0	82	71	139	94	134	160	124	92	119	122
ENSMUSG00000051817	chr2	Sox12	1.5E+08	1.5E+08	4453	0.283874061	0.895974094	0.3792513	0.478878207	0.09222	0	10	18	44	22	28	46	36	35	42	38
ENSMUSG00000023087	chr3	Ccrn4l	5.1E+07	5.1E+07	10658	0.25629887	4.128422411	0.3793935	0.479014646	0.09987	0	124	94	433	208	432	494	327	436	349	306
ENSMUSG00000050860	chr11	Phospho1	9.6E+07	9.6E+07	2029	-0.19366241	7.493403558	0.379733	0.479400116	0.05775	0	2422	1671	4325	2736	3869	2972	4407	2192	4437	3466
ENSMUSG00000049551	chr5	Fzd9	1.4E+08	1.4E+08	2293	0.249558649	4.492335076	0.3799654	0.479650288	0.0939	0	206	143	522	517	203	421	584	319	521	683
ENSMUSG00000025024	chr19	Smndc1	5.3E+07	5.3E+07	2125	-0.14480113	4.521332495	0.3800182	0.479673828	0.02962	0	350	236	445	404	393	530	526	360	420	413
ENSMUSG00000018858	chr11	Ict1	1.2E+08	1.2E+08	3332	0.143085416	4.846283541	0.3800623	0.479686274	0.03009	0	369	246	611	429	449	691	626	498	640	651

ENSMUSG00000037214	chr8	Thap1	2.6E+07	2.6E+07	1328	-0.27171843	1.175700533	0.3803412	0.479995078	0.07906	0	30	24	52	42	32	39	44	41	46	29
ENSMUSG00000043411	chr4	Usp48	1.4E+08	1.4E+08	9686	-0.13709012	4.731169902	0.3804663	0.480109815	0.02706	0	347	336	492	405	517	643	526	399	524	524
ENSMUSG00000029569	chr6	Tmem168	1.4E+07	1.4E+07	5825	-0.16519655	3.982392165	0.3806423	0.480288697	0.03822	0	283	164	276	246	289	350	374	255	238	313
ENSMUSG00000023147	chr16	Wrb	9.6E+07	9.6E+07	4261	-0.18311269	3.659329642	0.380709	0.480329591	0.04716	0	181	171	194	157	302	288	262	204	254	203
ENSMUSG00000052962	chr6	Mrpl35	7.2E+07	7.2E+07	3715	-0.14810026	4.702145345	0.3808874	0.480511483	0.03125	0	331	262	603	461	443	552	501	412	525	547
ENSMUSG00000034951	chr7	Cog7	1.2E+08	1.2E+08	3328	0.140478253	4.829464424	0.3810166	0.480631306	0.02887	0	395	255	462	400	554	653	616	494	651	648
ENSMUSG00000050373	chr2	Snx21	1.6E+08	1.6E+08	4760	0.151867922	5.266797153	0.3812859	0.480927744	0.03456	0	462	350	835	497	678	915	1030	537	833	912
ENSMUSG00000024423	chr18	Impact	1.3E+07	1.3E+07	3432	-0.1511603	4.047798092	0.3814103	0.481041334	0.03188	0	236	191	302	244	344	405	372	245	279	320
ENSMUSG00000092327	chr5	Gm20488	1.5E+08	1.5E+08	2996	0.192399903	3.389212086	0.3816207	0.481263393	0.05056	0	124	126	155	123	201	309	282	184	202	172
ENSMUSG00000027428	chr2	Rbbp9	1.4E+08	1.4E+08	2362	-0.21229732	2.879500776	0.3818248	0.48147751	0.06059	0	118	84	118	93	181	188	174	106	98	136
ENSMUSG00000042705	chr18	Commd10	4.7E+07	4.7E+07	1561	0.203229273	3.10349997	0.3818961	0.481524118	0.05607	0	115	85	135	80	190	273	182	144	172	176
ENSMUSG00000083567	chr2	Gm11451	1.6E+08	1.6E+08	630	0.267036673	1.756151479	0.3819899	0.481599122	0.09019	0	37	36	30	58	60	67	68	64	102	63
ENSMUSG00000040731	chr5	Eif4h	1.3E+08	1.3E+08	2425	0.164435174	7.229427559	0.382266	0.481903918	0.042	0	1902	1505	2554	2043	2802	3572	3517	2467	3667	3190
ENSMUSG00000016253	chr2	Nelfcd	1.7E+08	1.7E+08	2883	0.142126561	5.012551104	0.3824867	0.482138815	0.03015	0	382	300	679	435	570	775	793	559	725	636
ENSMUSG00000020163	chr10	Uqcr11	8E+07	8E+07	641	0.176923365	8.186149848	0.3825645	0.482170718	0.04897	0	3606	2392	5962	4777	4383	6570	6442	4914	7271	6697
ENSMUSG00000032504	chr9	Pdcd6ip	1.1E+08	1.1E+08	6903	0.15252191	6.060826174	0.3825808	0.482170718	0.03565	0	894	624	1231	908	1189	1760	1515	1099	1457	1457
ENSMUSG00000017167	chr11	Cntnap1	1E+08	1E+08	5875	-0.27827419	1.285537428	0.3832782	0.483006286	0.08998	0	30	24	38	29	78	44	50	27	46	53
ENSMUSG00000005374	chr5	Tbl2	1.4E+08	1.4E+08	5968	0.173750576	3.699439842	0.3834438	0.483171607	0.04253	0	151	130	192	168	286	384	247	214	292	284
ENSMUSG00000036442	chr8	Thap11	1.1E+08	1.1E+08	1848	0.137916284	4.848677446	0.3835517	0.483264107	0.02785	0	342	306	571	387	483	712	632	486	684	597
ENSMUSG00000026399	chr1	Cd55	1.3E+08	1.3E+08	4853	-0.2015318	6.370937574	0.3836613	0.483330045	0.06348	0	1396	1366	1143	1228	1274	1811	2255	1175	1492	1272
ENSMUSG00000039990	chr7	Edrf1	1.3E+08	1.3E+08	5992	-0.16881307	3.491328791	0.3836729	0.483330045	0.0396	0	166	144	216	181	179	278	232	181	183	212
ENSMUSG00000035725	chrX	Prkx	7.8E+07	7.8E+07	5807	0.18184052	3.527480336	0.3837826	0.483424803	0.04509	0	165	136	165	120	218	302	304	180	215	264
ENSMUSG00000090222	chr1	Gm16340	1.7E+08	1.7E+08	2164	-0.28989994	0.906274616	0.3839164	0.483549884	0.10891	0	30	22	47	26	23	59	31	12	27	42
ENSMUSG00000022476	chr15	Polr3h	8.2E+07	8.2E+07	2514	0.169487036	3.886629775	0.3841281	0.483773033	0.04057	0	224	157	208	171	283	369	279	260	375	319
ENSMUSG00000098661	chr7	Mir7052	4.4E+07	4.4E+07	65	0.329562769	0.497494008	0.3848546	0.484644572	0.10378	0	12	13	19	21	22	33	16	18	39	44
ENSMUSG00000005262	chr16	Ufd1l	1.9E+07	1.9E+07	4336	-0.15179802	5.835249974	0.385063	0.484863476	0.03551	0	908	678	946	833	1166	1230	1151	860	1090	1257
ENSMUSG00000037827	chr6	Gm5884	1.3E+08	1.3E+08	2259	-0.19459509	2.772043753	0.3851456	0.484923856	0.04813	0	99	61	161	111	124	133	140	106	128	140
ENSMUSG00000044030	chr7	Irf2bp1	1.9E+07	1.9E+07	2697	0.153976967	4.777059684	0.3853122	0.485090152	0.03571	0	299	249	493	430	523	614	527	447	754	628
ENSMUSG00000033170	chr15	Card10	7.9E+07	7.9E+07	4952	-0.18546514	3.432114314	0.3856173	0.485430609	0.04831	0	148	108	191	143	292	249	216	138	201	242
ENSMUSG00000022515	chr16	Anks3	4941415	4941797	2483	0.161165197	3.861509269	0.3858598	0.485648693	0.03592	0	193	166	238	184	246	438	270	225	328	329
ENSMUSG00000097303	chr14	3110083C13Rik	5.8E+07	5.8E+07	856	0.374359162	0.529295452	0.3858476	0.485648693	0.13401	0	14	24	7	17	21	30	31	19	39	37
ENSMUSG00000055523	chr19	Gucy2g	5.5E+07	5.5E+07	3690	-0.424189	0.252466488	0.3861456	0.485964815	0.21054	0	43	11	8	18	11	29	14	13	27	15
ENSMUSG00000008435	chr7	Rdh13	4424770	4425638	6595	-0.18257941	4.489221454	0.3862671	0.48603058	0.04953	0	257	203	669	390	345	490	545	324	394	424
ENSMUSG00000053600	chr17	Zfp472	3.3E+07	3.3E+07	2376	-0.26807947	1.330811989	0.3862427	0.48603058	0.08899	0	31	36	34	52	43	70	51	36	28	44
ENSMUSG00000007279	chr7	Scube2	1.1E+08	1.1E+08	4153	-0.41527784	0.679347997	0.3863501	0.486091374	0.21817	0	18	5	60	42	11	40	31	11	29	25
ENSMUSG00000067276	chrX	Capn6	1.4E+08	1.4E+08	7795	-0.23471745	1.582637766	0.3865012	0.486237867	0.05939	0	40	35	70	43	51	65	57	52	47	52
ENSMUSG00000099881	chr8	2810013P06Rik	1.2E+08	1.2E+08	2137	-0.21654244	2.936429067	0.3865675	0.486277605	0.06419	0	104	67	218	102	147	193	152	100	105	182
ENSMUSG00000020070	chr10	Rufy2	6.3E+07	6.3E+07	8108	-0.22903193	2.018457539	0.3867364	0.486402808	0.06979	0	57	67	62	55	74	109	83	56	73	59
ENSMUSG00000023044	chr15	Csad	1E+08	1E+08	2265	-0.45044967	3.78655732	0.3867183	0.486402808	0.31337	0	227	151	48	53	765	399	132	149	226	318
ENSMUSG00000080893	chr5	Gm15920	1.3E+08	1.3E+08	402	0.159907375	5.698305897	0.3870992	0.486815502	0.03989	0	625	457	1012	849	823	1034	1187	871	1298	1240
ENSMUSG00000037138	chr1	Aff3	3.8E+07	3.8E+07	6579	0.309078419	3.385002364	0.3872676	0.486983613	0.14084	0	82	184	67	209	102	348	168	190	252	231
ENSMUSG00000071172	chr17	Srsf3	2.9E+07	2.9E+07	5109	0.162912113	5.989159202	0.3873422	0.487033769	0.04164	0	727	618	1075	935	1236	1794	1212	1246	1301	1338
ENSMUSG00000022913	chr16	Psmg1	9.6E+07	9.6E+07	1344	0.171048047	3.432877188	0.3874277	0.487097598	0.04081	0	152	106	171	131	206	291	206	198	224	249
ENSMUSG00000052056	chr2	Zfp217	1.7E+08	1.7E+08	6139	0.207018462	3.412552654	0.3877584	0.487469726	0.06095	0	147	134	119	114	214	345	245	185	188	214
ENSMUSG00000100642	chr2	Gm28230	7.5E+07	7.5E+07	3527	0.35949335	0.120970194	0.3878211	0.487504783	0.08991	0	11	16	15	8	13	31	25	15	19	24
ENSMUSG00000103922	chr1	RP23-34E15.4	4771131	4772199	1069	-0.25137376	1.442751968	0.3879582	0.487633458	0.0708	0	45	25	57	43	48	41	65	28	60	55
ENSMUSG00000047989	chr18	Ino80c	2.4E+07	2.4E+07	2828	-0.14811832	5.431444795	0.388297	0.488015548	0.034	0	712	525	726	668	764	950	1019	656	750	858
ENSMUSG00000073791	chr4	Efcab7	1E+08	1E+08	2252	0.347254501	0.158642365	0.3885623	0.488305194	0.11498	0	10	15	13	7	21	32	23	24	22	14
ENSMUSG00000031167	chrX	Rbm3	8138975	8141208	4698	0.185257127	5.334371137	0.3886594	0.488383464	0.05406	0	427	368	1008	355	812	1124	971	680	720	960
ENSMUSG00000023832	chr17	Acat2	1.3E+07	1.3E+07	2544	-0.39668648	3.139407492	0.3890419	0.488820398	0.23929	0	149	67	63	41	473	220	111	119	184	147
ENSMUSG00000025512	chr7	Chid1	1.4E+08	1.4E+08	10799	0.185975496	3.669041732	0.389077	0.488820631	0.05213	0	128	93	303	157	253	370	321	185	282	250
ENSMUSG00000029366	chr5	Dck	8.9E+07	8.9E+07	3078	-0.24889372	1.765078883	0.3893274	0.489091489	0.08453	0	40	38	83	51	64	99	76	23	67	58
ENSMUSG00000014767	chr17	Tbp	1.5E+07	1.6E+07	13399	-0.18967313	2.845231223	0.3894595	0.489213644	0.04951	0	117	72	128	110	150	144	161	98	112	173
ENSMUSG00000035681	chr10	Kcnc2	1.1E+08	1.1E+08	6196	0.397533028	-0.08457301	0.3896966	0.489457965	0.13892	0	6	9	6	11	22	31	10	14	19	24
ENSMUSG00000050608	chr4	Minos1	1.4E+08	1.4E+08	2766	0.166927675	7.05335881	0.3897238	0.489457965	0.04471	0	1726	1108	2844	1939	2068	3329	2835	2313	3050	2978
ENSMUSG00000091803	chr12	Cox16	8.1E+07	8.1E+07	3751	-0.15765843	5.463860812	0.3903275	0.490172209	0.03907	0	798	578	761	600	719	1061	842	729	832	831
ENSMUSG00000029554	chr5	Mad1l1	1.4E+08	1.4E+08	3390	0.187363656	2.98029146	0.3906851	0.490577371	0.0492	0	91	68	158	132	109	181	167	133	201	173
ENSMUSG00000022136	chr14	Dnajc3	1.2E+08	1.2E+08	5190	-0.15615188	5.583803457	0.3911104	0.490996964	0.03855	0	695	599	869	757	882	1388	1029	711	763	846
ENSMUSG00000030616	chr7	Sytl2	9E+07	9E+07	6888	0.258529194	2.060055239	0.3910945	0.490996964	0.08919	0	78	41	37	42	77	131	106	64	71	91
ENSMUSG00000058761	chr7	Rnf169	1E+08	1E+08	7647	0.171885356	3.174297797	0.3911243	0.490996964	0.03972	0	115	100	162	113	145	229	180	156	195	216
ENSMUSG00000032607	chr9	Amt	1.1E+08	1.1E+08	2437	0.389432318	0.044294426	0.3913234	0.491202981	0.15198	0	9	11	12	6	22	30	9	10	26	34
ENSMUSG00000033545	chr8	Znrf1	1.1E+08	1.1E+08	7018	-0.17566478	6.495265807	0.3914395	0.491304677	0.04948	0	1132	957	2365	1544	1379	1666	2043	1301	1921	1817
ENSMUSG00000095832	chr3	Supt20	5.5E+07	5.5E+07	2112	0.184561651	2.917370756	0.3916788	0.491561046	0.04489	0	112	73	112	103	127	225	161	120	152	168
ENSMUSG00000044408	chr12	Sptssa	5.5E+07	5.5E+07	1363	0.142587211	4.83366471	0.3918507	0.491688862	0.03082	0	434	281	460	357	521	851	618	474	543	620
ENSMUSG00000052566	chr8	Hook2	8.5E+07	8.5E+07	2617	0.219567292	2.530693063	0.3918347	0.491688862	0.06371	0	67	71	105	48	106	153	115	80	137	152
ENSMUSG00000022400	chr15	Rbx1	8.1E+07	8.1E+07	1655	0.152930086	6.343583286	0.3920133	0.491848868	0.03741	0	1112	848	1420	1122	1322	1988	1769	1413	1911	1735
ENSMUSG00000020496	chr11	Rnf187	5.9E+07	5.9E+07	1949	0.157857913	6.601763686	0.3920566	0.491859204	0.04005	0	1152	1034	1581	1476	1715	2201	2142	1641	2288	2290

ENSMUSG00000038569	chr5	Rad9b	1.2E+08	1.2E+08	2920	-0.36998724	0.944842777	0.3923032	0.492124613	0.18806	0	20	11	60	25	49	28	31	7	40	62
ENSMUSG00000084799	chr1	Ino80dos	6.3E+07	6.3E+07	2880	-0.32182083	0.718715277	0.392368	0.492161789	0.12039	0	22	19	53	14	25	20	35	18	27	42
ENSMUSG00000031996	chr9	Aplp2	3.1E+07	3.1E+07	3694	0.220227016	8.143262248	0.3925116	0.492297928	0.07906	0	3854	2631	3220	2492	7972	6615	6874	4842	6853	6250
ENSMUSG00000059173	chr2	Pde1a	8E+07	8E+07	6012	0.284539741	2.03446589	0.3925566	0.492310345	0.11153	0	42	44	38	37	113	127	71	86	95	70
ENSMUSG00000010554	chr11	Mettl16	7.5E+07	7.5E+07	13817	-0.13854288	4.417373606	0.3928387	0.492582222	0.02852	0	293	252	410	358	375	479	455	331	440	389
ENSMUSG00000020715	chr11	Ern1	1.1E+08	1.1E+08	8173	-0.18191222	3.84178206	0.3928436	0.492582222	0.04918	0	174	155	353	281	195	249	309	209	289	320
ENSMUSG00000031377	chrX	Bmx	1.6E+08	1.6E+08	3092	0.368130401	-0.14978453	0.3929339	0.492651388	0.10931	0	10	12	14	6	9	15	29	11	21	16
ENSMUSG00000028034	chr3	Fubp1	1.5E+08	1.5E+08	6491	0.134529502	4.686703531	0.3930837	0.49279511	0.02732	0	320	260	444	377	464	660	617	454	490	555
ENSMUSG00000029433	chr5	Diablo	1.2E+08	1.2E+08	6155	0.145153491	5.748101513	0.3931556	0.492841195	0.03333	0	677	565	1008	795	825	1364	1207	866	1235	1177
ENSMUSG00000038605	chr2	Samd10	1.8E+08	1.8E+08	2448	0.233204362	2.712263962	0.3932974	0.492974902	0.08065	0	51	55	163	70	129	141	211	86	151	139
ENSMUSG00000001911	chr8	Nfix	8.5E+07	8.5E+07	7351	-0.17747876	7.87177078	0.3934885	0.49317044	0.0515	0	3116	2502	4847	4661	3816	4254	4824	3127	5572	4996
ENSMUSG00000057880	chr16	Abat	8513429	8513574	7748	-0.22038182	1.757041264	0.3935505	0.493204065	0.06348	0	52	43	60	61	48	78	73	33	65	70
ENSMUSG00000062683	chr15	Atp5g2	1E+08	1E+08	1675	0.166493336	7.098842488	0.3937497	0.493409626	0.04517	0	1745	1290	2650	2065	2136	3157	2833	2037	3616	3412
ENSMUSG00000066306	chr7	Numa1	1E+08	1E+08	7195	0.153992475	6.269885687	0.3938475	0.493488062	0.03819	0	959	774	1400	1143	1290	1867	1723	1122	1899	1850
ENSMUSG00000068966	chr2	Zbtb34	3.3E+07	3.3E+07	6604	-0.19724349	2.564924524	0.394013	0.49365128	0.05337	0	92	80	87	84	122	136	115	81	96	136
ENSMUSG00000022814	chr16	Umps	3.4E+07	3.4E+07	3484	-0.17329224	3.134642325	0.3945066	0.494225599	0.04181	0	132	84	167	126	201	205	178	121	179	167
ENSMUSG00000094497	chr1	Gm8210	4.3E+07	4.3E+07	483	-0.1871049	2.877278738	0.3947853	0.494530565	0.04974	0	121	87	152	109	114	150	131	92	174	158
ENSMUSG00000063060	chr14	Sox7	6.4E+07	6.4E+07	3298	-0.23503722	2.544387887	0.3950344	0.494798399	0.07586	0	86	50	127	58	167	98	137	81	118	110
ENSMUSG00000048814	chr1	Lonrf2	3.9E+07	3.9E+07	7506	0.373547535	0.028957169	0.3952847	0.495067649	0.13643	0	11	6	6	22	14	25	30	11	27	14
ENSMUSG00000031816	chr8	Mthfsd	1.2E+08	1.2E+08	4894	-0.16119065	3.635969661	0.3953476	0.495102317	0.0374	0	213	117	261	179	230	286	235	167	273	252
ENSMUSG00000032026	chr9	Rexo2	4.8E+07	4.8E+07	1075	0.160141831	5.75206834	0.3955547	0.495252019	0.04112	0	791	615	732	721	939	1414	1046	998	1293	1093
ENSMUSG00000032624	chr17	Eml4	8.3E+07	8.3E+07	5445	0.21657781	2.456855968	0.3955176	0.495252019	0.06364	0	71	58	105	44	103	149	116	95	98	141
ENSMUSG00000092341	chr19	Malat1	5795690	5802672	6983	-0.22690922	7.819159387	0.3955731	0.495252019	0.085	0	3687	2938	3813	2418	5603	6033	4949	1957	2903	6418
ENSMUSG00000032598	chr9	Nckipsd	1.1E+08	1.1E+08	4656	0.176339589	2.955640741	0.3958281	0.495482783	0.04319	0	115	77	121	96	135	213	162	138	165	161
ENSMUSG00000037148	chr8	Arhgap10	7.7E+07	7.7E+07	3038	-0.17934199	5.328825266	0.3958018	0.495482783	0.05137	0	506	324	1075	810	613	762	956	535	876	778
ENSMUSG00000042918	chr7	Mamstr	4.6E+07	4.6E+07	4877	0.190670784	4.885010677	0.3959497	0.49559083	0.05701	0	422	377	332	498	376	694	548	399	900	731
ENSMUSG00000032867	chr5	Fbxw8	1.2E+08	1.2E+08	4978	-0.15462638	5.792015166	0.3961181	0.495757335	0.03847	0	691	546	1184	1008	1069	1148	1195	738	1253	1113
ENSMUSG00000022982	chr16	Sod1	9E+07	9E+07	646	0.180462165	7.45537491	0.3961646	0.495771356	0.05384	0	2269	1515	2911	1940	4162	4569	3444	2959	4173	4158
ENSMUSG00000004642	chr5	Slbp	3.4E+07	3.4E+07	4472	0.176654508	3.143981673	0.3963809	0.495997665	0.04597	0	102	73	173	114	175	240	168	160	186	203
ENSMUSG00000021650	chr13	Ptcd2	9.9E+07	9.9E+07	1675	-0.14979814	4.932143927	0.3964841	0.496038388	0.03484	0	395	287	752	554	489	671	676	455	620	569
ENSMUSG00000022044	chr14	Stmn4	6.6E+07	6.6E+07	1916	-0.30885349	0.75803748	0.3964557	0.496038388	0.12673	0	29	24	21	15	43	34	49	11	25	32
ENSMUSG00000003235	chr16	Eif2b5	2E+07	2E+07	3209	-0.15143536	6.109384647	0.3967171	0.496285574	0.03723	0	948	716	1421	1204	1272	1466	1523	1024	1392	1362
ENSMUSG00000006784	chr11	Ttc25	1E+08	1E+08	6147	-0.41047174	-0.30222799	0.3967755	0.496314404	0.16028	0	16	3	13	8	23	19	9	4	20	12
ENSMUSG00000024325	chr17	Ring1	3.4E+07	3.4E+07	3243	0.138776372	4.386834939	0.3968125	0.49631638	0.0292	0	276	206	378	280	375	515	412	346	502	482
ENSMUSG00000022594	chr15	Lynx1	7.5E+07	7.5E+07	4662	-0.30620617	7.639763389	0.3968944	0.496330262	0.15494	0	2146	812	8689	3683	2851	3229	6124	2392	3195	3660
ENSMUSG00000047604	chr19	Frat2	4.2E+07	4.2E+07	2155	-0.18385358	3.739494494	0.3968682	0.496330262	0.05051	0	167	152	265	244	246	226	223	227	356	232
ENSMUSG00000018841	chr11	Rad51d	8.3E+07	8.3E+07	3714	-0.23012362	2.870772341	0.3975538	0.496905234	0.07796	0	106	83	107	72	233	177	137	99	148	131
ENSMUSG00000021038	chr12	Vipas39	8.7E+07	8.7E+07	2701	0.163617562	3.568808233	0.3975577	0.496905234	0.0401	0	168	91	235	149	218	304	278	169	256	292
ENSMUSG00000030110	chr6	Ret	1.2E+08	1.2E+08	7341	0.198830129	2.615291565	0.397546	0.496905234	0.05386	0	81	62	93	88	99	145	174	121	106	114
ENSMUSG00000038909	chr11	Kat7	9.5E+07	9.5E+07	5536	-0.13098997	4.977641642	0.3975514	0.496905234	0.02665	0	431	328	640	508	613	763	710	423	619	620
ENSMUSG00000066152	chr4	Slc31a2	6.2E+07	6.2E+07	2033	0.201007398	3.303713857	0.3974931	0.496905234	0.05831	0	152	125	143	90	166	301	271	126	198	207
ENSMUSG00000097974	chr7	Gm10605	1E+08	1E+08	3569	0.274932247	2.651976204	0.3975667	0.496905234	0.10715	0	80	106	57	93	58	144	130	98	199	129
ENSMUSG00000028023	chr3	Pitx2	1.3E+08	1.3E+08	4726	-0.22370826	2.949585891	0.3980229	0.497431038	0.07588	0	128	82	215	120	83	197	161	99	101	180
ENSMUSG00000022184	chr15	Fbxo4	3965445	3965792	2047	0.210364779	2.569394114	0.3983203	0.497714121	0.06193	0	77	57	78	69	131	189	119	112	113	114
ENSMUSG00000078815	chr7	Cacng6	3424195	3424992	1977	-0.16036821	7.284895056	0.3982863	0.497714121	0.0428	0	2618	1780	2824	2513	2666	3440	3415	2195	3306	2946
ENSMUSG00000012705	chr8	Retn	3655770	3655843	1579	0.711286451	4.862601628	0.3984394	0.497808847	0.80704	0	492	314	0	25	784	1023	181	644	1102	743
ENSMUSG00000068206	chr15	Pick1	7.9E+07	7.9E+07	7770	-0.1554228	5.573421794	0.3984671	0.497808847	0.03922	0	790	520	1018	741	733	869	1140	670	1052	923
ENSMUSG00000028163	chr3	Nfkb1	1.4E+08	1.4E+08	4779	-0.13169893	4.868411238	0.3986873	0.498039507	0.02675	0	388	317	633	450	548	651	608	436	597	588
ENSMUSG00000018362	chr11	Kpna2	1.1E+08	1.1E+08	2873	0.164086316	3.343570726	0.3989355	0.498305253	0.03876	0	127	103	169	144	177	281	204	191	210	208
ENSMUSG00000080848	chr9	Gm9385	1.2E+08	1.2E+08	472	0.150697538	4.255044568	0.3991142	0.498484012	0.03498	0	263	176	294	295	342	441	353	321	500	445
ENSMUSG00000037351	chr1	Actr1b	3.7E+07	3.7E+07	4274	-0.17840245	7.510284376	0.3992416	0.498598815	0.05326	0	2693	1953	4076	3626	2329	3870	4047	2613	3597	3615
ENSMUSG00000048445	chr11	Ccdc57	1.2E+08	1.2E+08	3743	-0.22260639	2.044920834	0.3995873	0.498986015	0.06559	0	57	46	85	72	70	69	113	42	83	82
ENSMUSG00000031788	chr8	Kifc3	9.5E+07	9.5E+07	3758	0.208229076	3.659704438	0.3997484	0.499142826	0.06973	0	130	87	210	127	371	338	280	216	286	272
ENSMUSG00000025878	chr13	Uimc1	5.5E+07	5.5E+07	5085	0.159189066	3.7773612	0.3998828	0.499266219	0.03697	0	169	163	200	183	251	381	291	227	268	324
ENSMUSG00000049643	chr7	2310022A10Rik	2.8E+07	2.8E+07	4780	0.172172517	6.554240262	0.4000096	0.49938007	0.04947	0	1088	856	1911	1589	1331	1857	2115	1505	2486	2300
ENSMUSG00000079511	chr6	Ccdc142	8.3E+07	8.3E+07	3763	0.145686879	5.882779742	0.4001899	0.4995607	0.0348	0	804	578	1062	931	871	1397	1319	980	1375	1329
ENSMUSG00000021748	chr14	Pdhb	8165991	8166481	1485	-0.16755165	8.333527319	0.4003628	0.499732062	0.0473	0	4731	2925	7413	5715	5608	6903	7103	4789	5958	6727
ENSMUSG00000030739	chr7	Myh14	4.5E+07	4.5E+07	7273	-0.2058056	5.739877165	0.4004664	0.499778928	0.07016	0	622	406	1566	1151	749	1010	1316	608	1100	1154
ENSMUSG00000034867	chr7	Ankrd27	3.6E+07	3.6E+07	5258	0.146620608	4.32137036	0.400477	0.499778928	0.03274	0	218	211	351	320	336	550	420	279	434	506
ENSMUSG00000068184	chr13	Ndufaf2	1.1E+08	1.1E+08	679	0.171269957	3.234892834	0.4005073	0.499778928	0.04285	0	126	95	185	107	156	227	177	170	222	218
ENSMUSG00000029111	chr5	Nelfa	3.4E+07	3.4E+07	4927	0.164996697	3.386315727	0.4009324	0.500264907	0.04205	0	123	87	198	130	221	248	229	179	240	234
ENSMUSG00000040875	chr9	Osbpl10	1.1E+08	1.1E+08	5139	0.265797201	1.624855545	0.4014139	0.500821206	0.09215	0	30	28	64	36	50	72	105	34	86	44
ENSMUSG00000029098	chr5	Acox3	3.6E+07	3.6E+07	9093	-0.13924747	4.924431072	0.4019077	0.501392658	0.0308	0	406	298	686	528	527	664	696	388	613	650
ENSMUSG00000060981	chr13	Hist1h4h	2.4E+07	2.4E+07	473	-0.20992795	3.062953108	0.4021355	0.501632147	0.06418	0	96	57	231	147	172	177	159	111	181	168
ENSMUSG00000016356	chr2	Col20a1	1.8E+08	1.8E+08	4193	0.211973613	2.755048945	0.4022452	0.501724398	0.06219	0	77	87	87	105	99	205	140	85	135	186
ENSMUSG00000024077	chr17	Strn	7.9E+07	7.9E+07	8858	-0.16325374	3.572762503	0.4023403	0.501780652	0.03985	0	168	124	227	192	244	316	274	170	177	227
ENSMUSG00000024382	chr18	Ercc3	3.2E+07	3.2E+07	2835	-0.14631977	4.051200761	0.4023618	0.501780652	0.03307	0	230	211	321	280	259	386	355	255	320	304

ENSMUSG00000031378	chrX	Abcd1	7.4E+07	7.4E+07	4192	0.174272804	5.247804128	0.4025774	0.501967615	0.05073	0	418	242	873	663	608	848	935	524	996	889
ENSMUSG00000036356	chr8	Csgalnact1	6.8E+07	6.8E+07	4774	0.22750085	2.11009161	0.4025833	0.501967615	0.06876	0	62	53	62	48	63	130	78	92	80	85
ENSMUSG00000017778	chr13	Cox7c	8.6E+07	8.6E+07	1131	0.170529771	7.95062565	0.4026938	0.502060673	0.0495	0	3322	2128	5473	3598	3435	6114	4948	4416	5570	5951
ENSMUSG00000045502	chr5	Hcar2	1.2E+08	1.2E+08	1947	-0.66564202	0.764597675	0.4029666	0.502356173	0.68355	0	27	6	3	0	125	51	16	14	27	22
ENSMUSG00000054580	chr2	Pla2r1	6E+07	6E+07	9618	0.220621012	2.123873723	0.403709	0.503237004	0.06486	0	54	50	62	40	91	133	98	66	83	98
ENSMUSG00000030279	chr6	C2cd5	1.4E+08	1.4E+08	4468	0.165553798	3.69197089	0.4043093	0.503940523	0.04223	0	217	108	226	192	174	337	287	239	258	276
ENSMUSG00000022555	chr15	Dgat1	7.7E+07	7.7E+07	3054	0.298708636	4.799603389	0.4047332	0.504379199	0.15101	0	377	163	209	189	1044	832	408	469	766	702
ENSMUSG00000030108	chr6	Slc6a13	1.2E+08	1.2E+08	2904	-0.36150555	0.620349377	0.4047245	0.504379199	0.16541	0	7	23	18	20	56	28	24	20	22	36
ENSMUSG00000032309	chr9	Fbxo22	5.5E+07	5.5E+07	2394	-0.13618451	4.66371211	0.4049852	0.504648429	0.02975	0	398	324	501	364	398	567	549	403	510	455
ENSMUSG00000041794	chr9	Myrip	1.2E+08	1.2E+08	5440	-0.30086422	0.365537908	0.4050373	0.504668475	0.08615	0	18	15	28	15	24	15	31	14	22	28
ENSMUSG00000022503	chr16	Nubp1	1E+07	1E+07	3637	0.176129294	3.55543173	0.4050904	0.504689776	0.04638	0	134	161	164	144	210	287	254	220	274	234
ENSMUSG00000020257	chr9	Wdr82	1.1E+08	1.1E+08	6338	0.129869001	5.120223895	0.4052026	0.504748493	0.02742	0	419	355	668	469	628	895	770	568	796	731
ENSMUSG00000025810	chr8	Nrp1	1.3E+08	1.3E+08	5907	-0.18319381	5.934615954	0.4052095	0.504748493	0.05645	0	773	401	1635	992	1388	1487	1282	886	1124	1175
ENSMUSG00000021493	chr13	Pdlim7	5.5E+07	5.5E+07	4849	0.193444607	8.150263126	0.4054341	0.504983469	0.06437	0	4051	3503	3326	4143	4505	6119	5440	4535	9078	6102
ENSMUSG00000017386	chr11	Traf4	7.8E+07	7.8E+07	3292	0.24781109	2.917980565	0.4054785	0.50499396	0.09893	0	97	50	74	92	218	190	115	141	181	203
ENSMUSG00000072889	chr5	Nfxl1	7.3E+07	7.3E+07	4919	0.220374133	2.351833505	0.4056061	0.505108028	0.06584	0	61	67	71	49	97	155	112	88	114	89
ENSMUSG00000042895	chr15	Abra	4.2E+07	4.2E+07	1762	-0.25447373	7.417067784	0.4057763	0.505275093	0.11126	0	1880	1036	5323	4513	1954	2939	3532	2194	3886	3597
ENSMUSG00000072770	chr6	Acrbp	1.3E+08	1.3E+08	3277	0.361209786	0.936051356	0.4058838	0.505364065	0.1759	0	16	27	10	21	42	41	20	40	39	66
ENSMUSG00000032035	chr9	Ets1	3.3E+07	3.3E+07	8476	-0.16898168	4.728199055	0.4059418	0.505391431	0.04596	0	306	210	664	400	637	540	618	410	423	579
ENSMUSG00000006920	chr11	Ezh1	1E+08	1E+08	7440	-0.14017823	5.422575165	0.4061591	0.505546815	0.0328	0	667	482	805	597	867	1018	943	519	876	918
ENSMUSG00000028487	chr4	Bnc2	8.4E+07	8.4E+07	8174	-0.28624641	0.603104402	0.4061748	0.505546815	0.10671	0	27	25	24	23	15	42	32	16	18	27
ENSMUSG00000103436	chrX	RP23-135F22.6	7558602	7560883	5727	0.144995849	4.422637874	0.4061719	0.505546815	0.03344	0	255	208	344	371	363	513	421	347	539	499
ENSMUSG00000019952	chr10	Poc1b	9.9E+07	9.9E+07	3748	0.196905768	2.413241026	0.4062556	0.50555766	0.05585	0	66	45	94	60	111	157	140	72	100	117
ENSMUSG00000097554	chr5	Gm26825	5781530	5783469	2026	0.795234577	0.732842045	0.4062323	0.50555766	1.01193	0	1	0	55	25	13	0	42	1	80	79
ENSMUSG00000030560	chr7	Ctsc	8.8E+07	8.8E+07	5801	0.182059343	5.902139271	0.4065877	0.505926048	0.05607	0	947	736	776	620	1076	2080	1431	917	1184	1071
ENSMUSG00000053886	chr8	Sh2d4a	6.8E+07	6.8E+07	2718	0.193210423	3.674846225	0.4066244	0.505926951	0.05857	0	210	127	246	174	131	374	239	200	225	372
ENSMUSG00000020492	chr11	Ska2	8.7E+07	8.7E+07	3272	-0.19903088	2.398226285	0.406754	0.505983318	0.05708	0	93	66	71	78	105	110	118	76	85	110
ENSMUSG00000025545	chr14	Clybl	1.2E+08	1.2E+08	1239	-0.1436924	5.85682764	0.406778	0.505983318	0.03471	0	947	600	1061	848	1183	1314	1209	922	1135	1100
ENSMUSG00000037921	chr8	Ddx60	6.2E+07	6.2E+07	6931	0.322942794	0.888003353	0.4067215	0.505983318	0.1287	0	27	21	19	18	29	86	41	16	29	36
ENSMUSG00000005804	chr2	Bloc1s6	1.2E+08	1.2E+08	3899	0.133955976	5.245972291	0.407027	0.506248189	0.02951	0	490	394	697	586	570	967	865	662	833	766
ENSMUSG00000029632	chr6	Ndufa4	1.2E+07	1.2E+07	492	-0.16542294	8.892455246	0.4071166	0.506314688	0.04754	0	7012	4541	10906	8306	7942	10065	10741	6726	9200	9799
ENSMUSG00000097251	chr1	5033417F24Rik	9.3E+07	9.3E+07	1787	0.30009307	0.193698792	0.4073118	0.506512583	0.07418	0	13	13	14	13	16	32	27	13	24	23
ENSMUSG00000028187	chr3	Rpf1	1.5E+08	1.5E+08	1263	-0.16312275	3.626404482	0.4077351	0.506994046	0.042	0	209	163	217	168	210	325	259	192	192	233
ENSMUSG00000021134	chr12	Srsf5	8.1E+07	8.1E+07	3988	0.170894643	6.770689215	0.4079605	0.507229318	0.05043	0	1283	1195	1834	1393	2113	2992	2003	1867	1930	3193
ENSMUSG00000066357	chr9	Wdr6	1.1E+08	1.1E+08	4163	0.151631227	4.275706874	0.4080775	0.507329845	0.03659	0	229	209	302	243	409	519	380	286	504	425
ENSMUSG00000027859	chr3	Ngf	1E+08	1E+08	1187	0.369525607	-0.15835326	0.4081431	0.50736639	0.12593	0	7	7	8	10	20	26	8	15	17	25
ENSMUSG00000024566	chr18	Atp9b	8.1E+07	8.1E+07	5397	0.130666675	4.628714591	0.4083692	0.507589623	0.02726	0	319	251	409	361	450	544	614	390	581	538
ENSMUSG00000089726	chr14	Mir17hg	1.2E+08	1.2E+08	3536	0.399194606	0.075313031	0.408395	0.507589623	0.17824	0	4	13	14	18	11	46	12	18	11	25
ENSMUSG00000010025	chr11	Aldh3a2	6.1E+07	6.1E+07	5619	-0.14841104	4.057749376	0.4085757	0.5077692	0.03428	0	244	163	351	224	365	419	371	228	312	312
ENSMUSG00000028454	chr4	Pigo	4.3E+07	4.3E+07	4283	-0.18211224	3.627283848	0.4086226	0.50778244	0.05222	0	148	105	308	248	205	288	278	138	274	230
ENSMUSG00000017774	chr11	Myo1c	7.6E+07	7.6E+07	6585	0.168799046	6.318749157	0.4089235	0.508111324	0.04937	0	819	714	1397	1012	1920	2177	1915	1303	1796	1589
ENSMUSG00000015217	chrX	Hmgb3	7.2E+07	7.2E+07	2234	-0.23713859	3.197182917	0.4090207	0.508187142	0.08763	0	89	54	303	136	215	190	195	141	160	173
ENSMUSG00000023286	chr4	Ube2j2	1.6E+08	1.6E+08	4409	-0.13458912	5.416654893	0.4091715	0.508329492	0.03032	0	622	492	890	633	758	959	852	651	894	849
ENSMUSG00000069117	chr13	Gm10260	9.8E+07	9.8E+07	459	0.145091631	5.390659093	0.4092203	0.508345017	0.03525	0	551	468	619	640	707	1049	798	742	1034	906
ENSMUSG00000000561	chr3	Wdr77	1.1E+08	1.1E+08	6644	0.142798955	5.463404606	0.4093561	0.508351182	0.03425	0	562	517	783	589	702	1086	886	811	915	1054
ENSMUSG00000004270	chr6	Lpcat3	1.2E+08	1.2E+08	3268	0.158383131	4.481011425	0.4093268	0.508351182	0.04198	0	237	181	415	276	541	580	531	325	474	541
ENSMUSG00000044783	chr1	Hjurp	8.8E+07	8.8E+07	8331	0.185979755	2.938918983	0.4092981	0.508351182	0.05144	0	114	76	124	92	130	215	131	142	144	198
ENSMUSG00000090077	chr2	Lime1	1.8E+08	1.8E+08	2304	0.173399449	3.335997859	0.4093702	0.508351182	0.04515	0	135	116	149	137	167	268	172	160	226	273
ENSMUSG00000020123	chr10	Avpr1a	1.2E+08	1.2E+08	2671	0.282684565	0.311898121	0.4094782	0.508440245	0.0718	0	11	12	16	17	21	30	30	20	27	21
ENSMUSG00000001143	chr1	Lman2l	3.6E+07	3.6E+07	7359	-0.13149335	5.0979711	0.4095505	0.508485067	0.02866	0	537	374	632	597	559	726	692	499	754	705
ENSMUSG00000047613	chr4	A430005L14Rik	1.5E+08	1.5E+08	1552	-0.14282208	4.046610658	0.4100141	0.508970516	0.03209	0	244	196	318	237	313	378	314	249	379	296
ENSMUSG00000086845	chr4	Gm13010	1.4E+08	1.4E+08	828	0.323694058	4.22252751	0.4100134	0.508970516	0.17696	0	306	340	77	215	187	582	203	371	583	384
ENSMUSG00000049516	chr7	Spty2d1	4.7E+07	4.7E+07	5223	-0.17333779	3.002037945	0.4105694	0.509614742	0.04706	0	110	106	124	136	152	204	170	96	147	164
ENSMUSG00000041879	chr1	Ipo9	1.4E+08	1.4E+08	8233	-0.13220658	5.195397814	0.4107697	0.509818241	0.02934	0	540	435	613	554	749	911	757	549	734	673
ENSMUSG00000027474	chr2	Ccm2l	1.5E+08	1.5E+08	2407	0.221475427	2.441160071	0.4108479	0.509870209	0.07275	0	41	56	88	68	126	162	99	76	122	141
ENSMUSG00000035047	chr9	Kri1	2.1E+07	2.1E+07	4182	0.155789357	3.67785469	0.4109689	0.509952882	0.03807	0	135	134	264	183	203	330	255	223	281	293
ENSMUSG00000049504	chr3	Proser1	5.3E+07	5.3E+07	5084	-0.17502687	3.118556784	0.4110082	0.509952882	0.04525	0	105	86	169	153	189	183	160	130	161	200
ENSMUSG00000067722	chr17	BC003965	2.5E+07	2.5E+07	3022	-0.14237099	5.389383922	0.4110236	0.509952882	0.03414	0	592	398	957	734	701	930	911	618	862	803
ENSMUSG00000041025	chr4	Iffo2	1.4E+08	1.4E+08	6216	0.260514886	2.844199987	0.4111011	0.510003918	0.11107	0	72	52	76	65	243	211	162	98	157	181
ENSMUSG00000079283	chr1	2310009B15Rik	1.4E+08	1.4E+08	1750	0.191449525	2.828044012	0.4111836	0.510061141	0.05346	0	96	71	96	91	141	181	145	97	201	154
ENSMUSG00000072258	chr1	Taf1a	1.8E+08	1.8E+08	2409	-0.19360565	2.839701012	0.4112379	0.510083404	0.05863	0	129	91	154	73	122	174	164	105	119	123
ENSMUSG00000028648	chr4	Ndufs5	1.2E+08	1.2E+08	860	0.153116713	6.675051239	0.4113803	0.510214898	0.04102	0	1419	955	2076	1401	1561	2484	2163	1696	2497	2283
ENSMUSG00000020923	chr11	Ubtf	1E+08	1E+08	6552	0.14810393	6.098997769	0.4117687	0.510651484	0.03808	0	782	703	1273	971	1246	1770	1391	1114	1642	1548
ENSMUSG00000041975	chr2	Mettl8	7.1E+07	7.1E+07	5594	-0.17672564	2.668798076	0.4119246	0.510799633	0.0481	0	94	74	109	112	112	154	117	73	146	126
ENSMUSG00000079036	chr12	Alkbh1	8.7E+07	8.7E+07	6574	0.184896354	2.816206138	0.4120569	0.510918556	0.04987	0	90	83	108	84	123	209	137	126	133	159
ENSMUSG00000032392	chr9	Parp16	6.5E+07	6.5E+07	2483	-0.19334668	2.8936143	0.4125494	0.511483983	0.05599	0	110	68	150	86	196	173	154	107	136	141
ENSMUSG00000029524	chr5	Sirt4	1.2E+08	1.2E+08	2398	-0.16946038	3.270033557	0.412752	0.51168986	0.04318	0	103	109	208	152	207	240	191	138	180	187

ENSMUSG00000036553	chr5	Sh3tc1	3.6E+07	3.6E+07	5705	0.301517998	2.860760147	0.4128422	0.511756511	0.15314	0	60	53	65	51	282	201	143	123	161	190
ENSMUSG00000037251	chr8	Pomk	2.6E+07	2.6E+07	3601	0.181102736	3.8025444	0.4129306	0.51182079	0.05167	0	194	181	143	209	225	388	309	235	332	262
ENSMUSG00000017428	chr11	Psmd11	8E+07	8E+07	6383	-0.15432728	6.861241963	0.4131492	0.512046575	0.04205	0	1882	1328	2233	1940	1848	2550	2576	1854	2232	2140
ENSMUSG00000002280	chr17	Narfl	2.6E+07	2.6E+07	3826	-0.16548077	5.28890611	0.4132112	0.512078166	0.04691	0	483	319	999	790	627	847	940	526	806	713
ENSMUSG00000024456	chr18	Diap1	3.8E+07	3.8E+07	6339	0.198029235	7.029934956	0.4134244	0.512297024	0.06974	0	1212	896	3351	2278	1879	3319	3860	1897	2738	2797
ENSMUSG00000022858	chr16	Tra2b	2.2E+07	2.2E+07	5383	-0.13146462	5.04494687	0.4135893	0.512414984	0.02864	0	427	338	704	499	691	782	720	512	639	604
ENSMUSG00000030170	chr6	Wnt5b	1.2E+08	1.2E+08	2654	-0.22143998	2.491369311	0.4136291	0.512414984	0.07466	0	119	64	123	77	63	109	92	84	132	108
ENSMUSG00000031577	chr8	Tti2	3.1E+07	3.1E+07	5039	0.17672368	3.021404587	0.4136076	0.512414984	0.04767	0	98	90	143	113	124	179	159	164	161	204
ENSMUSG00000002289	chr17	Angptl4	3.4E+07	3.4E+07	3286	-0.50282179	5.171996976	0.4138136	0.512598166	0.43984	0	626	252	89	112	2339	812	217	778	370	792
ENSMUSG00000058076	chr1	Sdhc	1.7E+08	1.7E+08	3250	-0.17921511	8.347241176	0.4140834	0.512887136	0.05738	0	4539	2653	8687	5910	5258	6338	7494	4536	6603	6705
ENSMUSG00000004127	chr3	Trmt10a	1.4E+08	1.4E+08	7976	0.232477833	1.454586231	0.4143267	0.51309857	0.06972	0	41	24	32	33	53	65	50	53	55	68
ENSMUSG00000027253	chr2	Lrp4	9.1E+07	9.1E+07	10504	-0.18901923	4.171001641	0.4143557	0.51309857	0.05987	0	248	160	495	365	207	381	431	262	277	387
ENSMUSG00000032649	chr1	Colgalt2	1.5E+08	1.5E+08	4245	0.184387832	3.122148544	0.4143639	0.51309857	0.05186	0	95	99	170	125	120	260	175	115	172	240
ENSMUSG00000026708	chr1	Cenpl	1.6E+08	1.6E+08	5695	0.345374761	0.249497567	0.4146356	0.513389753	0.11502	0	18	15	11	13	12	44	18	13	29	23
ENSMUSG00000014859	chr8	E2f4	1.1E+08	1.1E+08	1992	-0.1322451	5.122571105	0.4147752	0.513426558	0.02989	0	464	416	719	558	602	850	738	454	792	633
ENSMUSG00000030996	chr7	Art1	1E+08	1E+08	1417	-0.17290606	8.326937499	0.414769	0.513426558	0.05355	0	5170	2821	8451	4669	5393	6999	6703	5371	5582	6396
ENSMUSG00000032420	chr9	Nt5e	8.8E+07	8.8E+07	8411	-0.23107857	1.826668774	0.4147735	0.513426558	0.07856	0	63	50	80	37	49	79	87	36	60	72
ENSMUSG00000033022	chr18	Cdo1	4.7E+07	4.7E+07	1530	-0.65264008	5.999038771	0.4148609	0.513487341	0.7343	0	1511	665	16	43	3890	1686	326	903	1192	1029
ENSMUSG00000098543	chr19	Gm27533	5844286	5844437	152	-0.23172709	5.00076964	0.4151661	0.513819766	0.09524	0	558	551	320	281	810	878	631	309	498	811
ENSMUSG00000031839	chr8	Hsbp1	1.2E+08	1.2E+08	1163	0.152943104	6.639674618	0.4153738	0.513986143	0.04145	0	1430	1158	1550	1259	1677	2449	2102	1714	2376	2192
ENSMUSG00000069682	chr10	Gm10275	3E+07	3E+07	635	0.16164556	4.57869906	0.4153717	0.513986143	0.04294	0	335	335	278	318	376	669	486	392	520	543
ENSMUSG00000031563	chr8	Wwc2	4.8E+07	4.8E+07	6546	-0.18012017	3.777988552	0.4154135	0.513989861	0.0523	0	175	110	331	182	347	312	353	179	241	251
ENSMUSG00000020010	chr10	Vnn3	2.4E+07	2.4E+07	1811	0.636039016	0.338726857	0.4156686	0.514260189	0.65408	0	18	2	0	2	50	50	4	31	29	27
ENSMUSG00000019297	chr14	Nop9	5.6E+07	5.6E+07	3694	0.144584844	4.073658028	0.4157287	0.514289203	0.03458	0	179	162	335	251	297	382	365	296	399	367
ENSMUSG00000038503	chr7	Mesdc2	8.4E+07	8.4E+07	5081	0.130523235	5.312977647	0.4158639	0.514411116	0.02921	0	556	400	696	540	690	1052	906	684	859	791
ENSMUSG00000032526	chr9	Deb1	1.2E+08	1.2E+08	517	-0.12974235	5.131973297	0.4160873	0.514642068	0.02858	0	539	391	686	534	626	778	641	549	780	699
ENSMUSG00000020467	chr11	Efemp1	2.9E+07	2.9E+07	2037	-0.25380549	3.862043165	0.4162187	0.514759187	0.11114	0	206	156	150	148	560	469	254	206	254	201
ENSMUSG00000046020	chr2	Pofut1	1.5E+08	1.5E+08	9912	-0.14216458	4.517425963	0.4162563	0.514760264	0.03451	0	395	279	343	334	441	607	435	298	465	467
ENSMUSG00000037095	chr17	Lrg1	5.6E+07	5.6E+07	1351	0.25401297	4.722966778	0.4165404	0.515066128	0.11546	0	164	144	471	294	889	689	448	578	698	496
ENSMUSG00000091509	chr14	Gm17066	1.1E+08	1.1E+08	1113	0.204507595	2.485717866	0.4166468	0.515152346	0.06305	0	67	53	89	68	114	131	96	73	152	161
ENSMUSG00000064254	chr7	Ethe1	2.5E+07	2.5E+07	1484	0.156484161	4.586459781	0.4168277	0.515330512	0.04263	0	269	166	571	398	372	587	563	354	552	573
ENSMUSG00000071072	chr10	Ptges3	1.3E+08	1.3E+08	2217	0.148713833	6.047699136	0.4171045	0.515627356	0.03915	0	946	714	1107	848	1121	1859	1385	1188	1238	1519
ENSMUSG00000052456	chr8	Asna1	8.5E+07	8.5E+07	1250	-0.13984593	5.618108415	0.4173818	0.515924683	0.03427	0	661	526	1028	836	882	987	1146	667	1010	1040
ENSMUSG00000028677	chr4	Rnf220	1.2E+08	1.2E+08	7229	0.141259078	5.955517184	0.4177286	0.516274611	0.03531	0	769	651	1071	945	1037	1401	1389	1025	1422	1479
ENSMUSG00000041890	chr5	Git2	1.1E+08	1.1E+08	7233	0.131378275	4.521108154	0.4177753	0.516274611	0.02902	0	281	206	425	358	408	518	567	353	523	520
ENSMUSG00000050777	chr1	Tmem37	1.2E+08	1.2E+08	1311	0.254764798	6.148690572	0.4177552	0.516274611	0.11739	0	554	360	2291	674	1459	1576	2525	958	1418	1610
ENSMUSG00000087177	chr10	E130307A14Rik	4E+07	4E+07	7141	-0.16717223	2.998747759	0.4180193	0.516530643	0.04255	0	119	93	161	130	129	163	184	114	141	169
ENSMUSG00000020873	chr11	Slc35b1	9.5E+07	9.5E+07	2223	0.135822692	5.352975644	0.4182319	0.516747819	0.03205	0	563	422	633	635	680	1010	809	734	952	890
ENSMUSG00000024740	chr19	Ddb1	1.1E+07	1.1E+07	4155	0.156623709	8.039709709	0.4185963	0.51715243	0.04469	0	3251	2379	5266	4171	4059	6629	5841	4591	5709	5894
ENSMUSG00000009630	chr8	Ppp2cb	3.4E+07	3.4E+07	1826	-0.13745551	5.200746229	0.4186882	0.517210415	0.03287	0	462	425	680	550	824	752	885	481	771	752
ENSMUSG00000040389	chr3	Wdr47	1.1E+08	1.1E+08	4394	-0.17338642	2.757266685	0.418717	0.517210415	0.04658	0	89	74	138	122	115	173	149	84	119	132
ENSMUSG00000045598	chr7	Zfp553	1.3E+08	1.3E+08	3373	-0.1647373	3.186134468	0.4187803	0.517243026	0.04137	0	116	96	182	168	165	189	191	144	185	166
ENSMUSG00000020811	chr11	Wscd1	7.2E+07	7.2E+07	4287	0.282704898	0.401444868	0.4188478	0.51728089	0.08985	0	14	9	32	16	13	31	22	20	32	32
ENSMUSG00000034194	chr14	R3hcc1	7E+07	7E+07	2768	-0.13394313	4.264425186	0.4194841	0.518021176	0.02978	0	300	217	372	297	330	391	406	266	410	419
ENSMUSG00000038510	chr10	Rpf2	4E+07	4E+07	1924	0.159429398	3.786621502	0.4196664	0.518200616	0.04072	0	166	170	193	211	224	367	256	251	294	321
ENSMUSG00000028609	chr4	Magoh	1.1E+08	1.1E+08	770	0.158881725	4.05623127	0.4199638	0.518522225	0.04304	0	240	160	341	189	267	481	332	348	316	311
ENSMUSG00000004565	chr8	Pnpla6	3515384	3515556	4496	0.174919874	3.247631967	0.4202255	0.518799616	0.04969	0	104	91	134	131	217	259	182	143	219	235
ENSMUSG00000049882	chr12	Vcpkmt	7E+07	7E+07	1027	-0.20187018	2.379448116	0.420739	0.519387951	0.06533	0	71	89	71	71	99	113	112	75	98	94
ENSMUSG00000018921	chr11	Pelp1	7E+07	7E+07	3561	0.135413849	4.57252485	0.4217079	0.520507045	0.03174	0	262	213	446	385	436	558	495	370	553	597
ENSMUSG00000034807	chr8	Colgalt1	7.2E+07	7.2E+07	3179	0.13741208	5.851128522	0.4217198	0.520507045	0.03387	0	755	567	985	909	959	1559	1257	921	1340	1203
ENSMUSG00000035356	chr16	Nfkbiz	5.6E+07	5.6E+07	5018	0.253715012	1.039077359	0.4218073	0.520569185	0.08432	0	23	17	36	17	44	72	45	29	35	41
ENSMUSG00000098907	chr9	Mir7082	2.1E+07	2.1E+07	92	0.22834557	1.265351107	0.422011	0.520774838	0.06178	0	30	20	43	34	34	68	56	28	49	59
ENSMUSG00000006763	chr7	Saal1	4.7E+07	4.7E+07	8108	0.200111319	2.191090986	0.4222329	0.520956968	0.05879	0	62	41	59	65	88	127	107	55	116	96
ENSMUSG00000036867	chr9	Smad6	6.4E+07	6.4E+07	3205	-0.23538743	2.651252053	0.4222306	0.520956968	0.08676	0	66	49	123	83	211	123	137	89	94	145
ENSMUSG00000029681	chr5	Bcl7b	1.4E+08	1.4E+08	2404	0.130174135	4.826296541	0.4223577	0.520992089	0.02929	0	389	276	455	366	579	686	621	431	670	663
ENSMUSG00000031239	chrX	Itm2a	1.1E+08	1.1E+08	1744	-0.2557628	6.829496288	0.4223728	0.520992089	0.1207	0	2609	2064	1010	1578	1414	2802	1603	2088	2551	1533
ENSMUSG00000059482	chr4	2610301B20Rik	1.1E+07	1.1E+07	2391	-0.19293012	2.336001447	0.4223339	0.520992089	0.05568	0	69	56	128	62	92	128	112	67	87	89
ENSMUSG00000024006	chr17	Stk38	2.9E+07	2.9E+07	8489	0.136097163	5.362896436	0.4227036	0.521354261	0.03276	0	570	429	669	511	798	1211	919	618	838	915
ENSMUSG00000034663	chr5	Bmp2k	9.7E+07	9.7E+07	8480	-0.15687726	3.931107491	0.4228374	0.521473401	0.04275	0	210	229	220	251	269	384	327	234	256	287
ENSMUSG00000023106	chr5	Denr	1.2E+08	1.2E+08	2844	-0.13756955	5.743219863	0.4229369	0.521550296	0.03411	0	811	616	1139	763	935	1179	1235	786	1062	1023
ENSMUSG00000041540	chr6	Sox5	1.4E+08	1.4E+08	14376	-0.32121989	-0.00813853	0.4231171	0.521726691	0.11673	0	15	17	12	14	15	25	17	17	7	16
ENSMUSG00000097059	chr13	Fam120aos	4.9E+07	4.9E+07	1780	-0.21147612	1.742336707	0.4233078	0.521915915	0.05991	0	50	35	61	49	71	76	49	60	60	63
ENSMUSG00000037243	chr11	Zfp692	5.8E+07	5.8E+07	1963	0.200799931	2.667990396	0.4240157	0.522742697	0.06045	0	76	74	83	80	124	174	107	91	140	185
ENSMUSG00000101174	chr2	Hoxd4	7.5E+07	7.5E+07	2948	0.284193152	0.47759415	0.4240719	0.522766047	0.07902	0	17	18	18	11	22	35	30	19	34	28
ENSMUSG00000031725	chr8	Ces1f	9.3E+07	9.3E+07	3285	-0.69198982	2.534408488	0.4242122	0.522893055	0.83847	0	116	33	0	6	418	159	23	74	94	102
ENSMUSG00000030825	chr7	Hsd17b14	4.6E+07	4.6E+07	2046	0.392521647	0.662786868	0.4244223	0.523106103	0.21666	0	20	24	4	9	35	32	25	25	55	35
ENSMUSG00000004500	chr7	Zfp324	1.3E+07	1.3E+07	4776	-0.21395741	1.885900618	0.424588	0.523256012	0.06451	0	53	35	59	63	86	102	77	51	66	52

ENSMUSG00000038324	chr2	Trpc4ap	1.6E+08	1.6E+08	8753	-0.16002631	7.250108381	0.4246186	0.523256012	0.04763	0	2004	1543	3268	2924	2574	2977	3245	2174	3506	2970
ENSMUSG00000030714	chr7	Ccdc101	1.3E+08	1.3E+08	1802	0.141588557	4.251686884	0.4247227	0.523303147	0.03412	0	244	189	289	273	378	418	414	280	445	507
ENSMUSG00000048652	chr3	Samd13	1.5E+08	1.5E+08	2591	-0.30833816	0.002156517	0.4247687	0.523303147	0.09901	0	15	13	23	13	11	22	25	11	9	17
ENSMUSG00000049287	chr11	Iba57	5.9E+07	5.9E+07	4885	-0.17471258	4.392698108	0.4247535	0.523303147	0.05339	0	239	179	611	407	300	426	458	285	399	474
ENSMUSG00000025277	chr14	Abhd6	8002902	8002963	2157	-0.22627352	2.618449736	0.4248778	0.523391558	0.08069	0	54	50	187	89	140	119	148	79	121	112
ENSMUSG00000044465	chr7	Fam160a2	1.1E+08	1.1E+08	11569	-0.13560404	4.251436221	0.4249337	0.523414401	0.03086	0	252	199	398	306	369	379	436	262	415	383
ENSMUSG00000023755	chr15	Rhebl1	9.9E+07	9.9E+07	1940	0.284770023	0.963229192	0.4251353	0.523616802	0.1059	0	16	26	37	15	31	46	30	29	38	66
ENSMUSG00000057130	chr18	Txnl4a	8E+07	8E+07	2185	-0.13626116	4.353428784	0.4252415	0.523701583	0.03208	0	323	248	417	307	310	466	399	306	460	376
ENSMUSG00000072381	chr3	Gm10355	1E+08	1E+08	519	-0.24025141	0.63293337	0.4257329	0.524260692	0.06823	0	23	22	24	24	24	32	31	19	29	27
ENSMUSG00000059602	chr10	Syn3	8.6E+07	8.6E+07	12282	0.622041255	0.865042293	0.4259172	0.52444159	0.67349	0	10	1	49	13	39	1	43	5	70	94
ENSMUSG00000078762	chr7	Haus5	3.1E+07	3.1E+07	3455	-0.2165651	2.120309771	0.4260064	0.524497845	0.07311	0	38	54	98	58	105	83	92	52	102	80
ENSMUSG00000104011	chr1	RP24-272N10.3	1.6E+08	1.6E+08	540	0.391066269	0.772393547	0.4260376	0.524497845	0.25001	0	17	1	59	22	13	42	60	25	25	35
ENSMUSG00000030982	chr7	9030624J02Rik	1.2E+08	1.2E+08	8969	0.12814892	4.775441647	0.4261946	0.52464502	0.02927	0	351	225	521	415	506	713	581	444	617	604
ENSMUSG00000071659	chr19	Hnrnpul2	8819401	8820813	5726	-0.14469448	6.789353789	0.426423	0.524880083	0.03907	0	1558	1248	2262	1838	1926	2637	2382	1647	2066	2177
ENSMUSG00000075279	chr2	Mrpl23-ps1	7.5E+07	7.5E+07	580	0.190983155	3.198363074	0.426583	0.525031045	0.05882	0	142	107	103	136	137	208	166	150	259	214
ENSMUSG00000030979	chr7	Uros	1.3E+08	1.3E+08	3576	-0.12928136	4.389067931	0.4267817	0.525222583	0.02871	0	318	222	407	326	389	509	461	284	449	377
ENSMUSG00000051331	chr6	Cacna1c	1.2E+08	1.2E+08	21191	-0.20805315	1.566016905	0.4268136	0.525222583	0.06171	0	49	40	55	36	50	64	64	43	43	61
ENSMUSG00000036964	chr11	Trim17	5.9E+07	5.9E+07	3736	0.159981617	3.118424616	0.4272094	0.525663597	0.03944	0	115	94	141	112	151	235	205	130	195	179
ENSMUSG00000026447	chr1	Pik3c2b	1.3E+08	1.3E+08	9237	-0.13971683	5.032933374	0.4274982	0.525921343	0.03563	0	584	422	535	473	530	685	808	467	682	582
ENSMUSG00000027173	chr2	Depdc7	1E+08	1E+08	2096	0.224014048	1.723879808	0.4274683	0.525921343	0.07625	0	38	26	74	35	56	102	56	67	55	74
ENSMUSG00000036646	chr2	Man1b1	2.5E+07	2.5E+07	5391	0.128280811	5.059802874	0.4275314	0.525921343	0.02906	0	423	368	507	477	628	903	769	523	787	634
ENSMUSG00000029134	chr5	Plb1	3.2E+07	3.2E+07	8859	0.326267876	0.859873492	0.4275887	0.52594573	0.14805	0	14	18	35	38	8	41	28	33	50	42
ENSMUSG00000039461	chr9	Tcta	1.1E+08	1.1E+08	1838	0.142852873	5.376259817	0.4279056	0.526268114	0.03748	0	522	361	900	646	610	1098	1055	635	758	995
ENSMUSG00000041632	chr13	Mrps27	9.9E+07	9.9E+07	1848	-0.14642028	5.2915071	0.4279258	0.526268114	0.03879	0	500	343	879	729	738	748	849	536	906	807
ENSMUSG00000017837	chr11	Nkiras2	1E+08	1E+08	3578	-0.14041478	4.634256553	0.4280434	0.526366576	0.03447	0	317	242	643	392	420	557	563	351	530	447
ENSMUSG00000078201	chr2	Tmem203	2.5E+07	2.5E+07	854	0.160826927	3.188605059	0.4283062	0.526643482	0.04207	0	115	95	147	112	179	215	187	158	228	192
ENSMUSG00000004768	chr1	Rab23	3.4E+07	3.4E+07	8285	0.175500782	2.681411208	0.4285455	0.526891533	0.04782	0	68	71	123	72	119	173	157	99	130	138
ENSMUSG00000034163	chr10	Zfc3h1	1.2E+08	1.2E+08	7848	-0.15607848	4.130368002	0.4289473	0.527339362	0.04431	0	264	274	295	240	279	494	324	236	301	372
ENSMUSG00000015377	chr15	Dennd6b	8.9E+07	8.9E+07	4607	-0.14606379	3.940118717	0.4296025	0.528092861	0.03652	0	200	161	335	263	270	330	278	196	342	363
ENSMUSG00000018427	chr11	Ypel2	8.7E+07	8.7E+07	4847	-0.15718669	4.295270476	0.4296355	0.528092861	0.04395	0	254	213	433	381	288	358	544	276	385	352
ENSMUSG00000032187	chr9	Smarca4	2.2E+07	2.2E+07	6475	-0.15251997	5.897314842	0.4296815	0.528103076	0.04354	0	689	686	1270	1148	979	1167	1367	848	1343	1113
ENSMUSG00000022883	chr16	Robo1	7.3E+07	7.3E+07	7563	-0.23204596	0.956824414	0.4304171	0.528878742	0.08186	0	35	25	23	35	29	46	40	19	33	40
ENSMUSG00000028614	chr4	Ndc1	1.1E+08	1.1E+08	4924	-0.16909517	3.689009035	0.4304257	0.528878742	0.04893	0	161	114	337	251	188	301	279	183	248	243
ENSMUSG00000047976	chr6	Kcna1	1.3E+08	1.3E+08	8970	0.211663776	2.176488061	0.4303771	0.528878742	0.06857	0	52	53	68	59	75	170	97	67	70	95
ENSMUSG00000021823	chr14	Vcl	2.1E+07	2.1E+07	5229	-0.14817296	6.775366976	0.4305141	0.528896278	0.04171	0	1500	1231	2298	1734	2031	2593	2710	1610	1975	1920
ENSMUSG00000039660	chr2	D2Wsu81e	3E+07	3E+07	3010	0.167390417	3.047186413	0.4305154	0.528896278	0.04594	0	117	84	122	95	166	217	167	125	201	188
ENSMUSG00000032586	chr9	Traip	1.1E+08	1.1E+08	6281	0.323619819	0.24765077	0.4307617	0.529152572	0.11098	0	12	13	8	16	22	42	21	21	23	17
ENSMUSG00000039474	chr5	Wfs1	3.7E+07	3.7E+07	3564	0.268625551	6.953816867	0.4310257	0.529430502	0.13828	0	1107	475	3975	2402	1136	2586	3634	1807	2673	3405
ENSMUSG00000018770	chr2	Atp5g3	7.4E+07	7.4E+07	2181	0.191276625	9.49559353	0.4310676	0.529435521	0.07052	0	7721	4879	18414	12647	9404	15938	18114	11721	16119	17803
ENSMUSG00000029404	chr5	Arl6ip4	1.2E+08	1.2E+08	1438	0.122954672	5.097404219	0.4311109	0.529442344	0.02711	0	436	371	577	514	575	786	752	535	811	804
ENSMUSG00000027358	chr2	Bmp2	1.3E+08	1.3E+08	3555	0.240436346	1.773437292	0.4312578	0.529564992	0.07979	0	44	45	31	51	51	98	63	59	65	86
ENSMUSG00000033565	chr15	Rbfox2	7.7E+07	7.7E+07	7358	-0.15080587	6.158884744	0.4312862	0.529564992	0.04305	0	1062	763	1637	1257	1001	1590	1621	1038	1371	1405
ENSMUSG00000078851	chr11	Hist3h2a	5.9E+07	5.9E+07	2146	0.150161335	3.409240449	0.4316059	0.529911103	0.03755	0	135	113	184	132	195	291	240	157	247	220
ENSMUSG00000033318	chr10	Gstt2	7.6E+07	7.6E+07	1370	0.31605755	2.704425546	0.4317279	0.530014484	0.18269	0	96	44	50	28	231	186	101	127	137	179
ENSMUSG00000045969	chr8	Ing1	1.2E+07	1.2E+07	2813	-0.15182234	3.742656713	0.432489	0.530902404	0.03946	0	180	137	298	232	226	318	335	197	238	222
ENSMUSG00000073374	chr17	C030034I22Rik	6.9E+07	6.9E+07	4231	-0.27276187	0.475984744	0.4328597	0.531310939	0.08378	0	22	13	25	18	30	36	22	25	19	18
ENSMUSG00000079555	chr5	Haus3	3.4E+07	3.4E+07	1950	0.208513136	1.960138624	0.4330171	0.531457646	0.06679	0	50	36	63	58	59	138	60	65	77	83
ENSMUSG00000038235	chr1	F11r	1.7E+08	1.7E+08	2663	0.257758251	4.322538151	0.4333185	0.531781074	0.1269	0	176	120	272	135	771	564	388	332	426	542
ENSMUSG00000037239	chr7	Spred3	2.9E+07	2.9E+07	5997	0.250791148	1.451337682	0.4336562	0.53214893	0.08983	0	34	34	39	20	53	79	83	38	42	57
ENSMUSG00000037773	chr2	Pced1a	1.3E+08	1.3E+08	5072	-0.17600122	2.896782852	0.433818	0.53230087	0.05376	0	107	92	104	147	132	199	143	105	136	137
ENSMUSG00000064368	chrMT	mt-Nd6	13552	14070	519	-0.37161851	7.439312968	0.43408	0.532531169	0.26621	0	1412	361	8208	3590	2907	1949	4389	1152	3162	5337
ENSMUSG00000078607	chr11	1810010H24Rik	1.1E+08	1.1E+08	1205	-0.28913386	0.259255032	0.4340816	0.532531169	0.10761	0	16	21	13	14	25	34	23	12	20	15
ENSMUSG00000017639	chr11	Rab11fip4	8E+07	8E+07	7451	-0.52419937	0.853992524	0.434143	0.53255986	0.47622	0	13	10	4	9	129	45	22	14	18	48
ENSMUSG00000059343	chr4	Aldoart1	7.3E+07	7.3E+07	2052	-0.23890141	2.394879859	0.434691	0.533185518	0.09876	0	75	61	63	89	135	64	98	65	162	98
ENSMUSG00000097772	chr5	5430416N02Rik	1E+08	1E+08	3691	0.362789477	0.066185235	0.4348286	0.533307621	0.1584	0	9	14	15	6	17	33	6	16	24	30
ENSMUSG00000040112	chr6	Mrps35	1.5E+08	1.5E+08	5543	0.135932812	4.540757921	0.4350896	0.533581057	0.03444	0	279	187	537	331	389	584	496	389	477	568
ENSMUSG00000039233	chr13	Tbce	1.4E+07	1.4E+07	4540	-0.14271062	4.39966456	0.4351426	0.5335994	0.03735	0	383	273	349	265	375	520	391	346	405	400
ENSMUSG00000030966	chr7	Trim21	1E+08	1E+08	2775	0.240396471	2.109214926	0.4352508	0.533685484	0.08799	0	58	55	42	60	68	170	98	55	73	88
ENSMUSG00000043384	chrX	Gprasp1	1.4E+08	1.4E+08	8119	0.138625114	4.558531938	0.4353272	0.533732477	0.03394	0	332	285	386	361	295	635	569	374	483	498
ENSMUSG00000045761	chr17	Fam179a	7.2E+07	7.2E+07	5624	0.304755249	2.942126063	0.4354489	0.533788362	0.17592	0	92	32	287	92	45	238	160	180	121	154
ENSMUSG00000089875	chr13	Etohd2	6E+07	6E+07	3136	-0.22668067	1.071111214	0.4354121	0.533788362	0.06911	0	30	26	46	32	29	37	51	23	42	39
ENSMUSG00000073563	chr18	Csnk1g3	5.4E+07	5.4E+07	4394	0.149459776	3.609700388	0.4359206	0.534319875	0.03893	0	147	113	209	192	217	330	286	211	203	290
ENSMUSG00000031913	chr8	Vps4a	1.1E+08	1.1E+08	2522	-0.13829976	6.360988931	0.436025	0.534401107	0.03699	0	1225	942	1566	1300	1492	1716	1751	1205	1717	1707
ENSMUSG00000054302	chr12	Eapp	5.5E+07	5.5E+07	4448	-0.12541163	4.582807127	0.4365372	0.534982145	0.0281	0	368	239	509	381	410	571	524	373	440	459
ENSMUSG00000075268	chr19	Gm10819	1.6E+07	1.6E+07	561	-0.23867451	1.489110463	0.4366307	0.535050003	0.08534	0	32	31	53	50	58	41	71	27	74	46
ENSMUSG00000018893	chr15	Mb	7.7E+07	7.7E+07	1252	-0.41981696	11.92993544	0.4366926	0.535079124	0.34277	0	33987	5114	204897	106946	22237	68582	101539	46579	49546	82231
ENSMUSG00000024558	chr18	Mapk4	7.4E+07	7.4E+07	5400	-0.49423168	0.568324011	0.4367922	0.5351077	0.39866	0	8	3	74	42	5	17	36	24	11	27

ENSMUSG00000062963	chr1	Ufc1	1.7E+08	1.7E+08	2070	0.129762858	5.616035204	0.4367633	0.5351077	0.03214	0	629	492	896	653	910	1264	1033	851	1053	1087
ENSMUSG00000019428	chr8	Fkbp8	7.1E+07	7.1E+07	4529	0.148961064	6.860452203	0.4370181	0.535290904	0.04335	0	1525	1227	1709	1753	2106	2738	2494	1735	3005	2721
ENSMUSG00000054499	chr7	Dedd2	2.5E+07	2.5E+07	1828	-0.18557465	2.671529365	0.436993	0.535290904	0.05441	0	83	60	150	119	102	111	141	93	140	120
ENSMUSG00000028582	chr4	Cc2d1b	1.1E+08	1.1E+08	4771	-0.12305739	4.761429689	0.4374269	0.535744833	0.02818	0	434	325	452	435	468	668	557	390	515	564
ENSMUSG00000043999	chr11	Gpr75	3.1E+07	3.1E+07	2926	-0.37450407	0.58472801	0.4375036	0.535792007	0.22559	0	36	17	24	5	38	52	22	22	8	24
ENSMUSG00000039804	chr2	Ncoa5	1.7E+08	1.7E+08	4383	0.142227874	3.963552525	0.4375845	0.535844293	0.0366	0	184	135	275	283	251	371	345	282	328	348
ENSMUSG00000035504	chr10	Reep6	8E+07	8E+07	2506	0.202033779	2.075425947	0.4377025	0.535942016	0.06972	0	52	33	69	47	95	92	72	73	117	97
ENSMUSG00000039958	chr6	Mettl20	1.5E+08	1.5E+08	2496	-0.19541849	3.388443697	0.4384674	0.53683173	0.07197	0	244	138	146	111	177	236	222	134	161	258
ENSMUSG00000025780	chr2	Itih5	1E+07	1E+07	7900	-0.21883007	6.134338911	0.4385554	0.536892557	0.09444	0	1112	1081	598	781	2017	1818	1091	1155	1302	1330
ENSMUSG00000030780	chr7	BC017158	1.3E+08	1.3E+08	5526	0.205564554	2.358170844	0.4386205	0.536925344	0.06896	0	60	56	60	54	124	130	113	79	131	105
ENSMUSG00000026353	chr1	Ubxn4	1.3E+08	1.3E+08	4659	-0.14355149	5.983080401	0.4388894	0.537207726	0.04016	0	935	709	1378	1069	943	1486	1489	979	1157	1113
ENSMUSG00000030751	chr7	Psma1	1.1E+08	1.1E+08	2103	-0.13853912	6.231120085	0.4390937	0.53741082	0.03754	0	1148	860	1493	1157	1306	1788	1618	1188	1453	1347
ENSMUSG00000078202	chr2	Nrarp	2.5E+07	2.5E+07	2582	0.20443394	2.745237443	0.4393166	0.537636737	0.0777	0	52	52	111	103	162	142	117	135	156	169
ENSMUSG00000022450	chr15	Ndufa6	8.2E+07	8.2E+07	560	-0.15515926	7.574167479	0.4393945	0.537685128	0.04785	0	2735	1915	4627	3265	2893	3951	4304	2660	3869	3941
ENSMUSG00000049892	chr11	Rasd1	6E+07	6E+07	1611	-0.5511422	2.479849768	0.4394535	0.537710402	0.57494	0	65	54	8	6	394	146	32	70	99	115
ENSMUSG00000049097	chr3	Ankrd34a	9.7E+07	9.7E+07	2583	-0.34917254	0.346894444	0.4398217	0.538113964	0.18006	0	24	16	13	9	37	14	26	7	37	24
ENSMUSG00000019906	chr10	Lin7a	1.1E+08	1.1E+08	5952	-0.27739761	0.81000791	0.4399548	0.538229979	0.11231	0	37	13	43	23	23	22	40	22	24	46
ENSMUSG00000028729	chr4	Ebna1bp2	1.2E+08	1.2E+08	3553	0.130917578	5.152331625	0.4400354	0.538234575	0.0323	0	511	396	520	493	623	940	658	625	785	820
ENSMUSG00000038975	chr3	Rabggtb	1.5E+08	1.5E+08	1509	0.141115016	6.193093403	0.4400027	0.538234575	0.03907	0	988	772	1420	993	1107	1686	1575	1229	1570	1857
ENSMUSG00000037296	chr8	Lsm1	2.6E+07	2.6E+07	2360	0.151841341	3.33213757	0.4401168	0.5382872	0.04087	0	136	84	165	137	205	262	212	183	211	214
ENSMUSG00000062184	chrX	Hs6st2	5.1E+07	5.1E+07	7807	0.289477875	1.866303087	0.4402942	0.538457236	0.1346	0	73	52	30	27	46	100	60	86	84	65
ENSMUSG00000065954	chr8	Tacc1	2.5E+07	2.5E+07	7695	0.174341533	4.92365966	0.4403339	0.538458819	0.05946	0	321	253	450	305	910	834	669	478	683	678
ENSMUSG00000023495	chr9	Pcbp4	1.1E+08	1.1E+08	4242	0.166556861	5.800761347	0.4407259	0.538844229	0.05497	0	559	424	1379	926	828	1228	1550	768	1366	1234
ENSMUSG00000034437	chr3	Gm9761	1.2E+08	1.2E+08	342	-0.25935625	0.519158886	0.4406973	0.538844229	0.08081	0	17	17	21	23	32	26	31	20	31	17
ENSMUSG00000027635	chr2	Dsn1	1.6E+08	1.6E+08	3354	-0.24773123	0.850409778	0.4407855	0.538870109	0.07604	0	27	19	32	24	39	43	34	31	32	20
ENSMUSG00000093483	chr11	AA465934	8.3E+07	8.3E+07	711	0.246377289	1.241380232	0.4411534	0.539272897	0.09931	0	32	17	54	28	28	49	35	54	41	68
ENSMUSG00000022099	chr14	Dmtn	7.1E+07	7.1E+07	4629	-0.3596932	2.398224752	0.4413104	0.539370784	0.23911	0	61	33	37	40	301	107	73	68	104	116
ENSMUSG00000041623	chr11	D11Wsu47e	1.1E+08	1.1E+08	2382	0.190912472	2.48333383	0.4412747	0.539370784	0.06212	0	68	51	110	96	64	119	120	105	145	109
ENSMUSG00000021277	chr12	Traf3	1.1E+08	1.1E+08	7350	0.149787668	5.136282836	0.441749	0.539812851	0.04389	0	417	285	850	564	468	754	966	514	786	819
ENSMUSG00000031153	chrX	Gripap1	7789765	7790068	5502	0.128380107	4.808110545	0.4417166	0.539812851	0.03059	0	350	315	528	410	413	625	650	408	616	733
ENSMUSG00000015202	chr10	Cnksr3	7119063	7120586	3837	0.171681952	2.617012112	0.4420363	0.540069738	0.04694	0	84	66	108	72	99	159	119	114	123	142
ENSMUSG00000050088	chr17	1600012H06Rik	1.5E+07	1.5E+07	3294	-0.13725601	3.884444915	0.4420163	0.540069738	0.03452	0	188	200	254	240	270	359	303	220	267	302
ENSMUSG00000055302	chr5	Mrfap1	3.7E+07	3.7E+07	1648	0.146409178	7.728003441	0.4422602	0.540296248	0.04315	0	2895	2349	3904	2763	3304	5559	4375	3715	4745	4624
ENSMUSG00000062077	chr5	Trim54	3.1E+07	3.1E+07	1436	-0.15758625	8.238492322	0.4429734	0.541120492	0.05026	0	3928	2815	7145	5108	5769	5656	6690	4287	6965	5932
ENSMUSG00000039328	chr8	Rnf122	3.1E+07	3.1E+07	7080	-0.17469961	3.877928093	0.4430679	0.541188779	0.05765	0	170	158	303	357	184	299	329	191	329	280
ENSMUSG00000030051	chr6	Aplf	8.8E+07	8.8E+07	3278	-0.17728294	2.288055452	0.4432071	0.541311586	0.05127	0	83	55	87	64	96	113	83	62	105	105
ENSMUSG00000028252	chr4	Ccnc	2.2E+07	2.2E+07	5115	-0.16239721	3.091936139	0.4435531	0.541687026	0.04704	0	148	110	139	116	152	177	200	135	161	147
ENSMUSG00000053536	chr19	Cstf2t	3.1E+07	3.1E+07	3750	-0.12722905	4.820996734	0.4436135	0.541713621	0.03035	0	405	283	677	438	462	661	619	436	521	555
ENSMUSG00000041229	chrX	Phf8	1.5E+08	1.5E+08	9318	-0.15268329	3.781675523	0.444215	0.542400896	0.04219	0	187	153	227	183	353	270	292	211	271	290
ENSMUSG00000019797	chr10	1700021F05Rik	4.4E+07	4.4E+07	1339	0.149536425	5.973531468	0.4443266	0.54241718	0.04503	0	777	457	1313	1040	1052	1412	1354	980	1506	1587
ENSMUSG00000021772	chr14	Nkiras1	1.8E+07	1.8E+07	5430	-0.14701562	5.95676756	0.4443443	0.54241718	0.04308	0	879	609	1502	1117	903	1310	1414	878	1191	1322
ENSMUSG00000025872	chr13	Thoc3	5.4E+07	5.4E+07	2428	-0.14582072	4.046521901	0.4443386	0.54241718	0.03858	0	234	164	353	196	394	378	358	250	333	298
ENSMUSG00000021290	chr12	2010107E04Rik	1.1E+08	1.1E+08	365	0.1480677	7.677962748	0.4444994	0.542559301	0.04462	0	2690	1853	4187	3209	2961	4912	4736	3380	4537	4723
ENSMUSG00000030533	chr7	Unc45a	8E+07	8E+07	3991	0.139021322	3.700925057	0.4445637	0.542590573	0.03472	0	172	116	234	190	230	321	292	188	328	280
ENSMUSG00000020474	chr11	Polm	5827860	5829115	3658	0.205708751	2.289235064	0.44479	0.54281956	0.07017	0	65	53	68	44	107	138	95	70	92	140
ENSMUSG00000097121	chr12	D130020L05Rik	1E+08	1E+08	2431	0.238677721	0.876582494	0.44487	0.542869902	0.08542	0	19	10	36	27	31	51	39	25	27	53
ENSMUSG00000042535	chr15	Gtpbp1	8E+07	8E+07	3398	-0.13604495	5.207108158	0.4450787	0.543077308	0.03595	0	476	347	826	690	639	776	819	512	867	673
ENSMUSG00000028114	chr3	Mettl14	1.2E+08	1.2E+08	5119	-0.13251787	3.961881962	0.4452001	0.543178192	0.03186	0	225	186	331	221	267	353	289	239	312	335
ENSMUSG00000022701	chr16	2610015P09Rik	4.4E+07	4.4E+07	4230	-0.22592496	1.525150226	0.4453196	0.543276684	0.07949	0	49	27	53	30	72	80	53	27	55	56
ENSMUSG00000026991	chr2	Pkp4	5.9E+07	5.9E+07	5707	-0.1500512	4.283815808	0.4454674	0.543409793	0.04244	0	262	185	518	313	304	397	504	252	348	417
ENSMUSG00000053333	chr1	Dis3l2	8.7E+07	8.7E+07	8901	-0.15252242	4.127971665	0.4455642	0.543480592	0.04378	0	278	151	352	369	247	408	389	248	348	321
ENSMUSG00000036437	chr8	Npy1r	6.7E+07	6.7E+07	3007	-0.2759194	1.22394502	0.4457612	0.54367363	0.11986	0	13	37	50	30	57	42	57	36	44	29
ENSMUSG00000097099	chr9	Gm9917	1.1E+08	1.1E+08	6021	0.25624061	0.73309296	0.4465142	0.544544672	0.09989	0	20	9	30	11	41	39	35	27	38	35
ENSMUSG00000022498	chr16	Txndc11	1.1E+07	1.1E+07	8835	0.143777452	3.546041116	0.4467856	0.544767001	0.03726	0	142	112	195	157	238	329	234	183	250	270
ENSMUSG00000033653	chr16	Vps8	2.1E+07	2.1E+07	8670	0.14463385	3.639618732	0.446813	0.544767001	0.03849	0	154	113	209	194	229	332	263	219	304	223
ENSMUSG00000034371	chr19	Dak	1.1E+07	1.1E+07	2253	0.21442077	1.889985297	0.4467676	0.544767001	0.08068	0	32	23	73	49	86	111	68	65	84	72
ENSMUSG00000014402	chr7	Tsg101	4.7E+07	4.7E+07	2730	0.128526726	5.611703736	0.4470264	0.544979808	0.03279	0	708	523	781	658	852	1160	1108	859	1065	1063
ENSMUSG00000060044	chr10	Tmem26	6.9E+07	6.9E+07	5052	0.356501834	0.52711613	0.4471688	0.545106002	0.19404	0	9	17	9	10	43	48	49	15	25	21
ENSMUSG00000004748	chr11	Mtfp1	4091480	4092299	1738	-0.20295823	5.881531587	0.4472412	0.545138673	0.0836	0	691	369	1981	1130	872	979	1481	784	1138	1291
ENSMUSG00000028024	chr3	Enpep	1.3E+08	1.3E+08	4706	-0.21338421	3.153164104	0.4472733	0.545138673	0.08809	0	150	137	106	80	229	260	172	137	132	149
ENSMUSG00000027263	chr2	Tubgcp4	1.2E+08	1.2E+08	8395	-0.13260228	3.861237899	0.4474991	0.545359865	0.03249	0	190	172	293	220	275	366	326	187	288	276
ENSMUSG00000042105	chr7	Inpp5f	1.3E+08	1.3E+08	8323	0.18661522	2.207919354	0.4475326	0.545359865	0.05685	0	60	37	77	54	98	119	126	75	86	93
ENSMUSG00000028861	chr4	Mrps15	1.3E+08	1.3E+08	1693	0.128851651	5.727037432	0.4476593	0.545466936	0.03334	0	738	486	977	782	884	1268	1213	839	1134	1278
ENSMUSG00000003810	chr4	Mast2	1.2E+08	1.2E+08	7645	-0.17799149	6.659430167	0.4482095	0.546023241	0.06511	0	1171	877	2793	2119	1399	1921	2459	1303	2072	2113
ENSMUSG00000020321	chr11	Mdh1	2.2E+07	2.2E+07	2567	-0.21789338	9.802531676	0.4482327	0.546023241	0.09847	0	11110	5921	30422	18370	10523	18085	21780	12846	14035	18920
ENSMUSG00000031521	chr8	Aga	5.4E+07	5.4E+07	1289	0.132430175	4.268172629	0.448187	0.546023241	0.03263	0	268	215	297	230	373	478	422	308	466	404
ENSMUSG00000085787	chr4	Gm13092	1.5E+08	1.5E+08	260	0.292369448	-0.0585631	0.4484553	0.54624703	0.08623	0	11	8	14	8	17	22	13	16	18	27

ENSMUSG00000097571	chrX	Jpx	1E+08	1E+08	4785	-0.31055724	0.507183445	0.4486837	0.546477702	0.14137	0	32	19	19	25	12	36	14	23	17	32
ENSMUSG00000085667	chr4	Gm12992	1.3E+08	1.3E+08	5873	0.378619089	0.208061015	0.4487511	0.546512415	0.23335	0	5	5	41	8	14	15	30	8	35	34
ENSMUSG00000021504	chr13	B4galt7	5.6E+07	5.6E+07	2896	0.154827405	3.216031185	0.4490266	0.546752943	0.04249	0	117	78	157	151	164	256	215	120	210	216
ENSMUSG00000027952	chr3	Pmvk	8.9E+07	8.9E+07	1514	-0.18166164	4.095799345	0.4489922	0.546752943	0.0638	0	286	142	240	208	532	352	314	259	395	323
ENSMUSG00000013997	chr1	Nit1	1.7E+08	1.7E+08	4932	-0.11833775	4.812541559	0.4491521	0.546858328	0.02681	0	420	286	561	414	556	616	593	388	602	595
ENSMUSG00000020107	chr10	Anapc16	6E+07	6E+07	4890	0.126347918	5.452572659	0.4497032	0.547366785	0.03184	0	614	458	680	629	779	1108	948	732	1019	914
ENSMUSG00000030806	chr7	Stx1b	1.3E+08	1.3E+08	4802	0.315649391	1.590716868	0.4497259	0.547366785	0.17956	0	39	27	13	23	95	104	53	38	66	78
ENSMUSG00000037965	chr16	Zc3h7a	1.1E+07	1.1E+07	9160	0.149377628	4.328062375	0.4496553	0.547366785	0.0423	0	272	232	273	243	407	641	447	257	381	496
ENSMUSG00000070509	chr7	Rgma	7.3E+07	7.3E+07	3782	0.148566485	5.421634447	0.449721	0.547366785	0.04439	0	530	462	606	793	645	960	852	666	1221	953
ENSMUSG00000026275	chr1	Ppp1r7	9.3E+07	9.3E+07	10495	0.11778191	4.753916592	0.4499373	0.547576679	0.02703	0	354	248	481	411	482	659	583	453	631	567
ENSMUSG00000012428	chr5	Steap4	7960472	7960541	3140	-0.26010329	6.008243643	0.4499972	0.547601986	0.13984	0	809	742	765	414	2770	1658	1141	1198	1018	975
ENSMUSG00000009035	chr15	Tmem184b	7.9E+07	7.9E+07	3434	0.148430533	5.245768297	0.4501387	0.5477122	0.04478	0	438	340	543	494	968	944	887	574	985	751
ENSMUSG00000035342	chr19	Lzts2	4.5E+07	4.5E+07	2921	0.123615503	5.046695733	0.4501659	0.5477122	0.03027	0	381	320	555	506	658	817	666	508	801	778
ENSMUSG00000005674	chr1	Tomm40l	1.7E+08	1.7E+08	5135	-0.14905013	5.853470217	0.4503836	0.547929566	0.04533	0	771	492	1471	1062	932	1364	1335	786	1180	1051
ENSMUSG00000066892	chr9	Fbxl12	2.1E+07	2.1E+07	5090	0.176400304	2.503515242	0.4505534	0.548088586	0.05207	0	66	63	100	60	109	153	144	91	101	125
ENSMUSG00000002104	chr2	Rapsn	9.1E+07	9.1E+07	1802	0.125914959	5.057239276	0.4509229	0.548490608	0.03122	0	410	355	582	545	509	707	736	505	838	802
ENSMUSG00000010054	chr9	Tusc2	1.1E+08	1.1E+08	1785	0.128614858	5.744340992	0.4512277	0.548813687	0.03374	0	717	509	938	838	898	1294	1159	880	1279	1173
ENSMUSG00000026189	chr1	Pecr	7.2E+07	7.2E+07	1516	-0.1389539	4.089600874	0.4515854	0.549201195	0.03742	0	260	225	278	262	299	388	280	272	387	333
ENSMUSG00000022122	chr14	Ednrb	1E+08	1E+08	4037	0.194895717	3.674468108	0.4518248	0.549444695	0.07625	0	104	115	256	123	335	410	324	231	228	213
ENSMUSG00000030534	chr7	Vps33b	8E+07	8E+07	3343	-0.18654214	2.323852909	0.4519704	0.549574017	0.06089	0	87	58	78	58	115	135	98	58	92	100
ENSMUSG00000022052	chr14	Ppp2r2a	6.7E+07	6.7E+07	4036	-0.13499181	6.054342006	0.4520899	0.54967176	0.03749	0	916	690	1425	969	1358	1428	1514	971	1373	1276
ENSMUSG00000049792	chr12	Bag5	1.1E+08	1.1E+08	2508	-0.12145946	4.336935929	0.4525405	0.550124194	0.02814	0	260	237	407	321	370	492	414	303	389	403
ENSMUSG00000097290	chr16	1300002E11Rik	2.2E+07	2.2E+07	3955	0.180739012	2.781833483	0.45252	0.550124194	0.05883	0	104	62	99	69	152	192	135	100	161	163
ENSMUSG00000015994	chr8	Fnta	2.6E+07	2.6E+07	1874	-0.13308804	6.381473625	0.4527561	0.550338624	0.0369	0	1257	969	1599	1300	1471	1874	1751	1238	1746	1628
ENSMUSG00000046380	chr15	Jrk	7.5E+07	7.5E+07	5853	-0.18594328	1.787234554	0.4529681	0.550548571	0.05363	0	55	36	73	56	51	80	73	44	67	63
ENSMUSG00000009210	chr11	2310007L24Rik	1.1E+08	1.1E+08	1724	-0.19142506	2.059072312	0.4531684	0.550744252	0.06328	0	60	55	62	53	97	84	90	62	91	65
ENSMUSG00000031490	chr8	Eif4ebp1	2.7E+07	2.7E+07	981	0.176902765	5.489300318	0.4532881	0.550842046	0.06557	0	598	355	729	398	1228	1293	778	879	998	944
ENSMUSG00000028420	chr4	Tmem38b	5.4E+07	5.4E+07	3807	-0.15090821	6.216255998	0.4533789	0.550904706	0.04763	0	985	846	1665	1258	1207	1625	2110	1050	1213	1338
ENSMUSG00000081228	chr5	Gm16089	1.4E+08	1.4E+08	336	0.214011817	1.749243736	0.4534581	0.550953187	0.07983	0	31	20	70	60	54	76	71	43	86	88
ENSMUSG00000020265	chr10	Sumo3	7.8E+07	7.8E+07	3826	0.137489585	6.169214105	0.4536745	0.551168358	0.03919	0	871	871	1159	1037	1197	1815	1705	1165	1670	1459
ENSMUSG00000023066	chr18	Rttn	8.9E+07	8.9E+07	7268	-0.24412215	0.903764214	0.4538502	0.55133404	0.09357	0	26	29	46	20	23	48	42	26	24	29
ENSMUSG00000019761	chr11	Krt10	9.9E+07	9.9E+07	2094	0.207749394	1.386818035	0.4544341	0.551995527	0.06655	0	33	25	49	24	47	64	45	40	62	67
ENSMUSG00000031196	chrX	F8	7.5E+07	7.5E+07	9905	0.294494889	0.029897357	0.4544924	0.552018588	0.09425	0	15	9	8	12	17	23	15	16	29	20
ENSMUSG00000039405	chr7	Prss23	9E+07	9E+07	3226	0.160792899	6.845178437	0.4547796	0.552319605	0.0546	0	1326	1457	1887	1922	1454	2747	3330	1798	2654	2087
ENSMUSG00000000399	chr6	Ndufa9	1.3E+08	1.3E+08	1322	-0.18050275	8.295171956	0.4550797	0.552588359	0.06956	0	3929	2338	9307	6061	4702	5984	7099	4611	6295	6439
ENSMUSG00000052374	chr13	Actn2	1.2E+07	1.2E+07	3694	0.404957874	10.11913721	0.4550562	0.552588359	0.34577	0	5685	1058	41798	25986	5217	25732	29848	17382	24418	34575
ENSMUSG00000002307	chr17	Daxx	3.4E+07	3.4E+07	3058	-0.13593494	3.968408202	0.4554404	0.552978496	0.0364	0	228	181	313	265	245	382	350	181	356	289
ENSMUSG00000028886	chr4	Eya3	1.3E+08	1.3E+08	5647	0.129549563	4.371584876	0.4556841	0.553226412	0.03323	0	261	179	400	352	318	467	482	307	480	501
ENSMUSG00000070729	chr4	Gm12966	1.3E+08	1.3E+08	810	0.215993083	1.320391342	0.4560242	0.553591474	0.06902	0	31	25	32	31	48	61	53	31	49	74
ENSMUSG00000036309	chr11	Skp1a	5.2E+07	5.2E+07	2211	-0.14174971	7.517982661	0.456223	0.553784866	0.04301	0	2799	2222	3489	2863	3114	4145	3659	3032	3389	3726
ENSMUSG00000001943	chr9	Vsig2	3.8E+07	3.8E+07	1170	0.315933926	0.501586957	0.4563206	0.553855362	0.15668	0	10	16	10	11	41	48	24	17	25	38
ENSMUSG00000024790	chr19	Sac3d1	6116004	6116587	1374	0.163941636	3.471068981	0.4565223	0.554052189	0.05038	0	160	122	175	169	148	290	218	176	327	192
ENSMUSG00000047905	chr6	Gm8566	6.7E+07	6.7E+07	465	0.268872577	0.622250614	0.456614	0.55411553	0.10038	0	16	11	18	15	40	27	35	21	41	37
ENSMUSG00000021631	chr17	Mrps36-ps1	5.4E+07	5.4E+07	306	-0.21436331	1.389420388	0.456766	0.55425203	0.06677	0	42	27	66	35	37	56	53	43	43	45
ENSMUSG00000020216	chr10	Jsrp1	8.1E+07	8.1E+07	1333	0.146425434	8.695762576	0.4573555	0.554919385	0.04632	0	5719	4204	6814	6374	6674	9565	8622	6354	10788	9864
ENSMUSG00000042699	chr1	Dhx9	1.5E+08	1.5E+08	9603	-0.12530855	5.579319337	0.4574424	0.55492885	0.03264	0	697	506	860	745	997	1125	1067	712	854	986
ENSMUSG00000079184	chr14	Mphosph8	5.7E+07	5.7E+07	3586	-0.13380123	4.009665842	0.4574078	0.55492885	0.03453	0	248	162	362	253	258	384	380	228	320	279
ENSMUSG00000021007	chr12	Spata7	9.9E+07	9.9E+07	4642	-0.20300392	1.635181378	0.4575091	0.554958233	0.06109	0	51	29	60	47	59	49	68	51	53	65
ENSMUSG00000047547	chr13	Cltb	5.5E+07	5.5E+07	4868	0.134799699	6.742127702	0.4575458	0.554958233	0.03883	0	1333	1079	1938	1550	1892	2580	2318	1693	2565	2457
ENSMUSG00000069633	chr8	Pex11g	3457105	3459434	3397	0.216903196	2.078349886	0.4579099	0.555351895	0.08826	0	47	37	62	40	109	144	63	63	97	96
ENSMUSG00000102158	chr1	RP23-433P9.4	1.8E+08	1.8E+08	335	-0.37730457	-0.30896282	0.4580697	0.555497588	0.18398	0	18	13	9	2	17	11	16	7	20	10
ENSMUSG00000015474	chr17	Ppt2	3.5E+07	3.5E+07	2614	0.125778544	5.374969619	0.4581686	0.555569478	0.03296	0	546	384	696	641	763	925	902	634	1043	975
ENSMUSG00000051736	chr10	Fam229b	3.9E+07	3.9E+07	3331	0.232693128	1.080698024	0.4582238	0.555588481	0.07107	0	33	24	25	23	32	58	43	39	43	40
ENSMUSG00000054474	chr6	Thnsl2	7.1E+07	7.1E+07	2071	-0.18321261	2.616684993	0.4584688	0.55583746	0.06367	0	100	85	85	65	146	134	117	90	117	127
ENSMUSG00000086429	chr6	Gt(ROSA)26Sor	1.1E+08	1.1E+08	1695	-0.21520822	2.04456268	0.4585169	0.555847754	0.08112	0	75	43	68	59	83	50	93	50	79	113
ENSMUSG00000002728	chr2	Naa20	1.5E+08	1.5E+08	3705	-0.11919362	5.319739135	0.4587477	0.556079415	0.0294	0	619	465	788	580	690	921	832	636	753	807
ENSMUSG00000038253	chr6	Hoxa5	5.2E+07	5.2E+07	1877	0.202587466	1.206359416	0.4587896	0.556082226	0.05701	0	27	21	43	29	36	54	52	34	45	59
ENSMUSG00000047182	chr5	Irs3	1.4E+08	1.4E+08	2337	0.38702451	1.836454751	0.4592742	0.556621474	0.30266	0	43	28	16	8	140	120	38	71	77	97
ENSMUSG00000040562	chr3	Gstm2	1.1E+08	1.1E+08	1679	0.248450982	6.264342747	0.4597716	0.557176164	0.13314	0	1298	1154	378	1141	957	1904	1034	1413	2103	2108
ENSMUSG00000022437	chr15	Samm50	8.4E+07	8.4E+07	1673	-0.16480519	7.670457813	0.4602218	0.557608985	0.05918	0	2379	1676	5506	3827	3532	3952	4353	2780	4469	4368
ENSMUSG00000031467	chr8	Agpat5	1.9E+07	1.9E+07	10783	0.1271459	4.838217921	0.4601931	0.557608985	0.03281	0	417	311	434	470	404	650	610	526	611	657
ENSMUSG00000081999	chr2	Gm13461	4.2E+07	4.2E+07	662	0.181140606	2.545823308	0.4602481	0.557608985	0.06001	0	61	57	93	95	103	167	133	121	112	92
ENSMUSG00000003526	chr16	Prodh	1.8E+07	1.8E+07	3461	-0.20398633	2.913021599	0.4605675	0.557899655	0.0803	0	116	50	126	100	236	168	140	110	119	179
ENSMUSG00000020044	chr10	Timp3	8.6E+07	8.6E+07	8144	-0.15149161	6.920373826	0.4605581	0.557899655	0.04985	0	1864	1291	2265	1395	3010	3068	2318	1864	2165	2494
ENSMUSG00000031925	chr9	Maml2	1.4E+07	1.4E+07	6138	0.168585168	2.525335456	0.4606441	0.557944209	0.04872	0	76	50	99	83	99	171	131	88	98	137
ENSMUSG00000084319	chr6	Tpt1-ps3	1E+08	1E+08	519	-0.14399915	7.546880857	0.4607537	0.558028779	0.04536	0	3071	2376	3178	3006	2996	4359	4084	2899	3306	3756
ENSMUSG00000020377	chr11	Ltc4s	5E+07	5E+07	736	0.458196214	2.305133699	0.460807	0.558045184	0.43666	0	35	32	10	10	242	180	45	92	147	113

ENSMUSG00000049957	chr11	Ccdc137	1.2E+08	1.2E+08	3803	-0.15103262	3.100277612	0.4609665	0.558190079	0.04274	0	129	107	136	134	164	210	198	124	155	149
ENSMUSG00000022615	chr15	Tymp	8.9E+07	8.9E+07	2037	0.168844964	3.544139134	0.4610164	0.558202322	0.05849	0	119	89	311	181	153	268	249	179	285	288
ENSMUSG00000040658	chr17	Dnph1	4.6E+07	4.6E+07	1106	-0.23749338	2.236631111	0.4611159	0.558274675	0.10929	0	82	83	46	53	99	93	62	89	108	78
ENSMUSG00000026377	chr1	Nifk	1.2E+08	1.2E+08	1965	0.126122873	4.610657111	0.4611704	0.558292399	0.03202	0	327	296	395	295	436	626	488	464	506	524
ENSMUSG00000065124	chr2	Snora65	3.3E+07	3.3E+07	130	0.284947269	0.593536289	0.4618903	0.559115666	0.10776	0	12	21	23	14	24	54	19	20	31	37
ENSMUSG00000061559	chr9	Wdr61	5.5E+07	5.5E+07	4669	-0.12086185	4.151570196	0.4621857	0.559424954	0.02873	0	270	191	320	281	338	422	377	260	357	344
ENSMUSG00000074890	chr2	Lcmt2	1.2E+08	1.2E+08	3350	0.177342259	2.663678127	0.4627711	0.560085172	0.06303	0	57	52	153	74	124	169	158	110	119	129
ENSMUSG00000066361	chr12	Serpina3c	1E+08	1E+08	2213	-0.31875197	3.182865593	0.4628191	0.560094964	0.21491	0	107	92	82	42	472	211	113	143	164	191
ENSMUSG00000031534	chr8	Smim19	2.2E+07	2.2E+07	1458	0.125538937	5.456369168	0.4629407	0.560193846	0.03388	0	586	396	902	558	799	1088	914	736	934	1059
ENSMUSG00000029452	chr5	Tmem116	1.2E+08	1.2E+08	3732	0.333343158	0.292914979	0.4631405	0.56038728	0.18416	0	7	10	34	20	5	23	25	32	26	18
ENSMUSG00000010021	chr11	Kif19a	1.1E+08	1.1E+08	4068	0.299507047	0.44810362	0.4634057	0.560659729	0.10905	0	17	17	23	15	11	53	23	16	23	31
ENSMUSG00000039684	chr10	Gm5422	3.1E+07	3.1E+07	2906	-0.2177746	1.335854875	0.4636399	0.560894649	0.06986	0	34	23	60	40	44	56	52	44	46	32
ENSMUSG00000002428	chr3	Hltf	2E+07	2E+07	5931	0.169428269	2.712112853	0.4637341	0.560911906	0.05291	0	87	72	107	66	129	202	158	100	127	127
ENSMUSG00000027834	chr3	Serpini1	7.6E+07	7.6E+07	7286	-0.22826456	0.489395003	0.4637288	0.560911906	0.07285	0	18	19	27	18	24	29	33	16	19	28
ENSMUSG00000043290	chr7	Zfp784	5034439	5036479	2153	0.215664317	2.042628927	0.4638364	0.560987323	0.09231	0	32	28	107	60	66	99	86	54	78	133
ENSMUSG00000048277	chr11	Syngr2	1.2E+08	1.2E+08	1776	0.140859919	7.879214132	0.4639994	0.561135967	0.04404	0	3126	2347	4063	3605	3879	5142	5127	3805	6045	5385
ENSMUSG00000076437	chr2	2700094K13Rik	8.5E+07	8.5E+07	1131	0.162568688	3.084555147	0.4640442	0.561141832	0.05139	0	127	71	120	133	150	248	143	151	195	178
ENSMUSG00000080374	chr2	Gm22953	1.2E+08	1.2E+08	101	0.589143868	-0.12834216	0.4641907	0.561270587	0.67187	0	0	0	34	11	8	3	22	3	33	37
ENSMUSG00000058444	chr9	Map2k5	6.3E+07	6.3E+07	2309	-0.12571617	4.289540383	0.4643553	0.561372848	0.03116	0	310	187	378	287	398	398	386	318	388	425
ENSMUSG00000063696	chr8	Gm8730	1E+08	1E+08	1075	0.146270791	7.396647065	0.4643383	0.561372848	0.04733	0	2360	2074	2618	2426	2392	4633	3343	2892	3596	3876
ENSMUSG00000081281	chrX	Gm6274	3.7E+07	3.7E+07	797	0.296137546	0.213996141	0.4646651	0.56169891	0.12249	0	12	10	17	18	14	18	15	22	43	19
ENSMUSG00000024902	chr19	Mrpl11	4962306	4962515	2882	0.122869921	5.696184489	0.4648608	0.561887099	0.03262	0	716	519	934	726	880	1212	1119	859	1229	1157
ENSMUSG00000019738	chr7	Polr2i	3E+07	3E+07	1212	0.120102156	4.508592088	0.4650783	0.562081715	0.02942	0	292	240	369	322	427	545	442	377	531	544
ENSMUSG00000047166	chr15	Tigd5	7.6E+07	7.6E+07	2387	0.212005307	1.27327133	0.465102	0.562081715	0.07885	0	21	18	56	29	43	63	43	39	65	46
ENSMUSG00000000355	chrX	Mcts1	3.9E+07	3.9E+07	1571	0.123193099	4.9351548	0.4654068	0.562401632	0.03172	0	466	335	488	381	530	838	588	555	607	694
ENSMUSG00000032757	chr6	Bet1	4076899	4078036	3656	-0.12710052	4.3929255	0.4654934	0.562409318	0.03372	0	335	276	340	309	368	531	405	349	379	401
ENSMUSG00000087467	chr2	Gm13601	6.7E+07	6.7E+07	404	-0.80207041	0.69470044	0.4654894	0.562409318	1.28781	0	0	0	136	17	15	1	57	0	19	38
ENSMUSG00000025217	chr19	Btrc	4.5E+07	4.5E+07	6323	-0.12685684	4.654011127	0.465957	0.562921065	0.03341	0	327	264	618	397	411	524	582	336	574	480
ENSMUSG00000029084	chr5	Cd38	4.4E+07	4.4E+07	3014	0.166060891	2.632921188	0.4661705	0.563130408	0.05221	0	80	58	121	63	121	181	130	107	117	134
ENSMUSG00000082908	chr2	Gm13736	8.8E+07	8.8E+07	253	0.124773212	4.425882847	0.4662449	0.563171857	0.032	0	344	216	348	286	352	526	448	404	433	481
ENSMUSG00000058407	chr1	Txndc9	3.8E+07	3.8E+07	9102	-0.11728047	5.197078504	0.4670391	0.564053492	0.02948	0	561	419	760	537	614	965	710	549	676	755
ENSMUSG00000064264	chr7	Zfp428	2.5E+07	2.5E+07	1308	0.185924569	1.804665739	0.4670553	0.564053492	0.06503	0	33	26	73	54	60	81	65	63	84	77
ENSMUSG00000020105	chr10	Lrig3	1.3E+08	1.3E+08	4050	0.175576602	2.394247202	0.4673254	0.564282509	0.0568	0	68	57	93	58	91	130	114	110	85	119
ENSMUSG00000034484	chr18	Snx2	5.3E+07	5.3E+07	2013	0.16951295	4.869193463	0.4673192	0.564282509	0.06194	0	419	377	335	275	637	1042	642	488	558	502
ENSMUSG00000035722	chr10	Abca7	8E+07	8E+07	6752	-0.15532735	4.128993072	0.4678899	0.564915529	0.04998	0	173	153	455	320	339	352	404	215	385	363
ENSMUSG00000051652	chr10	Lrrc3	7.8E+07	7.8E+07	4296	0.279693847	0.531740442	0.4680036	0.565004151	0.10977	0	11	19	18	9	34	41	30	22	26	33
ENSMUSG00000032913	chr3	Lrig2	1E+08	1E+08	7111	0.14784431	3.431400095	0.4684256	0.565465009	0.04262	0	154	119	153	132	206	250	241	169	218	286
ENSMUSG00000022414	chr15	Tab1	8E+07	8E+07	2931	-0.13528694	4.584218996	0.4686327	0.565631341	0.03898	0	317	241	562	464	331	526	563	302	506	484
ENSMUSG00000027519	chr2	Rab22a	1.7E+08	1.7E+08	7206	-0.13496449	6.178286963	0.4686441	0.565631341	0.04062	0	1027	785	1628	1197	1146	1514	1754	1024	1427	1445
ENSMUSG00000097479	chr5	Gm26582	9.2E+07	9.2E+07	3135	-0.49476295	-0.13948132	0.4690246	0.566041887	0.41412	0	4	2	35	22	13	2	22	2	25	18
ENSMUSG00000050697	chr15	Prkaa1	5143861	5143995	4655	-0.122207	4.173766513	0.4690817	0.566062108	0.03074	0	279	191	304	294	353	458	386	252	334	365
ENSMUSG00000025139	chr7	Tollip	1.4E+08	1.4E+08	4333	-0.12224662	5.862864962	0.4693575	0.566346154	0.03313	0	857	691	1097	880	1058	1250	1212	880	1147	1269
ENSMUSG00000033486	chr2	Catsper2	1.2E+08	1.2E+08	3695	0.203792205	2.092399908	0.4694698	0.566433009	0.08036	0	42	32	109	47	74	100	74	71	85	129
ENSMUSG00000042055	chr7	Wdr11	1.3E+08	1.3E+08	10372	-0.11035418	4.960818842	0.4695269	0.566453115	0.02566	0	446	317	619	503	584	729	666	448	609	655
ENSMUSG00000020021	chr10	Fgd6	9.4E+07	9.4E+07	8241	-0.18412245	2.233086686	0.4698158	0.566752928	0.06412	0	85	59	105	52	68	97	113	62	96	80
ENSMUSG00000024826	chr19	Dpf2	5896516	5898631	6501	-0.12395339	5.838706441	0.4715651	0.568814198	0.03426	0	744	623	1157	903	1143	1208	1171	833	1234	1220
ENSMUSG00000007610	chr8	Gtpbp3	7.1E+07	7.1E+07	3984	-0.12399525	4.229087336	0.4717251	0.568958304	0.03186	0	280	199	421	262	330	431	427	262	407	332
ENSMUSG00000029048	chr4	Rer1	1.6E+08	1.6E+08	1814	0.129212661	6.110475725	0.4719629	0.569196131	0.03764	0	978	723	1115	922	1260	1862	1440	1184	1545	1435
ENSMUSG00000033722	chr1	BC034090	1.6E+08	1.6E+08	8222	0.288259517	1.645330932	0.4720693	0.569275596	0.16078	0	22	42	22	23	96	105	57	45	68	73
ENSMUSG00000048756	chr10	Foxo3	4.2E+07	4.2E+07	7571	-0.13124462	5.106120211	0.4721333	0.569303797	0.0383	0	579	391	604	662	444	803	677	515	728	676
ENSMUSG00000015879	chr5	Fam184b	4.6E+07	4.6E+07	4122	-0.33450562	1.931493225	0.472221	0.569360587	0.23476	0	58	27	109	113	10	74	115	47	58	49
ENSMUSG00000018347	chr11	Zkscan6	6.6E+07	6.6E+07	2371	0.185185275	2.07012207	0.4723086	0.569368333	0.06238	0	48	42	54	57	90	121	78	78	86	86
ENSMUSG00000050192	chr3	Eif5a2	2.9E+07	2.9E+07	5027	0.252322983	0.759403649	0.4722982	0.569368333	0.11067	0	18	12	42	11	30	54	47	24	24	31
ENSMUSG00000018677	chr11	Slc25a39	1E+08	1E+08	2756	0.152817693	6.239671153	0.4725781	0.569644269	0.0536	0	904	546	1415	1045	1712	1639	1678	1090	2161	1688
ENSMUSG00000020303	chr11	Stc2	3.1E+07	3.1E+07	5175	-0.30256727	2.643184643	0.4733831	0.570565606	0.20525	0	110	129	24	128	80	151	53	87	153	129
ENSMUSG00000062906	chr15	Hdac10	8.9E+07	8.9E+07	3379	-0.14237009	3.281997333	0.4737122	0.570913216	0.04123	0	140	114	149	159	201	240	176	133	193	212
ENSMUSG00000031834	chr8	Pik3r2	7.1E+07	7.1E+07	4176	0.115626604	4.78760983	0.4738591	0.571041152	0.02853	0	340	301	437	404	521	681	593	416	673	613
ENSMUSG00000091957	chr18	Rps2-ps10	6.1E+07	6.1E+07	965	0.210302462	1.673156958	0.4742576	0.571472281	0.07833	0	34	27	56	60	40	75	66	41	100	62
ENSMUSG00000060475	chr17	Wtap	1.3E+07	1.3E+07	5651	-0.11533589	4.708401727	0.4746293	0.571870971	0.02859	0	375	302	470	353	564	654	531	413	502	492
ENSMUSG00000019082	chr7	Slc25a22	1.4E+08	1.4E+08	4041	-0.20583135	4.518270878	0.4746837	0.571884584	0.0942	0	269	114	744	306	566	444	350	318	420	660
ENSMUSG00000027210	chr2	Meis2	1.2E+08	1.2E+08	12043	0.298326741	0.661567776	0.4748036	0.571884584	0.16068	0	10	15	13	12	52	49	30	30	26	32
ENSMUSG00000032289	chr9	Thsd4	6E+07	6E+07	13986	0.247384649	0.577385571	0.4747844	0.571884584	0.0791	0	15	19	24	20	16	27	34	28	31	33
ENSMUSG00000075028	chr2	Prdm11	9.3E+07	9.3E+07	17044	0.252039047	0.622599369	0.4747975	0.571884584	0.11224	0	8	12	42	19	21	31	28	26	41	33
ENSMUSG00000039230	chr11	Tbcd	1.2E+08	1.2E+08	8096	-0.12965153	4.359862243	0.4751288	0.572227052	0.03531	0	277	170	444	366	403	470	474	299	423	363
ENSMUSG00000037697	chr14	Ddhd1	4.6E+07	4.6E+07	6759	0.194171701	2.492934373	0.4755031	0.572628651	0.07303	0	85	57	67	50	132	166	126	78	111	137
ENSMUSG00000038717	chr9	Atp5l	4.5E+07	4.5E+07	511	0.142628726	8.440070328	0.4756001	0.57269639	0.04771	0	4515	2995	7521	5303	5160	8209	8313	5705	7164	8365
ENSMUSG00000003617	chr3	Cp	2E+07	2E+07	9566	-0.16504127	4.391196331	0.4758692	0.572884691	0.06148	0	328	287	249	242	549	631	423	303	319	389

ENSMUSG00000036046	chr15	5031439G07Rik	8.5E+07	8.5E+07	9604	-0.1546985	7.736692305	0.4758184	0.572884691	0.05605	0	3293	2488	5006	3319	2931	4328	5850	2929	4425	3467
ENSMUSG00000049047	chrX	Armcx3	1.3E+08	1.3E+08	3540	-0.14511737	3.833280827	0.475879	0.572884691	0.04544	0	263	168	276	213	193	368	323	228	220	256
ENSMUSG00000100214	chr7	6230415J03Rik	4E+07	4E+07	4560	-0.27970355	0.130118645	0.4759636	0.572937345	0.12977	0	13	21	13	12	21	27	12	12	13	30
ENSMUSG00000095403	chr8	Gm21092	2.1E+07	2.1E+07	4132	-0.1887538	2.653343949	0.4760362	0.572975469	0.07508	0	110	78	105	75	129	204	127	92	69	116
ENSMUSG00000020099	chr10	Unc5b	6.1E+07	6.1E+07	5852	0.165054428	3.059202201	0.4761399	0.573051125	0.0584	0	86	63	194	103	165	165	190	142	179	219
ENSMUSG00000070476	chr2	Fam217b	1.8E+08	1.8E+08	4559	-0.18264038	2.590650514	0.4761818	0.573052457	0.06777	0	93	56	75	95	164	161	109	85	105	119
ENSMUSG00000061887	chr4	Ssbp3	1.1E+08	1.1E+08	6582	0.116681906	4.655259335	0.4763691	0.573228629	0.02964	0	321	262	446	358	447	666	443	443	583	560
ENSMUSG00000060260	chr7	Pwwp2b	1.4E+08	1.4E+08	2640	0.170073323	2.630364783	0.4767063	0.573585229	0.05973	0	58	42	123	106	119	157	143	101	141	126
ENSMUSG00000022684	chr16	Bfar	1.4E+07	1.4E+07	4451	-0.12390524	5.833050233	0.4769179	0.573790621	0.03522	0	922	634	1181	822	950	1344	1150	863	1022	1273
ENSMUSG00000025466	chr7	Fuom	1.4E+08	1.4E+08	3272	0.135679275	4.485973627	0.4775737	0.574530275	0.04207	0	278	142	447	365	437	558	451	362	499	552
ENSMUSG00000031107	chrX	Rbmx2	4.9E+07	4.9E+07	1872	0.185791199	1.512135145	0.4777986	0.574751574	0.06181	0	38	22	52	31	55	63	54	50	67	66
ENSMUSG00000030084	chr6	Plxna1	8.9E+07	8.9E+07	9025	0.119738844	5.062682015	0.4780752	0.575035005	0.03203	0	400	379	503	448	692	729	853	565	715	719
ENSMUSG00000024191	chr17	Bnip1	2.7E+07	2.7E+07	5097	0.129445504	4.488933218	0.478455	0.575442437	0.03631	0	234	274	434	337	332	547	450	333	558	540
ENSMUSG00000099226	chrX	Mir7091	7.4E+07	7.4E+07	79	-0.24255325	1.490316979	0.4786049	0.575573416	0.12631	0	60	47	23	45	35	68	40	31	61	61
ENSMUSG00000036661	chr15	Dennd3	7.4E+07	7.4E+07	5703	0.205040376	2.09848237	0.4786658	0.575597275	0.09162	0	32	29	115	51	82	110	74	86	92	95
ENSMUSG00000101970	chr7	RP23-32A8.1	7.4E+07	7.4E+07	3778	0.165266986	3.040137056	0.4787193	0.575612218	0.05754	0	91	94	158	95	145	225	133	148	147	233
ENSMUSG00000020088	chr10	Sar1a	6.2E+07	6.2E+07	2611	-0.13150557	7.345578982	0.4787911	0.575649237	0.04091	0	2403	1797	3142	2674	2902	4000	3469	2440	3105	3116
ENSMUSG00000032481	chr9	Smarcc1	1.1E+08	1.1E+08	5672	-0.12032046	4.907247507	0.4791591	0.576001165	0.03284	0	444	360	488	576	459	689	637	455	608	581
ENSMUSG00000047656	chr19	Trpt1	6996131	6996524	1142	-0.13364635	3.766964656	0.479207	0.576001165	0.03695	0	189	142	293	215	245	280	233	213	281	321
ENSMUSG00000047789	chr13	Slc38a9	1.1E+08	1.1E+08	8904	-0.14689287	3.121457757	0.4791893	0.576001165	0.04551	0	129	108	176	136	132	204	213	113	141	183
ENSMUSG00000038227	chr6	Hoxa9	5.2E+07	5.2E+07	5580	-0.13398318	3.616758414	0.4796503	0.576484572	0.03738	0	199	124	204	179	266	279	254	173	225	276
ENSMUSG00000068923	chr3	Syt11	8.9E+07	8.9E+07	5205	0.143747797	3.209249777	0.4797497	0.576554687	0.04123	0	136	89	173	128	134	241	242	138	203	177
ENSMUSG00000034101	chr2	Ctnnd1	8.5E+07	8.5E+07	7319	0.119611129	5.820848577	0.4799724	0.576692764	0.03314	0	690	611	987	782	1049	1388	1307	913	1255	1232
ENSMUSG00000035459	chr10	Stab2	8.7E+07	8.7E+07	8757	-0.15346465	4.564321614	0.479988	0.576692764	0.0539	0	248	335	447	315	537	748	339	356	382	509
ENSMUSG00000038152	chr13	5033430I15Rik	4.6E+07	4.6E+07	952	-0.21315577	1.586353798	0.4799689	0.576692764	0.07595	0	39	18	77	53	58	66	66	35	55	59
ENSMUSG00000035456	chr5	Prdm8	9.8E+07	9.8E+07	3119	0.247917022	0.902835473	0.4802062	0.576905544	0.1126	0	12	9	44	36	25	46	45	24	35	49
ENSMUSG00000076281	chr9	Gm24270	5.6E+07	5.6E+07	57	-0.22800169	3.046171396	0.4803984	0.577087065	0.11199	0	139	46	280	138	95	209	134	161	150	112
ENSMUSG00000026621	chr1	Marc1	1.8E+08	1.8E+08	2246	0.400816078	0.598036477	0.4804774	0.577132457	0.31802	0	17	23	9	1	39	36	12	29	50	36
ENSMUSG00000021629	chr13	Slc30a5	1E+08	1E+08	3178	-0.1327131	3.888973249	0.4808554	0.577537103	0.03775	0	212	165	268	217	312	421	303	239	240	257
ENSMUSG00000056459	chr12	Zbtb25	7.6E+07	7.6E+07	3131	-0.17243949	2.139302287	0.481	0.577661316	0.05538	0	57	47	97	79	68	99	98	68	67	87
ENSMUSG00000022215	chr14	Fitm1	5.6E+07	5.6E+07	969	0.149186187	7.567471639	0.4811712	0.577817455	0.05337	0	2343	1705	3779	3127	2855	3640	4468	2786	5435	4319
ENSMUSG00000024667	chr19	Tmem216	1.1E+07	1.1E+07	1977	0.211269315	1.862251721	0.481237	0.577844401	0.08609	0	40	41	42	36	89	111	60	66	85	69
ENSMUSG00000085622	chr12	3110056K07Rik	7.1E+07	7.1E+07	1504	0.245025042	0.710071064	0.4812761	0.577844401	0.08778	0	18	17	22	21	27	56	29	16	29	45
ENSMUSG00000020843	chr11	Timm22	7.6E+07	7.6E+07	3183	0.116927739	5.258846555	0.481408	0.577953322	0.03141	0	557	371	772	546	547	899	880	651	874	799
ENSMUSG00000029735	chr6	Tpk1	4.3E+07	4.3E+07	4329	-0.22944147	0.485835195	0.4816674	0.578215206	0.08267	0	17	17	23	22	27	33	38	12	22	21
ENSMUSG00000009907	chr1	Vps4b	1.1E+08	1.1E+08	8905	-0.11396437	4.65736843	0.4818999	0.578444788	0.02927	0	368	296	420	390	502	651	596	358	441	477
ENSMUSG00000004462	chr16	Tbccd1	2.3E+07	2.3E+07	2702	-0.13828403	3.320385276	0.4821711	0.578607768	0.03961	0	126	114	205	154	193	241	206	162	160	205
ENSMUSG00000021276	chr12	Cinp	1.1E+08	1.1E+08	2029	0.120311078	4.127688335	0.4822006	0.578607768	0.0309	0	227	194	285	233	322	449	369	291	402	363
ENSMUSG00000061981	chr11	Flot2	7.8E+07	7.8E+07	2740	0.130398019	6.609681461	0.4821642	0.578607768	0.04057	0	1218	963	1691	1410	1851	2293	2220	1484	2537	2058
ENSMUSG00000093242	chr2	Gm24574	7.6E+07	7.6E+07	74	-0.32784465	1.574026365	0.4821554	0.578607768	0.21811	0	23	50	113	31	29	35	34	67	32	85
ENSMUSG00000030647	chr7	Ndufc2	9.7E+07	9.7E+07	754	0.134065338	6.935860021	0.482821	0.5793026	0.04331	0	1498	1023	2533	1859	2146	2922	2677	2017	2737	2899
ENSMUSG00000018167	chr11	Stard3	9.8E+07	9.8E+07	3557	0.120675862	3.986208606	0.4833821	0.579876571	0.03125	0	220	156	277	202	298	407	334	237	375	355
ENSMUSG00000026806	chr2	Ddx31	2.9E+07	2.9E+07	3534	0.152304207	3.018329408	0.4833437	0.579876571	0.04813	0	117	82	152	123	97	175	196	135	188	174
ENSMUSG00000047205	chr11	Dusp18	3895240	3895517	4632	0.297510381	4.2874117	0.483512	0.579982871	0.212	0	136	42	771	344	155	477	582	270	314	601
ENSMUSG00000040746	chr11	Rnf167	7.1E+07	7.1E+07	3539	0.122497004	5.648328532	0.4841122	0.580653137	0.03535	0	734	483	867	654	924	1243	1014	715	1171	1301
ENSMUSG00000043085	chr4	Tmem82	1.4E+08	1.4E+08	3991	0.327486893	0.456003841	0.4841579	0.580658276	0.22129	0	16	4	38	25	4	30	27	18	21	49
ENSMUSG00000037086	chrX	Prr32	4.5E+07	4.5E+07	1110	-0.59879764	0.472395492	0.4843905	0.580887582	0.7662	0	12	30	0	0	76	12	15	25	12	39
ENSMUSG00000026270	chr1	Capn10	9.3E+07	9.3E+07	4346	0.151169158	2.845007172	0.4845604	0.581010391	0.04647	0	100	71	98	100	139	162	160	115	172	161
ENSMUSG00000065399	chr18	Mir133a-1	1.1E+07	1.1E+07	87	-0.21881263	1.201310964	0.4845758	0.581010391	0.08936	0	33	41	31	31	37	49	48	36	28	49
ENSMUSG00000040331	chr7	Nsmce4a	1.3E+08	1.3E+08	2597	-0.11573925	5.038913905	0.4846382	0.581035585	0.03123	0	562	408	586	484	507	794	693	525	617	627
ENSMUSG00000034120	chr11	Srsf2	1.2E+08	1.2E+08	2958	0.128672566	6.246982574	0.4847908	0.581119206	0.03991	0	895	726	1397	1076	1492	1912	1513	1331	1603	1821
ENSMUSG00000057176	chr7	Gm166	1.3E+08	1.3E+08	2535	0.222940706	1.418004085	0.48478	0.581119206	0.10341	0	34	11	58	50	31	73	56	37	47	75
ENSMUSG00000025173	chr11	Wdr45b	1.2E+08	1.2E+08	4562	-0.1100478	4.57358478	0.4849545	0.581265805	0.02702	0	355	268	482	326	446	537	548	343	484	459
ENSMUSG00000024604	chr18	Rbm22	6.1E+07	6.1E+07	5338	0.117254204	4.183739503	0.4850863	0.581324416	0.03033	0	238	184	350	257	293	444	435	321	350	391
ENSMUSG00000028116	chr3	Myoz2	1.2E+08	1.2E+08	3399	0.588188673	7.517995841	0.4850849	0.581324416	0.81281	0	599	9	6492	4959	111	4199	5166	2683	2614	8379
ENSMUSG00000031982	chr8	Arv1	1.2E+08	1.2E+08	1165	0.204734073	1.174447597	0.4852213	0.581386823	0.06401	0	37	18	30	28	38	53	49	38	51	46
ENSMUSG00000044037	chr9	Als2cl	1.1E+08	1.1E+08	5848	-0.16513401	2.72434194	0.4852003	0.581386823	0.05594	0	73	82	131	85	157	174	123	85	113	148
ENSMUSG00000022956	chr16	Atp5o	9.2E+07	9.2E+07	2259	-0.15324816	9.066511587	0.4856296	0.581799932	0.05767	0	6985	4706	13519	10511	8103	10597	11573	7666	11145	11601
ENSMUSG00000029408	chr5	Abcb9	1.2E+08	1.2E+08	5817	-0.17676475	3.811189632	0.4856491	0.581799932	0.06991	0	147	93	424	271	243	264	292	179	316	309
ENSMUSG00000044991	chr2	1110034G24Rik	1.3E+08	1.3E+08	2117	0.166258739	2.3536127	0.4860005	0.582171187	0.05296	0	81	47	74	71	83	127	92	86	125	116
ENSMUSG00000022994	chr15	Adcy6	9.9E+07	9.9E+07	6017	-0.15377922	5.461206186	0.4860788	0.582215365	0.05632	0	513	408	743	620	1347	1114	702	680	873	945
ENSMUSG00000033111	chr14	3830406C13Rik	1.2E+07	1.2E+07	2477	0.133015777	3.80858541	0.4863835	0.582530581	0.03794	0	198	163	217	173	246	397	256	243	295	315
ENSMUSG00000059208	chr17	Hnrnpm	3.4E+07	3.4E+07	4701	0.125085448	6.563811612	0.4865486	0.582678493	0.03801	0	1254	954	1592	1328	1768	2498	2103	1543	1944	2157
ENSMUSG00000032198	chr9	Dock6	2.2E+07	2.2E+07	6556	0.144038148	4.017994403	0.4866491	0.582749113	0.04721	0	154	166	342	208	314	413	329	202	353	478
ENSMUSG00000082284	chrX	H3f3a-ps1	1E+08	1E+08	410	-0.32494276	-0.1742801	0.4869415	0.583049523	0.13718	0	16	12	13	12	12	13	18	20	14	5
ENSMUSG00000052040	chr7	Klf13	6.4E+07	6.4E+07	7535	-0.1259513	5.493952559	0.4869869	0.583054	0.03808	0	501	564	845	837	800	1004	1051	604	940	887
ENSMUSG00000097431	chr14	Gm26782	5.1E+07	5.1E+07	2650	0.230665233	0.772095168	0.4870873	0.583124514	0.0805	0	31	19	22	15	22	39	39	27	39	34

ENSMUSG00000063849	chr9	Ppcdc	5.7E+07	5.7E+07	2747	-0.13786563	3.241480181	0.4873955	0.583443707	0.04207	0	123	120	157	143	198	244	188	119	187	196
ENSMUSG00000032523	chr9	Hhatl	1.2E+08	1.2E+08	1911	-0.15073476	7.110995863	0.4875439	0.58357144	0.056	0	2118	1797	2209	2510	2157	2396	2612	2136	3634	2652
ENSMUSG00000024798	chr19	Htr7	3.6E+07	3.6E+07	3399	-0.25006084	0.4144111	0.487984	0.583985505	0.08417	0	19	12	29	16	27	22	31	22	25	15
ENSMUSG00000029454	chr5	Mapkapk5	1.2E+08	1.2E+08	6209	-0.12561449	6.278035629	0.4879866	0.583985505	0.03853	0	1190	851	1512	1314	1262	1769	1808	1071	1555	1526
ENSMUSG00000054387	chr1	Mdm4	1.3E+08	1.3E+08	14798	-0.1337725	5.180388076	0.4880147	0.583985505	0.04331	0	540	556	560	490	643	851	645	558	596	922
ENSMUSG00000043024	chr6	Gm16433	1.1E+08	1.1E+08	2248	-0.26641635	0.581996799	0.4887462	0.584810966	0.11094	0	20	23	23	26	21	23	23	34	30	17
ENSMUSG00000052713	chr18	Zfp608	5.5E+07	5.5E+07	6112	0.162607664	2.388874355	0.4891055	0.58518327	0.05101	0	67	48	97	74	84	171	108	75	101	114
ENSMUSG00000068394	chr2	Cep152	1.3E+08	1.3E+08	5768	-0.19292798	1.45797593	0.4891408	0.58518327	0.066	0	55	33	44	35	44	61	59	36	46	55
ENSMUSG00000021497	chr13	Txndc15	5.6E+07	5.6E+07	1521	-0.11065455	5.189894694	0.4892754	0.585294426	0.02921	0	594	433	676	506	643	846	818	502	782	701
ENSMUSG00000030286	chr6	Emc3	1.1E+08	1.1E+08	2422	0.121880971	6.20250991	0.4895062	0.58550932	0.03635	0	1013	747	1266	1062	1267	1825	1540	1241	1643	1679
ENSMUSG00000071661	chr19	Zbtb3	8802530	8802685	2037	0.266498399	0.779856064	0.4895386	0.58550932	0.1167	0	14	23	40	13	20	42	50	18	46	28
ENSMUSG00000073436	chr17	Eme2	2.5E+07	2.5E+07	6000	-0.16974071	2.953295183	0.4898606	0.585844571	0.06018	0	83	75	220	124	130	192	155	116	120	165
ENSMUSG00000075053	chr13	Vdac3-ps1	1.8E+07	1.8E+07	1306	-0.18613319	4.854884519	0.489918	0.585863179	0.08447	0	447	287	594	503	520	456	1217	307	456	405
ENSMUSG00000027394	chr2	Ttl	1.3E+08	1.3E+08	5945	0.123963498	4.09484564	0.4901124	0.586045703	0.03486	0	224	154	360	267	242	458	421	256	348	367
ENSMUSG00000032125	chr9	Robo4	3.7E+07	3.7E+07	4107	0.141688196	3.735800938	0.4905896	0.586566349	0.04707	0	139	117	249	155	323	312	282	223	293	323
ENSMUSG00000030738	chr7	Eif3c	1.3E+08	1.3E+08	3383	-0.13872562	7.378253836	0.4908817	0.58681554	0.04813	0	2224	1678	3617	3259	2554	3519	3610	2363	3537	3402
ENSMUSG00000036181	chr13	Hist1h1c	2.4E+07	2.4E+07	1560	-0.13376051	6.895189006	0.4908533	0.58681554	0.04452	0	1616	1210	2656	1796	2339	2460	2334	1587	2916	2494
ENSMUSG00000022386	chr15	Trmu	8.6E+07	8.6E+07	3974	-0.14757398	3.281691913	0.4911971	0.58710234	0.04526	0	129	84	227	154	194	224	199	146	155	224
ENSMUSG00000037455	chr10	Slc18b1	2.4E+07	2.4E+07	3258	-0.22490639	2.487822342	0.4912053	0.58710234	0.11336	0	86	71	47	56	191	115	108	82	118	102
ENSMUSG00000071180	chr13	Smim15	1.1E+08	1.1E+08	1852	0.133239087	3.960055896	0.4915589	0.587474917	0.04109	0	224	145	266	171	328	468	343	275	300	293
ENSMUSG00000034110	chr5	Kctd7	1.3E+08	1.3E+08	4368	0.146655758	2.831377647	0.4922917	0.588300582	0.04413	0	106	71	113	96	117	181	151	128	159	140
ENSMUSG00000046861	chr4	Hectd3	1.2E+08	1.2E+08	4901	-0.10799869	5.037022609	0.4923651	0.588338064	0.02768	0	407	380	676	510	621	723	744	459	654	699
ENSMUSG00000064342	chrMT	mt-Ti	3706	3774	69	0.20799318	6.728795451	0.4925885	0.588554923	0.10897	0	1263	790	1308	2026	2175	1373	3338	958	3299	2972
ENSMUSG00000025085	chr19	Ablim1	5.7E+07	5.7E+07	11949	0.139386933	5.977977205	0.4927401	0.588585675	0.04861	0	668	513	1221	1035	1230	1443	1549	906	1167	1818
ENSMUSG00000051351	chr4	Zfp46	1.4E+08	1.4E+08	5212	-0.12845912	4.67071808	0.4927323	0.588585675	0.03916	0	389	237	517	490	391	479	627	353	436	622
ENSMUSG00000089798	chr5	1700028K03Rik	1.1E+08	1.1E+08	8149	0.271306921	0.540250179	0.4926568	0.588585675	0.11085	0	28	14	18	8	23	36	41	24	21	30
ENSMUSG00000045410	chr13	Akr1e1	4590757	4593298	3514	-0.12097903	4.369720502	0.4928033	0.588611047	0.03487	0	319	292	333	279	370	493	388	325	428	404
ENSMUSG00000028932	chr5	Psmc2	2.2E+07	2.2E+07	5031	0.127002185	7.017893025	0.4933318	0.589192067	0.04063	0	1859	1353	2291	1801	2075	3278	2659	2250	2852	2928
ENSMUSG00000002129	chr11	Sf3a1	4160350	4160550	6147	0.122605612	4.732197184	0.4935618	0.589416618	0.03665	0	283	224	596	458	406	639	628	451	585	551
ENSMUSG00000022205	chr15	Sub1	1.2E+07	1.2E+07	3930	-0.12948937	5.588003886	0.4941581	0.590078406	0.04133	0	666	488	891	598	1247	1163	1066	702	929	913
ENSMUSG00000055943	chr2	Emc7	1.1E+08	1.1E+08	5826	0.116623822	5.744970662	0.4943235	0.590225736	0.0336	0	772	558	897	758	904	1349	1154	953	1156	1133
ENSMUSG00000026179	chr1	Pnkd	7.4E+07	7.4E+07	7832	0.123711083	5.356366252	0.4944805	0.590362867	0.0382	0	457	341	925	615	715	867	984	638	982	942
ENSMUSG00000024038	chr17	Ndufv3	3.2E+07	3.2E+07	2490	0.145820179	7.018031905	0.4947837	0.590656194	0.05427	0	1411	993	2702	2128	2388	2547	2846	2036	3354	3264
ENSMUSG00000034248	chr14	Slc25a37	6.9E+07	6.9E+07	6021	-0.11611574	4.625941514	0.4948104	0.590656194	0.03269	0	387	348	417	332	416	570	540	395	470	464
ENSMUSG00000019194	chr7	Scn1b	3.1E+07	3.1E+07	1801	0.145160293	9.398660836	0.4949384	0.590706402	0.05406	0	9932	6575	10937	10849	10122	13215	15571	10378	19270	14813
ENSMUSG00000028464	chr4	Tpm2	4.4E+07	4.4E+07	2909	0.1787571	12.35672097	0.4949152	0.590706402	0.082	0	67954	30245	129109	97109	62154	139336	95442	82591	118509	143560
ENSMUSG00000054770	chr1	Kctd18	5.8E+07	5.8E+07	12973	-0.15548078	2.540157723	0.4949788	0.590706402	0.05024	0	64	76	110	90	117	146	122	71	110	118
ENSMUSG00000099375	chr1	Gm28187	1E+08	1E+08	2134	-0.25330697	0.258362022	0.4951375	0.590845516	0.11584	0	25	19	20	14	9	27	22	11	21	24
ENSMUSG00000033446	chr14	Lpar6	7.3E+07	7.3E+07	5400	0.286020271	2.911338824	0.4951882	0.590855804	0.20116	0	94	51	62	33	291	279	100	135	141	193
ENSMUSG00000039347	chr6	Atp6v0e2	4.9E+07	4.9E+07	1832	0.116953273	5.787461545	0.4953757	0.591029226	0.03404	0	736	560	968	761	1012	1221	1317	838	1255	1324
ENSMUSG00000021963	chr14	Sap18	5.8E+07	5.8E+07	3781	0.113624767	5.67857355	0.495781	0.591462494	0.03198	0	693	531	895	717	899	1288	1088	813	1150	1177
ENSMUSG00000028851	chr4	Nudc	1.3E+08	1.3E+08	1425	0.1188648	5.697117997	0.4959024	0.591556954	0.03541	0	689	473	972	690	1007	1198	1178	778	1302	1146
ENSMUSG00000075467	chr2	Dnlz	2.6E+07	2.6E+07	2916	-0.1181165	5.381670291	0.4964604	0.592172253	0.03431	0	612	396	880	743	690	929	821	616	955	813
ENSMUSG00000020451	chr11	Limk2	3344256	3345884	6099	-0.11101975	4.268964661	0.4966351	0.592330281	0.02911	0	302	233	335	279	351	440	420	276	376	405
ENSMUSG00000003033	chr8	Ap1m1	7.2E+07	7.2E+07	3150	0.111920068	4.935060441	0.4969041	0.5926007	0.03086	0	398	258	668	444	504	735	690	454	726	692
ENSMUSG00000032298	chr9	Neil1	5.7E+07	5.7E+07	1871	0.142404545	3.128437459	0.4970675	0.5927452	0.0452	0	126	81	139	118	162	199	185	133	243	179
ENSMUSG00000038860	chr2	Garnl3	3.3E+07	3.3E+07	12352	0.308683845	0.297666139	0.4972019	0.592855074	0.18003	0	17	5	12	6	38	47	20	14	25	24
ENSMUSG00000024778	chr19	Fas	3.4E+07	3.4E+07	1801	0.174362397	2.527296062	0.4972941	0.592864135	0.06963	0	78	47	98	54	136	177	108	106	100	130
ENSMUSG00000024998	chr19	Plce1	3.8E+07	3.8E+07	15998	-0.12716118	3.863088104	0.4972924	0.592864135	0.03757	0	191	164	344	222	234	365	358	197	258	268
ENSMUSG00000021537	chr13	Cetn3	8.2E+07	8.2E+07	999	-0.1250375	3.919213826	0.497611	0.593191521	0.03662	0	244	161	288	250	245	416	335	223	237	291
ENSMUSG00000047098	chr14	Rnf31	5.6E+07	5.6E+07	4838	0.130826797	4.08306837	0.4977217	0.593273046	0.04153	0	185	134	382	268	286	443	365	232	426	377
ENSMUSG00000032452	chr9	Clstn2	9.7E+07	9.7E+07	5691	0.271127835	0.377239212	0.4979809	0.593493719	0.13295	0	18	8	14	11	32	24	14	28	32	33
ENSMUSG00000039220	chr17	Ppp1r10	3.6E+07	3.6E+07	5623	-0.14637906	4.010067586	0.4980274	0.593493719	0.05048	0	185	141	328	363	280	278	391	247	328	321
ENSMUSG00000040913	chr19	Fbxw4	4.6E+07	4.6E+07	3158	-0.11200522	5.011404334	0.4980337	0.593493719	0.03045	0	437	318	686	557	569	691	736	447	741	599
ENSMUSG00000034911	chr8	Ushbp1	7.1E+07	7.1E+07	3549	0.144776605	4.522938559	0.4985191	0.594021639	0.05263	0	248	195	413	234	622	629	465	326	503	593
ENSMUSG00000034341	chr11	Wbp2	1.2E+08	1.2E+08	3177	0.133471699	6.750840921	0.4985717	0.594033871	0.04599	0	1378	1042	1786	1540	2115	2177	2407	1578	2968	2539
ENSMUSG00000043635	chr5	Adamts3	9E+07	9E+07	7663	0.315460337	0.891562121	0.4986352	0.594059047	0.18767	0	32	29	9	24	15	71	24	38	29	39
ENSMUSG00000021149	chr13	Gtpbp4	8972071	8973274	2977	-0.1141942	5.536632176	0.4987846	0.594186613	0.03279	0	630	560	923	755	774	1071	992	738	834	967
ENSMUSG00000053279	chr19	Aldh1a1	2.1E+07	2.1E+07	2053	-0.15705851	6.61634958	0.4988807	0.594250533	0.06364	0	1264	692	2362	2197	1564	2556	1970	1449	1581	2107
ENSMUSG00000045007	chr11	Tubg2	1E+08	1E+08	1754	0.246914615	0.468059107	0.4991645	0.594516277	0.09959	0	12	8	20	28	21	28	33	14	37	32
ENSMUSG00000047907	chr2	Tshz2	1.7E+08	1.7E+08	7781	-0.13284188	4.049021009	0.4991885	0.594516277	0.04147	0	213	163	300	221	440	415	361	233	294	336
ENSMUSG00000030298	chr6	Sec13	1.1E+08	1.1E+08	1663	-0.11638312	5.942997753	0.4992979	0.594596087	0.03449	0	924	678	1167	970	1117	1435	1316	923	1319	1123
ENSMUSG00000038215	chr8	Cep44	5.7E+07	5.7E+07	2817	-0.14601381	2.694361037	0.4994186	0.594638809	0.04626	0	95	85	112	84	128	134	135	101	116	138
ENSMUSG00000083022	chr11	Rps15a-ps6	6172644	6173036	393	0.162821303	3.171841946	0.4993804	0.594638809	0.06017	0	116	107	192	101	119	237	135	137	227	241
ENSMUSG00000003527	chr16	Dgcr14	1.8E+07	1.8E+07	2819	0.135481248	3.42928557	0.4996457	0.594783106	0.04219	0	120	111	200	130	221	244	237	159	257	263
ENSMUSG00000028698	chr4	Pik3r3	1.2E+08	1.2E+08	5300	0.158697682	3.483857712	0.499667	0.594783106	0.06204	0	90	87	277	183	187	236	306	179	241	248
ENSMUSG00000029427	chr5	Zcchc8	1.2E+08	1.2E+08	4286	-0.12940485	3.616033291	0.4996603	0.594783106	0.0389	0	181	154	244	156	227	301	269	185	255	196

ENSMUSG00000053950	chr18	Adnp2	8E+07	8E+07	5012	-0.14843664	2.791310868	0.4997673	0.594801557	0.04886	0	101	74	137	103	133	179	133	105	99	157
ENSMUSG00000095325	chr17	Zfp870	3.3E+07	3.3E+07	5126	-0.14041752	3.156019212	0.4997311	0.594801557	0.04395	0	104	104	194	156	146	190	194	135	187	161
ENSMUSG00000097164	chr10	Cep83os	9.5E+07	9.5E+07	4135	-0.19782908	1.47135039	0.5005928	0.595733501	0.07588	0	41	19	58	52	51	82	47	36	41	55
ENSMUSG00000079469	chr9	Pigb	7.3E+07	7.3E+07	10434	-0.18060306	2.284787651	0.5010245	0.596196593	0.07351	0	58	74	97	66	85	81	113	46	108	121
ENSMUSG00000036751	chr7	Cox6b1	3.1E+07	3.1E+07	505	0.14461009	8.842786483	0.5011015	0.596237712	0.05522	0	5479	3475	10691	7545	6874	10325	10605	7520	10624	10782
ENSMUSG00000035770	chr8	Dync1li2	1E+08	1E+08	4633	-0.12171377	6.688209314	0.5011461	0.596240197	0.03861	0	1529	1168	2071	1649	1730	2318	2285	1515	1955	2176
ENSMUSG00000058586	chr15	Serhl	8.3E+07	8.3E+07	7393	0.124613694	5.113699985	0.5012753	0.596343333	0.03985	0	446	266	832	554	472	855	775	591	759	744
ENSMUSG00000102422	chr3	SCHIP1	6.8E+07	6.8E+07	2369	0.129740815	6.434239125	0.5013635	0.596397623	0.04397	0	1130	753	1855	1288	1347	2091	2353	1470	1656	1779
ENSMUSG00000043687	chr8	1190005I06Rik	1.2E+08	1.2E+08	1083	-0.38535552	1.198037705	0.5014296	0.596425682	0.33827	0	27	14	16	8	137	48	19	33	47	47
ENSMUSG00000010097	chr19	Nxf1	8757073	8757259	5980	0.122407736	6.543288859	0.502148	0.597190207	0.039	0	1259	1054	1521	1343	1538	2351	1917	1533	2062	2201
ENSMUSG00000027222	chr2	Pex16	9.2E+07	9.2E+07	1775	0.142827217	4.396928142	0.5021575	0.597190207	0.05144	0	294	193	299	219	533	528	369	344	562	473
ENSMUSG00000024163	chr17	Mapk8ip3	2.5E+07	2.5E+07	14558	-0.10681579	5.056301312	0.5023794	0.597332056	0.02841	0	430	368	744	532	559	789	675	459	684	724
ENSMUSG00000041219	chr2	Arhgap11a	1.1E+08	1.1E+08	5332	-0.19096219	1.412865778	0.5023998	0.597332056	0.07064	0	50	26	45	44	41	60	59	36	34	60
ENSMUSG00000074182	chr3	Znhit6	1.5E+08	1.5E+08	2813	-0.11715323	3.904761558	0.5024046	0.597332056	0.03296	0	239	189	258	212	263	342	287	216	319	317
ENSMUSG00000028295	chr4	Smim8	3.5E+07	3.5E+07	1510	0.135756919	3.530612321	0.5028036	0.597755854	0.04436	0	156	99	265	150	174	345	228	203	229	239
ENSMUSG00000032398	chr9	Snapc5	6.4E+07	6.4E+07	757	-0.1199397	4.164123912	0.5029783	0.597912887	0.03475	0	313	199	324	272	291	444	342	297	367	314
ENSMUSG00000020922	chr11	Lsm12	1E+08	1E+08	2388	-0.11218449	5.550303344	0.5032277	0.598158643	0.03229	0	665	565	827	749	859	1021	926	752	978	957
ENSMUSG00000038604	chr8	Fam65a	1.1E+08	1.1E+08	4109	0.11265552	5.038651286	0.5035656	0.598509597	0.03262	0	361	289	675	514	604	718	736	547	793	719
ENSMUSG00000036904	chr18	Fzd8	9212856	9216201	3346	0.154839126	2.474548706	0.5042948	0.599325425	0.05352	0	63	49	101	92	90	156	108	90	98	145
ENSMUSG00000035202	chr9	Lars2	1.2E+08	1.2E+08	3881	-0.16819759	8.422256642	0.5048017	0.599814407	0.07577	0	6460	2339	8213	6156	5016	7149	6852	6547	7405	4880
ENSMUSG00000046562	chr5	Unc119b	1.2E+08	1.2E+08	4603	-0.11266561	4.501669455	0.5048345	0.599814407	0.03179	0	335	294	396	296	443	520	537	331	460	404
ENSMUSG00000085172	chr18	Gm6542	3.7E+07	3.7E+07	772	-0.20855924	0.75406412	0.5047611	0.599814407	0.0808	0	25	19	28	36	19	37	31	25	25	34
ENSMUSG00000051041	chr7	Olfml1	1.1E+08	1.1E+08	1685	0.220996904	2.841495239	0.5051709	0.600163214	0.11898	0	95	92	50	54	196	238	163	105	148	145
ENSMUSG00000035329	chr12	Fbxo33	5.9E+07	5.9E+07	4466	0.168907997	2.075583655	0.5058238	0.600887978	0.05961	0	47	37	67	66	79	133	98	70	80	72
ENSMUSG00000002812	chr11	Flii	6.1E+07	6.1E+07	5039	-0.12950365	6.686231871	0.5060456	0.601100538	0.04466	0	1332	974	2301	1960	1722	2345	2292	1515	2127	1926
ENSMUSG00000017858	chr2	Ift52	1.6E+08	1.6E+08	2802	-0.11005513	4.328271888	0.5066058	0.601715049	0.03004	0	327	232	337	299	369	504	428	300	406	361
ENSMUSG00000086877	chrX	A230072C01Rik	2.1E+07	2.1E+07	1581	-0.21254754	0.984851943	0.5067283	0.601809636	0.09001	0	19	35	37	25	34	51	27	31	33	38
ENSMUSG00000017715	chr11	Pgs1	1.2E+08	1.2E+08	5333	0.10486629	4.93613157	0.5068211	0.601868793	0.028	0	432	293	562	429	532	726	713	525	721	579
ENSMUSG00000032232	chr9	Cgnl1	7.2E+07	7.2E+07	7844	-0.23573799	3.963542196	0.5069699	0.601994597	0.14478	0	225	132	151	131	689	497	212	200	253	339
ENSMUSG00000029192	chr5	Tbc1d14	3.6E+07	3.6E+07	9802	-0.10789188	4.488325129	0.5071478	0.602154859	0.02954	0	324	276	415	336	398	559	530	289	429	448
ENSMUSG00000050730	chr9	Arhgap42	8994329	8997685	7113	0.151681874	2.734241595	0.5075748	0.602610836	0.05155	0	75	75	129	81	112	193	129	128	126	134
ENSMUSG00000024451	chr18	Arap3	3.8E+07	3.8E+07	5224	0.120143162	4.284802709	0.5076745	0.602678209	0.03705	0	225	156	385	268	419	555	389	297	428	440
ENSMUSG00000047749	chr6	Zc3hav1l	3.8E+07	3.8E+07	6536	0.248653204	0.49746915	0.5079002	0.602848426	0.09896	0	22	15	14	10	28	36	36	19	34	22
ENSMUSG00000056228	chr8	Cars2	1.2E+07	1.2E+07	1846	-0.11223218	4.3886859	0.5079039	0.602848426	0.0313	0	330	230	410	341	328	423	494	315	437	403
ENSMUSG00000015337	chr2	Endog	3E+07	3E+07	1063	0.133338502	5.132517615	0.5080276	0.602944218	0.04755	0	382	253	856	583	547	711	727	584	873	872
ENSMUSG00000030612	chr7	Mrpl46	7.9E+07	7.9E+07	1392	-0.12296847	4.601345848	0.5081182	0.603000714	0.03782	0	324	214	609	424	386	551	583	363	490	416
ENSMUSG00000028894	chr4	Inpp5b	1.2E+08	1.2E+08	4657	-0.12084007	3.65510978	0.508163	0.603002883	0.03496	0	180	152	216	174	265	307	254	187	241	255
ENSMUSG00000060166	chr16	Zdhhc8	1.8E+07	1.8E+07	4867	0.115375711	5.145958041	0.5084402	0.603280799	0.03481	0	426	314	637	540	701	780	891	473	924	766
ENSMUSG00000099875	chr1	Gm15453	1.5E+08	1.5E+08	465	0.266334284	0.371186594	0.5086672	0.60349912	0.16808	0	15	6	28	7	29	36	38	27	10	21
ENSMUSG00000027030	chr2	Stk39	6.8E+07	6.8E+07	4955	0.196199495	2.296010788	0.5094752	0.604406626	0.09411	0	48	30	103	50	126	180	90	74	90	105
ENSMUSG00000028476	chr4	Reck	4.4E+07	4.4E+07	4779	-0.18027694	2.845581079	0.5101187	0.605118792	0.08279	0	120	113	89	73	161	221	121	90	117	152
ENSMUSG00000028684	chr4	Urod	1.2E+08	1.2E+08	2591	-0.11797016	5.857541286	0.5102904	0.605271355	0.03721	0	774	586	1208	1018	1038	1163	1290	785	1321	1211
ENSMUSG00000073643	chr1	Wdfy1	8E+07	8E+07	6488	-0.10827055	4.247964377	0.510549	0.605526854	0.02927	0	263	233	342	290	353	445	416	292	387	345
ENSMUSG00000095762	chr8	Gm16378	1.2E+08	1.2E+08	342	0.258361589	0.496476671	0.5107458	0.605709015	0.09875	0	17	20	14	15	21	34	20	26	39	26
ENSMUSG00000091625	chr6	Lsm5	5.7E+07	5.7E+07	774	0.181782217	1.896128559	0.5108163	0.605741425	0.06739	0	45	42	68	44	57	132	60	58	72	80
ENSMUSG00000055817	chr17	Mta3	8.4E+07	8.4E+07	5319	-0.15872647	3.0416736	0.5109476	0.605845893	0.06052	0	124	91	153	82	211	237	147	111	152	159
ENSMUSG00000031820	chr8	Babam1	7.1E+07	7.1E+07	1592	0.117762753	5.919925886	0.5112864	0.606145106	0.03734	0	801	617	966	922	1097	1293	1395	932	1521	1374
ENSMUSG00000064215	chr12	Ifi27	1E+08	1E+08	1467	0.253275292	6.156007701	0.511249	0.606145106	0.17602	0	932	427	579	380	2903	2223	1215	1202	1923	1494
ENSMUSG00000034168	chr12	Irf2bpl	8.7E+07	8.7E+07	4112	0.105588619	5.0733018	0.5113817	0.606206894	0.0289	0	384	361	583	497	642	756	831	496	748	788
ENSMUSG00000020908	chr11	Myh3	6.7E+07	6.7E+07	6057	0.404586612	7.738616354	0.5114759	0.606216015	0.44444	0	2595	16	3913	4210	4288	4189	4977	3934	6906	4917
ENSMUSG00000028795	chr4	Ccdc28b	1.3E+08	1.3E+08	2026	-0.16928884	3.440669355	0.5114409	0.606216015	0.07352	0	177	161	104	137	262	240	214	144	260	196
ENSMUSG00000030278	chr6	Cidec	1.1E+08	1.1E+08	1856	-0.52592704	6.389879504	0.5115441	0.60624573	0.73789	0	1400	730	19	66	5762	2211	563	1155	1776	1417
ENSMUSG00000029203	chr5	Ube2k	6.6E+07	6.6E+07	5173	0.112047574	5.769018276	0.5117162	0.606398398	0.03373	0	667	570	914	804	1032	1312	1176	914	1210	1234
ENSMUSG00000024277	chr18	Mapre2	2.4E+07	2.4E+07	10202	-0.11262531	5.310695304	0.5123205	0.607063163	0.03373	0	530	401	791	752	669	966	953	542	753	764
ENSMUSG00000035367	chr13	Rmi1	5.8E+07	5.8E+07	3522	-0.14284061	2.662976294	0.5127022	0.607464157	0.04792	0	88	78	97	99	131	145	127	104	104	131
ENSMUSG00000055723	chr7	Rras2	1.1E+08	1.1E+08	2272	0.109400022	4.654635976	0.5128822	0.607626115	0.03096	0	311	266	444	367	449	710	489	474	457	555
ENSMUSG00000005198	chr11	Polr2a	7E+07	7E+07	7067	-0.11868747	6.14177458	0.5130316	0.607649154	0.03845	0	935	746	1328	1218	1388	1455	1546	983	1453	1587
ENSMUSG00000017707	chr2	Serinc3	1.6E+08	1.6E+08	3840	0.139585027	7.71008926	0.5130053	0.607649154	0.05424	0	2511	1938	4350	2330	4402	5951	5916	3142	3849	4153
ENSMUSG00000040102	chr6	Klhl42	1.5E+08	1.5E+08	6267	0.157571838	2.506413591	0.5129636	0.607649154	0.05853	0	68	51	81	69	137	159	114	92	112	134
ENSMUSG00000031400	chrX	G6pdx	7.4E+07	7.4E+07	3080	0.294401629	4.360948506	0.5131198	0.607702346	0.23589	0	235	242	68	77	782	568	375	359	598	429
ENSMUSG00000038828	chr5	Tmem214	3.1E+07	3.1E+07	6024	-0.11609874	4.919988977	0.5133827	0.607962335	0.03537	0	360	288	588	620	556	668	641	400	674	637
ENSMUSG00000021687	chr13	Scamp1	9.4E+07	9.4E+07	4582	0.103106705	5.17952577	0.5136857	0.608269831	0.02822	0	544	344	635	483	656	873	842	620	752	781
ENSMUSG00000081249	chr11	Gm11517	9.7E+07	9.7E+07	387	0.223963884	1.181810764	0.5137545	0.608299856	0.1138	0	19	10	66	28	36	65	49	26	50	54
ENSMUSG00000022185	chr14	Acin1	5.5E+07	5.5E+07	8649	0.113244954	5.741037576	0.5138204	0.608326582	0.03463	0	695	568	884	836	898	1280	1107	827	1214	1331
ENSMUSG00000096173	chr15	Gm3150	7.3E+07	7.3E+07	204	-0.20552797	1.120635305	0.5138849	0.608351606	0.08402	0	41	19	31	44	32	39	53	31	31	45
ENSMUSG00000001663	chr10	Gstt1	7.6E+07	7.6E+07	1528	0.238624161	3.904839531	0.5141413	0.608603708	0.1545	0	158	149	115	80	563	501	246	253	351	327
ENSMUSG00000035642	chr7	Aamdc	9.8E+07	9.8E+07	1615	0.133862352	6.461901998	0.5147596	0.609284184	0.04955	0	1416	1066	1115	1063	1575	2232	1826	1586	2037	1814

ENSMUSG00000079560	chr6	Hoxa3	5.2E+07	5.2E+07	6014	-0.20538848	1.585899747	0.5149494	0.609457474	0.08608	0	35	32	66	53	52	55	66	42	31	85
ENSMUSG00000020448	chr11	Rnf185	3415982	3418087	2906	0.101720283	4.95463348	0.5151456	0.609638168	0.02745	0	406	285	625	442	539	731	771	471	680	675
ENSMUSG00000034203	chr6	Chchd4	9.1E+07	9.1E+07	1245	0.106263174	4.591216346	0.515246	0.60970554	0.02989	0	271	219	508	368	423	598	563	394	513	513
ENSMUSG00000041945	chr1	Mfsd9	4.1E+07	4.1E+07	5125	0.256703251	0.766382493	0.5153002	0.609718234	0.12312	0	23	16	9	33	26	32	46	32	39	28
ENSMUSG00000024269	chr18	Tpgs2	2.5E+07	2.5E+07	6840	-0.12963464	3.250527377	0.5153834	0.609720942	0.04147	0	149	102	148	157	189	214	209	121	211	184
ENSMUSG00000031060	chrX	Rbm10	2.1E+07	2.1E+07	3714	-0.11658964	4.113213325	0.5153894	0.609720942	0.03408	0	262	157	368	293	297	429	322	242	379	349
ENSMUSG00000030530	chr7	Furin	8E+07	8E+07	9178	-0.11691443	6.041244162	0.5155009	0.609801411	0.03783	0	926	762	1166	1097	1228	1394	1549	893	1444	1289
ENSMUSG00000022178	chr14	Ajuba	5.5E+07	5.5E+07	3503	0.202764585	2.022604758	0.5158647	0.610180318	0.0995	0	43	34	54	36	120	115	75	81	92	71
ENSMUSG00000014786	chr8	Slc9a5	1.1E+08	1.1E+08	5222	0.233319021	0.997177573	0.5169472	0.61140921	0.10592	0	16	28	31	18	37	48	29	26	43	66
ENSMUSG00000063568	chr6	Jazf1	5.3E+07	5.3E+07	2536	0.253970863	0.187679057	0.5170171	0.611440333	0.1093	0	16	11	12	6	26	30	19	20	26	20
ENSMUSG00000019295	chr5	Tmem129	3.4E+07	3.4E+07	2740	0.113484207	4.021467433	0.5170937	0.611442772	0.03198	0	222	170	296	226	263	489	349	249	348	318
ENSMUSG00000056820	chr8	Tsnax	1.3E+08	1.3E+08	2391	-0.12105868	7.042251675	0.5171064	0.611442772	0.04129	0	1954	1386	2732	2175	2227	2819	3022	2017	2528	2674
ENSMUSG00000024563	chr18	Smad2	7.6E+07	7.6E+07	3549	-0.12167553	3.728062852	0.5172399	0.611446017	0.0364	0	195	133	238	188	299	318	284	202	273	230
ENSMUSG00000092368	chr17	A930015D03Rik	3.6E+07	3.6E+07	1111	0.199393454	0.928190058	0.5172219	0.611446017	0.0652	0	26	18	23	31	27	52	42	29	37	39
ENSMUSG00000096917	chr8	2500002B13Rik	5.7E+07	5.7E+07	2618	0.167170956	2.247895889	0.5172187	0.611446017	0.06388	0	77	42	64	80	65	119	85	74	100	131
ENSMUSG00000049999	chr2	Ppp1r3d	1.8E+08	1.8E+08	3267	-0.23129951	2.735237733	0.5173531	0.6114768	0.14008	0	92	77	45	121	200	158	63	128	156	108
ENSMUSG00000060038	chr8	Dhps	8.5E+07	8.5E+07	2324	0.103504204	4.543227403	0.5173236	0.6114768	0.02736	0	300	245	426	363	364	604	501	348	547	505
ENSMUSG00000061601	chr5	Pclo	1.5E+07	1.5E+07	19182	-0.24278583	0.819483651	0.5174723	0.611566125	0.13789	0	28	31	13	39	18	37	37	27	31	26
ENSMUSG00000029430	chr5	Ran	1.3E+08	1.3E+08	2646	0.118666406	6.779948957	0.5175807	0.611591204	0.03963	0	1429	1224	1955	1492	1878	2864	2431	1928	2396	2197
ENSMUSG00000097919	chr8	Gm27021	1.2E+08	1.2E+08	758	-0.23725534	2.192572105	0.5175557	0.611591204	0.13709	0	56	33	70	41	187	89	62	77	106	84
ENSMUSG00000070697	chr5	Utp3	8.9E+07	8.9E+07	1601	0.101789417	5.048144055	0.5185838	0.612724861	0.02739	0	428	390	598	435	552	866	742	546	655	734
ENSMUSG00000036281	chr2	Snapc4	2.6E+07	2.6E+07	6622	-0.1583763	2.552936341	0.5187502	0.612869779	0.06119	0	87	79	78	78	134	152	97	79	110	131
ENSMUSG00000100680	chr6	1810044D09Rik	9.1E+07	9.1E+07	486	0.1764715	1.649400364	0.5190327	0.613151856	0.06325	0	43	35	45	41	49	76	49	49	77	81
ENSMUSG00000042207	chr1	Kdm5b	1.3E+08	1.3E+08	16555	0.115143663	3.745986843	0.519122	0.613205801	0.03316	0	184	140	233	173	242	308	294	229	278	319
ENSMUSG00000021938	chr14	Pspc1	5.7E+07	5.7E+07	4003	-0.11811716	3.544125188	0.5193334	0.613352109	0.03427	0	166	132	209	186	220	277	221	188	220	240
ENSMUSG00000025939	chr1	Ube2w	1.7E+07	1.7E+07	4930	-0.16232008	3.738669908	0.5193156	0.613352109	0.0694	0	170	144	207	137	430	333	276	221	204	259
ENSMUSG00000007589	chr14	Tinf2	5.6E+07	5.6E+07	1736	-0.11400414	3.782302499	0.5194319	0.613365187	0.03314	0	200	164	248	194	270	318	273	190	307	277
ENSMUSG00000078652	chr11	Psme3	1E+08	1E+08	2949	-0.11563846	6.111737482	0.5194051	0.613365187	0.03752	0	930	738	1361	1156	1308	1385	1531	1051	1455	1426
ENSMUSG00000020902	chr11	Ntn1	6.8E+07	6.8E+07	6277	0.139479567	4.376243016	0.5201006	0.61410307	0.05255	0	280	198	242	273	510	611	438	267	395	573
ENSMUSG00000028849	chr4	Map7d1	1.3E+08	1.3E+08	3652	0.129100218	8.072803634	0.5202206	0.614193118	0.04807	0	3292	2303	5302	4243	4762	6092	7459	3916	6145	5702
ENSMUSG00000059439	chr11	Bcas3	8.5E+07	8.5E+07	6085	-0.11316445	5.136400152	0.5204148	0.614370667	0.03499	0	495	333	731	686	544	734	731	508	805	714
ENSMUSG00000032375	chr9	Aph1b	6.7E+07	6.7E+07	5163	0.168600359	2.187656335	0.520478	0.614393529	0.06427	0	66	54	79	37	80	117	113	78	84	95
ENSMUSG00000031948	chr8	Kars	1.1E+08	1.1E+08	2249	-0.12014368	6.782599836	0.5207409	0.614652138	0.04134	0	1654	1183	2094	1978	1772	2339	2310	1596	2300	2387
ENSMUSG00000039046	chr2	Usp6nl	6322667	6322954	8059	0.139903241	3.020982185	0.5209322	0.614826252	0.04821	0	126	73	119	124	135	233	170	141	140	187
ENSMUSG00000032606	chr9	Nicn1	1.1E+08	1.1E+08	2835	-0.11685287	4.076076675	0.5212345	0.615131272	0.03627	0	313	193	282	220	304	374	341	243	361	350
ENSMUSG00000034957	chr7	Cebpa	3.5E+07	3.5E+07	2634	-0.39057964	5.684653183	0.521362	0.615229921	0.4328	0	719	447	119	90	3335	1354	575	785	948	933
ENSMUSG00000017446	chr11	C1qtnf1	1.2E+08	1.2E+08	3131	-0.1767668	3.819896123	0.5222935	0.616277359	0.08823	0	205	238	133	146	372	402	316	158	253	266
ENSMUSG00000038622	chr15	Med30	5.3E+07	5.3E+07	871	0.128347334	3.348056861	0.5225697	0.616551421	0.04205	0	136	102	183	119	197	249	194	196	211	229
ENSMUSG00000024069	chr17	Slc30a6	7.4E+07	7.4E+07	2171	0.138289629	2.737980857	0.5226639	0.616567388	0.04528	0	92	62	98	94	130	185	147	108	137	138
ENSMUSG00000028524	chr4	Sgip1	1E+08	1E+08	10136	-0.24517622	-0.10038505	0.5226712	0.616567388	0.12477	0	17	16	9	8	16	25	17	14	10	13
ENSMUSG00000068039	chr17	Tcp1	1.3E+07	1.3E+07	5030	-0.11986111	7.52792416	0.5229108	0.616798154	0.04179	0	2621	2102	3722	3028	3114	4155	3618	2976	3745	3748
ENSMUSG00000020652	chr12	Cenpo	4196004	4197106	7263	0.186402434	1.700318737	0.5229889	0.616838462	0.06987	0	40	38	38	48	55	96	81	38	79	58
ENSMUSG00000024855	chr19	Pacs1	5133688	5135025	4339	0.150148013	4.078527763	0.5231813	0.61701344	0.06385	0	172	99	444	281	270	383	439	220	431	375
ENSMUSG00000027865	chr3	Gdap2	1E+08	1E+08	3507	-0.13414642	3.030687384	0.5232779	0.617075516	0.0464	0	106	117	156	106	149	174	169	134	156	159
ENSMUSG00000067274	chr5	Rplp0	1.2E+08	1.2E+08	1659	0.125383483	7.999531564	0.5234611	0.61723962	0.04592	0	3797	2958	4179	3583	3778	6724	5020	4181	6024	5744
ENSMUSG00000002797	chr6	Ggct	5.5E+07	5.5E+07	4437	-0.14508092	2.476037517	0.523747	0.617524779	0.05134	0	77	73	92	94	93	129	91	89	107	119
ENSMUSG00000028576	chr4	Ift74	9.5E+07	9.5E+07	2656	0.155859356	2.469224395	0.5238751	0.617624009	0.0546	0	77	66	92	83	64	137	131	98	110	114
ENSMUSG00000057113	chr11	Npm1	3.3E+07	3.3E+07	2665	0.129267056	6.90520958	0.5239489	0.617659009	0.04861	0	1932	1301	1968	1621	1753	3528	2386	2247	2135	2636
ENSMUSG00000027559	chr3	Car3	1.5E+07	1.5E+07	2865	-0.19262477	10.83073457	0.5251994	0.619081115	0.10967	0	29641	16521	17601	23151	63791	38134	25487	34977	34848	38976
ENSMUSG00000090626	chr9	Tex9	7.2E+07	7.2E+07	8798	0.221667311	0.880336843	0.5253737	0.619234545	0.09731	0	21	23	15	20	40	57	35	25	33	45
ENSMUSG00000020515	chr11	Cnot8	5.8E+07	5.8E+07	2636	0.107876281	5.527804647	0.5256146	0.619466425	0.03298	0	690	502	821	602	732	1184	967	790	941	1058
ENSMUSG00000078126	chr14	Rpl23a-ps3	3.4E+07	3.4E+07	514	0.214177413	1.10886757	0.5256954	0.61950965	0.08284	0	19	31	30	31	29	56	51	27	37	59
ENSMUSG00000015937	chr13	H2afy	5.6E+07	5.6E+07	6809	0.113004725	6.046311271	0.5258658	0.619658387	0.03697	0	856	673	1071	1054	1159	1591	1388	1095	1486	1533
ENSMUSG00000097162	chr7	2310010J17Rik	9E+07	9E+07	451	0.223031768	1.306527091	0.5259193	0.619669378	0.12447	0	29	20	38	18	65	57	31	63	53	51
ENSMUSG00000027087	chr2	Itgav	8.4E+07	8.4E+07	10744	0.110973694	5.092685527	0.525992	0.619703	0.0344	0	518	364	658	506	416	874	824	596	691	668
ENSMUSG00000057103	chr6	Cml1	8.6E+07	8.6E+07	1345	0.228144593	0.504364561	0.5261121	0.619792455	0.09406	0	22	13	16	11	29	41	26	19	37	24
ENSMUSG00000001847	chr5	Rac1	1.4E+08	1.4E+08	2652	-0.1187204	7.576697321	0.5262226	0.619870483	0.04169	0	2805	2096	3629	2858	3770	4409	4493	2787	3791	3549
ENSMUSG00000029781	chr6	Fkbp9	5.7E+07	5.7E+07	3314	0.129632867	6.941087779	0.5264085	0.619985414	0.04936	0	1812	1525	1560	1615	2191	3547	2707	1991	2678	2445
ENSMUSG00000033707	chr15	Lrrc24	7.7E+07	7.7E+07	3912	-0.12817165	5.268173012	0.5263699	0.619985414	0.04669	0	474	303	885	740	738	693	910	480	884	858
ENSMUSG00000056305	chr6	Usp39	7.2E+07	7.2E+07	2425	-0.10531626	4.573164591	0.5265373	0.620085027	0.02946	0	326	239	505	382	436	509	443	407	498	488
ENSMUSG00000057098	chr11	Ebf1	4.5E+07	4.5E+07	9756	-0.16905294	4.210344359	0.5269118	0.620473977	0.08069	0	267	198	231	184	629	485	282	312	323	387
ENSMUSG00000045409	chr17	Trim39	3.6E+07	3.6E+07	7223	-0.11795398	3.568069635	0.5270241	0.620554012	0.03618	0	165	130	214	175	251	298	256	159	208	259
ENSMUSG00000029179	chr5	Zcchc4	5.3E+07	5.3E+07	10890	0.143006544	2.560553554	0.5271333	0.620630487	0.05095	0	65	45	123	90	105	142	140	90	118	142
ENSMUSG00000028745	chr4	Capzb	1.4E+08	1.4E+08	3299	0.120768432	7.868514535	0.5273198	0.620797972	0.04339	0	3262	2609	3852	3418	3691	5391	5051	3806	5757	5165
ENSMUSG00000027833	chr3	Shox2	6.7E+07	6.7E+07	3311	0.274512257	1.965647236	0.5275181	0.620927219	0.20267	0	52	39	26	18	128	168	55	56	65	96
ENSMUSG00000028978	chr5	Nos3	2.4E+07	2.4E+07	4132	-0.1510477	3.441698924	0.5274819	0.620927219	0.05827	0	107	101	223	160	299	217	195	179	237	219
ENSMUSG00000080989	chr2	Gm14048	1.3E+08	1.3E+08	1268	-0.2370076	0.224487826	0.5276766	0.621061697	0.10873	0	15	18	21	15	17	16	30	10	31	15

ENSMUSG00000029670	chr6	Ing3	2.2E+07	2.2E+07	4806	-0.14194106	2.64563311	0.5278419	0.621204126	0.04912	0	91	68	101	93	139	138	129	86	104	152
ENSMUSG00000025316	chr8	Banp	1.2E+08	1.2E+08	6632	0.159904483	2.686555276	0.5280706	0.621421056	0.06437	0	98	59	81	116	94	181	178	113	112	109
ENSMUSG00000047777	chr4	Phf13	1.5E+08	1.5E+08	3205	0.134471566	3.16372755	0.528184	0.621502377	0.04468	0	109	96	125	132	177	224	194	135	230	180
ENSMUSG00000027940	chr3	Tpm3	9E+07	9E+07	6085	-0.52852088	7.214658535	0.5284531	0.621766875	0.80579	0	157	93	8491	5717	300	2148	673	2114	929	6544
ENSMUSG00000057337	chr10	Chst3	6E+07	6E+07	6497	-0.25992585	0.358255449	0.5285598	0.621840273	0.12515	0	11	6	38	29	17	24	22	15	23	27
ENSMUSG00000028899	chr4	Taf12	1.3E+08	1.3E+08	4038	0.103689336	5.030088568	0.5287932	0.622062642	0.03	0	445	375	488	513	530	769	701	584	726	691
ENSMUSG00000063698	chr19	Sfxn4	6.1E+07	6.1E+07	2975	0.155360335	2.343856386	0.5290099	0.622265385	0.05907	0	61	49	101	73	75	166	92	78	86	126
ENSMUSG00000090136	chr9	Gm10177	3.7E+07	3.7E+07	444	-0.17092675	2.296873291	0.5295238	0.622817666	0.07323	0	89	68	102	56	65	122	70	87	89	97
ENSMUSG00000001472	chr8	Tcf25	1.2E+08	1.2E+08	3765	-0.11882447	7.126918791	0.5297799	0.623066615	0.04246	0	1870	1791	2488	2315	2459	3064	3041	1962	2988	2871
ENSMUSG00000028232	chr4	Tmem68	3549041	3550579	3462	0.151407722	2.472890096	0.5298581	0.623106377	0.05625	0	71	60	77	66	117	131	105	103	111	138
ENSMUSG00000020072	chr10	Pbld1	6.3E+07	6.3E+07	4889	0.250575	0.785689349	0.5299061	0.623110545	0.11919	0	30	14	19	22	25	56	38	12	27	54
ENSMUSG00000025364	chr10	Pa2g4	1.3E+08	1.3E+08	2751	0.112144643	5.913637614	0.5299642	0.623126645	0.03691	0	847	675	966	889	969	1588	1273	1114	1222	1245
ENSMUSG00000005225	chr6	Plekha8	5.5E+07	5.5E+07	7005	-0.14440094	2.574046501	0.5301172	0.623254289	0.05052	0	83	68	115	91	110	128	120	115	105	99
ENSMUSG00000072915	chr11	Gm12258	5.9E+07	5.9E+07	4429	0.209391135	0.771587928	0.5301934	0.623291692	0.06956	0	17	16	24	28	27	48	37	22	30	42
ENSMUSG00000018143	chr5	Mafk	1.4E+08	1.4E+08	3901	-0.11309033	4.42376645	0.5303597	0.623434864	0.03575	0	304	228	478	381	299	475	507	313	375	463
ENSMUSG00000026638	chr1	Irf6	1.9E+08	1.9E+08	7069	0.295941553	0.270248814	0.5306464	0.623719683	0.14641	0	18	11	15	24	4	26	20	16	33	30
ENSMUSG00000021868	chr14	Ppif	2.6E+07	2.6E+07	3641	-0.15485108	5.674113809	0.5306968	0.62372666	0.07095	0	583	332	1661	952	761	1067	1114	706	1085	1039
ENSMUSG00000025736	chr17	Jmjd8	2.6E+07	2.6E+07	2758	-0.11651557	3.945203136	0.5308085	0.623760017	0.0363	0	188	164	303	253	314	330	261	228	346	354
ENSMUSG00000057897	chr11	Camk2b	5969644	5971826	9125	-0.13405763	7.93621955	0.5308142	0.623760017	0.05447	0	3223	2619	5350	4736	3596	4246	6046	3643	5364	4779
ENSMUSG00000030735	chr8	Gm9755	6.8E+07	6.8E+07	1607	0.158525423	3.376080474	0.5310226	0.623952666	0.07153	0	89	86	244	196	139	171	264	182	258	234
ENSMUSG00000027881	chr3	Prpf38b	1.1E+08	1.1E+08	4750	0.112875297	4.635731813	0.5311627	0.624064996	0.03564	0	348	286	354	286	523	657	551	398	460	609
ENSMUSG00000098496	chr7	1810026B05Rik	7.4E+07	7.4E+07	5140	0.141350958	3.059578569	0.531312	0.624188153	0.05318	0	93	93	161	103	147	233	136	149	152	222
ENSMUSG00000069049	chrY	Eif2s3y	1010543	1010685	4161	-1.07941854	3.972689345	0.531468	0.624319089	3.01205	0	3	1	1140	1	786	1	1093	1	1	0
ENSMUSG00000034345	chr17	Gtf2h5	6079786	6079911	3855	0.11210582	5.607630334	0.5316448	0.624474449	0.03706	0	712	537	788	583	920	1250	1018	926	1020	980
ENSMUSG00000022340	chr15	Sybu	4.5E+07	4.5E+07	3599	0.224769037	1.278019563	0.5320618	0.624911919	0.1166	0	23	26	43	12	61	80	50	32	52	48
ENSMUSG00000025204	chr19	Ndufb8	4.5E+07	4.5E+07	3146	-0.13806764	8.618168528	0.5325994	0.625490998	0.05837	0	5177	3164	10667	7090	6163	8318	8713	5714	7908	8144
ENSMUSG00000037640	chr7	Zfp60	2.8E+07	2.8E+07	8390	-0.13446321	3.147284739	0.5329026	0.625794701	0.04702	0	146	97	196	134	122	197	204	136	145	183
ENSMUSG00000030246	chr6	Ldhb	1.4E+08	1.4E+08	1570	-0.36149722	8.199326335	0.5334526	0.626388079	0.3954	0	2508	228	15256	8045	1654	5126	7490	3478	3285	7495
ENSMUSG00000028102	chr3	Pex11b	9.7E+07	9.7E+07	5615	-0.09971857	4.620739135	0.5336505	0.626568094	0.02748	0	368	254	484	332	508	548	516	393	485	502
ENSMUSG00000014633	chr8	Cmc2	1.2E+08	1.2E+08	2043	-0.11349858	4.318476385	0.533974	0.626633117	0.03573	0	307	182	482	323	296	432	411	300	404	428
ENSMUSG00000021076	chr12	Actr10	7.1E+07	7.1E+07	4022	-0.10542813	5.72744848	0.5339323	0.626633117	0.03325	0	762	625	1005	855	894	1237	1123	826	1080	1010
ENSMUSG00000022808	chr16	Snx4	3.3E+07	3.3E+07	2442	0.103809827	4.356350536	0.5339007	0.626633117	0.03019	0	300	197	333	294	371	562	439	360	415	409
ENSMUSG00000027175	chr2	Tcp11l1	1E+08	1E+08	6877	0.145094032	2.41736813	0.5338312	0.626633117	0.05133	0	77	50	91	84	74	128	139	84	124	95
ENSMUSG00000030022	chr6	Adamts9	9.3E+07	9.3E+07	12527	-0.20170765	2.711562744	0.5338588	0.626633117	0.10784	0	68	63	119	70	225	173	87	137	111	101
ENSMUSG00000086825	chr1	Gm15675	1.3E+08	1.3E+08	3681	0.186183111	2.954520841	0.5337663	0.626633117	0.09134	0	103	128	65	81	138	221	138	123	160	205
ENSMUSG00000050490	chr10	Gm8394	8.5E+07	8.5E+07	952	0.190838956	0.851589786	0.5342646	0.626921756	0.07263	0	16	14	39	27	26	38	44	26	43	36
ENSMUSG00000027208	chr2	Fgf7	1.3E+08	1.3E+08	3248	-0.16299467	2.789107494	0.5350249	0.627754748	0.07352	0	133	69	168	81	99	180	177	96	86	134
ENSMUSG00000032512	chr9	Wdr48	1.2E+08	1.2E+08	3821	-0.10308456	4.027875946	0.535064	0.627754748	0.02974	0	244	197	298	234	295	387	349	226	328	339
ENSMUSG00000035473	chr17	Galm	8E+07	8E+07	2476	-0.23929391	2.487343487	0.5351798	0.627838103	0.15939	0	82	60	52	34	237	137	92	81	105	109
ENSMUSG00000061474	chr13	Mrps36	1E+08	1E+08	1274	-0.10322168	5.070253407	0.5354633	0.628118116	0.03094	0	499	329	702	609	509	729	711	535	697	662
ENSMUSG00000002109	chr2	Ddb2	9.1E+07	9.1E+07	2736	-0.15896912	1.76877535	0.536017	0.628714992	0.05767	0	44	36	75	48	65	79	60	39	66	83
ENSMUSG00000031841	chr8	Cdh13	1.2E+08	1.2E+08	11144	0.122423703	6.800927406	0.5360889	0.62874675	0.04632	0	1538	968	2048	2029	1554	2541	2617	1866	2447	2529
ENSMUSG00000030423	chr7	Pop4	3.8E+07	3.8E+07	1214	0.115619279	3.583477581	0.5362384	0.628869596	0.03713	0	163	113	243	143	216	302	249	208	240	278
ENSMUSG00000040532	chr5	Abhd11	1.4E+08	1.4E+08	2172	0.107338261	5.573588176	0.5364324	0.629044472	0.0351	0	576	415	981	736	835	1133	1004	778	1102	1084
ENSMUSG00000055334	chr9	Snupn	5.7E+07	5.7E+07	1391	-0.11931665	3.433050285	0.5365163	0.629090279	0.03771	0	169	123	212	163	176	234	249	169	213	195
ENSMUSG00000026740	chr2	Dnajc1	1.8E+07	1.8E+07	11651	0.105564438	4.097764048	0.5366676	0.629169525	0.03055	0	222	180	325	262	255	438	393	268	355	380
ENSMUSG00000032306	chr9	Mpi	5.8E+07	5.8E+07	3142	-0.13116334	5.847060321	0.5367185	0.629169525	0.05246	0	707	516	1444	1184	797	1102	1360	864	1179	1162
ENSMUSG00000039914	chr10	Coq10a	1.3E+08	1.3E+08	2502	-0.15115796	8.535286866	0.5366824	0.629169525	0.07136	0	5020	2853	10862	7112	4757	7874	8896	5385	6659	7683
ENSMUSG00000061100	chr16	Retnla	4.9E+07	4.9E+07	598	-0.34873296	5.590504047	0.5368422	0.62926192	0.37329	0	659	692	114	246	2425	1526	263	522	576	1605
ENSMUSG00000029993	chr6	Nfu1	8.7E+07	8.7E+07	2078	0.101131226	5.324817998	0.5370945	0.62948915	0.03053	0	528	432	691	540	742	957	804	708	890	902
ENSMUSG00000042198	chr4	Chchd7	3938888	3938962	4060	-0.10488091	4.226061995	0.5371258	0.62948915	0.03054	0	272	180	384	308	337	408	396	264	361	436
ENSMUSG00000062234	chr5	Gak	1.1E+08	1.1E+08	5938	0.110792549	4.519317515	0.5377955	0.630221395	0.03597	0	274	232	378	269	539	605	547	346	458	518
ENSMUSG00000007646	chr11	Rad51c	8.7E+07	8.7E+07	4384	-0.28267428	-0.28899404	0.5378667	0.630252123	0.16813	0	12	6	20	5	18	26	5	6	11	20
ENSMUSG00000046806	chr6	3110062M04Rik	3.5E+07	3.5E+07	4269	0.148442987	2.468983161	0.5383285	0.630740562	0.05401	0	63	68	80	72	104	138	100	90	134	128
ENSMUSG00000001016	chr3	Ilf2	9E+07	9E+07	1973	0.106001035	5.12209887	0.5384206	0.63079578	0.03284	0	497	433	481	487	589	900	726	578	796	728
ENSMUSG00000039286	chr3	Fndc3b	2.7E+07	2.7E+07	11485	-0.12414356	4.234188802	0.5391988	0.63165471	0.04595	0	228	263	309	254	416	399	535	267	300	364
ENSMUSG00000062691	chr17	Cebpzos	7.9E+07	7.9E+07	1131	0.114746034	3.728040632	0.5393344	0.631760816	0.03609	0	201	141	215	181	213	328	248	233	303	296
ENSMUSG00000026826	chr2	Nr4a2	5.7E+07	5.7E+07	4059	0.244734552	0.115411472	0.5395395	0.6319483	0.09604	0	10	9	16	20	12	30	31	10	17	23
ENSMUSG00000033282	chr8	Rpgrip1l	9.1E+07	9.1E+07	9855	-0.17262059	1.470899611	0.5397659	0.632160698	0.06697	0	44	35	50	42	41	58	70	44	48	39
ENSMUSG00000032604	chr9	Qars	1.1E+08	1.1E+08	7267	-0.11163071	6.58120091	0.5398454	0.63220102	0.03915	0	1411	1117	1716	1631	1612	2207	2104	1324	1972	1978
ENSMUSG00000028937	chr4	Acot7	1.5E+08	1.5E+08	2124	0.129595981	4.443543153	0.5401644	0.632521828	0.05202	0	247	132	526	389	337	490	492	346	470	546
ENSMUSG00000028389	chr4	Zfp37	6.2E+07	6.2E+07	3692	-0.20272366	0.434877245	0.5403243	0.632656145	0.08006	0	20	14	28	16	24	30	31	21	14	24
ENSMUSG00000020973	chr12	Dnaaf2	6.9E+07	6.9E+07	3390	-0.1664646	2.023646655	0.5407392	0.633089206	0.06576	0	62	29	94	56	87	102	85	61	79	61
ENSMUSG00000033450	chr17	Tagap	7926000	7926108	3076	-0.18988694	1.121590126	0.5409797	0.633317808	0.08011	0	27	20	49	44	29	39	55	32	31	43
ENSMUSG00000006678	chrX	Pola1	9.3E+07	9.3E+07	8813	0.211867668	1.138847018	0.5411681	0.633485506	0.08697	0	27	31	27	24	34	69	47	30	57	32
ENSMUSG00000024594	chr18	Prrc1	5.7E+07	5.7E+07	4801	-0.09774751	5.190820084	0.541709	0.634045619	0.0287	0	539	380	746	590	619	906	695	591	731	718
ENSMUSG00000024966	chr19	Stip1	7020696	7021171	2173	-0.11958679	6.733718427	0.541737	0.634045619	0.0452	0	1415	1063	2613	1653	1826	2149	2262	1653	2437	2009

ENSMUSG00000020430	chr11	Pes1	3963975	3964060	3024	0.101295643	5.509164485	0.5422307	0.634570491	0.03167	0	604	468	799	684	779	1109	927	800	986	1027
ENSMUSG00000035601	chr4	Trmt10b	4.5E+07	4.5E+07	2641	-0.14982708	2.22478315	0.5423466	0.634637323	0.05813	0	85	50	102	54	75	98	109	65	97	81
ENSMUSG00000079225	chr9	Gm9531	8.2E+07	8.2E+07	1080	-0.15271477	2.149923068	0.5423783	0.634637323	0.05424	0	66	38	97	72	79	98	89	77	82	76
ENSMUSG00000038742	chr9	Angptl6	2.1E+07	2.1E+07	1581	0.156187333	2.560953213	0.5425161	0.634745692	0.06365	0	89	58	78	77	112	153	118	74	182	112
ENSMUSG00000047735	chr6	Samd9l	3372257	3377281	5425	0.158030016	3.235523489	0.5432841	0.635591141	0.06895	0	149	120	110	113	157	335	232	117	147	213
ENSMUSG00000022899	chr16	Slc15a2	3.7E+07	3.7E+07	7360	-0.2525447	1.71908648	0.5434017	0.635675726	0.19452	0	53	80	16	29	64	99	64	35	65	48
ENSMUSG00000042406	chr15	Atf4	8E+07	8E+07	1724	0.115791333	7.873678772	0.5435148	0.63575507	0.04324	0	3023	2481	4230	3038	4416	5820	4647	4009	5154	5566
ENSMUSG00000024955	chr19	Esrra	6910977	6912010	2539	-0.15729287	6.730110027	0.5437699	0.635947364	0.07934	0	1155	710	3246	2048	1764	1978	2740	1247	2112	2416
ENSMUSG00000029614	chr5	Rpl6	1.2E+08	1.2E+08	2433	0.114531951	7.645854573	0.5437561	0.635947364	0.04222	0	2731	2244	3219	2961	3311	5035	4170	3165	4611	4632
ENSMUSG00000024304	chr18	Cdh2	1.7E+07	1.7E+07	8066	-0.26503107	1.037619013	0.5438778	0.635967465	0.16917	0	24	12	26	20	88	57	41	29	32	25
ENSMUSG00000047881	chr5	Rell1	6.4E+07	6.4E+07	3863	0.121830226	3.605384775	0.5438431	0.635967465	0.03988	0	172	159	189	165	171	294	273	195	268	272
ENSMUSG00000000320	chr11	Alox12	7E+07	7E+07	4085	0.35525033	1.409978992	0.5441642	0.63624938	0.40047	0	6	3	112	43	23	30	126	29	58	52
ENSMUSG00000000959	chr14	Oxa1l	5.4E+07	5.4E+07	2534	-0.1144785	6.108200436	0.5448857	0.637039878	0.04169	0	1009	615	1501	1188	1220	1440	1541	906	1429	1581
ENSMUSG00000081967	chr2	Gm14017	1.2E+08	1.2E+08	386	0.228735319	0.27007281	0.545222	0.637379918	0.09399	0	12	13	13	13	25	21	30	12	29	31
ENSMUSG00000026578	chr1	Ccdc181	1.6E+08	1.6E+08	1909	0.119256088	3.419846508	0.5453969	0.63753118	0.03922	0	139	109	205	151	170	231	287	153	242	235
ENSMUSG00000006050	chr18	Sra1	3.7E+07	3.7E+07	4684	0.099170843	5.402323488	0.545523	0.637574072	0.03093	0	561	381	819	600	782	1121	962	652	916	897
ENSMUSG00000030316	chr6	Tamm41	1.2E+08	1.2E+08	5276	0.129831454	2.719370505	0.5455245	0.637574072	0.04423	0	100	64	111	87	107	160	138	121	139	138
ENSMUSG00000024076	chr17	Vit	7.9E+07	7.9E+07	2720	0.214509555	1.810524301	0.5458382	0.637887547	0.13436	0	26	20	59	31	117	105	66	47	66	98
ENSMUSG00000079164	chr1	Tlr5	1.8E+08	1.8E+08	4790	-0.36616412	0.153554368	0.5464438	0.638542074	0.36338	0	7	19	3	3	55	27	19	14	19	13
ENSMUSG00000040289	chr3	Hey1	8663359	8665064	3265	-0.16763788	2.003769934	0.5465774	0.638644984	0.07033	0	32	44	87	74	82	82	93	49	82	78
ENSMUSG00000038070	chr4	Cntln	8.5E+07	8.5E+07	7102	0.171582221	1.819219791	0.5466405	0.638665528	0.07177	0	42	43	53	45	58	105	77	68	45	79
ENSMUSG00000039458	chr15	Mtmr12	1.2E+07	1.2E+07	4785	0.14948272	2.529918209	0.5470072	0.639040705	0.06566	0	48	48	114	90	119	155	153	83	135	97
ENSMUSG00000019802	chr10	Sec63	4.3E+07	4.3E+07	8787	0.104194012	5.599886805	0.5473545	0.639393212	0.03419	0	694	547	785	663	823	1390	1049	801	927	1051
ENSMUSG00000040599	chr11	Mis12	7.1E+07	7.1E+07	3003	0.123615415	3.095129384	0.5478561	0.63992581	0.04347	0	123	79	137	112	166	237	166	154	178	174
ENSMUSG00000033735	chr6	Spr	8.5E+07	8.5E+07	1230	-0.10317854	5.492259039	0.547912	0.639937894	0.03381	0	670	454	869	754	806	1010	886	602	1084	930
ENSMUSG00000070426	chr7	Rnf121	1E+08	1E+08	4427	0.104321702	5.421536833	0.5480343	0.640027407	0.03406	0	629	480	685	626	672	1059	1095	645	1002	813
ENSMUSG00000024953	chr19	Prdx5	6906697	6907127	2139	0.126476723	7.606470416	0.5480841	0.640032308	0.05286	0	2267	1511	4484	2970	3368	4168	4855	2786	4664	4690
ENSMUSG00000074754	chr2	Gm561	1.4E+08	1.4E+08	471	-0.10243256	4.593939422	0.5483151	0.640248717	0.03194	0	402	274	489	330	390	563	421	408	505	490
ENSMUSG00000096971	chr15	4930556M19Rik	1.1E+07	1.1E+07	4029	-0.19416986	1.189240238	0.5483898	0.640282631	0.08463	0	34	15	53	36	43	34	64	30	40	42
ENSMUSG00000057649	chr13	Brd9	7.4E+07	7.4E+07	2406	0.106193522	3.92593455	0.5489126	0.640839653	0.03191	0	201	173	255	217	250	427	317	236	300	351
ENSMUSG00000013593	chr1	Ndufs2	1.7E+08	1.7E+08	2313	-0.12735584	10.08997229	0.5494382	0.641399947	0.05413	0	14972	9873	27223	18790	17459	22077	27077	15600	21091	22300
ENSMUSG00000003208	chr17	Ccdc94	5.6E+07	5.6E+07	1311	0.136243348	2.747692729	0.5495748	0.641452634	0.04977	0	92	71	129	89	96	189	113	116	144	154
ENSMUSG00000056870	chr1	Gulp1	4.5E+07	4.5E+07	3758	-0.14899855	1.893031782	0.5495575	0.641452634	0.06016	0	58	46	60	44	79	71	77	46	85	77
ENSMUSG00000099519	chr1	Gm29253	7.5E+07	7.5E+07	5231	-0.12045345	7.215060893	0.549704	0.641549982	0.04813	0	2147	1646	2635	2777	2477	2803	3098	2054	3582	3202
ENSMUSG00000035305	chr4	Ror1	1E+08	1E+08	5762	0.218469019	0.9012844	0.55015	0.642017186	0.09731	0	27	27	20	17	28	42	60	25	38	32
ENSMUSG00000035351	chr10	Nup37	8.8E+07	8.8E+07	1362	0.162347093	2.299714784	0.5502676	0.642100911	0.07523	0	69	35	88	82	75	159	112	100	67	87
ENSMUSG00000046668	chr18	Cxxc5	3.6E+07	3.6E+07	2271	0.111701738	5.137520753	0.5504391	0.642247667	0.03968	0	427	377	457	663	608	828	687	606	857	778
ENSMUSG00000036782	chrX	Klhl13	2.3E+07	2.3E+07	4253	-0.16104693	3.092448398	0.5505375	0.642309059	0.0815	0	163	129	76	107	174	198	191	130	167	139
ENSMUSG00000008690	chr15	Ncaph2	8.9E+07	8.9E+07	4198	-0.1087087	6.084195154	0.5508706	0.642590703	0.03873	0	882	726	1367	1153	1251	1403	1436	961	1586	1376
ENSMUSG00000020224	chr10	Llph	1.2E+08	1.2E+08	1517	0.12024704	3.504299068	0.5508324	0.642590703	0.04063	0	160	139	201	135	173	313	216	182	255	250
ENSMUSG00000020740	chr11	Gga3	1.2E+08	1.2E+08	6245	0.10299057	4.23112984	0.5510962	0.642746958	0.03165	0	212	220	315	251	369	479	414	299	412	404
ENSMUSG00000053293	chr5	Pom121	1.4E+08	1.4E+08	5581	-0.1087356	4.208469792	0.5510682	0.642746958	0.03579	0	222	216	322	278	419	382	350	283	421	390
ENSMUSG00000098973	chr9	Mir6236	1.1E+08	1.1E+08	123	0.163202872	5.598249786	0.5512646	0.642889937	0.08904	0	816	218	1050	815	682	1113	838	1148	1245	793
ENSMUSG00000033985	chr4	Tesk2	1.2E+08	1.2E+08	4272	-0.17945973	1.302417945	0.5515493	0.643168533	0.07081	0	36	25	67	32	33	59	48	36	45	42
ENSMUSG00000047694	chrX	Yipf6	9.9E+07	9.9E+07	7149	-0.10512102	4.131544128	0.5522501	0.643932198	0.03433	0	270	218	278	234	360	423	343	252	334	395
ENSMUSG00000031059	chrX	Ndufb11	2.1E+07	2.1E+07	908	-0.12312793	8.273271798	0.5523348	0.643977372	0.05115	0	4480	2884	7392	5550	4537	6410	6547	4543	6775	6384
ENSMUSG00000036120	chr8	Rfxank	7E+07	7E+07	3676	0.114674398	3.417849195	0.5524347	0.644040377	0.03973	0	164	87	196	142	193	272	220	167	241	243
ENSMUSG00000040459	chr8	Arglu1	8666577	8667416	1711	-0.09684287	5.395103362	0.5526542	0.644242645	0.03039	0	617	464	791	654	773	933	882	581	852	976
ENSMUSG00000022779	chr16	Top3b	1.7E+07	1.7E+07	8340	-0.1014813	4.090483337	0.5532314	0.644861978	0.03154	0	235	210	292	257	329	377	390	259	351	315
ENSMUSG00000093677	chr15	Gm20712	5.9E+07	5.9E+07	1491	0.180069421	2.309620058	0.5533948	0.644998752	0.09955	0	54	20	124	84	80	98	110	66	115	146
ENSMUSG00000045629	chr18	Sh3tc2	6.2E+07	6.2E+07	4536	-0.20126327	1.045593394	0.5535302	0.645102969	0.0889	0	30	14	50	21	50	37	41	22	44	46
ENSMUSG00000055694	chr8	Gdf1	7E+07	7E+07	1349	-0.12997071	3.986449783	0.553769	0.645327728	0.05414	0	244	194	201	208	395	309	337	179	389	359
ENSMUSG00000027327	chr2	1700037H04Rik	1.3E+08	1.3E+08	2286	-0.34595816	3.87013471	0.5538282	0.645339601	0.39324	0	233	67	55	35	950	335	167	233	329	246
ENSMUSG00000029777	chr6	Gars	5.5E+07	5.5E+07	2390	-0.10815093	6.41907181	0.5538712	0.645339601	0.03899	0	1192	835	1763	1368	1678	1807	1726	1363	1771	1816
ENSMUSG00000049760	chr17	2410015M20Rik	5.7E+07	5.7E+07	755	0.100882046	5.593654698	0.5541259	0.645582676	0.03359	0	577	478	1013	700	809	1188	1088	755	1132	1017
ENSMUSG00000048796	chr3	Cyb561d1	1.1E+08	1.1E+08	5086	0.123609761	3.042491385	0.5550663	0.646624626	0.04219	0	107	80	163	111	135	232	196	109	168	186
ENSMUSG00000073775	chr4	Kti12	1.1E+08	1.1E+08	1629	0.098331488	4.757901727	0.555185	0.646709194	0.03021	0	383	317	402	393	453	613	567	482	604	598
ENSMUSG00000078247	chr17	Airn	1.3E+07	1.3E+07	3583	-0.14630548	2.370083085	0.5553753	0.646877054	0.05934	0	107	55	84	68	86	134	93	77	95	101
ENSMUSG00000044149	chrX	Nkrf	3.7E+07	3.7E+07	3268	-0.15939352	1.662789143	0.5557168	0.647221087	0.06548	0	39	30	50	68	59	59	60	48	67	64
ENSMUSG00000027221	chr2	Chst1	9.3E+07	9.3E+07	2680	0.285618679	2.815578801	0.5557929	0.647256015	0.26301	0	94	61	24	28	279	220	91	111	161	210
ENSMUSG00000024248	chr17	Cox7a2l	8.4E+07	8.4E+07	1147	0.111345913	6.340004969	0.5559813	0.647421594	0.04217	0	1054	692	1733	1268	1266	1845	1820	1250	1881	1922
ENSMUSG00000015488	chr2	Cacfd1	2.7E+07	2.7E+07	4693	-0.10895756	6.063364164	0.5560995	0.647505525	0.04017	0	1085	746	1157	1115	1116	1338	1523	913	1507	1395
ENSMUSG00000058301	chr8	Upf1	7E+07	7E+07	4616	-0.09941816	5.246120547	0.556179	0.647544367	0.03211	0	436	397	813	649	721	842	799	551	840	762
ENSMUSG00000006998	chr16	Psmd2	2.1E+07	2.1E+07	4038	-0.11175737	8.277847018	0.5563316	0.647668302	0.043	0	4320	3240	6228	5286	5570	6618	6756	4502	6572	6494
ENSMUSG00000031516	chr8	Dctn6	3.4E+07	3.4E+07	2853	0.099024786	5.186773906	0.5564078	0.647703206	0.03167	0	552	409	522	476	677	884	761	593	812	839
ENSMUSG00000011958	chr9	Bnip2	7E+07	7E+07	3455	-0.10795511	6.615770363	0.5566607	0.647890014	0.03974	0	1484	1086	1784	1686	1643	2279	2160	1569	1794	1955
ENSMUSG00000035227	chr7	Spcs2	1E+08	1E+08	2815	0.110551443	6.04804761	0.5566175	0.647890014	0.04094	0	1003	770	926	971	1061	1786	1365	1077	1429	1469

ENSMUSG00000054766	chr2	Set	3E+07	3E+07	4070	0.10553603	6.445868124	0.5567129	0.647897074	0.03782	0	1172	929	1557	1275	1428	2160	1847	1537	1900	1866
ENSMUSG00000100164	chr6	2610306M01Rik	8.7E+07	8.7E+07	1042	0.129756152	3.013667607	0.5570255	0.648207108	0.05195	0	83	69	194	110	138	217	169	135	155	188
ENSMUSG00000099843	chr1	Gm7160	1.1E+08	1.1E+08	1417	0.200905059	0.557327895	0.5571991	0.648355305	0.08967	0	10	12	24	18	34	35	25	20	32	39
ENSMUSG00000026209	chr1	Dnpep	7.5E+07	7.5E+07	4289	0.105196776	5.561755548	0.557438	0.648567919	0.03743	0	534	410	1000	778	798	1115	1097	714	1107	1046
ENSMUSG00000049659	chr11	Aftph	2.1E+07	2.1E+07	6979	-0.09394368	4.888082353	0.5574743	0.648567919	0.02877	0	393	366	583	444	520	629	712	428	552	644
ENSMUSG00000020389	chr11	Cdkl3	5.2E+07	5.2E+07	5360	-0.18144166	1.333885094	0.5582256	0.649388055	0.07842	0	30	18	55	47	50	64	40	31	39	63
ENSMUSG00000026385	chr1	Dbi	1.2E+08	1.2E+08	1422	0.188275751	7.611180212	0.5582957	0.649415805	0.12319	0	2322	1198	2368	1623	7175	5955	3248	3539	4029	4797
ENSMUSG00000019471	chr9	Cdc37	2.1E+07	2.1E+07	2456	0.113717733	6.804573297	0.5584718	0.649566755	0.04473	0	1400	979	2250	1857	1780	2460	2485	1709	2811	2569
ENSMUSG00000021428	chr13	Riok1	3.8E+07	3.8E+07	2744	0.126659637	3.114279309	0.5595859	0.650754702	0.04854	0	134	82	161	91	158	233	165	155	165	204
ENSMUSG00000041354	chr17	Rgl2	3.4E+07	3.4E+07	4625	0.09434353	5.063137007	0.5595416	0.650754702	0.02915	0	416	342	585	482	640	798	726	446	828	800
ENSMUSG00000029916	chr6	Agk	4E+07	4E+07	2225	-0.12968565	2.808881443	0.5596867	0.650817867	0.05026	0	105	82	128	87	147	166	138	97	170	115
ENSMUSG00000015806	chr5	Qdpr	4.5E+07	4.5E+07	1914	-0.10722801	5.741514137	0.5598702	0.650977277	0.03937	0	830	643	792	771	1135	1196	991	822	1182	1125
ENSMUSG00000057262	chr15	Gm10020	5.2E+07	5.2E+07	615	-0.11892001	4.19051214	0.5601955	0.651301581	0.0482	0	300	283	226	275	292	435	395	253	381	350
ENSMUSG00000072774	chr5	Zfp951	1E+08	1E+08	4730	-0.20778014	-0.05912395	0.5602429	0.651302731	0.09469	0	13	9	14	12	22	24	23	6	13	18
ENSMUSG00000026663	chr1	Atf6	1.7E+08	1.7E+08	9231	-0.09343246	5.257861077	0.5605212	0.651572248	0.02914	0	519	430	773	623	652	951	831	591	688	775
ENSMUSG00000020115	chr10	Tbk1	1.2E+08	1.2E+08	3031	-0.10573495	3.797509793	0.5606158	0.651628186	0.03409	0	201	141	282	212	261	367	288	214	230	285
ENSMUSG00000050912	chr9	Tmem123	7764041	7764312	3109	-0.10361048	5.189424459	0.5610963	0.652132623	0.03577	0	514	352	710	470	880	881	875	530	620	752
ENSMUSG00000044636	chr15	Csrnp2	1E+08	1E+08	4126	-0.15255791	2.008845169	0.5615329	0.652585993	0.06249	0	58	38	69	68	83	67	94	53	69	102
ENSMUSG00000022312	chr15	Eif3h	5.2E+07	5.2E+07	1253	-0.10767013	7.063036497	0.5619325	0.652966387	0.04088	0	2050	1641	2474	2011	2247	3118	2980	1944	2656	2683
ENSMUSG00000034714	chr11	Ttyh2	1.1E+08	1.1E+08	3739	0.12508755	5.574486467	0.5619533	0.652966387	0.05369	0	629	585	505	723	937	1056	1029	746	1373	927
ENSMUSG00000063015	chr5	Ccni	9.3E+07	9.3E+07	3303	-0.10894232	6.270042614	0.5623528	0.653376439	0.04129	0	1177	737	1471	1044	1754	1828	1707	1150	1390	1636
ENSMUSG00000024235	chr18	Map3k8	4331327	4332436	4504	0.203203559	1.08070711	0.5625051	0.653445145	0.08829	0	38	22	29	20	30	71	45	23	37	51
ENSMUSG00000024395	chr18	Lims2	3.2E+07	3.2E+07	1688	-0.13040891	4.783488138	0.5624807	0.653445145	0.05695	0	353	193	632	355	756	589	611	334	482	729
ENSMUSG00000022864	chr16	D16Ertd472e	7.9E+07	7.9E+07	2453	-0.2339113	0.316244772	0.563222	0.654169611	0.12053	0	12	10	30	27	16	23	20	14	14	38
ENSMUSG00000098798	chr8	Gm27288	1.9E+07	1.9E+07	80	-0.13532218	2.348913306	0.5632036	0.654169611	0.05429	0	82	64	104	64	80	114	101	59	104	120
ENSMUSG00000027968	chr3	Larp7	1.3E+08	1.3E+08	1880	0.114835117	3.743356476	0.5634732	0.654407099	0.04379	0	152	115	319	201	204	313	307	236	245	324
ENSMUSG00000101878	chr6	Gm8203	1.2E+08	1.2E+08	387	-0.16925495	1.255073427	0.564121	0.655105211	0.07415	0	41	24	40	37	41	56	65	29	45	30
ENSMUSG00000018126	chr15	Baiap2l2	7.9E+07	7.9E+07	2728	-0.16857139	1.095715399	0.5646593	0.655621757	0.07654	0	42	26	35	25	33	51	52	24	32	42
ENSMUSG00000064343	chrMT	mt-Tq	3772	3842	71	-0.39259605	1.0305712	0.564639	0.655621757	0.4678	0	8	0	89	47	40	21	31	11	30	81
ENSMUSG00000024457	chr17	Trim26	3.7E+07	3.7E+07	6868	-0.09370529	4.429236171	0.5647722	0.655698628	0.02941	0	285	261	402	326	404	541	487	271	439	439
ENSMUSG00000009863	chr4	Sdhb	1.4E+08	1.4E+08	2239	-0.14048077	9.063125948	0.5650673	0.65595275	0.07115	0	7319	3978	15006	10672	6936	10881	12120	7872	10462	11359
ENSMUSG00000020770	chr11	Unk	1.2E+08	1.2E+08	4438	0.133367614	3.192742724	0.5650846	0.65595275	0.05266	0	122	109	112	112	192	239	175	130	216	226
ENSMUSG00000024829	chr19	Mrpl21	3282901	3283171	2011	0.092340838	5.104943797	0.5652318	0.656069293	0.02898	0	467	359	690	506	503	866	740	613	714	719
ENSMUSG00000020190	chr10	Mknk2	8.1E+07	8.1E+07	3065	0.134186243	8.368465471	0.5655036	0.656320967	0.06515	0	3179	2167	7776	5847	6018	7427	7779	5401	7792	7362
ENSMUSG00000040877	chr12	Wdr25	1.1E+08	1.1E+08	4398	0.129952893	2.634343424	0.5655422	0.656320967	0.05181	0	85	55	134	69	107	128	137	99	156	138
ENSMUSG00000032567	chr9	Aste1	1.1E+08	1.1E+08	6367	-0.18522368	0.843467783	0.5656791	0.656401255	0.07862	0	25	17	32	18	47	44	33	27	27	33
ENSMUSG00000032612	chr9	Usp4	1.1E+08	1.1E+08	8628	-0.10607982	6.813553209	0.565705	0.656401255	0.04024	0	1514	1235	2238	1833	2075	2429	2627	1633	2425	2124
ENSMUSG00000022053	chr14	Ebf2	6.7E+07	6.7E+07	6928	-0.18202413	3.445947076	0.5659673	0.656651231	0.11269	0	147	112	121	104	410	339	239	104	192	207
ENSMUSG00000069565	chr10	Dazap1	8E+07	8E+07	2944	-0.09567366	5.010926726	0.566018	0.656655797	0.03098	0	437	310	661	563	582	749	623	428	776	666
ENSMUSG00000024948	chr19	Map4k2	6341135	6341345	6646	-0.12620496	3.202670566	0.5665073	0.657169124	0.05066	0	109	114	162	114	228	217	199	121	159	214
ENSMUSG00000038527	chr6	C1rl	1.2E+08	1.2E+08	3010	0.256606164	1.316646191	0.5671155	0.657820257	0.20408	0	43	16	9	18	81	66	49	50	49	51
ENSMUSG00000010205	chr9	Raver1	2.1E+07	2.1E+07	3440	0.097112819	4.978182494	0.5671817	0.657842623	0.03313	0	420	247	628	483	580	672	720	472	789	715
ENSMUSG00000052751	chr6	Repin1	4.9E+07	4.9E+07	3975	-0.09393839	4.814323603	0.5672449	0.657861445	0.02942	0	353	288	606	466	514	569	652	416	586	586
ENSMUSG00000042613	chr3	Pbxip1	8.9E+07	8.9E+07	4674	-0.11678837	8.85615368	0.5674561	0.658051997	0.04987	0	6968	5925	8604	7870	6597	10860	11156	6004	8967	9582
ENSMUSG00000032435	chr9	Dync1li1	1.1E+08	1.1E+08	2601	0.095951802	5.587230343	0.5675734	0.658133588	0.03216	0	618	518	932	693	766	1164	1152	710	1045	1094
ENSMUSG00000036395	chr9	Glb1l2	2.7E+07	2.7E+07	5031	-0.39860118	3.667683744	0.5678476	0.658397144	0.55941	0	196	211	12	11	659	412	93	209	164	252
ENSMUSG00000041895	chr11	Wipi1	1.1E+08	1.1E+08	4410	-0.14607052	6.16082471	0.567948	0.658459166	0.07688	0	976	497	2258	1321	878	1489	1899	955	1336	1397
ENSMUSG00000015120	chr17	Ube2i	2.5E+07	2.5E+07	5474	-0.09336375	4.464333493	0.5682233	0.658723862	0.02951	0	315	275	401	321	398	576	463	345	399	426
ENSMUSG00000028312	chr4	Smc2	5.2E+07	5.2E+07	5478	-0.16765335	1.193678624	0.5683864	0.658830836	0.08491	0	41	35	40	23	32	62	48	24	43	40
ENSMUSG00000030287	chr6	Itpr2	1.5E+08	1.5E+08	13484	-0.17204564	3.491139587	0.5684095	0.658830836	0.09939	0	152	85	161	111	430	267	224	170	170	256
ENSMUSG00000043300	chr3	B3galnt1	7E+07	7E+07	2028	0.167571828	2.409359565	0.5687376	0.659156653	0.08504	0	69	72	61	43	121	171	111	80	95	120
ENSMUSG00000048911	chr2	Rnf24	1.3E+08	1.3E+08	6801	-0.19639126	2.397059366	0.5691236	0.659549465	0.12455	0	66	60	48	52	200	132	121	68	97	86
ENSMUSG00000025049	chr19	Taf5	4.7E+07	4.7E+07	3258	-0.15216211	1.906904124	0.5693704	0.659672048	0.06165	0	60	38	75	65	53	81	85	65	68	56
ENSMUSG00000039886	chr5	Tmem120a	1.4E+08	1.4E+08	1553	-0.25633879	4.394000113	0.5693212	0.659672048	0.23548	0	276	153	146	103	1167	548	253	301	453	425
ENSMUSG00000053477	chr18	Tcf4	6.9E+07	6.9E+07	12250	0.103756745	5.699479709	0.5693364	0.659672048	0.03819	0	612	585	908	771	916	1237	1162	687	1104	1435
ENSMUSG00000022248	chr15	Rad1	1E+07	1E+07	7400	0.136504987	2.584758049	0.5695356	0.659808869	0.05718	0	82	59	101	57	132	163	120	108	123	123
ENSMUSG00000038542	chr8	Pcid2	1.3E+07	1.3E+07	3084	0.101575936	3.820313831	0.5695955	0.65982376	0.03336	0	191	145	250	168	281	358	313	219	308	311
ENSMUSG00000026273	chr1	Mterf4	9.3E+07	9.3E+07	5271	-0.11293816	3.333865654	0.5698415	0.660054215	0.03971	0	152	118	211	122	187	233	197	164	192	204
ENSMUSG00000035878	chr9	Hykk	5.5E+07	5.5E+07	8936	0.230443036	0.645418852	0.570138	0.660343144	0.11469	0	28	23	13	11	22	43	36	25	30	29
ENSMUSG00000036180	chr8	Gatad2a	7E+07	7E+07	5502	-0.09021465	4.745045834	0.570211	0.660344676	0.02749	0	351	308	498	413	527	599	560	441	567	501
ENSMUSG00000091243	chr16	Vgll3	6.6E+07	6.6E+07	3322	0.214534362	2.31014775	0.5702335	0.660344676	0.15284	0	44	53	37	39	174	136	110	110	93	82
ENSMUSG00000042111	chr1	Ccdc115	3.4E+07	3.4E+07	2543	0.101819477	4.257461903	0.5703238	0.660394805	0.0348	0	281	219	327	237	318	453	373	381	408	396
ENSMUSG00000005469	chr8	Prkaca	8.4E+07	8.4E+07	2293	-0.10890346	7.245909818	0.5707414	0.660804205	0.04364	0	2077	1448	3140	2432	3074	3071	3335	2247	3363	3087
ENSMUSG00000020547	chr12	Bzw2	3.6E+07	3.6E+07	1860	-0.11143517	6.674395075	0.5707716	0.660804205	0.04553	0	1550	1056	2268	1709	1503	2130	2544	1622	1845	1993
ENSMUSG00000002984	chr7	Tomm40	2E+07	2E+07	4239	0.101143128	5.303625301	0.5710521	0.661060047	0.03721	0	469	327	891	581	698	870	817	649	983	889
ENSMUSG00000058922	chr9	Gm10052	1.2E+08	1.2E+08	960	-0.14543742	1.84964048	0.5710869	0.661060047	0.05818	0	51	43	70	55	59	78	76	65	51	71
ENSMUSG00000066042	chr4	Med18	1.3E+08	1.3E+08	1998	-0.21627383	0.679060493	0.5718661	0.661907412	0.09314	0	24	16	31	15	38	34	19	31	27	30

ENSMUSG00000031951	chr8	Tmem231	1.1E+08	1.1E+08	2887	0.173046213	1.083336508	0.5725073	0.662594871	0.07318	0	33	18	31	27	34	72	36	34	40	40
ENSMUSG00000028896	chr4	Rcc1	1.3E+08	1.3E+08	3848	0.106949249	3.778550017	0.5725716	0.662614603	0.03836	0	193	139	247	199	217	357	247	274	274	294
ENSMUSG00000020167	chr10	Tcf3	8E+07	8E+07	4039	0.095022739	4.270340356	0.5728376	0.66277882	0.03012	0	262	204	307	253	386	488	452	295	427	401
ENSMUSG00000026277	chr1	Stk25	9.4E+07	9.4E+07	5812	-0.10122851	6.148421483	0.5729498	0.66277882	0.03782	0	1156	849	1245	1003	1264	1708	1453	1079	1371	1484
ENSMUSG00000051427	chr11	Ccdc157	4141123	4143935	5589	0.125069092	2.98520375	0.5728831	0.66277882	0.04722	0	114	84	102	115	147	216	171	112	162	191
ENSMUSG00000064816	chr1	Gm22357	1.6E+08	1.6E+08	83	0.247833803	-0.04808611	0.5729181	0.66277882	0.13597	0	9	6	21	16	8	29	8	20	16	22
ENSMUSG00000071528	chr19	Usmg5	4.7E+07	4.7E+07	341	-0.11163002	7.448313071	0.5728343	0.66277882	0.04655	0	2552	1864	3638	3207	2495	4018	3633	2674	3334	3733
ENSMUSG00000030960	chr7	Mettl10	1.3E+08	1.3E+08	1764	0.156670473	2.379118332	0.5731095	0.662908915	0.076	0	92	57	70	47	95	162	97	99	84	113
ENSMUSG00000034570	chr11	Inpp5j	3494375	3495166	5092	-0.36499077	2.13761614	0.5732673	0.662982127	0.45987	0	18	1	195	149	37	76	74	37	61	145
ENSMUSG00000092176	chr17	Gm20460	3.5E+07	3.5E+07	1572	-0.08790813	4.656059309	0.5732358	0.662982127	0.02658	0	372	267	448	413	467	538	557	356	549	529
ENSMUSG00000034480	chrX	Diap2	1.3E+08	1.3E+08	11553	-0.12892189	2.543445722	0.5733721	0.66304867	0.05062	0	87	73	107	81	103	144	147	85	92	102
ENSMUSG00000038375	chr2	Trp53inp2	1.6E+08	1.6E+08	5257	-0.13966234	9.184358351	0.5735546	0.663179131	0.07349	0	6215	4485	16744	10589	10336	10785	15877	7937	10579	12371
ENSMUSG00000049555	chr9	Tmie	1.1E+08	1.1E+08	2802	-0.26812105	0.539000976	0.5735795	0.663179131	0.1882	0	14	12	63	14	14	42	32	10	28	18
ENSMUSG00000001755	chr11	Coasy	1E+08	1E+08	2867	0.139455499	4.173738827	0.5737605	0.663333694	0.07126	0	225	118	239	233	531	525	297	315	440	370
ENSMUSG00000030471	chr7	Zdhhc13	4.9E+07	4.9E+07	2410	0.144479116	2.518907632	0.5742472	0.663841713	0.06169	0	98	73	90	60	74	150	129	93	133	107
ENSMUSG00000027498	chr2	Cstf1	1.7E+08	1.7E+08	3504	-0.09394049	4.351824741	0.5744138	0.663979536	0.02986	0	275	216	422	339	351	448	418	304	472	394
ENSMUSG00000035378	chr6	Shq1	1E+08	1E+08	2182	0.172146729	1.147388589	0.5744813	0.66400288	0.0864	0	22	14	39	40	38	61	45	32	62	32
ENSMUSG00000025408	chr10	Ddit3	1.3E+08	1.3E+08	1713	0.142145627	4.203582577	0.5745792	0.664061279	0.07553	0	146	98	514	284	368	439	432	288	386	451
ENSMUSG00000060380	chr9	C030014I23Rik	4.4E+07	4.4E+07	2446	-0.17924593	1.228455184	0.574655	0.664085516	0.07468	0	33	16	60	40	36	45	55	31	43	44
ENSMUSG00000102824	chr1	RP23-411B11.2	1.9E+08	1.9E+08	381	0.116384012	3.095843836	0.5746949	0.664085516	0.04201	0	101	90	125	135	163	202	203	139	188	177
ENSMUSG00000039697	chr10	Ncoa7	3.1E+07	3.1E+07	5336	-0.17197329	1.965703834	0.5748366	0.664194602	0.08842	0	46	50	74	34	106	74	105	61	61	68
ENSMUSG00000046658	chr5	Zfp316	1.4E+08	1.4E+08	6891	-0.12239828	3.265925274	0.5748969	0.664209509	0.04844	0	120	90	224	179	152	209	223	121	174	226
ENSMUSG00000026856	chr2	Dolpp1	3E+07	3E+07	3233	0.123968584	3.268826898	0.5749653	0.66423382	0.05139	0	115	99	126	135	220	225	191	168	248	191
ENSMUSG00000040270	chr4	Bach2	3.2E+07	3.2E+07	9940	-0.19332586	1.399680716	0.5752108	0.664462761	0.0958	0	47	15	72	29	50	58	67	36	39	46
ENSMUSG00000025575	chr11	Cant1	1.2E+08	1.2E+08	4358	0.095426352	4.727845987	0.5753357	0.664520711	0.03209	0	319	283	395	365	585	719	558	425	577	556
ENSMUSG00000062619	chr17	2310039H08Rik	4.7E+07	4.7E+07	773	0.11025631	3.882211023	0.5753557	0.664520711	0.04119	0	201	160	267	198	241	372	232	237	407	324
ENSMUSG00000026895	chr2	Ndufa8	3.6E+07	3.6E+07	861	0.123513012	7.700272455	0.5760857	0.665309061	0.05821	0	2346	1534	4920	3520	3287	4263	4839	3144	5122	5092
ENSMUSG00000015656	chr9	Hspa8	4.1E+07	4.1E+07	4156	0.117075389	9.544785584	0.5765678	0.66581095	0.05256	0	8493	7114	16639	12486	10383	19311	15668	12165	15808	17719
ENSMUSG00000089865	chr9	Dyx1c1Ccpg1	7.3E+07	7.3E+07	4383	-0.11044616	6.920748223	0.5769335	0.666178368	0.04634	0	1942	1141	2643	2077	1821	2771	2917	1697	2172	2585
ENSMUSG00000037808	chr9	Fam76b	1.4E+07	1.4E+07	4325	-0.13042766	2.715080184	0.5772823	0.666526282	0.05638	0	121	70	98	101	118	185	118	103	101	135
ENSMUSG00000082127	chr2	Gm13577	6.4E+07	6.4E+07	213	0.170735804	1.340406342	0.5774615	0.666678297	0.07894	0	47	26	31	33	32	69	48	48	43	56
ENSMUSG00000005057	chr5	Sh2b2	1.4E+08	1.4E+08	2848	0.281584274	2.531795703	0.5781919	0.667466679	0.29162	0	56	34	29	18	278	128	97	103	177	131
ENSMUSG00000049871	chr16	Nlrc3	3945007	3947539	7068	0.254855416	2.203410708	0.5788167	0.668132906	0.23657	0	24	20	122	132	24	101	82	72	74	176
ENSMUSG00000021481	chr13	Zfp346	5.5E+07	5.5E+07	4176	0.091904864	4.572697282	0.5791724	0.668223528	0.0296	0	321	249	457	331	389	595	506	328	492	635
ENSMUSG00000024914	chr19	Drap1	5422805	5423025	1741	0.11452244	8.111437115	0.5791855	0.668223528	0.05075	0	3882	3352	4050	3629	4944	5884	5892	4375	7558	5985
ENSMUSG00000025354	chr10	Dnajc14	1.3E+08	1.3E+08	4229	0.089008692	5.252929942	0.5792287	0.668223528	0.02922	0	516	368	673	525	745	1037	891	597	791	770
ENSMUSG00000025607	chr6	Copg2	3.1E+07	3.1E+07	4477	0.091966511	4.459929685	0.5789685	0.668223528	0.03009	0	273	230	391	295	433	510	554	374	461	436
ENSMUSG00000046949	chr13	Nqo2	3.4E+07	3.4E+07	3974	-0.08620314	4.99621646	0.579181	0.668223528	0.02703	0	502	365	574	493	537	735	704	506	634	614
ENSMUSG00000064725	chr11	Snord96a	4.9E+07	4.9E+07	81	0.223797314	-0.07010989	0.5790984	0.668223528	0.08189	0	12	9	13	15	9	22	15	17	18	21
ENSMUSG00000086003	chr11	B230206L02Rik	9.4E+07	9.4E+07	1042	0.20484685	-0.07471455	0.5790622	0.668223528	0.08507	0	13	5	14	8	20	22	18	13	21	19
ENSMUSG00000034353	chr1	Ramp1	9.1E+07	9.1E+07	3022	-0.13377244	4.901960723	0.5800027	0.669061402	0.06587	0	551	147	751	458	564	531	701	482	607	597
ENSMUSG00000021686	chr13	Ap3b1	9.4E+07	9.4E+07	4020	-0.08785399	4.589459786	0.5805014	0.669526529	0.02791	0	335	279	495	367	400	574	578	328	478	470
ENSMUSG00000098022	chr7	Zfp82	3E+07	3E+07	6041	-0.16652105	1.254024013	0.5804683	0.669526529	0.0742	0	38	28	40	27	50	69	55	30	34	38
ENSMUSG00000028763	chr4	Hspg2	1.4E+08	1.4E+08	14307	0.110813869	7.709901531	0.5805967	0.669581407	0.04792	0	2299	1991	4552	3240	3476	5028	4219	3545	5174	4468
ENSMUSG00000014907	chr8	Naf1	6.7E+07	6.7E+07	2990	0.123743997	2.606143733	0.5809259	0.669905959	0.04561	0	78	71	110	78	95	164	121	89	135	141
ENSMUSG00000026750	chr2	Psmb7	3.9E+07	3.9E+07	1214	-0.10570536	7.916270237	0.5815263	0.670543217	0.04382	0	3775	2936	4204	3820	4037	5040	5078	3814	5169	4892
ENSMUSG00000032397	chr9	Tipin	6.4E+07	6.4E+07	1211	-0.11573596	2.892666359	0.581908	0.670873098	0.04432	0	109	90	141	104	132	186	158	120	127	137
ENSMUSG00000058558	chr5	Rpl5	1.1E+08	1.1E+08	3920	-0.11194866	7.781152458	0.581886	0.670873098	0.0493	0	3490	3003	3455	3512	3417	5770	4336	3413	3941	4512
ENSMUSG00000030137	chr6	Tuba8	1.2E+08	1.2E+08	2225	-0.12506019	7.786539498	0.5821868	0.671139282	0.06152	0	3286	2173	4239	4263	3576	3962	4717	2746	6603	3910
ENSMUSG00000024870	chr19	Rab1b	5099207	5100572	1835	0.108563628	7.316946644	0.5823592	0.67117261	0.04632	0	1929	1417	3088	2560	2847	3473	3670	2324	4122	3592
ENSMUSG00000036327	chr2	Qsox2	2.6E+07	2.6E+07	4644	0.131897242	2.853655158	0.5822664	0.67117261	0.05849	0	94	70	97	88	171	204	158	134	133	140
ENSMUSG00000048787	chr7	Dcun1d3	1.2E+08	1.2E+08	6203	0.099451255	4.14455096	0.5823506	0.67117261	0.03536	0	209	195	286	232	372	410	449	310	343	364
ENSMUSG00000063445	chr16	Nmral1	4710059	4711603	3891	-0.12894403	2.428247206	0.5825423	0.671328414	0.05729	0	81	77	74	78	99	143	100	75	112	96
ENSMUSG00000031723	chr8	Txnl4b	1.1E+08	1.1E+08	1892	0.107186225	3.653024271	0.5826959	0.671450248	0.04113	0	178	102	191	184	270	309	278	202	305	247
ENSMUSG00000024330	chr17	Col11a2	3.4E+07	3.4E+07	6831	0.121309438	3.578898314	0.5827993	0.67151427	0.05281	0	169	123	206	118	253	323	216	209	321	205
ENSMUSG00000042165	chr3	Gm9774	9.2E+07	9.2E+07	1392	0.118511729	2.936138807	0.5832173	0.671940712	0.04574	0	89	81	127	97	159	165	166	124	176	180
ENSMUSG00000028954	chr5	Nub1	2.5E+07	2.5E+07	3455	-0.09322458	5.834681734	0.5833714	0.672062985	0.03364	0	871	642	1074	922	937	1373	1248	792	1113	1228
ENSMUSG00000029141	chr5	Slc4a1ap	3.2E+07	3.2E+07	4759	-0.09469428	4.196912841	0.5837359	0.672409888	0.03179	0	269	212	366	281	298	423	385	320	347	339
ENSMUSG00000057863	chr17	Rpl36	5.7E+07	5.7E+07	404	0.107690003	6.999194882	0.5837724	0.672409888	0.04567	0	1830	1389	2378	1755	1957	3272	2206	2120	3175	2945
ENSMUSG00000057963	chr12	Itpk1	1E+08	1E+08	3320	-0.16977856	3.975182195	0.5838163	0.672409888	0.10882	0	210	147	150	159	631	337	293	209	365	325
ENSMUSG00000080002	chr5	Gm5566	1.5E+08	1.5E+08	459	0.195864488	0.560609662	0.5838959	0.67244636	0.08996	0	22	8	21	24	22	29	29	18	44	31
ENSMUSG00000031546	chr8	Gins4	2.3E+07	2.3E+07	1364	0.101324736	3.833501379	0.5840516	0.672515199	0.0361	0	188	155	237	170	290	364	297	243	332	278
ENSMUSG00000040003	chr5	Magi2	1.9E+07	1.9E+07	7239	0.205747226	0.700433211	0.5840995	0.672515199	0.09823	0	18	25	26	13	22	55	30	23	26	36
ENSMUSG00000091512	chr3	Lamtor3	1.4E+08	1.4E+08	1295	-0.08829368	4.61239416	0.5840359	0.672515199	0.02865	0	369	277	458	403	388	609	541	389	429	481
ENSMUSG00000001017	chr3	Chtop	9E+07	9.1E+07	3637	-0.09985472	6.935677186	0.5842656	0.672651223	0.03936	0	1817	1395	2285	1913	2177	2675	2691	1893	2534	2423
ENSMUSG00000024487	chr18	Yipf5	4E+07	4E+07	2329	-0.10787145	3.71047888	0.5843518	0.67269522	0.04303	0	190	186	197	181	248	365	257	200	241	239
ENSMUSG00000019989	chr10	Enpp3	2.5E+07	2.5E+07	2815	0.157744595	2.015629043	0.5845306	0.672845811	0.07135	0	62	57	49	49	55	116	99	55	75	90

ENSMUSG00000021270	chr12	Hsp90aa1	1.1E+08	1.1E+08	3931	0.107873817	6.060672978	0.5846494	0.672927333	0.04583	0	829	603	1433	900	1214	2117	1514	1125	1108	1355
ENSMUSG00000059586	chr15	Nsmce2	5.9E+07	5.9E+07	3281	-0.10280429	3.785352029	0.585125	0.673419432	0.0367	0	201	132	325	217	216	332	309	199	255	280
ENSMUSG00000029647	chr5	Pan3	1.5E+08	1.5E+08	7316	0.111982013	3.658061631	0.5860791	0.674366745	0.04464	0	185	123	197	157	256	336	299	190	196	337
ENSMUSG00000045464	chr2	2810002D19Rik	9.4E+07	9.4E+07	2040	0.209625414	0.417276538	0.5860923	0.674366745	0.09599	0	18	19	20	11	16	29	33	28	21	23
ENSMUSG00000101680	chr14	Gm29015	5.5E+07	5.5E+07	207	-0.80763566	0.249839555	0.5860902	0.674366745	2.17249	0	0	0	94	24	0	0	0	0	3	78
ENSMUSG00000026676	chr2	Ccdc3	5137776	5138307	2670	-0.22677843	4.217148777	0.5864505	0.674723538	0.2009	0	200	128	143	144	1005	592	327	223	291	372
ENSMUSG00000001380	chr18	Hars	3.7E+07	3.7E+07	1987	0.088323265	5.294000086	0.586732	0.674992037	0.0304	0	489	363	737	573	764	937	832	668	838	890
ENSMUSG00000005951	chr11	Shpk	7.3E+07	7.3E+07	2985	-0.20035386	1.287897106	0.5868673	0.675039355	0.13353	0	35	32	25	19	79	66	35	27	44	57
ENSMUSG00000006392	chr4	Med8	1.2E+08	1.2E+08	3001	0.089392174	4.773003786	0.5868694	0.675039355	0.02936	0	407	313	470	370	423	695	555	470	622	558
ENSMUSG00000071547	chr14	Nt5dc2	3.1E+07	3.1E+07	1407	0.201856481	1.718754289	0.5869214	0.675043792	0.1501	0	17	16	119	42	47	92	74	51	71	65
ENSMUSG00000038383	chr2	Pigu	1.6E+08	1.6E+08	9326	0.092701371	4.614395969	0.5870571	0.675144543	0.03171	0	321	259	497	393	319	566	588	377	543	539
ENSMUSG00000020457	chr11	Drg1	3187360	3187410	3460	0.091494493	5.624951285	0.5872572	0.675319273	0.03264	0	685	517	867	719	830	1270	972	872	1047	1082
ENSMUSG00000025817	chr2	Nudt5	5845019	5845385	6484	0.183649088	2.592404425	0.5873698	0.675393422	0.12781	0	71	43	52	57	213	177	101	104	132	138
ENSMUSG00000028430	chr4	Nol6	4.1E+07	4.1E+07	5242	-0.09229663	4.989333953	0.5875226	0.67551375	0.03216	0	413	334	532	493	734	667	624	478	734	666
ENSMUSG00000022894	chr16	Adamts5	8.6E+07	8.6E+07	8091	0.159081475	5.199034725	0.5876897	0.675650513	0.10131	0	296	338	485	299	1330	850	1015	520	809	842
ENSMUSG00000038146	chr17	Notch3	3.2E+07	3.2E+07	8044	-0.09212252	5.021054349	0.5877983	0.675719976	0.03178	0	406	302	697	469	730	800	666	467	696	636
ENSMUSG00000031950	chr8	Gabarapl2	1.1E+08	1.1E+08	2325	-0.09808546	5.943199724	0.5878482	0.675721976	0.03815	0	1059	688	1213	807	1045	1493	1344	982	1125	1204
ENSMUSG00000050605	chr7	Zfp61	2.4E+07	2.4E+07	3431	-0.15436897	1.679924423	0.5881737	0.676040704	0.07891	0	42	43	60	51	49	79	46	36	52	95
ENSMUSG00000051344	chr1	Plekhm3	6.5E+07	6.5E+07	10921	-0.12381055	3.048260035	0.5882243	0.676043479	0.05303	0	91	85	183	133	167	189	211	106	123	190
ENSMUSG00000041609	chr5	Ccdc64	1.2E+08	1.2E+08	5932	0.154167877	1.647376308	0.5884714	0.676271954	0.07016	0	38	30	42	35	74	97	61	49	65	60
ENSMUSG00000045854	chr4	Lyrm2	3.3E+07	3.3E+07	1140	0.103707206	3.717973011	0.5887834	0.676575102	0.03782	0	205	134	198	168	248	387	284	206	269	265
ENSMUSG00000022377	chr15	Asap1	6.4E+07	6.4E+07	7482	0.098913921	3.981185687	0.588923	0.676639461	0.03657	0	225	148	294	180	320	419	359	273	282	348
ENSMUSG00000070327	chr11	Rnf213	1.2E+08	1.2E+08	16888	-0.10451233	4.524589726	0.5889359	0.676639461	0.04304	0	349	264	466	380	334	730	509	240	466	409
ENSMUSG00000041995	chr13	Zbed3	9.5E+07	9.5E+07	1894	-0.13895732	2.386270709	0.5893432	0.676996589	0.06769	0	79	46	107	77	106	103	95	52	108	154
ENSMUSG00000046743	chr3	Fat4	3.9E+07	3.9E+07	17165	-0.1157825	3.307232038	0.5893123	0.676996589	0.04956	0	130	133	184	129	193	304	223	124	176	166
ENSMUSG00000031545	chr8	Agpat6	2.3E+07	2.3E+07	3944	-0.10059861	6.120817077	0.5898701	0.67754637	0.04047	0	896	664	1368	1067	1584	1506	1462	998	1433	1566
ENSMUSG00000036298	chr15	Slc2a13	9.1E+07	9.1E+07	8367	-0.28840256	0.803884109	0.5900883	0.677685938	0.28979	0	22	25	8	7	76	59	17	25	27	27
ENSMUSG00000082516	chr2	Gm13342	2.2E+07	2.2E+07	207	-0.22336942	0.623104963	0.5900521	0.677685938	0.13646	0	15	18	39	28	18	13	30	15	37	42
ENSMUSG00000059981	chr7	Taok2	1.3E+08	1.3E+08	9247	-0.08687085	5.231968705	0.5902004	0.677759247	0.02916	0	496	395	783	603	683	786	804	541	807	833
ENSMUSG00000070424	chr7	Art5	1E+08	1E+08	1806	0.120636606	5.002019403	0.5903899	0.677921292	0.058	0	595	272	691	448	319	903	574	600	569	786
ENSMUSG00000001761	chr6	Smo	3E+07	3E+07	3779	0.115889208	3.621443889	0.5905903	0.678095942	0.04879	0	160	137	195	124	278	380	284	176	256	237
ENSMUSG00000057691	chr6	Zfp746	4.8E+07	4.8E+07	3651	-0.10531146	3.404957581	0.5907825	0.678261075	0.03914	0	157	133	202	148	179	234	203	169	195	242
ENSMUSG00000031865	chr6	Dctn1	8.3E+07	8.3E+07	6509	-0.11780629	7.270572319	0.5909382	0.678380808	0.05698	0	1954	1446	3615	3072	2291	2809	3664	2108	3649	3116
ENSMUSG00000044150	chrX	A830080D01Rik	1.6E+08	1.6E+08	4869	-0.18125235	0.933328205	0.5909835	0.678380808	0.09449	0	37	16	36	21	37	52	48	15	27	38
ENSMUSG00000044145	chr2	1810024B03Rik	1.3E+08	1.3E+08	3550	0.182998506	1.074463701	0.5911922	0.678564771	0.09705	0	18	22	32	24	47	59	30	22	52	60
ENSMUSG00000022360	chr15	Atad2	5.8E+07	5.8E+07	5683	0.166734591	1.22612477	0.5912927	0.67858166	0.07464	0	29	22	52	25	33	76	40	40	42	47
ENSMUSG00000027582	chr2	Zgpat	1.8E+08	1.8E+08	5624	-0.09212495	4.258729349	0.591352	0.67858166	0.03252	0	268	246	359	284	320	455	340	277	386	457
ENSMUSG00000029765	chr6	Plxna4	3.2E+07	3.2E+07	12877	-0.17009636	3.05831141	0.591342	0.67858166	0.10818	0	136	39	236	176	99	128	209	104	170	192
ENSMUSG00000009741	chr9	Ubp1	1.1E+08	1.1E+08	3850	-0.0842329	4.569341286	0.591444	0.678631635	0.02686	0	324	276	478	346	427	582	497	348	437	525
ENSMUSG00000023944	chr17	Hsp90ab1	4.6E+07	4.6E+07	2999	0.104778571	10.62133072	0.5918498	0.6790326	0.04571	0	20909	15430	32724	21831	25662	38469	33932	24028	36087	37237
ENSMUSG00000034795	chr14	Ccdc122	7.7E+07	7.7E+07	1985	-0.21419087	0.895979937	0.5919317	0.6790326	0.13046	0	45	11	37	15	38	38	47	25	19	40
ENSMUSG00000038762	chr17	Abcf1	3.6E+07	3.6E+07	4410	-0.10659341	6.890968881	0.5919387	0.6790326	0.0467	0	1522	1167	2566	2220	1974	2334	2769	1637	2663	2456
ENSMUSG00000090215	chr7	Trim34b	1E+08	1E+08	2068	0.235851235	0.206410406	0.5922538	0.6793385	0.15216	0	14	10	15	8	26	35	24	11	9	40
ENSMUSG00000068882	chr2	Ssb	7E+07	7E+07	2160	0.098716261	5.852517913	0.5927883	0.679896052	0.0394	0	868	661	937	748	972	1608	1171	1075	1037	1264
ENSMUSG00000060152	chr5	Pop5	1.2E+08	1.2E+08	2296	-0.08977198	4.500503807	0.5930628	0.680155262	0.03103	0	322	281	378	342	425	488	431	366	523	440
ENSMUSG00000022820	chr16	Ndufb4	3.8E+07	3.8E+07	1170	-0.09574248	6.27199183	0.5936635	0.680705689	0.03753	0	1168	752	1600	1198	1408	1751	1682	1187	1600	1510
ENSMUSG00000035354	chr7	Uvrag	9.9E+07	9.9E+07	3438	0.110076538	3.189474943	0.5936883	0.680705689	0.0427	0	118	93	178	113	162	265	223	136	157	199
ENSMUSG00000036023	chr14	Parp2	5.1E+07	5.1E+07	1788	0.109137753	3.366466321	0.593612	0.680705689	0.04075	0	147	124	167	120	180	274	215	177	198	232
ENSMUSG00000029053	chr4	Prkcz	1.6E+08	1.6E+08	6318	0.151195456	2.744202098	0.5940943	0.68111551	0.0831	0	87	69	162	89	69	102	215	103	160	135
ENSMUSG00000037013	chr18	Ss18	1.5E+07	1.5E+07	4523	0.098671501	4.310355921	0.5942044	0.681152547	0.03744	0	299	205	290	243	410	565	428	356	353	411
ENSMUSG00000053460	chr6	Ggcx	7.2E+07	7.2E+07	3244	0.103467119	3.561310473	0.5942238	0.681152547	0.03875	0	141	118	200	168	237	360	239	167	246	260
ENSMUSG00000038208	chr11	Pgap3	9.8E+07	9.8E+07	3248	0.135009932	2.127264686	0.5945391	0.681458364	0.05993	0	42	39	73	80	77	111	108	57	88	103
ENSMUSG00000028669	chr4	Pithd1	1.4E+08	1.4E+08	2477	-0.08279586	5.043417056	0.594622	0.681497682	0.02685	0	485	371	655	480	580	776	650	530	709	635
ENSMUSG00000020057	chr10	Dram1	8.8E+07	8.8E+07	3045	0.282717241	4.077080167	0.5947053	0.681537394	0.32815	0	161	170	41	44	773	560	251	357	378	345
ENSMUSG00000016520	chr5	Lnx2	1.5E+08	1.5E+08	4557	0.127582386	2.89060784	0.5955334	0.682430677	0.0624	0	60	73	138	98	174	167	172	135	164	146
ENSMUSG00000030225	chr6	Dera	1.4E+08	1.4E+08	1742	0.119610991	2.857509809	0.5956702	0.682531636	0.04864	0	80	79	111	128	118	194	147	112	169	151
ENSMUSG00000042831	chr7	Alkbh6	3E+07	3E+07	3123	0.094983237	3.851935098	0.5965325	0.683463925	0.03379	0	174	153	248	200	283	325	320	228	357	302
ENSMUSG00000015750	chr3	Aph1a	9.6E+07	9.6E+07	2863	0.0893375	4.877568205	0.5967124	0.683502492	0.03286	0	357	254	681	384	540	699	676	483	601	669
ENSMUSG00000028836	chr4	Slc30a2	1.3E+08	1.3E+08	3564	-0.48151488	4.492511096	0.5966919	0.683502492	0.93859	0	16	28	1548	114	639	80	1657	59	76	152
ENSMUSG00000043192	chr8	Gm1840	5639584	5640996	1413	0.111613801	5.92235217	0.596628	0.683502492	0.05213	0	706	552	1000	1130	1064	1108	1384	831	1773	1427
ENSMUSG00000068240	chr4	Gm11808	3973092	3973595	504	-0.09716042	4.920773765	0.5968151	0.683564306	0.03825	0	467	325	728	456	404	779	543	410	705	611
ENSMUSG00000026234	chr1	Ncl	8.6E+07	8.6E+07	10188	0.100485054	7.689683361	0.5971044	0.683839772	0.04297	0	3013	2150	3708	2696	3577	5306	4461	3733	4003	4525
ENSMUSG00000002372	chr17	Ranbp3	5.7E+07	5.7E+07	2511	-0.09179368	5.804594919	0.5972694	0.683972907	0.03484	0	758	605	1141	882	1015	1166	1216	820	1306	1087
ENSMUSG00000025949	chr1	Pikfyve	6.5E+07	6.5E+07	18504	-0.11341061	3.432772497	0.5975112	0.684184078	0.049	0	163	131	158	126	265	256	230	159	196	227
ENSMUSG00000028373	chr4	Astn2	6.5E+07	6.5E+07	4959	0.204518579	0.672420618	0.5975513	0.684184078	0.13152	0	23	11	31	26	14	37	20	43	22	37
ENSMUSG00000024084	chr17	Qpct	7.9E+07	7.9E+07	1924	-0.18460899	1.743199429	0.5976806	0.684276209	0.11095	0	47	34	43	28	116	81	56	49	57	72
ENSMUSG00000021809	chr14	Nudt13	2E+07	2E+07	2523	-0.10033998	4.705483726	0.5981185	0.684721649	0.03994	0	332	213	687	436	439	653	597	326	508	552

ENSMUSG00000036186	chr2	Fam69b	2.7E+07	2.7E+07	2476	-0.19410914	2.145669057	0.5983468	0.684871241	0.13245	0	57	14	110	62	132	111	66	81	74	80
ENSMUSG00000036580	chr3	Spg20	5.5E+07	5.5E+07	5362	-0.08891105	5.204404655	0.5983103	0.684871241	0.03216	0	558	373	752	657	542	816	834	567	720	754
ENSMUSG00000000811	chr6	Txnrd3	9E+07	9E+07	2836	0.117589966	3.012050858	0.5985342	0.68502984	0.05302	0	100	69	122	103	197	198	165	139	186	167
ENSMUSG00000029075	chr4	Tnfrsf4	1.6E+08	1.6E+08	1365	0.274828397	-0.09871973	0.5986515	0.685108244	0.18253	0	15	7	17	8	9	21	10	4	22	38
ENSMUSG00000031818	chr8	Cox4i1	1.2E+08	1.2E+08	1550	0.12122119	9.606874677	0.5988187	0.685243567	0.0635	0	8611	5529	20207	12366	12333	17138	17689	12214	18098	19024
ENSMUSG00000015083	chr2	C8g	2.5E+07	2.5E+07	1493	0.171253953	0.571932705	0.5991675	0.685586841	0.08029	0	23	12	27	12	25	33	26	29	28	33
ENSMUSG00000095334	chr7	Gm21984	1.3E+08	1.3E+08	822	0.238705571	-0.06312338	0.5992614	0.685638395	0.17177	0	15	3	15	3	25	24	11	15	19	25
ENSMUSG00000071256	chr17	Zfp213	2.4E+07	2.4E+07	2672	-0.14409049	1.82013632	0.5993589	0.685694005	0.0623	0	39	35	72	67	63	87	71	60	63	55
ENSMUSG00000008318	chr7	Relt	1E+08	1E+08	3279	-0.0922167	5.070972151	0.5994334	0.685723275	0.03481	0	361	380	709	579	621	670	854	453	701	699
ENSMUSG00000000884	chr16	Gnb1l	1.8E+07	1.8E+07	4164	-0.14373299	1.608495255	0.5995359	0.685784629	0.05918	0	53	25	57	46	56	79	56	45	58	53
ENSMUSG00000059288	chr13	Cdyl	3.6E+07	3.6E+07	4018	-0.12209553	2.427419122	0.5996216	0.685826625	0.0537	0	71	69	96	77	102	112	127	94	80	106
ENSMUSG00000021606	chr13	Ndufs6	7.3E+07	7.3E+07	629	0.103484806	7.326050856	0.5997811	0.68595318	0.04622	0	2156	1465	3500	2426	2351	3560	3664	2568	3848	3545
ENSMUSG00000042197	chr1	Zfp451	3.4E+07	3.4E+07	15839	-0.10807793	3.490671464	0.5998671	0.685995587	0.04464	0	206	128	183	142	211	274	237	192	188	215
ENSMUSG00000081219	chr2	Bambi-ps1	1.2E+08	1.2E+08	592	0.210803364	-0.00842021	0.6000743	0.686176649	0.11982	0	10	6	17	6	25	20	23	22	17	14
ENSMUSG00000050567	chr11	Maml1	5E+07	5E+07	5528	0.097372911	3.480537843	0.6007148	0.68685304	0.03619	0	132	108	207	159	215	273	241	188	232	248
ENSMUSG00000020841	chr11	Cpd	7.7E+07	7.7E+07	8332	-0.09650932	6.560830987	0.6015058	0.687701384	0.0402	0	1480	1038	1740	1329	1827	2142	2322	1407	1681	1922
ENSMUSG00000034449	chr11	Dhrs11	8.5E+07	8.5E+07	1603	-0.14064845	4.944634289	0.6017353	0.687907665	0.0831	0	278	202	1084	555	475	580	774	393	591	705
ENSMUSG00000020180	chr10	Snrpd3	7.6E+07	7.6E+07	3434	0.096663248	6.120936996	0.6019645	0.688092247	0.0401	0	1010	732	1278	1013	1050	1709	1301	1239	1457	1691
ENSMUSG00000033596	chr8	Rfwd3	1.1E+08	1.1E+08	4443	0.107690922	3.229320615	0.6020017	0.688092247	0.04229	0	130	84	160	140	169	282	231	134	172	191
ENSMUSG00000034906	chr2	Ncaph	1.3E+08	1.3E+08	4307	0.197898993	0.774689213	0.6020439	0.688092247	0.11467	0	11	22	29	26	24	54	30	38	33	20
ENSMUSG00000005378	chr5	Wbscr22	1.4E+08	1.4E+08	3386	0.085993432	4.316481265	0.6022114	0.688172306	0.03016	0	269	177	407	299	328	454	443	342	432	434
ENSMUSG00000040128	chr4	Pnrc1	3.3E+07	3.3E+07	2095	-0.09740317	6.106581426	0.6022121	0.688172306	0.04094	0	1107	760	1137	1237	1101	1432	1538	1047	1358	1503
ENSMUSG00000025422	chr10	Agap2	1.3E+08	1.3E+08	5633	0.184426535	1.213125993	0.6024958	0.688440443	0.11667	0	17	24	71	20	29	60	46	27	51	62
ENSMUSG00000061306	chr11	Slc38a10	1.2E+08	1.2E+08	6421	0.109995997	6.547155058	0.6026311	0.688538954	0.05303	0	1109	683	2319	1488	1463	2131	2299	1440	2244	1953
ENSMUSG00000020483	chr11	Dynll2	8.8E+07	8.8E+07	2736	-0.10485274	8.605144572	0.6028078	0.688684758	0.04845	0	5942	4040	7887	5815	7195	7497	9169	5052	9536	7794
ENSMUSG00000056598	chr11	Lrrc48	6E+07	6E+07	4519	0.156696147	1.393428438	0.6030571	0.688913407	0.07803	0	34	21	54	35	39	64	77	46	54	33
ENSMUSG00000040323	chr1	Gm15429	1.6E+08	1.6E+08	798	0.162647506	1.023936681	0.6031902	0.68898685	0.07668	0	22	12	44	25	39	52	51	24	39	47
ENSMUSG00000040520	chr4	Manea	2.6E+07	2.6E+07	4867	-0.1180215	2.554177251	0.6032327	0.68898685	0.04816	0	84	60	108	91	116	164	109	94	100	108
ENSMUSG00000051255	chr19	Gm6563	2.4E+07	2.4E+07	869	0.115830396	2.935163925	0.6032688	0.68898685	0.0497	0	109	89	140	87	121	231	161	134	137	151
ENSMUSG00000021771	chr14	Vdac2	2.2E+07	2.2E+07	4658	-0.1012937	8.309731845	0.6036302	0.689343577	0.04533	0	4161	3175	7085	5352	5521	6782	6524	4991	6418	6888
ENSMUSG00000052033	chr2	Pfdn4	1.7E+08	1.7E+08	2520	-0.1156926	2.97316498	0.6039942	0.689703037	0.05349	0	117	120	128	105	125	198	157	132	143	138
ENSMUSG00000033096	chr2	Apmap	1.5E+08	1.5E+08	2428	-0.1253246	5.455376266	0.604186	0.689865945	0.06778	0	709	379	620	457	1404	1100	783	642	865	967
ENSMUSG00000033032	chr18	Afap1l1	6.2E+07	6.2E+07	3680	-0.09142499	5.522859715	0.6042627	0.68989738	0.03585	0	651	571	854	676	817	884	1037	732	1066	852
ENSMUSG00000049411	chr18	Tmem241	1.2E+07	1.2E+07	3336	-0.14334842	1.794236106	0.6044138	0.689957487	0.06701	0	42	36	50	64	77	84	81	50	48	70
ENSMUSG00000093470	chr11	Gm20645	2.4E+07	2.4E+07	3511	0.118398718	2.390534931	0.6043761	0.689957487	0.0485	0	65	53	89	85	81	122	104	90	104	131
ENSMUSG00000053297	chr6	AI854703	4.9E+07	4.9E+07	4156	0.157693297	1.235745477	0.6049942	0.690485786	0.0711	0	43	20	34	35	27	56	51	37	48	53
ENSMUSG00000083899	chr11	Gm12346	7.7E+07	7.7E+07	2255	-0.15904663	1.564403317	0.6049951	0.690485786	0.08113	0	35	28	72	40	59	69	87	42	44	39
ENSMUSG00000092072	chr3	Gm4540	1.1E+08	1.1E+08	395	0.217502625	0.910800257	0.6050243	0.690485786	0.13646	0	27	24	8	36	23	37	48	32	40	39
ENSMUSG00000000751	chr11	Rpa1	7.5E+07	7.5E+07	5578	-0.09678919	6.408872581	0.6063892	0.691981929	0.04141	0	1342	963	1587	1379	1342	1759	1738	1496	1738	1669
ENSMUSG00000020692	chr11	Nle1	8.3E+07	8.3E+07	3233	-0.1093478	3.039911916	0.6064339	0.691981929	0.04522	0	106	101	153	104	178	170	169	138	164	162
ENSMUSG00000032239	chr9	Rp9	2.2E+07	2.2E+07	1142	0.080265155	5.095063526	0.6066101	0.692126729	0.02766	0	469	307	651	516	604	776	737	566	799	739
ENSMUSG00000003346	chr10	Abhd17a	8.1E+07	8.1E+07	1547	0.096555071	5.817396275	0.6067961	0.692282604	0.04097	0	689	549	963	867	1103	1225	1319	797	1580	1129
ENSMUSG00000013539	chr16	Tango2	1.8E+07	1.8E+07	7040	-0.12545464	5.267110786	0.6069606	0.692413892	0.06846	0	442	277	1239	651	582	824	998	478	606	945
ENSMUSG00000090698	chr6	Apold1	1.3E+08	1.3E+08	3284	0.256216801	1.774954982	0.6070299	0.692436667	0.27216	0	8	23	44	111	45	41	72	72	44	134
ENSMUSG00000046808	chr5	Atp10d	7.2E+07	7.2E+07	7848	-0.16194657	2.236036815	0.6071524	0.692520108	0.09965	0	65	62	55	48	139	143	87	79	71	72
ENSMUSG00000043644	chr11	0610009L18Rik	1.2E+08	1.2E+08	619	0.103055748	3.55470686	0.6072261	0.692547855	0.04242	0	144	116	215	169	216	292	189	182	307	280
ENSMUSG00000103839	chr1	RP24-191N24.2	5.8E+07	5.8E+07	2623	-0.23207815	0.224368382	0.6072916	0.692566224	0.16144	0	10	11	15	16	37	24	22	13	7	36
ENSMUSG00000018559	chr11	Ctdnep1	7E+07	7E+07	2182	0.101883189	7.595443814	0.6081465	0.693484795	0.04698	0	2342	1779	3863	3266	3084	4344	4058	2919	4802	4641
ENSMUSG00000008200	chr2	Fnbp4	9.1E+07	9.1E+07	6583	-0.10174696	3.868931316	0.6083966	0.693657197	0.04442	0	248	197	227	195	248	346	310	196	233	377
ENSMUSG00000020361	chr11	Hspa4	5.3E+07	5.3E+07	5528	-0.09757311	7.047964777	0.6083593	0.693657197	0.04284	0	1684	1357	2910	2263	2297	2999	3031	1975	2509	2753
ENSMUSG00000076275	chr7	Mir675	1.4E+08	1.4E+08	84	0.244505176	7.220672845	0.60927	0.69459655	0.27036	0	1076	605	3325	5215	353	3579	3809	2480	3487	3402
ENSMUSG00000071856	chr18	Mcc	4.4E+07	4.4E+07	8426	-0.15377177	1.713664519	0.6094512	0.694746613	0.07922	0	51	27	44	47	89	81	71	54	48	57
ENSMUSG00000029790	chr6	Cep41	3.1E+07	3.1E+07	4979	-0.19818823	0.699289445	0.609627	0.694890561	0.12044	0	14	16	20	21	55	47	28	21	27	25
ENSMUSG00000062488	chr19	I830012O16Rik	3.5E+07	3.5E+07	2000	-0.18027791	2.397585509	0.6098619	0.695101857	0.13527	0	127	65	45	41	129	165	110	51	106	85
ENSMUSG00000031214	chrX	Ophn1	9.9E+07	9.9E+07	13100	0.15391385	2.78669805	0.6100809	0.695238466	0.09578	0	98	72	60	64	195	215	148	107	142	136
ENSMUSG00000067825	chr6	Pex26	1.2E+08	1.2E+08	5667	-0.11089505	2.629462393	0.6100645	0.695238466	0.04476	0	81	71	105	97	126	136	122	82	132	137
ENSMUSG00000079562	chr5	Maea	3.3E+07	3.3E+07	2128	-0.09511206	6.128380542	0.6110618	0.696299732	0.04081	0	980	705	1525	1209	1107	1557	1636	1020	1531	1273
ENSMUSG00000086922	chr6	Gm13835	3.1E+07	3.1E+07	685	0.090042279	4.0978362	0.6113797	0.696605383	0.03268	0	249	183	248	245	319	389	403	263	381	384
ENSMUSG00000005656	chr12	Snx6	5.5E+07	5.5E+07	1928	0.095642177	4.944578534	0.6120677	0.697332595	0.03918	0	415	405	413	361	620	903	637	477	657	636
ENSMUSG00000054931	chr13	Zkscan4	2.1E+07	2.1E+07	2400	0.19821093	0.244075239	0.6128699	0.698189857	0.1067	0	15	8	16	10	28	43	18	17	19	23
ENSMUSG00000044086	chr6	Lmod3	9.7E+07	9.7E+07	2242	0.141436445	7.37738537	0.6129557	0.698230846	0.09324	0	1727	874	5109	2877	2105	3782	3769	2700	3354	4445
ENSMUSG00000022130	chr14	Tgds	1.2E+08	1.2E+08	2265	-0.11447183	2.692454771	0.6131319	0.698364329	0.05203	0	98	72	123	84	127	179	157	91	93	120
ENSMUSG00000053080	chr19	2700081O15Rik	7417625	7417917	7032	0.106235041	3.954871595	0.6131724	0.698364329	0.04799	0	180	173	203	200	373	439	290	270	299	356
ENSMUSG00000002103	chr2	Acp2	9.1E+07	9.1E+07	5186	-0.08036864	5.035756042	0.6135278	0.698671159	0.02875	0	521	359	560	549	545	807	752	458	614	689
ENSMUSG00000046694	chr4	Fam46b	1.3E+08	1.3E+08	2287	-0.22293986	0.157545944	0.6135415	0.698671159	0.12631	0	8	10	15	13	39	20	25	16	17	18
ENSMUSG00000063576	chr17	Klhdc3	4.7E+07	4.7E+07	2126	-0.0998352	6.672960478	0.6139626	0.699093926	0.04613	0	1290	1013	2139	1987	1652	2072	2078	1470	2298	2276
ENSMUSG00000033739	chr17	Fkbpl	3.5E+07	3.5E+07	1336	0.120216223	2.513337873	0.6141082	0.699202956	0.05849	0	79	43	99	80	114	135	93	85	146	146

ENSMUSG00000047409	chr9	Ctdspl	1.2E+08	1.2E+08	5190	0.157392987	3.642617621	0.6142069	0.699258572	0.11036	0	166	132	117	86	399	336	201	229	256	323
ENSMUSG00000029063	chr4	Nadk	1.6E+08	1.6E+08	3747	-0.12852229	5.122670296	0.6143467	0.699361018	0.07508	0	445	356	457	346	1230	899	608	549	685	700
ENSMUSG00000036278	chr19	Macrod1	7056768	7057182	1274	-0.10073177	7.695952301	0.6147768	0.699793783	0.04765	0	3041	2236	4137	3661	3194	4003	4374	2950	5015	4363
ENSMUSG00000007670	chr17	Khsrp	5.7E+07	5.7E+07	3990	0.0805799	4.798089325	0.6149652	0.699951514	0.02866	0	382	281	536	360	504	622	567	467	624	658
ENSMUSG00000020032	chr10	Nuak1	8.4E+07	8.4E+07	5625	0.101542908	4.682139552	0.6150394	0.699979172	0.0472	0	342	173	605	446	360	607	613	392	459	683
ENSMUSG00000020083	chr10	2010107G23Rik	6.2E+07	6.2E+07	2981	0.178175907	1.163411972	0.6152797	0.700166975	0.09882	0	33	26	44	14	34	67	55	26	56	34
ENSMUSG00000090086	chr5	AI480526	1.2E+08	1.2E+08	4725	0.171505836	2.773113379	0.6153043	0.700166975	0.11905	0	85	100	71	52	161	222	118	73	117	228
ENSMUSG00000004558	chr14	Ndrg2	5.2E+07	5.2E+07	2157	-0.10019161	11.06898652	0.6153811	0.700197526	0.04761	0	32303	22295	40540	39511	33917	46231	45849	31593	43834	47542
ENSMUSG00000020528	chr11	Prpsap2	6.2E+07	6.2E+07	1962	-0.11458773	2.831819206	0.6155318	0.700312258	0.04983	0	107	65	119	102	169	158	143	111	126	159
ENSMUSG00000001910	chr8	Nacc1	8.5E+07	8.5E+07	4300	-0.09381149	5.227844998	0.6158367	0.700602265	0.03963	0	391	395	828	707	647	742	896	552	834	719
ENSMUSG00000027276	chr2	Jag1	1.4E+08	1.4E+08	5827	-0.11454553	3.494121699	0.6159698	0.70069689	0.05432	0	151	120	172	145	305	294	200	199	197	215
ENSMUSG00000031536	chr8	Polb	2.3E+07	2.3E+07	1227	-0.09077664	6.019134009	0.6161244	0.700815876	0.0382	0	1018	689	1217	1131	995	1500	1350	1045	1255	1332
ENSMUSG00000038013	chr11	Wipf2	9.9E+07	9.9E+07	7819	-0.09802312	3.531176546	0.6162722	0.700870358	0.03932	0	169	111	216	158	260	285	260	142	243	232
ENSMUSG00000038046	chr11	Rnmtl1	7.6E+07	7.6E+07	1935	-0.11758161	3.84584197	0.6162403	0.700870358	0.0586	0	160	115	396	294	196	319	286	222	309	280
ENSMUSG00000028019	chr3	Pdgfc	8.1E+07	8.1E+07	5089	0.205069984	2.100218031	0.6169204	0.701550639	0.17307	0	47	47	33	24	147	157	110	45	73	93
ENSMUSG00000006732	chr10	Mettl1	1.3E+08	1.3E+08	2907	-0.11496689	4.125277603	0.6169897	0.701572522	0.06088	0	329	261	247	246	228	512	294	302	283	334
ENSMUSG00000021991	chr14	Cacna2d3	2.9E+07	2.9E+07	3695	0.224528827	0.370424762	0.6172713	0.701778939	0.13093	0	16	21	17	8	18	35	18	29	17	31
ENSMUSG00000078185	chr1	Chml	1.8E+08	1.8E+08	6117	-0.12953124	1.863600299	0.6172316	0.701778939	0.05433	0	53	36	71	58	64	87	65	61	77	58
ENSMUSG00000006221	chr4	Hspb7	1.4E+08	1.4E+08	2769	0.245431382	9.340343772	0.61741	0.701879739	0.28543	0	4354	1389	22735	17431	2385	17993	18686	9546	11925	15665
ENSMUSG00000006289	chr14	Osgep	5.1E+07	5.1E+07	4933	-0.08447527	5.532987484	0.617631	0.702074162	0.03263	0	607	523	946	705	849	972	917	734	985	1017
ENSMUSG00000049354	chr11	Dcaf7	1.1E+08	1.1E+08	6133	-0.08736294	5.773297545	0.6179005	0.702323509	0.03532	0	704	564	1154	933	960	1210	1305	811	1077	1094
ENSMUSG00000046856	chr1	Gpr1	6.3E+07	6.3E+07	2496	-0.21443968	-0.08138979	0.6180613	0.702449385	0.11724	0	10	11	9	17	21	12	27	9	13	20
ENSMUSG00000037735	chr12	2810032G03Rik	5375870	5376528	3173	-0.20123181	0.236603684	0.6181963	0.702545913	0.11157	0	12	13	14	14	35	33	22	17	13	19
ENSMUSG00000022234	chr15	Cct5	3.2E+07	3.2E+07	2809	-0.09402623	7.203066712	0.6183753	0.702692355	0.04226	0	2273	1782	2697	2217	2467	3464	3039	2398	2983	2832
ENSMUSG00000021136	chr12	Smoc1	8.1E+07	8.1E+07	3496	-0.35804728	3.086003716	0.6187299	0.703038411	0.58637	0	135	103	8	7	484	268	47	130	171	148
ENSMUSG00000020435	chr11	Osbp2	3703731	3705207	6361	0.185570849	0.344782537	0.6188258	0.703090414	0.0914	0	13	15	19	19	15	38	16	20	21	33
ENSMUSG00000030166	chr6	Rad52	1.2E+08	1.2E+08	3371	-0.10094176	3.436934177	0.6189081	0.703126974	0.04228	0	171	106	167	183	217	270	247	172	184	201
ENSMUSG00000058620	chr2	Adra2b	1.3E+08	1.3E+08	4014	-0.19299155	0.554833621	0.6189692	0.70313941	0.09835	0	17	9	36	23	29	37	16	24	31	23
ENSMUSG00000033883	chr3	D3Ertd254e	3.6E+07	3.6E+07	6503	-0.13588527	1.860466871	0.6191737	0.70330552	0.06695	0	57	34	45	67	77	98	74	51	64	64
ENSMUSG00000079055	chr12	Slc8a3	8.1E+07	8.1E+07	5332	-0.10849091	5.375915571	0.6192157	0.70330552	0.05583	0	902	456	622	619	590	936	1204	580	737	705
ENSMUSG00000029557	chr5	Ftsj2	1.4E+08	1.4E+08	1443	-0.10973166	3.300077888	0.6195848	0.703667772	0.04937	0	121	89	224	193	153	192	210	134	226	211
ENSMUSG00000087413	chr4	Gm11266	8.3E+07	8.3E+07	1271	-0.12898459	2.241550011	0.6199069	0.703976501	0.06337	0	84	56	93	53	79	108	90	65	72	125
ENSMUSG00000012422	chr13	Tmem167	9E+07	9E+07	10807	-0.09065402	4.966883558	0.6203144	0.704325296	0.03841	0	549	393	426	433	591	797	629	529	618	545
ENSMUSG00000035266	chr5	Helq	1E+08	1E+08	5056	0.119161755	2.027761694	0.620284	0.704325296	0.0516	0	42	43	76	55	75	105	83	64	82	95
ENSMUSG00000001918	chr7	Slc1a5	1.7E+07	1.7E+07	4156	-0.30889066	6.396747541	0.6204313	0.704400975	0.45448	0	942	660	165	193	5659	2352	822	1429	1442	1699
ENSMUSG00000000916	chr5	Nsun5	1.4E+08	1.4E+08	3142	-0.10914305	2.628958658	0.6207135	0.704664302	0.04537	0	70	68	134	94	119	141	124	95	121	125
ENSMUSG00000024170	chr17	Telo2	2.5E+07	2.5E+07	8006	0.09859414	3.320108039	0.6209055	0.70482522	0.0417	0	112	89	178	170	185	273	199	149	218	227
ENSMUSG00000002957	chr7	Ap2a2	1.4E+08	1.4E+08	4639	0.090371977	6.502644963	0.6210093	0.70482892	0.03921	0	1078	962	1547	1390	1710	2453	1978	1431	2014	1848
ENSMUSG00000027777	chr3	Schip1	6.8E+07	6.8E+07	5102	0.096362875	6.476686939	0.6209872	0.70482892	0.0449	0	1164	784	1958	1350	1391	2117	2423	1499	1678	1804
ENSMUSG00000064037	chr5	Gpn1	3.1E+07	3.1E+07	7845	0.07782932	4.659971183	0.6211054	0.704881037	0.02706	0	333	273	434	361	459	610	509	451	561	530
ENSMUSG00000041837	chr9	Pdcd7	6.5E+07	6.5E+07	2454	0.08609816	4.324289764	0.6212277	0.704962737	0.03284	0	264	194	332	355	322	448	425	326	412	510
ENSMUSG00000028015	chr3	Ctso	8.2E+07	8.2E+07	5123	-0.11146874	3.765946741	0.6215182	0.705190278	0.05714	0	230	176	175	161	307	381	329	198	201	250
ENSMUSG00000039252	chr5	Lgi2	5.3E+07	5.3E+07	1950	0.181271693	1.299515443	0.6215287	0.705190278	0.11374	0	38	37	23	20	43	72	46	53	46	39
ENSMUSG00000020781	chr11	Tsen54	1.2E+08	1.2E+08	2458	0.103805356	3.018783877	0.6216454	0.705265623	0.04724	0	82	71	161	131	152	184	179	122	186	189
ENSMUSG00000022564	chr15	Grina	7.6E+07	7.6E+07	1693	0.102653787	7.195322828	0.621747	0.705323758	0.05148	0	1659	1383	2613	1829	3505	3355	3099	2215	3571	3505
ENSMUSG00000033039	chr15	Micall1	7.9E+07	7.9E+07	6701	0.087643864	4.538359596	0.6221231	0.705693377	0.03623	0	267	186	509	364	425	502	551	356	467	597
ENSMUSG00000029310	chr5	Nudt9	1E+08	1E+08	2392	0.085190161	5.899010084	0.6226187	0.706198459	0.03478	0	768	611	1143	842	1060	1324	1352	916	1379	1388
ENSMUSG00000007033	chr17	Hspa1l	3.5E+07	3.5E+07	2472	-0.11474434	4.851161082	0.6227283	0.706265627	0.06193	0	381	194	727	660	370	731	650	343	552	633
ENSMUSG00000028759	chr4	Hp1bp3	1.4E+08	1.4E+08	8433	-0.08770359	6.437815133	0.6236231	0.707223301	0.03748	0	1275	940	1755	1325	1505	2052	1984	1279	1658	1762
ENSMUSG00000027746	chr3	Ufm1	5.4E+07	5.4E+07	4122	-0.07576981	5.067919732	0.6237512	0.707311382	0.02646	0	488	373	643	530	569	794	711	557	617	684
ENSMUSG00000042202	chr4	Slc35e2	1.6E+08	1.6E+08	6574	-0.10854918	2.706103517	0.6239595	0.707490388	0.04899	0	100	85	108	79	129	152	144	105	111	127
ENSMUSG00000021468	chr13	Sptlc1	5.3E+07	5.3E+07	2606	0.086548562	4.350714251	0.6240699	0.707558368	0.03363	0	262	226	310	256	444	498	430	322	470	448
ENSMUSG00000024312	chr17	Wdr46	3.4E+07	3.4E+07	2442	0.098588521	3.535631355	0.6244124	0.70788946	0.04079	0	155	132	191	171	186	236	233	172	299	289
ENSMUSG00000074305	chr9	Peak1	5.6E+07	5.6E+07	12351	-0.08247406	4.568142002	0.6245329	0.707911635	0.032	0	327	305	423	386	378	647	424	363	463	490
ENSMUSG00000075704	chr16	Txnrd2	1.8E+07	1.8E+07	3359	-0.08594003	4.572090724	0.6245206	0.707911635	0.03357	0	314	237	411	379	534	550	488	330	594	430
ENSMUSG00000019732	chr8	Calr3	7.2E+07	7.2E+07	1962	0.138575085	1.739089824	0.6246758	0.707938734	0.07053	0	47	30	71	30	59	86	53	58	69	83
ENSMUSG00000028013	chr3	Ppa2	1.3E+08	1.3E+08	2535	0.085821253	5.484529745	0.6246646	0.707938734	0.03586	0	561	388	977	696	735	1089	964	757	878	1069
ENSMUSG00000047434	chr16	Xxylt1	3.1E+07	3.1E+07	3412	0.118924737	2.720120918	0.6247082	0.707938734	0.06279	0	83	63	133	65	137	197	154	124	114	109
ENSMUSG00000078154	chr11	Gm12184	4.9E+07	4.9E+07	1310	-0.12898093	1.512197739	0.6249874	0.708197879	0.05909	0	45	31	53	32	58	65	53	35	57	64
ENSMUSG00000031578	chr8	Mak16	3.1E+07	3.1E+07	1857	-0.08757941	3.930839265	0.625359	0.70851744	0.03317	0	217	159	298	265	248	345	322	261	295	289
ENSMUSG00000034216	chr2	Vps18	1.2E+08	1.2E+08	4786	0.081667554	4.382598616	0.6253704	0.70851744	0.03027	0	279	222	364	286	383	418	490	345	487	458
ENSMUSG00000044337	chr1	Ackr3	9E+07	9E+07	3348	-0.08032317	4.68571203	0.6257877	0.70892415	0.02997	0	340	287	414	403	562	619	588	371	468	551
ENSMUSG00000079614	chr18	Seh1l	6.8E+07	6.8E+07	3516	0.079271286	4.923722144	0.6258305	0.70892415	0.02955	0	444	319	512	378	585	738	688	552	622	599
ENSMUSG00000027887	chr3	Sypl2	1.1E+08	1.1E+08	4377	0.10280081	8.955135541	0.626603	0.70974192	0.05331	0	6484	5450	8654	8304	7130	9404	10621	8024	13343	11493
ENSMUSG00000030243	chr6	Recql	1.4E+08	1.4E+08	7510	-0.10654854	2.985160948	0.6268779	0.709995969	0.05139	0	129	107	145	105	118	209	189	111	129	149
ENSMUSG00000022664	chr16	Slc35a5	4.5E+07	4.5E+07	8105	0.12003593	2.369627755	0.6270808	0.710168388	0.05469	0	66	60	62	78	97	138	109	86	100	113
ENSMUSG00000028159	chr3	Dapp1	1.4E+08	1.4E+08	3284	0.142916823	2.152381201	0.6271527	0.710192406	0.08745	0	84	31	92	64	43	143	87	69	75	102

ENSMUSG00000075486	chr14	Commd6	1E+08	1E+08	1322	0.10988407	3.079354355	0.6272117	0.710201956	0.05304	0	115	78	131	103	190	256	142	130	193	183
ENSMUSG00000040856	chr12	Dlk1	1.1E+08	1.1E+08	5657	-0.30678381	0.592820067	0.627438	0.710400877	0.40866	0	45	26	5	13	21	71	7	30	15	10
ENSMUSG00000022781	chr16	Pak2	3.2E+07	3.2E+07	6795	0.083259729	5.286489756	0.627638	0.710569947	0.03377	0	462	410	668	515	846	998	894	681	749	819
ENSMUSG00000021895	chr14	Arhgef3	2.7E+07	2.7E+07	3585	0.094945608	3.786056037	0.6282083	0.711158206	0.04133	0	186	124	286	188	237	401	355	210	213	302
ENSMUSG00000007603	chr17	Dus3l	5.7E+07	5.7E+07	2303	0.080182422	4.487518096	0.6283229	0.711230498	0.02969	0	277	244	417	305	413	501	502	344	558	473
ENSMUSG00000028671	chr4	Gale	1.4E+08	1.4E+08	2370	0.292887126	1.923478361	0.6286287	0.71151918	0.41837	0	44	22	9	6	185	147	49	70	83	71
ENSMUSG00000049744	chr2	Arhgap15	4.4E+07	4.4E+07	8818	0.165709026	0.823165031	0.6288161	0.711586489	0.07965	0	18	22	23	24	30	55	43	19	38	30
ENSMUSG00000071645	chr19	Tut1	8953850	8954021	2747	-0.09179624	3.56456631	0.6288403	0.711586489	0.03616	0	155	123	233	190	226	260	217	180	238	280
ENSMUSG00000085151	chr2	1110018N20Rik	1.7E+08	1.7E+08	1579	-0.21434695	0.060617252	0.6288017	0.711586489	0.09905	0	13	5	20	13	28	24	17	14	13	22
ENSMUSG00000038119	chr9	Cdon	3.5E+07	3.5E+07	7715	-0.10660085	4.805877256	0.6291868	0.711921114	0.05601	0	386	377	369	329	715	786	468	470	418	640
ENSMUSG00000029030	chr4	Tprgl	1.5E+08	1.5E+08	2242	0.087909956	6.708286711	0.6293585	0.712057921	0.03903	0	1337	1140	1872	1427	1937	2382	2453	1605	2312	2423
ENSMUSG00000020092	chr10	Pald1	6.1E+07	6.1E+07	4274	-0.11313376	3.793315623	0.6294883	0.712147362	0.05777	0	168	132	249	155	417	308	262	240	276	272
ENSMUSG00000093571	chr7	Gm24757	3E+07	3E+07	371	-0.12371376	2.102453084	0.6295884	0.712203121	0.0582	0	64	40	80	61	91	84	99	65	101	65
ENSMUSG00000049119	chr4	Fam110b	5644090	5644410	8164	0.110306753	2.924426506	0.6296693	0.712237275	0.05242	0	89	72	150	139	98	207	157	110	181	156
ENSMUSG00000019478	chr8	Rab4a	1.2E+08	1.2E+08	1757	-0.08096371	4.25238155	0.6298082	0.712336886	0.03045	0	287	209	361	303	317	391	452	268	419	383
ENSMUSG00000020439	chr11	Smtn	3517523	3517827	4380	0.096145354	6.75806524	0.630527	0.713040013	0.04728	0	1214	1011	2253	1789	1798	2280	2612	1495	2776	2473
ENSMUSG00000038187	chr7	Btbd10	1.1E+08	1.1E+08	5801	-0.09784766	3.196354563	0.6305315	0.713040013	0.04366	0	128	106	167	143	166	265	210	132	156	154
ENSMUSG00000025375	chr11	Aatk	1.2E+08	1.2E+08	7159	-0.13565624	3.639779834	0.6307698	0.713251971	0.08905	0	185	147	169	94	401	355	218	162	224	279
ENSMUSG00000045999	chr17	AY036118	4E+07	4E+07	1304	0.518415402	3.161135911	0.6310865	0.713502186	1.29736	0	2	3	530	60	54	2	219	6	500	365
ENSMUSG00000085028	chr2	Slc2a4rg-ps	1.8E+08	1.8E+08	2976	-0.15390661	1.386792935	0.6310928	0.713502186	0.10525	0	38	47	36	30	42	64	38	25	49	75
ENSMUSG00000021509	chr13	Slc25a48	5.6E+07	5.6E+07	3374	0.304255788	0.118548786	0.631247	0.713597676	0.37851	0	16	7	1	2	41	38	14	11	29	21
ENSMUSG00000037669	chr12	1110057K04Rik	8208107	8208192	2748	-0.09365543	3.824737951	0.6312791	0.713597676	0.04098	0	212	167	227	169	329	359	316	207	243	294
ENSMUSG00000032615	chr11	Nt5m	6E+07	6E+07	3361	0.089751179	4.207836505	0.6315368	0.713790243	0.03926	0	222	166	427	282	280	387	460	301	450	358
ENSMUSG00000058581	chr14	Gm5801	5.6E+07	5.6E+07	780	0.111281672	2.652300404	0.6315512	0.713790243	0.04997	0	78	78	91	91	106	148	118	111	128	155
ENSMUSG00000055553	chr8	Kxd1	7.1E+07	7.1E+07	3176	0.092728249	7.970808222	0.6316562	0.713851417	0.04457	0	3196	2378	5271	3882	3931	5997	5461	3786	5870	5798
ENSMUSG00000024785	chr19	Rcl1	2.9E+07	2.9E+07	1803	-0.11617826	2.974299438	0.6319468	0.714122329	0.05888	0	114	81	121	93	212	170	137	117	167	179
ENSMUSG00000029403	chr5	Cdkl2	9.2E+07	9.2E+07	4967	-0.09768315	3.559558392	0.6320027	0.714127879	0.04365	0	146	134	251	164	232	260	338	158	208	216
ENSMUSG00000005204	chr11	Senp3	7E+07	7E+07	3632	-0.07345492	4.890760872	0.6320706	0.714146241	0.02599	0	417	344	565	444	529	689	622	460	626	587
ENSMUSG00000025059	chrX	Gyk	8.6E+07	8.6E+07	7743	-0.21339404	1.471334191	0.6321207	0.714146241	0.18366	0	65	8	57	28	69	60	77	44	21	53
ENSMUSG00000031072	chr7	Oraov1	1.4E+08	1.4E+08	4400	0.090687054	4.129986755	0.6323789	0.714380304	0.03696	0	265	217	271	206	301	500	404	267	371	332
ENSMUSG00000103476	chr3	RP24-79E2.2	6.3E+07	6.3E+07	243	-0.4802975	1.682208199	0.6330346	0.715063471	1.103	0	6	0	157	135	0	30	16	45	14	156
ENSMUSG00000032892	chr11	Rangrf	6.9E+07	6.9E+07	1269	0.07995781	5.062140496	0.6331503	0.715136544	0.03169	0	398	322	666	587	504	744	770	506	805	726
ENSMUSG00000026494	chr1	Kif26b	1.8E+08	1.8E+08	14696	-0.25509923	1.8945113	0.6332918	0.715238767	0.30218	0	37	23	156	91	5	63	84	62	54	73
ENSMUSG00000010175	chr1	Prox1	1.9E+08	1.9E+08	8390	-0.31797499	1.085884345	0.6334909	0.71540609	0.45447	0	1	6	89	74	12	27	33	30	40	52
ENSMUSG00000033373	chr12	Fntb	7.7E+07	7.7E+07	3987	0.078881421	5.420091704	0.634251	0.716206839	0.03167	0	615	396	860	617	700	1044	925	731	934	899
ENSMUSG00000082575	chr4	Gm13050	1.4E+08	1.4E+08	1345	-0.13325002	1.95481568	0.634593	0.716535302	0.07009	0	54	34	75	70	70	53	78	57	97	84
ENSMUSG00000028517	chr4	Ppap2b	1.1E+08	1.1E+08	3159	-0.10599866	6.5147773	0.6346604	0.716553761	0.05856	0	889	938	2340	1272	1995	2129	2561	1236	1557	1728
ENSMUSG00000025925	chr1	Terf1	1.6E+07	1.6E+07	4608	0.126029549	2.424652079	0.6351602	0.717060281	0.06457	0	86	59	82	50	103	172	107	81	94	121
ENSMUSG00000041343	chr7	Ankrd42	9.3E+07	9.3E+07	5099	0.226709136	-0.00200906	0.6352256	0.717076452	0.16032	0	13	10	10	3	26	33	15	9	19	25
ENSMUSG00000030942	chr7	Thumpd1	1.2E+08	1.2E+08	2653	0.075111934	4.780169163	0.635472	0.717296781	0.0274	0	408	284	516	373	445	732	615	455	543	570
ENSMUSG00000008859	chr13	Rala	1.8E+07	1.8E+07	2684	-0.07713079	5.388628853	0.6356085	0.717393166	0.03024	0	609	472	765	654	752	987	989	631	831	788
ENSMUSG00000030007	chr6	Cct7	8.5E+07	8.5E+07	2452	0.088816095	7.168864017	0.6357181	0.717459166	0.04165	0	1999	1466	2612	2067	2473	3286	2913	2425	3381	3281
ENSMUSG00000068580	chr2	Zfyve19	1.2E+08	1.2E+08	3255	-0.10106003	3.131081547	0.6358458	0.717545498	0.04379	0	110	86	199	120	180	186	198	137	160	183
ENSMUSG00000064284	chr15	Cdpf1	8.6E+07	8.6E+07	1215	-0.07921628	4.111046239	0.6366026	0.718341813	0.02997	0	263	194	308	245	329	427	344	255	365	346
ENSMUSG00000001656	chr15	Hoxc11	1E+08	1E+08	2021	0.120063713	2.500488203	0.6367058	0.718400367	0.06926	0	55	57	93	79	125	89	112	105	140	142
ENSMUSG00000028568	chr4	Btf3l4	1.1E+08	1.1E+08	4546	-0.08475897	4.011309739	0.6369575	0.718538598	0.03487	0	258	196	299	215	274	429	320	262	318	283
ENSMUSG00000040174	chr2	Alkbh3	9.4E+07	9.4E+07	3159	-0.07656789	5.261426766	0.636978	0.718538598	0.02951	0	571	386	824	596	630	878	857	572	743	818
ENSMUSG00000051498	chr5	Tlr6	6.5E+07	6.5E+07	2603	0.147649773	1.570751696	0.636982	0.718538598	0.08274	0	45	38	45	23	52	83	79	51	48	51
ENSMUSG00000090625	chr2	Gm20721	1.7E+08	1.7E+08	1484	0.41354903	3.379394803	0.6372286	0.71875905	0.87114	0	15	8	498	122	126	8	276	9	443	505
ENSMUSG00000024067	chr17	Dpy30	7.4E+07	7.4E+07	974	0.083899836	4.334258541	0.6374417	0.71894151	0.03319	0	296	242	313	245	367	516	413	314	487	414
ENSMUSG00000022623	chr15	Shank3	8.9E+07	8.9E+07	8896	0.092890505	4.021743416	0.637658	0.719127743	0.04407	0	172	137	323	215	377	408	299	250	358	416
ENSMUSG00000030008	chr6	Pradc1	8.5E+07	8.5E+07	1594	-0.09085924	3.610729643	0.6380284	0.719487595	0.04058	0	189	155	220	162	213	273	281	158	296	216
ENSMUSG00000003299	chr9	Mrpl4	2.1E+07	2.1E+07	1285	0.094873332	5.685426472	0.6381603	0.719520625	0.04796	0	551	414	1227	857	837	1068	1159	779	1328	1159
ENSMUSG00000026473	chr1	Glul	1.5E+08	1.5E+08	3323	0.123625967	7.528008792	0.6381135	0.719520625	0.08206	0	3345	2101	1531	2506	3532	4776	2913	3459	4493	4110
ENSMUSG00000030120	chr6	Mlf2	1.2E+08	1.2E+08	1533	0.09188832	7.651340094	0.6386463	0.720010645	0.04548	0	2581	2226	3256	2888	3794	4266	4118	3190	5091	4749
ENSMUSG00000030433	chr7	Sbk2	4956134	4957713	2426	-0.11497823	4.953263909	0.6387146	0.720029836	0.06928	0	361	270	739	648	470	691	702	297	451	1001
ENSMUSG00000071103	chr8	1700029J07Rik	4.6E+07	4.6E+07	2740	0.257040489	-0.19534517	0.6387791	0.72004471	0.22842	0	3	15	5	7	21	33	7	13	14	20
ENSMUSG00000022545	chr16	Ercc4	1.3E+07	1.3E+07	6730	-0.0935002	3.194418594	0.6389929	0.72022779	0.04252	0	117	122	164	133	167	199	211	114	187	204
ENSMUSG00000097316	chr1	Gm10516	1.9E+08	1.9E+08	2788	0.112402236	2.064000421	0.6392016	0.720405155	0.05599	0	66	36	81	59	56	90	102	71	89	84
ENSMUSG00000021975	chr14	Ints9	6.5E+07	6.5E+07	2677	0.084568504	4.009255812	0.6393473	0.720511444	0.03489	0	191	147	324	261	273	378	413	215	352	365
ENSMUSG00000004187	chr15	Kifc2	7.7E+07	7.7E+07	3143	-0.11450222	2.052238827	0.6398204	0.720986684	0.05215	0	48	45	91	61	78	87	97	56	77	87
ENSMUSG00000002870	chr6	Mcm2	8.9E+07	8.9E+07	3370	-0.11329211	2.678266062	0.6401801	0.721334089	0.06358	0	118	87	79	90	108	160	135	97	137	99
ENSMUSG00000030611	chr7	Mrps11	7.9E+07	7.9E+07	2172	-0.08402176	4.25677905	0.6406434	0.721798066	0.03372	0	259	172	403	312	368	421	372	285	467	367
ENSMUSG00000020288	chr11	Ahsa2	2.3E+07	2.3E+07	4532	-0.08337519	5.33216549	0.6409832	0.722122875	0.03633	0	625	420	930	590	595	1060	844	658	770	714
ENSMUSG00000027080	chr2	Med19	8.5E+07	8.5E+07	2059	0.098203724	3.433399592	0.6411336	0.722210714	0.04398	0	135	146	180	123	189	260	242	185	243	211
ENSMUSG00000030201	chr6	Lrp6	1.3E+08	1.3E+08	9822	-0.08809482	6.40428431	0.6411641	0.722210714	0.04203	0	1199	930	1826	1145	1585	1955	1932	1038	1624	2059
ENSMUSG00000027522	chr2	Stx16	1.7E+08	1.7E+08	3962	-0.0792867	4.886771959	0.6413537	0.722311736	0.03348	0	406	409	495	400	555	789	548	402	604	657

ENSMUSG00000074030	chr8	Exoc8	1.2E+08	1.2E+08	7406	-0.08996512	3.79828168	0.6413568	0.722311736	0.03733	0	190	138	277	207	284	306	238	247	305	275
ENSMUSG00000062937	chr4	Mtap	8.9E+07	8.9E+07	3226	-0.09327398	4.321471108	0.6415817	0.722506968	0.04543	0	384	255	256	257	368	415	425	325	437	379
ENSMUSG00000073600	chr18	Prob1	3.6E+07	3.6E+07	4890	-0.10140641	6.693407075	0.6417661	0.722656609	0.05596	0	1327	844	2550	2055	1549	2066	2513	1406	2103	2292
ENSMUSG00000013787	chr17	Ehmt2	3.5E+07	3.5E+07	5489	0.077289363	5.500649582	0.6418237	0.722663484	0.03145	0	623	458	792	625	860	1099	1022	652	1046	1017
ENSMUSG00000057561	chr18	Eif1a	4.7E+07	4.7E+07	2879	0.096174322	4.177048936	0.6419049	0.722696935	0.04628	0	263	207	228	215	397	534	402	314	363	316
ENSMUSG00000020826	chr11	Nos2	7.9E+07	7.9E+07	4192	-0.14069758	2.412769717	0.6420551	0.722807964	0.08666	0	52	36	104	91	151	97	96	91	131	92
ENSMUSG00000000131	chr7	Xpo6	1.3E+08	1.3E+08	9692	-0.09290311	4.539389004	0.6426223	0.723388491	0.04631	0	352	350	322	281	460	508	418	335	449	614
ENSMUSG00000028700	chr4	Pomgnt1	1.2E+08	1.2E+08	5463	-0.08243833	6.271247451	0.6429044	0.723639686	0.03686	0	1143	798	1518	1241	1355	1755	1564	1220	1587	1622
ENSMUSG00000049044	chr2	Rapgef4	7.2E+07	7.2E+07	6677	-0.21598073	0.526182273	0.6429486	0.723639686	0.17837	0	10	8	50	35	10	30	28	18	21	31
ENSMUSG00000016552	chr15	Foxred2	7.8E+07	7.8E+07	5939	0.209086699	1.379516259	0.6431961	0.723860159	0.18002	0	32	43	11	17	65	73	46	38	67	55
ENSMUSG00000074170	chr7	Plekhf1	3.8E+07	3.8E+07	1559	-0.0863913	3.803787886	0.6435666	0.72421896	0.03537	0	172	140	288	251	244	301	306	223	266	293
ENSMUSG00000004394	chr11	Tmed4	6270369	6271800	2178	-0.08154486	6.109545605	0.6436694	0.724276561	0.03627	0	1006	747	1277	1117	1241	1515	1481	976	1473	1521
ENSMUSG00000000266	chrX	Mid2	1.4E+08	1.4E+08	8114	0.092611231	3.204244621	0.6439336	0.724515692	0.03966	0	134	87	178	114	163	259	198	141	184	199
ENSMUSG00000043153	chr12	Ispd	3.6E+07	3.6E+07	2690	-0.12516559	1.664468831	0.6444991	0.72509376	0.06002	0	44	38	53	51	55	74	76	52	55	46
ENSMUSG00000018339	chr11	Gpx3	5.5E+07	5.5E+07	1813	0.110843989	9.075100834	0.6446444	0.725199047	0.06891	0	5329	7571	6621	7961	11025	11349	13168	7366	11310	15229
ENSMUSG00000064138	chr13	Fam172a	7.8E+07	7.8E+07	4019	-0.09075427	3.343382628	0.6447214	0.72522753	0.04018	0	161	108	186	151	181	288	226	141	186	179
ENSMUSG00000038233	chr9	Fam198a	1.2E+08	1.2E+08	3622	0.208593447	0.24243195	0.6448989	0.725369051	0.10728	0	16	15	11	16	15	40	25	10	18	29
ENSMUSG00000079605	chr17	Zbtb9	2.7E+07	2.7E+07	2798	0.109776245	2.344832975	0.6451861	0.725633915	0.05621	0	59	43	84	80	102	117	93	99	99	120
ENSMUSG00000011179	chr12	Odc1	1.8E+07	1.8E+07	2547	0.123380727	6.525898673	0.6461337	0.726583118	0.0858	0	889	865	2079	721	2443	2094	3021	1425	1665	1792
ENSMUSG00000019505	chr11	Ubb	6.3E+07	6.3E+07	1675	-0.08890988	8.669701664	0.6461255	0.726583118	0.04478	0	6608	4767	7535	6086	6586	9903	8400	6188	8646	7832
ENSMUSG00000037259	chr2	Dzank1	1.4E+08	1.4E+08	8262	-0.18607641	-0.06180799	0.6464006	0.726825032	0.10733	0	17	6	15	9	23	21	25	12	10	15
ENSMUSG00000021340	chr13	Gpld1	2.5E+07	2.5E+07	3584	0.185086717	1.060320042	0.6466099	0.727002044	0.14718	0	15	17	22	18	73	59	33	31	49	46
ENSMUSG00000037034	chr2	Pax1	1.5E+08	1.5E+08	4492	0.412374005	0.385840184	0.6469426	0.727317806	0.84841	0	15	18	0	5	36	100	0	21	6	21
ENSMUSG00000052915	chr11	Msl1	9.9E+07	9.9E+07	5433	-0.08405351	6.389333038	0.6473432	0.727699989	0.03953	0	1207	850	1766	1415	1349	1825	1932	1229	1671	1783
ENSMUSG00000074364	chr7	Ehd2	1.6E+07	1.6E+07	5100	-0.13882739	6.774621206	0.6473863	0.727699989	0.10895	0	1153	955	1487	1112	4438	2900	1842	1802	2205	2021
ENSMUSG00000030335	chr6	Mrpl51	1.3E+08	1.3E+08	3357	-0.09194236	7.120837775	0.6476088	0.727891733	0.04779	0	1800	1338	3558	2226	2211	3181	2936	2154	2674	3004
ENSMUSG00000039349	chr1	C130074G19Rik	1.8E+08	1.8E+08	3035	0.132317978	5.244502873	0.6479088	0.728170538	0.09906	0	444	312	467	295	1337	910	631	652	1038	840
ENSMUSG00000027663	chr3	Zmat3	3.2E+07	3.2E+07	11435	0.097479812	4.008428063	0.6479823	0.72819481	0.04769	0	220	187	216	316	203	349	392	247	378	346
ENSMUSG00000037010	chrX	Apln	4.8E+07	4.8E+07	3149	0.149407117	1.744035407	0.6484985	0.728716525	0.11646	0	35	22	57	36	93	68	44	85	73	70
ENSMUSG00000097960	chr8	A330074K22Rik	1.2E+08	1.2E+08	2489	-0.19564038	1.669090015	0.648558	0.728725001	0.18656	0	39	10	116	70	28	62	91	30	61	57
ENSMUSG00000025792	chr11	Slc25a10	1.2E+08	1.2E+08	3455	0.189744979	4.250138236	0.6489799	0.729082216	0.20294	0	281	138	117	83	780	546	287	340	560	347
ENSMUSG00000028475	chr4	5430416O09Rik	4.4E+07	4.4E+07	4086	-0.14275776	1.842076287	0.6489533	0.729082216	0.08524	0	56	39	58	29	99	80	81	54	55	73
ENSMUSG00000039536	chr2	Stau1	1.7E+08	1.7E+08	6065	-0.07492398	5.523973644	0.6494341	0.729534091	0.03091	0	686	474	893	697	850	1117	1004	695	949	882
ENSMUSG00000022556	chr15	Hsf1	7.6E+07	7.6E+07	2018	-0.07893907	5.419703345	0.6497181	0.72979471	0.03462	0	532	467	866	745	738	894	983	562	960	931
ENSMUSG00000032348	chr9	Gsta4	7.8E+07	7.8E+07	957	-0.10891388	4.08840285	0.6501116	0.730178221	0.06223	0	232	141	282	234	484	403	219	284	410	357
ENSMUSG00000052406	chr2	Rexo4	2.7E+07	2.7E+07	3662	0.083689003	3.969021341	0.6502708	0.730298522	0.03408	0	239	177	230	242	240	388	369	236	333	339
ENSMUSG00000022106	chr14	Rcbtb2	7.3E+07	7.3E+07	9489	-0.09488013	4.588208894	0.6504108	0.730303256	0.05028	0	408	312	275	278	575	574	469	354	516	493
ENSMUSG00000028681	chr4	Ptch2	1.2E+08	1.2E+08	5974	0.212085531	1.60362415	0.6503485	0.730303256	0.2199	0	25	33	19	17	116	97	35	44	73	79
ENSMUSG00000031972	chr8	Acta1	1.2E+08	1.2E+08	1433	-0.09664102	14.90014876	0.6504312	0.730303256	0.05447	0	425123	303025	630436	571877	485103	587075	676166	410781	780406	614019
ENSMUSG00000043284	chr11	Tmem11	6.1E+07	6.1E+07	1745	0.077491538	5.590970929	0.6505283	0.730353829	0.03405	0	571	460	999	705	881	1111	1034	803	1085	1068
ENSMUSG00000031627	chr8	Irf2	4.7E+07	4.7E+07	2484	-0.07268064	4.353113829	0.6507641	0.730560027	0.02811	0	289	235	384	318	353	528	408	292	400	440
ENSMUSG00000027375	chr2	Mal	1.3E+08	1.3E+08	2778	0.164366613	1.443654779	0.6512313	0.730909025	0.11247	0	54	26	53	23	29	107	55	37	43	50
ENSMUSG00000029049	chr4	Morn1	1.6E+08	1.6E+08	4320	0.18324019	0.195641855	0.6511875	0.730909025	0.09349	0	20	7	11	17	18	28	31	13	22	21
ENSMUSG00000038042	chr13	Ptpdc1	4.9E+07	4.9E+07	4310	0.118552574	2.548741797	0.6512164	0.730909025	0.06735	0	58	73	95	62	131	152	138	70	111	158
ENSMUSG00000021395	chr13	Spin1	5.1E+07	5.1E+07	4434	-0.07915506	4.420422374	0.6515603	0.731219791	0.03329	0	303	242	357	346	409	496	514	374	352	399
ENSMUSG00000030058	chr6	Copg1	8.8E+07	8.8E+07	10905	0.077124763	5.825351132	0.651648	0.731259716	0.03371	0	770	559	1026	871	978	1513	1182	881	1329	1143
ENSMUSG00000001642	chr6	Akr1b3	3.4E+07	3.4E+07	3933	-0.08538495	7.293860172	0.6517811	0.731350542	0.04248	0	2223	1880	2986	2480	2616	3275	3491	2423	3426	3110
ENSMUSG00000037119	chr15	D15Ertd621e	5.8E+07	5.8E+07	5621	-0.09337311	3.78058751	0.6519242	0.731452545	0.04672	0	219	157	186	183	320	371	321	203	247	236
ENSMUSG00000061353	chr6	Cxcl12	1.2E+08	1.2E+08	8176	0.091946588	6.94518489	0.6520811	0.731570126	0.04937	0	1345	1159	2813	2047	1847	3329	2527	2197	2444	2634
ENSMUSG00000014592	chr4	Camta1	1.5E+08	1.5E+08	14570	-0.14083928	4.670683122	0.6535372	0.733115821	0.11256	0	251	130	875	613	261	490	617	364	479	550
ENSMUSG00000097885	chr3	5031434O11Rik	5.2E+07	5.2E+07	3731	0.195285926	0.401465029	0.6535634	0.733115821	0.1099	0	14	20	10	14	25	24	23	20	31	35
ENSMUSG00000074215	chr8	Gm10643	8.4E+07	8.4E+07	1577	0.170545883	0.381100619	0.6537932	0.733314996	0.09043	0	15	13	29	8	21	36	28	16	22	30
ENSMUSG00000020774	chr11	Aspa	7.3E+07	7.3E+07	5954	-0.14255639	3.372019286	0.6538468	0.733316439	0.10584	0	148	61	197	89	372	199	264	165	194	181
ENSMUSG00000015605	chr17	Srf	4.7E+07	4.7E+07	4093	-0.08995737	6.359591908	0.6540036	0.733358495	0.04733	0	971	894	1792	1370	1465	1526	2045	1043	2000	1662
ENSMUSG00000020255	chr10	D10Wsu102e	8.3E+07	8.3E+07	3509	-0.09466286	3.102284859	0.6540412	0.733358495	0.04731	0	116	112	132	120	179	198	207	137	159	148
ENSMUSG00000027752	chr3	Exosc8	5.5E+07	5.5E+07	3968	0.100537664	3.174023865	0.6540023	0.733358495	0.05079	0	91	120	159	128	148	257	163	163	186	184
ENSMUSG00000022070	chr14	Bora	9.9E+07	9.9E+07	2673	-0.1882275	0.004435536	0.6541525	0.733424745	0.09769	0	19	13	12	13	14	22	19	19	14	12
ENSMUSG00000031790	chr8	Mmp15	9.5E+07	9.5E+07	4348	-0.08369916	5.270278589	0.6544943	0.733749319	0.03965	0	459	387	824	621	772	721	862	494	1018	792
ENSMUSG00000095478	chr10	Gm9824	2.9E+07	2.9E+07	564	-0.20358679	-0.14208219	0.6551685	0.7344464	0.13459	0	5	12	11	15	22	13	19	10	25	10
ENSMUSG00000010651	chr9	Acaa1b	1.2E+08	1.2E+08	1962	0.182568105	1.714064805	0.6553374	0.734518356	0.17036	0	52	27	27	20	103	104	35	50	76	86
ENSMUSG00000032332	chr9	Col12a1	8E+07	8E+07	15228	0.118288893	4.957786817	0.6552952	0.734518356	0.08046	0	348	399	340	355	795	1319	577	451	535	547
ENSMUSG00000032376	chr9	Usp3	6.7E+07	6.7E+07	6848	0.084814154	3.661076128	0.6554062	0.734536761	0.03819	0	151	128	220	199	231	334	294	236	231	236
ENSMUSG00000046314	chr12	Stxbp6	4.5E+07	4.5E+07	4855	-0.10788301	2.906680297	0.6555497	0.734638872	0.06116	0	107	90	116	86	185	214	159	84	135	161
ENSMUSG00000051483	chr16	Cbr1	9.4E+07	9.4E+07	1237	-0.07950681	4.602967305	0.6558831	0.734953789	0.03459	0	363	243	423	341	538	558	403	363	597	516
ENSMUSG00000009894	chr11	Snap47	5.9E+07	5.9E+07	2651	-0.08100441	4.986286902	0.6559976	0.735023301	0.03729	0	414	312	711	613	435	722	670	421	700	692
ENSMUSG00000031166	chrX	Wdr13	8123301	8125729	5277	0.073648306	4.696096909	0.6566956	0.735746642	0.03029	0	343	250	513	371	455	689	707	386	476	511
ENSMUSG00000035799	chr12	Twist1	3.4E+07	3.4E+07	1616	0.2201727	1.957573278	0.6568125	0.735818866	0.25954	0	42	68	18	9	118	114	72	49	91	102

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ENSMUSG00000031169	chrX	Porcn	8193848	8194277	3000	0.114325558	2.567767646	0.6569418	0.735904901	0.06051	0	67	77	83	71	122	175	120	73	136	133
ENSMUSG00000054737	chrX	Zfp182	2.1E+07	2.1E+07	5733	-0.14063815	0.797582952	0.6572505	0.736191974	0.06967	0	19	21	29	26	35	42	38	27	24	30
ENSMUSG00000085525	chr4	Gm13166	1.5E+08	1.5E+08	1412	-0.17065014	0.181903773	0.657804	0.736753086	0.13372	0	22	15	17	18	8	34	22	9	25	13
ENSMUSG00000031708	chr8	Tecr	8.4E+07	8.4E+07	1334	0.094932668	8.197887031	0.6581365	0.737040664	0.05494	0	3150	2844	5099	4333	6530	5302	6541	4892	7140	7261
ENSMUSG00000082087	chr11	Gm12138	4.1E+07	4.1E+07	951	-0.16048161	0.600749014	0.6581659	0.737040664	0.07968	0	23	13	24	22	32	22	24	21	35	35
ENSMUSG00000031119	chrX	Gpc4	5.2E+07	5.2E+07	2651	0.082173563	4.745494944	0.6583021	0.73713438	0.03966	0	357	224	639	432	356	564	593	441	636	600
ENSMUSG00000029076	chr4	Sdf4	1.6E+08	1.6E+08	6115	0.081331211	6.97754683	0.6585768	0.737383108	0.03991	0	1766	1347	2126	1735	2316	3301	2878	1859	2605	2880
ENSMUSG00000046434	chr15	Hnrnpa1	1E+08	1E+08	1918	0.081963563	6.319824417	0.6586422	0.73739751	0.0404	0	1177	803	1628	1030	1287	2145	1755	1385	1487	1726
ENSMUSG00000079499	chr2	6530402F18Rik	2.9E+07	2.9E+07	5511	-0.11217778	2.632176104	0.6587691	0.7374807	0.06985	0	86	78	93	128	85	133	172	70	138	102
ENSMUSG00000030826	chr7	Bcat2	4.6E+07	4.6E+07	3899	-0.08772808	6.702207583	0.6590799	0.737769764	0.0467	0	1689	1126	1649	1761	1851	2270	1713	1601	2367	2465
ENSMUSG00000029334	chr5	Prkg2	9.9E+07	9.9E+07	5369	0.196424217	0.382178287	0.6592697	0.737923345	0.14829	0	12	18	16	21	15	34	17	33	11	34
ENSMUSG00000031422	chrX	Morf4l2	1.4E+08	1.4E+08	3135	-0.08320764	6.937106126	0.6595022	0.738124681	0.04229	0	1886	1468	2045	1835	2240	3298	2665	1845	2221	2375
ENSMUSG00000038861	chr3	Pi4kb	9.5E+07	9.5E+07	3880	0.070233095	4.81919364	0.6597398	0.738331641	0.02781	0	361	308	528	352	549	727	642	418	609	609
ENSMUSG00000075040	chr2	Zfp408	9.2E+07	9.2E+07	4008	-0.10084974	2.346407546	0.6605877	0.739221515	0.05394	0	64	70	89	78	85	130	120	77	85	88
ENSMUSG00000039205	chr2	Ciz1	3.2E+07	3.2E+07	8604	0.072794359	4.82072521	0.6613903	0.740060644	0.02988	0	330	320	455	457	514	666	628	403	661	649
ENSMUSG00000011658	chr7	Fuz	4.5E+07	4.5E+07	5003	-0.07638303	4.364692913	0.661464	0.740084076	0.03415	0	285	275	323	303	387	438	409	298	492	430
ENSMUSG00000026749	chr2	Nek6	3.9E+07	3.9E+07	4149	0.113953081	4.16120082	0.6617821	0.740380918	0.07766	0	186	184	300	150	514	531	500	298	346	253
ENSMUSG00000044167	chr3	Foxo1	5.2E+07	5.2E+07	8665	-0.08566048	4.646919278	0.6622047	0.740794584	0.04202	0	312	255	456	297	678	578	515	395	434	585
ENSMUSG00000020061	chr10	Mybpc1	8.9E+07	8.9E+07	4527	-0.14536816	11.02713846	0.6625453	0.741077036	0.13229	0	29401	11956	67847	48409	15155	51857	46745	30018	30815	47439
ENSMUSG00000021179	chr12	Nrde2	1E+08	1E+08	3723	-0.08667175	3.898460618	0.6626157	0.741077036	0.04056	0	174	140	354	269	243	301	338	227	322	297
ENSMUSG00000038172	chr4	Ttc39b	8.3E+07	8.3E+07	10199	0.11795884	2.234263498	0.6626062	0.741077036	0.06545	0	69	42	82	61	83	130	103	63	66	140
ENSMUSG00000023967	chr17	Mrps18a	4.6E+07	4.6E+07	3690	0.088887168	6.011835676	0.6628148	0.741240649	0.04907	0	681	546	1505	1141	985	1447	1307	1036	1538	1537
ENSMUSG00000003345	chr10	Csnk1g2	8.1E+07	8.1E+07	2511	-0.0828662	6.876229288	0.6630104	0.741361861	0.0427	0	1699	1250	2477	1927	1848	2403	2726	1683	2614	2402
ENSMUSG00000038563	chr7	Eftud1	8.3E+07	8.3E+07	4398	-0.08625462	3.25469553	0.6630289	0.741361861	0.03829	0	143	102	196	139	161	235	212	150	180	173
ENSMUSG00000022537	chr16	Tmem44	3.1E+07	3.1E+07	8822	0.1248542	2.032743495	0.6634689	0.741794698	0.07704	0	45	37	64	41	109	104	78	58	82	111
ENSMUSG00000026941	chr2	Mamdc4	2.6E+07	2.6E+07	4630	-0.0774088	5.843726238	0.6636128	0.741896505	0.03686	0	906	650	1044	963	863	1231	1164	897	1189	1282
ENSMUSG00000018169	chr15	Mfng	7.9E+07	7.9E+07	2839	0.191217709	3.351843935	0.663757	0.741998485	0.22448	0	110	69	56	54	468	304	149	194	229	232
ENSMUSG00000071041	chr8	Gm15210	1E+08	1E+08	1545	0.117486824	2.285864791	0.6639424	0.742146696	0.0607	0	66	68	72	61	71	114	95	92	116	91
ENSMUSG00000058318	chr2	Phf21a	9.2E+07	9.2E+07	8561	-0.07684374	4.319918866	0.6641739	0.742346302	0.03596	0	292	278	315	278	354	460	408	259	403	490
ENSMUSG00000002319	chr14	Ipo4	5.6E+07	5.6E+07	5362	0.079216988	6.016065711	0.6649094	0.743046921	0.03901	0	779	648	1095	1059	1220	1590	1236	1019	1537	1502
ENSMUSG00000004771	chr9	Rab11a	6.5E+07	6.5E+07	2992	-0.07284241	5.791409307	0.6649597	0.743046921	0.0327	0	842	612	1047	814	989	1258	1255	820	1090	1175
ENSMUSG00000081413	chr2	Gm14088	1.2E+08	1.2E+08	269	0.159815326	0.261377508	0.6649202	0.743046921	0.12509	0	10	6	31	15	19	25	18	26	32	15
ENSMUSG00000025147	chr7	Mob2	1.4E+08	1.4E+08	1456	-0.07672981	5.916875636	0.6656137	0.743718495	0.0368	0	930	728	990	915	1086	1226	1317	927	1274	1321
ENSMUSG00000035325	chr5	Sec31a	1E+08	1E+08	7884	0.078760295	6.012330147	0.6657103	0.743767104	0.03888	0	730	617	1311	1050	1123	1625	1385	986	1550	1340
ENSMUSG00000023030	chr15	Slc11a2	1E+08	1E+08	6354	-0.06969554	4.982182044	0.6660443	0.744081032	0.02927	0	401	354	609	552	535	708	722	436	722	614
ENSMUSG00000033439	chr3	Trmt13	1.2E+08	1.2E+08	5035	-0.10931775	1.631700665	0.6667854	0.744849581	0.05904	0	43	39	53	51	47	67	64	40	52	77
ENSMUSG00000038412	chr9	Higd1a	1.2E+08	1.2E+08	1873	0.079511093	6.189953993	0.666937	0.744915472	0.04014	0	971	691	1581	1082	1127	1710	1683	1267	1439	1630
ENSMUSG00000053647	chr5	Gper1	1.4E+08	1.4E+08	2537	0.139417581	1.023994513	0.6669506	0.744915472	0.09285	0	20	12	52	33	26	42	37	31	42	56
ENSMUSG00000051234	chr9	Rnf7	9.6E+07	9.6E+07	1328	0.078902119	6.536198785	0.6671077	0.745031608	0.03959	0	1417	938	1762	1198	1557	2255	2030	1626	1982	1930
ENSMUSG00000032580	chr9	Rbm5	1.1E+08	1.1E+08	15434	-0.0749216	5.450805821	0.6676063	0.745469763	0.03528	0	723	502	721	681	733	1107	827	648	818	1024
ENSMUSG00000048578	chr5	Mlec	1.2E+08	1.2E+08	6010	-0.0940705	7.728939447	0.6675874	0.745469763	0.05721	0	4006	2823	3164	2503	3707	4751	4615	3311	4888	3647
ENSMUSG00000038957	chr9	Edc3	5.8E+07	5.8E+07	5804	0.077099448	3.880510195	0.6680451	0.745900333	0.0322	0	199	169	253	226	223	364	342	234	325	292
ENSMUSG00000033788	chr6	Dysf	8.4E+07	8.4E+07	8333	-0.0805434	6.169250909	0.6682428	0.746046135	0.04128	0	925	789	1355	1264	1289	1517	1723	1071	1659	1268
ENSMUSG00000041797	chr11	Abca9	1.1E+08	1.1E+08	8048	-0.09569749	4.605403983	0.6683352	0.746046135	0.05898	0	388	362	318	337	433	785	651	285	356	418
ENSMUSG00000074406	chr7	Zfp628	4915217	4915405	3524	-0.09725477	3.032354041	0.6683306	0.746046135	0.05299	0	86	86	161	133	178	177	175	98	211	155
ENSMUSG00000035517	chr4	Tdrd7	4.6E+07	4.6E+07	3958	0.081491674	4.15739329	0.668467	0.746133831	0.0388	0	253	186	252	219	403	495	418	275	365	350
ENSMUSG00000052605	chr7	Isoc2b	4844959	4845365	1297	-0.11818417	2.809112599	0.6690515	0.746726841	0.07432	0	133	50	135	110	126	203	98	110	105	173
ENSMUSG00000026970	chr2	Rbms1	6.1E+07	6.1E+07	5473	0.07301087	5.208912523	0.6691076	0.746729989	0.0335	0	430	365	635	527	813	887	936	616	698	780
ENSMUSG00000021189	chr12	Atxn3	1E+08	1E+08	5407	0.092554398	3.190320694	0.6692423	0.746820986	0.04627	0	139	102	138	110	169	263	200	155	154	195
ENSMUSG00000001054	chr11	Rmnd5b	5.2E+07	5.2E+07	2161	0.075738557	3.921025963	0.6701829	0.747692112	0.03515	0	187	133	300	235	276	315	342	266	351	312
ENSMUSG00000022210	chr14	Dhrs4	5.5E+07	5.5E+07	1390	-0.13507092	5.191198634	0.6701677	0.747692112	0.11602	0	383	123	1295	699	629	770	823	472	677	882
ENSMUSG00000063172	chr4	Hspb11	1.1E+08	1.1E+08	2071	0.135997911	1.9149451	0.6701707	0.747692112	0.0886	0	50	53	48	42	65	121	48	74	79	73
ENSMUSG00000023175	chr10	Bsg	8E+07	8E+07	1814	-0.08885771	9.468038373	0.6708776	0.74840766	0.05231	0	9997	9667	11517	10696	12465	14573	14130	9208	16436	17146
ENSMUSG00000087579	chr19	1500017E21Rik	3.7E+07	3.7E+07	3977	0.139069608	3.488098853	0.6709912	0.7484748	0.11946	0	120	91	248	278	67	279	365	142	222	218
ENSMUSG00000103906	chr15	TIGD5	7.6E+07	7.6E+07	4801	0.125403587	1.533552472	0.6710814	0.748515935	0.0826	0	28	20	77	35	50	77	55	43	75	52
ENSMUSG00000025950	chr1	Idh1	6.5E+07	6.5E+07	2771	0.112112212	6.039325932	0.6711706	0.748555938	0.08249	0	818	628	885	541	2056	1898	1173	1143	1333	1524
ENSMUSG00000021047	chr12	Nova1	4.7E+07	4.7E+07	7000	0.121705878	2.881040696	0.6712892	0.748628596	0.08848	0	95	67	73	87	213	185	168	99	128	212
ENSMUSG00000031556	chr8	Tm2d2	2.5E+07	2.5E+07	1280	0.071139962	5.521796804	0.6717807	0.749117197	0.03191	0	665	515	776	611	811	1117	977	739	1043	990
ENSMUSG00000034880	chr8	Mrpl34	7.1E+07	7.1E+07	645	0.079270087	4.789666473	0.6720553	0.749363788	0.04078	0	309	218	663	466	438	610	583	435	689	612
ENSMUSG00000062704	chr8	9430002A10Rik	8.8E+07	8.8E+07	475	0.183311331	-0.16155702	0.6723175	0.749596641	0.11662	0	9	5	14	17	11	21	8	17	23	16
ENSMUSG00000015671	chr13	Psma2	1.5E+07	1.5E+07	944	0.077548685	6.621522571	0.6724453	0.749679495	0.03947	0	1436	1082	1695	1365	1653	2624	2108	1716	2015	1986
ENSMUSG00000016252	chr2	Atp5e	1.7E+08	1.7E+08	1756	0.08437075	8.525550781	0.673192	0.750309017	0.04776	0	4860	3484	7401	6152	5464	8658	7550	5944	9235	7840
ENSMUSG00000039130	chr6	Zc3hc1	3E+07	3E+07	4601	0.073051031	4.370413183	0.6730783	0.750309017	0.03168	0	254	233	385	338	305	470	456	322	499	438
ENSMUSG00000045932	chr19	Ifit2	3.5E+07	3.5E+07	3927	0.134305986	2.127806907	0.6732239	0.750309017	0.09673	0	54	50	95	34	78	163	115	43	70	87
ENSMUSG00000102805	chr3	RP24-559D1.1	8.4E+07	8.4E+07	2913	-0.0743578	4.40337296	0.6731278	0.750309017	0.03378	0	281	242	400	368	343	542	428	365	341	443
ENSMUSG00000037772	chr7	Mrpl23	1.4E+08	1.4E+08	1777	0.074780335	5.197140232	0.6732909	0.750324029	0.03522	0	553	407	569	558	585	845	651	607	950	816
ENSMUSG00000082192	chrX	Gm14719	5E+07	5E+07	231	-0.18150691	0.173236598	0.6736922	0.75065198	0.08744	0	12	11	21	11	29	22	19	15	26	17

ENSMUSG00000098905	chr13	Zfp953	6.7E+07	6.7E+07	4676	-0.14225105	0.572337398	0.6736512	0.75065198	0.09771	0	25	16	37	17	15	39	31	12	28	29
ENSMUSG00000085704	chr2	4921531C22Rik	1.8E+08	1.8E+08	1967	0.135787255	0.88094267	0.6737581	0.750665699	0.08838	0	29	10	40	21	28	44	52	29	26	37
ENSMUSG00000060679	chr1	Mrps9	4.3E+07	4.3E+07	5524	0.08589777	5.267929617	0.6738603	0.750719968	0.04917	0	472	260	999	656	546	957	853	631	803	858
ENSMUSG00000058239	chr7	Usf2	3.1E+07	3.1E+07	2647	-0.08327514	5.929813081	0.6742828	0.751130986	0.0457	0	849	572	1366	1130	890	1204	1406	787	1415	1346
ENSMUSG00000073633	chr1	Fbxo36	8.5E+07	8.5E+07	2148	0.127588871	1.451061989	0.6749288	0.751790955	0.08661	0	35	13	48	38	63	75	73	33	56	51
ENSMUSG00000028622	chr4	Mrpl37	1.1E+08	1.1E+08	4460	-0.08486675	6.583653712	0.6752694	0.752050853	0.04815	0	1330	848	2221	1730	1494	1867	2081	1381	2203	2096
ENSMUSG00000090137	chr8	Uba52	7.1E+07	7.1E+07	1498	0.080731938	7.687810532	0.6752438	0.752050853	0.04416	0	2690	1971	4319	3209	3187	5000	4401	3109	4904	4616
ENSMUSG00000051855	chr6	Mest	3.1E+07	3.1E+07	3935	0.237405373	3.562964654	0.6755386	0.752290992	0.37256	0	67	98	48	29	631	442	138	251	293	179
ENSMUSG00000038079	chr1	Tmem237	5.9E+07	5.9E+07	2389	0.122235366	1.934667982	0.6759536	0.752634773	0.06904	0	50	40	39	56	83	108	91	54	74	78
ENSMUSG00000048921	chr7	Zfp689	1.3E+08	1.3E+08	2005	-0.14245356	0.595120387	0.6759547	0.752634773	0.07342	0	16	15	33	25	24	28	33	17	35	26
ENSMUSG00000041757	chr1	Plekha6	1.3E+08	1.3E+08	10827	-0.09156369	4.199036654	0.6760102	0.75263686	0.05597	0	243	280	303	306	252	367	369	215	345	554
ENSMUSG00000032316	chr9	Clk3	5.8E+07	5.8E+07	2494	-0.06940776	5.403975391	0.6761238	0.752703579	0.03141	0	633	466	899	564	741	978	912	607	856	937
ENSMUSG00000050315	chr3	Synpo2	1.2E+08	1.2E+08	9403	-0.09748202	9.333336934	0.6762317	0.752763979	0.06506	0	8603	5318	15725	13040	9001	11827	14413	9503	12617	16047
ENSMUSG00000079610	chr1	Ankrd39	3.7E+07	3.7E+07	4654	-0.09745969	2.543182242	0.6763582	0.752844994	0.05213	0	80	58	100	80	137	107	137	91	115	120
ENSMUSG00000010797	chr6	Wnt2	1.8E+07	1.8E+07	2255	0.242186704	-0.00901798	0.676641	0.753100083	0.28413	0	4	7	5	19	27	43	8	20	7	21
ENSMUSG00000037885	chr2	Stk35	1.3E+08	1.3E+08	6195	-0.09835008	2.90826434	0.6769205	0.753351346	0.05555	0	99	80	127	95	188	175	193	89	151	143
ENSMUSG00000023571	chr4	Fam132a	1.6E+08	1.6E+08	1366	0.125659759	3.622888478	0.6770581	0.753444649	0.10052	0	175	158	95	113	332	294	202	230	340	239
ENSMUSG00000030088	chr6	Aldh1l1	9E+07	9E+07	4512	0.135808482	3.992281641	0.6777454	0.753970218	0.12335	0	250	138	130	133	513	367	194	322	426	373
ENSMUSG00000030630	chr7	Fah	8.5E+07	8.5E+07	2103	0.194695853	3.898499188	0.6777207	0.753970218	0.25553	0	184	111	90	40	680	450	213	293	332	336
ENSMUSG00000031381	chrX	Piga	1.6E+08	1.6E+08	6379	-0.12083508	1.16388829	0.677654	0.753970218	0.07933	0	29	28	54	21	38	52	55	24	36	48
ENSMUSG00000061130	chr17	Ppm1b	8.5E+07	8.5E+07	4971	-0.09095027	7.404989125	0.6777239	0.753970218	0.05672	0	2499	1340	4374	2926	2480	3650	4079	2578	3113	3583
ENSMUSG00000001014	chr9	Icam4	2.1E+07	2.1E+07	907	0.154171107	0.484800938	0.6781212	0.754328537	0.09273	0	14	14	21	16	28	21	37	23	38	20
ENSMUSG00000020135	chr10	Apc2	8E+07	8E+07	11281	-0.15125284	0.223637744	0.6784199	0.754600923	0.08193	0	17	13	20	20	14	29	19	19	14	23
ENSMUSG00000030409	chr7	Dmpk	1.9E+07	1.9E+07	4330	0.100831555	8.731776228	0.6785077	0.754638778	0.07067	0	4582	3717	10080	8034	5295	7489	10535	6328	11405	9698
ENSMUSG00000028140	chr3	Mrpl9	9.4E+07	9.4E+07	1601	-0.0769923	6.129606866	0.6789519	0.75498294	0.03999	0	957	650	1648	1026	1296	1616	1561	1094	1400	1379
ENSMUSG00000040181	chr1	Fmo1	1.6E+08	1.6E+08	6304	-0.11147272	4.240823534	0.6789787	0.75498294	0.08062	0	252	165	265	180	678	457	327	295	391	401
ENSMUSG00000040651	chr14	Fam208a	2.7E+07	2.7E+07	7574	-0.08753162	3.128314519	0.6788879	0.75498294	0.04722	0	160	89	142	130	151	202	193	131	141	203
ENSMUSG00000046079	chr5	Lrrc8d	1.1E+08	1.1E+08	12573	0.111145243	3.260917251	0.6790971	0.755054773	0.08064	0	130	77	148	75	286	267	190	150	193	225
ENSMUSG00000047342	chr11	Zfp286	6.3E+07	6.3E+07	4735	-0.133868	1.022252618	0.6793294	0.755253155	0.10167	0	46	23	24	21	36	54	52	25	32	30
ENSMUSG00000022313	chr15	Utp23	5.2E+07	5.2E+07	2992	0.094258587	2.531385167	0.6796893	0.755593373	0.04688	0	67	68	90	84	105	148	114	90	121	135
ENSMUSG00000013858	chr10	Tmem259	8E+07	8E+07	4663	0.083754508	6.500164223	0.6798327	0.755692891	0.04888	0	975	735	2086	1469	1611	1990	2205	1327	2125	2027
ENSMUSG00000075254	chr16	Heg1	3.4E+07	3.4E+07	12632	0.093765488	5.312932904	0.6799205	0.755730644	0.06041	0	439	410	621	403	1106	1166	804	730	619	918
ENSMUSG00000052446	chr8	Zfp961	7.2E+07	7.2E+07	3950	-0.12474407	1.653501346	0.6800466	0.755810955	0.08107	0	59	30	47	40	65	73	48	62	43	71
ENSMUSG00000048537	chr9	Phldb1	4.5E+07	4.5E+07	7179	0.081525183	5.610535031	0.6802532	0.755980631	0.0458	0	564	466	816	576	1264	1249	1061	756	1140	1008
ENSMUSG00000046572	chr5	Zfp518b	3.9E+07	3.9E+07	6882	-0.10097831	2.275771907	0.6803204	0.75599544	0.05968	0	58	61	73	82	95	96	104	82	112	75
ENSMUSG00000070002	chr8	Ell	7.1E+07	7.1E+07	3085	0.07429764	3.87120869	0.6813974	0.757094336	0.03376	0	185	157	253	210	272	365	291	227	282	383
ENSMUSG00000091845	chr6	Gm4604	1.1E+08	1.1E+08	390	0.193529924	0.125815914	0.6814173	0.757094336	0.13926	0	20	14	4	15	13	23	20	13	27	26
ENSMUSG00000028100	chr3	Nudt17	9.7E+07	9.7E+07	1362	0.138175461	0.402151325	0.6816294	0.75721001	0.08556	0	13	10	28	17	21	28	17	23	34	28
ENSMUSG00000028104	chr3	Polr3gl	9.7E+07	9.7E+07	1597	-0.06876547	5.514780599	0.6816271	0.75721001	0.03208	0	705	490	882	654	826	1019	1032	685	848	1038
ENSMUSG00000026688	chr1	Mgst3	1.7E+08	1.7E+08	1097	0.089328561	7.580931619	0.6817861	0.757270802	0.05666	0	2110	1362	4684	3035	3476	4582	4522	2755	4189	4535
ENSMUSG00000028139	chr3	Riiad1	9.4E+07	9.4E+07	813	-0.09738137	2.31789755	0.6818461	0.757270802	0.06137	0	90	62	71	78	73	103	107	63	122	96
ENSMUSG00000079470	chr1	Utp14b	7.9E+07	7.9E+07	7679	-0.14640729	1.213879463	0.6818039	0.757270802	0.11751	0	33	24	46	18	59	48	79	21	39	35
ENSMUSG00000032688	chr18	Malt1	6.5E+07	6.5E+07	5073	0.113538598	2.358306811	0.6821584	0.75737779	0.06743	0	85	67	72	58	74	113	149	74	88	119
ENSMUSG00000036863	chr3	Syde2	1.5E+08	1.5E+08	5495	-0.20345459	0.570397811	0.6821463	0.75737779	0.2189	0	16	20	7	9	61	36	25	22	21	29
ENSMUSG00000055538	chr14	Zcchc24	2.6E+07	2.6E+07	4557	-0.0832031	6.807146359	0.6820383	0.75737779	0.049	0	1783	1528	1537	1502	2189	2624	2181	1725	2424	2301
ENSMUSG00000084106	chr1	Gm6136	8.7E+07	8.7E+07	891	0.088717546	3.990361295	0.6821358	0.75737779	0.04962	0	265	203	271	176	221	453	272	310	316	321
ENSMUSG00000041390	chr6	Mdfic	1.6E+07	1.6E+07	7427	0.079613391	4.217381788	0.6822162	0.757381997	0.04092	0	275	199	278	200	418	515	442	300	347	375
ENSMUSG00000005397	chr13	Nid1	1.3E+07	1.3E+07	6046	0.095987788	6.812296711	0.6823931	0.757518506	0.06533	0	1231	1148	1742	1215	3094	3203	2751	2013	2108	1949
ENSMUSG00000047496	chr1	Rnf152	1.1E+08	1.1E+08	8532	-0.19847414	0.886507894	0.682469	0.75754279	0.22177	0	21	24	15	7	77	45	24	31	29	38
ENSMUSG00000019578	chr17	Ubxn6	5.6E+07	5.6E+07	5685	-0.07310577	5.993215615	0.6827152	0.757696117	0.03712	0	850	657	1258	1037	1196	1399	1353	860	1522	1323
ENSMUSG00000048481	chr7	Mypop	1.9E+07	1.9E+07	2175	-0.09313565	3.14961089	0.6826749	0.757696117	0.05187	0	120	76	181	159	163	195	208	116	227	139
ENSMUSG00000038141	chr17	Tmem181a	6270475	6270590	1869	0.153377483	1.03265758	0.6828596	0.757796442	0.10337	0	39	22	24	21	30	55	24	29	46	58
ENSMUSG00000068874	chr3	Selenbp1	9.5E+07	9.5E+07	2273	-0.08078449	4.639831551	0.6831204	0.758025873	0.04437	0	444	282	349	312	536	678	382	380	487	583
ENSMUSG00000097729	chr12	2310015A10Rik	8E+07	8E+07	4843	0.093893508	4.15511362	0.6833096	0.758175803	0.06092	0	189	153	545	237	224	424	457	289	323	404
ENSMUSG00000006281	chr14	Tep1	5.1E+07	5.1E+07	8168	0.070364503	4.595695578	0.6834597	0.758231718	0.03121	0	357	278	353	344	430	702	490	362	520	503
ENSMUSG00000050549	chr3	5730508B09Rik	1.3E+08	1.3E+08	1603	0.116068665	2.322574065	0.6834681	0.758231718	0.08895	0	50	28	113	53	133	122	121	70	94	124
ENSMUSG00000006435	chr19	Neurl1a	4.7E+07	4.7E+07	4411	0.084363856	7.647706991	0.6836071	0.758325908	0.05108	0	2455	1724	4468	3303	3130	3999	4811	3257	4967	4235
ENSMUSG00000020937	chr11	Plcd3	1E+08	1E+08	3393	0.102928639	3.216989157	0.6836804	0.758347249	0.06638	0	133	118	139	86	190	245	154	169	153	260
ENSMUSG00000062867	chr9	Impdh2	1.1E+08	1.1E+08	3077	0.07278518	5.586889808	0.6838418	0.758466339	0.03623	0	691	556	777	750	724	1235	901	807	1097	1045
ENSMUSG00000032579	chr9	Hemk1	1.1E+08	1.1E+08	3646	-0.07965973	3.609481472	0.6841857	0.758787749	0.03768	0	152	118	270	198	222	246	255	186	263	266
ENSMUSG00000035873	chr10	Pawr	1.1E+08	1.1E+08	1828	0.155625575	0.092554323	0.6843842	0.758907787	0.11674	0	12	9	19	4	26	29	18	13	21	24
ENSMUSG00000104496	chr1	RP23-13N24.1	1.4E+08	1.4E+08	1369	-0.15394398	0.045782439	0.6844022	0.758907787	0.08674	0	19	8	14	15	18	21	26	9	15	21
ENSMUSG00000028703	chr4	Lrrc41	1.2E+08	1.2E+08	3713	-0.07016289	4.58937069	0.6845495	0.759011212	0.03285	0	277	288	477	401	422	593	512	372	551	398
ENSMUSG00000074649	chr2	BC029722	1.6E+08	1.6E+08	1615	0.06585164	5.390624463	0.6846889	0.759105699	0.03013	0	564	401	787	618	768	962	953	671	884	963
ENSMUSG00000002981	chr7	Clptm1	2E+07	2E+07	4130	-0.07639793	6.251348598	0.6852292	0.759644727	0.04136	0	929	741	1589	1360	1401	1623	1669	1101	1736	1556
ENSMUSG00000022120	chr14	Rnf219	1E+08	1E+08	3456	-0.10099643	2.179422377	0.6854485	0.759827784	0.05554	0	71	52	94	66	63	104	79	69	82	108
ENSMUSG00000035478	chr10	Mbd3	8E+07	8E+07	1987	0.079204693	6.834962314	0.685742	0.760092993	0.04526	0	1420	1127	1984	1849	2101	2360	2567	1629	3049	2563

ENSMUSG00000022848	chr16	Dirc2	3.6E+07	3.6E+07	5395	-0.07325285	6.45565026	0.6863992	0.760701271	0.03856	0	1221	885	1837	1366	1598	2120	2076	1200	1786	1750
ENSMUSG00000053398	chr3	Phgdh	9.8E+07	9.8E+07	2486	0.206114968	3.17659383	0.6863874	0.760701271	0.29952	0	100	73	25	39	421	265	106	186	211	210
ENSMUSG00000032679	chr2	Cd59a	1E+08	1E+08	1811	0.076363874	5.534104008	0.6864631	0.760712026	0.04208	0	565	388	941	572	1064	1021	1099	677	1101	1036
ENSMUSG00000022983	chr16	Scaf4	9E+07	9E+07	4364	-0.07544513	3.739417644	0.6869435	0.761184144	0.03591	0	191	155	223	202	257	280	288	238	243	274
ENSMUSG00000019998	chr10	Stx7	2.4E+07	2.4E+07	2500	0.064516117	5.06838055	0.687273	0.761489125	0.02853	0	501	343	635	441	572	849	871	529	649	660
ENSMUSG00000027678	chr2	Ncoa3	1.7E+08	1.7E+08	7895	0.071283702	4.783164816	0.6874105	0.761571101	0.03611	0	346	228	682	391	442	695	650	411	539	637
ENSMUSG00000029328	chr5	Hnrnpdl	1E+08	1E+08	4818	-0.07295567	6.502844831	0.6874556	0.761571101	0.03861	0	1317	987	1752	1477	1520	2271	1752	1414	1751	1975
ENSMUSG00000021903	chr14	Galnt15	3.2E+07	3.2E+07	6326	-0.0775494	4.459408378	0.6878455	0.761942893	0.04208	0	336	232	361	305	482	619	575	257	339	467
ENSMUSG00000049300	chr3	Prmt6	1.1E+08	1.1E+08	4197	0.098796478	2.245130067	0.6881384	0.762207203	0.05615	0	67	56	68	63	81	99	95	86	88	123
ENSMUSG00000032718	chr6	Mansc1	1.3E+08	1.3E+08	2373	0.132782568	0.811090518	0.6882395	0.762258994	0.07339	0	15	21	28	21	34	40	35	22	44	38
ENSMUSG00000052631	chr6	Sh2d6	7.3E+07	7.3E+07	1737	-0.14998323	0.696255042	0.6883028	0.762261853	0.11012	0	15	27	30	14	34	21	29	25	33	39
ENSMUSG00000060739	chr13	Nsa2	9.7E+07	9.7E+07	2686	-0.06930831	5.313830337	0.6883508	0.762261853	0.03484	0	658	495	741	569	573	1037	885	559	746	822
ENSMUSG00000010045	chr9	Tmem115	1.1E+08	1.1E+08	2194	0.066539595	4.525364681	0.6885009	0.762367845	0.03047	0	278	209	402	394	438	550	491	345	540	512
ENSMUSG00000059669	chr12	Taf1b	2.4E+07	2.4E+07	2019	-0.08593807	2.928973955	0.6889622	0.762818449	0.04711	0	121	92	145	100	125	174	179	130	137	131
ENSMUSG00000026696	chr1	Vamp4	1.6E+08	1.6E+08	4565	-0.07088522	3.964140171	0.6893793	0.763219994	0.03402	0	246	187	271	235	253	343	382	245	278	317
ENSMUSG00000020620	chr11	Abca8b	1.1E+08	1.1E+08	7423	-0.07760964	5.521700732	0.6896692	0.763420386	0.04439	0	735	525	757	686	845	1366	1149	541	695	982
ENSMUSG00000057137	chr6	Tmem140	3.5E+07	3.5E+07	5687	0.082009551	5.652889156	0.6896325	0.763420386	0.04842	0	960	539	710	633	795	1499	1009	838	865	1166
ENSMUSG00000037643	chr3	Prkci	3.1E+07	3.1E+07	5551	-0.12023077	2.730628509	0.6897967	0.763501308	0.09678	0	94	83	90	49	205	194	127	93	123	119
ENSMUSG00000022241	chr15	Tars	1.1E+07	1.1E+07	2636	-0.06907539	5.536041685	0.6899661	0.763628504	0.03435	0	617	572	925	710	756	1032	946	814	922	926
ENSMUSG00000038990	chr2	Cables2	1.8E+08	1.8E+08	4597	0.075629901	3.828787095	0.6901366	0.763756953	0.03661	0	186	158	231	176	294	336	350	190	324	313
ENSMUSG00000071064	chr8	Zfp827	7.9E+07	7.9E+07	8944	-0.14966995	2.666518474	0.6904104	0.763999717	0.15031	0	60	28	200	171	63	148	117	65	131	162
ENSMUSG00000044906	chr18	4930503L19Rik	7E+07	7E+07	2291	-0.15412166	0.26072444	0.6905436	0.764062464	0.08837	0	14	11	23	20	20	32	26	20	17	12
ENSMUSG00000054720	chr5	Lrrc8c	1.1E+08	1.1E+08	7654	-0.08414639	3.524444588	0.6905761	0.764062464	0.04528	0	165	124	278	163	168	280	225	206	187	241
ENSMUSG00000027580	chr2	Helz2	1.8E+08	1.8E+08	11529	0.091412745	3.169000358	0.6907036	0.764103311	0.05362	0	107	88	163	100	208	253	204	102	201	209
ENSMUSG00000089979	chr16	Gm15954	1.8E+07	1.8E+07	466	-0.07655808	3.792212998	0.6907219	0.764103311	0.03759	0	190	135	248	193	323	298	277	197	295	323
ENSMUSG00000001942	chr9	Siae	3.8E+07	3.8E+07	3433	-0.08998809	2.76426489	0.6908907	0.764109689	0.05435	0	86	93	101	92	146	175	149	101	110	140
ENSMUSG00000038279	chr6	Nop2	1.3E+08	1.3E+08	2623	-0.08003611	4.481691826	0.6908911	0.764109689	0.04318	0	258	207	492	429	379	490	376	417	503	421
ENSMUSG00000070873	chr7	Lilra5	4237754	4237791	2109	0.241315625	-0.15972041	0.6908747	0.764109689	0.26891	0	9	7	1	5	33	24	15	8	17	25
ENSMUSG00000034278	chr2	Dnajc17	1.2E+08	1.2E+08	1308	0.087348504	2.827960904	0.6912708	0.764469333	0.04649	0	100	71	147	90	110	195	139	118	158	137
ENSMUSG00000030711	chr7	Sult1a1	1.3E+08	1.3E+08	1507	0.105987357	4.354981846	0.6916551	0.764834053	0.08047	0	289	262	224	163	538	640	311	358	430	451
ENSMUSG00000003032	chr4	Klf4	5.6E+07	5.6E+07	3049	0.091222465	4.369087571	0.6917368	0.764864054	0.05968	0	196	224	310	266	539	412	676	282	404	440
ENSMUSG00000026500	chr1	Cox20	1.8E+08	1.8E+08	883	-0.06723882	4.483668406	0.6918831	0.764947661	0.03105	0	363	240	413	308	407	581	413	371	413	473
ENSMUSG00000032583	chr9	Mon1a	1.1E+08	1.1E+08	2826	0.077911858	3.509692277	0.6920306	0.764947661	0.04108	0	131	105	217	205	183	270	228	195	262	240
ENSMUSG00000033917	chr7	Gde1	1.2E+08	1.2E+08	1692	-0.06729193	5.613406787	0.6919695	0.764947661	0.03289	0	693	515	865	730	1019	1041	1110	744	1031	1014
ENSMUSG00000047632	chr19	Fgfbp3	3.7E+07	3.7E+07	1772	-0.16931239	0.333728352	0.692017	0.764947661	0.10725	0	18	10	33	13	21	20	13	24	27	26
ENSMUSG00000024213	chr17	Nudt3	2.8E+07	2.8E+07	2985	-0.0753025	7.070897852	0.6921965	0.765070755	0.04265	0	1889	1311	2917	2226	2252	2965	2803	2165	2874	2696
ENSMUSG00000082691	chr6	Dynlt1-ps1	1.4E+08	1.4E+08	342	0.109419484	2.268092216	0.6924529	0.76529385	0.06132	0	50	63	74	77	74	112	123	60	122	94
ENSMUSG00000015112	chr6	Slc25a13	6041218	6042332	3122	-0.20398258	0.955482333	0.6925995	0.76532458	0.24799	0	17	5	100	25	15	44	40	21	33	39
ENSMUSG00000029062	chr4	Cdk11b	1.6E+08	1.6E+08	3752	0.070329322	6.019100603	0.6926444	0.76532458	0.03667	0	858	700	1266	936	1045	1447	1488	967	1398	1591
ENSMUSG00000101609	chr7	Kcnq1ot1	1.4E+08	1.4E+08	84395	0.169265937	1.142448473	0.6926208	0.76532458	0.16341	0	30	22	40	9	51	52	42	20	33	87
ENSMUSG00000036022	chrX	Fam122b	5.3E+07	5.3E+07	4409	-0.11412661	1.560202917	0.692859	0.765501368	0.08257	0	59	43	44	27	45	69	62	39	52	63
ENSMUSG00000021763	chr13	BC067074	1.1E+08	1.1E+08	8410	-0.10817205	2.44242085	0.6930306	0.765595373	0.06949	0	107	38	112	64	108	141	109	91	86	104
ENSMUSG00000063320	chr10	1190007I07Rik	8.3E+07	8.3E+07	1197	0.093344599	2.483749774	0.6930532	0.765595373	0.05635	0	66	44	135	71	99	126	118	86	118	139
ENSMUSG00000083364	chrX	Llph-ps2	1.3E+07	1.3E+07	393	-0.17352732	0.034724141	0.6933593	0.76587315	0.096	0	21	8	18	12	15	27	15	18	12	17
ENSMUSG00000026869	chr2	Psmd5	3.5E+07	3.5E+07	3750	0.065257068	4.432129922	0.6934488	0.76591173	0.02897	0	284	250	371	308	372	514	463	374	490	423
ENSMUSG00000004610	chr7	Etfb	4.3E+07	4.3E+07	1139	-0.08281541	8.064763815	0.6935616	0.765976021	0.0525	0	3531	2164	6361	4494	5001	5498	5561	3707	5806	6438
ENSMUSG00000024990	chr19	Rbp4	3.8E+07	3.8E+07	1297	0.25183945	4.153468074	0.6942426	0.76666768	0.47571	0	269	119	25	26	848	541	125	407	488	389
ENSMUSG00000021367	chr13	Edn1	4.2E+07	4.2E+07	2344	0.133604146	0.742878893	0.694333	0.766690314	0.088	0	21	13	29	17	35	59	37	23	24	29
ENSMUSG00000087236	chr1	Gm1305	1.8E+08	1.8E+08	3449	0.109411072	1.227679086	0.6943724	0.766690314	0.06988	0	24	18	43	29	53	47	52	41	45	53
ENSMUSG00000036427	chr7	Gpi1	3.4E+07	3.4E+07	4497	-0.08020877	9.399658628	0.6945375	0.766812297	0.04985	0	9270	6874	13081	11931	11876	12850	14735	9530	16732	14147
ENSMUSG00000043953	chr9	Ccrl2	1.1E+08	1.1E+08	2110	0.113918355	2.350895621	0.6947599	0.766997449	0.08083	0	72	61	96	45	89	88	150	64	89	150
ENSMUSG00000016503	chr5	Gtf3a	1.5E+08	1.5E+08	2548	0.069500616	4.000335908	0.6949996	0.767201719	0.0331	0	218	163	275	220	308	432	289	257	368	344
ENSMUSG00000015305	chr10	Sash1	8722219	8725760	7183	-0.08201005	4.849315529	0.6960492	0.768178888	0.0505	0	358	371	435	306	782	670	715	389	499	645
ENSMUSG00000028790	chr4	Khdrbs1	1.3E+08	1.3E+08	6419	-0.06174946	5.008713244	0.6960246	0.768178888	0.0279	0	451	363	583	537	545	825	693	521	612	605
ENSMUSG00000092868	chr15	Mir5113	8.1E+07	8.1E+07	82	-0.10830106	1.447645724	0.6959779	0.768178888	0.06813	0	47	28	44	31	57	68	63	32	42	60
ENSMUSG00000042272	chr2	Sestd1	7.7E+07	7.7E+07	9857	0.079493103	3.993553887	0.6964474	0.768557915	0.0424	0	234	194	309	228	184	384	412	236	293	369
ENSMUSG00000032519	chr9	Slc25a38	1.2E+08	1.2E+08	2747	0.074333853	3.812152661	0.6967871	0.768811837	0.03595	0	191	170	234	217	203	361	281	231	321	286
ENSMUSG00000085492	chr17	Trmt61b	7.2E+07	7.2E+07	2897	-0.18928822	0.042638975	0.6967449	0.768811837	0.1445	0	9	8	27	13	20	24	6	10	19	31
ENSMUSG00000022365	chr15	Derl1	5.8E+07	5.8E+07	3145	0.074049833	6.674393167	0.6970368	0.769026808	0.04254	0	1473	1121	1526	1310	2102	2493	2220	1719	2230	2158
ENSMUSG00000016619	chr15	Nup50	8.5E+07	8.5E+07	4741	0.062417408	4.431404205	0.6980043	0.770033675	0.02711	0	287	232	395	301	384	533	499	315	488	451
ENSMUSG00000024742	chr19	Fen1	1E+07	1E+07	2422	0.082725821	2.761564255	0.6982311	0.770223348	0.04444	0	87	59	117	111	123	179	142	102	149	143
ENSMUSG00000026280	chr1	Atg4b	9.4E+07	9.4E+07	8278	0.060811924	4.757240781	0.6983037	0.770242798	0.02794	0	378	234	501	400	521	650	587	451	581	576
ENSMUSG00000025321	chr12	Itgb8	1.2E+08	1.2E+08	11060	0.188805865	-0.04193309	0.6983815	0.770268108	0.17127	0	13	5	10	25	7	21	24	10	10	31
ENSMUSG00000032485	chr9	Scap	1.1E+08	1.1E+08	4275	0.063625521	4.567472846	0.6984581	0.770291976	0.03029	0	314	210	527	319	421	572	560	347	507	529
ENSMUSG00000049521	chr15	Cdc42ep1	7.9E+07	7.9E+07	2542	-0.11708799	4.282117275	0.6986248	0.770415273	0.10243	0	189	175	244	215	775	444	296	349	396	415
ENSMUSG00000024949	chr19	Sf1	6363690	6364118	6211	0.073008251	6.476487353	0.6986888	0.770425256	0.04164	0	1062	998	1489	1394	1628	2014	1806	1328	2178	2139
ENSMUSG00000078994	chr13	Zfp429	6.7E+07	6.7E+07	2134	-0.13163707	1.094350433	0.6989743	0.770679484	0.10704	0	30	32	43	26	27	79	43	22	26	37

ENSMUSG00000030435	chr7	U2af2	5062143	5062336	2266	0.065653781	5.76444305	0.6990881	0.770729911	0.03323	0	681	555	1032	802	991	1442	1179	814	1217	1136
ENSMUSG00000037072	chr3	Sep15	1.4E+08	1.4E+08	2104	0.081528947	6.460135386	0.6991299	0.770729911	0.05217	0	1405	1009	1196	938	1891	2538	1938	1430	1792	1722
ENSMUSG00000023572	chr2	Ccndbp1	1.2E+08	1.2E+08	3469	0.091225389	6.352806674	0.6993876	0.770953333	0.06512	0	1510	1147	876	1005	1178	1851	1758	1460	1805	1782
ENSMUSG00000016349	chr2	Eef1a2	1.8E+08	1.8E+08	2084	-0.08757709	10.57824177	0.6995145	0.771032659	0.06157	0	20140	13952	35651	29523	22162	27395	32442	21724	39325	32291
ENSMUSG00000026701	chr1	Prdx6	1.6E+08	1.6E+08	4804	0.073998315	6.589995926	0.7028947	0.774697596	0.04465	0	1146	860	2143	1499	1627	2264	1852	1650	2198	2210
ENSMUSG00000103659	chr1	RP23-152I6.2	1.6E+08	1.6E+08	823	0.179139039	0.459677328	0.7032734	0.775054018	0.19714	0	28	1	22	13	29	50	33	14	21	24
ENSMUSG00000056366	chr10	Fabp3-ps1	8.7E+07	8.7E+07	656	-0.18100596	6.291769934	0.7034055	0.775138698	0.26575	0	591	202	4150	1414	656	1513	2071	829	890	2425
ENSMUSG00000015243	chr4	Abca1	5.3E+07	5.3E+07	10363	0.107121004	4.623817142	0.7037242	0.77542901	0.09066	0	317	299	229	193	760	646	682	347	445	550
ENSMUSG00000025027	chr19	Xpnpep1	5.3E+07	5.3E+07	7120	0.069584122	5.488417021	0.7038572	0.775453668	0.03939	0	533	363	1020	755	733	1098	975	747	996	930
ENSMUSG00000062014	chr14	Gmfb	4.7E+07	4.7E+07	4446	0.072063933	4.954064275	0.7038469	0.775453668	0.04042	0	404	352	416	372	745	827	698	531	617	607
ENSMUSG00000097652	chr14	Mhrt	5.5E+07	5.5E+07	1214	-0.57678268	0.656486951	0.7041831	0.775751797	2.30334	0	0	0	120	31	0	1	0	0	4	117
ENSMUSG00000001674	chr1	Ddx18	1.2E+08	1.2E+08	2483	-0.0666689	4.137042807	0.7044439	0.77591723	0.03189	0	261	172	301	283	350	443	358	292	324	351
ENSMUSG00000026154	chr1	1110058L19Rik	2.4E+07	2.4E+07	874	0.071225859	4.263012767	0.704436	0.77591723	0.04021	0	257	146	451	313	281	471	409	310	382	457
ENSMUSG00000050017	chr5	Pitpnb	1.1E+08	1.1E+08	2761	-0.05934632	4.993103968	0.7047105	0.776089037	0.0273	0	473	350	520	474	641	731	706	478	619	694
ENSMUSG00000072964	chrX	Bhlhb9	1.4E+08	1.4E+08	2978	-0.11351787	2.224833595	0.7046659	0.776089037	0.0848	0	106	43	75	53	82	128	67	88	76	92
ENSMUSG00000037750	chr11	Fam222b	7.8E+07	7.8E+07	3490	0.074298208	3.387175216	0.7050084	0.776356066	0.03736	0	133	111	167	152	204	249	255	164	229	205
ENSMUSG00000038623	chr7	Tm6sf1	8.2E+07	8.2E+07	5921	-0.1421811	3.63865765	0.7054704	0.776768153	0.15822	0	96	79	586	168	135	311	359	119	192	267
ENSMUSG00000074398	chr3	Gm15441	9.7E+07	9.7E+07	1676	-0.21610787	0.572084266	0.7054933	0.776768153	0.27319	0	7	8	62	16	28	16	37	5	30	46
ENSMUSG00000014504	chr18	Srp19	3.4E+07	3.4E+07	3630	0.058940814	5.115008573	0.7057582	0.776998785	0.02729	0	472	364	683	490	571	831	792	594	705	719
ENSMUSG00000021474	chr13	Sfxn1	5.4E+07	5.4E+07	2811	-0.19351247	3.459821957	0.7059529	0.777091119	0.29817	0	157	74	55	39	616	317	130	188	214	199
ENSMUSG00000082044	chr2	Gm14284	1.3E+08	1.3E+08	279	0.129790584	0.69524183	0.7059442	0.777091119	0.08361	0	22	16	34	14	24	46	37	29	28	23
ENSMUSG00000029499	chr5	Pxmp2	1.1E+08	1.1E+08	1200	0.082258947	4.550573932	0.7060836	0.777173982	0.05398	0	324	205	502	457	238	525	484	400	426	639
ENSMUSG00000031371	chrX	Haus7	7.3E+07	7.3E+07	1438	0.081033541	3.549696402	0.7064356	0.777500397	0.04662	0	168	137	187	147	210	311	197	175	330	227
ENSMUSG00000004264	chr6	Phb2	1.2E+08	1.2E+08	3718	0.077458179	6.871728147	0.7066799	0.7776473	0.05041	0	1303	971	2804	1861	1970	2518	2604	1805	2728	2789
ENSMUSG00000015341	chr8	Golga7	2.3E+07	2.3E+07	2383	0.059173073	5.1486028	0.7066309	0.7776473	0.02805	0	503	330	694	471	671	887	802	543	748	776
ENSMUSG00000020898	chr11	Ctc1	6.9E+07	6.9E+07	6797	-0.06756122	4.333928902	0.7068966	0.777824708	0.03508	0	261	204	383	329	399	429	442	234	499	449
ENSMUSG00000087331	chr15	1810021B22Rik	8.9E+07	8.9E+07	896	0.099606139	1.775992215	0.7070444	0.777926336	0.06696	0	36	28	75	40	71	87	66	43	77	86
ENSMUSG00000004895	chr3	Prcc	8.8E+07	8.8E+07	2099	-0.0656305	5.447097239	0.7071108	0.777938405	0.03453	0	570	434	945	759	708	939	939	642	945	946
ENSMUSG00000055065	chr15	Ddx17	8E+07	8E+07	4761	-0.07483347	6.683247023	0.7071834	0.777957197	0.04714	0	1390	1444	1596	1439	1976	2753	1865	1541	1940	2321
ENSMUSG00000031628	chr8	Casp3	4.7E+07	4.7E+07	1455	0.137739847	0.946876046	0.7077632	0.778500528	0.10661	0	24	14	26	20	50	56	61	25	29	29
ENSMUSG00000034473	chr16	Sec22a	3.5E+07	3.5E+07	5221	-0.0784981	3.312227566	0.7077883	0.778500528	0.04494	0	131	121	167	123	226	266	181	153	192	202
ENSMUSG00000029125	chr5	Stx18	3.8E+07	3.8E+07	4194	-0.06792714	3.965651909	0.707844	0.778500701	0.03364	0	210	151	280	235	348	372	330	217	351	310
ENSMUSG00000023249	chr9	Parp3	1.1E+08	1.1E+08	3699	0.068867721	5.714853438	0.7082542	0.778890853	0.03922	0	675	508	1091	733	937	1549	1353	755	1031	951
ENSMUSG00000037993	chr8	Dhx38	1.1E+08	1.1E+08	4197	0.062845578	4.245740393	0.7083969	0.778986627	0.03052	0	216	183	362	303	356	484	421	283	413	408
ENSMUSG00000010362	chr11	Rdm1	1E+08	1E+08	1575	-0.06428667	4.727080431	0.7089261	0.779507537	0.03392	0	430	334	428	379	441	549	534	375	673	542
ENSMUSG00000063889	chr18	Crem	3266048	3267732	5895	-0.07679996	3.389437596	0.7090973	0.779634614	0.04047	0	162	89	197	180	190	214	242	156	212	222
ENSMUSG00000036504	chr2	Phpt1	2.6E+07	2.6E+07	1074	-0.0656693	5.828478291	0.709436	0.779945881	0.03609	0	887	644	1038	938	857	1223	1164	895	1175	1268
ENSMUSG00000027077	chr2	Smtnl1	8.5E+07	8.5E+07	1761	0.13924316	5.847872751	0.7096751	0.780000236	0.16587	0	643	180	1918	1144	551	1472	1647	707	678	1863
ENSMUSG00000030401	chr7	Rtn2	1.9E+07	1.9E+07	2034	-0.07890055	9.696669927	0.7096011	0.780000236	0.0537	0	13052	10445	13109	12743	14228	15463	16227	12285	21014	18258
ENSMUSG00000036528	chr7	Ppfibp2	1.1E+08	1.1E+08	4729	-0.07867911	4.122369253	0.7097079	0.780000236	0.04888	0	219	176	439	314	217	394	403	231	302	430
ENSMUSG00000052763	chr6	Zfp212	4.8E+07	4.8E+07	3002	-0.06740786	3.595062748	0.7096372	0.780000236	0.03311	0	173	130	216	194	218	284	240	184	251	254
ENSMUSG00000038216	chr11	Pnmt	9.8E+07	9.8E+07	1154	0.133246176	0.451843791	0.7098825	0.780130976	0.07505	0	12	18	23	18	19	33	32	22	25	24
ENSMUSG00000025265	chrX	Fgd1	1.5E+08	1.5E+08	4931	0.106458727	1.91824435	0.710237	0.780459457	0.069	0	57	47	48	46	65	120	67	66	71	71
ENSMUSG00000004934	chr10	Pias4	8.1E+07	8.1E+07	4582	0.062327267	4.305439968	0.7106757	0.780719779	0.0295	0	256	209	340	316	339	461	436	294	486	410
ENSMUSG00000024096	chr17	Ralbp1	6.6E+07	6.6E+07	4335	-0.06121202	5.321322937	0.7107841	0.780719779	0.03124	0	553	439	768	608	736	953	995	497	833	820
ENSMUSG00000026938	chr2	Fcna	2.6E+07	2.6E+07	1374	0.200672643	2.202735286	0.7108079	0.780719779	0.32668	0	36	59	7	37	178	218	75	63	99	58
ENSMUSG00000045435	chr5	Tmem60	2.1E+07	2.1E+07	1147	0.062934211	4.154952325	0.710769	0.780719779	0.02993	0	272	188	302	248	300	415	404	301	371	377
ENSMUSG00000047909	chr2	Ankrd16	1.2E+07	1.2E+07	5926	-0.07136877	3.902799938	0.7107003	0.780719779	0.04199	0	239	214	219	182	273	342	300	220	299	342
ENSMUSG00000048222	chr2	Mfap1b	1.2E+08	1.2E+08	3362	0.067300988	3.729940685	0.7108026	0.780719779	0.03497	0	167	130	263	195	231	326	291	229	235	311
ENSMUSG00000079139	chr1	Gm4204	1.4E+08	1.4E+08	1231	0.081983326	3.703672531	0.710871	0.780727951	0.05076	0	170	158	159	187	266	365	306	244	211	246
ENSMUSG00000000127	chr17	Fer	6.4E+07	6.4E+07	3473	-0.07148474	3.421067724	0.7113245	0.781164795	0.04003	0	142	131	198	175	173	297	221	147	221	197
ENSMUSG00000039640	chr11	Mrpl12	1.2E+08	1.2E+08	1532	0.07712802	7.340283882	0.7115478	0.781287777	0.05182	0	1814	1356	3874	2727	2520	3785	3725	2443	3681	3651
ENSMUSG00000098915	chr9	Rpl15-ps2	7.2E+07	7.2E+07	613	-0.07282629	3.565742641	0.7114923	0.781287777	0.03957	0	163	134	228	201	184	263	227	201	275	210
ENSMUSG00000024271	chr18	Elp2	2.5E+07	2.5E+07	2789	0.058091871	4.901755805	0.7117911	0.781493686	0.02687	0	441	318	498	424	529	771	623	496	624	634
ENSMUSG00000099835	chr1	Gm29668	1E+08	1E+08	315	-0.19775163	-0.07885299	0.7122655	0.781953357	0.20829	0	1	9	18	26	15	10	19	9	21	22
ENSMUSG00000010057	chr9	Nprl2	1.1E+08	1.1E+08	2013	0.071047088	3.686027046	0.7128946	0.782544011	0.03736	0	156	154	225	203	198	318	249	227	279	274
ENSMUSG00000037266	chr4	Rsrp1	1.3E+08	1.3E+08	3349	-0.09358169	7.266188862	0.7129151	0.782544011	0.0772	0	2242	2477	1602	2144	3095	4228	2546	2126	2624	4067
ENSMUSG00000097743	chr14	Gm16973	5.7E+07	5.7E+07	2421	-0.12963688	0.820281305	0.7130788	0.782662409	0.09238	0	36	11	23	23	40	43	32	20	32	39
ENSMUSG00000037503	chr1	Fam168b	3.5E+07	3.5E+07	5219	-0.06352557	5.803242144	0.7136345	0.783211093	0.03482	0	803	676	947	755	1126	1368	1203	856	1098	1137
ENSMUSG00000027937	chr3	Jtb	9E+07	9E+07	1531	0.064680616	6.044004259	0.7140746	0.783632725	0.03616	0	924	714	1164	915	1171	1666	1367	1133	1432	1361
ENSMUSG00000062931	chr10	Zfp938	8.2E+07	8.2E+07	2128	0.077426232	3.279289532	0.714131	0.783633332	0.04729	0	167	98	170	126	144	234	166	177	226	209
ENSMUSG00000092564	chr17	BC051226	3.4E+07	3.4E+07	979	-0.12843205	0.93293676	0.714368	0.783832132	0.11497	0	36	17	18	23	49	52	24	21	38	46
ENSMUSG00000029397	chr5	Rchy1	9.2E+07	9.2E+07	2894	-0.05823566	5.24069534	0.7151613	0.784641105	0.02882	0	545	443	663	547	712	956	815	609	692	759
ENSMUSG00000020307	chr10	Cdc34	8E+07	8E+07	1262	-0.07032579	8.013240026	0.7153997	0.784841359	0.04428	0	3776	2854	4848	4176	4402	5281	5614	3972	6101	5052
ENSMUSG00000021144	chr12	Mta1	1.1E+08	1.1E+08	3104	-0.05850599	4.921139679	0.7155965	0.784995858	0.02842	0	432	328	520	451	615	676	611	448	719	613
ENSMUSG00000019880	chr10	Rspo3	2.9E+07	2.9E+07	2394	0.272898181	1.743072868	0.7158751	0.785240049	0.63987	0	7	0	160	76	4	51	83	62	64	97
ENSMUSG00000053286	chr1	Trmt1l	1.5E+08	1.5E+08	8211	0.063241786	4.127809063	0.7160609	0.785382427	0.03093	0	266	182	300	246	293	460	388	263	398	341

ENSMUSG00000053604	chr6	Rpia	7.1E+07	7.1E+07	5359	0.06413975	4.67158433	0.7163278	0.785613661	0.03288	0	310	326	407	380	434	614	500	387	663	527
ENSMUSG00000019848	chr10	Popdc3	4.5E+07	4.5E+07	2083	0.062149985	5.356794138	0.7166627	0.785808813	0.03273	0	543	465	719	652	634	964	1093	642	773	866
ENSMUSG00000029106	chr5	Add1	3.5E+07	3.5E+07	6066	0.067606716	6.574766707	0.7166738	0.785808813	0.04084	0	1182	919	1984	1496	1570	2361	2362	1364	2112	1981
ENSMUSG00000062397	chr15	Zfp706	3.7E+07	3.7E+07	4413	0.064820658	6.047373439	0.7165827	0.785808813	0.03681	0	868	757	1111	895	1260	1728	1447	1029	1460	1361
ENSMUSG00000029389	chr5	Ddx55	1.2E+08	1.2E+08	5121	-0.0955858	2.408886997	0.7172866	0.78641933	0.06593	0	78	68	90	61	109	123	109	94	66	126
ENSMUSG00000032458	chr9	Copb2	9.9E+07	9.9E+07	6351	0.066716972	6.599884776	0.7173804	0.78646065	0.03972	0	1499	1037	1607	1414	1578	2639	2149	1556	2027	1943
ENSMUSG00000078813	chr7	Leng1	3660098	3661360	2222	0.073704895	3.492404088	0.7178574	0.786922081	0.04337	0	133	104	250	185	164	292	234	158	230	281
ENSMUSG00000029504	chr5	Ddx51	1.1E+08	1.1E+08	5248	-0.07086698	3.40180678	0.71822	0.787236202	0.03872	0	150	129	199	158	172	248	246	170	205	187
ENSMUSG00000071141	chr6	Rpl36a-ps3	1.4E+08	1.4E+08	321	-0.11269976	1.840780693	0.7182562	0.787236202	0.09238	0	68	44	76	39	44	85	45	72	77	61
ENSMUSG00000038593	chr5	Tctn1	1.2E+08	1.2E+08	4856	0.126239248	1.417806379	0.7183775	0.787307657	0.10076	0	30	35	38	21	61	78	39	31	68	65
ENSMUSG00000055137	chr13	Sugct	1.7E+07	1.7E+07	1311	-0.16667702	0.550052888	0.7186394	0.787533098	0.15397	0	21	11	15	13	52	34	14	21	31	32
ENSMUSG00000047037	chr7	Nipa1	5.6E+07	5.6E+07	3183	-0.09793494	2.408243424	0.718847	0.787699054	0.07788	0	110	64	70	55	102	134	107	83	122	75
ENSMUSG00000022095	chr14	Fam160b2	7.1E+07	7.1E+07	4033	-0.06428036	5.91158864	0.7191064	0.787921742	0.03719	0	794	682	1107	913	1183	1244	1494	795	1279	1316
ENSMUSG00000077220	chr1	Gm23436	1.6E+08	1.6E+08	66	0.166434828	0.08491186	0.7196741	0.788482136	0.11732	0	12	14	9	15	16	37	13	16	14	25
ENSMUSG00000029683	chr6	Lmod2	2.5E+07	2.5E+07	1967	0.207661892	6.514952739	0.7198131	0.788572851	0.39394	0	788	40	3822	1950	492	1956	2081	1580	1341	3143
ENSMUSG00000021764	chr13	Ndufs4	1.1E+08	1.1E+08	1534	-0.07462553	7.571708947	0.7201436	0.788838765	0.05136	0	2549	1602	4847	3116	3118	4339	4433	2965	3468	3995
ENSMUSG00000026185	chr1	Igfbp5	7.3E+07	7.3E+07	6006	-0.0827979	9.879755813	0.7201946	0.788838765	0.0639	0	15567	13313	14250	9772	19143	18699	22022	16329	20252	16483
ENSMUSG00000028532	chr4	Cachd1	1E+08	1E+08	6020	-0.09933611	2.401390537	0.7202245	0.788838765	0.07398	0	52	73	113	52	120	97	118	83	91	126
ENSMUSG00000042079	chr6	Hnrnpf	1.2E+08	1.2E+08	3047	0.060883385	5.09318073	0.7202889	0.788847681	0.03239	0	458	366	618	456	642	1032	769	583	575	658
ENSMUSG00000091896	chr18	Ube2d2a	3.6E+07	3.6E+07	2483	0.058671491	5.220454358	0.7207408	0.789281003	0.03055	0	521	382	609	547	712	943	786	684	734	758
ENSMUSG00000096210	chr15	H1f0	7.9E+07	7.9E+07	2287	0.067695729	7.079853307	0.7208532	0.789342373	0.04236	0	1960	1486	2373	1681	2526	3444	2689	2113	3053	3075
ENSMUSG00000097354	chr6	2310001H17Rik	1.3E+08	1.3E+08	5694	-0.06895915	4.003591829	0.7209222	0.789356347	0.04319	0	267	223	234	196	289	440	314	209	329	340
ENSMUSG00000086503	chrX	Xist	1E+08	1E+08	17923	-0.41240839	6.509105656	0.7210994	0.789488739	1.48266	0	2758	2378	3	1483	5	2824	4	1552	1635	2028
ENSMUSG00000032126	chr9	Hmbs	4.4E+07	4.4E+07	1755	-0.05704859	4.71732991	0.7218828	0.79028474	0.02777	0	339	300	477	383	538	613	528	412	597	508
ENSMUSG00000082491	chr8	Gm5909	8E+07	8E+07	1281	-0.12095075	0.42504121	0.7221966	0.790566591	0.09048	0	17	20	24	18	17	32	37	12	22	22
ENSMUSG00000005682	chr10	Pan2	1.3E+08	1.3E+08	4450	0.077485399	3.258350076	0.7223695	0.790632455	0.04476	0	133	117	142	131	166	255	195	157	162	239
ENSMUSG00000025933	chr1	Tmem14a	2.1E+07	2.1E+07	1351	-0.11193037	1.027940518	0.7223364	0.790632455	0.08711	0	34	23	23	27	44	61	38	26	43	27
ENSMUSG00000055041	chr15	Commd5	7.7E+07	7.7E+07	1060	0.074543549	3.352853508	0.7227415	0.790977912	0.0433	0	171	106	153	139	172	276	183	164	229	224
ENSMUSG00000013833	chr10	Med16	8E+07	8E+07	4663	-0.0682979	5.011558476	0.7232311	0.791390216	0.0417	0	355	334	698	619	518	557	775	457	748	710
ENSMUSG00000030929	chr7	Eri2	1.2E+08	1.2E+08	7170	-0.12185812	0.31003079	0.7231836	0.791390216	0.07808	0	18	15	17	15	24	35	20	18	18	22
ENSMUSG00000029090	chr5	Gpr125	5E+07	5E+07	4475	-0.06691245	3.657694233	0.7234775	0.791583319	0.03596	0	177	122	244	210	228	348	239	191	258	238
ENSMUSG00000038217	chr11	Tlcd2	7.5E+07	7.5E+07	1936	0.093762373	3.272928345	0.7235205	0.791583319	0.0708	0	140	125	122	83	224	300	182	168	190	185
ENSMUSG00000050619	chr2	Zscan29	1.2E+08	1.2E+08	7169	-0.08202646	2.658625375	0.7248893	0.793019088	0.05619	0	85	84	111	90	109	165	142	112	85	119
ENSMUSG00000037461	chr1	Ints7	1.9E+08	1.9E+08	7319	-0.06761926	3.436425435	0.7255518	0.793681885	0.03746	0	128	129	197	162	219	253	235	165	215	218
ENSMUSG00000019808	chr10	Adat2	1.4E+07	1.4E+07	1466	-0.12524375	0.827990058	0.7262603	0.794379632	0.10209	0	33	20	30	14	35	24	44	30	39	26
ENSMUSG00000044502	chr11	Bod1	3.2E+07	3.2E+07	1644	0.066179361	7.19245589	0.7263029	0.794379632	0.04232	0	2225	1452	2650	2119	2416	3185	3451	2398	3313	3094
ENSMUSG00000034083	chr6	Ccdc174	9.2E+07	9.2E+07	9188	-0.06549347	3.50879715	0.7264394	0.794405084	0.03664	0	164	133	198	168	209	310	244	172	203	220
ENSMUSG00000039047	chr3	Pigk	1.5E+08	1.5E+08	9367	-0.05805	5.476098943	0.7264303	0.794405084	0.03206	0	641	556	787	684	729	1095	957	645	912	924
ENSMUSG00000020156	chr10	Mum1	8E+07	8E+07	10361	0.053981932	4.742257995	0.7270536	0.795001086	0.02601	0	368	260	459	408	504	685	565	407	572	598
ENSMUSG00000027822	chr3	Slc33a1	6.4E+07	6.4E+07	3548	-0.0710073	3.444937078	0.7270978	0.795001086	0.04267	0	174	117	157	156	233	270	235	173	188	225
ENSMUSG00000091537	chr9	Tma7	1.1E+08	1.1E+08	1359	-0.06256708	5.646381105	0.7275909	0.795478163	0.03774	0	799	611	700	749	957	1148	1014	736	1092	1087
ENSMUSG00000037185	chr15	Krt80	1E+08	1E+08	1774	-0.12617039	1.518978719	0.7276803	0.795513997	0.13487	0	18	37	39	35	93	65	81	31	38	63
ENSMUSG00000020015	chr10	Cdk17	9.3E+07	9.3E+07	3643	0.074430537	3.17296368	0.7279505	0.795747316	0.05055	0	114	82	171	107	199	222	201	181	162	170
ENSMUSG00000024410	chr18	3110002H16Rik	1.2E+07	1.2E+07	5768	-0.06317623	3.829807665	0.7280375	0.795780368	0.03473	0	221	161	226	192	292	330	316	218	262	306
ENSMUSG00000020900	chr11	Myh10	6.9E+07	6.9E+07	10458	-0.11510071	4.686362991	0.7281091	0.795796585	0.12608	0	221	148	691	765	270	474	726	283	426	677
ENSMUSG00000001062	chr8	Vps9d1	1.2E+08	1.2E+08	5153	-0.05958425	4.530381188	0.7285836	0.796248372	0.03163	0	309	223	480	362	436	531	597	301	506	423
ENSMUSG00000078681	chr7	Tm2d3	6.6E+07	6.6E+07	1489	0.064004716	4.097088992	0.728636	0.796248372	0.03543	0	278	172	268	263	272	385	385	271	426	331
ENSMUSG00000050368	chr2	Hoxd10	7.5E+07	7.5E+07	1816	0.221456061	0.033069142	0.7287467	0.796307365	0.31629	0	11	12	10	24	4	4	40	14	33	10
ENSMUSG00000036091	chr9	Hyal3	1.1E+08	1.1E+08	1948	-0.08819477	1.800819296	0.7290384	0.796564048	0.06017	0	45	38	55	59	67	66	67	44	89	74
ENSMUSG00000038365	chr8	Fbxo25	1.4E+07	1.4E+07	2008	0.073216808	3.508016459	0.7295987	0.79711411	0.04331	0	187	135	173	152	171	272	275	184	263	202
ENSMUSG00000021696	chr13	Elovl7	1.1E+08	1.1E+08	5435	0.138069013	0.10446706	0.7297599	0.797228176	0.08536	0	10	10	24	15	11	24	18	13	26	24
ENSMUSG00000097868	chr2	A330069E16Rik	9.1E+07	9.1E+07	887	-0.09681162	1.101415396	0.7298645	0.797280302	0.06646	0	35	28	31	30	33	43	51	31	42	37
ENSMUSG00000025785	chr9	Exosc7	1.2E+08	1.2E+08	1843	0.062160033	4.026864486	0.7299503	0.797311997	0.03272	0	251	177	252	248	262	414	330	269	365	334
ENSMUSG00000078789	chr11	Dph1	7.5E+07	7.5E+07	2690	-0.08064552	2.84067112	0.730286	0.797616508	0.05175	0	80	80	132	103	162	182	133	127	125	140
ENSMUSG00000089902	chr2	Gm13625	7E+07	7E+07	480	0.131338185	0.849268909	0.7305074	0.797796202	0.10328	0	17	26	20	15	43	49	30	26	40	39
ENSMUSG00000028540	chr4	Dph2	1.2E+08	1.2E+08	3030	-0.08861629	2.231428768	0.7306164	0.797853143	0.05642	0	55	53	83	78	91	127	86	80	95	72
ENSMUSG00000003273	chr7	Car11	4.6E+07	4.6E+07	1926	-0.0703018	3.217606454	0.7307543	0.797941632	0.04324	0	113	119	155	139	185	184	196	133	210	206
ENSMUSG00000028741	chr4	Mrto4	1.4E+08	1.4E+08	2611	0.059227825	4.557048344	0.7313404	0.798519472	0.03198	0	295	271	435	344	393	632	395	397	535	515
ENSMUSG00000058838	chr9	Rps27a-ps2	8.3E+07	8.3E+07	467	0.077758138	3.889273276	0.7320885	0.799274055	0.05431	0	242	183	275	172	196	480	245	282	268	287
ENSMUSG00000018599	chr11	Mief2	6.1E+07	6.1E+07	2716	-0.07685376	6.786663281	0.7322029	0.799336692	0.05922	0	1229	879	2900	2049	1844	2051	2551	1611	2389	2503
ENSMUSG00000064307	chr7	Lrrc51	1E+08	1E+08	1210	0.091683669	1.97856371	0.7323706	0.799457524	0.06086	0	50	40	49	60	82	99	69	64	84	93
ENSMUSG00000011158	chr12	Brf1	1.1E+08	1.1E+08	2755	-0.06082633	4.229803632	0.7326482	0.799698314	0.03302	0	236	215	416	240	355	457	363	307	359	403
ENSMUSG00000028409	chr4	Smu1	4.1E+07	4.1E+07	3119	0.059194223	5.710265174	0.732854	0.799860773	0.03434	0	742	592	961	704	873	1374	1080	887	1018	1163
ENSMUSG00000006315	chr7	Tmem147	3.1E+07	3.1E+07	868	-0.06816019	6.774244079	0.7330726	0.800037078	0.04694	0	1470	1050	2326	1870	1901	2043	2257	1573	2792	2372
ENSMUSG00000041957	chr16	Pkp2	1.6E+07	1.6E+07	5360	-0.14738807	2.553002368	0.7333996	0.800331654	0.19989	0	79	53	36	41	268	118	146	104	80	112
ENSMUSG00000097048	chr6	1600020E01Rik	8.7E+07	8.7E+07	2092	0.094328721	1.917365476	0.7340621	0.800992249	0.06011	0	44	37	60	55	75	101	71	55	64	104
ENSMUSG00000045275	chr16	Lca5l	9.6E+07	9.6E+07	6521	-0.11924975	0.455613148	0.7343998	0.801298407	0.09709	0	14	18	17	22	28	38	15	16	27	31

ENSMUSG00000013646	chr11	Sh3bp5l	5.8E+07	5.8E+07	6352	-0.05471515	4.815175415	0.7345847	0.801375528	0.02783	0	338	300	544	454	555	626	588	448	583	599
ENSMUSG00000034111	chr12	Tmed8	8.7E+07	8.7E+07	7179	-0.07945252	2.561739554	0.7345604	0.801375528	0.05618	0	91	74	81	79	122	171	112	77	119	113
ENSMUSG00000025270	chrX	Alas2	1.5E+08	1.5E+08	2403	0.177125506	1.051267659	0.7347771	0.801523084	0.26687	0	1	15	34	50	44	37	37	28	73	39
ENSMUSG00000038156	chr7	Spon1	1.1E+08	1.1E+08	8177	-0.14760324	3.531784801	0.7350074	0.801674923	0.22427	0	116	362	59	76	185	321	206	156	258	203
ENSMUSG00000039065	chr15	Fam173b	3.2E+07	3.2E+07	5248	-0.06788841	3.339804543	0.7350306	0.801674923	0.03957	0	138	110	202	149	184	247	169	146	229	226
ENSMUSG00000001985	chr4	Grik3	1.3E+08	1.3E+08	8973	0.153756952	-0.30060931	0.7352102	0.801808483	0.13098	0	6	6	10	9	20	25	11	5	21	16
ENSMUSG00000041361	chr9	Myzap	7.2E+07	7.2E+07	5635	0.099049935	1.771714044	0.7354327	0.801988748	0.08748	0	27	27	93	55	48	65	87	56	65	79
ENSMUSG00000089083	chr6	Rnu7	1.2E+08	1.2E+08	62	-0.10817248	0.594773399	0.7359724	0.802514839	0.07665	0	19	22	28	19	21	25	30	23	26	35
ENSMUSG00000025357	chr10	Dgka	1.3E+08	1.3E+08	2808	0.068410897	3.551385986	0.7362101	0.802711681	0.03908	0	178	132	204	168	170	288	301	160	220	275
ENSMUSG00000004567	chr8	Mcoln1	3500457	3500627	3260	0.05287392	4.650225691	0.7370376	0.80353978	0.02591	0	363	265	441	354	441	630	562	352	547	569
ENSMUSG00000019132	chr13	BC005537	2.5E+07	2.5E+07	3665	0.063766647	6.825599563	0.7370858	0.80353978	0.04264	0	1640	1078	2193	1580	2013	3021	2844	1864	1965	2352
ENSMUSG00000030551	chr7	Nr2f2	7E+07	7E+07	4863	0.063314808	4.066764472	0.7371988	0.80353978	0.03653	0	252	186	230	215	346	424	359	255	354	378
ENSMUSG00000040165	chr8	Cd209c	3940222	3940430	1889	-0.19130127	-0.18019357	0.7371867	0.80353978	0.3799	0	8	24	1	5	20	26	12	10	4	26
ENSMUSG00000037740	chr2	Mrps26	1.3E+08	1.3E+08	4358	0.05663519	5.115650202	0.7374711	0.803712576	0.03315	0	444	289	743	556	597	770	731	531	852	768
ENSMUSG00000096780	chr17	Tmem181b-ps	6438524	6438843	4187	-0.08815253	1.915194635	0.7374719	0.803712576	0.06216	0	47	54	61	49	72	95	92	56	60	67
ENSMUSG00000014959	chr2	Gorasp2	7.1E+07	7.1E+07	4145	-0.06038783	6.542702192	0.7377559	0.803959639	0.03825	0	1218	1056	1742	1530	1675	2111	2102	1342	1978	1951
ENSMUSG00000049184	chr8	Purg	3.3E+07	3.3E+07	2119	0.104315006	1.079175963	0.7379809	0.804142282	0.07662	0	22	15	48	31	34	60	38	24	51	45
ENSMUSG00000071317	chr10	Bves	4.5E+07	4.5E+07	1607	-0.06361725	5.410983304	0.7381487	0.804262744	0.04145	0	667	431	964	691	551	896	1069	645	772	921
ENSMUSG00000045008	chr10	9030612E09Rik	4.3E+07	4.3E+07	1859	-0.10233544	1.021839302	0.7382514	0.804312164	0.06592	0	26	21	47	32	26	39	43	29	39	42
ENSMUSG00000032036	chr9	Kirrel3	3.4E+07	3.4E+07	6454	0.132145364	-0.10598283	0.7385217	0.804544054	0.08737	0	7	7	14	13	19	21	19	11	24	14
ENSMUSG00000029162	chr5	Khk	3.1E+07	3.1E+07	1670	-0.05975151	4.109646131	0.7388214	0.804808108	0.03318	0	253	175	304	276	327	339	349	269	357	419
ENSMUSG00000034035	chr4	Ccdc17	1.2E+08	1.2E+08	2634	-0.1557258	-0.10662966	0.7388865	0.804816512	0.14182	0	17	12	14	5	17	25	8	8	16	25
ENSMUSG00000095567	chr4	Noc2l	1.6E+08	1.6E+08	2867	-0.05490061	5.220619668	0.7391891	0.80508363	0.03096	0	531	458	671	595	588	829	763	623	806	735
ENSMUSG00000051864	chr15	Tbc1d22a	8.6E+07	8.6E+07	3229	0.055052839	5.0216935	0.7397663	0.805649697	0.0314	0	424	284	650	525	568	716	823	487	769	632
ENSMUSG00000041936	chr4	Agrn	1.6E+08	1.6E+08	9285	0.061050257	3.995528618	0.740334	0.806205385	0.03625	0	176	153	329	240	301	430	383	211	366	309
ENSMUSG00000022973	chr16	Synj1	9.1E+07	9.1E+07	8085	-0.0744027	3.51185123	0.7404269	0.806243949	0.0501	0	143	93	311	165	199	283	264	147	213	248
ENSMUSG00000020857	chr11	Nme2	9.4E+07	9.4E+07	1171	-0.06795135	8.472966582	0.7407162	0.806496252	0.05023	0	4483	3528	8808	5955	5290	8420	7511	5604	7076	7320
ENSMUSG00000032855	chr17	Pkd1	2.5E+07	2.5E+07	14170	0.056279992	5.486441786	0.7408007	0.806525659	0.03249	0	550	516	805	608	856	1169	1021	631	944	1006
ENSMUSG00000024309	chr17	Pfdn6	3.4E+07	3.4E+07	1193	-0.05506185	5.253162968	0.7411268	0.806818074	0.03174	0	531	456	634	580	723	776	779	552	887	870
ENSMUSG00000028773	chr4	Fabp3	1.3E+08	1.3E+08	823	-0.15286077	9.488298892	0.7413419	0.806989684	0.254	0	5803	2134	37202	12734	5642	15219	17429	8754	7992	21993
ENSMUSG00000029068	chr4	Ccnl2	1.6E+08	1.6E+08	5278	0.063917055	5.207461826	0.7414126	0.807003958	0.04182	0	422	472	575	478	771	1059	697	532	672	985
ENSMUSG00000020034	chr10	Tcp11l2	8.5E+07	8.5E+07	3438	-0.06391269	5.385712321	0.7416397	0.807188494	0.04292	0	727	401	910	612	604	912	1026	640	648	1005
ENSMUSG00000029014	chr5	Dnajc2	2.2E+07	2.2E+07	5029	-0.05423967	4.52402666	0.7417719	0.807269721	0.029	0	280	252	466	396	385	556	511	358	450	457
ENSMUSG00000101841	chr11	Gm11993	9149778	9150597	820	-0.12645381	0.42819917	0.7421285	0.80759514	0.07898	0	23	12	24	21	18	21	23	19	26	33
ENSMUSG00000033765	chr13	Calm4	3837757	3838671	915	-0.18221099	0.038896819	0.7423574	0.807781588	0.27509	0	34	16	6	5	9	23	17	25	13	10
ENSMUSG00000031505	chr8	Carkd	1.1E+07	1.1E+07	3694	0.052150197	5.015328643	0.7424751	0.80784698	0.02815	0	441	305	554	515	607	778	694	489	781	668
ENSMUSG00000028879	chr4	Stx12	1.3E+08	1.3E+08	3188	-0.05601588	5.457880199	0.7426579	0.807983226	0.03259	0	594	454	866	612	914	1034	999	713	821	883
ENSMUSG00000035285	chr7	Nat14	4922251	4922639	1612	0.095069339	1.261034429	0.7430546	0.808352071	0.07296	0	24	18	47	47	34	50	54	34	50	57
ENSMUSG00000023911	chr17	Flywch2	2.4E+07	2.4E+07	996	-0.10105371	0.383541645	0.7434452	0.808714263	0.08836	0	20	14	24	15	21	30	27	9	34	22
ENSMUSG00000019854	chr10	Reps1	1.8E+07	1.8E+07	5301	-0.05251688	4.435425503	0.7435319	0.80874595	0.02812	0	288	260	392	336	380	486	440	324	475	466
ENSMUSG00000028556	chr4	Dock7	9.9E+07	9.9E+07	8115	-0.05966187	3.846167242	0.7437803	0.808953387	0.03602	0	207	174	258	208	252	412	312	224	247	263
ENSMUSG00000041445	chr14	Mmrn2	3.4E+07	3.4E+07	3935	-0.06547769	4.675430323	0.7443207	0.809478292	0.04279	0	267	208	674	372	542	646	536	365	523	526
ENSMUSG00000086158	chr9	Ccpg1os	7.3E+07	7.3E+07	2404	-0.07650836	2.46004569	0.7443984	0.80950008	0.05497	0	88	67	88	79	93	132	86	99	113	109
ENSMUSG00000020340	chr11	Cyfip2	4.6E+07	4.6E+07	7103	-0.26837763	5.283223392	0.7445438	0.809595374	0.77918	0	18	427	262	2329	10	554	627	512	760	1180
ENSMUSG00000058886	chr7	Deaf1	1.4E+08	1.4E+08	2192	0.071639433	3.585458151	0.7449821	0.81000919	0.04996	0	155	135	141	182	261	244	257	194	304	257
ENSMUSG00000020484	chr11	Xbp1	5520659	5521200	3248	0.078622981	6.633526623	0.745145	0.810123582	0.06848	0	1385	1388	994	1787	1442	2833	1812	1698	2322	1894
ENSMUSG00000037762	chr10	Slc16a9	7E+07	7E+07	3869	-0.06589376	3.327224719	0.7455419	0.810492258	0.04187	0	125	112	157	171	206	222	245	156	196	186
ENSMUSG00000025981	chr1	Coq10b	5.5E+07	5.5E+07	4805	-0.07903934	3.74636963	0.7457008	0.810602104	0.05998	0	234	88	265	181	303	266	317	231	195	322
ENSMUSG00000031832	chr8	Taf1c	1.2E+08	1.2E+08	3386	-0.07809791	2.975427148	0.7460759	0.810821381	0.05583	0	104	79	176	108	148	145	147	110	227	151
ENSMUSG00000037440	chr10	Vnn1	2.4E+07	2.4E+07	2416	-0.22299246	-0.18465645	0.7460065	0.810821381	0.42519	0	11	15	0	3	33	26	5	12	10	22
ENSMUSG00000099681	chr11	1700052K11Rik	1.1E+08	1.1E+08	3708	-0.08114556	2.921123877	0.7460231	0.810821381	0.05669	0	117	57	168	89	171	163	147	121	162	156
ENSMUSG00000027531	chr3	Impa1	1E+07	1E+07	5437	-0.05687211	4.453607679	0.746303	0.811005362	0.0325	0	253	235	408	317	500	534	475	343	438	428
ENSMUSG00000015363	chr15	Trabd	8.9E+07	8.9E+07	5591	-0.05702341	5.540856327	0.7465564	0.811089293	0.03585	0	596	503	881	868	747	1051	1030	652	1063	944
ENSMUSG00000022391	chr15	Rangap1	8.2E+07	8.2E+07	3211	0.055641673	5.281747812	0.7464985	0.811089293	0.03317	0	466	441	676	650	642	976	734	642	917	821
ENSMUSG00000058267	chr1	Mrps14	1.6E+08	1.6E+08	3258	-0.05752052	6.001124479	0.746476	0.811089293	0.0364	0	933	626	1368	997	1084	1405	1411	992	1368	1310
ENSMUSG00000062944	chr7	9130023H24Rik	1.3E+08	1.3E+08	3581	-0.09004326	1.746580477	0.7466116	0.811089293	0.05796	0	36	41	69	50	59	69	64	58	71	61
ENSMUSG00000062591	chr17	Tubb4a	5.7E+07	5.7E+07	2228	0.152864717	1.076880287	0.7466776	0.811098152	0.19794	0	20	21	11	20	73	71	32	18	43	60
ENSMUSG00000039018	chr7	Mtg1	1.4E+08	1.4E+08	4019	-0.05507908	4.8152647	0.7469332	0.811313041	0.03213	0	435	312	445	414	556	624	511	459	683	557
ENSMUSG00000015944	chr5	Gatsl2	1.3E+08	1.3E+08	7560	-0.06720652	6.761800052	0.747015	0.811339013	0.05118	0	1599	1060	2599	1794	1457	2099	2607	1469	2339	2497
ENSMUSG00000029148	chr5	Nrbp1	3.1E+07	3.1E+07	3559	0.060382501	6.234098571	0.7473151	0.811602119	0.04109	0	976	749	1553	1270	1067	1863	1661	1219	1671	1541
ENSMUSG00000030922	chr7	Lyrm1	1.2E+08	1.2E+08	1513	-0.07105364	2.774717095	0.7476603	0.811914197	0.04975	0	99	81	145	100	97	152	157	96	116	163
ENSMUSG00000055897	chr2	Ppp4r1l-ps	1.7E+08	1.7E+08	12025	0.081740266	3.258794107	0.7477474	0.811945858	0.06179	0	146	131	115	95	195	241	190	132	213	240
ENSMUSG00000040028	chr8	Elavl1	4284782	4289924	6030	0.051815571	4.975613263	0.7479044	0.812025664	0.02899	0	417	333	505	460	628	666	677	535	690	717
ENSMUSG00000092981	chr17	Mir5125	2.4E+07	2.4E+07	79	0.151438195	1.056179955	0.7479367	0.812025664	0.17762	0	30	34	17	11	44	46	35	22	34	81
ENSMUSG00000021684	chr13	Pde8b	9.5E+07	9.5E+07	5879	0.108222662	0.723696299	0.7481325	0.812175386	0.09626	0	12	15	37	21	30	30	49	22	24	41
ENSMUSG00000039457	chr16	Ppl	5086291	5089828	6277	-0.08408481	2.366999937	0.7493175	0.813398882	0.07934	0	65	76	58	79	107	172	92	73	90	89
ENSMUSG00000029343	chr5	Crybb1	1.1E+08	1.1E+08	985	0.094549686	1.136439808	0.7505684	0.814693757	0.07917	0	23	19	51	37	25	49	40	33	57	44

ENSMUSG00000075528	chr11	Aarsd1	1E+08	1E+08	3052	-0.05454837	5.432702929	0.7506763	0.814747829	0.03299	0	564	435	911	696	768	972	842	669	1005	885
ENSMUSG00000022836	chr16	Mylk	3.5E+07	3.5E+07	10159	-0.05755241	4.718732904	0.7510284	0.815066916	0.03723	0	295	347	492	341	556	778	536	392	461	523
ENSMUSG00000039231	chrX	Suv39h1	8061171	8062983	5270	-0.06423171	2.871509093	0.751912	0.815962732	0.04117	0	106	84	132	113	122	169	158	108	152	145
ENSMUSG00000096935	chr3	1700113A16Rik	8.8E+07	8.8E+07	983	0.140109736	-0.09266565	0.7520408	0.816039348	0.1017	0	12	7	9	10	22	17	16	10	24	23
ENSMUSG00000052928	chr18	Ctif	7.5E+07	7.5E+07	6173	0.058436949	4.193229404	0.752172	0.816118517	0.0352	0	220	225	286	257	355	395	414	276	452	385
ENSMUSG00000001018	chr3	Snapin	9E+07	9E+07	2290	-0.05618751	6.069282091	0.752442	0.816335107	0.03708	0	1007	783	1128	978	1263	1534	1576	1041	1330	1334
ENSMUSG00000024352	chr18	Spata24	3.6E+07	3.6E+07	967	0.098316703	1.025031234	0.7525851	0.816335107	0.0777	0	24	17	47	22	34	38	34	31	47	55
ENSMUSG00000025728	chr17	Pigq	2.6E+07	2.6E+07	5769	0.061393921	5.038163008	0.7527208	0.816335107	0.0434	0	333	328	520	476	823	819	666	438	842	734
ENSMUSG00000029314	chr5	Agpat9	1E+08	1E+08	3502	0.098992637	3.953234189	0.7526337	0.816335107	0.11494	0	213	100	200	163	500	502	147	266	382	353
ENSMUSG00000051557	chr4	Pusl1	1.6E+08	1.6E+08	2329	-0.0727785	2.777237162	0.7526842	0.816335107	0.05202	0	88	84	118	81	156	172	121	104	138	148
ENSMUSG00000055652	chr7	Klhl25	7.6E+07	7.6E+07	3385	-0.08067637	2.588837537	0.7526909	0.816335107	0.05882	0	77	49	96	95	155	133	115	84	134	131
ENSMUSG00000035372	chr19	1810055G02Rik	3708333	3708436	1882	0.078087658	2.978150145	0.7531272	0.816712751	0.05924	0	89	100	112	105	163	220	172	134	186	115
ENSMUSG00000035049	chr19	Rrp12	4.2E+07	4.2E+07	4319	-0.06763442	5.402821723	0.7532479	0.816780496	0.05286	0	458	428	960	920	535	891	858	748	841	886
ENSMUSG00000037300	chr8	Ttc13	1.2E+08	1.2E+08	10190	-0.05393663	4.480418187	0.7537379	0.817248589	0.03241	0	341	248	333	327	463	578	468	351	454	413
ENSMUSG00000026510	chr1	Trp53bp2	1.8E+08	1.8E+08	4418	0.061534474	3.444248965	0.7539475	0.817412712	0.04022	0	124	98	194	186	210	269	257	163	242	215
ENSMUSG00000057363	chr1	Uxs1	4.4E+07	4.4E+07	5097	-0.05239985	4.326373986	0.7545536	0.818006502	0.03058	0	274	250	342	298	365	500	416	337	407	364
ENSMUSG00000048696	chr10	Mex3d	8E+07	8E+07	3266	0.080315488	2.350582137	0.7546846	0.818085379	0.0593	0	61	57	112	53	89	128	132	80	110	83
ENSMUSG00000028797	chr4	Tmem234	1.3E+08	1.3E+08	4273	0.05199059	5.364856141	0.754996	0.818359621	0.03152	0	507	430	719	577	861	1006	993	630	870	854
ENSMUSG00000026127	chr1	Imp4	3.4E+07	3.4E+07	8553	0.05503018	4.07604428	0.7552085	0.818463521	0.03305	0	208	169	300	236	350	463	354	254	325	387
ENSMUSG00000026276	chr1	Sept2	9.3E+07	9.3E+07	7979	-0.06022869	6.469819124	0.7551613	0.818463521	0.04405	0	1354	1062	1511	1293	1578	2640	1810	1425	1534	1629
ENSMUSG00000025959	chr1	Klf7	6.4E+07	6.4E+07	8131	-0.06012512	3.646009326	0.7554115	0.818620192	0.03751	0	154	154	255	168	233	284	263	217	223	264
ENSMUSG00000039810	chr10	Zc3h10	1.3E+08	1.3E+08	4384	-0.06348571	3.210018767	0.7560271	0.819224066	0.04311	0	127	117	174	138	147	227	153	147	206	192
ENSMUSG00000027560	chr2	Dok5	1.7E+08	1.7E+08	1768	0.131034604	1.771978289	0.7562031	0.819288133	0.20995	0	43	4	97	73	36	68	101	51	49	88
ENSMUSG00000038895	chr9	Zfp653	2.2E+07	2.2E+07	2132	0.08698642	2.31198255	0.7561784	0.819288133	0.06396	0	65	64	69	57	98	133	96	57	128	112
ENSMUSG00000055720	chr9	Ubl7	5.8E+07	5.8E+07	1364	-0.05668082	5.829549174	0.756398	0.819436051	0.03805	0	727	545	1212	834	1172	1144	1371	814	1269	1177
ENSMUSG00000030498	chr7	Gas2	5.2E+07	5.2E+07	4993	0.08545622	2.035155483	0.7565325	0.819518456	0.07059	0	46	40	86	66	58	140	86	69	66	68
ENSMUSG00000040713	chr1	Creg1	1.7E+08	1.7E+08	2362	0.06080107	5.904577807	0.756695	0.819631206	0.0441	0	1003	683	913	966	777	1387	1240	988	1341	1351
ENSMUSG00000016534	chrX	Lamp2	3.8E+07	3.8E+07	9552	0.0576805	6.680086152	0.7571705	0.820082863	0.04069	0	1441	1133	1788	1483	1749	2451	2746	1504	1934	2268
ENSMUSG00000031637	chr8	Lrp2bp	4.6E+07	4.6E+07	4338	-0.07664586	4.484098865	0.7575352	0.82035122	0.07135	0	450	312	283	329	285	383	583	423	496	319
ENSMUSG00000057836	chrX	Xlr3a	7.3E+07	7.3E+07	4045	-0.16127575	-0.09704217	0.7575294	0.82035122	0.23929	0	9	23	4	8	18	17	34	6	13	14
ENSMUSG00000004347	chr6	Pde1c	5.6E+07	5.6E+07	12803	0.141059472	0.010832744	0.7578358	0.820613344	0.14624	0	20	5	26	4	11	22	23	11	18	24
ENSMUSG00000091154	chr8	Proscos	2.7E+07	2.7E+07	666	0.121769997	0.508582	0.7579006	0.820620153	0.15871	0	8	6	50	20	17	24	31	25	31	28
ENSMUSG00000018102	chr13	Hist1h2bc	2.4E+07	2.4E+07	736	0.050373059	5.348833581	0.7583386	0.820874913	0.03058	0	520	424	756	559	802	960	848	657	965	849
ENSMUSG00000028833	chr4	Ncdn	1.3E+08	1.3E+08	3710	0.055090238	4.749884211	0.7582644	0.820874913	0.03464	0	330	305	402	430	519	579	543	389	710	612
ENSMUSG00000036073	chr4	Galt	4.2E+07	4.2E+07	2471	0.064153181	5.000700328	0.75837	0.820874913	0.05148	0	373	213	830	559	486	664	718	462	711	833
ENSMUSG00000079559	chr9	Gm684	5.1E+07	5.1E+07	1263	0.155633565	0.077620241	0.7582955	0.820874913	0.19079	0	17	6	6	5	35	30	17	12	20	25
ENSMUSG00000034109	chr3	Golim4	7.6E+07	7.6E+07	11072	-0.05744761	4.03566769	0.7584575	0.820906303	0.03769	0	259	182	275	205	342	446	398	243	283	299
ENSMUSG00000070282	chr9	3000002C10Rik	1.1E+08	1.1E+08	3981	0.13828981	-0.04627661	0.7586407	0.821041248	0.10018	0	16	9	16	14	6	18	17	17	23	17
ENSMUSG00000004268	chr6	Emg1	1.2E+08	1.2E+08	1404	0.05306717	5.835542521	0.7588868	0.821244165	0.03398	0	767	671	978	826	974	1396	1177	895	1331	1222
ENSMUSG00000039067	chr8	Psmd7	1.1E+08	1.1E+08	1599	-0.05843569	7.40116701	0.7589978	0.821300992	0.04295	0	2686	1780	3296	2561	2770	4012	3440	2850	3419	3350
ENSMUSG00000021715	chr13	Cwc27	1E+08	1E+08	2873	-0.05853262	3.765250879	0.7594714	0.821750092	0.03655	0	191	132	305	201	231	336	332	204	237	268
ENSMUSG00000031483	chr8	Erlin2	2.7E+07	2.7E+07	3943	-0.05523648	4.146113589	0.759937	0.822190385	0.0347	0	226	206	314	231	393	445	405	268	363	315
ENSMUSG00000020653	chr12	Klf11	2.5E+07	2.5E+07	4228	0.08801963	3.18887174	0.760074	0.822275195	0.08818	0	159	101	87	89	220	226	137	167	175	249
ENSMUSG00000039116	chr10	Gpr126	1.4E+07	1.4E+07	6505	0.100048478	1.590823913	0.7603193	0.822413652	0.08687	0	26	35	70	47	35	74	84	30	66	63
ENSMUSG00000054823	chr8	Whsc1l1	2.6E+07	2.6E+07	16513	-0.05171682	4.100783426	0.760309	0.822413652	0.03059	0	226	200	304	252	336	405	370	251	326	390
ENSMUSG00000039670	chr11	Oxld1	1.2E+08	1.2E+08	813	0.069242042	3.409159838	0.7605356	0.822584252	0.05878	0	137	64	253	170	185	238	226	166	200	286
ENSMUSG00000035790	chr16	Cep19	3.2E+07	3.2E+07	1751	-0.07403215	2.835871357	0.7607132	0.82271287	0.0643	0	97	103	105	137	87	164	134	102	143	169
ENSMUSG00000021750	chr14	Fam107a	8296274	8298797	3870	-0.1196155	0.913571932	0.7613869	0.823187604	0.10363	0	14	18	53	31	28	30	52	22	40	33
ENSMUSG00000024817	chr19	Uhrf2	3E+07	3E+07	8590	0.059767057	3.969513775	0.7612849	0.823187604	0.03752	0	218	201	274	217	227	384	405	230	276	361
ENSMUSG00000028995	chr5	Fam126a	2.4E+07	2.4E+07	7107	-0.05697862	3.558822531	0.7612696	0.823187604	0.03434	0	158	125	240	166	224	302	244	183	215	246
ENSMUSG00000049641	chr10	Vgll2	5.2E+07	5.2E+07	1650	0.108397619	6.155180038	0.761367	0.823187604	0.15116	0	634	331	1885	2031	509	1591	1255	1193	1581	1990
ENSMUSG00000024174	chr17	Pot1b	5.6E+07	5.6E+07	3499	-0.09915802	0.679178177	0.7621033	0.82389861	0.09005	0	19	23	27	19	28	46	30	14	23	40
ENSMUSG00000026020	chr1	Nop58	6E+07	6E+07	10758	0.061779841	4.206212214	0.7622955	0.823979434	0.04426	0	265	237	296	260	277	481	358	395	311	365
ENSMUSG00000030706	chr7	Mrpl48	1E+08	1E+08	6119	-0.05030164	5.611449112	0.7622738	0.823979434	0.03144	0	728	519	949	752	828	1134	1032	780	1010	1003
ENSMUSG00000024037	chr17	Wdr4	3.1E+07	3.1E+07	5432	-0.06191185	3.083198947	0.7628862	0.824554303	0.03916	0	112	85	154	139	164	204	183	130	173	160
ENSMUSG00000027495	chr2	Fam210b	1.7E+08	1.7E+08	3617	0.060160879	3.554075059	0.763422	0.82506991	0.03789	0	175	139	180	165	194	267	272	189	276	224
ENSMUSG00000040272	chr2	Accs	9.4E+07	9.4E+07	8364	0.079098338	2.28241018	0.7648206	0.826517713	0.0657	0	66	56	65	54	109	135	77	81	108	105
ENSMUSG00000001948	chr9	Spa17	3.8E+07	3.8E+07	689	-0.08940519	1.148912651	0.7648894	0.8265284	0.07146	0	40	22	33	26	44	54	46	34	46	32
ENSMUSG00000000776	chr14	Polr3d	7E+07	7E+07	2156	-0.05331176	4.386019356	0.7654287	0.827047484	0.03333	0	288	213	441	357	318	451	478	357	434	381
ENSMUSG00000095159	chr5	Tubb4b-ps1	7179365	7180699	1335	-0.13019493	0.477212543	0.7655267	0.827089609	0.09704	0	19	13	30	19	22	16	39	20	32	19
ENSMUSG00000020674	chr12	Pxdn	3E+07	3E+07	9517	0.061231425	4.975501642	0.7657795	0.827299035	0.04911	0	375	304	525	337	849	907	673	537	677	530
ENSMUSG00000026176	chr1	Ctdsp1	7.4E+07	7.4E+07	3334	0.056023138	6.971843289	0.7659368	0.827405213	0.04183	0	1675	1218	2172	2101	2218	2768	2743	1915	2913	2915
ENSMUSG00000102827	chr18	RP23-56B11.5	3.8E+07	3.8E+07	1740	0.114943385	0.568780596	0.7661828	0.827607272	0.11879	0	18	10	27	17	30	50	28	10	43	21
ENSMUSG00000028989	chr4	Angptl7	1.5E+08	1.5E+08	2157	0.093057717	4.186575164	0.7671254	0.828561621	0.11703	0	175	96	614	193	357	575	535	274	190	393
ENSMUSG00000005078	chr12	Jkamp	7.2E+07	7.2E+07	2692	0.064880444	3.673598113	0.7678447	0.829146901	0.04913	0	205	126	161	162	285	332	279	159	301	288
ENSMUSG00000029910	chr6	Mad2l1	6.7E+07	6.7E+07	2203	0.106656477	1.216749324	0.7677973	0.829146901	0.10239	0	52	17	36	25	31	73	43	42	33	47
ENSMUSG00000036158	chr15	Prickle1	9.3E+07	9.4E+07	4345	0.071806038	2.714632479	0.767839	0.829146901	0.05649	0	90	61	142	87	104	199	103	100	123	166

ENSMUSG00000026544	chr1	Dusp23	1.7E+08	1.7E+08	1410	-0.05491739	5.327148149	0.768168	0.82943226	0.03995	0	660	467	554	597	779	793	786	639	994	829
ENSMUSG00000099481	chr7	Xndc1	1E+08	1E+08	5278	0.066689641	2.711247371	0.7683496	0.829564399	0.04763	0	101	65	111	98	101	176	122	86	146	160
ENSMUSG00000041417	chr13	Pik3r1	1E+08	1E+08	10079	0.053265722	5.745796531	0.7685334	0.829699035	0.0377	0	656	595	873	824	1043	1481	1023	940	1042	1157
ENSMUSG00000032121	chr9	Tmem218	3.7E+07	3.7E+07	1019	-0.07511347	2.595641209	0.7686945	0.829749772	0.05702	0	91	55	150	91	82	135	122	108	109	120
ENSMUSG00000049969	chr4	Plekhf2	1.1E+07	1.1E+07	3039	-0.05310168	3.752322104	0.7686987	0.829749772	0.03456	0	183	167	214	200	261	306	293	212	259	288
ENSMUSG00000083396	chr7	Gm15542	1.4E+08	1.4E+08	1194	-0.11476474	0.776331517	0.7689205	0.829925267	0.11039	0	30	21	19	12	44	43	31	22	38	27
ENSMUSG00000040888	chr17	Gfer	2.5E+07	2.5E+07	1775	0.051366121	4.15300183	0.7690622	0.830014338	0.0324	0	244	179	290	263	348	420	346	278	442	378
ENSMUSG00000038855	chr1	Itpkb	1.8E+08	1.8E+08	10463	-0.06694323	5.308453723	0.7691524	0.83004071	0.05794	0	396	283	1163	581	821	862	770	589	835	945
ENSMUSG00000039630	chr1	Hnrnpu	1.8E+08	1.8E+08	8959	-0.05591826	7.226515418	0.769205	0.83004071	0.04293	0	1907	1663	2989	2403	2677	3782	3102	2466	2668	3180
ENSMUSG00000041396	chr1	Mettl18	1.6E+08	1.6E+08	1513	-0.08417863	1.852352189	0.7693197	0.830100681	0.08356	0	63	42	55	39	73	90	114	41	57	57
ENSMUSG00000024097	chr17	Srsf7	8E+07	8E+07	2279	-0.04947045	4.826761329	0.7699793	0.830613109	0.03132	0	401	317	531	476	449	728	539	515	538	539
ENSMUSG00000030271	chr6	Ogg1	1.1E+08	1.1E+08	2034	0.089686829	1.880513318	0.7700315	0.830613109	0.07004	0	49	44	40	51	75	112	70	48	74	83
ENSMUSG00000038400	chr2	Pmepa1	1.7E+08	1.7E+08	4913	0.100388157	5.74922039	0.7700161	0.830613109	0.14006	0	434	375	589	480	2318	1309	1041	976	1019	1370
ENSMUSG00000040957	chr18	Cables1	1.2E+07	1.2E+07	3397	-0.09488865	2.232427279	0.769918	0.830613109	0.09153	0	62	35	84	47	147	130	77	72	77	106
ENSMUSG00000026576	chr1	Atp1b1	1.6E+08	1.6E+08	3081	0.135495782	7.515770539	0.7701469	0.830627268	0.2548	0	1519	279	7256	3930	1494	4069	5957	2687	2854	4433
ENSMUSG00000031487	chr8	Brf2	2.7E+07	2.7E+07	1383	0.065159776	3.009110293	0.7701631	0.830627268	0.04719	0	111	81	139	121	138	151	167	130	215	172
ENSMUSG00000040250	chr6	Asun	1.5E+08	1.5E+08	3968	0.062585535	3.664674628	0.7702497	0.830656833	0.04477	0	204	147	185	210	166	302	312	219	239	254
ENSMUSG00000052684	chr4	Jun	9.5E+07	9.5E+07	3189	0.060243677	6.32843044	0.7703435	0.830694092	0.05074	0	1015	633	1406	1294	1771	1588	1530	1440	1964	1858
ENSMUSG00000029596	chr5	Sdsl	1.2E+08	1.2E+08	1497	0.141448149	0.160279746	0.7705798	0.830821166	0.18646	0	9	9	12	5	40	26	19	15	34	15
ENSMUSG00000061576	chr5	Dpp6	2.7E+07	2.7E+07	10030	0.113609665	0.463048808	0.7705646	0.830821166	0.14994	0	17	7	43	14	15	20	36	16	43	21
ENSMUSG00000104139	chr14	AC102815.1	1E+08	1E+08	3805	0.074944622	3.539773161	0.7707476	0.830938145	0.06963	0	160	124	166	144	260	323	393	160	222	146
ENSMUSG00000026248	chr1	Mrpl44	8E+07	8E+07	1644	-0.04864885	5.320494311	0.7711699	0.831265653	0.03087	0	571	385	858	612	692	854	867	607	826	904
ENSMUSG00000044982	chr18	Sft2d3	3.2E+07	3.2E+07	2810	-0.0876141	1.572912727	0.7711511	0.831265653	0.07203	0	35	23	56	41	76	75	68	32	56	62
ENSMUSG00000028416	chr4	Bag1	4.1E+07	4.1E+07	1349	0.055151433	7.486009275	0.7713355	0.831316362	0.04263	0	2476	1903	3238	2881	2808	4111	4002	2820	3687	4308
ENSMUSG00000091952	chr8	Gm17709	1.2E+08	1.2E+08	1096	-0.12672867	0.253703099	0.7712979	0.831316362	0.11002	0	15	8	29	9	28	20	22	11	30	25
ENSMUSG00000065987	chr8	Cd209b	3917655	3918827	2115	-0.13530877	2.711794677	0.7717362	0.831684355	0.2478	0	73	138	16	47	212	193	125	89	132	108
ENSMUSG00000021495	chr13	Fam193b	5.6E+07	5.6E+07	4338	-0.06179303	3.941867038	0.7719108	0.831808632	0.05388	0	226	233	205	206	276	432	257	192	292	398
ENSMUSG00000090523	chr18	Gypc	3.3E+07	3.3E+07	2331	0.064289789	5.163376633	0.7720142	0.831856126	0.05802	0	455	289	664	340	1014	907	998	525	715	673
ENSMUSG00000086350	chr1	B230369F24Rik	1.8E+08	1.8E+08	2560	-0.09248014	0.473548567	0.7724643	0.832277165	0.07174	0	14	17	27	23	19	31	26	18	24	30
ENSMUSG00000011752	chr19	Pgam1	4.2E+07	4.2E+07	1831	-0.08637962	3.631387239	0.7725931	0.832280491	0.09705	0	191	104	143	109	445	313	274	159	239	265
ENSMUSG00000026418	chr1	Tnni1	1.4E+08	1.4E+08	3600	0.323317957	6.773564867	0.7725835	0.832280491	1.39821	0	44	3	3978	3992	3	1976	586	2155	890	6755
ENSMUSG00000032842	chr17	Abcc10	4.6E+07	4.6E+07	6856	0.072323228	2.042444721	0.7727047	0.832280491	0.05587	0	56	33	84	51	79	95	79	60	91	102
ENSMUSG00000080059	chr4	Rps19-ps3	1.5E+08	1.5E+08	426	0.111587143	0.428942744	0.772679	0.832280491	0.07907	0	17	14	22	15	22	40	18	18	25	33
ENSMUSG00000020720	chr11	Psmd12	1.1E+08	1.1E+08	2649	-0.05317262	6.84536171	0.7731064	0.832649183	0.03992	0	1655	1191	2328	1821	1939	2633	2521	1899	2301	2288
ENSMUSG00000025377	chr11	Enthd2	1.2E+08	1.2E+08	3329	0.06346734	3.072524829	0.773887	0.833402103	0.04807	0	99	85	179	120	141	199	202	99	218	173
ENSMUSG00000079362	chr5	Gbp6	1.1E+08	1.1E+08	7842	-0.10599345	3.285252949	0.7739581	0.833402103	0.15203	0	111	74	305	147	156	427	200	63	84	245
ENSMUSG00000083044	chr4	Gm12416	8.4E+07	8.4E+07	1008	0.107730371	0.11906926	0.7739837	0.833402103	0.14536	0	8	5	26	17	18	10	17	20	23	32
ENSMUSG00000020042	chr10	Btbd11	8.5E+07	8.5E+07	10033	-0.09742529	0.786659602	0.7742817	0.833658937	0.0864	0	21	25	37	18	25	33	23	30	36	38
ENSMUSG00000097616	chr6	1110019D14Rik	1.4E+07	1.4E+07	1722	-0.07593466	1.587240747	0.7743859	0.833707131	0.05979	0	51	36	47	46	42	77	63	39	57	59
ENSMUSG00000032044	chr9	Rpusd4	3.5E+07	3.5E+07	2647	-0.05943542	3.525758817	0.7747407	0.834025095	0.04179	0	162	100	265	185	189	312	253	175	198	228
ENSMUSG00000038058	chr6	Nod1	5.5E+07	5.5E+07	4415	0.05244627	4.184989101	0.7750969	0.834301506	0.03632	0	231	177	378	218	371	495	438	234	398	372
ENSMUSG00000041329	chr11	Atp1b2	7E+07	7E+07	4085	-0.07640564	8.769114862	0.7751164	0.834301506	0.08543	0	8441	6104	4072	6259	7634	8783	8037	7262	11946	7505
ENSMUSG00000034403	chrX	Pja1	9.9E+07	9.9E+07	3324	0.047621582	4.551938192	0.7754181	0.834562132	0.02978	0	319	265	408	291	463	614	475	391	522	456
ENSMUSG00000024570	chr18	Rbfa	8E+07	8E+07	1377	-0.04543737	5.095534991	0.7758204	0.834674886	0.02776	0	446	354	696	565	588	778	675	523	775	724
ENSMUSG00000028952	chr4	Zbtb48	1.5E+08	1.5E+08	3199	0.088003706	1.742492705	0.7758075	0.834674886	0.06865	0	31	34	68	56	51	82	74	35	79	81
ENSMUSG00000031586	chr8	Rbpms	3.4E+07	3.4E+07	4022	0.065467799	3.801171719	0.7757633	0.834674886	0.05828	0	175	139	197	147	387	358	246	217	307	341
ENSMUSG00000035754	chr10	Wdr18	8E+07	8E+07	2954	-0.04973969	5.387788609	0.7757988	0.834674886	0.03437	0	540	435	802	712	758	836	989	613	1000	813
ENSMUSG00000037949	chr9	Ano10	1.2E+08	1.2E+08	2599	-0.04936682	5.271005796	0.7756893	0.834674886	0.03284	0	541	374	687	562	852	869	728	646	856	799
ENSMUSG00000057409	chr17	Zfp53	2.1E+07	2.1E+07	2058	0.11352537	1.1545689	0.7763849	0.835218184	0.10211	0	34	27	24	27	39	70	28	34	62	35
ENSMUSG00000026873	chr2	Phf19	3.5E+07	3.5E+07	5036	0.104490944	0.289151416	0.7766224	0.835409578	0.10933	0	7	7	30	20	20	24	21	16	32	26
ENSMUSG00000028917	chr4	Plekhm2	1.4E+08	1.4E+08	5186	-0.05489934	5.238622401	0.7769754	0.835725235	0.0422	0	502	341	930	699	486	871	813	544	789	826
ENSMUSG00000051768	chr7	Xrcc1	2.5E+07	2.5E+07	2155	0.050642855	4.145585177	0.7775818	0.8363133	0.0354	0	218	166	387	261	303	408	334	261	428	428
ENSMUSG00000018326	chr2	Ywhab	1.6E+08	1.6E+08	3382	0.076908587	6.861722934	0.7776752	0.83634972	0.08813	0	1581	1097	1201	1227	3647	3342	2062	2168	2386	2345
ENSMUSG00000086287	chr18	Gm15972	2.4E+07	2.4E+07	418	0.116357703	-0.21077983	0.7777912	0.836410314	0.10346	0	9	5	12	9	21	14	12	15	18	21
ENSMUSG00000032120	chr9	C2cd2l	4.4E+07	4.4E+07	4334	-0.05725297	3.970040021	0.7779998	0.836506295	0.0425	0	171	163	304	225	366	297	361	208	368	352
ENSMUSG00000056167	chr9	Cnot10	1.1E+08	1.1E+08	2979	0.045172296	4.592658941	0.7779687	0.836506295	0.02677	0	326	253	429	384	403	607	536	355	553	491
ENSMUSG00000031608	chr8	Galnt7	5.8E+07	5.8E+07	5253	0.075364357	2.461004818	0.7780625	0.836509613	0.07035	0	88	48	121	59	89	135	178	76	96	95
ENSMUSG00000028277	chr4	Ube2j1	3.3E+07	3.3E+07	3530	-0.04719181	5.174326526	0.779013	0.837467313	0.03078	0	432	361	723	528	789	858	835	541	739	710
ENSMUSG00000098702	chr18	1500015A07Rik	6.2E+07	6.2E+07	2296	0.09175218	1.240094585	0.7792284	0.837634665	0.1137	0	17	12	72	32	42	52	46	42	50	48
ENSMUSG00000034563	chr9	Ccpg1	7.3E+07	7.3E+07	7497	-0.05508593	6.982719887	0.77956	0.837926986	0.04567	0	1963	1164	2711	2120	1916	2989	3027	1818	2306	2786
ENSMUSG00000085348	chr11	Gm12300	6.7E+07	6.7E+07	2027	0.195722012	4.732138273	0.7799755	0.83830934	0.56971	0	83	64	1349	417	192	62	526	75	1123	1191
ENSMUSG00000005936	chr17	Kctd20	2.9E+07	2.9E+07	4379	0.047060834	5.607576515	0.7801972	0.838457023	0.03223	0	718	517	836	660	905	1241	1064	769	952	1113
ENSMUSG00000020397	chr11	Med7	4.6E+07	4.6E+07	2871	0.058435812	3.82788808	0.7802613	0.838457023	0.04558	0	168	165	215	270	215	285	280	266	302	335
ENSMUSG00000038256	chr3	Bcl9	9.7E+07	9.7E+07	8285	-0.0700744	2.83064653	0.7802923	0.838457023	0.0586	0	73	65	124	144	147	176	135	97	132	174
ENSMUSG00000083179	chr4	Gm12693	9.5E+07	9.5E+07	483	-0.07030133	1.61193386	0.7803905	0.838498335	0.06203	0	48	29	59	48	46	80	72	35	48	68
ENSMUSG00000000402	chrX	Egfl6	1.7E+08	1.7E+08	2704	-0.12106093	0.441903847	0.7812819	0.839391796	0.16991	0	25	18	18	19	16	54	19	20	7	27
ENSMUSG00000061787	chr7	Rps17	8.1E+07	8.1E+07	1274	0.054885608	7.706207745	0.7814126	0.839458739	0.04636	0	3198	2392	3684	2954	3147	5493	3774	3598	4580	4534

ENSMUSG00000072653	chr6	Zfp783	4.8E+07	4.8E+07	6848	-0.1175174	1.446365248	0.7814639	0.839458739	0.17481	0	68	33	24	18	59	60	33	55	33	75
ENSMUSG00000035152	chr11	Ap2b1	8.3E+07	8.3E+07	8755	-0.04819958	5.740714076	0.7816922	0.839639667	0.03508	0	722	606	946	945	876	1327	1134	823	1127	1039
ENSMUSG00000027999	chr3	Pla2g12a	1.3E+08	1.3E+08	1654	-0.09848301	5.94121251	0.7820053	0.839911695	0.14808	0	495	303	2373	1307	683	1070	1570	824	879	1816
ENSMUSG00000029592	chr5	Usp30	1.1E+08	1.1E+08	3372	-0.05221818	3.847485988	0.7824583	0.840333845	0.03529	0	183	152	325	215	242	285	322	226	297	318
ENSMUSG00000045005	chr1	Fzd5	6.5E+07	6.5E+07	6915	-0.09169501	1.982532184	0.782762	0.840595638	0.09041	0	34	26	114	59	84	102	81	47	70	91
ENSMUSG00000006024	chr7	Napa	1.6E+07	1.6E+07	3786	-0.0539866	6.911850713	0.7830125	0.840735877	0.04561	0	2049	1415	1859	1617	2256	2774	2344	1707	2750	2706
ENSMUSG00000020267	chr11	Hint1	5.5E+07	5.5E+07	872	0.054395941	7.23551346	0.7829707	0.840735877	0.04599	0	2155	1810	2521	2122	2471	3938	2681	2639	3361	3213
ENSMUSG00000029657	chr5	Hsph1	1.5E+08	1.5E+08	7042	-0.06346195	6.608227819	0.7834767	0.841105607	0.06252	0	1229	913	3071	1188	1436	2521	2277	1469	1806	1863
ENSMUSG00000080746	chr4	Rpsa-ps12	1.5E+08	1.5E+08	892	0.081856859	0.590445623	0.7834223	0.841105607	0.06759	0	19	12	29	20	24	33	26	20	34	36
ENSMUSG00000027349	chr2	Fam98b	1.2E+08	1.2E+08	3390	-0.04244192	4.639796939	0.7845024	0.84214224	0.02584	0	341	268	442	386	482	568	536	360	539	540
ENSMUSG00000027465	chr2	Tbc1d20	1.5E+08	1.5E+08	4171	0.059304676	5.950894696	0.7849059	0.842446422	0.05598	0	732	522	1014	713	1775	1531	1380	951	1325	1367
ENSMUSG00000029059	chr4	Fam213b	1.5E+08	1.5E+08	1027	-0.0571032	6.93806925	0.7848664	0.842446422	0.05154	0	1749	1334	2132	1576	2777	2335	2439	1943	3309	2318
ENSMUSG00000021974	chr14	Fgf9	5.8E+07	5.8E+07	4266	0.10760425	1.339099779	0.7850011	0.842484145	0.1688	0	17	11	83	51	24	58	51	36	39	76
ENSMUSG00000022544	chr16	Fam86	5244152	5245385	2649	0.052701683	3.492943408	0.7859019	0.843386339	0.03765	0	154	111	201	145	229	275	262	155	263	231
ENSMUSG00000098666	chr14	Mir6950	7E+07	7E+07	73	0.136429927	0.197902391	0.7860835	0.843516773	0.1445	0	9	17	13	15	19	44	31	15	11	14
ENSMUSG00000039221	chr3	Rpl22l1	2.9E+07	2.9E+07	1989	-0.04841065	5.921139792	0.7865272	0.843928235	0.03691	0	926	661	1088	852	1147	1625	1158	1001	1240	1139
ENSMUSG00000023723	chr11	Mrps23	8.8E+07	8.8E+07	1560	0.052150247	6.659316868	0.7867365	0.844088316	0.04402	0	1271	928	2352	1540	1585	2253	2380	1597	2097	2322
ENSMUSG00000038644	chr7	Pold1	4.5E+07	4.5E+07	4860	0.064118254	2.7090219	0.7872318	0.844555099	0.0586	0	89	49	166	98	87	145	146	104	143	142
ENSMUSG00000063296	chr15	Tmem117	9.5E+07	9.5E+07	2781	-0.04805366	4.965985024	0.7873472	0.844614318	0.03637	0	493	372	567	527	405	641	783	498	641	599
ENSMUSG00000070469	chr7	Adamtsl3	8.2E+07	8.2E+07	7732	0.064945741	2.843106813	0.7875142	0.84472879	0.05257	0	94	80	141	83	129	234	160	97	132	139
ENSMUSG00000028271	chr3	Gtf2b	1.4E+08	1.4E+08	1271	-0.04779236	4.00761592	0.7879575	0.845075129	0.03294	0	239	192	292	215	289	397	328	283	295	316
ENSMUSG00000032194	chr9	Kank2	2.2E+07	2.2E+07	4853	0.047697273	5.56017132	0.7879377	0.845075129	0.03534	0	555	560	742	746	890	1210	1024	747	1049	940
ENSMUSG00000022329	chr15	Stk3	3.5E+07	3.5E+07	3237	0.068740717	2.479582506	0.7885031	0.845595527	0.06249	0	89	60	82	54	120	128	125	106	103	112
ENSMUSG00000028133	chr3	Rwdd3	1.2E+08	1.2E+08	5063	0.064414834	2.359572958	0.7888555	0.845908808	0.05348	0	69	52	87	65	102	136	83	93	107	110
ENSMUSG00000055745	chr15	Ldoc1l	8.5E+07	8.5E+07	4426	0.05581127	3.310818866	0.7891428	0.846152218	0.04555	0	148	98	217	112	164	208	254	159	225	188
ENSMUSG00000022558	chr15	Mroh1	7.6E+07	7.6E+07	16533	0.055944487	4.684820901	0.7894578	0.846425231	0.0507	0	251	205	654	455	406	585	658	306	595	600
ENSMUSG00000061666	chr11	Gdpd1	8.7E+07	8.7E+07	2336	-0.07448565	2.643812941	0.7895614	0.846471627	0.0791	0	104	55	179	71	80	148	155	65	113	151
ENSMUSG00000068739	chr3	Sars	1.1E+08	1.1E+08	3653	-0.05451309	6.684409168	0.7899611	0.846835378	0.04899	0	1211	927	2453	1793	1759	2121	2162	1411	2306	2481
ENSMUSG00000035086	chr11	Becn1	1E+08	1E+08	7065	-0.04639863	6.008234456	0.7902775	0.846991084	0.03536	0	922	736	1206	901	1194	1400	1458	950	1310	1445
ENSMUSG00000038984	chr15	Tspyl5	3.4E+07	3.4E+07	4008	0.097567644	1.584436245	0.7902691	0.846991084	0.08763	0	44	46	31	27	57	73	62	46	58	71
ENSMUSG00000085396	chrX	Firre	5.1E+07	5.1E+07	1439	-0.10021456	1.4987785	0.7902875	0.846991084	0.15525	0	49	61	30	31	26	73	49	32	40	84
ENSMUSG00000081600	chr11	Gm12286	6.3E+07	6.3E+07	1002	0.093105388	0.943940004	0.7903868	0.847032779	0.08148	0	19	20	34	33	27	48	29	40	43	31
ENSMUSG00000025938	chr1	Slco5a1	1.3E+07	1.3E+07	13137	0.05943998	5.281208994	0.7906764	0.847278401	0.05864	0	501	350	959	702	406	821	1002	743	637	849
ENSMUSG00000033128	chr15	Gga1	7.9E+07	7.9E+07	3034	-0.05133205	6.033367908	0.7911106	0.847614163	0.04337	0	799	616	1408	1134	1189	1338	1492	854	1603	1407
ENSMUSG00000062861	chr7	Zfp28	6383318	6383601	4142	-0.07185627	1.923231519	0.7910516	0.847614163	0.07186	0	50	47	96	48	46	111	78	48	74	67
ENSMUSG00000032571	chr9	Pik3r4	1.1E+08	1.1E+08	9660	-0.04973512	4.192659359	0.7913831	0.847841373	0.03582	0	223	170	395	334	303	437	423	293	338	361
ENSMUSG00000029034	chr4	Cpsf3l	1.6E+08	1.6E+08	3067	0.043822501	4.394458901	0.7914909	0.84789214	0.02926	0	304	202	388	303	380	515	431	302	513	452
ENSMUSG00000025825	chr5	Iscu	1.1E+08	1.1E+08	2176	0.050709625	6.559568284	0.7916928	0.848043574	0.04356	0	1272	858	2033	1370	1623	1920	2428	1365	2139	2108
ENSMUSG00000028771	chr5	Ptpn12	2.1E+07	2.1E+07	3509	-0.04770493	4.223268103	0.7922163	0.848539549	0.03401	0	235	189	368	306	351	416	508	276	356	344
ENSMUSG00000048503	chr9	Tmem136	4.3E+07	4.3E+07	3500	-0.08509557	1.821222027	0.7923117	0.848577012	0.0858	0	64	24	81	33	74	87	86	50	50	74
ENSMUSG00000017300	chr2	Tnnc2	1.6E+08	1.6E+08	800	0.054911263	13.32231292	0.7926933	0.848920797	0.05228	0	160999	122074	159327	135681	173169	216353	205980	160593	268558	226442
ENSMUSG00000020228	chr10	Helb	1.2E+08	1.2E+08	5011	-0.07267625	2.887016546	0.7927539	0.848920871	0.07209	0	115	46	205	113	109	203	170	102	130	140
ENSMUSG00000058254	chrX	Tspan7	1E+07	1E+07	7067	0.048688368	6.763622663	0.7935746	0.84973485	0.04064	0	1569	1129	2084	1601	1731	2378	2602	1623	2589	2266
ENSMUSG00000037686	chr12	Aspg	1.1E+08	1.1E+08	2732	-0.16737657	0.099449104	0.7936653	0.849767118	0.35309	0	26	10	3	2	36	24	13	7	36	16
ENSMUSG00000042873	chr6	Lhfpl4	1.1E+08	1.1E+08	4762	-0.1186883	0.057735797	0.7937724	0.849816932	0.13165	0	7	20	13	11	21	26	14	16	12	25
ENSMUSG00000002833	chr17	Hdgfrp2	5.6E+07	5.6E+07	2251	0.042920226	4.963405071	0.7940842	0.85008587	0.03044	0	403	299	660	522	463	734	654	496	711	673
ENSMUSG00000032744	chr4	Heyl	1.2E+08	1.2E+08	5113	-0.05206368	3.839825772	0.794167	0.850109662	0.03944	0	147	150	326	200	301	353	302	208	301	290
ENSMUSG00000025137	chr11	Pcyt2	1.2E+08	1.2E+08	4346	-0.04825198	5.129234116	0.7943874	0.850192959	0.03667	0	409	288	811	573	700	746	750	515	758	790
ENSMUSG00000039683	chr5	Sdk1	1.4E+08	1.4E+08	11087	0.087870126	1.547767984	0.7943812	0.850192959	0.08132	0	39	40	29	37	57	74	51	37	70	71
ENSMUSG00000054920	chr5	Klhl5	6.5E+07	6.5E+07	4866	-0.07361771	3.307492272	0.7944267	0.850192959	0.08217	0	136	101	133	88	322	263	194	158	174	202
ENSMUSG00000020918	chr11	Kat2a	1E+08	1E+08	3480	-0.04457044	4.317605223	0.7946289	0.850228039	0.03206	0	263	262	346	291	348	456	412	346	418	376
ENSMUSG00000021124	chr12	Vti1b	7.9E+07	7.9E+07	1612	0.046378425	6.168597498	0.7945739	0.850228039	0.03678	0	1031	741	1234	1104	1256	1813	1653	1166	1536	1403
ENSMUSG00000097617	chr9	Gm10687	4.4E+07	4.4E+07	1651	-0.1517993	0.911845478	0.7946413	0.850228039	0.30838	0	14	17	8	16	93	49	12	35	41	34
ENSMUSG00000026374	chr1	Tsn	1.2E+08	1.2E+08	9046	-0.0438903	5.712622369	0.7949512	0.85049468	0.03291	0	771	598	965	736	959	1282	1199	795	1021	1063
ENSMUSG00000005360	chr15	Slc1a3	8634124	8636339	8537	-0.14799097	3.036646895	0.7950635	0.850549978	0.36808	0	140	93	18	22	385	257	72	150	149	164
ENSMUSG00000030079	chr6	Ruvbl1	8.8E+07	8.8E+07	1899	0.045101695	4.385152032	0.7955092	0.850961879	0.03194	0	292	238	369	313	330	444	431	371	504	415
ENSMUSG00000086784	chr7	Isoc2a	4877053	4877193	1088	0.050814065	5.179024881	0.7956871	0.851087234	0.04329	0	602	384	541	476	673	904	526	573	890	912
ENSMUSG00000026887	chr2	Mrrf	3.6E+07	3.6E+07	2853	-0.04515301	4.359225349	0.795846	0.851192367	0.03178	0	265	223	430	340	322	415	462	329	448	418
ENSMUSG00000000120	chr11	Ngfr	9.6E+07	9.6E+07	3446	0.142946733	1.045804965	0.7960296	0.851258859	0.24912	0	23	39	5	42	20	51	27	34	70	31
ENSMUSG00000026755	chr2	Arpc5l	3.9E+07	3.9E+07	4438	0.04761823	6.934268482	0.7960071	0.851258859	0.04	0	1737	1262	2372	1836	1939	2954	2586	2057	2565	2674
ENSMUSG00000032551	chr9	1110059G10Rik	1.2E+08	1.2E+08	3361	0.05641552	2.989975831	0.7961844	0.851359455	0.04635	0	127	85	136	97	136	206	161	148	154	153
ENSMUSG00000021365	chr13	Nedd9	4.1E+07	4.1E+07	4712	0.060196548	3.60771726	0.7962956	0.8514135	0.06034	0	111	100	305	202	211	309	334	149	210	298
ENSMUSG00000005716	chr15	Pvalb	7.8E+07	7.8E+07	1041	-0.07792773	13.35732035	0.7964509	0.851433034	0.10902	0	224297	161413	90664	100349	200054	217742	177369	184819	274695	188805
ENSMUSG00000041477	chr6	Dcp1b	1.2E+08	1.2E+08	6339	-0.06994126	2.008854996	0.7963915	0.851433034	0.06709	0	52	39	99	43	79	93	83	48	102	74
ENSMUSG00000047067	chr1	Dusp28	9.3E+07	9.3E+07	1314	0.040720001	4.672331362	0.796496	0.851433034	0.02758	0	339	243	516	403	419	595	519	398	566	591
ENSMUSG00000015980	chr7	Lrrc27	1.4E+08	1.4E+08	3637	-0.12215044	1.085049609	0.7967023	0.851487485	0.20639	0	28	25	10	16	82	46	31	43	33	43
ENSMUSG00000018199	chr1	Trove2	1.4E+08	1.4E+08	9541	-0.05532867	3.207107722	0.7967249	0.851487485	0.04328	0	143	78	194	145	157	214	232	136	168	182

ENSMUSG00000029394	chr5	Cdk2ap1	1.2E+08	1.2E+08	1945	-0.04353545	5.527752489	0.7967898	0.851487485	0.03286	0	667	559	820	658	817	982	1020	733	1025	920
ENSMUSG00000033845	chr1	Mrpl15	4773206	4774516	8487	-0.04793102	6.035562487	0.7967772	0.851487485	0.0395	0	893	591	1461	1064	1145	1462	1304	1048	1428	1410
ENSMUSG00000021285	chr12	Ppp1r13b	1.1E+08	1.1E+08	4658	0.050204849	3.626634446	0.7972332	0.851896493	0.04264	0	170	102	295	166	203	338	276	206	235	239
ENSMUSG00000039853	chr4	Trim14	4.6E+07	4.6E+07	4338	0.149129609	-0.13892854	0.797296	0.851898611	0.12075	0	9	14	6	7	20	20	21	13	14	19
ENSMUSG00000028927	chr4	Padi2	1.4E+08	1.4E+08	5013	0.051926738	7.226493312	0.7976165	0.852176146	0.0486	0	2033	1400	2942	2573	2293	2953	3923	2194	3178	3564
ENSMUSG00000083833	chr5	Gm13841	1.2E+08	1.2E+08	483	0.124572627	0.596309175	0.7979612	0.85247957	0.11869	0	26	20	11	18	23	42	19	19	32	41
ENSMUSG00000015961	chr1	Adss	1.8E+08	1.8E+08	4531	0.053166187	3.679329318	0.7980644	0.852524841	0.04183	0	168	150	187	183	252	393	236	197	249	277
ENSMUSG00000058240	chr16	Cryzl1	9.2E+07	9.2E+07	4353	0.048219909	3.921566452	0.7988358	0.853283943	0.03387	0	236	182	247	186	259	374	337	224	327	330
ENSMUSG00000052712	chr17	BC004004	2.9E+07	2.9E+07	6017	0.046620809	6.671507808	0.7989817	0.85337481	0.03939	0	1472	996	1947	1561	1672	2472	2045	1586	2329	2304
ENSMUSG00000051177	chr2	Plcb1	1.3E+08	1.3E+08	8685	-0.08380308	1.651276339	0.7990811	0.853415978	0.10331	0	46	45	37	27	79	86	49	59	60	49
ENSMUSG00000046671	chr4	Mtfr1l	1.3E+08	1.3E+08	5370	-0.04832561	7.167911131	0.7992737	0.853556594	0.04265	0	1977	1530	3019	2278	2352	3077	3432	2144	3116	2884
ENSMUSG00000043716	chr1	Rpl7	1.6E+07	1.6E+07	2687	0.050913782	8.368693908	0.7995229	0.85375781	0.04772	0	5061	4123	5162	4678	5105	8996	6708	5413	6597	7217
ENSMUSG00000064372	chrMT	mt-Tp	15356	15422	67	-0.16053911	1.821184147	0.799646	0.853824197	0.40088	0	10	3	186	54	57	80	33	58	43	115
ENSMUSG00000022338	chr15	Eny2	4.4E+07	4.4E+07	2429	-0.0435509	4.771942869	0.8003622	0.854458845	0.03187	0	399	286	583	427	410	702	516	474	497	578
ENSMUSG00000042506	chr11	Usp22	6.1E+07	6.1E+07	4886	-0.0405743	4.565474721	0.8003517	0.854458845	0.02789	0	353	256	382	375	443	550	530	363	515	452
ENSMUSG00000036854	chr7	Hspb6	3.1E+07	3.1E+07	2299	0.086433556	10.03525688	0.8006635	0.854715441	0.13973	0	9873	4064	29334	26985	11059	26244	20362	14961	21656	29612
ENSMUSG00000039623	chr5	Ap5z1	1.4E+08	1.4E+08	3817	0.057123007	2.740724263	0.8009693	0.85497683	0.04867	0	99	58	106	102	128	180	152	84	130	159
ENSMUSG00000030553	chr7	Pgpep1l	6.8E+07	6.8E+07	955	0.094873738	0.655517859	0.8016464	0.855629273	0.11379	0	29	12	34	10	24	40	34	32	19	30
ENSMUSG00000035545	chr7	Leng8	4137039	4137122	6391	0.062772602	5.843534243	0.8018246	0.855629273	0.07155	0	700	920	693	592	1212	1515	1131	731	1053	1729
ENSMUSG00000045287	chr11	Rtn4rl1	7.5E+07	7.5E+07	3525	-0.12574362	2.327143886	0.8017823	0.855629273	0.26488	0	60	44	33	17	255	140	72	78	83	114
ENSMUSG00000063458	chr14	1700112E06Rik	2.2E+07	2.2E+07	2714	0.075567001	1.603411526	0.8017621	0.855629273	0.06703	0	44	32	37	48	53	79	49	42	75	68
ENSMUSG00000032584	chr9	Mst1r	1.1E+08	1.1E+08	5007	0.116327927	1.732082263	0.8025711	0.856360789	0.20345	0	28	41	21	20	127	112	58	54	50	75
ENSMUSG00000042660	chr18	Wdr55	3.7E+07	3.7E+07	1498	-0.04875112	3.724205666	0.8026762	0.856407751	0.04313	0	207	179	179	174	251	337	271	204	279	247
ENSMUSG00000037260	chr8	Hgsnat	2.6E+07	2.6E+07	2679	-0.0436384	4.062970995	0.8027675	0.856439982	0.03358	0	272	193	268	235	300	412	382	247	358	303
ENSMUSG00000047710	chr8	Champ1	1.4E+07	1.4E+07	4040	-0.04770285	3.722180124	0.8031685	0.856802685	0.03864	0	196	160	223	198	222	335	290	234	211	258
ENSMUSG00000018446	chr11	C1qbp	7.1E+07	7.1E+07	2826	-0.04754073	6.29287416	0.8037806	0.85736808	0.04226	0	975	755	1738	1365	1303	1722	1607	1289	1538	1786
ENSMUSG00000025577	chr11	Cbx2	1.2E+08	1.2E+08	4257	0.087172995	1.066946502	0.8038208	0.85736808	0.07924	0	28	19	26	39	33	53	29	31	51	48
ENSMUSG00000018239	chr11	Zcchc10	5.3E+07	5.3E+07	1391	0.058280706	2.855401637	0.8039082	0.857396078	0.05174	0	104	75	111	104	135	157	159	140	115	173
ENSMUSG00000020639	chr12	Pfn4	4769295	4770269	1306	0.124041974	-0.06285066	0.8043033	0.857752298	0.11724	0	18	5	21	10	8	27	13	17	17	17
ENSMUSG00000037376	chr2	Trmt6	1.3E+08	1.3E+08	5384	0.050581556	3.638204971	0.8050363	0.858468692	0.03997	0	193	146	173	188	204	307	275	222	239	251
ENSMUSG00000092021	chr5	Gbp11	1.1E+08	1.1E+08	2692	0.208292731	0.007172392	0.8053731	0.858762577	0.60193	0	15	13	0	1	32	58	6	14	6	19
ENSMUSG00000061024	chr1	Rrs1	9545408	9547455	2048	-0.04774519	3.896934214	0.8059848	0.859349457	0.03648	0	219	126	300	256	257	354	289	239	274	350
ENSMUSG00000019718	chr12	L3hypdh	7.2E+07	7.2E+07	2679	0.12060475	1.53097156	0.8060714	0.859376466	0.23029	0	40	31	14	13	106	92	35	47	60	67
ENSMUSG00000028344	chr4	Invs	4.8E+07	4.8E+07	11431	0.07940631	1.658803841	0.8065207	0.859790214	0.0797	0	54	27	34	46	63	97	71	49	62	48
ENSMUSG00000035048	chr9	Anapc13	1E+08	1E+08	2377	-0.04140871	5.569386064	0.8065908	0.859799589	0.03252	0	725	520	826	688	885	1115	925	773	1022	989
ENSMUSG00000059878	chr6	Zfp422	1.2E+08	1.2E+08	3625	0.052814325	3.478445795	0.806698	0.859848446	0.04436	0	172	134	171	123	215	295	223	179	210	260
ENSMUSG00000042210	chr9	Abhd14a	1.1E+08	1.1E+08	2087	0.046276395	3.659509577	0.8068786	0.859910308	0.03473	0	168	147	225	164	230	279	287	198	294	259
ENSMUSG00000052395	chr14	Rft1	3.1E+07	3.1E+07	4355	-0.05958198	3.054230758	0.8068754	0.859910308	0.05657	0	126	67	145	102	212	230	188	112	153	160
ENSMUSG00000056144	chr7	Trim34a	1E+08	1E+08	4255	-0.09047007	0.759228447	0.8072806	0.860273298	0.14126	0	26	16	29	18	36	50	49	10	14	42
ENSMUSG00000000378	chr11	Ccm2	6546887	6547029	3666	0.04084041	4.783119957	0.8076495	0.860535685	0.03002	0	371	293	458	412	521	660	663	394	679	503
ENSMUSG00000030556	chr7	Lrrc28	6.8E+07	6.8E+07	4834	0.040878337	4.165718557	0.8076412	0.860535685	0.03131	0	249	158	327	269	352	407	402	286	407	371
ENSMUSG00000014313	chr15	Cox6c	3.6E+07	3.6E+07	3567	-0.05147482	8.873003854	0.8082292	0.86108791	0.05357	0	6712	3949	11720	7721	6977	10982	9977	7688	9077	9856
ENSMUSG00000041840	chr18	Haus1	7.8E+07	7.8E+07	1004	-0.05027875	3.335140019	0.8085325	0.861345635	0.04428	0	141	115	189	120	211	290	185	150	179	221
ENSMUSG00000025076	chr19	Casp7	5.6E+07	5.6E+07	2350	-0.05984561	2.403479884	0.8086618	0.861352504	0.05596	0	87	52	85	67	113	149	117	63	110	96
ENSMUSG00000095597	chrX	Gm6472	1.5E+08	1.5E+08	651	-0.04242328	4.912153482	0.8086014	0.861352504	0.03612	0	445	389	508	441	490	921	671	443	488	579
ENSMUSG00000041747	chr13	Utp15	9.8E+07	9.8E+07	4071	-0.05410899	2.891935793	0.8087838	0.861417117	0.04704	0	100	83	136	102	147	194	137	132	146	131
ENSMUSG00000056328	chr11	Myh1	6.7E+07	6.7E+07	6353	-0.10257787	12.71687781	0.8092747	0.861874492	0.21456	0	74775	14185	247699	176207	54815	168062	156719	88593	132390	134974
ENSMUSG00000038530	chr1	Rgs4	1.7E+08	1.7E+08	3098	0.060852704	3.685045499	0.8093758	0.86191676	0.07603	0	146	79	412	144	225	341	299	197	223	298
ENSMUSG00000047819	chr3	Tigd4	8.5E+07	8.5E+07	3459	0.059930044	4.188320994	0.8102812	0.862815413	0.06689	0	420	179	306	235	176	468	449	296	363	345
ENSMUSG00000019303	chr11	Psmc3ip	1E+08	1E+08	1818	-0.08508302	0.89326786	0.8103971	0.862873314	0.08491	0	36	19	40	22	19	43	33	28	30	42
ENSMUSG00000005718	chr16	Tfap4	4544661	4545747	2113	-0.08463216	2.128327087	0.8110607	0.863514341	0.12306	0	100	57	49	40	77	90	54	84	67	127
ENSMUSG00000032355	chr9	Mlip	7.7E+07	7.7E+07	8916	-0.05202701	6.454942834	0.8113284	0.863733764	0.05609	0	1237	981	1683	1809	969	1797	2039	1368	1863	1822
ENSMUSG00000038624	chr10	Nepn	5.2E+07	5.2E+07	1981	-0.13757029	0.35546733	0.8118238	0.864129934	0.15714	0	13	10	19	8	47	19	18	19	26	32
ENSMUSG00000082745	chr1	Gm15181	7.6E+07	7.6E+07	177	-0.07738756	0.847898718	0.8118178	0.864129934	0.12638	0	24	29	17	34	22	31	54	18	43	27
ENSMUSG00000001524	chr17	Gtf2h4	3.6E+07	3.6E+07	3313	-0.04790278	3.691309431	0.8119493	0.864198	0.04014	0	158	134	247	216	242	281	232	194	337	259
ENSMUSG00000020251	chr10	Glt8d2	8.3E+07	8.3E+07	5773	0.097350439	1.269255898	0.8127454	0.864979691	0.1322	0	28	38	26	15	58	71	40	26	64	50
ENSMUSG00000025887	chr9	Casp12	5345430	5345525	3840	0.067524891	3.465707976	0.8128901	0.865065766	0.09228	0	152	90	271	86	245	338	350	172	150	165
ENSMUSG00000097573	chr1	G730003C15Rik	5.9E+07	5.9E+07	2309	-0.13500402	0.032026071	0.8129497	0.865065766	0.11454	0	6	5	27	15	23	18	20	13	22	17
ENSMUSG00000001134	chrX	Uxt	2.1E+07	2.1E+07	1639	0.04427418	4.130080313	0.8131031	0.865163463	0.03583	0	282	198	290	234	283	406	316	304	413	378
ENSMUSG00000007739	chr11	Cct4	2.3E+07	2.3E+07	4201	0.043712098	6.810598812	0.8132216	0.865223862	0.03998	0	1647	1283	2058	1596	1739	2844	2413	1815	2325	2413
ENSMUSG00000028809	chr4	Srrm1	1.4E+08	1.4E+08	7299	-0.04204705	5.780687236	0.813357	0.86523669	0.03651	0	837	588	954	750	1112	1225	1086	792	1152	1363
ENSMUSG00000059810	chr4	Rgs3	6.3E+07	6.3E+07	10801	0.0549452	3.671578033	0.8133139	0.86523669	0.06005	0	198	113	213	119	318	389	220	212	237	282
ENSMUSG00000003868	chr7	Ruvbl2	4.5E+07	4.5E+07	2573	-0.03780409	4.695063863	0.8135383	0.86536393	0.02723	0	362	266	493	418	455	542	578	381	594	544
ENSMUSG00000047910	chr18	Pcdhb16	3.7E+07	3.7E+07	5225	0.104737014	0.46417834	0.8138581	0.865638419	0.08518	0	21	20	17	15	17	31	33	22	22	28
ENSMUSG00000023988	chr17	Bysl	4.8E+07	4.8E+07	3854	-0.03743213	4.985833468	0.8143196	0.865866674	0.02758	0	405	341	650	512	535	717	664	475	724	653
ENSMUSG00000026553	chr1	Copa	1.7E+08	1.7E+08	9427	-0.04306066	6.803388159	0.8142883	0.865866674	0.03959	0	1484	1195	2050	1880	2013	2916	2388	1636	2205	2327
ENSMUSG00000029086	chr5	Prom1	4.4E+07	4.4E+07	4517	-0.0615027	2.472414793	0.8143095	0.865866674	0.06908	0	96	66	105	67	84	147	116	79	68	147

ENSMUSG00000047921	chr15	Trappc9	7.3E+07	7.3E+07	6363	-0.0441885	5.559476668	0.8141631	0.865866674	0.03964	0	596	423	899	866	901	955	1027	689	1176	951
ENSMUSG00000026078	chr1	Pdcl3	3.9E+07	3.9E+07	4219	-0.0376454	5.214616276	0.8148122	0.866324756	0.02861	0	530	387	783	553	615	958	814	561	706	768
ENSMUSG00000027176	chr2	Cstf3	1E+08	1E+08	5879	0.053757111	3.134406981	0.8149118	0.866364969	0.04676	0	99	105	185	120	138	232	218	120	154	202
ENSMUSG00000057738	chr2	Sptan1	3E+07	3E+07	11428	0.045336388	6.340234806	0.8150165	0.866410646	0.04432	0	884	801	1648	1083	1775	2202	1657	1244	1618	1848
ENSMUSG00000028826	chr4	Tmem57	1.3E+08	1.3E+08	6744	-0.04137873	4.486626859	0.8154774	0.866834876	0.03187	0	317	201	417	316	502	509	497	323	491	468
ENSMUSG00000023153	chr4	Tmem52	1.6E+08	1.6E+08	1157	-0.05430755	6.305083197	0.8167526	0.868109001	0.06464	0	1046	797	1333	1678	1233	1248	1532	993	2129	2130
ENSMUSG00000092274	chr19	Neat1	5824708	5845478	20771	0.066226805	8.715493292	0.8167998	0.868109001	0.09723	0	6373	6121	4069	3875	9815	12833	7433	5526	7328	12235
ENSMUSG00000019494	chr5	Cops6	1.4E+08	1.4E+08	2525	-0.04132536	6.382941033	0.8169887	0.868243925	0.03722	0	1267	878	1475	1309	1489	1898	1850	1285	1780	1702
ENSMUSG00000063810	chr6	Alms1	8.6E+07	8.6E+07	9986	0.096203656	0.390719524	0.8173623	0.868575173	0.10587	0	22	9	17	19	21	40	20	17	15	38
ENSMUSG00000052512	chr7	Nav2	4.9E+07	4.9E+07	32073	0.054042147	4.207151416	0.8178353	0.869011965	0.06407	0	190	167	453	353	229	286	432	363	386	429
ENSMUSG00000022974	chr16	Paxbp1	9.1E+07	9.1E+07	5508	0.049869736	3.462037995	0.8179854	0.869105591	0.04357	0	142	137	190	143	196	337	223	172	185	243
ENSMUSG00000013822	chr9	Elof1	2.2E+07	2.2E+07	1092	0.039894329	4.868852259	0.818484	0.869569504	0.03236	0	430	347	472	359	556	719	579	484	707	561
ENSMUSG00000056313	chr8	1810011O10Rik	2.4E+07	2.4E+07	1805	0.053930633	3.9376061	0.8186689	0.869700046	0.06652	0	168	118	302	154	446	384	266	283	336	323
ENSMUSG00000002455	chr2	Prpf6	1.8E+08	1.8E+08	3859	-0.0407839	5.436357998	0.8189058	0.869885894	0.03565	0	519	424	905	743	785	950	976	570	929	1022
ENSMUSG00000000325	chr16	Arvcf	1.8E+07	1.8E+07	6425	0.041209207	4.197620176	0.8191819	0.870113234	0.03604	0	214	169	370	311	322	369	441	273	440	394
ENSMUSG00000031840	chr8	Rab3a	7.1E+07	7.1E+07	2226	0.039920147	5.120537046	0.8194222	0.870302545	0.03501	0	427	320	727	589	572	696	763	494	849	847
ENSMUSG00000041308	chr8	Sntb2	1.1E+08	1.1E+08	4423	0.070891852	2.25742641	0.8197177	0.870550546	0.08043	0	63	68	74	40	96	129	95	75	127	71
ENSMUSG00000015468	chr17	Notch4	3.5E+07	3.5E+07	8061	0.046299244	4.012835517	0.8198738	0.870650355	0.05012	0	159	124	368	229	369	355	306	274	351	392
ENSMUSG00000047911	chr14	Npm2	7.1E+07	7.1E+07	997	0.087492773	0.111736566	0.8202668	0.871001708	0.10784	0	7	12	20	13	20	11	22	17	26	26
ENSMUSG00000029152	chr5	Ociad1	7.3E+07	7.3E+07	4132	-0.04274459	7.240820484	0.8211518	0.871875527	0.04237	0	2302	1782	2740	2213	2514	3643	3195	2532	2953	3058
ENSMUSG00000003531	chr16	Dgcr6	1.8E+07	1.8E+07	2985	0.039488994	5.213456528	0.8216777	0.872367787	0.03582	0	446	324	668	563	834	798	808	535	895	860
ENSMUSG00000025854	chr5	Fam20c	1.4E+08	1.4E+08	4223	-0.04156872	4.766970542	0.8221243	0.872709899	0.03842	0	371	312	350	444	598	566	566	405	654	575
ENSMUSG00000054733	chr14	Msra	6.4E+07	6.4E+07	1862	-0.03795853	4.766135172	0.822091	0.872709899	0.02955	0	430	250	527	392	511	653	561	432	622	502
ENSMUSG00000088559	chr1	Mir1981	1.8E+08	1.8E+08	82	-0.08188971	0.805509516	0.8230404	0.873616242	0.08432	0	20	15	25	26	44	45	23	23	39	36
ENSMUSG00000078908	chr8	Mon1b	1.1E+08	1.1E+08	5156	0.050807082	2.836900716	0.8231135	0.873627722	0.04989	0	90	74	120	116	125	148	207	111	131	145
ENSMUSG00000056687	chr11	Gm11696	1.1E+08	1.1E+08	4250	0.105247688	0.422330891	0.8234003	0.873865937	0.16993	0	6	8	40	12	29	37	15	14	30	37
ENSMUSG00000064128	chr14	Cenpj	5.7E+07	5.7E+07	4363	-0.07194614	1.545416661	0.823746	0.874166715	0.08005	0	58	30	55	30	45	76	73	40	38	60
ENSMUSG00000020198	chr10	Ap3d1	8.1E+07	8.1E+07	4730	-0.03898302	5.697738311	0.8247473	0.875005633	0.03527	0	690	514	924	849	1049	1133	1249	712	1139	1093
ENSMUSG00000026083	chr1	Eif5b	3.8E+07	3.8E+07	9753	-0.04297212	7.149364765	0.8248137	0.875005633	0.04454	0	2120	1468	2824	2350	2182	2858	3323	2054	3038	3222
ENSMUSG00000028385	chr4	Snx30	6E+07	6E+07	7795	-0.04747424	3.030983413	0.8248485	0.875005633	0.05168	0	143	106	115	108	136	216	176	127	144	162
ENSMUSG00000031883	chr8	Car7	1E+08	1E+08	2459	0.072322193	1.361881032	0.8247091	0.875005633	0.08698	0	33	20	39	35	58	83	59	26	36	64
ENSMUSG00000034729	chr17	Mrps10	4.7E+07	4.7E+07	8079	-0.03537869	4.74184117	0.8246645	0.875005633	0.02775	0	395	320	486	364	471	637	529	460	540	546
ENSMUSG00000013973	chr1	Dedd	1.7E+08	1.7E+08	5861	0.036737983	5.217074356	0.8252497	0.875365102	0.03043	0	499	396	737	501	667	852	882	486	867	842
ENSMUSG00000038690	chr5	Atp5j2	1.5E+08	1.5E+08	1231	0.044288669	8.494081754	0.8255343	0.875536277	0.0482	0	4925	3257	7976	5868	5306	8246	7985	5757	8292	7598
ENSMUSG00000051510	chr11	Mafg	1.2E+08	1.2E+08	5613	-0.04001069	6.455563057	0.825536	0.875536277	0.03823	0	1200	896	1834	1274	1629	1949	2038	1314	1890	1780
ENSMUSG00000037020	chr7	Wdr62	3E+07	3E+07	5743	0.08701598	1.499540805	0.825791	0.875740532	0.15833	0	24	20	42	22	102	59	67	23	64	82
ENSMUSG00000025488	chr7	Cox8b	1.4E+08	1.4E+08	362	0.04345447	8.516488686	0.826148	0.876052933	0.04672	0	4868	3321	7594	5897	6115	7829	8762	5278	8280	8489
ENSMUSG00000038900	chr2	Rpl12	3.3E+07	3.3E+07	3598	0.044950602	7.400287877	0.8268179	0.876697007	0.04964	0	2475	2204	2758	2423	2463	4764	3203	2920	3519	3353
ENSMUSG00000039196	chr4	Orm1	6.3E+07	6.3E+07	775	-0.1858871	3.098702636	0.8272976	0.877139368	0.80779	0	169	65	2	2	478	229	45	198	211	109
ENSMUSG00000039376	chr14	Synpo2l	2.1E+07	2.1E+07	4629	0.047359667	7.89661462	0.8275013	0.877222718	0.05624	0	2938	2217	4704	4710	3323	4422	5885	3674	5626	5391
ENSMUSG00000096255	chr17	Dynlt1b	6430112	6430238	768	0.089234459	1.668117223	0.8274927	0.877222718	0.12268	0	48	47	25	42	54	125	51	42	45	73
ENSMUSG00000029089	chr5	Pacrgl	4.8E+07	4.8E+07	1464	0.074702417	1.106119008	0.8278324	0.877507389	0.07775	0	17	24	36	31	44	53	61	29	35	41
ENSMUSG00000097624	chr17	Gm5091	1.5E+07	1.5E+07	1179	-0.05366917	1.557323007	0.8279106	0.877523963	0.06528	0	50	37	41	34	54	62	65	40	68	54
ENSMUSG00000018340	chr11	Anxa6	5.5E+07	5.5E+07	2930	-0.04200048	8.140884745	0.8283642	0.877938328	0.04453	0	3580	2726	5497	4368	5963	6806	6351	4263	6175	5303
ENSMUSG00000098792	chr11	Gm27401	1.2E+08	1.2E+08	173	0.116369091	0.110996572	0.8284799	0.877994594	0.12433	0	5	14	22	18	11	32	27	13	13	21
ENSMUSG00000087589	chr1	D430040D24Rik	3.7E+07	3.7E+07	2830	0.077516126	0.558551028	0.8286367	0.878094475	0.09397	0	12	9	25	26	31	37	28	14	35	33
ENSMUSG00000000194	chr2	Gpr107	3.1E+07	3.1E+07	12766	0.03711121	5.586604618	0.828766	0.878165172	0.03319	0	700	484	826	799	778	1151	1115	743	1070	964
ENSMUSG00000059534	chr11	Uqcr10	4701973	4702220	584	0.041889826	8.07109616	0.8292898	0.878653761	0.04502	0	3680	2473	5701	4273	4258	6134	6104	4444	5807	5690
ENSMUSG00000029028	chr4	Lrrc47	1.5E+08	1.5E+08	3510	-0.04071519	5.271539053	0.8298776	0.87921011	0.03892	0	452	325	897	692	679	817	928	572	801	823
ENSMUSG00000039166	chr10	Akap7	2.5E+07	2.5E+07	4375	-0.05191859	3.58772598	0.8305042	0.879807529	0.05293	0	152	76	291	181	263	285	249	180	251	251
ENSMUSG00000032330	chr9	Cox7a2	8E+07	8E+07	754	-0.04416179	7.434084104	0.8310361	0.880238059	0.05042	0	2300	1389	4084	2988	2927	3719	4000	2556	3676	3709
ENSMUSG00000084941	chr11	Gm11944	3308996	3309323	873	-0.11164537	-0.08098188	0.8310156	0.880238059	0.09729	0	11	5	15	19	17	26	12	12	14	20
ENSMUSG00000059183	chr9	Mtfmt	6.5E+07	6.5E+07	3655	0.056993435	2.195313955	0.8311048	0.880244322	0.06783	0	71	35	91	46	98	127	114	70	73	92
ENSMUSG00000011877	chr11	Git1	7.7E+07	7.7E+07	4838	0.045259256	5.807867689	0.8314347	0.880448662	0.05359	0	618	415	1363	1004	923	1210	1428	733	1399	1164
ENSMUSG00000022787	chr16	Wdr53	3.2E+07	3.2E+07	1523	-0.04794143	2.937985856	0.8314536	0.880448662	0.04279	0	120	72	146	111	139	172	145	125	153	172
ENSMUSG00000026269	chr1	Rnpepl1	9.3E+07	9.3E+07	9467	-0.04109423	6.227777343	0.8317226	0.880448662	0.04328	0	903	712	1513	1294	1440	1556	1785	977	1749	1630
ENSMUSG00000027722	chr3	Spata5	3.7E+07	3.7E+07	3788	-0.04981885	3.144992205	0.8315497	0.880448662	0.04765	0	106	94	197	142	142	204	160	170	167	177
ENSMUSG00000028029	chr3	Aimp1	1.3E+08	1.3E+08	1122	0.039622776	6.324876804	0.8318471	0.880448662	0.03997	0	1214	956	1309	1148	1280	1893	1623	1267	1768	1856
ENSMUSG00000028982	chr4	Slc25a33	1.5E+08	1.5E+08	1887	0.042463115	3.589907813	0.8315127	0.880448662	0.04288	0	193	109	204	169	223	243	244	214	225	316
ENSMUSG00000045252	chr7	Zfp574	2.5E+07	2.5E+07	4236	-0.04620276	3.433805152	0.8319254	0.880448662	0.04527	0	119	108	199	178	234	225	217	150	274	227
ENSMUSG00000060579	chr14	Fhit	9550092	9550398	1491	0.092607713	0.030298981	0.8318913	0.880448662	0.07698	0	9	11	14	12	21	21	21	16	16	23
ENSMUSG00000070953	chr2	Rabepk	3.5E+07	3.5E+07	3814	0.045715728	3.092272836	0.8316545	0.880448662	0.04697	0	116	77	151	115	180	242	196	106	198	159
ENSMUSG00000086040	chr6	Wipf3	5.4E+07	5.4E+07	7114	0.060997813	3.666530945	0.8318771	0.880448662	0.09824	0	113	69	413	222	175	232	369	177	278	279
ENSMUSG00000011171	chr12	Vipr2	1.2E+08	1.2E+08	4463	-0.06583013	2.421722671	0.8321839	0.880655792	0.10459	0	106	63	85	60	87	115	193	44	119	75
ENSMUSG00000034220	chr1	Gpc1	9.3E+07	9.3E+07	5159	0.046909165	8.263721309	0.8323685	0.8807847	0.05867	0	3379	2630	7094	5161	5320	5849	8821	4403	7124	6232
ENSMUSG00000083902	chr5	Gm15975	5.6E+07	5.6E+07	1406	0.124799443	-0.07359698	0.8324935	0.880850514	0.09665	0	18	9	9	9	15	20	24	12	21	14
ENSMUSG00000068040	chr2	Tm9sf4	1.5E+08	1.5E+08	7281	0.034524949	4.960796096	0.8325636	0.8808582	0.03044	0	402	274	672	522	497	785	709	474	656	646

ENSMUSG00000032062	chr9	2310030G06Rik	5.1E+07	5.1E+07	1242	-0.05077515	3.219505733	0.833088	0.881346478	0.06145	0	141	91	181	190	104	250	164	135	164	231
ENSMUSG00000004980	chr6	Hnrnpa2b1	5.1E+07	5.1E+07	4086	-0.04070616	9.13996483	0.8332008	0.881399424	0.04458	0	8383	5977	11549	7916	9879	13147	11732	9439	10893	12178
ENSMUSG00000052783	chr5	Grk4	3.5E+07	3.5E+07	4830	-0.09120797	0.483867942	0.8333974	0.881540861	0.11296	0	18	21	28	12	21	29	37	23	28	12
ENSMUSG00000034893	chr14	Cog3	7.6E+07	7.6E+07	4222	0.035675143	4.176380876	0.833714	0.881793804	0.02967	0	224	195	339	249	351	466	389	273	382	385
ENSMUSG00000037257	chr9	Aagab	6.4E+07	6.4E+07	2600	0.034248511	4.710797834	0.8337623	0.881793804	0.02694	0	392	303	443	374	425	599	582	415	545	591
ENSMUSG00000027698	chr3	Nceh1	2.7E+07	2.7E+07	5253	0.094113878	5.412240736	0.8340223	0.882002353	0.23909	0	308	86	1957	782	314	1059	1212	570	729	1034
ENSMUSG00000050147	chr8	F2rl3	7.3E+07	7.3E+07	1751	-0.06909173	1.471219653	0.8343492	0.882215001	0.08301	0	37	29	39	39	64	60	71	36	71	33
ENSMUSG00000078919	chr2	Dpm1	1.7E+08	1.7E+08	7489	-0.03599453	5.62697145	0.8343364	0.882215001	0.03439	0	744	608	918	650	839	1283	1019	796	926	1029
ENSMUSG00000033852	chr2	Gm28042	1.2E+08	1.2E+08	5188	-0.05194837	2.237695997	0.8347252	0.88254604	0.05655	0	73	54	96	57	76	106	122	62	75	108
ENSMUSG00000000339	chr3	Rtca	1.2E+08	1.2E+08	1880	0.035109634	4.532928964	0.8348217	0.882581492	0.03061	0	310	223	430	416	354	504	542	367	497	503
ENSMUSG00000053730	chr4	Tmem39b	1.3E+08	1.3E+08	2286	0.063304183	1.431714172	0.8354102	0.883070627	0.06941	0	39	21	36	39	59	56	56	35	68	60
ENSMUSG00000063785	chrX	Utp14a	4.8E+07	4.8E+07	4130	-0.04980711	3.982695356	0.8354057	0.883070627	0.06606	0	255	195	234	331	157	427	243	268	316	341
ENSMUSG00000061859	chr4	Inadl	9.8E+07	9.8E+07	13086	-0.07852227	1.209131318	0.8355462	0.883147813	0.1008	0	22	18	65	46	25	55	55	33	43	37
ENSMUSG00000025439	chr7	Clns1a	9.8E+07	9.8E+07	1515	-0.0367321	4.456931854	0.8361791	0.883750117	0.03494	0	332	275	366	316	367	501	406	378	532	400
ENSMUSG00000055917	chr12	Zfp277	4E+07	4E+07	2454	-0.05395262	2.048855571	0.8363035	0.883814989	0.065	0	50	48	63	60	91	122	101	58	69	65
ENSMUSG00000027649	chr2	Ctnnbl1	1.6E+08	1.6E+08	2705	-0.03897897	3.853870165	0.836427	0.883878939	0.03762	0	193	174	240	247	238	332	246	244	315	320
ENSMUSG00000038194	chr7	Lhb	4.5E+07	4.5E+07	2501	-0.08887784	0.030813564	0.8372005	0.884629671	0.16209	0	18	18	14	5	14	16	18	12	34	12
ENSMUSG00000018541	chr11	Cwc25	9.8E+07	9.8E+07	5053	-0.03943666	3.278077005	0.837527	0.88487293	0.04243	0	128	119	143	165	174	243	210	125	197	216
ENSMUSG00000025231	chr19	Sufu	4.6E+07	4.6E+07	6945	0.041578098	3.373894677	0.8375733	0.88487293	0.04414	0	140	81	191	140	236	263	212	155	215	239
ENSMUSG00000067713	chr15	Prkag1	9.9E+07	9.9E+07	1638	-0.03535897	5.834761633	0.83762	0.88487293	0.03393	0	782	597	1179	921	923	1277	1256	880	1184	1233
ENSMUSG00000021754	chr13	Map3k1	1.1E+08	1.1E+08	7447	-0.0460199	3.644467254	0.8382916	0.885515724	0.04701	0	148	106	289	201	239	315	253	205	188	304
ENSMUSG00000021257	chr12	Angel1	8.7E+07	8.7E+07	4463	-0.04113345	3.56296358	0.8385969	0.885771477	0.03739	0	163	115	242	176	217	244	250	184	290	224
ENSMUSG00000031819	chr8	Emc8	1.2E+08	1.2E+08	6295	-0.03955958	4.268214524	0.8386652	0.885776977	0.03626	0	239	174	365	273	461	420	390	309	412	421
ENSMUSG00000028565	chr4	Nfia	9.8E+07	9.8E+07	10891	-0.03660377	5.328111725	0.8387339	0.885782859	0.03674	0	559	438	613	578	902	1044	707	586	867	918
ENSMUSG00000020022	chr10	Ndufa12	9.4E+07	9.4E+07	1334	0.040295481	7.377911182	0.8388426	0.885830917	0.04661	0	2256	1523	3034	2985	2736	3390	3718	2624	3785	3890
ENSMUSG00000029480	chr5	Dhx37	1.3E+08	1.3E+08	4139	0.047373792	3.143877653	0.8390168	0.88588151	0.05301	0	91	81	149	176	161	197	173	131	223	196
ENSMUSG00000054604	chr16	Cggbp1	6.5E+07	6.5E+07	4522	0.036114813	4.80002089	0.8389715	0.88588151	0.03624	0	392	264	420	365	667	654	636	488	528	591
ENSMUSG00000040136	chr7	Abcc8	4.6E+07	4.6E+07	4952	-0.05728387	1.894706823	0.8392157	0.886024762	0.08593	0	53	52	44	71	50	96	49	64	74	82
ENSMUSG00000021555	chr13	Naa35	6E+07	6E+07	5780	-0.0318148	4.603302245	0.8397343	0.886417888	0.02632	0	346	256	456	398	403	599	534	375	496	482
ENSMUSG00000034908	chr9	Sidt2	4.6E+07	4.6E+07	5135	-0.03647098	6.073529038	0.8397776	0.886417888	0.03724	0	891	672	1388	1111	1162	1480	1460	1039	1424	1471
ENSMUSG00000078484	chr4	Klhl17	1.6E+08	1.6E+08	3014	-0.04058252	3.623629003	0.8397671	0.886417888	0.04214	0	175	135	165	187	277	279	263	174	280	257
ENSMUSG00000022468	chr15	Endou	9.8E+07	9.8E+07	2718	0.07104001	-0.03630121	0.8400952	0.886423725	0.1052	0	9	6	16	8	27	22	16	17	16	20
ENSMUSG00000025200	chr19	Cwf19l1	4.4E+07	4.4E+07	3574	0.051286749	2.398916024	0.8400277	0.886423725	0.04755	0	76	55	100	79	74	139	113	87	100	106
ENSMUSG00000025324	chr7	Atp10a	5.9E+07	5.9E+07	5469	-0.06972966	1.715361496	0.8401255	0.886423725	0.11471	0	46	49	24	38	84	81	61	63	57	56
ENSMUSG00000026235	chr1	Epha4	7.7E+07	7.7E+07	8054	-0.06216428	1.451165681	0.8401623	0.886423725	0.07203	0	45	28	60	35	36	55	51	49	65	43
ENSMUSG00000036402	chr6	Gng12	6.7E+07	6.7E+07	4694	-0.03208038	4.939611756	0.840108	0.886423725	0.02874	0	458	378	499	414	575	721	622	482	650	656
ENSMUSG00000045211	chr14	Nudt18	7.1E+07	7.1E+07	3716	-0.05791998	4.303807989	0.8399403	0.886423725	0.08673	0	204	136	377	192	710	481	357	304	397	457
ENSMUSG00000024525	chr18	Impa2	6.7E+07	6.7E+07	1661	0.064395612	2.701093473	0.8405224	0.886670259	0.12452	0	69	28	239	79	95	168	105	105	128	170
ENSMUSG00000063229	chr7	Ldha	4.7E+07	4.7E+07	2982	-0.04218713	11.60424297	0.8404982	0.886670259	0.05261	0	43814	35713	49549	51450	57573	60617	73500	44192	81199	58461
ENSMUSG00000018166	chr10	Erbb3	1.3E+08	1.3E+08	6016	0.056846513	2.842319378	0.8407566	0.886850544	0.08507	0	84	43	207	118	96	219	177	102	114	145
ENSMUSG00000024260	chr18	Sap130	3.2E+07	3.2E+07	4050	-0.04214988	3.493448935	0.8409071	0.886942632	0.04005	0	141	97	224	174	244	274	257	154	236	228
ENSMUSG00000040177	chr7	2310057M21Rik	1.3E+08	1.3E+08	2214	0.040823828	3.986354195	0.8415697	0.887507972	0.04594	0	187	150	372	277	207	360	338	262	280	410
ENSMUSG00000050271	chr8	D8Ertd82e	3.6E+07	3.6E+07	9606	0.058127785	2.31410499	0.8415238	0.887507972	0.10012	0	47	24	98	64	151	129	102	68	106	113
ENSMUSG00000096549	chr17	Prickle4	4.8E+07	4.8E+07	1962	-0.07554492	0.0639024	0.8417354	0.887616015	0.08899	0	9	14	17	11	22	24	24	9	18	21
ENSMUSG00000001700	chr18	Gramd3	5.6E+07	5.6E+07	2605	0.038694162	3.62253498	0.8420832	0.887915972	0.03849	0	183	116	272	150	207	332	282	175	246	260
ENSMUSG00000006715	chr13	Gmnn	2.5E+07	2.5E+07	1465	0.06016649	2.563480377	0.8427359	0.888492385	0.10933	0	64	37	196	88	67	177	169	75	113	91
ENSMUSG00000064369	chrMT	mt-Te	14071	14139	69	0.163276366	3.123625077	0.8427565	0.888492385	0.76667	0	12	1	383	160	143	22	277	20	204	438
ENSMUSG00000040485	chr1	Lrrc52	1.7E+08	1.7E+08	1143	-0.19575438	0.049479228	0.8437186	0.889439792	0.74233	0	0	0	48	32	1	10	36	7	17	19
ENSMUSG00000031090	chr7	Nadsyn1	1.4E+08	1.4E+08	3306	-0.06141369	1.758462304	0.8438514	0.889512935	0.06082	0	40	34	64	44	76	65	66	48	67	86
ENSMUSG00000021621	chr13	Zcchc9	9.2E+07	9.2E+07	3422	-0.03826055	3.474914166	0.8442529	0.88980395	0.04181	0	137	153	178	174	190	251	262	177	207	227
ENSMUSG00000026283	chr1	Ing5	9.4E+07	9.4E+07	4729	-0.04764367	2.805396573	0.8442543	0.88980395	0.04938	0	104	67	137	97	132	185	110	115	134	157
ENSMUSG00000030787	chr7	Lyve1	1.1E+08	1.1E+08	2607	0.059556447	2.99919898	0.8445585	0.889991288	0.09162	0	88	100	92	94	211	236	223	146	122	108
ENSMUSG00000036306	chr8	Lzts1	6.9E+07	6.9E+07	6993	0.087919078	1.714269786	0.844559	0.889991288	0.22763	0	21	8	114	77	29	54	97	46	51	89
ENSMUSG00000021752	chr14	Kctd6	8214148	8214342	3253	-0.0439789	3.010745453	0.8447214	0.890095619	0.04644	0	112	94	120	117	167	187	161	146	156	154
ENSMUSG00000065037	chr9	Rn7sk	7.8E+07	7.8E+07	331	0.102069489	-0.05462568	0.8451287	0.890457827	0.12059	0	21	7	9	15	9	28	16	14	13	21
ENSMUSG00000002274	chr17	Metrn	2.6E+07	2.6E+07	1434	-0.03414264	4.777552186	0.8453805	0.890547579	0.03437	0	365	322	469	415	521	543	664	379	713	504
ENSMUSG00000028736	chr4	Pax7	1.4E+08	1.4E+08	5860	-0.08302229	0.8252614	0.8453808	0.890547579	0.07699	0	21	16	45	19	32	39	29	31	36	31
ENSMUSG00000037922	chr3	Bank1	1.4E+08	1.4E+08	3248	0.125545281	-0.23870824	0.8454615	0.890547579	0.17336	0	9	12	2	8	21	28	14	10	16	13
ENSMUSG00000042029	chr12	Ncapg2	1.2E+08	1.2E+08	6604	-0.07586469	1.312034582	0.8454678	0.890547579	0.09858	0	43	26	53	17	48	62	62	43	38	34
ENSMUSG00000007877	chr11	Tcap	9.8E+07	9.8E+07	948	0.047719814	11.11326727	0.8456614	0.89068459	0.07192	0	29770	13207	54104	37476	37866	41778	53037	32073	46635	59969
ENSMUSG00000020658	chr12	Efr3b	3962554	3966547	6547	-0.0787411	4.130217566	0.8460807	0.891059304	0.18064	0	89	61	582	497	224	278	416	273	368	402
ENSMUSG00000040265	chr1	Dnm3	1.6E+08	1.6E+08	24452	0.062215264	2.08804381	0.8462532	0.891174077	0.07121	0	58	62	56	53	70	128	86	49	80	104
ENSMUSG00000022761	chr16	Lztr1	1.8E+07	1.8E+07	5445	0.034189703	5.194001752	0.8464713	0.891302317	0.03324	0	556	430	533	486	704	1007	720	560	808	753
ENSMUSG00000058440	chr6	Nrf1	3E+07	3E+07	10282	-0.0360216	3.589537947	0.8465021	0.891302317	0.03498	0	150	140	241	179	209	267	260	171	252	275
ENSMUSG00000042549	chr11	Map2k3os	6.1E+07	6.1E+07	1291	0.059603441	1.957430291	0.8466522	0.891326557	0.08814	0	50	25	98	67	48	94	110	64	76	55
ENSMUSG00000084819	chr11	Gm11967	5915315	5915396	480	-0.06905517	2.681492773	0.8466162	0.891326557	0.12762	0	31	54	162	107	161	157	203	58	100	137
ENSMUSG00000051169	chr6	Rpusd3	1.1E+08	1.1E+08	2161	-0.05360721	2.716097728	0.8473013	0.891942956	0.06715	0	70	43	139	103	167	152	147	88	146	129

ENSMUSG00000042138	chr9	Msantd2	3.7E+07	3.7E+07	2289	0.069574442	1.506011369	0.847493	0.89207784	0.09641	0	34	39	42	40	43	87	63	56	27	56
ENSMUSG00000026896	chr2	Ifih1	6.3E+07	6.3E+07	8165	0.057771478	2.195216851	0.8476243	0.892149059	0.07351	0	59	52	89	44	91	123	138	62	64	92
ENSMUSG00000051043	chr11	Gprc5c	1.1E+08	1.1E+08	5245	-0.04050163	5.799172253	0.8477524	0.89221693	0.05135	0	941	662	804	622	1216	1035	1267	1045	1166	1068
ENSMUSG00000041126	chr11	H2afv	6427229	6428432	1633	-0.03295916	5.343943461	0.8478997	0.89230504	0.03494	0	668	495	636	626	624	923	859	587	938	854
ENSMUSG00000004151	chr12	Etv1	3.9E+07	3.9E+07	5889	0.082567905	1.27494999	0.848296	0.892655076	0.11014	0	48	25	22	32	39	56	62	19	50	65
ENSMUSG00000015748	chr3	Prpf3	9.6E+07	9.6E+07	5661	0.032659486	3.930567416	0.8484867	0.89272184	0.0317	0	211	137	304	222	280	348	352	233	309	348
ENSMUSG00000027956	chr3	Tmem144	8E+07	8E+07	3487	-0.05650518	1.41240623	0.8484633	0.89272184	0.06507	0	31	34	49	36	47	45	61	33	58	63
ENSMUSG00000074272	chr7	Ceacam1	2.5E+07	2.5E+07	3736	0.046693236	2.378110011	0.8486308	0.892806452	0.05636	0	62	50	119	78	76	130	130	75	83	122
ENSMUSG00000001627	chr12	Ifrd1	4E+07	4E+07	5858	0.045030941	5.789759955	0.8491603	0.893162507	0.06722	0	453	418	1307	901	1247	1429	1185	932	813	1455
ENSMUSG00000017781	chr11	Pitpna	7.6E+07	7.6E+07	4129	0.037112383	7.043663657	0.8490747	0.893162507	0.04441	0	1714	1720	2125	1976	2165	3015	2780	2243	2924	2800
ENSMUSG00000030672	chr7	Mylpf	1.3E+08	1.3E+08	885	0.044313923	13.28473816	0.8491543	0.893162507	0.06497	0	183320	135247	137138	125757	135701	222697	219183	167043	247438	188174
ENSMUSG00000021040	chr12	Slirp	8.7E+07	8.7E+07	3104	0.03165637	5.094180151	0.8494558	0.89340133	0.02979	0	512	382	569	550	514	825	686	597	736	702
ENSMUSG00000054021	chr13	Sirt5	4.3E+07	4.3E+07	1367	-0.05008086	3.658102824	0.8495612	0.89340133	0.06515	0	146	75	363	216	215	283	288	184	235	289
ENSMUSG00000097989	chr15	Gm4335	9.3E+07	9.3E+07	1004	-0.08143789	0.342969156	0.8495784	0.89340133	0.1872	0	18	20	6	19	24	15	14	14	36	38
ENSMUSG00000054855	chr15	Rnd1	9.9E+07	9.9E+07	2967	-0.06221534	0.969769753	0.8499068	0.893612699	0.09746	0	26	30	22	31	30	39	25	33	36	53
ENSMUSG00000061904	chr10	Slc25a3	9.1E+07	9.1E+07	5550	-0.04676647	9.910760409	0.8498619	0.893612699	0.07284	0	10364	7049	27107	17895	14967	18633	24147	13607	19988	21938
ENSMUSG00000040688	chr17	Tbl3	2.5E+07	2.5E+07	5686	0.034712936	4.490313681	0.8502063	0.89386053	0.03776	0	245	208	445	430	371	489	513	336	548	462
ENSMUSG00000085289	chr18	Gm15337	3.9E+07	3.9E+07	3888	-0.0916652	3.719041843	0.8503284	0.893921927	0.27664	0	187	296	32	300	87	276	122	237	314	344
ENSMUSG00000029176	chr5	Anapc4	5.3E+07	5.3E+07	5902	-0.03108951	5.430240522	0.850481	0.894015314	0.0307	0	605	461	842	693	705	1059	996	658	832	880
ENSMUSG00000040987	chr7	Mill2	1.9E+07	1.9E+07	1121	0.076825504	1.635585131	0.8506337	0.894108855	0.1037	0	54	47	30	26	56	93	72	41	50	68
ENSMUSG00000002741	chr11	Ykt6	5955693	5956004	2984	0.036112522	6.471629969	0.8509224	0.894278254	0.04382	0	1047	782	2040	1344	1612	2154	2095	1315	2022	1761
ENSMUSG00000028456	chr4	Unc13b	4.3E+07	4.3E+07	13497	0.056195954	2.176445728	0.8509862	0.894278254	0.08009	0	39	48	130	57	62	116	103	63	78	110
ENSMUSG00000066838	chr7	Zfp772	7202122	7204359	2772	-0.055804	1.697585205	0.8509742	0.894278254	0.05795	0	53	28	69	40	56	86	70	43	61	62
ENSMUSG00000069917	chr11	Hba-a2	3.2E+07	3.2E+07	667	0.108613596	-0.00233425	0.8511297	0.894362115	0.35364	0	1	5	12	21	29	9	5	21	36	20
ENSMUSG00000041353	chrX	Tmem29	1.5E+08	1.5E+08	7621	-0.0509301	1.861226864	0.8512103	0.894379733	0.07354	0	59	42	55	41	74	111	50	59	72	68
ENSMUSG00000022771	chr16	Ppil2	1.7E+07	1.7E+07	6171	-0.0292253	5.066558769	0.8517314	0.894860265	0.02717	0	516	366	551	470	655	856	697	518	671	695
ENSMUSG00000073236	chr2	2500004C02Rik	1.5E+08	1.5E+08	2147	-0.0680628	0.533692037	0.8519063	0.894977036	0.08768	0	23	10	23	23	26	44	20	19	21	33
ENSMUSG00000020387	chr11	Jade2	5.2E+07	5.2E+07	10760	-0.04643816	2.958280496	0.8532204	0.89622324	0.06387	0	59	100	156	123	157	170	189	104	140	184
ENSMUSG00000024571	chr18	Gm16286	8E+07	8E+07	3075	0.032910964	6.107663129	0.8532047	0.89622324	0.03649	0	980	738	1275	1017	1158	1580	1425	1114	1588	1491
ENSMUSG00000063286	chr7	Gm8995	1.1E+08	1.1E+08	7280	-0.05990021	2.383305432	0.8535505	0.896502822	0.1206	0	58	65	128	89	54	220	106	39	95	84
ENSMUSG00000096952	chr8	Gm26572	1.2E+08	1.2E+08	3231	0.055304849	0.928605583	0.8539295	0.896833752	0.07605	0	27	15	39	19	36	35	39	23	44	49
ENSMUSG00000001995	chr8	Sipa1l2	1.3E+08	1.3E+08	6365	0.039653645	3.611958268	0.8541086	0.896954725	0.05465	0	142	93	322	208	170	268	252	207	250	289
ENSMUSG00000027423	chr2	Snx5	1.4E+08	1.4E+08	4177	-0.03502642	6.31465399	0.8548616	0.897678291	0.04337	0	1282	954	1335	1146	1308	2235	1803	1276	1352	1514
ENSMUSG00000038301	chr6	Snx10	5.2E+07	5.2E+07	4912	0.067987863	2.975018693	0.8553341	0.898039975	0.14829	0	128	89	49	48	261	197	172	133	149	170
ENSMUSG00000039164	chr2	Naif1	3.2E+07	3.2E+07	4650	-0.04066864	2.578867189	0.8552765	0.898039975	0.046	0	77	63	116	95	103	144	127	73	140	122
ENSMUSG00000031812	chr8	Map1lc3b	1.2E+08	1.2E+08	7517	0.034266133	7.710615239	0.8560137	0.898608812	0.04208	0	2987	2365	3693	3253	3285	5086	4773	3236	4558	4358
ENSMUSG00000036438	chr17	Calm2	8.7E+07	8.7E+07	1467	0.038112026	7.621306722	0.8560079	0.898608812	0.05204	0	2891	2411	2570	2457	4237	4567	4820	2979	4016	4350
ENSMUSG00000101795	chr1	Gm5835	1.4E+08	1.4E+08	1270	-0.05313866	2.276079543	0.8560681	0.898608812	0.07431	0	65	49	72	87	93	88	135	54	133	76
ENSMUSG00000022009	chr14	Nufip1	7.6E+07	7.6E+07	3974	0.04012479	2.979250689	0.856229	0.898689039	0.04568	0	115	83	164	108	113	223	166	128	155	148
ENSMUSG00000049305	chr9	Ccdc71	1.1E+08	1.1E+08	3267	-0.03021488	4.247771548	0.8562727	0.898689039	0.02876	0	265	197	358	298	338	466	420	273	428	361
ENSMUSG00000022843	chr16	Clcn2	2.1E+07	2.1E+07	6022	0.067005517	1.247912798	0.8564651	0.898718428	0.06992	0	36	23	33	35	40	77	43	30	41	53
ENSMUSG00000031144	chrX	Syp	7638471	7638728	5211	-0.09522564	1.862127054	0.8564929	0.898718428	0.24424	0	30	23	31	23	189	108	49	45	76	79
ENSMUSG00000097493	chr15	9930014A18Rik	6.1E+07	6.1E+07	7043	0.048776751	0.917456881	0.8563928	0.898718428	0.08104	0	24	13	33	22	44	41	29	36	35	44
ENSMUSG00000054715	chr7	Zscan22	1.3E+07	1.3E+07	3501	-0.06085809	1.960602966	0.8565753	0.898737711	0.08535	0	66	20	99	48	72	91	92	44	83	79
ENSMUSG00000025158	chr11	Rfng	1.2E+08	1.2E+08	2489	-0.03239084	4.339674467	0.8569716	0.898976248	0.03243	0	229	218	414	307	398	425	426	300	474	438
ENSMUSG00000084929	chr4	Foxo6os	1.2E+08	1.2E+08	2291	-0.08168374	0.484712172	0.856995	0.898976248	0.10568	0	19	13	38	18	14	19	30	16	28	37
ENSMUSG00000100291	chr6	2310069B03Rik	8.3E+07	8.3E+07	1902	0.087298953	0.454053237	0.856958	0.898976248	0.1833	0	18	4	39	24	11	32	29	21	11	41
ENSMUSG00000028958	chr5	Tmub1	2.4E+07	2.4E+07	1879	-0.03244892	4.135617505	0.8571354	0.899056332	0.03376	0	241	187	306	285	324	372	340	251	446	382
ENSMUSG00000030327	chr6	Necap1	1.2E+08	1.2E+08	2386	0.031525831	4.080231376	0.8574162	0.899283629	0.03119	0	232	174	293	230	342	453	369	256	331	363
ENSMUSG00000048833	chr12	Slc39a9	8.1E+07	8.1E+07	5229	-0.03113934	4.266722635	0.8578231	0.899643075	0.03036	0	259	205	366	251	404	481	418	293	365	413
ENSMUSG00000013936	chr5	Myl2	1.2E+08	1.2E+08	1950	-0.19244507	7.60868401	0.8580244	0.899786959	1.30011	0	267	4	9165	7854	20	2886	1313	2554	846	11211
ENSMUSG00000021807	chr14	2700060E02Rik	2E+07	2E+07	1510	0.033352523	6.494428527	0.8582421	0.899922881	0.04021	0	1358	1055	1531	1271	1469	2321	1733	1482	1979	1920
ENSMUSG00000040537	chr5	Adam22	8072352	8078706	12231	-0.0520506	1.936467837	0.8582824	0.899922881	0.07361	0	68	40	87	48	44	102	63	51	73	93
ENSMUSG00000035671	chr8	Zswim4	8.4E+07	8.4E+07	4348	0.034304432	3.580762316	0.8587735	0.900334896	0.03968	0	155	111	222	209	199	257	284	209	266	218
ENSMUSG00000052906	chr8	Ubxn8	3.4E+07	3.4E+07	2817	0.047585832	2.589922166	0.8588037	0.900334896	0.05641	0	95	73	75	76	115	138	118	106	118	138
ENSMUSG00000031365	chrX	Zfp275	7.3E+07	7.3E+07	6745	-0.04856368	3.459781483	0.8589009	0.900369521	0.08903	0	240	167	106	132	149	294	202	182	176	257
ENSMUSG00000022231	chr15	Sema5a	3.2E+07	3.2E+07	10809	0.044037856	2.776219836	0.8590129	0.900419575	0.04956	0	100	80	88	101	128	169	141	112	149	137
ENSMUSG00000034748	chr10	Sirt6	8.2E+07	8.2E+07	2785	-0.04342968	2.300576119	0.8591709	0.900469773	0.05234	0	70	39	100	75	95	128	114	60	100	97
ENSMUSG00000037003	chr15	Tenc1	1E+08	1E+08	4728	0.040974349	5.767987459	0.8591891	0.900469773	0.06366	0	563	438	967	641	1648	1398	1080	805	1108	1360
ENSMUSG00000030871	chr7	Ears2	1.2E+08	1.2E+08	5152	-0.03688591	3.453823444	0.8593387	0.900559255	0.03821	0	138	119	222	153	210	245	215	195	223	222
ENSMUSG00000007379	chr3	Dennd2c	1E+08	1E+08	6858	0.045806779	3.370365871	0.8596133	0.900779706	0.06144	0	162	140	148	94	207	278	270	167	168	199
ENSMUSG00000004096	chr9	Cwc15	1.5E+07	1.5E+07	1111	-0.03202485	6.037918967	0.8598136	0.9008	0.03835	0	1016	794	1134	909	1129	1482	1304	1103	1331	1464
ENSMUSG00000037847	chr19	Nmrk1	1.9E+07	1.9E+07	3345	-0.04789966	1.396635279	0.8598254	0.9008	0.08158	0	51	30	31	35	44	71	40	36	63	49
ENSMUSG00000068250	chr6	Amn1	1.5E+08	1.5E+08	4300	-0.04941104	1.948521716	0.8597869	0.9008	0.05881	0	61	42	67	45	75	94	83	66	57	81
ENSMUSG00000019558	chrX	Slc6a8	7.4E+07	7.4E+07	5210	-0.03936945	7.146645322	0.8601595	0.900991624	0.0589	0	2005	1323	3518	2483	1702	3185	3803	2104	2820	2614
ENSMUSG00000061536	chr9	Sec22c	1.2E+08	1.2E+08	6301	0.046716194	3.222488792	0.860201	0.900991624	0.05893	0	146	104	119	158	149	199	276	114	225	168
ENSMUSG00000082488	chr13	1700119I11Rik	9.2E+07	9.2E+07	405	-0.20231887	0.668364729	0.8601403	0.900991624	1.35528	0	0	0	118	14	6	1	38	0	41	62

ENSMUSG00000031216	chrX	Stard8	9.9E+07	9.9E+07	5499	-0.02833369	4.894395076	0.8602746	0.901001419	0.02969	0	388	333	566	514	465	773	652	394	633	624
ENSMUSG00000074797	chr2	Itpa	1.3E+08	1.3E+08	1963	-0.02825783	4.644526723	0.8605723	0.901245915	0.02805	0	369	296	439	354	438	627	485	431	500	501
ENSMUSG00000038539	chr7	Atf5	4.5E+07	4.5E+07	1992	-0.03756692	7.137538327	0.8607644	0.901379785	0.05367	0	1769	1090	3147	2543	2593	2912	2851	1932	3339	3400
ENSMUSG00000017999	chr2	Ddx27	1.7E+08	1.7E+08	4817	0.033239231	3.884290579	0.8613198	0.901894097	0.03786	0	176	166	253	178	337	339	316	240	319	319
ENSMUSG00000022965	chr16	Ifngr2	9.2E+07	9.2E+07	3313	-0.03269984	6.628800925	0.8614895	0.901937138	0.04117	0	1630	1036	1691	1551	1643	2175	2048	1590	2256	2019
ENSMUSG00000027641	chr2	Rbl1	1.6E+08	1.6E+08	5993	-0.05990531	1.620517912	0.8614815	0.901937138	0.07946	0	52	25	57	27	74	84	61	42	51	66
ENSMUSG00000029227	chr5	Fip1l1	7.5E+07	7.5E+07	10442	0.029133761	4.685352286	0.8617753	0.902058982	0.03157	0	364	254	539	399	381	620	491	473	525	549
ENSMUSG00000029298	chr5	Gbp9	1.1E+08	1.1E+08	3693	0.084139136	2.007264042	0.8618619	0.902058982	0.2124	0	57	48	63	62	51	251	83	21	41	54
ENSMUSG00000034343	chr1	Ube2f	9.1E+07	9.1E+07	8842	-0.03024625	5.92119281	0.8618631	0.902058982	0.03494	0	854	678	1172	969	955	1464	1332	952	1247	1213
ENSMUSG00000043629	chr1	1700019D03Rik	5.3E+07	5.3E+07	4330	0.072843481	0.785751972	0.8618282	0.902058982	0.06796	0	22	16	31	23	28	45	46	19	29	35
ENSMUSG00000027673	chr3	Ndufb5	3.3E+07	3.3E+07	4995	0.036483387	8.661258287	0.8621334	0.902274503	0.05274	0	5497	3352	9265	7083	5718	9393	9006	6295	8874	8942
ENSMUSG00000031504	chr8	Rab20	1.1E+07	1.1E+07	1446	0.043577103	2.189255626	0.8622552	0.902309953	0.06574	0	48	45	111	57	79	97	81	64	101	126
ENSMUSG00000034105	chr8	Tldc1	1.2E+08	1.2E+08	2574	-0.05587916	2.544425872	0.8622959	0.902309953	0.09698	0	58	42	170	114	75	111	173	75	133	93
ENSMUSG00000091478	chr11	Gm10039	1E+08	1E+08	411	-0.03865414	5.449911759	0.8625025	0.902458804	0.05568	0	488	352	1165	839	612	886	1103	583	955	957
ENSMUSG00000021840	chr14	Mapk1ip1l	4.7E+07	4.7E+07	4608	0.028566102	4.399011261	0.8625975	0.902490871	0.02972	0	313	211	408	282	375	541	416	368	420	444
ENSMUSG00000043993	chr11	2900052L18Rik	1.2E+08	1.2E+08	1588	0.06338984	0.248723827	0.8628373	0.902674377	0.09904	0	10	10	27	11	24	35	21	12	18	30
ENSMUSG00000029110	chr5	Rnf4	3.4E+07	3.4E+07	7287	0.031792844	4.962547774	0.8632382	0.902999017	0.03919	0	370	323	482	392	803	737	676	529	618	684
ENSMUSG00000032841	chr2	Prr5l	1E+08	1E+08	4967	0.109687051	0.471132427	0.8632763	0.902999017	0.28558	0	19	12	5	3	56	32	27	16	27	36
ENSMUSG00000053740	chr18	Gm6457	1.5E+07	1.5E+07	815	-0.09342446	0.074893074	0.8633529	0.903011767	0.13643	0	10	8	13	28	15	13	32	16	15	18
ENSMUSG00000036957	chr7	Lrfn3	3E+07	3E+07	2861	-0.05227885	2.115014117	0.8636798	0.90328631	0.07559	0	47	37	114	60	79	78	108	55	115	75
ENSMUSG00000026753	chr2	Ppp6c	3.9E+07	3.9E+07	4219	0.03087082	6.211354221	0.8638737	0.903421727	0.03765	0	1016	829	1383	1021	1311	1716	1588	1325	1474	1587
ENSMUSG00000089788	chr1	Gm16586	1.8E+08	1.8E+08	2640	0.045747693	3.616722244	0.8639572	0.903441715	0.07159	0	102	155	189	222	234	303	206	163	213	407
ENSMUSG00000034453	chr10	Polr3b	8.5E+07	8.5E+07	4829	-0.02968394	4.443786368	0.8640775	0.903500176	0.02953	0	310	196	449	341	391	555	449	325	426	478
ENSMUSG00000004791	chr12	Pgf	8.5E+07	8.5E+07	1582	-0.07965451	1.032795656	0.8643185	0.903684774	0.15974	0	11	20	20	40	63	42	24	38	37	51
ENSMUSG00000066057	chr17	Gm1976	9.5E+07	9.5E+07	1912	0.072843166	0.706984998	0.8645494	0.903858813	0.08331	0	20	18	27	15	33	40	45	22	21	35
ENSMUSG00000073434	chr17	Wdr90	2.6E+07	2.6E+07	8466	0.075624061	0.736358448	0.8646361	0.903882116	0.07904	0	18	19	24	19	35	50	28	22	39	28
ENSMUSG00000034126	chr12	Pomt2	8.7E+07	8.7E+07	5059	-0.03350476	3.357738406	0.865037	0.904233793	0.03814	0	132	115	219	154	162	249	238	141	213	206
ENSMUSG00000027998	chr3	Plrg1	8.3E+07	8.3E+07	2816	-0.02596724	4.678449366	0.8653958	0.904541451	0.02551	0	378	287	483	378	422	612	560	394	509	548
ENSMUSG00000074793	chr2	Hspa12b	1.3E+08	1.3E+08	3685	0.036679402	4.031940036	0.8656355	0.904724521	0.05436	0	151	152	331	201	427	442	314	239	412	310
ENSMUSG00000007837	chr7	Prrg2	4.5E+07	4.5E+07	2091	0.033158252	3.677982735	0.8659118	0.904945898	0.04336	0	152	102	267	191	269	342	247	172	300	284
ENSMUSG00000024858	chr19	Adrbk1	4286001	4287264	4476	-0.03266256	6.537210498	0.8660863	0.905060854	0.04402	0	1199	1002	1741	1685	1491	1856	2092	1303	2229	2040
ENSMUSG00000037470	chr1	Uggt1	3.6E+07	3.6E+07	12853	0.031211605	5.861815026	0.8663783	0.905298504	0.03923	0	744	618	1158	1028	806	1505	1363	937	1137	1154
ENSMUSG00000024036	chr17	Slc37a1	3.1E+07	3.1E+07	3626	-0.07918733	0.408973914	0.8666637	0.905529233	0.14869	0	15	12	46	10	15	35	38	13	23	16
ENSMUSG00000032582	chr9	Rbm6	1.1E+08	1.1E+08	13944	-0.02619082	4.936667755	0.8668247	0.905630023	0.02845	0	445	369	553	436	517	843	631	440	580	669
ENSMUSG00000027546	chr2	Atp9a	1.7E+08	1.7E+08	5917	0.031606059	5.668417554	0.8671244	0.905875649	0.04176	0	662	451	925	655	1216	1345	1276	715	1005	1036
ENSMUSG00000047767	chr7	Atg16l2	1E+08	1E+08	3881	0.050288332	2.672229346	0.8674335	0.906131062	0.06699	0	84	83	69	108	111	181	138	74	120	160
ENSMUSG00000050248	chr5	Evc2	3.7E+07	3.7E+07	5837	0.046353463	3.789853323	0.8676394	0.906278737	0.09014	0	146	86	458	242	143	342	347	180	294	299
ENSMUSG00000032180	chr9	Tmed1	2.2E+07	2.2E+07	1487	-0.02876607	5.396741779	0.867714	0.906289118	0.03428	0	574	485	765	741	629	1022	844	663	952	829
ENSMUSG00000020372	chr11	Gnb2l1	4.9E+07	4.9E+07	5119	0.032181833	8.582461868	0.868239	0.906769969	0.04467	0	5389	4569	6461	5842	6159	9300	7877	5797	8820	8477
ENSMUSG00000046062	chr1	Ppp1r15b	1.3E+08	1.3E+08	5594	-0.03302771	4.99765722	0.8687794	0.907266783	0.04289	0	451	315	465	389	865	761	635	528	650	678
ENSMUSG00000024963	chr19	Dnajc4	6987911	6988108	1074	0.029746299	4.071614715	0.8693721	0.907818083	0.0324	0	233	184	311	241	286	344	367	251	409	376
ENSMUSG00000028107	chr3	Tars2	9.6E+07	9.6E+07	4438	-0.02803819	5.042939686	0.8695687	0.907888271	0.03127	0	408	326	626	598	582	689	698	475	762	752
ENSMUSG00000044122	chr11	Proca1	7.8E+07	7.8E+07	2088	-0.10643184	1.647255304	0.8695056	0.907888271	0.40177	0	47	35	10	6	145	107	19	44	71	64
ENSMUSG00000033705	chr2	Stard9	1.2E+08	1.2E+08	19408	-0.03589419	2.911151809	0.87017	0.90844837	0.05633	0	131	88	130	98	116	196	161	79	148	190
ENSMUSG00000043311	chr17	D17H6S53E	3.5E+07	3.5E+07	2280	-0.0380713	3.776524229	0.8709615	0.909207024	0.04966	0	151	104	360	231	239	305	307	195	305	284
ENSMUSG00000020189	chr10	Osbpl8	1.1E+08	1.1E+08	7152	0.034285731	4.295444076	0.8710516	0.909233478	0.04472	0	271	231	386	324	235	378	566	284	380	444
ENSMUSG00000037104	chr17	Socs5	8.7E+07	8.7E+07	4392	0.030422647	4.490386878	0.8712693	0.909392992	0.04123	0	292	180	554	368	329	600	539	362	427	424
ENSMUSG00000035011	chr10	Zbtb7a	8.1E+07	8.1E+07	6808	-0.02667674	5.238552784	0.8714104	0.909472643	0.02873	0	483	384	752	558	747	827	836	584	816	799
ENSMUSG00000034175	chr11	Rhbdd3	5098926	5099566	2790	-0.02721359	4.705702885	0.8719189	0.909935638	0.03112	0	325	290	455	436	487	557	531	361	665	561
ENSMUSG00000064210	chr15	Ano6	9.6E+07	9.6E+07	5640	0.030101608	6.167907619	0.8727144	0.910630261	0.04085	0	1013	794	1201	1025	1351	1962	1541	1311	1366	1307
ENSMUSG00000081189	chr4	Gm12725	1.1E+08	1.1E+08	1668	0.145133521	0.648893543	0.8726842	0.910630261	0.62758	0	35	37	1	2	18	59	3	35	38	25
ENSMUSG00000017314	chr11	Mpp2	1E+08	1E+08	4807	-0.08302135	1.101471128	0.8728676	0.91072242	0.17058	0	20	10	25	26	87	61	32	25	49	40
ENSMUSG00000097277	chr7	2900076A07Rik	8.2E+07	8.2E+07	1993	-0.03813579	2.343454259	0.8732937	0.911099234	0.0512	0	63	62	80	76	99	110	95	74	104	125
ENSMUSG00000004897	chr3	Hdgf	8.8E+07	8.8E+07	2873	-0.0303567	8.278074235	0.8737915	0.911550724	0.04348	0	4303	3539	5369	4837	5679	6454	6728	4867	6805	6858
ENSMUSG00000080850	chr4	Gm12439	4.9E+07	4.9E+07	365	0.034787458	4.525906182	0.8738805	0.911575794	0.04644	0	295	357	382	328	296	438	542	349	495	574
ENSMUSG00000018697	chr11	Aatf	8.4E+07	8.4E+07	2869	0.031038568	3.9093746	0.8740766	0.911644731	0.03835	0	158	180	278	254	246	385	292	271	302	303
ENSMUSG00000027510	chr2	Rbm38	1.7E+08	1.7E+08	2869	-0.03674954	7.313926776	0.8740399	0.911644731	0.06319	0	1998	1225	3810	3102	2420	2978	3805	2112	4094	3328
ENSMUSG00000020412	chr11	Ascc2	4637747	4637822	4964	-0.02480032	4.829054375	0.8741424	0.911645555	0.02822	0	395	345	523	449	434	653	628	422	624	588
ENSMUSG00000004815	chr5	Dgkq	1.1E+08	1.1E+08	7189	-0.03991769	2.258399953	0.8745103	0.911893614	0.06006	0	54	61	93	57	96	133	107	61	75	109
ENSMUSG00000016257	chr2	Slmo2	1.7E+08	1.7E+08	1860	0.031032076	5.818944216	0.8744582	0.911893614	0.04652	0	650	429	1346	910	1051	1157	1405	875	1237	1220
ENSMUSG00000068686	chr2	Cd59b	1E+08	1E+08	1300	0.036546556	3.033960947	0.8753142	0.91266408	0.05133	0	125	75	122	124	162	189	199	150	175	128
ENSMUSG00000032301	chr9	Psma4	5.5E+07	5.5E+07	2370	0.029178739	6.864998464	0.875562	0.912786694	0.04066	0	1813	1233	2042	1629	2019	2999	2471	2001	2318	2375
ENSMUSG00000078429	chr10	Ctdsp2	1.3E+08	1.3E+08	5065	-0.02911221	7.281095601	0.8755413	0.912786694	0.04083	0	2137	1699	2811	2470	2811	3573	3342	2337	3133	3592
ENSMUSG00000064262	chr6	Gimap8	4.9E+07	4.9E+07	3654	0.043225126	2.080435238	0.8758467	0.913015707	0.06469	0	60	36	87	44	88	104	109	56	69	100
ENSMUSG00000028348	chr4	Murc	4.9E+07	4.9E+07	2054	-0.03548784	7.502520273	0.8761904	0.913129245	0.06186	0	2591	2390	3420	3296	1859	3795	3843	3054	3697	4022
ENSMUSG00000035495	chr4	Tstd2	4.6E+07	4.6E+07	5570	-0.02912803	3.90346216	0.8762161	0.913129245	0.03617	0	202	145	300	261	240	345	347	181	327	343
ENSMUSG00000048495	chr1	Tyw5	5.7E+07	5.7E+07	2672	-0.05021215	1.433165014	0.8761543	0.913129245	0.07549	0	41	27	45	35	53	81	47	48	33	55

ENSMUSG00000064354	chrMT	mt-Co2	7013	7696	684	-0.0606819	4.745888233	0.8760845	0.913129245	0.17368	0	281	152	328	701	670	299	814	147	936	576
ENSMUSG00000024169	chr17	Ift140	2.5E+07	2.5E+07	7572	-0.03960747	2.303247898	0.8765712	0.913363632	0.05806	0	57	64	85	67	97	143	98	70	110	77
ENSMUSG00000079658	chr1	Tceb1	1.7E+07	1.7E+07	3026	-0.02832307	6.347779084	0.876568	0.913363632	0.03895	0	1238	914	1314	1279	1442	1876	1615	1282	1811	1749
ENSMUSG00000024743	chr19	Syt7	1E+07	1E+07	6966	-0.04991095	1.475237829	0.8766891	0.913418581	0.07122	0	33	27	56	54	37	64	71	38	41	60
ENSMUSG00000030494	chr7	Rhpn2	3.5E+07	3.5E+07	6304	-0.05136479	3.521886659	0.8772861	0.913922768	0.13477	0	155	230	87	237	91	302	192	193	250	220
ENSMUSG00000081683	chr5	Fzd10	1.3E+08	1.3E+08	3250	0.079974933	0.161606297	0.8773033	0.913922768	0.16028	0	10	7	30	19	10	17	24	10	15	42
ENSMUSG00000043505	chr6	Gimap5	4.9E+07	4.9E+07	2353	0.057205189	0.779019217	0.8774589	0.914016986	0.09775	0	15	15	39	30	22	48	24	19	33	48
ENSMUSG00000033272	chr18	Slc35a4	3.7E+07	3.7E+07	3275	-0.03015279	6.261951447	0.8776427	0.914140504	0.04387	0	913	725	1738	1262	1364	1607	1957	1100	1671	1548
ENSMUSG00000032498	chr9	Mlh1	1.1E+08	1.1E+08	4818	-0.03284457	2.883125725	0.8778896	0.914261905	0.04327	0	110	81	121	106	139	174	163	96	163	155
ENSMUSG00000035944	chr15	Ttc38	8.6E+07	8.6E+07	3842	-0.04445517	2.238933484	0.8778465	0.914261905	0.05244	0	53	43	89	71	107	116	94	68	95	100
ENSMUSG00000049588	chr11	Ccdc69	5.5E+07	5.5E+07	1848	0.050446149	2.620496927	0.8779863	0.914294757	0.09917	0	100	73	52	67	152	179	123	109	143	82
ENSMUSG00000033326	chr4	Kdm4a	1.2E+08	1.2E+08	5782	-0.02677519	5.099896817	0.8782107	0.914460539	0.03179	0	440	330	727	598	555	785	688	569	799	652
ENSMUSG00000032869	chr2	Psmf1	1.5E+08	1.5E+08	6441	-0.02511734	4.304581833	0.8787933	0.914931359	0.02761	0	291	212	351	276	379	476	421	306	391	428
ENSMUSG00000037139	chr4	Myom3	1.4E+08	1.4E+08	6038	0.108351886	6.438713035	0.8787826	0.914931359	0.58747	0	361	20	3667	2700	193	1859	2316	1169	1135	2926
ENSMUSG00000026848	chr2	Tor1b	3.1E+07	3.1E+07	5327	0.029521257	5.418101761	0.8793075	0.91519497	0.04065	0	682	535	586	663	654	1075	878	756	929	802
ENSMUSG00000026971	chr2	Itgb6	6.1E+07	6.1E+07	7111	0.034545831	5.43591476	0.8793034	0.91519497	0.06161	0	789	324	932	712	514	811	1025	922	792	869
ENSMUSG00000031935	chr9	Med17	1.5E+07	1.5E+07	3899	0.030351435	3.568829859	0.8791405	0.91519497	0.03747	0	175	132	205	160	208	298	275	209	202	243
ENSMUSG00000078440	chr10	Dohh	8.1E+07	8.1E+07	3202	0.027497348	5.569888721	0.8792844	0.91519497	0.03733	0	592	475	908	800	816	1005	1035	674	1247	1008
ENSMUSG00000094530	chr8	Gm21399	1.3E+08	1.3E+08	600	-0.05043265	0.947876555	0.8795058	0.915333438	0.07571	0	23	19	36	20	45	36	38	23	48	41
ENSMUSG00000003038	chr4	Hmgn2	1.3E+08	1.3E+08	3060	0.034698984	2.865087541	0.8799618	0.915691317	0.04631	0	90	78	135	105	133	149	190	99	169	149
ENSMUSG00000066491	chr12	Gm6265	5.6E+07	5.6E+07	231	0.055010677	0.857437255	0.8799803	0.915691317	0.14406	0	13	8	49	39	23	28	31	33	35	49
ENSMUSG00000028688	chr4	Toe1	1.2E+08	1.2E+08	2979	-0.03766812	2.921485035	0.8800616	0.915707964	0.04997	0	94	84	133	91	179	193	156	110	167	142
ENSMUSG00000038982	chr13	Bloc1s5	3.9E+07	3.9E+07	1766	-0.02658327	3.928586777	0.8802485	0.915834493	0.03248	0	212	175	301	190	285	390	321	212	330	312
ENSMUSG00000025371	chr11	Chmp6	1.2E+08	1.2E+08	2432	0.024055437	5.111101939	0.8805826	0.916114196	0.02704	0	462	380	637	552	557	840	757	538	747	724
ENSMUSG00000028798	chr4	Eif3i	1.3E+08	1.3E+08	3702	0.027386379	6.640848353	0.8807169	0.916185946	0.03859	0	1409	1144	1707	1414	1785	2289	2131	1621	2212	2149
ENSMUSG00000057315	chr5	Arhgap24	1E+08	1E+08	8791	-0.04635613	4.161485477	0.8819732	0.917424779	0.09847	0	162	79	532	331	365	317	490	241	328	443
ENSMUSG00000020739	chr11	Nup85	1.2E+08	1.2E+08	3385	-0.0235197	4.716958185	0.8825267	0.917932502	0.02891	0	407	299	442	391	450	665	485	378	602	576
ENSMUSG00000023345	chr9	Poc1a	1.1E+08	1.1E+08	2995	-0.05295131	0.908611046	0.8827274	0.918073125	0.0881	0	24	12	43	24	38	34	42	17	41	48
ENSMUSG00000045968	chr1	Teddm2	1.5E+08	1.5E+08	4905	-0.06297615	0.369844118	0.8829092	0.918194197	0.12276	0	21	10	15	27	18	18	43	13	20	27
ENSMUSG00000026240	chr1	Cops7b	8.7E+07	8.7E+07	5515	0.027992094	3.788037742	0.8831157	0.918272696	0.0343	0	189	148	267	219	206	324	273	215	292	330
ENSMUSG00000055707	chr8	Klhl26	7E+07	7E+07	3069	-0.02793429	4.122566407	0.8830932	0.918272696	0.03427	0	284	149	331	255	326	467	367	269	324	359
ENSMUSG00000027575	chr2	Arfgap1	1.8E+08	1.8E+08	5367	-0.02346128	5.106049303	0.8837847	0.918900232	0.02748	0	505	345	666	510	622	866	723	520	774	659
ENSMUSG00000044155	chr6	Lsm8	1.9E+07	1.9E+07	4108	0.033535938	3.315186868	0.8841477	0.919209493	0.04537	0	166	114	192	110	152	258	218	171	189	194
ENSMUSG00000003955	chr16	Fam162a	3.6E+07	3.6E+07	635	0.024129249	5.395136349	0.8848223	0.919748681	0.03181	0	595	404	911	611	678	1013	921	664	866	927
ENSMUSG00000024427	chr18	Spry4	3.9E+07	3.9E+07	4587	0.038784688	2.957700338	0.8849286	0.919748681	0.08784	0	69	67	108	123	223	165	118	162	151	191
ENSMUSG00000039768	chr4	Dnajc11	1.5E+08	1.5E+08	10678	-0.03088373	5.805412722	0.8849114	0.919748681	0.05036	0	628	443	1477	995	888	1201	1252	852	1187	1228
ENSMUSG00000046070	chr17	Igfals	2.5E+07	2.5E+07	2111	0.058862694	1.641169488	0.8847775	0.919748681	0.15001	0	43	37	24	29	90	69	32	70	64	75
ENSMUSG00000039159	chr6	Ube2h	3E+07	3E+07	4780	0.026639841	6.330902561	0.885406	0.920176722	0.03924	0	1216	852	1354	1273	1319	1761	1733	1233	1756	1923
ENSMUSG00000052298	chr11	Cdc42se2	5.5E+07	5.5E+07	3661	0.02531885	5.312225603	0.8855254	0.920232607	0.03327	0	553	481	710	463	767	962	952	608	859	774
ENSMUSG00000084803	chr4	5830444B04Rik	1.6E+08	1.6E+08	5410	0.068717708	0.270239259	0.8856444	0.920288095	0.15801	0	16	12	23	7	24	49	9	17	17	26
ENSMUSG00000014771	chr17	Pdcd2	1.6E+07	1.6E+07	2582	0.031021491	3.488643753	0.8859521	0.92053958	0.04225	0	168	130	183	155	191	323	197	199	216	227
ENSMUSG00000027778	chr3	Ift80	6.9E+07	6.9E+07	12428	-0.03383398	2.410341501	0.8872789	0.921849929	0.07471	0	78	85	82	66	75	165	119	60	85	117
ENSMUSG00000070713	chr8	Gm10282	7.2E+07	7.2E+07	1159	-0.05234482	0.910815237	0.8874716	0.921913521	0.09703	0	31	14	44	31	18	59	37	20	35	33
ENSMUSG00000071014	chr4	Ndufb6	4E+07	4E+07	659	-0.02710855	6.896964147	0.8874267	0.921913521	0.04251	0	1650	1100	2599	1920	2003	2580	2576	1850	2629	2567
ENSMUSG00000019951	chr10	Uhrf1bp1l	9E+07	9E+07	6446	0.028129778	4.153850962	0.8876176	0.921928683	0.04765	0	205	130	467	273	308	478	429	256	319	389
ENSMUSG00000031283	chrX	Chrdl1	1.4E+08	1.4E+08	6755	-0.05630319	2.916047616	0.8875548	0.921928683	0.17406	0	104	132	42	65	210	287	106	130	99	143
ENSMUSG00000037972	chr16	Snn	1.1E+07	1.1E+07	2902	0.046294783	3.071765885	0.8877266	0.921935204	0.11827	0	119	65	96	60	304	232	174	147	161	158
ENSMUSG00000100215	chr1	Gm8292	5.5E+07	5.5E+07	396	0.0654106	0.431737701	0.8877554	0.921935204	0.12341	0	23	15	25	12	16	43	20	26	12	30
ENSMUSG00000042305	chr1	Tmem183a	1.3E+08	1.3E+08	3564	-0.02431016	4.169145973	0.8884786	0.922617992	0.03151	0	238	201	282	280	367	450	367	273	381	372
ENSMUSG00000074743	chr2	Thbd	1.5E+08	1.5E+08	3723	0.028219295	5.050683225	0.8885848	0.92265995	0.04442	0	416	382	503	487	690	1087	740	586	520	542
ENSMUSG00000071037	chr17	Camkmt	8.5E+07	8.5E+07	972	0.090726306	-0.15376728	0.8889036	0.922922673	0.16765	0	8	13	5	6	25	26	16	8	13	23
ENSMUSG00000015312	chr10	Gadd45b	8.1E+07	8.1E+07	1266	0.026682929	4.591806714	0.8892578	0.923153209	0.04444	0	421	169	432	318	508	498	465	396	513	624
ENSMUSG00000031075	chr7	Ano1	1.4E+08	1.4E+08	5206	0.03310215	2.566261188	0.8893528	0.923153209	0.06188	0	68	56	133	59	133	149	152	82	121	111
ENSMUSG00000045045	chr19	Lrfn4	4611785	4612638	3366	-0.06299262	2.772134048	0.8892264	0.923153209	0.22117	0	63	61	101	246	40	141	83	89	272	96
ENSMUSG00000048076	chr11	Arf1	5.9E+07	5.9E+07	2089	-0.02588794	7.944421878	0.8893889	0.923153209	0.04115	0	3610	2679	4333	3666	4574	5822	5500	3741	5261	5019
ENSMUSG00000031605	chr8	Klhl2	6.5E+07	6.5E+07	3025	-0.04813213	3.555941816	0.8897616	0.923471641	0.121	0	123	99	137	98	487	270	233	199	224	254
ENSMUSG00000022179	chr14	4931414P19Rik	5.5E+07	5.5E+07	2585	-0.03840541	2.016441781	0.8901694	0.923758257	0.05599	0	54	40	89	47	78	81	98	55	84	86
ENSMUSG00000030905	chr7	Crym	1.2E+08	1.2E+08	3391	0.051999727	1.933954431	0.8901046	0.923758257	0.08462	0	52	46	48	41	88	108	86	38	103	65
ENSMUSG00000023980	chr17	Taf8	4.7E+07	4.7E+07	2779	-0.02314743	3.943548444	0.8903491	0.923807976	0.03309	0	237	183	241	228	266	373	344	209	315	342
ENSMUSG00000031822	chr8	Gse1	1.2E+08	1.2E+08	8098	-0.02441143	5.011393048	0.8902973	0.923807976	0.03228	0	376	326	657	463	687	653	757	461	729	709
ENSMUSG00000022681	chr16	Ntan1	1.4E+07	1.4E+07	2174	-0.02334947	4.767104088	0.8914084	0.924838653	0.03208	0	427	271	402	433	542	756	582	407	519	546
ENSMUSG00000097906	chr13	Gm9625	6.8E+07	6.8E+07	955	0.025153909	5.156458199	0.8915315	0.924897955	0.03494	0	498	418	573	557	601	783	766	456	964	776
ENSMUSG00000099338	chr8	2810030D12Rik	1.3E+07	1.3E+07	1422	0.073241689	0.179451255	0.8917652	0.925072007	0.09373	0	19	12	13	9	22	26	27	20	17	18
ENSMUSG00000021286	chr12	Zfyve21	1.1E+08	1.1E+08	1310	0.028973913	3.827687724	0.8923568	0.925565009	0.04324	0	213	160	183	203	290	375	241	232	315	311
ENSMUSG00000024099	chr17	Ndufv2	6.6E+07	6.6E+07	1990	-0.02735763	8.533335131	0.8923724	0.925565009	0.04853	0	4937	3336	7899	6746	5879	8242	8593	5664	7316	8237
ENSMUSG00000070371	chr7	Prss36	1.3E+08	1.3E+08	3221	0.031704235	2.859407736	0.8924634	0.925590948	0.05086	0	111	71	125	80	155	164	138	118	171	155
ENSMUSG00000072582	chr11	Ptrh2	8.7E+07	8.7E+07	3132	0.024648188	4.105517614	0.8925463	0.925608444	0.03171	0	266	193	306	227	289	416	335	281	369	383

ENSMUSG00000049577	chr8	Zfpm1	1.2E+08	1.2E+08	3503	0.039440253	2.263249068	0.8929974	0.925939357	0.10582	0	40	28	159	60	87	108	126	69	109	82
ENSMUSG00000057143	chr7	Trim12c	1E+08	1E+08	3740	0.034091527	3.464514041	0.8929795	0.925939357	0.05138	0	170	149	177	117	192	340	229	143	209	245
ENSMUSG00000041351	chr4	Rap1gap	1.4E+08	1.4E+08	6429	0.034976229	4.28229524	0.8934036	0.926168286	0.08291	0	199	91	545	347	359	436	541	217	454	415
ENSMUSG00000063480	chr15	Nhp2l1	8.2E+07	8.2E+07	2130	0.023622198	5.64689159	0.8933103	0.926168286	0.03457	0	771	549	831	737	851	1290	1101	888	920	1005
ENSMUSG00000093185	chr4	Gm25692	4.5E+07	4.5E+07	125	-0.03803099	2.287253388	0.8934163	0.926168286	0.0673	0	68	64	63	53	116	117	86	78	105	101
ENSMUSG00000073478	chr1	D730003I15Rik	1.9E+08	1.9E+08	1687	0.070535319	0.882137778	0.8940697	0.926777123	0.11877	0	23	29	13	27	31	65	31	26	32	33
ENSMUSG00000021694	chr13	Ercc8	1.1E+08	1.1E+08	7657	0.033003171	2.396949227	0.8945383	0.927110916	0.04521	0	73	52	95	82	86	137	103	75	116	113
ENSMUSG00000047867	chr6	Gimap6	4.9E+07	4.9E+07	3496	0.02108256	5.028653197	0.89459	0.927110916	0.02863	0	493	310	606	478	584	767	677	544	610	789
ENSMUSG00000097320	chr7	C630016N16Rik	3.1E+07	3.1E+07	1416	-0.05661603	0.796243711	0.8945672	0.927110916	0.07663	0	26	14	32	20	36	34	49	23	33	27
ENSMUSG00000037787	chr12	Apopt1	1.1E+08	1.1E+08	3945	-0.02127068	5.068515533	0.8947991	0.927190649	0.02719	0	481	341	607	506	639	736	710	506	798	690
ENSMUSG00000039033	chr2	Tasp1	1.4E+08	1.4E+08	3652	-0.03333807	2.603444817	0.894762	0.927190649	0.06528	0	99	78	115	88	69	159	135	112	96	106
ENSMUSG00000028452	chr4	Vcp	4.3E+07	4.3E+07	4851	0.025333991	9.057908274	0.8948852	0.927211284	0.04391	0	7464	5278	10238	8212	9204	12346	11539	8920	11878	10800
ENSMUSG00000079017	chr12	Ifi27l2a	1E+08	1E+08	463	0.097487395	6.274868109	0.8950558	0.927319564	0.63231	0	863	696	42	61	4321	3484	784	1002	1900	1372
ENSMUSG00000060227	chr2	Casc4	1.2E+08	1.2E+08	5858	0.034627493	2.35894501	0.8952243	0.927425616	0.09604	0	63	28	160	53	95	121	124	89	82	108
ENSMUSG00000018604	chr5	Tbx3	1.2E+08	1.2E+08	5365	-0.03960025	2.769720502	0.8953869	0.927525639	0.0733	0	59	70	122	83	198	170	139	104	124	151
ENSMUSG00000031755	chr8	Bbs2	9.4E+07	9.4E+07	3194	0.035856291	2.619647103	0.8955156	0.927590398	0.06503	0	104	60	85	72	132	173	127	103	87	145
ENSMUSG00000033706	chr6	Smyd5	8.5E+07	8.5E+07	3169	0.024612132	3.529598863	0.8960558	0.928081473	0.03716	0	151	110	223	181	205	268	265	192	264	203
ENSMUSG00000101599	chr1	Gm20342	6.3E+07	6.3E+07	9720	-0.05447376	0.447951947	0.8963736	0.928342038	0.14645	0	27	20	17	10	20	26	30	12	16	46
ENSMUSG00000032264	chr9	Zw10	4.9E+07	4.9E+07	2895	0.025855604	3.189811002	0.8968488	0.928765623	0.04035	0	117	83	184	143	161	191	221	144	193	192
ENSMUSG00000020381	chr11	3010026O09Rik	5E+07	5E+07	2039	-0.04890539	1.426147413	0.8976106	0.929451984	0.08426	0	32	29	55	29	57	42	69	47	64	37
ENSMUSG00000079179	chr12	Rab10os	3235504	3235929	6144	-0.02873674	2.976869136	0.8976441	0.929451984	0.04773	0	96	100	130	116	149	176	155	112	148	208
ENSMUSG00000103983	chr1	RP23-395H6.2	1.7E+08	1.7E+08	5577	0.093612624	-0.08146791	0.8977326	0.929474966	0.17891	0	13	16	7	5	18	15	15	10	14	36
ENSMUSG00000032479	chr9	Map4	1.1E+08	1.1E+08	10576	0.026598871	9.154465988	0.8983874	0.930054009	0.05185	0	7628	4903	12314	10118	8582	12977	14611	8557	11273	12391
ENSMUSG00000032657	chr3	Fam189b	8.9E+07	8.9E+07	3649	-0.02452206	4.424447948	0.8984245	0.930054009	0.04534	0	347	274	245	339	387	472	491	284	528	434
ENSMUSG00000043909	chr2	Trp53bp1	1.2E+08	1.2E+08	14164	-0.02410781	4.491379496	0.8985159	0.930079977	0.03946	0	288	260	525	337	308	544	610	315	455	396
ENSMUSG00000033047	chr15	Eif3l	7.9E+07	7.9E+07	1893	0.02259464	6.020304858	0.8988718	0.930379705	0.0371	0	859	595	1251	1067	1176	1495	1350	1023	1387	1509
ENSMUSG00000024079	chr17	Eif2ak2	7.9E+07	7.9E+07	5113	-0.03090213	2.886028263	0.8991161	0.930426575	0.05656	0	94	89	157	75	149	209	155	96	165	132
ENSMUSG00000048758	chr9	Rpl29	1.1E+08	1.1E+08	796	0.022277266	4.27867389	0.8990687	0.930426575	0.03199	0	254	196	353	337	317	407	417	305	466	414
ENSMUSG00000099411	chr16	2310015D24Rik	1.4E+07	1.4E+07	3035	0.027592412	5.209268517	0.8990416	0.930426575	0.05058	0	668	449	480	490	617	904	918	618	895	516
ENSMUSG00000021108	chr12	Prkch	7.4E+07	7.4E+07	4519	-0.03188351	3.162573275	0.8994833	0.93073792	0.05224	0	109	68	218	144	162	214	211	113	205	174
ENSMUSG00000000028	chr16	Cdc45	1.9E+07	1.9E+07	2252	0.040768386	1.937583986	0.899569	0.930757988	0.05682	0	66	38	55	49	69	98	80	62	81	70
ENSMUSG00000022863	chr16	Btg3	7.8E+07	7.8E+07	1439	0.057165747	0.687062931	0.8998919	0.931023414	0.10735	0	24	15	13	23	36	36	37	34	27	22
ENSMUSG00000031955	chr8	Bcar1	1.1E+08	1.1E+08	3171	0.023871403	3.917399516	0.900099	0.931100278	0.03782	0	153	155	279	277	275	347	323	239	334	323
ENSMUSG00000070972	chr4	Dnajc25	5.9E+07	5.9E+07	4542	-0.02800915	3.642511443	0.9000975	0.931100278	0.04545	0	137	118	308	211	195	308	314	177	240	242
ENSMUSG00000008540	chr6	Mgst1	1.4E+08	1.4E+08	2013	0.04399611	5.861208087	0.9001813	0.931116727	0.14692	0	647	381	1450	219	1996	1552	1322	915	1134	1209
ENSMUSG00000025731	chr17	0610011F06Rik	2.6E+07	2.6E+07	1109	0.025338635	4.848758954	0.9004601	0.931271068	0.04099	0	439	358	360	449	504	613	555	438	772	615
ENSMUSG00000036781	chr9	Rps27l	6.7E+07	6.7E+07	816	0.024061	5.806070146	0.9004633	0.931271068	0.04078	0	902	684	786	808	935	1335	1111	990	1202	1155
ENSMUSG00000042121	chr5	Ssh1	1.1E+08	1.1E+08	8892	0.0255757	3.508684561	0.9006673	0.93141336	0.04175	0	128	115	203	164	251	298	225	163	221	281
ENSMUSG00000032051	chr9	Fdx1	5.2E+07	5.2E+07	861	-0.02626273	4.94789488	0.9008183	0.931432196	0.04292	0	389	231	841	413	586	699	704	486	647	621
ENSMUSG00000045414	chr9	1190002N15Rik	9.5E+07	9.5E+07	3950	-0.03164277	2.817604254	0.900778	0.931432196	0.05435	0	112	64	137	79	150	191	169	106	116	135
ENSMUSG00000039246	chr1	Lyplal1	1.9E+08	1.9E+08	1578	0.045611129	2.231381108	0.9014618	0.932000618	0.13296	0	68	34	48	41	163	158	78	79	95	75
ENSMUSG00000089736	chr8	Tgfbr3l	4248214	4248352	1870	0.071348239	0.19106765	0.901501	0.932000618	0.12462	0	15	11	19	7	25	35	15	8	28	26
ENSMUSG00000021811	chr14	Dnajc9	2E+07	2E+07	1631	-0.02069932	4.339748767	0.901646	0.932081854	0.02784	0	292	221	383	271	379	483	428	321	407	433
ENSMUSG00000015697	chr3	Setdb1	9.5E+07	9.5E+07	6853	0.021273292	4.276682154	0.9020276	0.932391241	0.03046	0	232	206	374	320	327	487	443	313	406	365
ENSMUSG00000021831	chr14	Ero1l	4.5E+07	4.5E+07	4413	0.034642745	2.790053251	0.9021314	0.932391241	0.05833	0	88	98	104	95	114	188	155	110	101	163
ENSMUSG00000025264	chrX	Tsr2	1.5E+08	1.5E+08	3805	0.026320723	3.657729254	0.9021744	0.932391241	0.04627	0	194	143	205	133	266	327	239	239	242	250
ENSMUSG00000037710	chr10	Cisd1	7.1E+07	7.1E+07	1084	0.023838334	7.525274048	0.9022777	0.932391241	0.04483	0	2429	1733	3980	2976	2938	3968	4096	2887	4112	4140
ENSMUSG00000060121	chr12	Gemin2	5.9E+07	5.9E+07	2415	-0.03371767	2.72360676	0.9022718	0.932391241	0.0646	0	122	78	92	79	120	160	112	131	111	142
ENSMUSG00000051314	chr7	Ffar2	3.1E+07	3.1E+07	2790	-0.11240036	1.127569378	0.9023574	0.932404988	0.7963	0	28	20	0	0	123	81	20	38	23	45
ENSMUSG00000011096	chr7	Akt1s1	4.5E+07	4.5E+07	3201	0.023921875	7.146331048	0.9026384	0.932489256	0.04497	0	1825	1460	2640	2351	2429	2928	3156	2036	3628	3062
ENSMUSG00000026564	chr1	Dusp27	1.7E+08	1.7E+08	4049	0.024252735	6.519464627	0.9025997	0.932489256	0.04662	0	1035	878	2181	1522	1415	2032	2140	1512	2002	1855
ENSMUSG00000036009	chr10	Mettl25	1.1E+08	1.1E+08	2688	0.035852578	1.710430937	0.9026043	0.932489256	0.06029	0	51	27	63	42	57	86	68	48	51	81
ENSMUSG00000051444	chr3	Bbs12	3.7E+07	3.7E+07	2436	-0.05103417	0.377570789	0.9028996	0.932690352	0.08886	0	17	18	21	13	22	28	21	24	16	31
ENSMUSG00000020400	chr11	Tnip1	5.5E+07	5.5E+07	3539	0.022969345	6.159891496	0.9033339	0.932932865	0.04035	0	934	832	1277	1066	1247	1465	1779	982	1687	1578
ENSMUSG00000041153	chr4	Osgin2	1.6E+07	1.6E+07	5571	0.033972281	2.695237939	0.9032114	0.932932865	0.05655	0	71	84	142	75	106	163	170	90	110	141
ENSMUSG00000078173	chr3	Lenep	8.9E+07	8.9E+07	1806	-0.02933638	3.149074481	0.9033068	0.932932865	0.04971	0	99	89	192	151	150	188	185	108	193	233
ENSMUSG00000055368	chr8	Slc6a2	9.3E+07	9.3E+07	6176	-0.031859	0.983636003	0.9038524	0.933399612	0.07159	0	28	22	38	27	28	50	35	22	33	54
ENSMUSG00000001508	chr11	Sgca	9.5E+07	9.5E+07	1735	-0.02508413	7.598532892	0.9040119	0.9334734	0.05094	0	2568	1861	4218	3377	2981	3591	4491	2892	4808	4051
ENSMUSG00000038965	chr16	Ube2l3	1.7E+07	1.7E+07	5599	-0.02323399	7.236833738	0.9040853	0.9334734	0.04393	0	2231	1630	2491	2531	2587	3222	3419	2322	3501	3006
ENSMUSG00000087178	chr7	A230056P14Rik	5.6E+07	5.6E+07	2354	0.065902644	0.766816863	0.9041235	0.9334734	0.10334	0	24	23	20	30	17	33	48	32	27	27
ENSMUSG00000040749	chrX	Siah1b	1.6E+08	1.6E+08	2119	-0.04156153	1.369339388	0.9043662	0.933655293	0.06858	0	51	23	38	33	45	59	60	39	51	44
ENSMUSG00000005514	chr5	Por	1.4E+08	1.4E+08	4021	-0.04009787	5.323576473	0.9049339	0.934172569	0.12695	0	452	316	452	321	1701	1086	603	667	890	827
ENSMUSG00000052676	chrX	Zmat1	1.3E+08	1.3E+08	5391	0.035947043	0.988949138	0.9053048	0.934486732	0.07475	0	30	13	32	26	42	58	32	29	38	41
ENSMUSG00000006057	chr11	Atp5g1	9.6E+07	9.6E+07	4912	0.030517406	8.844047072	0.9053874	0.934503132	0.07874	0	4682	3472	11456	9812	6094	8794	11916	6027	10604	11058
ENSMUSG00000018820	chr19	Zfyve27	4.2E+07	4.2E+07	8623	-0.02258535	4.236332238	0.9055434	0.934595402	0.03333	0	249	180	347	249	437	446	423	275	396	396
ENSMUSG00000055003	chr6	Lrtm2	1.2E+08	1.2E+08	4102	-0.08550942	0.743570735	0.90597	0.93496692	0.43446	0	10	14	12	4	89	65	57	11	11	20
ENSMUSG00000068732	chr3	Tmem167b	1.1E+08	1.1E+08	2948	0.01973598	4.867730435	0.9063105	0.935249484	0.02835	0	414	327	497	382	574	770	630	442	557	654

ENSMUSG00000041133	chrX	Smc1a	1.5E+08	1.5E+08	5769	-0.02103253	5.536823223	0.9066795	0.93556148	0.03585	0	637	481	854	790	787	1312	958	788	828	885
ENSMUSG00000020319	chr11	Wdpcp	2.2E+07	2.2E+07	5934	0.041250936	1.635162809	0.9068677	0.935584751	0.07602	0	55	33	37	41	55	103	58	38	60	62
ENSMUSG00000021079	chr12	Timm9	7.1E+07	7.1E+07	1018	-0.02251036	4.067978104	0.9068981	0.935584751	0.03592	0	202	189	336	282	267	421	300	296	336	350
ENSMUSG00000085379	chr11	2310058D17Rik	5.9E+07	5.9E+07	3201	-0.03682632	0.513976828	0.9069022	0.935584751	0.08039	0	19	15	22	22	23	28	40	12	29	28
ENSMUSG00000027634	chr2	Ndrg3	1.6E+08	1.6E+08	8388	0.018778519	5.169963487	0.9069977	0.935614473	0.02767	0	501	379	660	517	662	946	856	562	695	703
ENSMUSG00000028549	chr4	Itgb3bp	1E+08	1E+08	4632	-0.03641634	1.851752182	0.9073539	0.935913058	0.05423	0	60	31	62	58	59	79	75	51	80	74
ENSMUSG00000048939	chr16	Atp13a5	2.9E+07	2.9E+07	4661	0.037249627	1.56798167	0.9076282	0.936127185	0.12576	0	44	17	75	23	65	72	90	53	49	34
ENSMUSG00000000568	chr5	Hnrnpd	1E+08	1E+08	4863	-0.0198583	5.424063572	0.9079237	0.936320281	0.03285	0	532	510	857	653	719	1064	877	729	800	924
ENSMUSG00000031351	chrX	Zfp185	7.3E+07	7.3E+07	3707	0.054852741	2.028172802	0.9079608	0.936320281	0.20762	0	59	40	31	17	155	150	56	57	86	77
ENSMUSG00000042763	chr4	Maneal	1.2E+08	1.2E+08	2727	0.060012784	0.16577712	0.9080157	0.936320281	0.15906	0	10	8	13	13	33	21	42	16	10	18
ENSMUSG00000002767	chr17	Mrpl2	4.7E+07	4.7E+07	1170	0.023074478	6.131228391	0.9081524	0.936388886	0.0479	0	875	541	1502	1262	1229	1463	1445	1047	1679	1672
ENSMUSG00000032336	chr9	Nptn	5.9E+07	5.9E+07	6168	0.023791879	6.522341162	0.9082825	0.936388886	0.04815	0	1522	1200	1259	1160	1596	2241	2243	1435	1870	1830
ENSMUSG00000054226	chr6	Tprkb	8.6E+07	8.6E+07	3491	0.024801475	4.781891655	0.9082388	0.936388886	0.04281	0	427	412	364	353	427	724	553	447	568	574
ENSMUSG00000073422	chr17	H2-Ke6	3.4E+07	3.4E+07	1533	0.019964298	5.699058118	0.9085676	0.936613932	0.03436	0	706	524	949	862	881	1197	1011	833	1177	1179
ENSMUSG00000026199	chr1	Ankzf1	7.5E+07	7.5E+07	5142	-0.02495796	2.837540192	0.9087997	0.936762385	0.05229	0	93	100	107	94	136	180	132	105	138	171
ENSMUSG00000058835	chr2	Abi1	2.3E+07	2.3E+07	4032	-0.01899708	4.388822328	0.9088452	0.936762385	0.03176	0	320	241	346	301	373	587	489	308	377	405
ENSMUSG00000044864	chr3	Ankrd50	3.8E+07	3.8E+07	8488	0.021479444	3.638883257	0.9090594	0.936914285	0.04073	0	135	107	269	195	250	327	278	187	241	265
ENSMUSG00000025185	chr19	Loxl4	4.3E+07	4.3E+07	4213	0.043611979	1.059893427	0.9094664	0.937264896	0.13323	0	31	6	41	43	31	62	46	38	35	26
ENSMUSG00000020775	chr11	Mrpl38	1.2E+08	1.2E+08	2550	0.021681515	5.970638427	0.9099538	0.937687029	0.04363	0	760	534	1404	1035	1102	1296	1412	878	1528	1442
ENSMUSG00000044881	chr7	Coa4	1E+08	1E+08	1425	-0.02665546	2.890845655	0.9100097	0.937687029	0.04985	0	105	68	171	112	112	212	148	112	146	138
ENSMUSG00000045104	chr19	Gm5514	2.2E+07	2.2E+07	306	-0.07255065	1.679260708	0.9105309	0.938155157	0.37248	0	23	3	151	66	20	43	98	19	67	90
ENSMUSG00000015354	chr9	Pcolce2	9.6E+07	9.6E+07	4625	0.031373195	4.064040375	0.9107939	0.938357226	0.0836	0	237	181	166	167	506	553	310	263	285	349
ENSMUSG00000020160	chr11	Meis1	1.9E+07	1.9E+07	10532	-0.03049362	2.231862797	0.9109225	0.938420747	0.06623	0	41	61	80	83	85	101	119	80	82	86
ENSMUSG00000040717	chr14	Il17rd	2.7E+07	2.7E+07	8220	-0.02508548	2.620986612	0.9110275	0.938459987	0.04836	0	79	62	112	88	127	177	143	78	116	117
ENSMUSG00000026303	chr1	Mlph	9.1E+07	9.1E+07	5357	0.062925802	0.843911225	0.9111378	0.938504687	0.42961	0	4	7	99	4	26	32	72	19	20	35
ENSMUSG00000021520	chr13	Uqcrb	6.7E+07	6.7E+07	876	-0.02225142	8.410576402	0.9114001	0.938637037	0.04739	0	4947	3157	7231	5836	5114	7519	7350	5354	6908	7794
ENSMUSG00000103041	chr3	RP24-372I24.4	6.6E+07	6.6E+07	4279	-0.03830944	0.568624598	0.9113812	0.938637037	0.08392	0	20	18	27	11	30	40	33	19	23	27
ENSMUSG00000003477	chr6	Inmt	5.5E+07	5.5E+07	1600	-0.04016229	3.902206787	0.9116639	0.938839809	0.15485	0	121	284	146	127	428	393	479	157	146	385
ENSMUSG00000062761	chr5	Zfp512	3.1E+07	3.1E+07	3293	-0.0185928	4.382689379	0.9119482	0.939063643	0.02755	0	281	224	430	302	359	482	452	320	425	460
ENSMUSG00000030495	chr7	Slc7a10	3.5E+07	3.5E+07	2463	-0.09447348	1.865972436	0.9122553	0.93924189	0.73453	0	57	44	0	2	178	151	25	49	57	81
ENSMUSG00000040652	chr9	Oaz2	6.6E+07	6.6E+07	2990	-0.02146105	7.690839307	0.9122285	0.93924189	0.0448	0	3392	2086	4137	3002	3212	4745	4827	3201	4552	3927
ENSMUSG00000030816	chr7	Rnf40	1.3E+08	1.3E+08	4154	-0.02029929	5.585567417	0.9125888	0.939510217	0.03695	0	587	461	1099	811	765	1096	1034	729	1027	1050
ENSMUSG00000032590	chr9	Apeh	1.1E+08	1.1E+08	5651	0.018308656	5.206002669	0.9127168	0.939510217	0.0318	0	506	336	710	638	614	842	766	564	903	764
ENSMUSG00000073535	chr1	Gm5532	1.6E+08	1.6E+08	2206	-0.08065705	2.19682859	0.9126941	0.939510217	0.47427	0	24	3	258	88	17	95	153	63	32	108
ENSMUSG00000031303	chrX	Map3k15	1.6E+08	1.6E+08	4348	0.07146941	2.175784367	0.9130404	0.939705335	0.49305	0	25	17	186	63	65	17	138	5	91	228
ENSMUSG00000059327	chrX	Eda	1E+08	1E+08	6825	0.036716236	1.980845528	0.9130373	0.939705335	0.07576	0	59	44	46	47	90	113	79	44	98	76
ENSMUSG00000026687	chr1	Aldh9a1	1.7E+08	1.7E+08	3383	0.035286814	3.637376671	0.9133118	0.939915759	0.12004	0	187	96	154	82	443	407	199	203	222	272
ENSMUSG00000046574	chr7	Prr12	4.5E+07	4.5E+07	6879	0.018129266	4.544279898	0.9134979	0.940038274	0.02772	0	308	248	419	370	410	516	510	345	564	490
ENSMUSG00000041375	chr7	Ccdc9	1.6E+07	1.6E+07	5507	0.01786584	4.737811238	0.9138133	0.940293827	0.02589	0	374	295	465	404	461	635	567	387	588	606
ENSMUSG00000038370	chr1	Pcp4l1	1.7E+08	1.7E+08	1577	0.045784487	3.289459898	0.9141673	0.940451084	0.21201	0	56	43	433	185	65	168	248	134	187	280
ENSMUSG00000098220	chr13	Gm27031	9.6E+07	9.6E+07	2578	0.073443508	-0.2053289	0.9141638	0.940451084	0.11821	0	10	12	6	8	19	18	22	15	12	13
ENSMUSG00000098234	chr1	Snhg6	9941959	9942155	1146	-0.03431178	2.15973834	0.914108	0.940451084	0.08056	0	67	61	83	50	69	103	55	95	83	101
ENSMUSG00000031642	chr8	Sh3rf1	6.1E+07	6.1E+07	5181	0.025313901	1.843502518	0.9150628	0.941273033	0.06862	0	46	33	68	39	81	63	67	56	86	89
ENSMUSG00000039735	chr3	Fnbp1l	1.2E+08	1.2E+08	5408	0.027034387	2.249595979	0.9151005	0.941273033	0.05261	0	66	44	98	57	90	140	100	69	92	90
ENSMUSG00000017221	chr11	Psmd3	9.9E+07	9.9E+07	4967	0.019930928	7.133811035	0.9160567	0.942127065	0.04215	0	1880	1401	2758	2281	2336	3071	3150	2194	3281	2926
ENSMUSG00000030505	chr7	Prmt3	5E+07	5E+07	3361	-0.01810618	4.246274475	0.9160651	0.942127065	0.03243	0	255	245	317	279	326	434	382	327	415	371
ENSMUSG00000078546	chr17	2210404O09Rik	2.2E+07	2.2E+07	3167	-0.05666614	0.050658209	0.9162032	0.942199997	0.07668	0	10	8	21	15	19	24	23	12	14	22
ENSMUSG00000000827	chr2	Tpd52l2	1.8E+08	1.8E+08	4982	-0.01823452	5.680865939	0.9163472	0.942279057	0.03511	0	799	594	867	696	928	1349	1180	799	986	981
ENSMUSG00000021514	chr13	Zfp369	6.5E+07	6.5E+07	5896	-0.02502966	2.178524306	0.9164625	0.942328451	0.0612	0	72	63	77	54	65	117	84	63	85	108
ENSMUSG00000020936	chr11	Nmt1	1E+08	1E+08	5017	-0.0190607	6.401842013	0.9168813	0.942690047	0.03783	0	1161	878	1741	1152	1599	1999	1810	1374	1713	1783
ENSMUSG00000023795	chr17	Pisd-ps2	3076578	3076782	2108	0.037583899	2.791199104	0.9169964	0.942739269	0.10023	0	113	107	75	60	137	234	137	81	104	178
ENSMUSG00000032271	chr9	Nnmt	4.9E+07	4.9E+07	1576	0.07405478	3.224502542	0.9176709	0.943363561	0.55113	0	95	103	7	15	488	341	55	198	197	181
ENSMUSG00000013495	chr5	Tmem175	1.1E+08	1.1E+08	3875	0.026542604	3.189993732	0.9186314	0.944281744	0.04887	0	151	94	137	121	173	235	233	101	193	199
ENSMUSG00000030056	chr6	Isy1	8.8E+07	8.8E+07	1620	0.019897361	4.196817384	0.9187411	0.944325316	0.03353	0	233	232	337	275	282	470	345	304	385	395
ENSMUSG00000020638	chr12	Cmpk2	2.6E+07	2.6E+07	3198	-0.03996879	1.809763327	0.9190187	0.944541352	0.08177	0	53	25	69	35	88	104	79	50	63	55
ENSMUSG00000001924	chrX	Uba1	2.1E+07	2.1E+07	4819	-0.02036221	7.460384152	0.9192751	0.944724219	0.04723	0	2119	1675	3570	3286	2976	3836	3769	2728	4030	3718
ENSMUSG00000016496	chr19	Cd274	2.9E+07	2.9E+07	3622	0.042833411	3.113872523	0.9193313	0.944724219	0.18469	0	94	68	111	92	300	456	128	57	110	205
ENSMUSG00000039611	chr4	Tmem246	5E+07	5E+07	3325	0.020709416	5.083048301	0.9195696	0.944899854	0.04864	0	374	298	830	606	498	657	1011	446	737	701
ENSMUSG00000009090	chr11	Ap1b1	4986824	4987051	4957	0.019696734	6.130702949	0.9196719	0.944935804	0.04517	0	754	627	1569	1253	1192	1750	1511	1053	1584	1433
ENSMUSG00000046947	chr6	Adck2	4E+07	4E+07	4095	-0.01959738	7.08229534	0.9199812	0.945115126	0.04458	0	2098	1388	2685	2229	1938	3010	2821	2203	3014	2832
ENSMUSG00000075266	chr10	Cenpw	3E+07	3E+07	1510	-0.02523771	-0.13841579	0.9199752	0.945115126	0.12708	0	15	13	8	13	10	23	8	10	20	22
ENSMUSG00000084830	chrX	Gm14539	2.1E+07	2.1E+07	174	0.017750853	4.531257694	0.9202293	0.945300719	0.0314	0	304	236	464	410	325	573	528	353	456	499
ENSMUSG00000024906	chr19	Mus81	5482345	5483029	3567	-0.0161596	4.791226261	0.9204609	0.945469444	0.02803	0	370	305	521	442	468	636	557	408	667	579
ENSMUSG00000043929	chrX	Klhl15	9.4E+07	9.4E+07	9741	-0.02876569	1.696921202	0.9208105	0.945759248	0.06571	0	53	31	57	43	57	78	62	43	49	92
ENSMUSG00000032425	chr9	Zfp949	8.9E+07	8.9E+07	4110	-0.02234351	3.870024882	0.9209553	0.945838742	0.05974	0	249	179	200	184	280	422	261	199	203	428
ENSMUSG00000038160	chr10	Atg5	4.4E+07	4.4E+07	2352	-0.01844727	4.051366583	0.9214192	0.946245806	0.03395	0	234	164	338	242	294	414	438	229	294	339
ENSMUSG00000053769	chr3	Lysmd1	9.5E+07	9.5E+07	2394	-0.02978687	1.787551653	0.9216577	0.946421443	0.05799	0	55	30	57	46	71	94	66	48	61	77

ENSMUSG00000032839	chr9	Trpc1	9.6E+07	9.6E+07	8030	-0.0658269	0.093487905	0.9225773	0.947296393	0.09122	0	9	7	22	19	19	26	19	11	26	16
ENSMUSG00000019235	chr12	Rps6kl1	8.5E+07	8.5E+07	2534	0.033279766	-0.08717561	0.9226821	0.947334706	0.13161	0	5	10	20	6	23	22	13	18	13	20
ENSMUSG00000028036	chr3	Ptgfr	1.5E+08	1.5E+08	4362	0.051088139	1.340871588	0.92292	0.947509583	0.12278	0	39	37	29	27	43	48	87	33	26	64
ENSMUSG00000053094	chr5	Tmem248	1.3E+08	1.3E+08	3845	-0.01664148	5.767178118	0.9231429	0.947669103	0.03328	0	719	588	1004	849	1006	1249	1249	838	1211	1057
ENSMUSG00000023092	chrX	Fhl1	5.7E+07	5.7E+07	3714	-0.0431991	10.43738787	0.9233581	0.947820568	0.23902	0	16565	3132	46083	38781	8617	39190	39926	17181	16992	31408
ENSMUSG00000041849	chr15	Card6	5095981	5101095	6101	-0.02935365	2.235134344	0.9245501	0.948974777	0.07178	0	56	38	104	96	64	116	130	62	90	79
ENSMUSG00000042348	chr13	Arl15	1.1E+08	1.1E+08	3364	0.023982355	3.041395101	0.9247923	0.949084471	0.04826	0	140	92	115	103	155	190	174	141	175	164
ENSMUSG00000043998	chr12	Mgat2	6.9E+07	6.9E+07	2614	-0.02006049	3.516268077	0.924747	0.949084471	0.04439	0	171	130	201	138	227	326	270	182	214	181
ENSMUSG00000072762	chr5	4930522L14Rik	1.1E+08	1.1E+08	2409	-0.04974039	-0.0703543	0.9250221	0.949250827	0.13488	0	24	11	7	9	12	22	20	15	17	12
ENSMUSG00000037363	chr8	Letm2	2.6E+07	2.6E+07	2098	-0.02196969	1.876958054	0.9253444	0.949512107	0.05689	0	45	40	80	55	54	98	82	44	67	81
ENSMUSG00000011306	chr8	Sugp1	7E+07	7E+07	2287	-0.01680189	4.525232648	0.9254321	0.949532566	0.03008	0	310	211	469	376	410	512	498	320	481	563
ENSMUSG00000024346	chr18	Pfdn1	3.6E+07	3.6E+07	1077	0.016684524	6.280509344	0.9255319	0.9495655	0.03716	0	1085	780	1474	1150	1418	1691	1705	1259	1726	1681
ENSMUSG00000030098	chr6	Grip2	9.2E+07	9.2E+07	5849	-0.02047609	3.425816446	0.925961	0.94986679	0.04525	0	167	109	229	173	135	235	249	167	202	241
ENSMUSG00000056537	chrX	Rlim	1E+08	1E+08	8917	-0.01525584	4.914746493	0.9259229	0.94986679	0.02706	0	458	310	521	444	566	705	618	500	598	667
ENSMUSG00000020537	chr11	Drg2	6E+07	6E+07	2716	0.01496464	4.783935027	0.9261332	0.949974	0.02706	0	379	284	491	396	536	637	619	407	643	561
ENSMUSG00000019978	chr10	Epb4.1l2	2.5E+07	2.5E+07	4464	-0.02561406	5.523831237	0.9262048	0.949977904	0.08758	0	576	549	493	419	1517	1327	802	735	885	986
ENSMUSG00000057156	chr14	Homez	5.5E+07	5.5E+07	5907	0.027192208	2.50871278	0.9263176	0.950024163	0.04953	0	70	70	99	92	84	127	141	85	104	128
ENSMUSG00000060989	chr4	Gm11847	1.2E+07	1.2E+07	1119	-0.07853951	-0.05273883	0.9267209	0.950368343	0.40837	0	20	4	1	17	24	30	25	2	28	5
ENSMUSG00000021266	chr12	Wars	1.1E+08	1.1E+08	3447	-0.01699253	5.249056897	0.9269969	0.950581807	0.03928	0	481	380	790	637	639	1235	843	453	706	768
ENSMUSG00000031255	chrX	Sytl4	1.3E+08	1.3E+08	5125	0.056818759	0.420751219	0.9279977	0.951538555	0.19565	0	6	8	15	19	47	51	24	12	28	18
ENSMUSG00000053581	chr5	Zfand2a	1.4E+08	1.4E+08	3407	0.01769143	3.991343916	0.9283506	0.95183081	0.03364	0	238	168	259	231	294	375	428	231	306	317
ENSMUSG00000027478	chr2	Dnmt3b	1.5E+08	1.5E+08	5106	-0.04563509	0.22609861	0.9284826	0.951890508	0.09033	0	13	15	20	9	25	29	19	19	16	25
ENSMUSG00000046618	chr2	Olfml2a	3.9E+07	3.9E+07	5579	-0.01735768	2.795433933	0.9285446	0.951890508	0.04706	0	92	89	126	85	127	180	156	100	123	150
ENSMUSG00000027166	chr2	Dnajc24	1.1E+08	1.1E+08	1369	0.029440533	1.884686245	0.9290371	0.95218667	0.06375	0	59	39	52	40	79	101	86	51	64	77
ENSMUSG00000058799	chr10	Nap1l1	1.1E+08	1.1E+08	4086	0.01854483	6.611438941	0.9289703	0.95218667	0.04913	0	1585	1239	1358	1195	1849	2559	2019	1705	1780	2097
ENSMUSG00000067567	chrX	Hdac8	1E+08	1E+08	4839	0.027593384	2.244667095	0.9289335	0.95218667	0.05629	0	72	51	65	72	85	120	85	60	109	115
ENSMUSG00000053580	chr11	Tanc2	1.1E+08	1.1E+08	16494	0.019141456	3.524360371	0.9295903	0.952684073	0.04031	0	143	147	221	161	180	247	241	211	242	234
ENSMUSG00000036352	chr2	Ubac1	2.6E+07	2.6E+07	2632	0.017156271	8.025568765	0.9302334	0.953273476	0.04541	0	3501	2797	4802	4426	4088	5424	5952	4183	6104	5376
ENSMUSG00000019849	chr10	Prep	4.5E+07	4.5E+07	2729	-0.01758903	4.800745237	0.9304832	0.953320454	0.03857	0	340	251	657	516	392	661	609	472	560	547
ENSMUSG00000058587	chr9	Tmod3	7.5E+07	7.6E+07	3578	0.015605577	4.383303229	0.9304732	0.953320454	0.03779	0	278	196	404	233	495	536	475	330	426	403
ENSMUSG00000097388	chr7	Gm3200	1E+08	1E+08	1002	0.036065205	-0.04852093	0.9304509	0.953320454	0.16738	0	3	4	17	26	16	17	18	14	25	15
ENSMUSG00000027628	chr2	Aar2	1.6E+08	1.6E+08	3615	0.014184323	5.10210243	0.9310233	0.953804122	0.03101	0	398	363	667	579	596	762	739	626	723	679
ENSMUSG00000029094	chr5	Afap1	3.6E+07	3.6E+07	8543	-0.02827887	3.53033026	0.9311079	0.953821144	0.10504	0	140	130	148	79	401	320	200	187	204	266
ENSMUSG00000059540	chr2	Tcea2	1.8E+08	1.8E+08	2704	-0.02509652	2.022614576	0.9312559	0.953903077	0.05551	0	56	34	80	54	85	104	70	63	83	87
ENSMUSG00000021972	chr14	Hmbox1	6.5E+07	6.5E+07	9681	-0.01475716	4.08177487	0.9314326	0.953984225	0.03384	0	203	218	301	239	315	411	355	239	392	347
ENSMUSG00000093156	chr14	Mir3076	3.1E+07	3.1E+07	60	-0.05606969	3.779166412	0.9314711	0.953984225	0.46117	0	247	65	29	24	762	371	120	289	352	220
ENSMUSG00000039813	chr4	Tbc1d2	4.7E+07	4.7E+07	5425	0.041739139	0.899103836	0.9321625	0.954622613	0.09929	0	27	15	27	14	51	45	44	23	43	31
ENSMUSG00000029228	chr5	Lnx1	7.5E+07	7.5E+07	3988	0.019883781	1.75229782	0.9323347	0.954659547	0.08871	0	35	20	95	49	58	83	64	66	58	65
ENSMUSG00000070610	chr4	Gm13127	1.4E+08	1.4E+08	1389	0.035788599	1.026447819	0.9323133	0.954659547	0.08029	0	28	13	34	39	32	49	54	22	45	35
ENSMUSG00000048100	chr3	Taf13	1.1E+08	1.1E+08	3155	-0.01374654	4.542240771	0.9324233	0.954680543	0.03023	0	351	289	396	293	423	555	492	365	438	543
ENSMUSG00000027198	chr2	Ext2	9.4E+07	9.4E+07	7328	0.015104317	5.611600452	0.9325881	0.954779592	0.03471	0	669	517	794	738	975	1236	981	713	1190	989
ENSMUSG00000042570	chr10	Mier2	8E+07	8E+07	4497	0.016120174	4.298756897	0.9326726	0.954796401	0.03325	0	279	204	330	305	361	443	393	256	509	453
ENSMUSG00000035572	chr4	Dcaf10	4.5E+07	4.5E+07	7305	-0.01556782	3.913451821	0.9339283	0.955948363	0.03079	0	219	156	265	210	298	334	339	234	320	314
ENSMUSG00000044627	chr2	Swi5	3.2E+07	3.2E+07	5551	0.015775255	6.598739894	0.9339342	0.955948363	0.04182	0	1520	1013	1728	1428	1604	2585	1737	1667	2025	2048
ENSMUSG00000028799	chr4	Zfp362	1.3E+08	1.3E+08	3052	-0.01540308	3.914985492	0.9341618	0.956111579	0.03268	0	194	164	253	230	306	333	309	221	332	351
ENSMUSG00000020277	chr10	Pfkl	7.8E+07	7.8E+07	4395	-0.02457084	4.8489443	0.9344994	0.956387329	0.09099	0	456	164	329	365	979	638	492	490	708	596
ENSMUSG00000029402	chr5	Snrnp35	1.2E+08	1.2E+08	1347	-0.01566916	4.031016082	0.9347879	0.956590624	0.0357	0	262	165	295	253	263	345	323	241	424	339
ENSMUSG00000034164	chr11	Emid1	5106265	5106969	2890	-0.01794559	3.261336268	0.9348344	0.956590624	0.04807	0	143	111	135	138	191	185	195	136	249	210
ENSMUSG00000001441	chr11	Npepps	9.7E+07	9.7E+07	7206	-0.01728181	6.524754551	0.9355008	0.957063622	0.05161	0	1100	828	2298	1635	1315	2004	2312	1415	1762	1988
ENSMUSG00000026014	chr1	Raph1	6E+07	6E+07	20498	0.017063358	4.695005026	0.9356378	0.957063622	0.05443	0	290	191	735	441	365	626	706	365	469	548
ENSMUSG00000030768	chr1	Disp1	1.8E+08	1.8E+08	5224	0.022214877	2.411671512	0.9355637	0.957063622	0.05494	0	59	65	84	67	118	138	117	82	113	96
ENSMUSG00000032105	chr9	Pdzd3	4.4E+07	4.4E+07	2181	0.031402292	0.98530645	0.9355907	0.957063622	0.09835	0	19	14	42	46	21	44	44	25	45	39
ENSMUSG00000033767	chr3	D930015E06Rik	8.4E+07	8.4E+07	10572	0.022863514	3.687455334	0.9355291	0.957063622	0.10367	0	113	70	480	187	182	275	278	190	264	328
ENSMUSG00000098004	chr2	Gm27027	9.4E+07	9.4E+07	547	0.016283513	3.705627612	0.9362492	0.95761909	0.03672	0	198	128	253	192	210	359	285	199	221	294
ENSMUSG00000025544	chr14	Tm9sf2	1.2E+08	1.2E+08	3107	-0.01504632	6.787335283	0.9363782	0.957681281	0.0408	0	1499	1116	2364	1593	1960	2711	2704	1686	2045	2280
ENSMUSG00000027637	chr2	1110008F13Rik	1.6E+08	1.6E+08	2871	-0.01400094	5.569521054	0.9364846	0.957720232	0.03221	0	643	474	962	726	849	1196	997	789	931	968
ENSMUSG00000023923	chr17	Tbc1d5	5.1E+07	5.1E+07	5613	0.015113346	3.846142047	0.9365541	0.957721514	0.03379	0	188	145	258	241	250	344	312	223	344	265
ENSMUSG00000078350	chr4	Smim1	1.5E+08	1.5E+08	5761	-0.03727945	2.53874597	0.93718	0.958291641	0.18453	0	51	60	56	32	258	177	111	84	113	104
ENSMUSG00000014748	chr6	Tex261	8.4E+07	8.4E+07	4088	0.014394361	6.466989264	0.9374941	0.958542969	0.03801	0	1163	969	1565	1397	1580	2067	2019	1258	1997	1913
ENSMUSG00000024112	chr17	Cacna1h	2.5E+07	2.5E+07	9763	0.032391927	1.140365798	0.9378974	0.958885438	0.08289	0	30	20	55	22	33	60	36	26	57	43
ENSMUSG00000020538	chr11	Srebf1	6E+07	6E+07	5634	0.028076806	6.404734637	0.9384878	0.959069594	0.15745	0	647	568	1063	825	3721	1550	2785	987	2046	1591
ENSMUSG00000025260	chrX	Hsd17b10	1.5E+08	1.5E+08	1298	0.014014467	5.706875391	0.9384585	0.959069594	0.03575	0	719	616	854	774	944	1134	1029	883	1225	1117
ENSMUSG00000031158	chrX	Timm17b	7899357	7899469	2557	-0.01357669	5.002567135	0.9383308	0.959069594	0.03533	0	532	373	504	453	542	713	605	504	845	616
ENSMUSG00000033423	chr4	Eri3	1.2E+08	1.2E+08	3007	0.014620314	6.399155531	0.9382171	0.959069594	0.04016	0	1100	944	1471	1416	1407	1810	1856	1277	2022	1810
ENSMUSG00000034850	chr2	Tmem127	1.3E+08	1.3E+08	4811	0.013222613	5.877869227	0.9382773	0.959069594	0.03295	0	824	612	1184	846	998	1423	1290	939	1170	1292
ENSMUSG00000039725	chr2	2810408M09Rik	1.7E+08	1.7E+08	2118	0.015347067	3.587132578	0.9383609	0.959069594	0.03788	0	158	129	228	184	202	285	230	213	285	218
ENSMUSG00000029387	chr5	Gtf2h3	1.2E+08	1.2E+08	3840	-0.01645559	3.557422332	0.9386114	0.959126032	0.03658	0	179	104	229	188	200	315	261	177	227	230

ENSMUSG00000007476	chr2	Lrrc8a	3E+07	3E+07	4308	0.014390568	4.128980777	0.9391857	0.959642984	0.05002	0	191	119	436	274	353	416	412	278	305	403
ENSMUSG00000027018	chr2	Hat1	7.1E+07	7.1E+07	2886	0.013776739	4.339322668	0.9393331	0.959723669	0.03341	0	282	213	436	308	287	511	453	352	384	390
ENSMUSG00000030584	chr7	Dpf1	2.9E+07	2.9E+07	3529	0.025090747	0.743092955	0.9398822	0.960214704	0.17808	0	8	9	48	14	47	27	52	20	37	27
ENSMUSG00000032643	chr4	Fhl3	1.2E+08	1.2E+08	1683	0.016822921	6.809512201	0.9400426	0.960308641	0.06059	0	1393	761	2569	1413	2754	2711	2710	1466	2383	2547
ENSMUSG00000031994	chr9	Adamts8	3.1E+07	3.1E+07	4613	0.062779721	1.832026697	0.9403913	0.960594926	0.67729	0	1	2	105	155	7	62	64	38	78	124
ENSMUSG00000063870	chr6	Chd4	1.3E+08	1.3E+08	8019	-0.01415857	7.06321906	0.9406204	0.96075894	0.04173	0	1711	1338	2739	1987	2576	3134	2992	1893	3087	2751
ENSMUSG00000019779	chr10	Frk	3.4E+07	3.4E+07	4799	-0.04133285	0.57464602	0.9408017	0.960824021	0.08284	0	12	16	31	18	31	43	26	21	29	23
ENSMUSG00000038725	chr15	Pkhd1l1	4.4E+07	4.4E+07	12754	-0.01088783	0.374921355	0.9408211	0.960824021	0.1173	0	24	17	12	21	13	22	36	13	24	29
ENSMUSG00000027430	chr2	Dtd1	1.4E+08	1.4E+08	2353	0.017856687	3.41702236	0.9410634	0.961001499	0.04271	0	153	117	139	172	210	249	251	158	221	227
ENSMUSG00000017764	chr2	Zswim1	1.6E+08	1.6E+08	2781	-0.0169544	3.213041644	0.9411548	0.96102482	0.03927	0	121	100	175	142	164	206	183	163	205	179
ENSMUSG00000021368	chr13	Tbc1d7	4.3E+07	4.3E+07	1259	-0.01564769	4.139669827	0.9413649	0.961099398	0.03516	0	229	151	364	308	309	379	367	271	414	372
ENSMUSG00000071757	chr15	Zhx2	5.8E+07	5.8E+07	4434	-0.01348264	5.522721318	0.941303	0.961099398	0.03964	0	621	597	754	761	695	871	1038	760	1005	1017
ENSMUSG00000030870	chr7	Ubfd1	1.2E+08	1.2E+08	9629	0.01319774	5.151938782	0.9414886	0.961155758	0.03174	0	541	419	595	532	556	910	696	626	764	675
ENSMUSG00000030774	chr7	Pak1	9.8E+07	9.8E+07	3065	0.017272996	6.184888255	0.9415575	0.961156107	0.06144	0	1390	944	843	955	1151	1455	1574	1302	1756	1391
ENSMUSG00000074811	chr19	Hps6	4.6E+07	4.6E+07	2696	-0.0185906	2.481107219	0.941665	0.961195942	0.06244	0	61	67	120	96	73	125	136	81	134	89
ENSMUSG00000039318	chr1	Rab3gap2	1.9E+08	1.9E+08	10800	-0.01164213	4.913242038	0.9419179	0.961384135	0.02761	0	414	328	546	507	487	685	721	461	612	624
ENSMUSG00000045671	chr11	Spred2	2E+07	2E+07	4619	0.013891687	3.532143529	0.9422117	0.961614022	0.04059	0	165	106	233	143	235	299	278	190	196	233
ENSMUSG00000025395	chr10	Prim1	1.3E+08	1.3E+08	3868	0.034823427	0.453730209	0.9423035	0.961637754	0.11021	0	29	12	21	11	21	42	20	24	27	19
ENSMUSG00000021710	chr13	Nln	1E+08	1E+08	3780	0.013507317	3.510382267	0.9425329	0.961665625	0.05076	0	133	86	256	144	269	293	242	188	219	234
ENSMUSG00000025037	chrX	Maoa	1.7E+07	1.7E+07	4167	-0.01497528	3.818003206	0.9425087	0.961665625	0.05795	0	237	210	146	177	256	351	293	228	281	289
ENSMUSG00000027079	chr2	Clp1	8.5E+07	8.5E+07	2672	-0.0204515	2.400441984	0.9425365	0.961665625	0.04744	0	72	58	91	79	95	147	104	87	95	100
ENSMUSG00000078784	chr3	1810022K09Rik	1.5E+07	1.5E+07	1753	0.016644658	3.579497674	0.9427041	0.961766626	0.0384	0	184	141	179	162	218	316	240	194	227	259
ENSMUSG00000054200	chr19	Ffar4	3.8E+07	3.8E+07	1393	-0.07115354	0.148892665	0.9428893	0.961885656	0.51945	0	18	6	0	1	56	28	15	13	25	20
ENSMUSG00000002250	chr17	Ppard	2.8E+07	2.8E+07	4631	0.01158414	4.772744027	0.9434202	0.96235724	0.03298	0	336	239	602	451	475	585	569	416	633	628
ENSMUSG00000019826	chr10	Zbtb24	4.1E+07	4.1E+07	2828	-0.01283389	2.341836419	0.9444892	0.96337766	0.05644	0	67	74	81	72	75	126	118	81	93	94
ENSMUSG00000020964	chr12	Sel1l	9.2E+07	9.2E+07	8555	-0.0122211	6.084693787	0.9447532	0.963576768	0.03581	0	942	745	1229	1058	1189	1689	1550	1026	1296	1464
ENSMUSG00000085037	chr4	4933421O10Rik	3.3E+07	3.3E+07	3847	-0.02569616	0.697596237	0.944852	0.963607527	0.0808	0	20	16	18	32	29	45	34	21	29	28
ENSMUSG00000057342	chr7	Sphk2	4.6E+07	4.6E+07	4159	-0.01126615	4.711651032	0.945918	0.964554434	0.02932	0	343	294	495	414	442	584	542	377	671	525
ENSMUSG00000063145	chr2	Bbs5	7E+07	7E+07	2445	-0.01670045	1.866053296	0.945875	0.964554434	0.07359	0	55	53	67	41	48	85	70	73	71	60
ENSMUSG00000003234	chr16	Abcf3	2.1E+07	2.1E+07	3557	-0.01221055	6.112061127	0.9460036	0.964571579	0.03635	0	970	712	1312	1115	1176	1551	1504	1073	1526	1468
ENSMUSG00000052911	chr9	Lamb2	1.1E+08	1.1E+08	6082	0.014325576	7.802908621	0.946124	0.964624195	0.05341	0	2757	1907	4211	4640	3542	5060	4701	3296	5447	4788
ENSMUSG00000040016	chr3	Ptger3	1.6E+08	1.6E+08	2107	0.054175127	2.072076253	0.9463006	0.964734134	0.68453	0	51	50	1	3	207	133	23	95	109	63
ENSMUSG00000025608	chr6	Podxl	3.2E+07	3.2E+07	5488	0.01544144	5.673363634	0.9469718	0.965168298	0.06566	0	521	383	1500	924	672	1290	1056	812	904	1255
ENSMUSG00000027122	chr2	Arl14ep	1.1E+08	1.1E+08	5313	-0.0157929	3.011782402	0.9470932	0.965168298	0.04995	0	103	103	148	93	159	195	170	147	134	168
ENSMUSG00000027959	chr3	Sass6	1.2E+08	1.2E+08	4241	-0.02727076	0.702330749	0.9472082	0.965168298	0.08993	0	21	22	33	20	19	39	23	32	24	36
ENSMUSG00000030086	chr6	Chchd6	8.9E+07	8.9E+07	1126	-0.03395051	2.267869795	0.9471596	0.965168298	0.20083	0	59	41	38	27	212	131	63	76	123	88
ENSMUSG00000032641	chr6	Gpr19	1.3E+08	1.3E+08	2637	0.026976611	0.798863656	0.9472016	0.965168298	0.07676	0	24	13	32	26	29	51	36	24	39	22
ENSMUSG00000040564	chr7	Apoc1	2E+07	2E+07	537	0.059384319	2.747988748	0.9471638	0.965168298	0.85524	0	137	42	0	4	329	227	26	151	192	88
ENSMUSG00000091898	chr14	Tnnc1	3.1E+07	3.1E+07	1041	-0.08157014	6.748405086	0.9470068	0.965168298	1.65686	0	24	1	4833	4328	1	1481	249	1901	592	6348
ENSMUSG00000061461	chr5	Smim20	5.3E+07	5.3E+07	6494	0.012121109	6.052686718	0.9474308	0.965325013	0.04011	0	926	604	1417	1035	1106	1359	1443	1044	1521	1505
ENSMUSG00000068290	chr2	Ddrgk1	1.3E+08	1.3E+08	2084	0.012633826	6.366081258	0.9477875	0.965618319	0.04151	0	1252	893	1342	1227	1484	1910	1526	1196	1981	1985
ENSMUSG00000021484	chr13	Lman2	5.5E+07	5.5E+07	4315	0.011909586	6.75702866	0.9480423	0.965807734	0.0386	0	1414	1107	1975	1656	2086	2705	2453	1605	2322	2221
ENSMUSG00000072847	chr11	A530017D24Rik	6.2E+07	6.2E+07	2614	-0.01553243	2.775029269	0.9481402	0.965837322	0.05238	0	112	79	124	92	102	145	145	133	119	142
ENSMUSG00000022353	chr15	Mtss1	5.9E+07	5.9E+07	4965	-0.01401618	4.471434304	0.9486517	0.966288226	0.04083	0	256	200	415	299	564	578	455	303	434	531
ENSMUSG00000005069	chr6	Pex5	1.2E+08	1.2E+08	3943	-0.01168813	5.291329894	0.9489997	0.966572488	0.03105	0	551	347	741	591	801	939	814	614	853	813
ENSMUSG00000021681	chr13	Aggf1	9.5E+07	9.5E+07	3697	0.010982347	5.019901552	0.9490924	0.96659674	0.03087	0	418	339	661	522	519	852	803	519	634	568
ENSMUSG00000022754	chr16	Tmem45a	5.7E+07	5.7E+07	3056	-0.03148211	2.617224567	0.9495305	0.966932846	0.21241	0	66	61	38	40	274	178	81	118	142	92
ENSMUSG00000026975	chr2	Dph7	2.5E+07	2.5E+07	2365	0.015989236	2.628252984	0.9496293	0.966932846	0.04581	0	79	72	94	93	118	157	119	95	137	126
ENSMUSG00000045503	chr2	Sys1	1.6E+08	1.6E+08	4958	-0.01169241	4.727714433	0.9496219	0.966932846	0.02862	0	354	248	506	398	538	580	563	399	632	550
ENSMUSG00000058392	chr17	Rrp1b	3.2E+07	3.2E+07	7702	-0.01823329	2.880232954	0.9498552	0.967092674	0.04834	0	102	68	138	117	135	192	162	122	110	162
ENSMUSG00000039680	chr16	Mrps6	9.2E+07	9.2E+07	1053	-0.01433163	4.250021959	0.9502528	0.967427319	0.03768	0	270	168	395	231	416	493	365	335	384	366
ENSMUSG00000027944	chr3	Hax1	9E+07	9E+07	1117	-0.01006748	4.862178899	0.9506525	0.967764017	0.029	0	456	326	544	399	473	724	547	450	649	626
ENSMUSG00000032078	chr9	Zpr1	4.6E+07	4.6E+07	3583	0.010367312	4.899336769	0.9508024	0.967846293	0.02749	0	385	321	548	503	492	699	628	465	656	645
ENSMUSG00000054752	chr4	Fsd1l	5.4E+07	5.4E+07	9739	0.013938505	3.921572684	0.951881	0.968873974	0.04761	0	246	158	308	220	201	354	425	248	215	326
ENSMUSG00000006464	chr19	Bbs1	4886898	4890758	5581	0.024870631	1.765893427	0.9520098	0.968934702	0.05731	0	40	33	50	56	70	80	81	44	67	75
ENSMUSG00000099647	chr7	Gm5776	5.4E+07	5.4E+07	321	0.021884539	1.654677533	0.9521128	0.968969275	0.06907	0	43	27	65	58	37	82	63	43	55	77
ENSMUSG00000033540	chr5	Idua	1.1E+08	1.1E+08	4204	-0.01443675	3.361772701	0.9521916	0.968979132	0.05038	0	137	80	229	193	152	260	236	130	199	238
ENSMUSG00000019302	chr11	Atp6v0a1	1E+08	1E+08	6556	0.011777171	6.488786207	0.9525641	0.969278774	0.0431	0	1332	1057	1403	1415	1478	1891	1877	1343	2253	1961
ENSMUSG00000035513	chr2	Ntng2	2.9E+07	2.9E+07	3990	0.016822758	3.963442374	0.9526243	0.969278774	0.07643	0	163	149	350	365	145	337	377	184	377	359
ENSMUSG00000068742	chr2	Cry2	9.2E+07	9.2E+07	6320	-0.0121242	5.167698357	0.9528009	0.969388202	0.03978	0	482	353	683	385	895	798	853	548	758	745
ENSMUSG00000097656	chr6	Gm26712	5.8E+07	5.8E+07	217	0.009297274	4.529516326	0.9532325	0.969756952	0.02871	0	321	233	440	346	411	466	531	399	500	473
ENSMUSG00000058013	chr5	Sept11	9.3E+07	9.3E+07	5008	0.015014107	6.152724345	0.9533654	0.969821815	0.0701	0	1392	1004	774	1011	909	1990	1313	1179	1550	1377
ENSMUSG00000002342	chr8	Tmem161a	7E+07	7E+07	3673	0.010990427	6.438990427	0.9536138	0.96998007	0.04024	0	1260	923	1576	1396	1380	1812	1875	1339	2059	1908
ENSMUSG00000085558	chr4	4930412C18Rik	9770585	9770821	6148	-0.03602754	0.533980153	0.9536593	0.96998007	0.17335	0	21	15	13	13	41	33	16	9	33	49
ENSMUSG00000028018	chr3	Gstcd	1.3E+08	1.3E+08	4731	0.037347408	1.100161626	0.9543814	0.970503438	0.06756	0	35	26	31	25	33	49	50	35	34	45
ENSMUSG00000053963	chr1	6330403A02Rik	1.8E+08	1.8E+08	6552	-0.02146569	0.794058429	0.9543588	0.970503438	0.11255	0	18	33	21	29	17	34	41	23	38	32
ENSMUSG00000062762	chr9	Ei24	3.7E+07	3.7E+07	3459	-0.0106591	6.6100809	0.9542758	0.970503438	0.03888	0	1393	1020	1836	1470	1749	2031	2192	1616	2009	2168

ENSMUSG00000091471	chr19	Gm20538	4.5E+07	4.5E+07	225	-0.01231669	7.890724905	0.955317	0.971384374	0.05584	0	2991	1823	6140	4050	3683	5426	5363	3622	4822	5282
ENSMUSG00000086583	chr7	Gm15500	1.1E+08	1.1E+08	1019	0.011938959	4.53362884	0.9556144	0.971616337	0.03154	0	354	298	364	328	363	567	538	352	436	514
ENSMUSG00000085498	chr2	Gm14023	1.3E+08	1.3E+08	1781	0.039088929	-0.05869013	0.9557011	0.971634102	0.07972	0	11	7	15	16	15	19	23	15	12	20
ENSMUSG00000038648	chr6	Creb3l2	3.7E+07	3.7E+07	7283	-0.00879653	4.766113246	0.9559146	0.971780691	0.03396	0	404	344	387	424	463	765	581	428	498	543
ENSMUSG00000097343	chr7	9030407P20Rik	1.2E+08	1.2E+08	2347	0.021968085	0.967415928	0.9564074	0.972211237	0.09812	0	20	10	38	25	52	48	37	24	50	35
ENSMUSG00000092367	chr7	Gm20479	2.7E+07	2.7E+07	556	-0.05393505	-0.04471353	0.9569014	0.972642855	0.08479	0	11	6	16	12	23	24	14	12	17	21
ENSMUSG00000066043	chr4	Phactr4	1.3E+08	1.3E+08	4960	0.009015573	3.899536495	0.9571198	0.972794421	0.03415	0	192	142	330	207	271	368	328	249	270	324
ENSMUSG00000073755	chr4	5730409E04Rik	1.3E+08	1.3E+08	2891	0.010056727	5.532258061	0.9576585	0.973271398	0.03537	0	722	530	723	642	844	973	1078	680	1072	1003
ENSMUSG00000039617	chr3	Gm7488	2.1E+07	2.1E+07	684	-0.02437665	0.009330957	0.9578659	0.973411628	0.07959	0	10	14	19	13	12	24	20	11	21	17
ENSMUSG00000023032	chr15	Slc4a8	1E+08	1E+08	13021	-0.03995526	0.807595441	0.9580333	0.973511178	0.14148	0	17	7	59	28	22	34	37	25	24	47
ENSMUSG00000056716	chr10	Gm5420	2.2E+07	2.2E+07	992	-0.03359932	1.088569176	0.9581222	0.97353104	0.22924	0	55	15	47	32	4	32	46	33	39	55
ENSMUSG00000026388	chr1	3110009E18Rik	1.2E+08	1.2E+08	2428	0.026917536	1.175711225	0.9583181	0.973588976	0.0761	0	27	30	28	39	34	62	35	36	46	46
ENSMUSG00000029482	chr5	Aacs	1.3E+08	1.3E+08	3668	-0.02987729	4.414150689	0.9582843	0.973588976	0.3478	0	206	127	70	75	1287	588	304	403	517	338
ENSMUSG00000016427	chrX	Ndufa1	3.7E+07	3.7E+07	419	0.010132044	6.925845634	0.9586732	0.973667616	0.04503	0	1872	1184	2654	1714	1850	2927	2253	2052	2702	2642
ENSMUSG00000024190	chr17	Dusp1	2.7E+07	2.7E+07	2697	0.011915971	5.570947006	0.9585602	0.973667616	0.06531	0	532	416	982	887	841	667	896	943	895	1405
ENSMUSG00000034334	chr13	Fam151b	9.2E+07	9.2E+07	1381	-0.02534828	1.302666553	0.958622	0.973667616	0.06262	0	39	26	44	26	46	55	56	42	45	43
ENSMUSG00000038797	chr7	Zscan2	8.1E+07	8.1E+07	2712	-0.0398094	0.993974281	0.9585449	0.973667616	0.10564	0	31	8	50	31	30	47	33	38	30	42
ENSMUSG00000097042	chr8	Gm17491	2.2E+07	2.2E+07	2309	0.037024589	0.74557179	0.9589729	0.973901558	0.1645	0	14	21	18	14	51	53	22	17	23	53
ENSMUSG00000003444	chr7	Med29	2.8E+07	2.8E+07	1281	0.011811395	4.000149221	0.9595041	0.974088367	0.03501	0	230	178	270	262	252	355	371	203	386	353
ENSMUSG00000025089	chr19	Gfra1	5.8E+07	5.8E+07	5476	-0.01081991	2.756560397	0.9593983	0.974088367	0.06215	0	111	97	102	80	102	164	107	110	149	154
ENSMUSG00000025184	chr19	R3hcc1l	4.3E+07	4.3E+07	7397	-0.00960053	3.967595573	0.9594765	0.974088367	0.03489	0	239	167	312	227	238	447	343	245	286	294
ENSMUSG00000034430	chr6	Zxdc	9E+07	9E+07	8564	-0.01165213	4.044031928	0.9593064	0.974088367	0.03523	0	227	144	384	249	271	376	374	248	322	376
ENSMUSG00000037152	chr3	Ndufc1	5.1E+07	5.1E+07	1495	0.009630517	7.157006944	0.9594142	0.974088367	0.04222	0	1977	1395	2832	2313	2360	3168	3111	2345	3220	2922
ENSMUSG00000028646	chr4	Rragc	1.2E+08	1.2E+08	3341	0.009094439	5.223642641	0.9596926	0.974209143	0.03346	0	487	406	633	472	848	966	876	550	732	778
ENSMUSG00000034501	chr12	Pcnxl4	7.3E+07	7.3E+07	4420	0.012272724	3.078034016	0.960334	0.974789697	0.04047	0	130	84	148	113	158	230	183	122	164	176
ENSMUSG00000070604	chr7	Vsig10l	4.3E+07	4.3E+07	3730	0.027785853	0.823538639	0.9604076	0.974793919	0.16062	0	26	10	30	14	49	48	33	8	37	53
ENSMUSG00000002660	chr17	Clpp	5.7E+07	5.7E+07	1207	0.007985608	5.044292728	0.9606411	0.97496038	0.02996	0	424	306	652	525	623	703	737	459	771	762
ENSMUSG00000020238	chr10	Ncln	8.1E+07	8.1E+07	3465	-0.0091295	5.805004428	0.9609117	0.97516443	0.03956	0	727	624	1000	972	909	1235	1172	815	1480	1069
ENSMUSG00000003528	chr16	Slc25a1	1.8E+07	1.8E+07	2176	0.032701487	5.219024037	0.9610726	0.975186609	0.51794	0	596	183	49	55	2111	850	333	792	1193	616
ENSMUSG00000026202	chr1	Tuba4a	7.5E+07	7.5E+07	3701	0.011092585	9.2409631	0.9610456	0.975186609	0.06143	0	8104	5578	13059	10873	8632	13074	14204	7989	17553	10506
ENSMUSG00000033059	chr2	Pygb	1.5E+08	1.5E+08	4809	-0.02133464	4.879641502	0.9612504	0.975225894	0.20825	0	334	261	203	134	1428	886	430	479	578	654
ENSMUSG00000096232	chr16	0610012G03Rik	3.2E+07	3.2E+07	417	-0.01019982	5.342356501	0.9612031	0.975225894	0.04021	0	500	353	1012	673	621	856	911	620	871	917
ENSMUSG00000022964	chr16	Tmem50b	9.2E+07	9.2E+07	2446	0.009768779	4.260686488	0.9614018	0.975308992	0.03475	0	248	212	316	240	437	490	450	269	390	401
ENSMUSG00000028243	chr4	Ubxn2b	6191098	6191213	6642	-0.00681285	1.206470698	0.9616927	0.975533463	0.09047	0	31	30	29	35	39	64	67	22	31	49
ENSMUSG00000020328	chr11	Nudcd2	4.1E+07	4.1E+07	2054	0.011793054	3.70577323	0.9618536	0.975626159	0.04458	0	198	162	204	163	239	360	270	247	218	243
ENSMUSG00000081944	chr11	Gm12276	6.2E+07	6.2E+07	301	-0.03950589	0.09135331	0.96201	0.975714276	0.09584	0	17	9	20	12	16	20	10	16	25	26
ENSMUSG00000027012	chr2	Dync1i2	7.1E+07	7.1E+07	8280	-0.00849345	5.920366907	0.9621089	0.975744013	0.03592	0	883	655	1159	962	933	1478	1363	969	1121	1321
ENSMUSG00000001436	chr10	Slc19a1	7.7E+07	7.7E+07	4644	-0.01588054	2.898370709	0.9626598	0.976232128	0.09094	0	108	71	91	76	225	207	147	137	159	103
ENSMUSG00000027472	chr2	Pdrg1	1.5E+08	1.5E+08	2443	0.009089841	6.416497365	0.9627402	0.976243035	0.04064	0	1404	990	1443	1196	1338	1917	1924	1353	1787	1877
ENSMUSG00000038637	chr7	Lrrc56	1.4E+08	1.4E+08	6068	0.022269389	1.485897879	0.9628538	0.976287699	0.06164	0	32	29	53	35	56	67	65	31	54	68
ENSMUSG00000027583	chr2	Zbtb46	1.8E+08	1.8E+08	8508	0.011130585	2.983457975	0.9630573	0.976352846	0.05496	0	100	81	168	76	178	206	173	109	174	157
ENSMUSG00000081272	chr2	Gm13509	4.9E+07	4.9E+07	1308	0.014917493	3.024041429	0.9630124	0.976352846	0.05154	0	96	82	131	164	132	205	186	100	184	172
ENSMUSG00000035168	chr2	Tanc1	6E+07	6E+07	14570	-0.01323612	3.715840512	0.963265	0.976492871	0.04048	0	160	109	274	191	289	307	262	225	261	283
ENSMUSG00000028955	chr4	Vamp3	1.5E+08	1.5E+08	2889	0.008412311	6.085600153	0.9633483	0.976506753	0.03624	0	982	746	1181	1002	1210	1665	1503	1104	1464	1307
ENSMUSG00000019899	chr10	Lama2	2.7E+07	2.7E+07	16338	-0.00857849	5.760299447	0.9634892	0.976578922	0.04384	0	697	695	1004	881	781	1487	1426	779	884	1080
ENSMUSG00000015134	chr7	Aldh1a3	6.6E+07	6.6E+07	4615	-0.02461683	1.932892074	0.9636696	0.976691219	0.16617	0	44	37	44	39	127	135	56	86	31	69
ENSMUSG00000019256	chr12	Ahr	3.5E+07	3.6E+07	6163	-0.01908943	1.540033377	0.9640877	0.976903149	0.06181	0	28	28	55	48	58	67	73	40	51	59
ENSMUSG00000025373	chr10	Rnf41	1.3E+08	1.3E+08	4374	0.009870916	4.205296608	0.9640237	0.976903149	0.03443	0	278	202	300	249	356	413	456	240	444	370
ENSMUSG00000036959	chrX	Bcorl1	4.8E+07	4.8E+07	8516	-0.00924368	3.837702956	0.9640625	0.976903149	0.03685	0	190	148	230	247	266	293	327	205	353	289
ENSMUSG00000002416	chr6	Ndufb2	4E+07	4E+07	5628	-0.00905373	7.221022459	0.9642116	0.976951893	0.04693	0	2289	1490	2975	2506	2095	3285	3024	2474	3419	3111
ENSMUSG00000029518	chr5	Rab35	1.2E+08	1.2E+08	2799	-0.00815131	5.401188749	0.9642751	0.976951893	0.03131	0	513	422	874	660	788	1005	952	637	873	903
ENSMUSG00000005320	chr13	Fgfr4	5.5E+07	5.5E+07	3542	-0.02295042	1.336203978	0.964638	0.977107847	0.09054	0	27	17	63	27	59	65	45	33	64	43
ENSMUSG00000009905	chr1	Kdsr	1.1E+08	1.1E+08	8147	-0.01403519	3.178049113	0.9645814	0.977107847	0.09447	0	132	94	87	93	283	253	161	132	153	231
ENSMUSG00000033233	chr3	Trim45	1E+08	1E+08	6005	0.013312564	2.247953094	0.964547	0.977107847	0.05658	0	73	44	108	58	72	105	98	62	116	105
ENSMUSG00000031962	chr8	Cdh15	1.2E+08	1.2E+08	2843	0.008822554	4.69173575	0.965	0.977403999	0.0389	0	333	260	492	519	339	614	506	411	623	517
ENSMUSG00000015222	chr1	Map2	6.6E+07	6.6E+07	16449	-0.02622865	0.21849101	0.9652546	0.977520701	0.10048	0	25	9	14	15	17	25	31	10	21	23
ENSMUSG00000034771	chr10	Tle2	8.2E+07	8.2E+07	6221	0.016296096	2.645100811	0.9652154	0.977520701	0.06302	0	71	84	90	84	130	183	129	70	115	157
ENSMUSG00000019891	chr10	Dcbld1	5.2E+07	5.2E+07	7282	-0.02500015	1.353697822	0.965426	0.977580039	0.0928	0	31	15	55	51	40	50	53	41	35	71
ENSMUSG00000031754	chr8	Nudt21	9.4E+07	9.4E+07	2726	-0.00910436	3.339145466	0.9654526	0.977580039	0.03753	0	148	123	184	131	171	234	227	161	200	211
ENSMUSG00000029623	chr5	Pdap1	1.5E+08	1.5E+08	3201	0.008342425	6.235807066	0.9656026	0.977661306	0.03997	0	1118	840	1233	1177	1284	1624	1599	1139	1867	1586
ENSMUSG00000027195	chr2	Hsd17b12	9.4E+07	9.4E+07	2407	0.018398518	4.455112573	0.9658383	0.97779188	0.21082	0	369	159	140	88	964	663	369	389	458	394
ENSMUSG00000033697	chr15	Arhgap39	7.7E+07	7.7E+07	7367	0.012232893	2.357826967	0.965871	0.97779188	0.05221	0	70	43	102	69	103	125	107	63	123	110
ENSMUSG00000032834	chr10	Pwp2	7.8E+07	7.8E+07	3871	-0.00754223	4.545828912	0.9660322	0.977843658	0.03091	0	277	274	438	406	366	532	490	388	512	470
ENSMUSG00000040105	chr19	Ppapdc2	2.9E+07	2.9E+07	2859	-0.02183416	2.557774913	0.9661123	0.977843658	0.12503	0	67	49	79	48	218	197	105	90	91	118
ENSMUSG00000042389	chr6	Tsen2	1.2E+08	1.2E+08	6437	0.01354887	2.928846181	0.9661313	0.977843658	0.0436	0	95	95	128	107	138	191	144	122	162	162
ENSMUSG00000027829	chr3	Ccnl1	6.6E+07	6.6E+07	5997	0.010773692	3.963892612	0.9662846	0.977872853	0.04342	0	181	189	235	253	306	413	312	220	257	425
ENSMUSG00000029600	chr5	Rita1	1.2E+08	1.2E+08	2836	-0.01516083	2.417573098	0.9662996	0.977872853	0.04902	0	73	50	98	73	111	112	121	69	117	124

ENSMUSG00000002486	chr5	Tchp	1.1E+08	1.1E+08	3851	0.009670548	2.706923244	0.9664531	0.977887156	0.0626	0	57	56	155	97	138	154	136	83	149	152
ENSMUSG00000030869	chr7	Ndufab1	1.2E+08	1.2E+08	6883	0.009174777	7.765310628	0.9664033	0.977887156	0.05761	0	2575	1674	5717	3705	3364	5006	4514	3682	4461	4833
ENSMUSG00000027341	chr2	Tmem230	1.3E+08	1.3E+08	3267	0.007187557	4.711700574	0.9677851	0.979164286	0.02661	0	385	274	463	371	489	629	536	371	600	590
ENSMUSG00000044043	chr18	Pcdhb14	3.7E+07	3.7E+07	8695	0.009588302	0.267032705	0.9686898	0.980008876	0.12599	0	20	6	18	9	32	19	24	12	29	30
ENSMUSG00000021037	chr12	Ahsa1	8.7E+07	8.7E+07	1347	-0.00731637	6.965475373	0.9690676	0.980320346	0.04006	0	1803	1263	2620	1783	2127	2968	2703	1915	2693	2651
ENSMUSG00000057788	chr8	Ddx49	7E+07	7E+07	2928	0.006917657	4.326686923	0.9693986	0.980584519	0.02937	0	256	209	347	305	405	446	430	296	451	454
ENSMUSG00000018909	chr7	Arrb1	1E+08	1E+08	11175	0.008214476	5.219710718	0.969586	0.980703379	0.03795	0	545	469	477	519	756	862	835	545	860	772
ENSMUSG00000022354	chr15	Ndufb9	5.9E+07	5.9E+07	651	-0.00775763	8.842402269	0.9700845	0.981136797	0.05015	0	6343	4029	10525	7755	6904	10108	10062	7181	9865	10149
ENSMUSG00000039543	chr14	Cfap70	2E+07	2E+07	4315	-0.03834014	0.27543202	0.9703897	0.981374765	0.1399	0	20	14	19	13	18	24	15	26	36	9
ENSMUSG00000007080	chr5	Pole	1.1E+08	1.1E+08	11160	0.017195456	0.515287357	0.9706518	0.981537142	0.09548	0	20	9	30	23	19	47	31	21	21	19
ENSMUSG00000038241	chr2	Cep250	1.6E+08	1.6E+08	10373	0.010573554	3.536440441	0.9706903	0.981537142	0.04227	0	141	138	201	163	226	278	243	136	249	306
ENSMUSG00000035530	chr11	Eif1	1E+08	1E+08	2098	0.007035087	9.530416867	0.9708621	0.981640157	0.044	0	10743	7895	13130	11035	13210	17288	15711	11035	15960	17038
ENSMUSG00000018848	chr11	Rars	3.6E+07	3.6E+07	3228	-0.00603942	5.66780937	0.9711012	0.98174037	0.03366	0	777	598	864	743	835	1266	1162	793	1001	1038
ENSMUSG00000024535	chr18	Snx24	5.3E+07	5.3E+07	1880	-0.00609077	3.765720351	0.9710666	0.98174037	0.04006	0	233	172	218	172	211	342	298	218	265	273
ENSMUSG00000014601	chr3	Strip1	1.1E+08	1.1E+08	3231	-0.0066471	5.045959004	0.9715688	0.981987007	0.02951	0	427	323	705	556	521	740	731	497	727	714
ENSMUSG00000026643	chr2	Nmt2	3284212	3284406	6556	-0.00673749	4.185082195	0.9716252	0.981987007	0.04338	0	291	227	247	215	377	475	426	290	374	309
ENSMUSG00000043858	chr7	Nup62	4.5E+07	4.5E+07	2851	0.006416264	5.169368621	0.9715435	0.981987007	0.03431	0	420	387	667	639	611	724	750	588	896	742
ENSMUSG00000066554	chr5	Gm10167	1.5E+08	1.5E+08	1479	0.02310348	0.549490959	0.9714826	0.981987007	0.09741	0	15	11	29	21	28	28	24	12	38	41
ENSMUSG00000026885	chr2	Ttll11	3.6E+07	3.6E+07	4024	-0.0094756	1.757207578	0.9718795	0.982102425	0.08019	0	44	39	57	68	37	76	60	44	63	97
ENSMUSG00000029073	chr4	Cptp	1.6E+08	1.6E+08	2709	-0.00840121	3.849222811	0.9718168	0.982102425	0.04067	0	175	149	270	203	307	310	378	198	352	248
ENSMUSG00000053964	chr7	Lgals4	2.9E+07	2.9E+07	2315	0.016399876	1.938568647	0.9720337	0.982187481	0.15759	0	33	20	79	40	128	103	67	46	44	133
ENSMUSG00000016128	chr5	Stard13	1.5E+08	1.5E+08	8044	-0.00870311	3.193246702	0.9724757	0.982492577	0.04719	0	134	95	171	95	202	244	188	144	181	180
ENSMUSG00000031145	chrX	Prickle3	7657260	7657500	4902	-0.0116312	3.763313616	0.972421	0.982492577	0.05506	0	168	91	350	190	275	302	265	180	336	316
ENSMUSG00000060938	chr11	Rpl26	6.9E+07	6.9E+07	1444	0.006847256	7.963831938	0.97266	0.982607983	0.04555	0	3832	3032	4079	3654	4003	6490	4762	4113	5246	5301
ENSMUSG00000003848	chr8	Nob1	1.1E+08	1.1E+08	3486	-0.00781647	4.324558076	0.9728012	0.98260912	0.03373	0	268	210	370	329	343	465	378	397	393	395
ENSMUSG00000007122	chr1	Casq1	1.7E+08	1.7E+08	1951	-0.00859788	11.90522007	0.9727433	0.98260912	0.07576	0	75532	49827	43519	46352	66843	72914	73219	66980	100374	77372
ENSMUSG00000020153	chr10	Ndufs7	8E+07	8E+07	1718	-0.00780498	8.346867536	0.9730567	0.982725582	0.06171	0	3771	2597	8190	5985	4985	6248	7302	4735	7895	7423
ENSMUSG00000091475	chr17	2810468N07Rik	2.6E+07	2.6E+07	1349	0.014162882	0.650166971	0.9730385	0.982725582	0.09565	0	15	14	30	15	39	52	27	21	25	29
ENSMUSG00000020877	chr11	Scrn2	9.7E+07	9.7E+07	2050	-0.00762817	3.79550414	0.9733403	0.982941229	0.04035	0	187	145	258	232	228	269	270	200	375	307
ENSMUSG00000085888	chr11	Gm12224	5.4E+07	5.4E+07	1091	0.006515119	5.759099794	0.9734653	0.982996691	0.03659	0	893	583	895	840	844	1288	1152	828	1258	1099
ENSMUSG00000025157	chr19	Zdhhc16	4.2E+07	4.2E+07	1830	0.006315267	4.112990007	0.9736091	0.983000398	0.03134	0	213	195	322	272	301	376	376	298	361	362
ENSMUSG00000032294	chr9	Pkm	6E+07	6E+07	2599	0.007064063	11.92640673	0.9735816	0.983000398	0.05444	0	49779	39966	69982	68197	67883	71537	94614	58582	103595	74511
ENSMUSG00000036873	chr3	2410004B18Rik	1.5E+08	1.5E+08	2029	0.004758998	4.165557956	0.974314	0.98350378	0.03202	0	264	154	340	277	337	398	392	302	365	386
ENSMUSG00000042854	chr2	Trp53rk	1.7E+08	1.7E+08	5755	-0.01631157	1.957502561	0.974304	0.98350378	0.07279	0	45	33	67	78	68	72	66	70	102	73
ENSMUSG00000091989	chr7	Gm17257	8.1E+07	8.1E+07	468	-0.03302406	0.767293101	0.9743181	0.98350378	0.08831	0	22	13	46	23	21	34	27	31	38	31
ENSMUSG00000025477	chr7	Inpp5a	1.4E+08	1.4E+08	3529	0.006856233	6.743425778	0.9744505	0.983566659	0.05577	0	1238	854	2674	1878	1719	2133	2826	1524	2363	2304
ENSMUSG00000023932	chr17	Cdc5l	4.5E+07	4.5E+07	2989	-0.00608541	5.72250869	0.9746889	0.983736502	0.03739	0	719	528	1182	829	791	1261	1280	783	999	1154
ENSMUSG00000025068	chr19	Gsto1	4.8E+07	4.8E+07	1968	0.005387014	4.529492226	0.9748556	0.983834004	0.04636	0	292	181	566	394	357	469	469	403	402	622
ENSMUSG00000031246	chrX	Sh3bgrl	1.1E+08	1.1E+08	3298	0.008333079	4.787022292	0.9749617	0.9838703	0.07636	0	414	257	323	245	891	747	681	404	493	561
ENSMUSG00000027132	chr2	Katnbl1	1.1E+08	1.1E+08	4051	0.010726039	2.131555848	0.975082	0.983900625	0.05951	0	63	46	61	60	93	122	92	71	67	94
ENSMUSG00000039781	chr11	Cep131	1.2E+08	1.2E+08	3833	-0.00999981	2.929628906	0.9751321	0.983900625	0.04576	0	108	69	154	108	142	183	146	97	179	178
ENSMUSG00000020212	chr10	Mdm1	1.2E+08	1.2E+08	3149	-0.01919035	0.901849142	0.9753259	0.983927228	0.07728	0	19	20	43	17	38	48	41	27	35	31
ENSMUSG00000028211	chr4	Trp53inp1	1.1E+07	1.1E+07	6475	0.009046638	3.711289096	0.9753689	0.983927228	0.04605	0	199	153	200	183	238	279	403	190	222	263
ENSMUSG00000040151	chr3	Hs2st1	1.4E+08	1.4E+08	4916	-0.00538467	4.271590781	0.9752969	0.983927228	0.02962	0	262	235	340	277	336	440	395	325	398	418
ENSMUSG00000020089	chr10	Ppa1	6.2E+07	6.2E+07	2902	0.005870665	5.797409284	0.9755502	0.984039327	0.05005	0	664	439	1101	703	1472	1418	1145	924	1107	1166
ENSMUSG00000028578	chr4	Caap1	9.5E+07	9.5E+07	3591	0.010971649	0.969988382	0.9759364	0.984358095	0.07343	0	27	17	26	26	45	38	41	36	41	34
ENSMUSG00000034820	chr19	Cpsf7	1.1E+07	1.1E+07	3604	-0.00431895	4.585500489	0.9765222	0.984878162	0.02989	0	302	304	432	357	406	622	561	364	424	516
ENSMUSG00000031155	chrX	Pim2	7878262	7878556	2795	-0.01420792	1.002219725	0.976638	0.9849241	0.07526	0	25	20	33	30	37	67	29	27	34	41
ENSMUSG00000031373	chrX	Car5b	1.6E+08	1.6E+08	6354	-0.01830669	3.546000994	0.9773913	0.985542039	0.39106	0	192	103	23	27	571	308	102	233	290	237
ENSMUSG00000067995	chr14	Gtf2f2	7.6E+07	7.6E+07	1467	-0.00780925	3.596233863	0.977323	0.985542039	0.04016	0	156	132	240	196	189	280	222	229	261	231
ENSMUSG00000024593	chr18	Megf10	5.7E+07	5.7E+07	7718	-0.01793236	0.787548971	0.9776119	0.985622799	0.12125	0	22	24	44	21	11	48	28	31	32	27
ENSMUSG00000027313	chr2	Chac1	1.2E+08	1.2E+08	1637	-0.00946523	4.882845017	0.9775725	0.985622799	0.09062	0	452	163	623	398	710	420	930	436	381	861
ENSMUSG00000097006	chr17	9530082P21Rik	2.4E+07	2.4E+07	4842	0.008839615	3.075737453	0.9781759	0.986120545	0.04958	0	107	86	184	111	151	263	197	102	152	170
ENSMUSG00000030231	chr6	Plekha5	1.4E+08	1.4E+08	5133	-0.00360548	2.236748536	0.9783639	0.986239182	0.07082	0	62	59	77	75	72	122	145	47	76	98
ENSMUSG00000074282	chr7	Zfp94	2.4E+07	2.4E+07	3510	0.018864633	1.025150959	0.9788751	0.986683569	0.09465	0	26	25	34	13	48	43	47	37	33	39
ENSMUSG00000022247	chr15	Brix1	1E+07	1E+07	2731	0.006169809	4.203384166	0.9789899	0.98672844	0.0336	0	257	221	307	272	317	491	386	331	331	355
ENSMUSG00000074212	chr3	Dnajb14	1.4E+08	1.4E+08	12553	0.00582078	4.807255884	0.9797248	0.987398154	0.02997	0	407	335	431	430	482	614	636	415	560	676
ENSMUSG00000002763	chr17	Pex6	4.7E+07	4.7E+07	3796	-0.00565129	5.411762485	0.9811835	0.988785422	0.04121	0	515	332	885	767	820	986	798	641	996	975
ENSMUSG00000033488	chr1	BC026585	1.6E+08	1.6E+08	2534	0.031487234	0.304419863	0.9812423	0.988785422	0.41027	0	19	9	1	3	55	32	12	23	20	29
ENSMUSG00000042569	chr11	Dhrs7b	6.1E+07	6.1E+07	3325	0.004594021	4.858622907	0.9813814	0.988854581	0.04414	0	367	280	464	344	786	654	604	401	687	670
ENSMUSG00000056724	chr9	Nbeal2	1.1E+08	1.1E+08	9554	0.004530658	2.755440127	0.9817789	0.989183998	0.04796	0	79	63	151	91	131	156	146	93	140	159
ENSMUSG00000054863	chr15	Fam19a5	8.8E+07	8.8E+07	2575	0.001209212	2.558884113	0.9822522	0.989521936	0.06892	0	74	33	141	91	119	146	109	96	112	136
ENSMUSG00000099041	chr2	Gm28035	3E+07	3E+07	4238	0.006989268	4.596998223	0.9822554	0.989521936	0.13288	0	172	115	922	398	370	514	833	289	366	540
ENSMUSG00000064179	chr7	Tnnt1	4504570	4504800	2204	-0.02376538	7.535042995	0.9826906	0.989889325	1.33363	0	92	9	9471	6219	13	2368	922	3405	1296	10588
ENSMUSG00000085436	chr2	Zfp335os	1.6E+08	1.6E+08	1273	0.011048623	1.653930613	0.9828955	0.990024616	0.05785	0	34	35	61	38	64	69	72	51	66	57
ENSMUSG00000021546	chr13	Hnrnpk	5.8E+07	5.8E+07	5634	0.004052433	7.453081137	0.9834414	0.990503293	0.04379	0	2415	1940	3270	2254	3473	4570	3684	2998	3330	3561
ENSMUSG00000026648	chr2	Dclre1c	3424131	3424326	9316	0.0196896	1.34065955	0.9839064	0.990829372	0.11119	0	42	41	43	22	28	84	59	36	43	35

ENSMUSG00000039887	chr3	Alg14	1.2E+08	1.2E+08	910	0.006456693	2.821147176	0.9838812	0.990829372	0.05756	0	95	76	88	108	159	207	150	107	120	145
ENSMUSG00000003438	chr7	Timm50	2.8E+07	2.8E+07	2684	-0.00452293	5.600145148	0.9839861	0.990838462	0.03941	0	607	420	1074	845	811	1045	1062	704	1164	1042
ENSMUSG00000043155	chr4	Hpdl	1.2E+08	1.2E+08	1804	-0.02652623	1.164043929	0.984535	0.991320011	0.1677	0	18	7	81	33	36	53	47	20	42	60
ENSMUSG00000048175	chr15	Asb8	9.8E+07	9.8E+07	2410	-0.00365337	6.805402	0.9848506	0.991453312	0.03879	0	1569	1118	2155	1687	2041	2516	2544	1710	2383	2422
ENSMUSG00000087174	chrX	5530601H04Rik	1.1E+08	1.1E+08	9005	-0.00831767	1.497132935	0.9847971	0.991453312	0.09993	0	44	34	28	45	51	102	49	45	37	51
ENSMUSG00000091228	chr11	Gm20390	9.4E+07	9.4E+07	991	-0.0040029	8.617040867	0.9848794	0.991453312	0.0511	0	4844	3752	9654	6397	5750	9570	8364	6367	8041	8253
ENSMUSG00000035171	chr19	1110059E24Rik	2.2E+07	2.2E+07	3067	0.008020453	3.137830747	0.9851404	0.991644869	0.04304	0	114	111	145	112	172	231	200	136	172	168
ENSMUSG00000022557	chr15	Bop1	7.6E+07	7.6E+07	2476	-0.00376367	4.919002391	0.9852203	0.991654085	0.03034	0	362	306	511	530	599	702	657	446	698	626
ENSMUSG00000016487	chr6	Ppfibp1	1.5E+08	1.5E+08	9790	0.004156106	5.506930544	0.9862279	0.992547152	0.0425	0	725	531	817	618	713	1009	1374	652	771	935
ENSMUSG00000028964	chr4	Park7	1.5E+08	1.5E+08	2479	0.003533343	8.485948011	0.9862491	0.992547152	0.04785	0	5324	4396	5580	5053	6452	7394	7405	5940	8538	7642
ENSMUSG00000019564	chr10	Arid3a	8E+07	8E+07	5562	0.009376551	2.017731005	0.9864162	0.992591173	0.05775	0	46	44	62	74	71	80	85	63	82	98
ENSMUSG00000046916	chr10	Myct1	5593728	5593901	2775	-0.00803269	3.222137085	0.9864344	0.992591173	0.04673	0	146	74	205	113	182	228	188	151	181	205
ENSMUSG00000027615	chr3	Hps3	2E+07	2E+07	9103	-0.00301524	2.962088027	0.9867192	0.992806595	0.07185	0	103	119	96	97	152	231	169	144	123	127
ENSMUSG00000074652	chr2	Myh7b	1.6E+08	1.6E+08	6634	0.012996072	2.374132965	0.9871068	0.993125265	0.74904	0	17	1	235	164	1	127	93	57	64	193
ENSMUSG00000089718	chr9	2310075C17Rik	1.1E+08	1.1E+08	326	-0.01007915	1.773286456	0.9885226	0.994478441	0.12643	0	63	20	75	69	27	115	59	51	48	73
ENSMUSG00000041530	chr4	Ago1	1.3E+08	1.3E+08	8120	-0.00279801	4.195725487	0.9892421	0.995130876	0.03027	0	248	201	298	278	359	418	387	277	387	419
ENSMUSG00000001158	chr6	Snrnp27	8.7E+07	8.7E+07	1767	-0.0025924	5.648483766	0.9898551	0.995533332	0.0341	0	799	527	978	699	801	1218	1014	867	993	1065
ENSMUSG00000031758	chr8	Cdyl2	1.2E+08	1.2E+08	8087	0.00934273	2.476476872	0.9897447	0.995533332	0.05558	0	58	67	94	83	111	113	149	79	101	127
ENSMUSG00000074781	chr10	Ube2n	9.6E+07	9.6E+07	3851	-0.00235276	5.758429242	0.989831	0.995533332	0.03695	0	878	620	878	727	964	1354	1179	918	1123	1005
ENSMUSG00000026090	chr1	2010300C02Rik	3.8E+07	3.8E+07	5075	-0.01752715	1.640535783	0.9902145	0.995751945	0.22212	0	16	17	126	34	56	39	119	34	76	42
ENSMUSG00000061950	chr17	Ppp4r1	6.6E+07	6.6E+07	5449	0.002049675	4.458930082	0.9901831	0.995751945	0.03156	0	282	235	409	298	452	546	495	391	393	434
ENSMUSG00000032816	chr9	Igdcc4	6.5E+07	6.5E+07	6366	0.002961361	5.988092001	0.9905541	0.995950644	0.04745	0	966	714	1205	1122	730	1499	1609	956	1297	1238
ENSMUSG00000054517	chr11	Trim65	1.2E+08	1.2E+08	5883	0.007649719	2.510542733	0.9905425	0.995950644	0.06395	0	55	65	116	91	99	170	151	67	113	92
ENSMUSG00000045538	chr8	Ddx28	1.1E+08	1.1E+08	2262	0.002189341	4.04469025	0.9910362	0.996363952	0.03353	0	206	166	308	265	310	349	381	259	396	311
ENSMUSG00000038520	chr7	Tbc1d17	4.5E+07	4.5E+07	3448	-0.00210966	5.610755965	0.9912016	0.996458836	0.03435	0	740	512	863	700	895	1125	942	695	1161	1145
ENSMUSG00000024891	chr19	Slc29a2	5024006	5024277	2472	-0.00682959	2.748241317	0.9918481	0.997037323	0.06258	0	85	56	174	117	81	168	150	99	134	136
ENSMUSG00000024968	chr19	Rcor2	7267325	7267424	3135	0.003122547	2.796888578	0.9919905	0.997108989	0.06058	0	67	65	107	120	169	165	144	93	155	158
ENSMUSG00000021248	chr12	Tmed10	8.5E+07	8.5E+07	3526	0.002021521	6.952551732	0.9922326	0.997209443	0.03977	0	1838	1337	2124	1913	2144	3170	2819	1849	2481	2593
ENSMUSG00000035027	chr10	Map2k2	8.1E+07	8.1E+07	3722	-0.00204601	7.331232392	0.992168	0.997209443	0.04694	0	2169	1732	2886	2506	2962	3257	3394	2349	4388	3260
ENSMUSG00000021607	chr13	Mrpl36	7.3E+07	7.3E+07	899	0.002429432	4.93886802	0.9927182	0.99762597	0.02999	0	424	359	590	416	525	781	644	475	739	538
ENSMUSG00000028407	chr4	Toporsos	4E+07	4E+07	1054	0.003131752	3.299528482	0.9931773	0.997944329	0.04103	0	159	98	162	143	176	218	190	139	222	244
ENSMUSG00000035521	chr17	Gnptg	2.5E+07	2.5E+07	2249	-0.00074375	3.608420415	0.9931266	0.997944329	0.04204	0	169	155	164	177	239	307	240	174	282	256
ENSMUSG00000034781	chr10	Gna11	8.2E+07	8.2E+07	4097	-0.00183991	5.656459046	0.9935855	0.998211503	0.03267	0	648	511	1009	719	991	1206	1140	712	1119	1070
ENSMUSG00000039081	chr14	Zfp503	2.2E+07	2.2E+07	4213	-0.00199868	3.964309592	0.9935705	0.998211503	0.0923	0	348	194	121	200	265	382	214	259	353	390
ENSMUSG00000020929	chr11	Eftud2	1E+08	1E+08	8395	0.00112896	5.030203638	0.9948407	0.999289522	0.02732	0	406	338	656	513	582	781	673	513	738	672
ENSMUSG00000073838	chr7	Tufm	1.3E+08	1.3E+08	1776	-0.00183639	6.992940037	0.9947969	0.999289522	0.06001	0	1462	939	3372	2276	1982	2718	3039	1878	2856	2711
ENSMUSG00000074218	chr7	Cox7a1	3E+07	3E+07	364	0.001676309	7.911673142	0.9948723	0.999289522	0.08667	0	2664	1516	7593	4314	3107	4845	6393	3570	4977	5200
ENSMUSG00000018659	chr11	Pnpo	9.7E+07	9.7E+07	2925	0.000294339	4.348818449	0.9956337	0.999982685	0.03451	0	275	184	398	253	466	484	424	313	456	427
ENSMUSG00000000942	chr6	Hoxa4	5.2E+07	5.2E+07	1594	0.004663979	1.338986581	1	1	0.10663	0	36	16	30	34	72	51	58	34	37	72
ENSMUSG00000001767	chr2	Crnkl1	1.5E+08	1.5E+08	3844	-9.5935E-05	4.427703161	0.9989996	1	0.03102	0	291	272	371	313	359	523	459	372	389	466
ENSMUSG00000020684	chr11	Rasl10b	8.3E+07	8.3E+07	4010	-0.01970268	-0.19263749	1	1	0.49459	0	2	1	42	16	2	21	33	8	4	13
ENSMUSG00000020728	chr11	Cep112	1.1E+08	1.1E+08	6175	-0.02676573	0.040783821	1	1	0.12318	0	13	5	22	16	16	31	23	11	7	24
ENSMUSG00000022325	chr15	Pop1	3.4E+07	3.4E+07	3795	0.004904321	1.212863418	1	1	0.07123	0	31	24	29	41	41	56	40	44	39	48
ENSMUSG00000024246	chr17	Thumpd2	8.1E+07	8.1E+07	1856	0.012739078	1.714982292	1	1	0.08627	0	46	41	37	58	52	82	39	54	76	78
ENSMUSG00000024942	chr19	Capn1	5988546	5989387	3190	0.000888605	6.780083928	0.997468	1	0.04208	0	1555	1239	1956	1766	1763	2446	2649	1586	2634	2107
ENSMUSG00000026768	chr2	Itga8	1.2E+07	1.2E+07	7368	0.005831509	1.613673918	1	1	0.08546	0	54	37	67	31	32	86	56	44	50	73
ENSMUSG00000027160	chr2	Ccdc34	1.1E+08	1.1E+08	6558	0.000653815	1.739845858	1	1	0.06521	0	49	37	61	35	64	102	78	44	61	55
ENSMUSG00000028068	chr3	Iqgap3	8.8E+07	8.8E+07	11384	0.012112102	0.358158603	1	1	0.11259	0	15	14	19	27	12	29	22	10	36	27
ENSMUSG00000028121	chr3	Bcar3	1.2E+08	1.2E+08	3298	-0.00504685	3.249918339	0.9959264	1	0.13457	0	101	95	96	66	383	225	194	148	174	232
ENSMUSG00000028542	chr4	Slc6a9	1.2E+08	1.2E+08	5141	0.002281932	3.293975771	1	1	0.07224	0	137	144	116	155	157	243	139	135	292	201
ENSMUSG00000028883	chr5	Sema3a	1.3E+07	1.3E+07	6470	0.008521794	1.410899162	1	1	0.09115	0	39	36	42	21	53	66	80	35	46	41
ENSMUSG00000028975	chr4	Pex14	1.5E+08	1.5E+08	6272	-0.00195643	4.855640491	0.9965032	1	0.03119	0	370	277	503	441	633	645	617	430	701	598
ENSMUSG00000029708	chr6	Gcc1	2.8E+07	2.8E+07	5287	-0.00189545	3.636962918	0.9989329	1	0.03228	0	168	126	241	182	228	311	271	186	258	257
ENSMUSG00000032077	chr9	Bud13	4.6E+07	4.6E+07	3980	0.005901537	2.92017274	1	1	0.05167	0	88	100	151	93	131	189	169	99	186	139
ENSMUSG00000032251	chr9	Irak1bp1	8.3E+07	8.3E+07	2158	-0.00460399	1.526445187	1	1	0.06076	0	47	25	43	38	59	75	52	42	62	57
ENSMUSG00000032469	chr9	Dbr1	1E+08	1E+08	2488	-0.00145435	2.540107192	1	1	0.04572	0	72	55	113	90	109	143	112	100	112	122
ENSMUSG00000032531	chr9	Amotl2	1E+08	1E+08	6289	0.001696769	4.644287287	0.9967606	1	0.10564	0	268	297	210	270	864	434	468	414	501	737
ENSMUSG00000033543	chr9	Gtf2a2	7E+07	7E+07	4047	0.001028285	4.883745212	1	1	0.03369	0	446	387	482	381	496	772	591	508	524	647
ENSMUSG00000034575	chr13	Papd7	6.9E+07	7E+07	3972	-0.00109211	3.230134098	1	1	0.03969	0	113	94	192	155	157	225	205	156	178	195
ENSMUSG00000036678	chr15	Aaas	1E+08	1E+08	1816	0.000732157	2.922584713	1	1	0.04551	0	114	80	127	107	139	194	160	94	187	149
ENSMUSG00000036840	chr8	Siah1a	8.7E+07	8.7E+07	2107	-0.00176064	3.325702954	1	1	0.041	0	131	109	191	136	191	247	218	182	163	211
ENSMUSG00000037624	chr1	Kcnk2	1.9E+08	1.9E+08	4943	0.004467934	1.601842495	1	1	0.07581	0	53	31	67	32	39	79	50	41	58	78
ENSMUSG00000037703	chr2	Lzts3	1.3E+08	1.3E+08	4252	0.000804335	2.166156859	1	1	0.05503	0	73	52	65	68	69	101	103	59	86	108
ENSMUSG00000037991	chr16	Rmi2	1.1E+07	1.1E+07	4495	-0.0040278	1.438824401	1	1	0.13691	0	49	20	40	22	71	47	68	38	86	29
ENSMUSG00000039801	chr15	2410089E03Rik	8169106	8169489	13017	0.006554994	2.660067267	1	1	0.04639	0	95	78	107	77	109	169	137	87	133	125
ENSMUSG00000040429	chr5	Mterf1a	3890581	3891897	2442	0.022402531	0.055000543	1	1	0.0972	0	11	8	13	21	17	30	16	13	13	26
ENSMUSG00000040860	chr4	Crocc	1.4E+08	1.4E+08	8266	0.004301938	1.497358884	1	1	0.06884	0	35	30	47	36	59	66	76	27	54	64

ENSMUSG00000043279	chr5	Trim56	1.4E+08	1.4E+08	9281	0.001567694	4.282239017	1	1	0.03987	0	269	218	299	264	419	542	451	249	313	485
ENSMUSG00000046280	chr3	She	9E+07	9E+07	5733	-0.0016103	3.259088211	1	1	0.04416	0	109	87	209	131	202	215	202	164	198	196
ENSMUSG00000047227	chr12	Gm527	6.5E+07	6.5E+07	1463	0.010041581	0.210327384	1	1	0.10364	0	17	15	13	12	21	26	22	26	13	20
ENSMUSG00000048997	chr3	Atxn7l2	1.1E+08	1.1E+08	4817	0.001662704	2.942416304	1	1	0.0588	0	121	113	108	93	122	177	141	109	168	193
ENSMUSG00000050394	chrX	Armcx6	1.3E+08	1.3E+08	2486	0.004685552	0.896221433	1	1	0.10598	0	31	29	25	14	30	40	36	38	39	26
ENSMUSG00000050663	chr10	Trhde	1.1E+08	1.1E+08	8065	0.044250337	0.10751292	1	1	0.19053	0	27	17	5	6	13	23	22	14	16	28
ENSMUSG00000051154	chr2	Commd3	1.9E+07	1.9E+07	2330	-0.00087779	5.956214993	0.9974825	1	0.03444	0	910	610	1152	983	1077	1479	1441	962	1253	1299
ENSMUSG00000052921	chr11	Arhgef15	6.9E+07	6.9E+07	6483	-0.00244753	3.919935369	1	1	0.05446	0	148	113	397	237	298	329	294	223	318	394
ENSMUSG00000053353	chr2	2310001K24Rik	1.6E+08	1.6E+08	740	-0.03408341	-0.08265049	1	1	0.12504	0	4	5	20	20	17	18	19	9	21	19
ENSMUSG00000056832	chr6	Ttc26	3.8E+07	3.8E+07	4673	-0.00493854	0.451316077	1	1	0.10419	0	24	19	21	8	22	34	30	23	20	23
ENSMUSG00000056962	chr11	Jmjd6	1.2E+08	1.2E+08	4698	-0.00149544	4.914119577	0.9996755	1	0.04156	0	322	272	763	536	444	678	631	459	681	664
ENSMUSG00000059842	chr2	Zfp341	1.5E+08	1.5E+08	3299	0.000153313	2.068392986	1	1	0.06477	0	48	36	86	80	64	95	70	69	104	83
ENSMUSG00000060639	chr13	Hist1h4i	2.2E+07	2.2E+07	727	-9.3236E-05	4.072568444	1	1	0.03355	0	234	177	320	230	317	438	380	251	390	283
ENSMUSG00000061740	chr15	Cyp2d22	8.2E+07	8.2E+07	2771	-0.00177194	3.604389395	0.9988974	1	0.0638	0	152	119	197	139	329	325	245	137	212	354
ENSMUSG00000062012	chr17	Zfp13	2.4E+07	2.4E+07	2439	-0.00871836	1.192293657	1	1	0.07134	0	35	18	49	24	43	51	45	26	50	55
ENSMUSG00000063254	chr7	B230325K18Rik	1.3E+08	1.3E+08	2623	0.008256685	0.043324004	1	1	0.12964	0	12	12	8	14	23	18	12	16	15	34
ENSMUSG00000067928	chr17	Zfp760	2.2E+07	2.2E+07	4209	0.001233182	1.71298729	1	1	0.09578	0	48	36	36	38	82	110	48	47	52	76
ENSMUSG00000070883	chr2	Ccdc173	7E+07	7E+07	2558	-0.02458288	0.096044095	1	1	0.11847	0	7	16	23	14	13	20	21	22	11	23
ENSMUSG00000072966	chrX	Gprasp2	1.4E+08	1.4E+08	4540	0.022116507	0.214636952	1	1	0.12357	0	24	14	14	11	14	38	18	17	12	26
ENSMUSG00000074623	chr2	Gm826	1.6E+08	1.6E+08	1493	-0.00976348	0.762783254	1	1	0.38993	0	11	1	90	18	14	26	47	17	16	57
ENSMUSG00000074918	chr2	Inafm2	1.2E+08	1.2E+08	3053	-0.0042181	3.01018619	1	1	0.13622	0	68	71	99	65	332	185	160	151	152	164
ENSMUSG00000075394	chr15	Hoxc4	1E+08	1E+08	2568	-0.00070263	2.641546671	1	1	0.05622	0	73	56	107	92	147	142	130	83	116	169
ENSMUSG00000078580	chr7	E430018J23Rik	1.3E+08	1.3E+08	3334	-0.00265629	1.500462084	1	1	0.06968	0	32	19	57	43	62	78	52	39	62	53
ENSMUSG00000081476	chr2	Itpa-ps1	9.4E+07	9.4E+07	597	-0.01932364	0.124200932	1	1	0.09528	0	19	8	19	7	23	28	21	12	22	19
ENSMUSG00000085971	chr5	Gm15411	1.5E+08	1.5E+08	3488	-0.02125294	-0.19307859	1	1	0.13509	0	11	7	7	10	24	29	10	14	13	13
ENSMUSG00000087698	chr4	Gm13031	1.4E+08	1.4E+08	924	0.006028055	0.403899784	1	1	0.10969	0	29	7	25	12	20	27	33	15	20	32
ENSMUSG00000089698	chr16	Gm2541	8.6E+07	8.6E+07	711	-0.00253457	0.843554317	1	1	0.0672	0	18	19	29	32	30	42	36	21	39	38
ENSMUSG00000093880	chr17	Tmem181c-ps	6612952	6613027	1288	0.050001788	-0.18250673	1	1	0.1431	0	6	16	9	15	9	19	24	7	12	21
ENSMUSG00000094568	chr8	Gm1815	4.2E+07	4.2E+07	1077	0.016337048	0.276656514	1	1	0.0782	0	18	13	23	12	17	31	24	18	26	16
ENSMUSG00000097660	chr7	Gm26762	3.4E+07	3.4E+07	5284	-0.024333	-0.04823112	1	1	0.9491	0	0	1	63	6	4	0	19	2	38	27
ENSMUSG00000098715	chr6	Gm28053	4.9E+07	4.9E+07	350	-0.03292526	-0.00782153	1	1	0.13061	0	13	3	24	18	12	16	20	19	11	23
ENSMUSG00000098816	chr7	Gm27786	1.4E+08	1.4E+08	70	-0.006626	0.166138833	1	1	0.87429	0	4	0	64	16	1	3	25	1	31	44

Table S9. Pathways predicted to be affected by differentially expressed genes in B10-mdx versus B10-WT samples. Differentially expressed genes were input into Enrichr at maayanlab.cloud/Enrichr/ and pathways were identified using BioPlanet 2019 ontology.

Term	Overlap	P-value	Adjusted P-value	Old P-value	Old Adjusted P-value	Odds Ratio	Combined Score	Genes
Lck and Fyn tyrosine kinases in initiation of T cell receptor activation	2/13	0.000315	0.02553	0	0	92.99767	749.7563133	ZAP70;PTPRC
Hyaluronan metabolism	2/14	0.000367	0.02553	0	0	85.24359	674.2124591	HEXB;CD44
Inhibition of T cell receptor signaling by activated Csk	2/19	0.000686	0.031775	0	0	60.15686	438.2385475	ZAP70;PTPRC
Ascorbate and aldarate metabolism	2/26	0.001292	0.044884	0	0	42.59615	283.3431573	ALDH1B1;UGT1A1
PD-1 signaling	2/31	0.001836	0.046411	0	0	35.24315	222.0359748	ZAP70;PTPRC
MEF2D role in T cell apoptosis	2/35	0.002337	0.046411	0	0	30.96503	187.6102131	ZAP70;PTPRC
Primary immunodeficiency	2/35	0.002337	0.046411	0	0	30.96503	187.6102131	ZAP70;PTPRC
T cell receptor signaling in naive CD8+ T cells	2/55	0.005684	0.098765	0	0	19.26076	99.57896455	ZAP70;PTPRC
T cell receptor signaling in naive CD4+ T cells	2/67	0.008333	0.128702	0	0	15.69546	75.14212226	ZAP70;PTPRC
Heme degradation	1/5	0.010209	0.140636	0	0	124.7188	571.7716334	UGT1A1
T cell signal transduction	2/83	0.012564	0.140636	0	0	12.585	55.08344639	ZAP70;PTPRC
Codeine and morphine metabolism	1/8	0.016286	0.140636	0	0	71.25714	293.3998472	UGT1A1
Binding of RNA by insulin-like growth factor 2 mRNA binding proteins (IGF2BPs/IMPs/VICKZs)	1/8	0.016286	0.140636	0	0	71.25714	293.3998472	CD44

Transport of glucose and other sugars, bile salts and organic acids, metal ions and amine compounds	2/96	0.016557	0.140636	0	0	10.83742	44.44397661	SLC44A4;SLC11A1
MAP kinase pathway regulation through dual specificity phosphatases	1/9	0.018303	0.140636	0	0	62.34688	249.430818	DUSP9
Alpha-4 beta-7 integrin signaling	1/9	0.018303	0.140636	0	0	62.34688	249.430818	CD44
Glycosaminoglycan metabolism	2/110	0.021379	0.140636	0	0	9.425926	36.24594615	HEXB;CD44
Keratan sulfate degradation	1/11	0.022326	0.140636	0	0	49.8725	189.6162115	HEXB
Monocyte and its surface molecules	1/11	0.022326	0.140636	0	0	49.8725	189.6162115	CD44
B lymphocyte cell surface molecules	1/11	0.022326	0.140636	0	0	49.8725	189.6162115	PTPRC
Nucleotide G-protein coupled receptors (GPCRs)	1/12	0.024331	0.140636	0	0	45.33636	168.4701655	P2RY6
Lysosome	2/121	0.025528	0.140636	0	0	8.549881	31.3609071	SLC11A1;HEXB
Irinotecan pathway	1/13	0.026332	0.140636	0	0	41.55625	151.1383993	UGT1A1
Chondroitin sulfate/dermatan sulfate degradation	1/13	0.026332	0.140636	0	0	41.55625	151.1383993	HEXB
Activation of DNA fragmentation factor	1/13	0.026332	0.140636	0	0	41.55625	151.1383993	HIST1H1E
T helper cell surface molecules	1/13	0.026332	0.140636	0	0	41.55625	151.1383993	PTPRC
Porphyrin metabolism	1/14	0.02833	0.140636	0	0	38.35769	136.7009949	UGT1A1
Glycosphingolipid biosynthesis: globo series	1/14	0.02833	0.140636	0	0	38.35769	136.7009949	HEXB

Glycosphingolipid biosynthesis: ganglio series	1/15	0.030323	0.143153	0	0	35.61607	124.5085078	HEXB
Nucleotide-like (purinergic) G-protein coupled receptors	1/16	0.032312	0.143153	0	0	33.24	114.0899655	P2RY6
Other glycan degradation	1/16	0.032312	0.143153	0	0	33.24	114.0899655	HEXB
T cell receptor signaling pathway	2/139	0.032956	0.143153	0	0	7.419802	25.32064804	ZAP70;PTPRC
Estrogen metabolism	1/17	0.034298	0.144466	0	0	31.16094	105.0958914	UGT1A1
Phosphatidylcholine biosynthesis	1/18	0.036279	0.148317	0	0	29.32647	97.26176224	SLC44A4
Glycosaminoglycan degradation	1/19	0.038256	0.151932	0	0	27.69583	90.38385304	HEXB
Beta-alanine metabolism	1/22	0.044165	0.170525	0	0	23.73571	74.05131012	ALDH1B1
Metal ion solute carrier family (SLC) transporters	1/25	0.050038	0.182411	0	0	20.76563	62.19251854	SLC11A1
Interaction between L1-type proteins and ankyrins	1/26	0.051988	0.182411	0	0	19.934	58.93979602	SPTBN5
Interleukin-9 regulation of target genes	1/26	0.051988	0.182411	0	0	19.934	58.93979602	CCL7
Glucuronidation	1/27	0.053934	0.182411	0	0	19.16635	55.96572434	UGT1A1
Pentose and glucuronate interconversions	1/29	0.057814	0.182411	0	0	17.79554	50.72663121	UGT1A1
Amine compound SLC transporters	1/29	0.057814	0.182411	0	0	17.79554	50.72663121	SLC44A4
Histidine metabolism	1/29	0.057814	0.182411	0	0	17.79554	50.72663121	ALDH1B1

Sema4D in semaphorin signaling	1/29	0.057814	0.182411	0	0	17.79554	50.72663121	PTPRC
Inflammatory response pathway	1/30	0.059748	0.182411	0	0	17.18103	48.40956011	ZAP70
Keratan sulfate/keratin metabolism	1/31	0.061679	0.182411	0	0	16.6075	46.26547336	HEXB
Alpha-V beta-3 integrin/OPN pathway	1/31	0.061679	0.182411	0	0	16.6075	46.26547336	CD44
Propanoate metabolism	1/33	0.065528	0.187406	0	0	15.56797	42.42707813	ALDH1B1
Phospholipid metabolism	2/205	0.066064	0.187406	0	0	4.990779	13.56059125	SLC44A4;HEXB
EPO receptor signaling	1/34	0.067447	0.187502	0	0	15.09545	40.70365761	PTPRC
Generation of second messenger molecules	1/36	0.071273	0.194253	0	0	14.23143	37.58862573	ZAP70
Latent infection of Homo sapiens with Mycobacterium tuberculosis	1/37	0.07318	0.195616	0	0	13.83542	36.17728305	SLC11A1
Glycosphingolipid metabolism	1/38	0.075084	0.196917	0	0	13.46081	34.852097	HEXB
Lipid and lipoprotein metabolism	3/489	0.078261	0.200217	0	0	3.163255	8.059041147	GLIPR1;SLC44A4;HEXB
Fatty acid metabolism	1/42	0.08266	0.200217	0	0	12.14512	30.27809233	ALDH1B1
Carbohydrate metabolism	2/235	0.083638	0.200217	0	0	4.341587	10.77258241	HEXB;CD44
Porphyrin and chlorophyll metabolism	1/43	0.084544	0.200217	0	0	11.85536	29.2884537	UGT1A1
Lysine degradation	1/44	0.086425	0.200217	0	0	11.57907	28.35113154	ALDH1B1

Gastrin pathway	1/44	0.086425	0.200217	0	0	11.57907	28.35113154	CD44
Valine, leucine and isoleucine degradation	1/44	0.086425	0.200217	0	0	11.57907	28.35113154	ALDH1B1
Amino sugar and nucleotide sugar metabolism	1/45	0.088302	0.201212	0	0	11.31534	27.46228274	HEXB
SLC-mediated transmembrane transport	2/251	0.093537	0.205614	0	0	4.059314	9.618117133	SLC44A4;SLC11A1
Chondroitin sulfate/dermatan sulfate metabolism	1/48	0.09391	0.205614	0	0	10.59149	25.05329844	HEXB
Glycerolipid metabolism	1/49	0.095772	0.205614	0	0	10.37031	24.32652283	ALDH1B1
Type I interferon (interferon-alpha/beta) pathway	1/51	0.099485	0.205614	0	0	9.9545	22.97251088	PTPRC
Pyruvate metabolism	1/52	0.101335	0.205614	0	0	9.758824	22.34105716	ALDH1B1
Apoptotic execution phase	1/52	0.101335	0.205614	0	0	9.758824	22.34105716	HIST1H1E
Drug metabolism: other enzymes	1/52	0.101335	0.205614	0	0	9.758824	22.34105716	UGT1A1
Starch and sucrose metabolism	1/53	0.103183	0.205614	0	0	9.570673	21.73744506	UGT1A1
Arginine and proline metabolism	1/54	0.105026	0.205614	0	0	9.389623	21.15996827	ALDH1B1
Binding of chemokines to chemokine receptors	1/54	0.105026	0.205614	0	0	9.389623	21.15996827	CCL7
Steroid hormone biosynthesis	1/56	0.108702	0.209854	0	0	9.047273	20.07724991	UGT1A1
Tryptophan metabolism	1/58	0.112362	0.21395	0	0	8.728947	19.08170254	ALDH1B1

Shigellosis	1/62	0.11964	0.22473	0	0	8.154918	17.31505749	CD44
Retinol metabolism	1/65	0.12506	0.228493	0	0	7.771484	16.156591	UGT1A1
ERK1/ERK2 MAPK pathway	1/65	0.12506	0.228493	0	0	7.771484	16.156591	DUSP9
Semaphorin interactions	1/66	0.12686	0.228493	0	0	7.651538	15.79791644	PTPRC
SIDS susceptibility pathways	1/67	0.128656	0.228493	0	0	7.535227	15.4518494	CDCA7L
NCAM signaling for neurite out-growth	1/70	0.134022	0.228493	0	0	7.206522	14.48332969	SPTBN5
Phase II of biological oxidations: conjugation	1/71	0.135803	0.228493	0	0	7.103214	14.18190957	UGT1A1
RIG-I-like receptor signaling pathway	1/71	0.135803	0.228493	0	0	7.103214	14.18190957	DHX58
Sphingolipid metabolism	1/72	0.137581	0.228493	0	0	7.002817	13.89037664	HEXB
Myc repressed pathway	1/73	0.139355	0.228493	0	0	6.905208	13.60828094	SLC11A1
RANKL regulation of apoptosis and immune response	1/74	0.141126	0.228493	0	0	6.810274	13.33519869	CD44
Prolactin activation of MAPK signaling	1/75	0.142894	0.228493	0	0	6.717905	13.07073043	ZAP70
Glycolysis and gluconeogenesis	1/75	0.142894	0.228493	0	0	6.717905	13.07073043	ALDH1B1
Axon guidance	2/325	0.143087	0.228493	0	0	3.117568	6.061487757	SPTBN5;PTPRC
RIG-I/MDA5-mediated induction of interferon-alpha/beta pathways	1/76	0.144657	0.228493	0	0	6.628	12.81449936	DHX58

Immune system	4/998	0.146456	0.228735	0	0	2.062646	3.962401844	ZAP70;PTPRC;DHX58;CD44
Drug metabolism: cytochrome P450	1/83	0.156904	0.242279	0	0	6.060061	11.22395966	UGT1A1
ECM-receptor interaction	1/84	0.15864	0.242279	0	0	5.986747	11.0223164	CD44
NOD signaling pathway	1/85	0.160372	0.242279	0	0	5.915179	10.8263173	CCL7
Glycerophospholipid biosynthesis	1/86	0.1621	0.242279	0	0	5.845294	10.63574365	SLC44A4
Hematopoietic cell lineage	1/88	0.165547	0.244798	0	0	5.710345	10.2700514	CD44
L1CAM interactions	1/94	0.175805	0.25455	0	0	5.340323	9.283521129	SPTBN5
Fc gamma receptor-mediated phagocytosis	1/94	0.175805	0.25455	0	0	5.340323	9.283521129	PTPRC
Interferon-gamma signaling pathway	1/97	0.180887	0.258706	0	0	5.172656	8.844632572	CD44
Wnt signaling pathway and pluripotency	1/98	0.182574	0.258706	0	0	5.119072	8.705479391	CD44
Senescence and autophagy	1/99	0.184258	0.258706	0	0	5.066582	8.569696843	CD44
GPCR ligand binding	2/410	0.205148	0.283291	0	0	2.457391	3.892565676	P2RY6;CCL7
Lipid metabolism regulation by peroxisome proliferator-activated receptor alpha (PPAR-alpha)	1/112	0.205844	0.283291	0	0	4.47027	7.065863017	GLIPR1
CXCR4 signaling pathway	1/116	0.212373	0.285438	0	0	4.313913	6.684015202	PTPRC
Developmental biology	2/420	0.212666	0.285438	0	0	2.397375	3.711216746	SPTBN5;PTPRC

Prolactin regulation of apoptosis	1/118	0.215618	0.285438	0	0	4.239744	6.504807607	GLIPR1
p53 activity regulation	1/118	0.215618	0.285438	0	0	4.239744	6.504807607	GTSE1
Interleukin-1 regulation of extracellular matrix	1/120	0.21885	0.286983	0	0	4.168067	6.332829	CCL7
Transmembrane transport of small molecules	2/432	0.221725	0.288036	0	0	2.32904	3.508268307	SLC44A4;SLC11A1
Metabolism	5/1615	0.233686	0.300763	0	0	1.582902	2.301184795	GLIPR1;UGT1A1;ALDH1B1;HEXB;CD44
Cell adhesion molecules (CAMs)	1/133	0.239542	0.305056	0	0	3.755114	5.366151639	PTPRC
TNF-alpha effects on cytokine activity, cell motility, and apoptosis	1/135	0.242678	0.305056	0	0	3.698694	5.237425219	CD44
Diabetes pathways	1/137	0.245801	0.305056	0	0	3.643934	5.11328983	CD44
Natural killer cell-mediated cytotoxicity	1/137	0.245801	0.305056	0	0	3.643934	5.11328983	ZAP70
Biological oxidations	1/139	0.248911	0.306183	0	0	3.590761	4.99352278	UGT1A1
Interleukin-5 regulation of apoptosis	1/144	0.256633	0.312912	0	0	3.464336	4.71187607	CD44
Integrin signaling pathway	1/155	0.273348	0.330395	0	0	3.215097	4.170011448	PTPRC
Interferon signaling	1/168	0.29263	0.350652	0	0	2.962874	3.640914861	CD44
Fatty acid, triacylglycerol, and ketone body metabolism	1/173	0.299913	0.354992	0	0	2.876017	3.463483654	GLIPR1
Metapathway biotransformation	1/174	0.30136	0.354992	0	0	2.859249	3.429520906	UGT1A1

Chemokine signaling pathway	1/189	0.322729	0.376969	0	0	2.629122	2.973388909	CCL7
Peptide G-protein coupled receptors	1/192	0.326925	0.378688	0	0	2.587435	2.892814637	CCL7
Jak-STAT signaling pathway	1/199	0.336618	0.386694	0	0	2.495076	2.7166517	PTPRC
Gastrin-CREB signaling pathway via PKC and MAPK	1/206	0.346176	0.394413	0	0	2.409024	2.555515658	P2RY6
Antigen-activated B-cell receptor generation of second messengers	1/211	0.35292	0.39683	0	0	2.351071	2.448675972	PTPRC
Adaptive immune system	2/606	0.354007	0.39683	0	0	1.643318	1.706487021	ZAP70;PTPRC
Apoptosis	1/242	0.393244	0.437287	0	0	2.045436	1.909058834	HIST1H1E
Disease	2/674	0.40422	0.445406	0	0	1.471841	1.333186561	SLC11A1;CD44
Class A GPCRs (rhodopsin-like)	1/253	0.406954	0.445406	0	0	1.95506	1.757706059	P2RY6
FSH regulation of apoptosis	1/263	0.419156	0.454246	0	0	1.879485	1.634236662	DUSP9
Cytokine-cytokine receptor interaction	1/265	0.421566	0.454246	0	0	1.865057	1.610995379	CCL7
Neuroactive ligand-receptor interaction	1/272	0.429927	0.459691	0	0	1.816236	1.533156061	P2RY6
Immune system signaling by interferons, interleukins, prolactin, and growth hormones	1/280	0.439338	0.466168	0	0	1.763441	1.450404318	CD44
Oncostatin M	1/311	0.474395	0.499221	0	0	1.584597	1.18165597	CCL7
MAPK signaling pathway	1/314	0.477672	0.499221	0	0	1.569169	1.159349846	DUSP9

Innate immune system	1/319	0.48309	0.501115	0	0	1.544104	1.123417849	DHX58
Interleukin-2 signaling pathway	2/847	0.523055	0.538553	0	0	1.160006	0.75176256	PTPRC;DUSP9
Signaling by GPCR	2/977	0.601823	0.615098	0	0	0.998501	0.507031068	P2RY6;CCL7
TGF-beta regulation of extracellular matrix	1/565	0.691525	0.701621	0	0	0.859707	0.317107759	CCL7
T cell receptor regulation of apoptosis	1/603	0.715335	0.720518	0	0	0.803862	0.269297602	PTPRC
Signal transduction	1/1020	0.883329	0.883329	0	0	0.464671	0.057645768	CCL7

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Table S10. Pathways predicted to be affected by differentially expressed genes in D2-mdx versus D2-WT samples. Differentially expressed genes were input into Enrichr at maayanlab.cloud/Enrichr/ and pathways were identified using BioPlanet 2019 ontology.

Term	Overlap	P-value	Adjusted P-value	Old P-value	Old Adjusted P-value	Odds Ratio	Combine Score	Genes
Selective expression of chemokine receptors during T-cell polarization	2/26	0.001292	0.172707	0	0	42.59615	283.3432	CCR1;TGFB1
Cytokine-cytokine receptor interaction	4/265	0.002076	0.172707	0	0	8.159056	50.40215	CCR1;TGFB1;CCL8;TNFRSF1B
G alpha 12 pathway	2/49	0.004537	0.172707	0	0	21.72613	117.2251	PLD5;VAV1
Amyotrophic lateral sclerosis (ALS)	2/53	0.005288	0.172707	0	0	20.0181	104.9397	NOS1;TNFRSF1B
Chemokine signaling pathway	3/189	0.006801	0.172707	0	0	8.392615	41.88443	CCR1;CCL8;VAV1
T cell receptor regulation of apoptosis	5/603	0.007493	0.172707	0	0	4.496702	22.00577	CCR1;CCNB2;TGFB1;NLRP3;TNFRSF1B
Cyclin B2-mediated events	1/5	0.010209	0.172707	0	0	124.7188	571.7716	CCNB2
Influenza factor interactions with host	1/6	0.012239	0.172707	0	0	99.77	439.3038	TGFB1
Interleukin-1-beta (IL-1b) processing pathway	1/6	0.012239	0.172707	0	0	99.77	439.3038	NLRP3
NOD signaling pathway	2/85	0.013147	0.172707	0	0	12.28051	53.19401	CCL8;NLRP3
Non-class A, B, C GPCRs	2/86	0.013442	0.172707	0	0	12.1337	52.2882	GPR162;LGR6
Thymic stromal lymphopoietin (TSLP) pathway	2/90	0.014654	0.172707	0	0	11.57984	48.90207	CCR1;TGFB1

Hemostasis pathway	4/468	0.015139	0.172707	0	0	4.542171	19.03398	TGFB1;SELPLG;NOS1;VAV1
Transcription factor regulation of microRNAs related to cardiac hypertrophy	1/8	0.016286	0.172707	0	0	71.25714	293.3998	TGFB1
Nitric oxide effects	1/9	0.018303	0.172707	0	0	62.34688	249.4308	NOS1
Amoebiasis	2/105	0.019596	0.172707	0	0	9.885985	38.87571	TGFB1;LAMC3
Phospholipase C signaling pathway	1/10	0.020316	0.172707	0	0	55.41667	215.9217	VAV1
Leptin influence on immune response	2/110	0.021379	0.172707	0	0	9.425926	36.24595	CCR1;PTAFR
SUMOylation as a mechanism to modulate CtBP-dependent gene responses	1/11	0.022326	0.172707	0	0	49.8725	189.6162	NOS1
Serotonin transporter activity	1/11	0.022326	0.172707	0	0	49.8725	189.6162	NOS1
CD28-dependent Vav1 pathway	1/11	0.022326	0.172707	0	0	49.8725	189.6162	VAV1
TGF-beta signaling in gastrointestinal stem cells	1/11	0.022326	0.172707	0	0	49.8725	189.6162	TGFB1
SODD/TNFR1 signaling pathway	1/12	0.024331	0.172707	0	0	45.33636	168.4702	TNFRSF1B
Interleukin-1 regulation of extracellular matrix	2/120	0.025138	0.172707	0	0	8.622773	31.76094	GDF10;CCL8
Adhesion and diapedesis of granulocytes	1/15	0.030323	0.172707	0	0	35.61607	124.5085	SELPLG
Cyclin A/B1-associated events during G2/M transition	1/15	0.030323	0.172707	0	0	35.61607	124.5085	CCNB2

Erythrocyte differentiation pathway	1/15	0.030323	0.172707	0	0	35.61607	124.5085	TGFB1
Adipogenesis	2/133	0.030395	0.172707	0	0	7.761989	27.11638	GDF10;TGFB1
Acetylation and deacetylation of RelA in the nucleus	1/16	0.032312	0.172707	0	0	33.24	114.09	TNFRSF1B
Control of cell cycle and breast tumor growth by estrogen-responsive protein Efp	1/16	0.032312	0.172707	0	0	33.24	114.09	CCNB2
TGF-beta receptor signaling in EMT (epithelial to mesenchymal transition)	1/16	0.032312	0.172707	0	0	33.24	114.09	TGFB1
ACE inhibitor pathway	1/17	0.034298	0.172707	0	0	31.16094	105.0959	TGFB1
Post-chaperonin tubulin folding pathway	1/17	0.034298	0.172707	0	0	31.16094	105.0959	TUBB3
Inflammasomes	1/17	0.034298	0.172707	0	0	31.16094	105.0959	NLRP3
Cells and molecules involved in local acute inflammatory response	1/17	0.034298	0.172707	0	0	31.16094	105.0959	SELPLG
Interleukin-5 regulation of apoptosis	2/144	0.035153	0.172707	0	0	7.156735	23.961	CCR1;PTAFR
CBL signaling regulation	1/18	0.036279	0.172707	0	0	29.32647	97.26176	VAV1
TNFR2 signaling pathway	1/18	0.036279	0.172707	0	0	29.32647	97.26176	TNFRSF1B
Transcriptional activity regulation by PML	1/18	0.036279	0.172707	0	0	29.32647	97.26176	TNFRSF1B
Small ligand GPCRs	1/19	0.038256	0.172707	0	0	27.69583	90.38385	PTAFR

Tob role in T-cell activation	1/19	0.038256	0.172707	0	0	27.69583	90.38385	TGFB1
EGFR1 pathway	2/152	0.038784	0.172707	0	0	6.772308	22.00825	COTL1;NOS1
Phagosome	2/154	0.039714	0.172707	0	0	6.682524	21.55824	TUBB3;NOS1
Interleukin-3 regulation of hematopoietic cells	1/20	0.04023	0.172707	0	0	26.23684	84.30285	TGFB1
Prion pathway	1/21	0.042199	0.172707	0	0	24.92375	78.89244	LAMC3
E-cadherin keratinocyte pathway	1/21	0.042199	0.172707	0	0	24.92375	78.89244	FMN1
PKC-catalyzed phosphorylation of inhibitory phosphoprotein of myosin phosphatase	1/21	0.042199	0.172707	0	0	24.92375	78.89244	VAV1
Nitric oxide signaling pathway	1/22	0.044165	0.172707	0	0	23.73571	74.05131	NOS1
Interleukin-11 pathway	1/23	0.046126	0.172707	0	0	22.65568	69.69723	TGFB1
Modulation of interferon signaling by chaperones	1/23	0.046126	0.172707	0	0	22.65568	69.69723	TNFRSF1B
Ras-independent pathway in NK cell-mediated cytotoxicity	1/24	0.048084	0.172707	0	0	21.66957	65.76286	VAV1
NF-kappaB signaling pathway	1/24	0.048084	0.172707	0	0	21.66957	65.76286	TNFRSF1B
Calcium signaling pathway	2/178	0.051505	0.172707	0	0	5.764277	17.09728	PTAFR;NOS1
ALK1 pathway	1/26	0.051988	0.172707	0	0	19.934	58.9398	TGFB1

RXR/VDR pathway	1/26	0.051988	0.172707	0	0	19.934	58.9398	TGFB1
Ras signaling pathway	1/26	0.051988	0.172707	0	0	19.934	58.9398	VAV1
Interleukin-27-mediated signaling events	1/26	0.051988	0.172707	0	0	19.934	58.9398	TGFB1
TGF-beta signaling in development	1/26	0.051988	0.172707	0	0	19.934	58.9398	TGFB1
Proteins and DNA sequences in cardicac structures	1/27	0.053934	0.172707	0	0	19.16635	55.96572	TGFB1
Insulin regulation of blood glucose	1/27	0.053934	0.172707	0	0	19.16635	55.96572	PPP1R3A
CTCF pathway	1/27	0.053934	0.172707	0	0	19.16635	55.96572	TGFB1
Cooperation of prefoldin and TriC/CCT in actin and tubulin folding	1/27	0.053934	0.172707	0	0	19.16635	55.96572	TUBB3
TGF-beta signaling pathway	2/185	0.055155	0.172707	0	0	5.541824	16.05804	CCNB2;TGFB1
Cell cycle: G1/S checkpoint	1/28	0.055876	0.172707	0	0	18.45556	53.23735	TGFB1
TGF-beta receptor activation of SMADs	1/28	0.055876	0.172707	0	0	18.45556	53.23735	TGFB1
Nitric oxide stimulation of guanylate cyclase	1/28	0.055876	0.172707	0	0	18.45556	53.23735	NOS1
Inflammatory response pathway	1/30	0.059748	0.179245	0	0	17.18103	48.40956	TNFRSF1B
Tumor necrosis factor (TNF) pathway	1/30	0.059748	0.179245	0	0	17.18103	48.40956	TNFRSF1B

CD28 co-stimulation	1/31	0.061679	0.179749	0	0	16.6075	46.26547	VAV1
NF-kappaB activation by non-typeable Hemophilus influenzae	1/31	0.061679	0.179749	0	0	16.6075	46.26547	TGFB1
Glycoprotein VI-mediated activation cascade	1/33	0.065528	0.183455	0	0	15.56797	42.42708	VAV1
Syndecan 2 pathway	1/33	0.065528	0.183455	0	0	15.56797	42.42708	TGFB1
Platelet activation, signaling and aggregation	2/205	0.066064	0.183455	0	0	4.990779	13.56059	TGFB1;VAV1
Interleukin-7 interactions in immune response	1/34	0.067447	0.183455	0	0	15.09545	40.70366	CCL8
Monoamine transport	1/34	0.067447	0.183455	0	0	15.09545	40.70366	NOS1
Cytokines and inflammatory response	1/35	0.069362	0.186181	0	0	14.65074	39.09433	TGFB1
ALK in cardiac myocytes	1/37	0.07318	0.191394	0	0	13.83542	36.17728	TGFB1
Latent infection of Homo sapiens with Mycobacterium tuberculosis	1/37	0.07318	0.191394	0	0	13.83542	36.17728	NOS1
RAC1 activity regulation	1/38	0.075084	0.191463	0	0	13.46081	34.8521	VAV1
Signal transduction through IL-1R	1/38	0.075084	0.191463	0	0	13.46081	34.8521	TGFB1
Alpha-M beta-2 integrin signaling	1/41	0.080771	0.195342	0	0	12.44938	31.3243	SELPLG
FOXM1 transcription factor network	1/41	0.080771	0.195342	0	0	12.44938	31.3243	CCNB2

Fc epsilon receptor I signaling in mast cells	1/41	0.080771	0.195342	0	0	12.44938	31.3243	VAV1
Focal adhesion	2/233	0.082425	0.195342	0	0	4.37962	10.93094	LAMC3;VAV1
Urokinase-type plasminogen activator (uPA) and uPAR-mediated signaling	1/42	0.08266	0.195342	0	0	12.14512	30.27809	TGFB1
G2/M checkpoints	1/43	0.084544	0.195342	0	0	11.85536	29.28845	CCNB2
PI3K class IB pathway in neutrophils	1/43	0.084544	0.195342	0	0	11.85536	29.28845	VAV1
Interleukin-12/STAT4 pathway	1/45	0.088302	0.195342	0	0	11.31534	27.46228	TGFB1
Interleukin-3 signaling pathway	1/45	0.088302	0.195342	0	0	11.31534	27.46228	TGFB1
Interleukin-3, interleukin-5, and GM-CSF signaling	1/45	0.088302	0.195342	0	0	11.31534	27.46228	VAV1
Alpha-6 beta-1 and alpha-6 beta-4 integrin signaling	1/46	0.090175	0.195342	0	0	11.06333	26.61842	LAMC3
RhoA activity regulation	1/46	0.090175	0.195342	0	0	11.06333	26.61842	VAV1
Syndecan 1 pathway	1/46	0.090175	0.195342	0	0	11.06333	26.61842	TGFB1
Agrin in postsynaptic differentiation	1/47	0.092044	0.195342	0	0	10.82228	25.81639	LAMC3
Delta Np63 pathway	1/47	0.092044	0.195342	0	0	10.82228	25.81639	CCNB2
Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) signaling pathways	1/47	0.092044	0.195342	0	0	10.82228	25.81639	NLRP3

Intestinal immune network for IgA production	1/48	0.09391	0.195342	0	0	10.59149	25.0533	TGFB1
Diurnally regulated genes with circadian orthologs	1/48	0.09391	0.195342	0	0	10.59149	25.0533	TUBB3
Class A GPCRs (rhodopsin-like)	2/253	0.094798	0.195342	0	0	4.02656	9.486596	CCR1;PTAFR
Malaria	1/51	0.099485	0.202949	0	0	9.9545	22.97251	TGFB1
Signaling events mediated by stem cell factor receptor (c-Kit)	1/52	0.101335	0.20405	0	0	9.758824	22.34106	VAV1
Protein folding	1/53	0.103183	0.20405	0	0	9.570673	21.73745	TUBB3
Arginine and proline metabolism	1/54	0.105026	0.20405	0	0	9.389623	21.15997	NOS1
Binding of chemokines to chemokine receptors	1/54	0.105026	0.20405	0	0	9.389623	21.15997	CCR1
Kit receptor signaling pathway	1/54	0.105026	0.20405	0	0	9.389623	21.15997	VAV1
T cell receptor signaling in naive CD8+ T cells	1/55	0.106866	0.205666	0	0	9.215278	20.60705	VAV1
Pathogenic Escherichia coli infection	1/57	0.110534	0.208381	0	0	8.885268	19.56921	TUBB3
Keratinocyte differentiation	1/57	0.110534	0.208381	0	0	8.885268	19.56921	TNFRSF1B
Immune system signaling by interferons, interleukins, prolactin, and growth hormones	2/280	0.112286	0.208381	0	0	3.630511	7.93885	PTAFR;VAV1
HIV-1 Nef as negative effector of Fas and TNF	1/58	0.112362	0.208381	0	0	8.728947	19.0817	TNFRSF1B

RAGE pathway	1/60	0.116009	0.211301	0	0	8.432203	18.16373	TGFB1
Natural killer cell receptor signaling pathway	1/60	0.116009	0.211301	0	0	8.432203	18.16373	VAV1
Colorectal cancer	1/62	0.11964	0.215988	0	0	8.154918	17.31506	TGFB1
Signaling by TGF-beta receptor complex	1/66	0.12686	0.217012	0	0	7.651538	15.79792	TGFB1
Endochondral ossification	1/66	0.12686	0.217012	0	0	7.651538	15.79792	TGFB1
G alpha 13 pathway	1/67	0.128656	0.217012	0	0	7.535227	15.45185	PLD5
Adipocytokine signaling pathway	1/67	0.128656	0.217012	0	0	7.535227	15.45185	TNFRSF1B
T cell receptor signaling in naive CD4+ T cells	1/67	0.128656	0.217012	0	0	7.535227	15.45185	VAV1
Telomerase regulation	1/67	0.128656	0.217012	0	0	7.535227	15.45185	TGFB1
Pancreatic cancer	1/70	0.134022	0.217012	0	0	7.206522	14.48333	TGFB1
G alpha q pathway	1/70	0.134022	0.217012	0	0	7.206522	14.48333	PLD5
AP-1 transcription factor network	1/70	0.134022	0.217012	0	0	7.206522	14.48333	TGFB1
Renal cell carcinoma	1/70	0.134022	0.217012	0	0	7.206522	14.48333	TGFB1
Long-term depression	1/70	0.134022	0.217012	0	0	7.206522	14.48333	NOS1

MicroRNA regulation of DNA damage response	1/70	0.134022	0.217012	0	0	7.206522	14.48333	CCNB2
Rac1 cell motility signaling pathway	1/71	0.135803	0.217012	0	0	7.103214	14.18191	VAV1
Interleukin-6 signaling pathway	1/71	0.135803	0.217012	0	0	7.103214	14.18191	VAV1
Leishmaniasis	1/72	0.137581	0.217012	0	0	7.002817	13.89038	TGFB1
Costimulation by the CD28 family	1/72	0.137581	0.217012	0	0	7.002817	13.89038	VAV1
Innate immune system	2/319	0.138878	0.217012	0	0	3.177546	6.272984	CD180;NLRP3
Chronic myeloid leukemia	1/73	0.139355	0.217012	0	0	6.905208	13.60828	TGFB1
Prolactin activation of MAPK signaling	1/75	0.142894	0.219472	0	0	6.717905	13.07073	VAV1
Pathways in cancer	2/325	0.143087	0.219472	0	0	3.117568	6.061488	TGFB1;LAMC3
G alpha (12/13) signaling events	1/77	0.146417	0.219569	0	0	6.540461	12.56615	VAV1
Transcriptional regulation of white adipocyte differentiation	1/77	0.146417	0.219569	0	0	6.540461	12.56615	TGFB1
Immune system	4/998	0.146456	0.219569	0	0	2.062646	3.962402	CD180;PTAFR;NLRP3;VAV1
Signaling by SCF-KIT	1/78	0.148174	0.219569	0	0	6.455195	12.32535	VAV1
Fc epsilon receptor I signaling pathway	1/79	0.149927	0.219569	0	0	6.372115	12.09177	VAV1

Apoptosis modulation and signaling	1/80	0.151677	0.219569	0	0	6.291139	11.86512	TNFRSF1B
MAP kinase signaling pathway	1/81	0.153423	0.219569	0	0	6.212188	11.64511	TGFB1
ATM-dependent DNA damage response	1/82	0.155165	0.219569	0	0	6.135185	11.43148	TGFB1
Platelet homeostasis	1/82	0.155165	0.219569	0	0	6.135185	11.43148	NOS1
Response to elevated platelet cytosolic calcium	1/83	0.156904	0.219569	0	0	6.060061	11.22396	TGFB1
T cell signal transduction	1/83	0.156904	0.219569	0	0	6.060061	11.22396	VAV1
Small cell lung cancer	1/84	0.15864	0.219569	0	0	5.986747	11.02232	LAMC3
ECM-receptor interaction	1/84	0.15864	0.219569	0	0	5.986747	11.02232	LAMC3
Integrin cell surface interactions	1/85	0.160372	0.219569	0	0	5.915179	10.82632	LAMC3
TGF-beta regulation of skeletal system development	1/85	0.160372	0.219569	0	0	5.915179	10.82632	TGFB1
MicroRNAs in cardiomyocyte hypertrophy	1/85	0.160372	0.219569	0	0	5.915179	10.82632	TGFB1
Progesterone-mediated oocyte maturation	1/86	0.1621	0.220457	0	0	5.845294	10.63574	CCNB2
Mitotic G2-G2/M phases	1/87	0.163825	0.221327	0	0	5.777035	10.45039	CCNB2
Salivary secretion	1/89	0.167265	0.224488	0	0	5.64517	10.09455	NOS1

Gap junction pathway	1/90	0.16898	0.225307	0	0	5.581461	9.923695	TUBB3
Cell surface interactions at the vascular wall	1/94	0.175805	0.231382	0	0	5.340323	9.283521	SELPLG
Fc gamma receptor-mediated phagocytosis	1/94	0.175805	0.231382	0	0	5.340323	9.283521	VAV1
Interferon-gamma signaling pathway	1/97	0.180887	0.236545	0	0	5.172656	8.844633	PTAFR
Senescence and autophagy	1/99	0.184258	0.239419	0	0	5.066582	8.569697	TGFB1
Dilated cardiomyopathy	1/100	0.185939	0.240073	0	0	5.015152	8.437172	TGFB1
TNF-alpha signaling pathway	1/101	0.187616	0.240715	0	0	4.96475	8.307798	TNFRSF1B
Chagas disease	1/104	0.192628	0.2456	0	0	4.819417	7.937562	TGFB1
Signaling by interleukins	1/109	0.200913	0.254573	0	0	4.595139	7.37466	VAV1
Epidermal growth factor receptor (EGFR) pathway	1/111	0.204204	0.25675	0	0	4.511136	7.166553	VAV1
GPCR ligand binding	2/410	0.205148	0.25675	0	0	2.457391	3.892566	CCR1;PTAFR
Oocyte meiosis	1/113	0.207482	0.258087	0	0	4.430134	6.967326	CCNB2
CXCR4 signaling pathway	1/116	0.212373	0.26141	0	0	4.313913	6.684015	VAV1
Cell cycle checkpoints	1/117	0.213998	0.26141	0	0	4.276509	6.593482	CCNB2

Leukocyte transendothelial migration	1/117	0.213998	0.26141	0	0	4.276509	6.593482	VAV1
p53 activity regulation	1/118	0.215618	0.261822	0	0	4.239744	6.504808	CCNB2
Rho GTPase cycle	1/123	0.223673	0.269996	0	0	4.064959	6.087553	VAV1
p75 neurotrophin receptor-mediated signaling	1/124	0.225275	0.27033	0	0	4.031707	6.008996	VAV1
Cell cycle	2/453	0.237661	0.283525	0	0	2.218205	3.187365	CCNB2;TGFB1
Cell adhesion molecules (CAMs)	1/133	0.239542	0.284108	0	0	3.755114	5.366152	SELPLG
TNF-alpha effects on cytokine activity, cell motility, and apoptosis	1/135	0.242678	0.286164	0	0	3.698694	5.237425	CCR1
Natural killer cell-mediated cytotoxicity	1/137	0.245801	0.28818	0	0	3.643934	5.11329	VAV1
T cell receptor signaling pathway	1/139	0.248911	0.290159	0	0	3.590761	4.993523	VAV1
EGF/EGFR signaling pathway	1/141	0.252009	0.290589	0	0	3.539107	4.877915	VAV1
Influenza infection	1/142	0.253553	0.290589	0	0	3.51383	4.821609	TGFB1
Toll-like receptor signaling pathway regulation	1/142	0.253553	0.290589	0	0	3.51383	4.821609	CD180
Signaling by the B cell receptor (BCR)	1/151	0.267313	0.304647	0	0	3.3015	4.35579	VAV1
Myometrial relaxation and contraction pathways	1/155	0.273348	0.309794	0	0	3.215097	4.170011	NOS1

Toll receptor cascades	1/159	0.279335	0.314831	0	0	3.13307	3.99574	CD180
Interferon signaling	1/168	0.29263	0.327841	0	0	2.962874	3.640915	PTAFR
Alzheimer's disease	1/169	0.294093	0.327841	0	0	2.945089	3.604379	NOS1
TGF-beta regulation of extracellular matrix	2/565	0.323091	0.357324	0	0	1.766726	1.996086	TGFB1;CCL8
Signaling by GPCR	3/977	0.324044	0.357324	0	0	1.538825	1.734065	CCR1;PTAFR;VAV1
Peptide G-protein coupled receptors	1/192	0.326925	0.358563	0	0	2.587435	2.892815	CCR1
G alpha (i) signaling events	1/199	0.336618	0.36722	0	0	2.495076	2.716652	CCR1
Endocytosis	1/201	0.339363	0.368245	0	0	2.469875	2.669158	TGFB1
Gastrin-CREB signaling pathway via PKC and MAPK	1/206	0.346176	0.37365	0	0	2.409024	2.555516	PTAFR
Antigen-activated B-cell receptor generation of second messengers	1/211	0.35292	0.378924	0	0	2.351071	2.448676	VAV1
Signaling by NGF	1/221	0.366205	0.39113	0	0	2.243068	2.253302	VAV1
Actin cytoskeleton regulation	1/226	0.372747	0.396044	0	0	2.192667	2.163843	VAV1
Apoptosis	1/242	0.393244	0.415656	0	0	2.045436	1.909059	TNFRSF1B
Disease	2/674	0.40422	0.425056	0	0	1.471841	1.333187	TGFB1;NOS1

Neuroactive ligand-receptor interaction	1/272	0.429927	0.44977	0	0	1.816236	1.533156	PTAFR
Insulin signaling pathway	1/277	0.435827	0.453616	0	0	1.78288	1.480699	PPP1R3A
Oncostatin M	1/311	0.474395	0.491252	0	0	1.584597	1.181656	CCL8
MAPK signaling pathway	1/314	0.477672	0.492147	0	0	1.569169	1.15935	TGFB1
Interleukin-2 signaling pathway	2/847	0.523055	0.536198	0	0	1.160006	0.751763	CCR1;TNFRSF1B
Developmental biology	1/420	0.581487	0.593117	0	0	1.165871	0.632096	TGFB1
Protein metabolism	1/442	0.600359	0.609319	0	0	1.106463	0.564548	TUBB3
Signal transduction	2/1020	0.625721	0.631916	0	0	0.954158	0.447358	CCR1;LAMC3
Adaptive immune system	1/606	0.717136	0.720669	0	0	0.799752	0.265909	VAV1
Metabolism	1/1615	0.968433	0.968433	0	0	0.284154	0.009115	NOS1

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